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(54) **NUCLEIC ACID DETECTION EMPLOYING CHARGED ADDUCTS**

6,001,567, which is a continuation-in-part of application No. 08/599,491, filed on Jan. 24, 1996, now Pat. No. 5,846,717.

(76) Inventors: **Mary Ann D. Brow**, Madison, WI (US); **Jeff Steven Grotelueschen Hall**, Madison, WI (US); **Victor Lyamichev**, Madison, WI (US); **David Michael Olive**, Madison, WI (US); **James Robert Prudent**, Madison, WI (US)

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Correspondence Address:
MEDLEN & CARROLL, LLP
Suite 350
101 Howard Street
San Francisco, CA 94105 (US)

(57) **ABSTRACT**

The present invention relates to means for the detection and characterization of nucleic acid sequences, as well as variations in nucleic acid sequences. The present invention also relates to methods for forming a nucleic acid cleavage structure on a target sequence and cleaving the nucleic acid cleavage structure in a site-specific manner. The 5' nuclease activity of a variety of enzymes is used to cleave the target-dependent cleavage structure, thereby indicating the presence of specific nucleic acid sequences or specific variations thereof. The present invention further relates to methods and devices for the separation of nucleic acid molecules based by charge.

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Related U.S. Application Data

(63) Continuation of application No. 09/333,145, filed on Jun. 14, 1999, which is a continuation of application No. 08/682,853, filed on Jul. 12, 1996, now Pat. No.

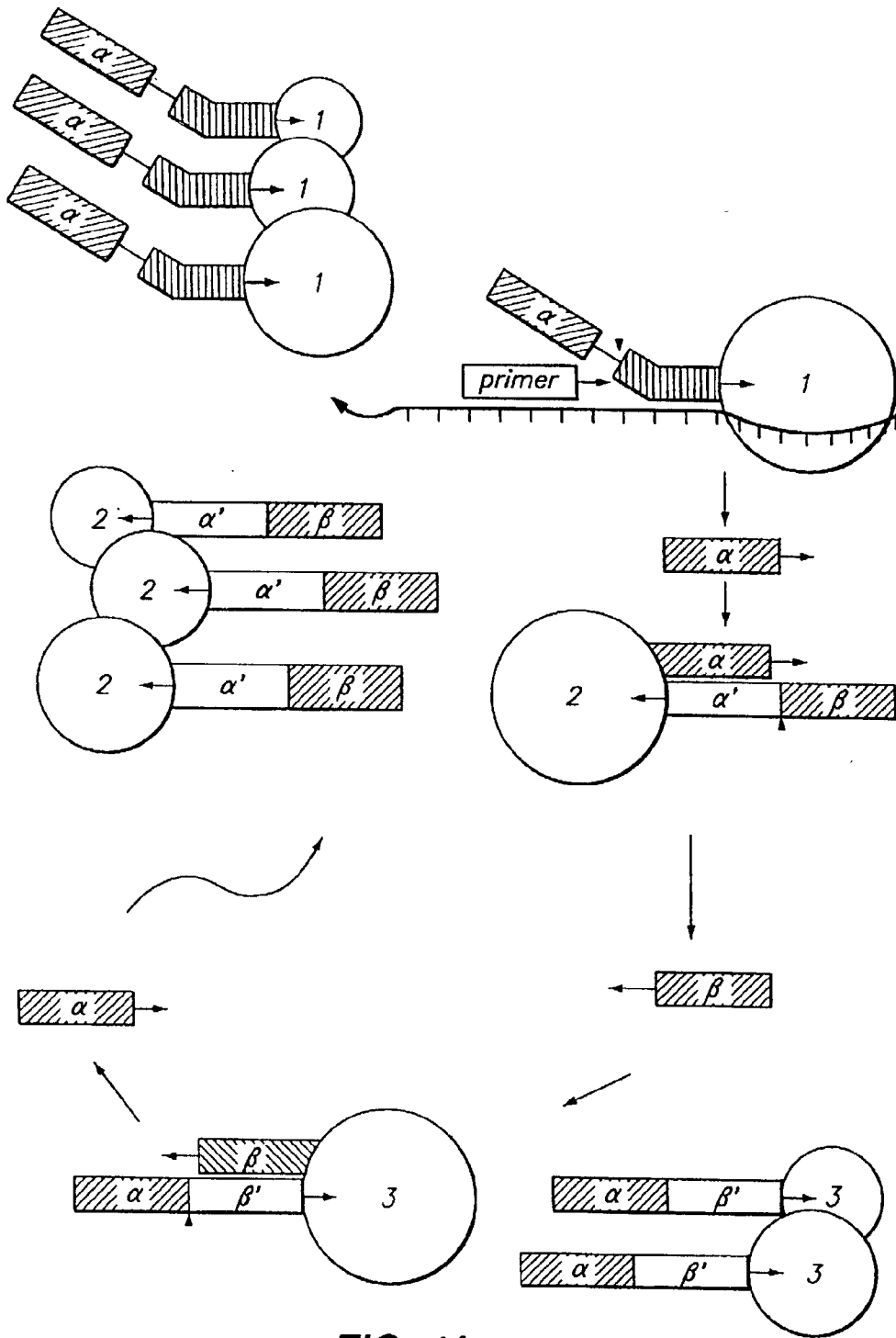


FIG. 1A

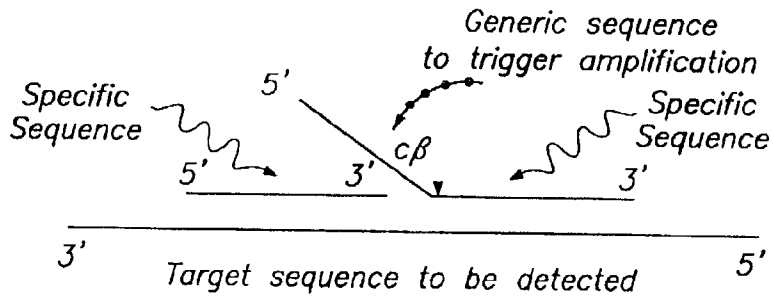


FIG. 1B PART ONE: TRIGGER REACTION

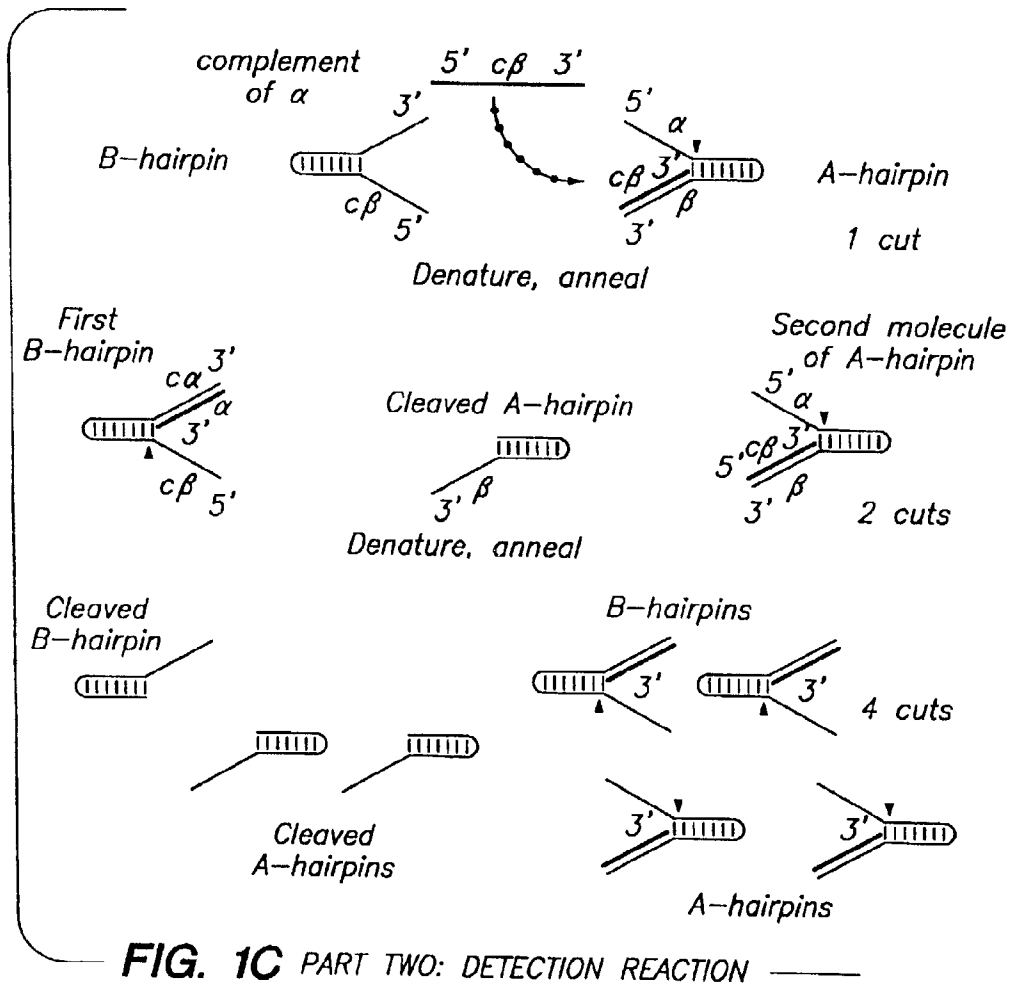


FIG. 1C PART TWO: DETECTION REACTION

FIG. 2B

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MAJORITY [SEQ ID NO: 7] CGAGGGGGAGGACGTXCTGGCCACCCTGCCCAAGAAAGGGGAAAGGGGGTACGAGGTGGGCATCCTC
DNAPTAA [SEQ ID NO: 1] .....C.....G.....C.....C..... 417
DNAPTFL [SEQ ID NO: 2] T.....G.....CG.....T..... 414
DNAPTTR [SEQ ID NO: 3] .....T..C..... 420

MAJORITY ACCGGCCGACGGGACCTCTACGAGCTCCTTCCGACCGCATCGCCGTCCTCCACCCGGAGGGGTACCTCA
DNAPTAA .....AAA.....T.....CA..... 487
DNAPTFL ..T.....G..G.....A.....T.....G.. 484
DNAPTTR .....A..G.C.....G.....CC..... 490

MAJORITY TCACCCGGGGCTGGCTTGGGAGAAGTACGGCCCTGAGCCCGGAGCACTGGGTGGACTACCGGGCCCTGGC
DNAPTAA .....C.....A.....C..C.....CC.....A.. 557
DNAPTFL .....AG.....C.C..... 554
DNAPTTR .....A.....C.....T..C.....C.T 560

MAJORITY GGGGACCCCTCGGACCAACCTCCCCGGGTCAGGGGCATCGGGGAGAAAGACCCGCCXGAAGCTCCTCXAG
DNAPTAA C.....GAG.....T.....G..GAG.....T..GG.. 627
DNAPTFL .....G..T..A.....G.....A..G.....A..GGC.. 624
DNAPTTR .....A.....C.....TC.....A... 630

MAJORITY GAGTCGGGGAGGCTGGAAAACCTCCTCAAGAACCTGGACCGGCTGAAGGGCGG...CXTCCGGGGAGGAAGA
DNAPTAA .....GC.....C.....A..... 694
DNAPTFL .....T..C..C.....A.....T..G.....C 691
DNAPTTR .....A.....A.AAAA.G..... 700
    
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FIG. 2C

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MAJORITY [SEQ ID NO:7] TCCAGGCCCCACATGGAXGACCTGAXGCTCTCCTGGGAGCTXTCGCCAGGTCGGCAGCGGACCTGCCCCCTGGA
DNAPTAO [SEQ ID NO:1] . . . T . . . . . C . T . . . . . A . . . . . C . G . . . . . A . . . . . 764
DNAPTFL [SEQ ID NO:2] . . . . . GGG . . . . . G . C . . . . . GCC . T . . . . . C . A . . . . . T . . . . . A . . . . . T . . . . . 761
DNAPTTR [SEQ ID NO:3] . . . . . A . . . . . C . . . . . A . . . . . C . G . . . . . T . . . . . C . . . . . G . . . . . C . . . . . 770

MAJORITY GCTGGACTTCGCCAAGXGGGGGAGCCCGAGCCGGAGGGGCTTAGGGCCCTTCTGGAGAGCCTGGAGTTT
DNAPTAO . . . . . AA . . . . . AA . . . . . A . . . . . A . . . . . T . . . . . T . . . . . 834
DNAPTFL . . . . . GG . G . C . C . CACA . . . . . A . . . . . T . . . . . T . . . . . GG . . . . . T . . . . . C . . . . . T . . . . . 831
DNAPTTR . . . . . C . . . . . C . G . . . . . G . . . . . C . . . . . C . . . . . C . . . . . C . . . . . C . . . . . 840

MAJORITY GGCAGCCCTCCTCCACGAGTTCGGGCTCCTGGAGGGGCCCAAGGCCCTGGAGGAGGCCCCCTGGCCCGCCG
DNAPTAO . . . . . T . . . . . AA . . . . . T . . . . . AA . . . . . T . . . . . T . . . . . T . . . . . T . . . . . 904
DNAPTFL . . . . . A . . . . . G . . . . . G . . . . . G . G . . . . . GGCA . . . . . T . . . . . T . . . . . T . . . . . 901
DNAPTTR . . . . . . . . . . C . . . . . C . . . . . GCCC . . . . . T . . . . . T . . . . . T . . . . . T . . . . . 910

MAJORITY CCGAAGGGCCCTCCTGGGCTTTGTCCCTTCCCGCCCGCCGAGCCCATGTGGCCCGGAGCTTCTGGCCCTGGC
DNAPTAO . . . . . G . . . . . G . . . . . AAG . . . . . T . . . . . T . . . . . T . . . . . T . . . . . 974
DNAPTFL . . . . . T . . . . . TT . . . . . TG . T . . . . . T . . . . . T . . . . . T . . . . . T . . . . . T . . . . . 971
DNAPTTR . . . . . . . . . . C . . . . . C . . . . . G . . . . . AAA . . . . . T . . . . . T . . . . . T . . . . . 980

MAJORITY CCGCCCGCAGGGAGGGCCGGGTCCACCGGGCACCAGACCCCTTAXGGGCCCTXAGGGACCTXAAGGAGGTG
DNAPTAO . . . . . G . . . . . G . . . . . C . . . . . C . G . . . . . T . A . . . . . AA . C . . . . . C . . . . . G . . . . . C . . . . . 1044
DNAPTFL T . GG . . GT . . . . . G . . . . . CC . . . . . T . . . . . A . . . . . C . . . . . G . . . . . G . . . . . T . . . . . G . . . . . 1041
DNAPTTR . . . . . TG . . . . . C . . . . . G . . . . . G . . . . . GGG . . . . . G . . . . . G . . . . . A . A . . . . . C . . . . . C . . . . . 1050
    
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FIG. 2D

MAJORITY [SEQ ID NO:7]	CGGGGXCTCCTCGCAAGGAGCCTGGCCGTTTTGGCCCTGAGCGAGCCCTXGACCTCXTGCCGGGGGAGCG	
DNAPTAQ [SEQ ID NO:1]G..T.....A.....AG.....C.....A.....T.G.....CC.....C.....	1174
DNAPTFL [SEQ ID NO:2]AA.....G.....G.....C.....G.....T.C.....A.A.....	1171
DNAPTTR [SEQ ID NO:3]C.....C.....C.....TC.....G.A.....G.....	1120
MAJORITY	ACCCCATGCTCCTGCCCTACCTCCTGGACCCCTCCACACACCACCCCGGAGGGGGTGGCCCGGGCGCTACGG	
DNAPTAQT.....	1184
DNAPTFLG.....T.....T.....	1181
DNAPTTRG.....G.....	1190
MAJORITY	GGGGGAGTGGACGGAGGAXGCGGGGGAGGGGGCGCTGCTXTCGAGAGGCTCTCCXGAACGCTXXXGGAG	
DNAPTAQG.....G.....GC..T.....GCC.....GTG..G..	1254
DNAPTFLT.....A.....GG.....C.C.....A..C.....AAA.....	1251
DNAPTTRG..C.CCC.C.....C..G.....CAT.G.....CCTTA..	1260
MAJORITY	CGCCTTGAGGGGAGGAGAGGCTCCTTGGCTTTACGACGAGCTGGAGAGCGGCTTCCCGGGTCCCTGG	
DNAPTAQ	A.G.....A.A..A.A.C.C.G.....G.....G.....GCT.....	1324
DNAPTFLC.....A.....A.....G.....G.....G.....GT.....	1321
DNAPTTRC.....C.....C.....C.....A.....G.....	1330
MAJORITY	CCACATGGAGCCACCGGGGCTXCGGCTGGAGCTGGAGCTACCTCCAGGCCCTXTCCTGGAGGTGGCGGA	
DNAPTAQG.C.....G.C.....T..AG.....T.G.....C..	1394
DNAPTFLGG.....C.....C.....C.....C.....A..G	1391
DNAPTTRC.....A.....A.....T.....T.....C.T.....	1400

FIG. 2E

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MAJORITY [SEQ ID NO:7]  GGAGATCCGCCGCCCTCGAGGAGGAGGTCTTCGGCTGGCCGGCCACCCCTTCAACCTCAACTCCCGGGCAG
DNAPTAQ [SEQ ID NO:1]  .....GC.....CC.....1464
DNAPTFL [SEQ ID NO:2]  ....G.G....AG..G.....G.....C.....1461
DNAPTTR [SEQ ID NO:3]  .....T.....G.....1470

MAJORITY  CAOCTGGAAGGCTGCTCTTTGACGAGGCTXGGGCTTCCGGCCATCGGCAAGACGGAGAGACXGGCAAGC
DNAPTAQ .....G.....A.....1534
DNAPTFL ....GC.....G.C.G.T.....G.G.A.....1531
DNAPTTR .....TA.....T.G.G.....C.A.....A.....1540

MAJORITY  GCTCCAGCAGCCGCCGCTGCTGGAGGCTXCGXGAGGCCACCCCATCGTGGAGAAAGATCCTGCAGTA
DNAPTAQ .....G.....G.C.....1604
DNAPTFL .....T.....G.A.....CCGC.....1601
DNAPTTR .....G.....A..G.....C..C.....1610

MAJORITY  CCGGGAGGTCACCAAGCTCAGAAACACCTACATXGACCCCTGCCXGXCCTCGTCCACCCGAGGACGGGGC
DNAPTAQ .....G...G.....T...G.A...A.....1674
DNAPTFL .....A.....C.C...G.....A..C.....1671
DNAPTTR .....G.G.....C..AAG.....G.....1680

MAJORITY  CGCCTCCACACCCGCTTCAACGACGCGCCACCGCCAGGCTTAGTAGCTCCGAGCCCAACCTGC
DNAPTAQ .....A.....T.....C..1744
DNAPTFL .....G.....C.....TCC.....1741
DNAPTTR .....G.....G.....1750
    
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FIG. 2F

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MAJORITY [SEQ ID NO:7]  AGAACATCCCCTCCGCACCCXCTGGCCGACAGGATCCGCCGGCCCTTGGTGGCCGAGGAGGGXTGGGT
DNAPTAQ [SEQ ID NO:1]  .....G..T..G.....A..C.....G....C. 1814
DNAPTFL [SEQ ID NO:2]  .....G.....T.....C..G.....A.....C..... 1817
DNAPTTH [SEQ ID NO:3]  .....CT.....C.....T.....C.....T.....G 1820

MAJORITY  GTTGGTGGCCCTGGACTATAGCCACATAGAGCTCCGGTCCCTGGCCCACTCTCCGGGACCGAAGACTG
DNAPTAQ  A.....T.....A....G.....G.....C..... 1884
DNAPTFL  .C.....T.....C.....T.....T.....A..... 1881
DNAPTTH  .....C.....C.....C.....A..... 1890

MAJORITY  ATCCGGTCTTCCAGGAGGGGAGGACATCCACACCCAGCCGCGAGCTGGATGTTCCGGCTCCGCCCGG
DNAPTAQ  .....G.....G.....G.....G.....G... 1954
DNAPTFL  .....T.....T.....T.....T.....T... 1951
DNAPTTH  ..A.....A.....A.....A..... 1960

MAJORITY  AGCCGTGGACCCCTGATGGCCCGGGCCCAAGACCATCAAGTGGGGTGGTGTACGGCATGTCCGC
DNAPTAQ  .....G.....G.....G.....G.....G... 2024
DNAPTFL  .A.GG..A.....T.....G.....G..... 2021
DNAPTTH  .....GG..G.....GG..G.....C..... 2030

MAJORITY  CCACCCCTCTCCAGGAGCTTCCCATCCCTACGAGAGCCGGTGGCCTTACTTCCAG
DNAPTAQ  .....A.....T.....CCA.....T.... 2094
DNAPTFL  .....GG.....T.....T.....T..... 2091
DNAPTTH  ...TA.G.....T.....A.....A 2100
    
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FIG. 2G

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MAJORITY [SEQ ID NO:7] AGCTTCCCCAAGCTCGGGGCTGGATTGAGAACACCCCTCGAGGAGCCGAGGGGGGTACGCTCCACA
DNAPTAQ [SEQ ID NO:1] ..... 2164
DNAPTFL [SEQ ID NO:2] .....A.....GG.....C.....C.CC.....T..... 2161
DNAPTTR [SEQ ID NO:3] .....A.A.....G.....A.....C.....A..... 2170

MAJORITY CCTCTTCGGCCGCGCCGCTACCTGCCCGACCTCAACGCCCGGGTGAAGAGCGGTGGCGGACCGCCGCGGGA
DNAPTAQ .....C.....A.....AG.G.....C... 2234
DNAPTFL .....T.....T.....G.....C..... 2231
DNAPTTR .....AA.AA.....CA.....C..... 2240

MAJORITY GCGCATGGCCTTCAACATGCCCCGTCCAGGGCACCGCGGACCTCATGAAGCTGGCCATGGTGAAGCTC
DNAPTAQ ..... 2304
DNAPTFL .....G.....G.....T..... 2301
DNAPTTR ..... 2310

MAJORITY TTCGGCCGCTXCAGGAAATGGGGCCAGGATGCTCCTXCAGGTCCAGGACGAGCTGGTCCCTCGAGGCGCC
DNAPTAQ .....A.....GG.....T..... 2374
DNAPTFL .....T.....C.....G.....TT.G.....G..... 2371
DNAPTTR .....C.C.G.....G.....C.G.....C.....G..... 2380

MAJORITY CCAAAGCGCGCGGAGCGGTGGCCGCTTGGCCAGGAGGT CATGGAGGGGCTCTATCCGCTGGCCGT
DNAPTAQ .....A.....A.....CC.....GGG.....G..... 2444
DNAPTFL .....G.C.....AG.....A.....GG.....CAG... 2441
DNAPTTR .....C.....C.....A.....G.....C.....AA.C.....C..... 2450
    
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FIG. 3A

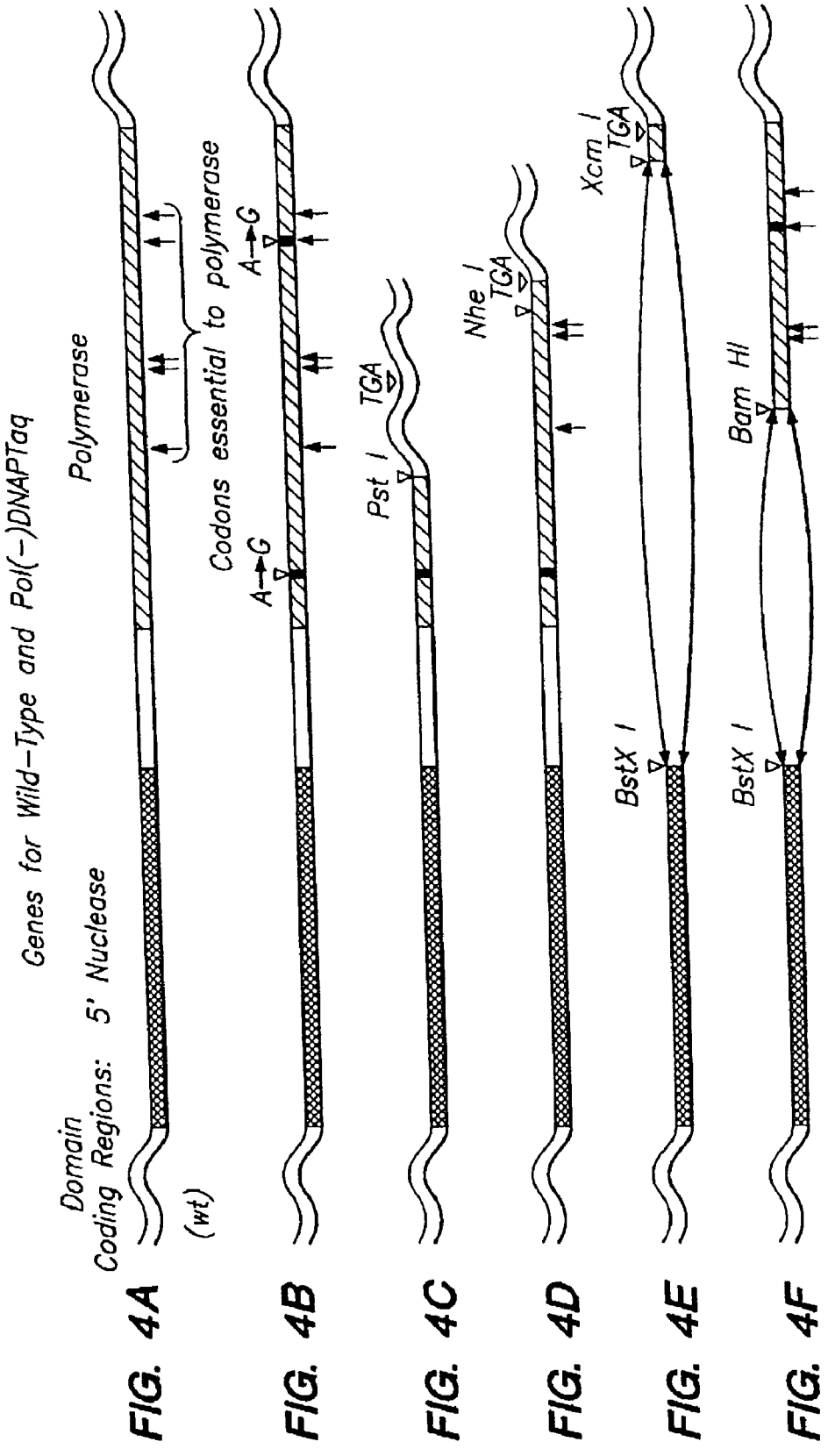
MAJORITY	[SEQ ID NO:8]	MXAMLPLEFEPKGRVLLVDGHHLAYRTFFALKGLTTSRGEVQAVYGFAKSLIKALKEDG-DAVXVVVFDK	
TAO PRO	[SEQ ID NO:4]	.RG.....H.....I.....	69
TFL PRO	[SEQ ID NO:5]V.V.....	68
TTR PRO	[SEQ ID NO:6]YK.F.....	70
MAJORITY	APSF8HEAYEAYKACRAPTPEDFPROLALI KELVDLLGLXRLEVPGEADDVLATLAKKAEKEGYEVRI L		
TAO PRO	GG.....A.....S.....	139	
TFL PROV.....F.....R.....	138	
TTR PROFT.....	140	
MAJORITY	TADRDLYQLLSDRIAVLHPGEYLI TPAWLWEKYGLRPEQWVDYRALXGDPSONLPGVKGI GEKTXKLLX		
TAO PRO	K.....H.....D..A.....T..E.....R...E	209	
TFL PROE..I.....Y.....A.....I.....OR..IR	208	
TTR PROV...V.....H...E.....F...V.....L...K	210	
MAJORITY	EWGSLENLLKNLDRVKP·XXREKIXAHMEDLXLSXLSXVRTDLPLEVDFAXRREPDREGLRAFLELEF		
TAO PROA.....L...AI...L...D...K..WD..AK.....K.....R.....	278	
TFL PROFOH..O...SL...LO.G..A.A..RK..Q.H.....GR..T.NL.....	277	
TTR PROENV...K..L...R..LE..R.....L..QG.....	280	
MAJORITY	GSLLEHFGLLXPKALEEAPWPPPEGAFVGFVLSRPEPMVAELLALAAARXGRVHRAXDPLXGLRDLKEV		
TAO PROS.....K.....D.....G.....PE.YKA.....A	348	
TFL PROG...A.....L..SF.....G.WE..L...Q...R.....G.	347	
TTR PROA.AP.....K...C.D.....A...A...K.....	350	

FIG. 3B

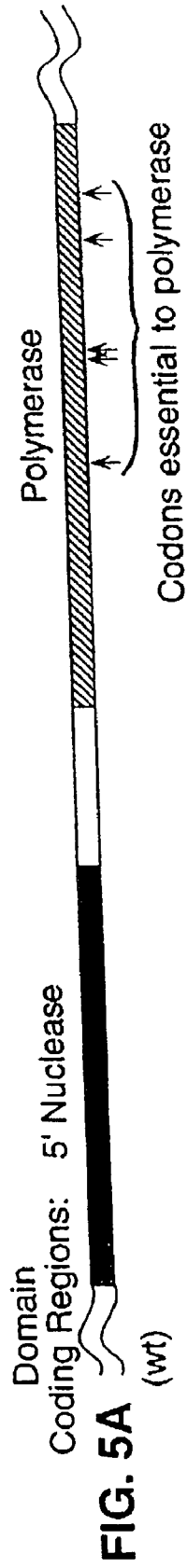
MAJORITY	[SEQ ID NO:8]	RGLLAKDLAVLALREGDLXPDDPMLLAYLLDPSNTTPEGVARRYGGEWTEADGERALLSERLFXNLXX	
TAQ PRO	[SEQ ID NO:4]S.....G.P.....E.....A.....A.....WG	418
TFL PRO	[SEQ ID NO:5]I.....F.E.....A.....QT.KE	417
TTH PRO	[SEQ ID NO:6]S.....V.....AH.....HR..LK	420
MAJORITY		RLEGEERLLWLYXEVEKPLSRVLHMEATGURLDVAYLQALSLEVAEEI RRLEEEVFRLAGHPFNLSRD	
TAQ PRO	R..R..A.....R.....A.....A.....	488
TFL PRO	K.....E.....R.....EA.V.O.....	487
TTH PRO	K.....H.....L.....	490
MAJORITY		QLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILOYRELTCLKNTYIDPLPXLVHPRTG	
TAQ PRO	S.....S.....D.I.....	558
TFL PRO	DR.....A.....K..	557
TTH PRO	R..L..Q.....H.....V.....S.....	560
MAJORITY		RLHTRFNOTATATGRSSDPNLQNI PVRTPLGQRI RRAFVAEEGWXLVALDYSOIELRVLAHLSCDENL	
TAQ PRO	I.....L.....	628
TFL PRO	V..V.....	627
TTH PRO	A..A.....	630
MAJORITY		IRVFOEGRDIHTOTASWHF GVPPEAVDPLMRRAAKTI NFGULYGMSAHLRSOELAI PYEEAVAFI ERYFO	
TAQ PRO	E.....R.....G.....	698
TFL PRO	S..G.....G..S.....	697
TTH PRO	K.....V.....	700

FIG. 3C

MAJORITY [SEQ ID NO: 8]	SFPKVRAWIEKTL EGRRRGYVETLFGRRRYVPDLNARVKSAREAAERMAFNMPVVOGTAADLMKLA MVKL	768
TAD PRO [SEQ ID NO: 4] E.....	767
TFL PRO [SEQ ID NO: 5]	Y..... G..... R.....	770
TTH PRO [SEQ ID NO: 6] K.....	
MAJORITY	FPRLXEHGARM LQVHDELVL EAPKXRAEXVAALAKEVME GUYPLAVPLEVEVGXGEDWLSAKEX	
TAD PRO E..... A..... R..... I.....	833
TFL PRO O..... L..... D..... R..... W..... Q..... L.....	831
TTH PRO R..... L..... QA..... E..... A..... KA..... M..... G.....	835



Genes for Wild-Type and Pol(-) DNAPTf1



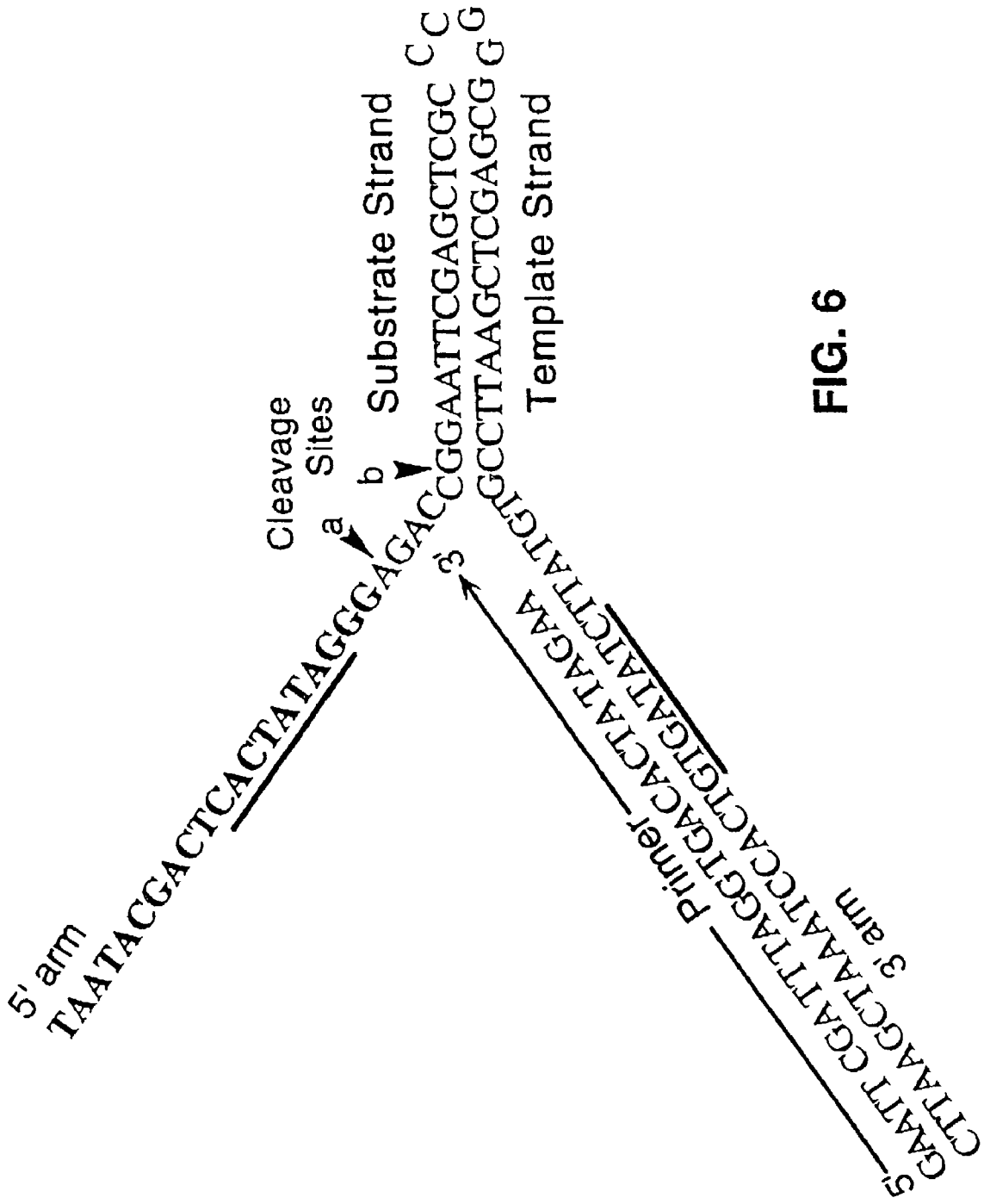


FIG. 6

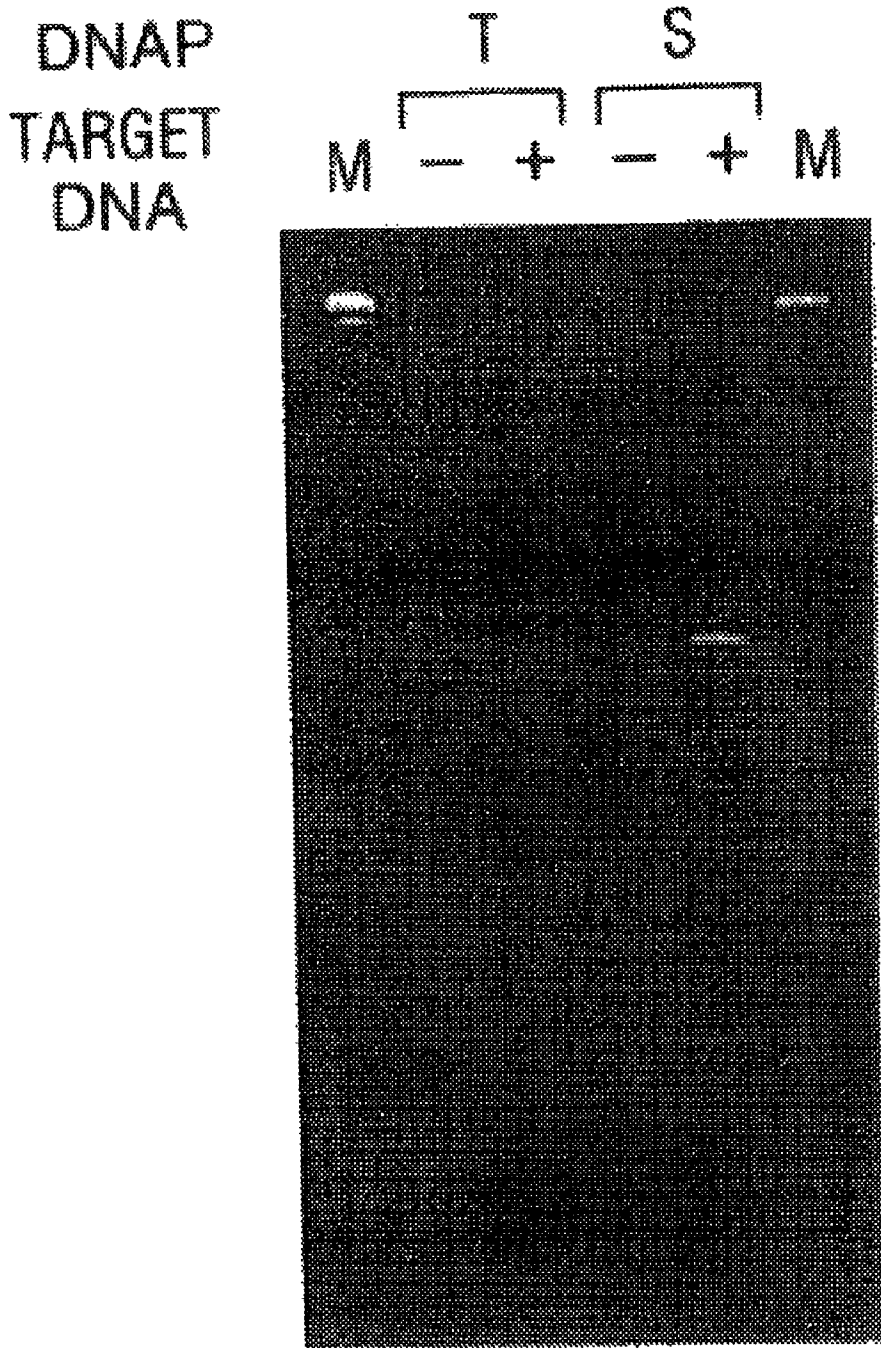


FIG. 7

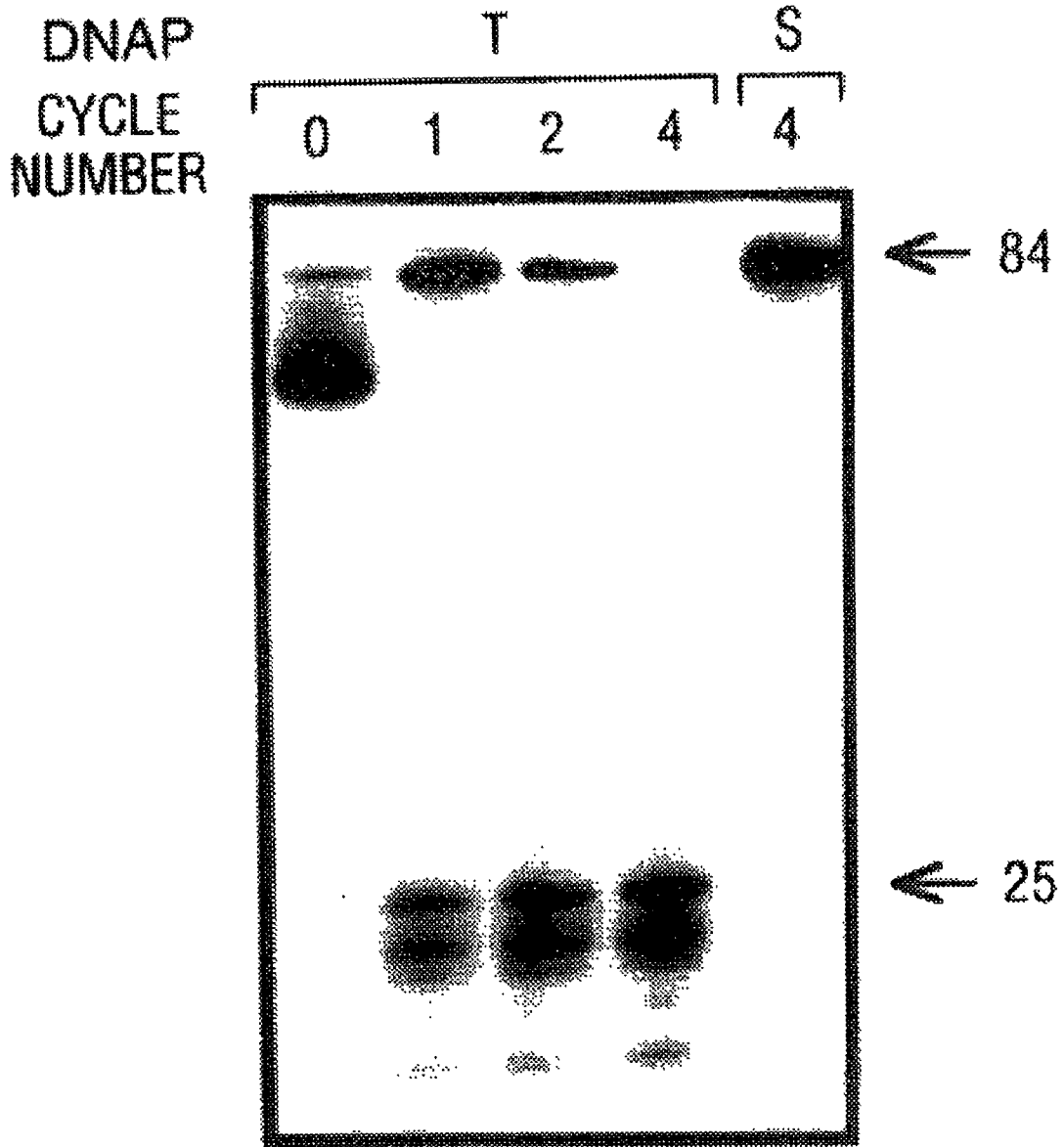


FIG. 8

	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl ₂ :	+	-	+	+	+	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-

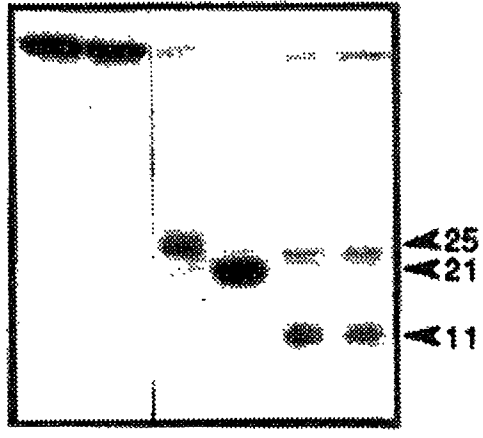


FIG. 9A

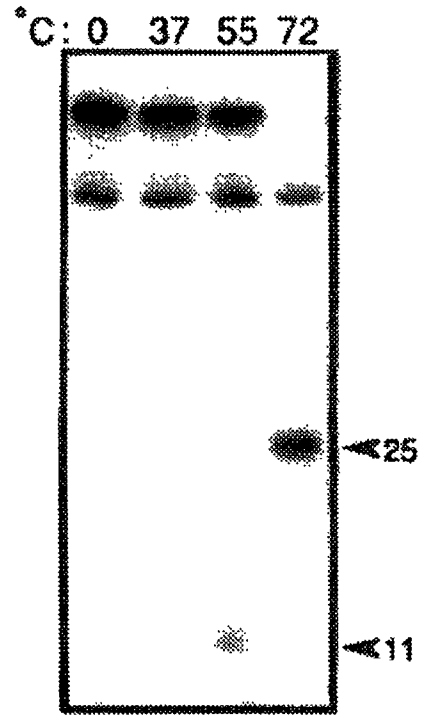


FIG. 9B

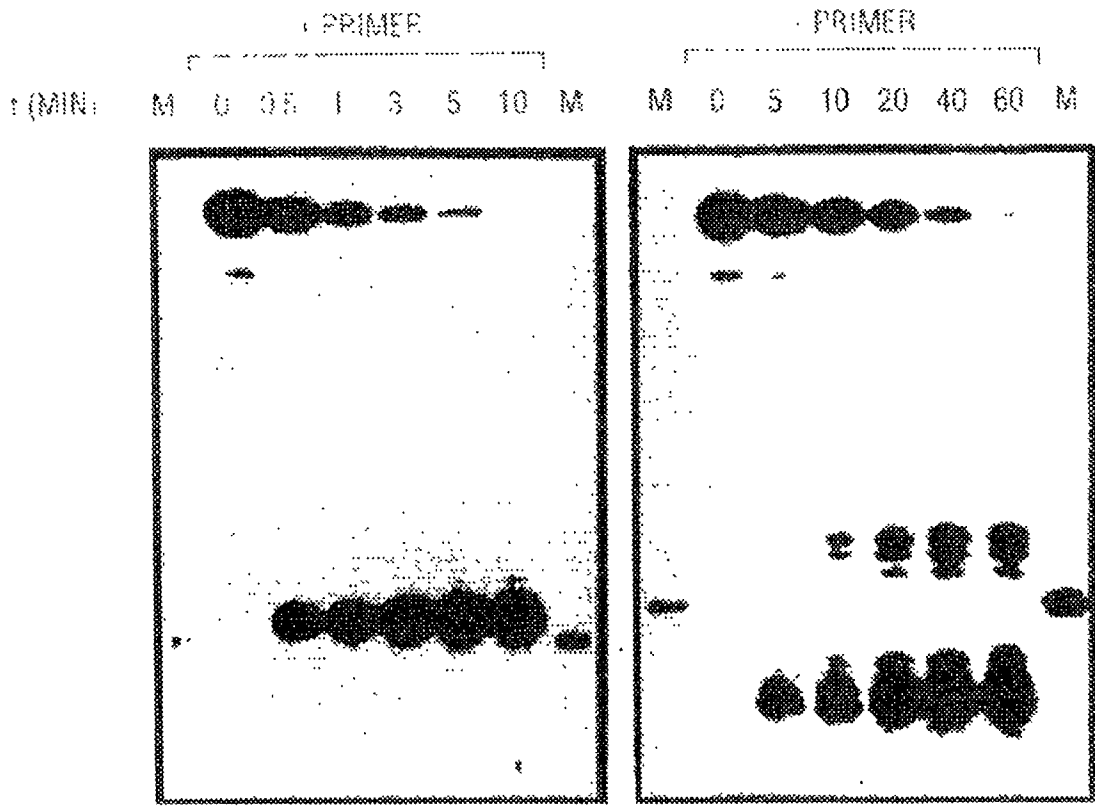


FIG. 10A

FIG. 10B

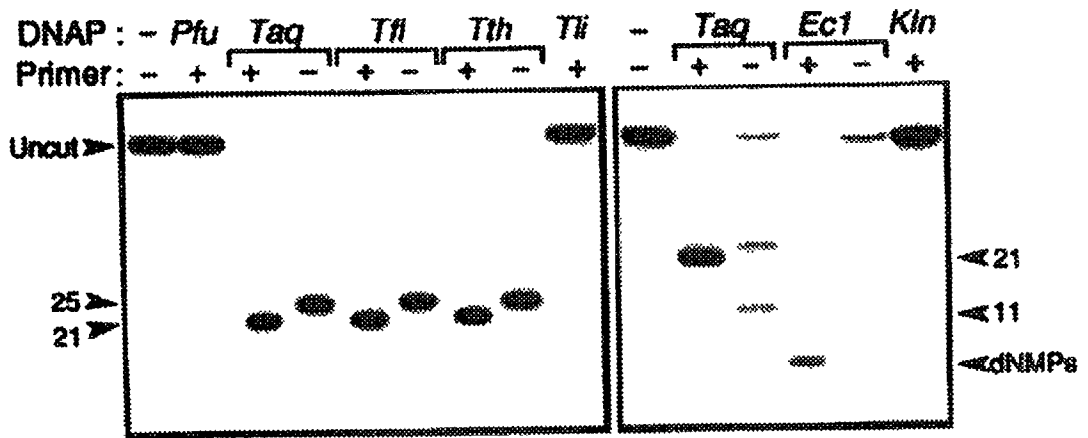
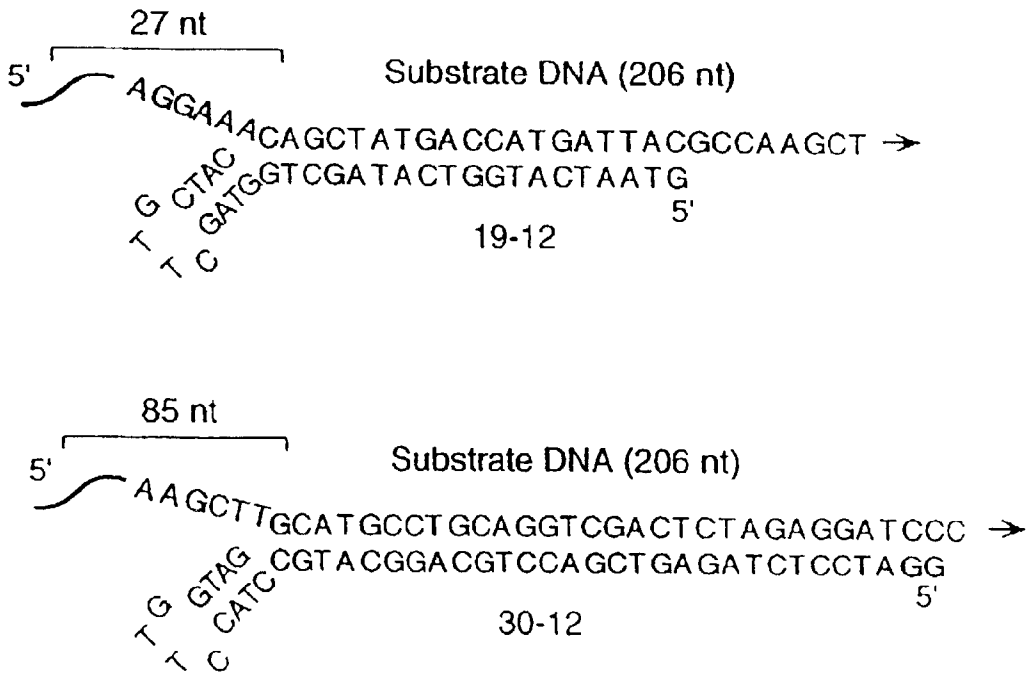


FIG. 11A

FIG. 11B

FIG. 12A



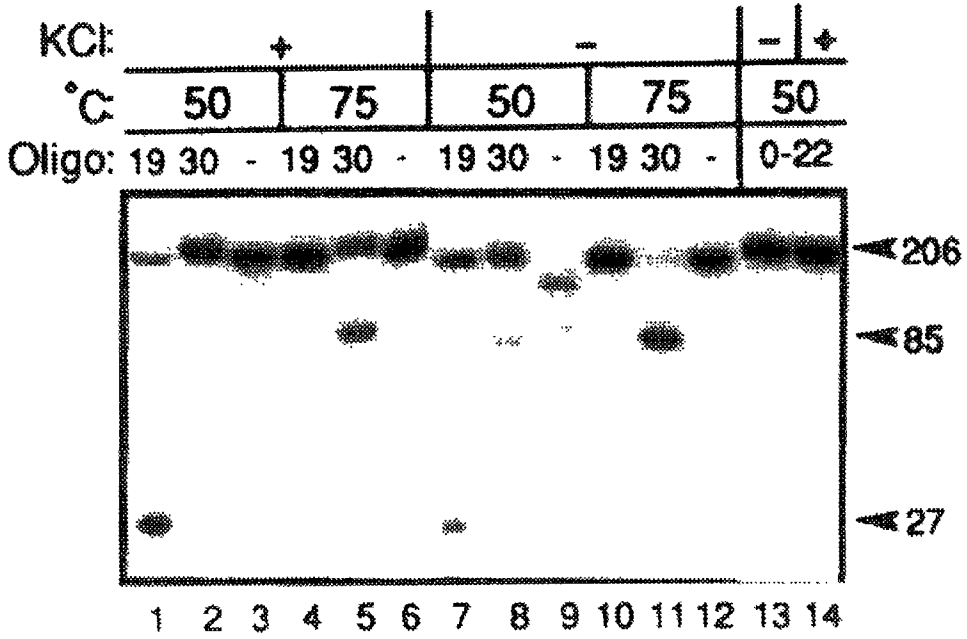


FIG. 12B

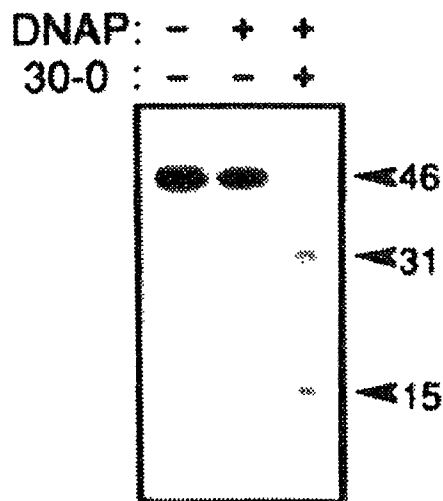


FIG. 13B

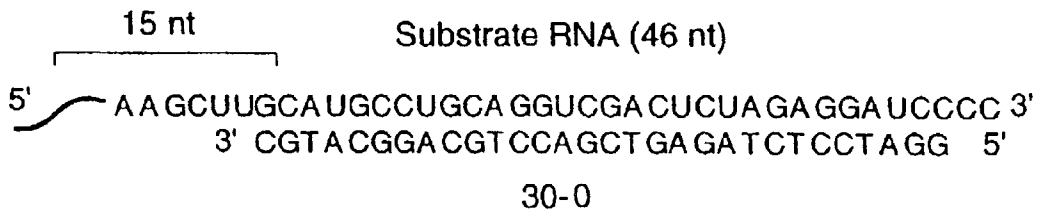


FIG. 13A

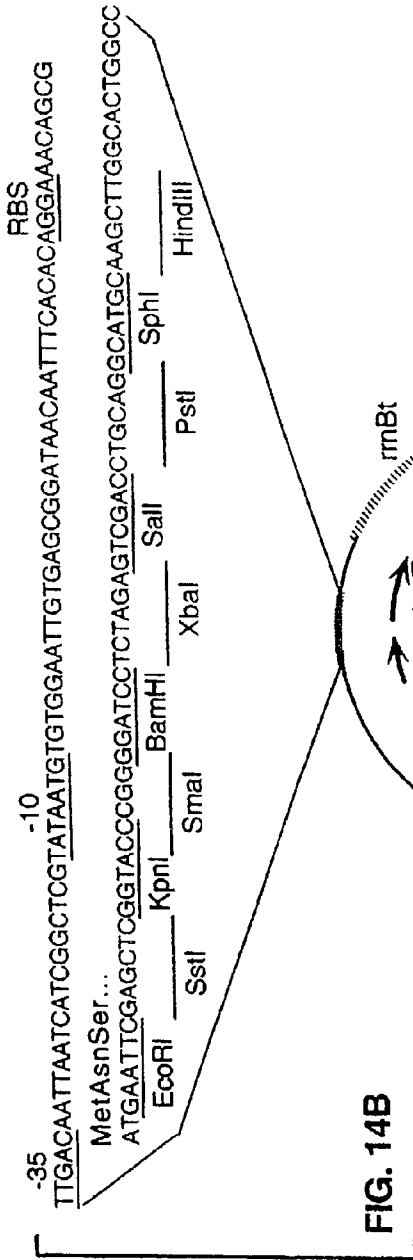


FIG. 14B

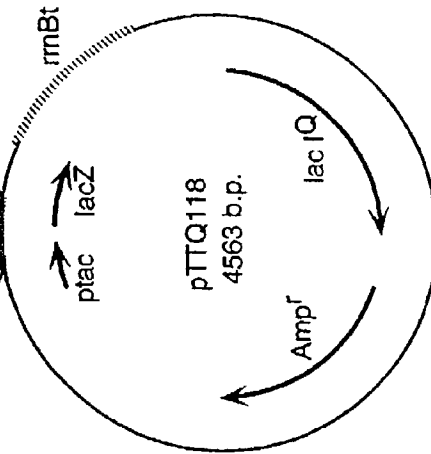
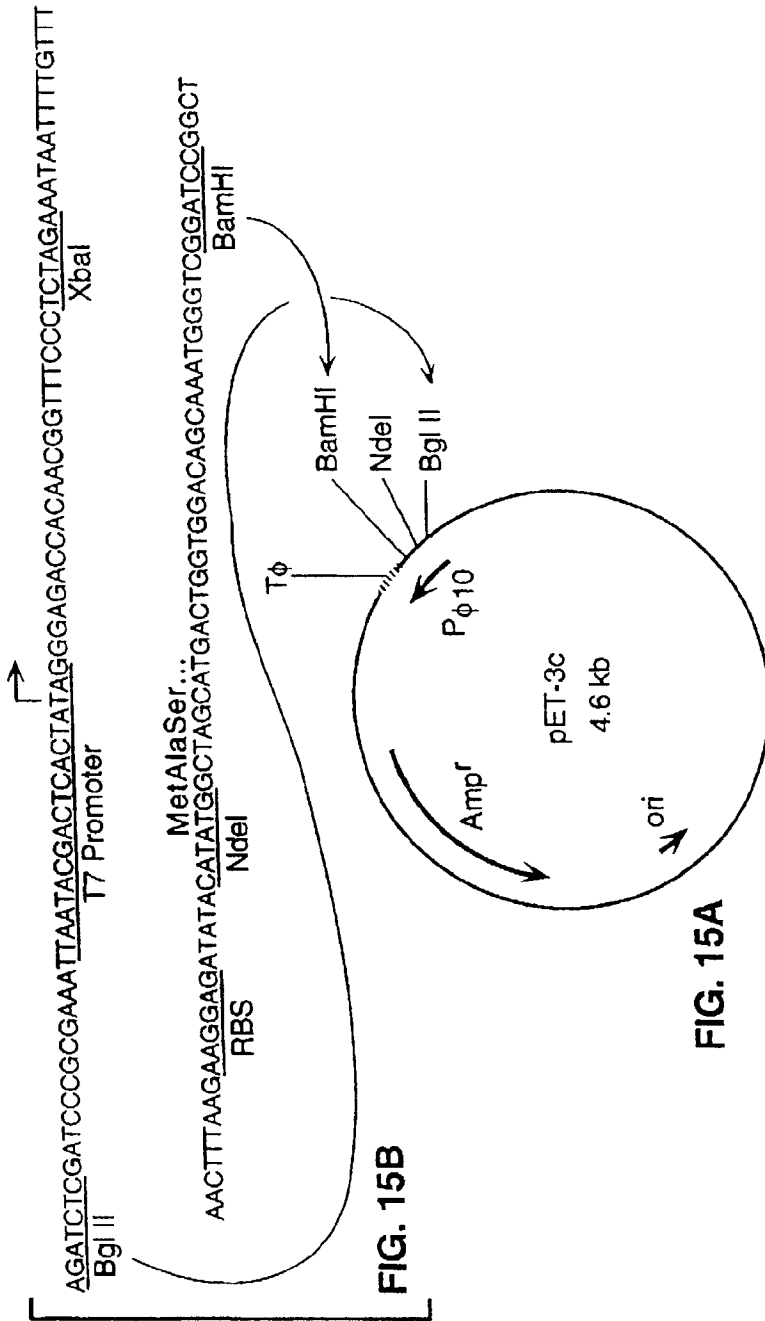


FIG. 14A

RBS: Ribosome binding site
 ptac: Synthetic tac promoter
 lac I^Q: Lac repressor gene
 lacZ: Beta-galactosidase alpha fragment
 rmBt: E. coli rmB transcription terminator

FIG. 14C



P_{φ10}: Bacteriophage T7 φ10 promoter
 Tφ: T7 φ Terminator
FIG. 15C

RBS: Ribosome binding site

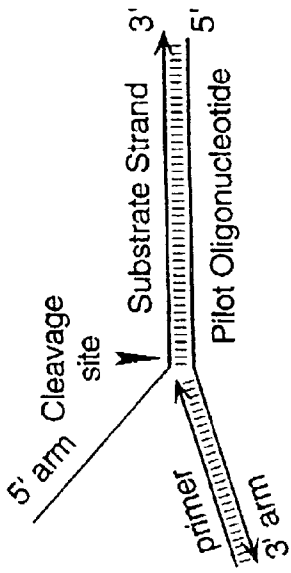


FIG. 16B

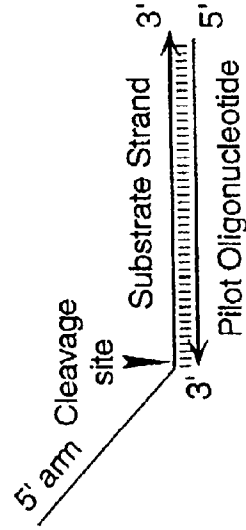


FIG. 16D

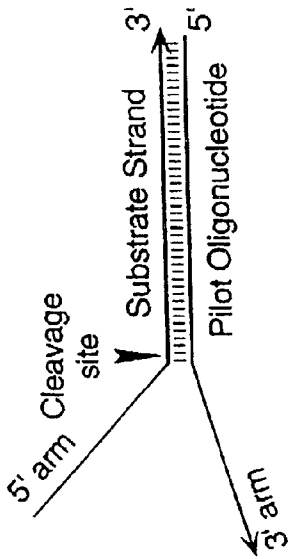


FIG. 16A

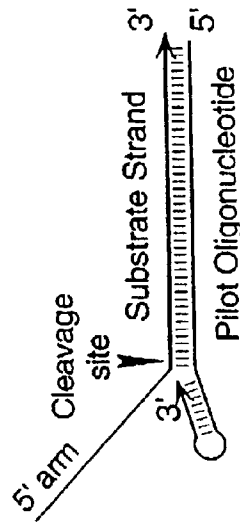


FIG. 16C

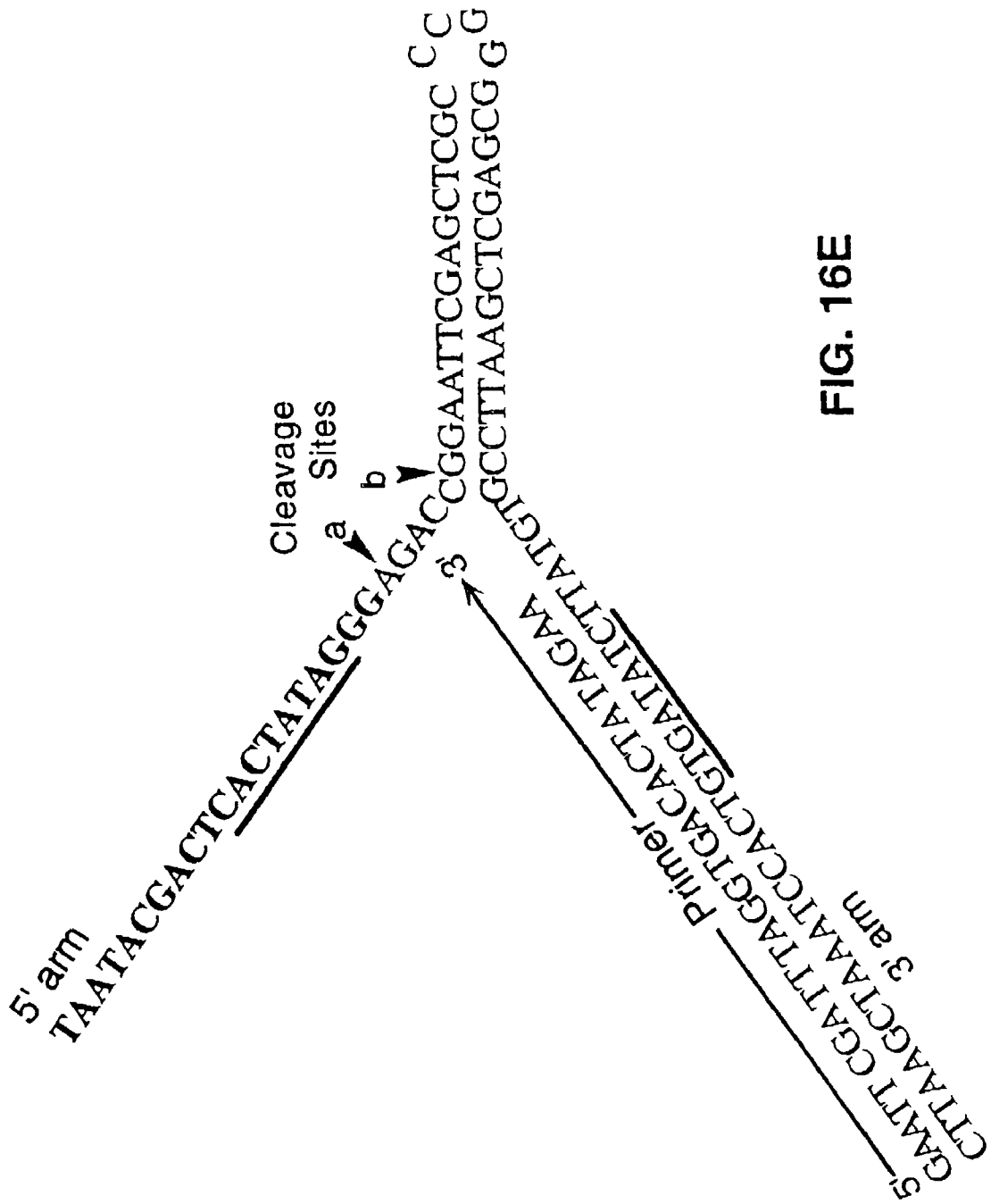


FIG. 16E

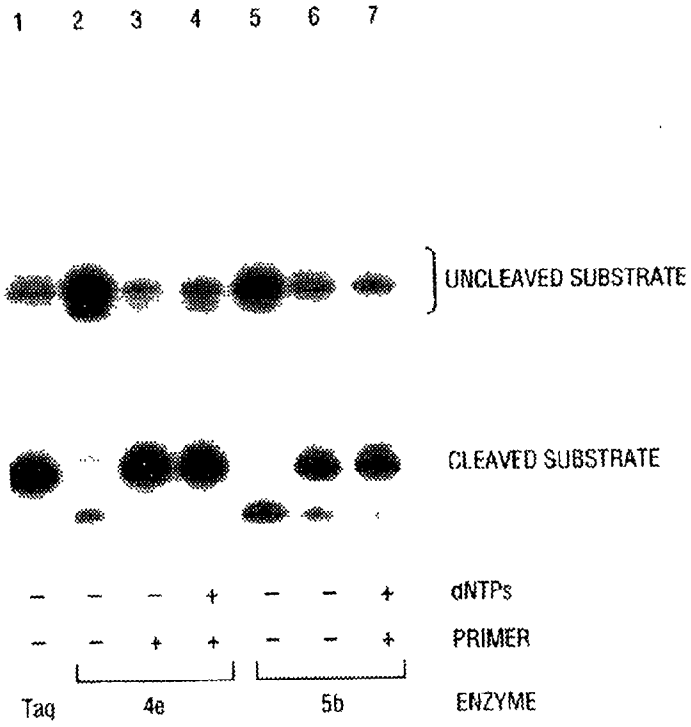


FIG. 17

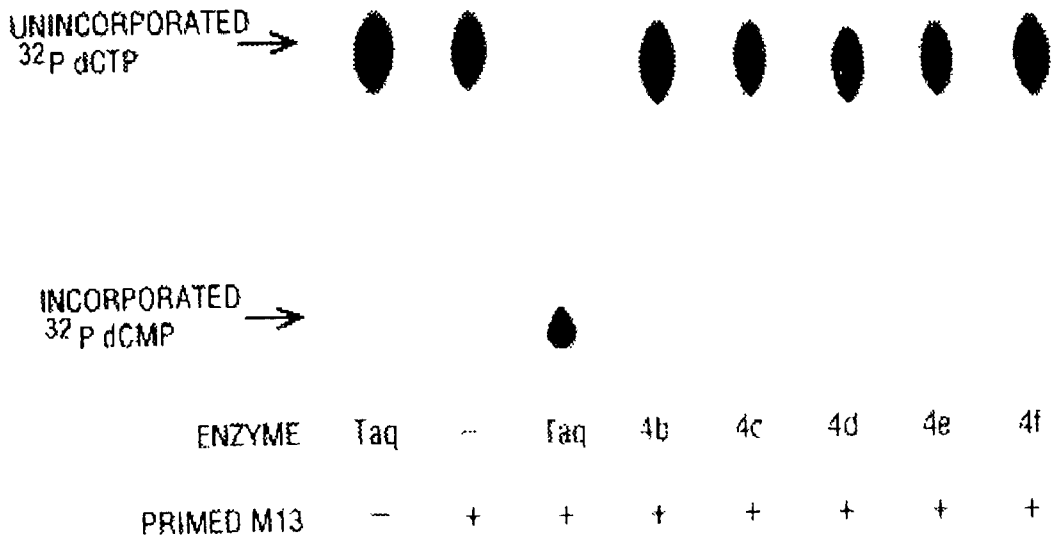


FIG. 18

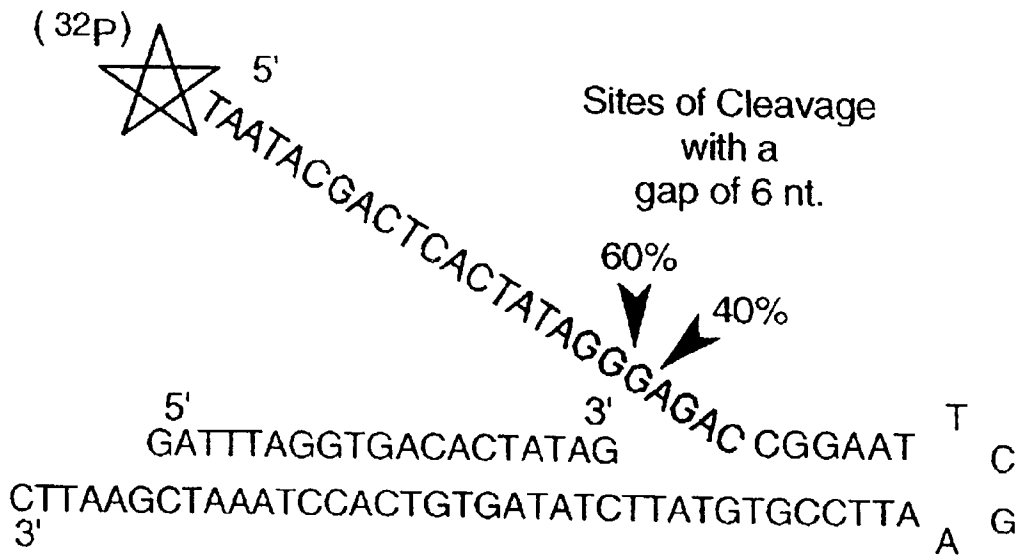


FIG. 19A

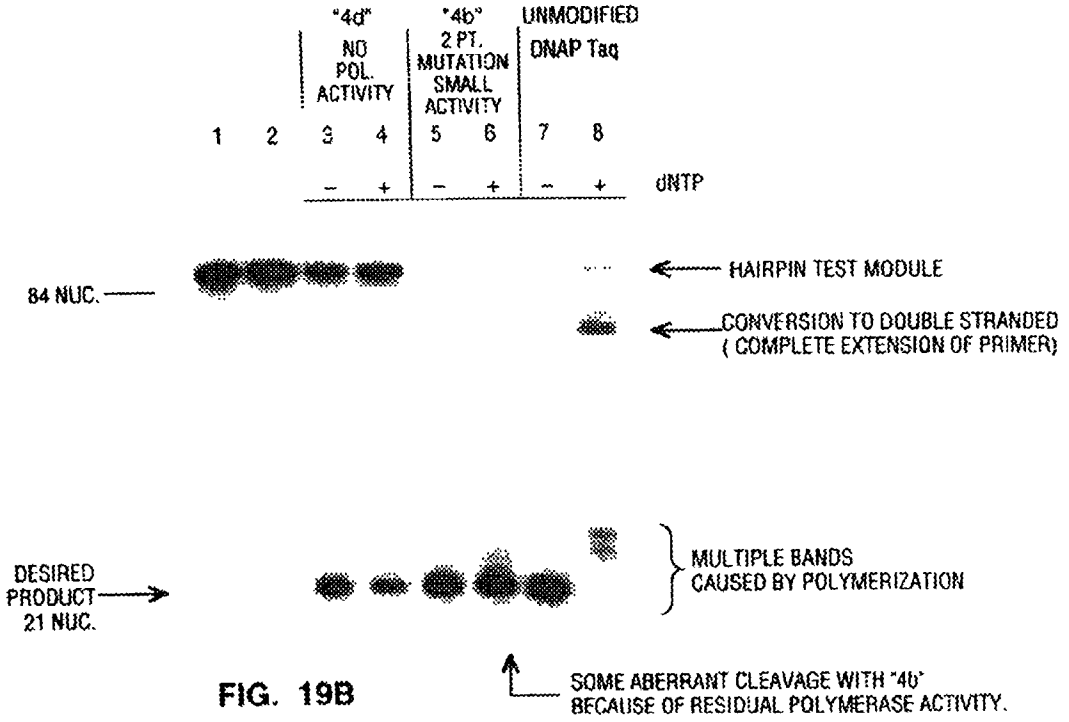


FIG. 19B

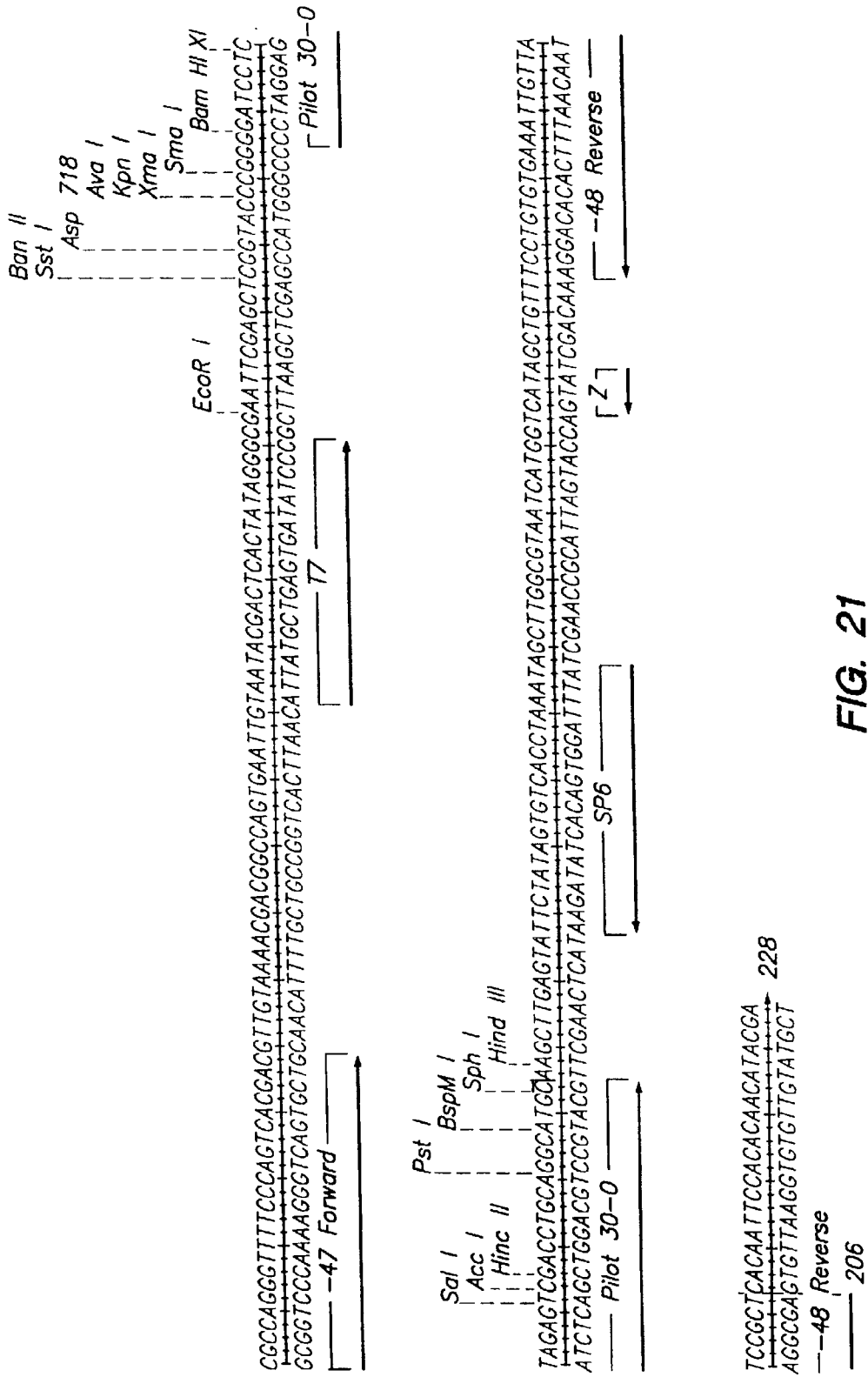


FIG. 21

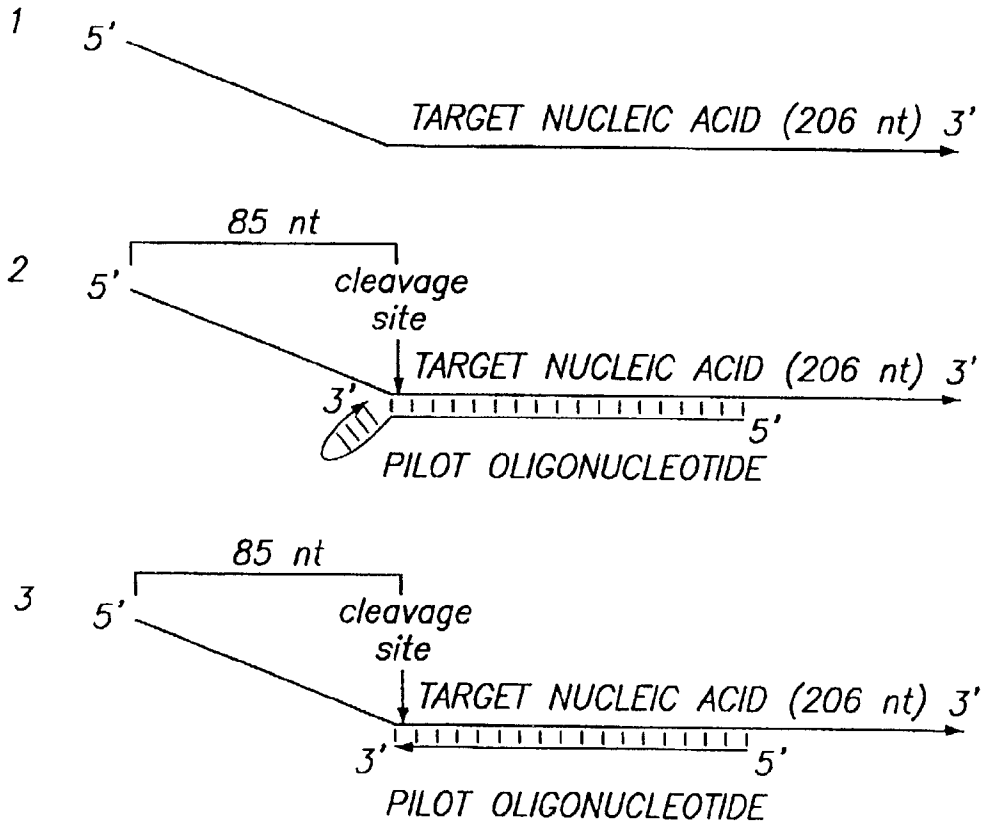


FIG. 22A

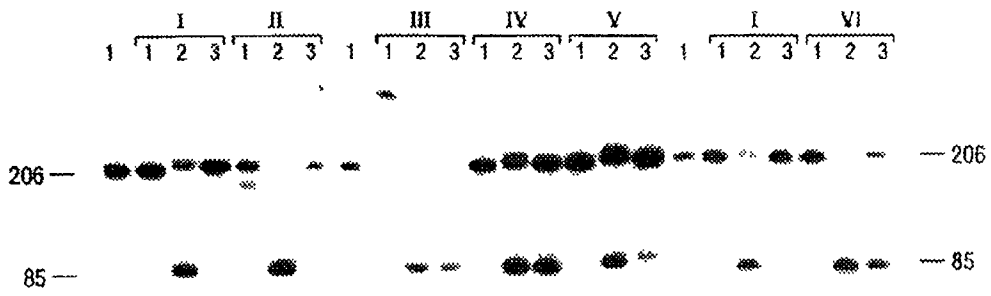


FIG. 22B

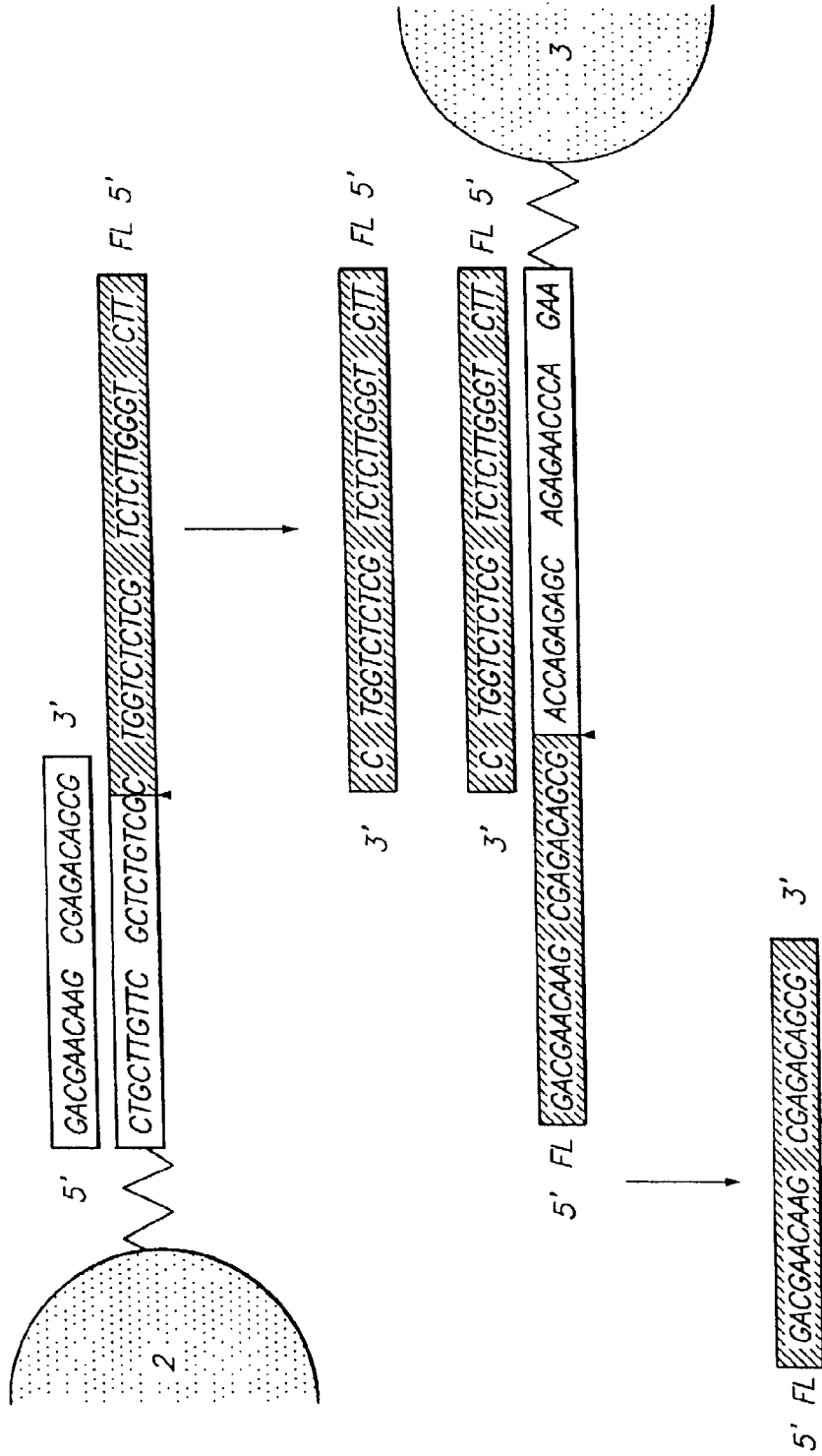


FIG. 23

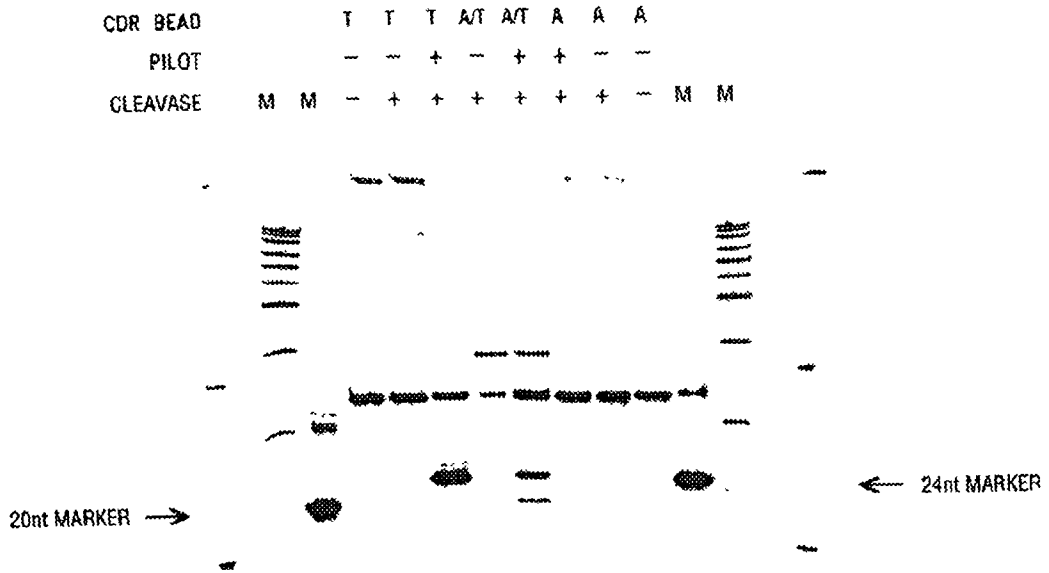


FIG. 24

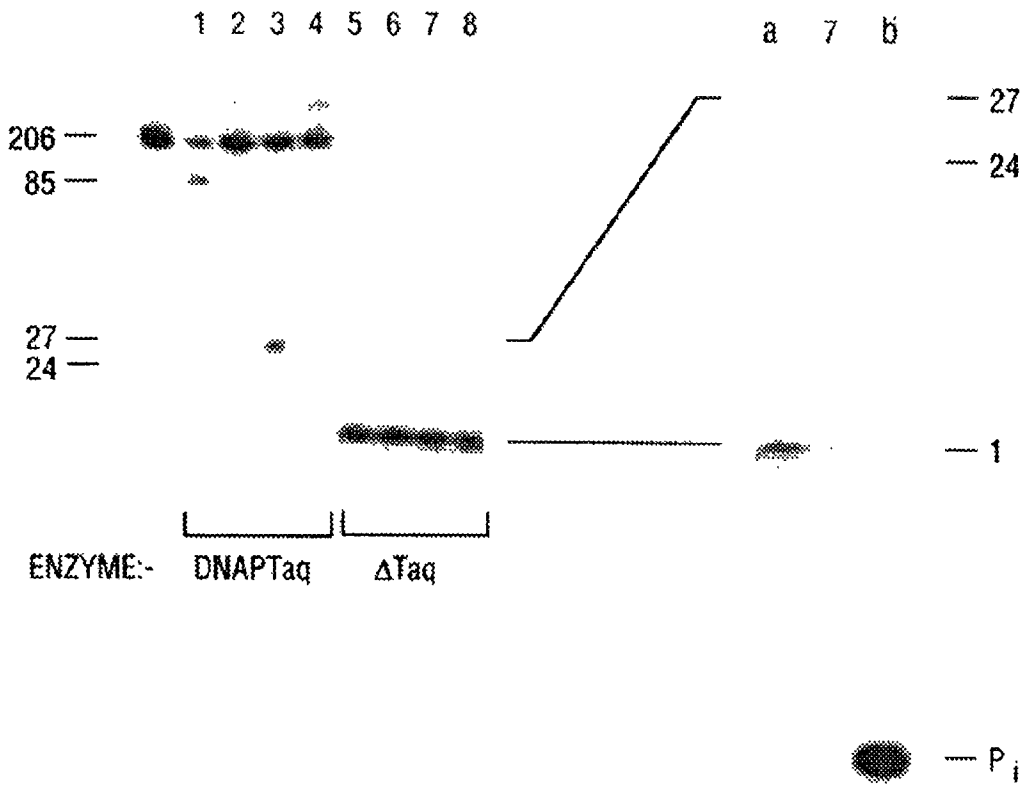
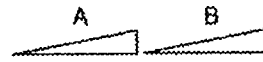
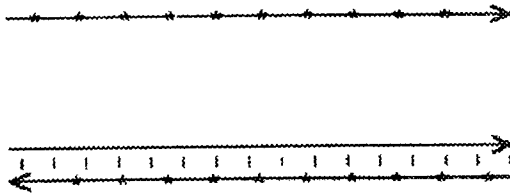


FIG. 25A

FIG. 25B

FIG. 26A



— 206

FIG. 26B

+ = 32p

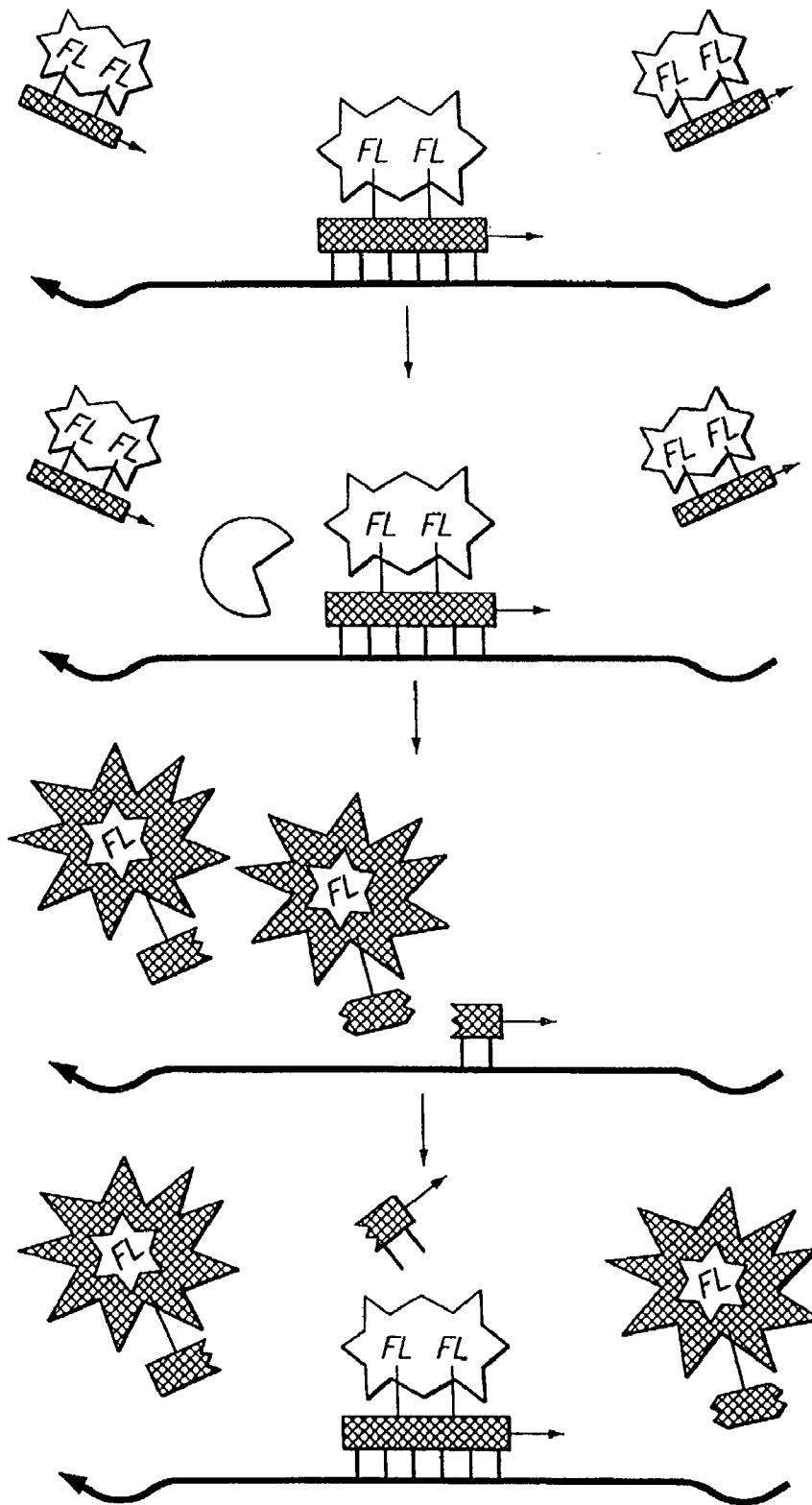


FIG. 27

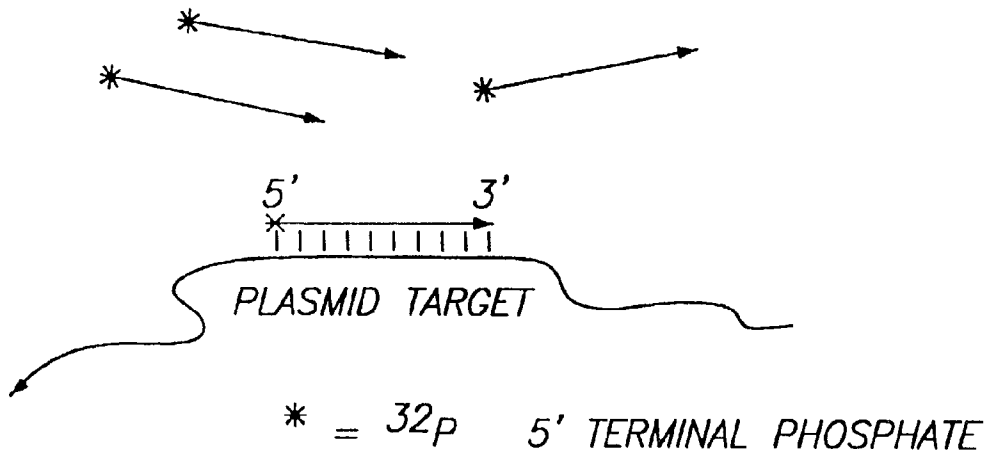


FIG. 28A

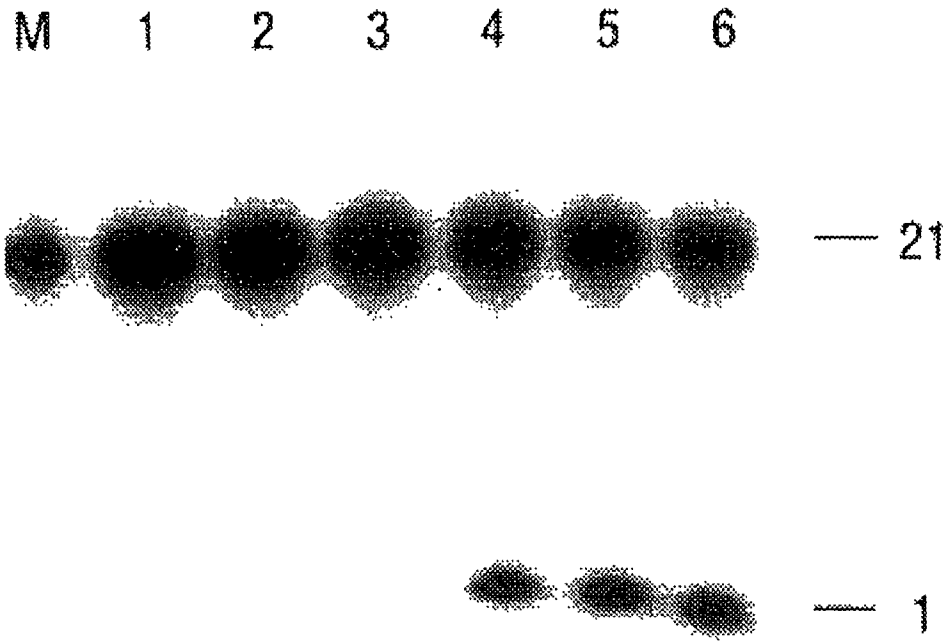


FIG. 28B

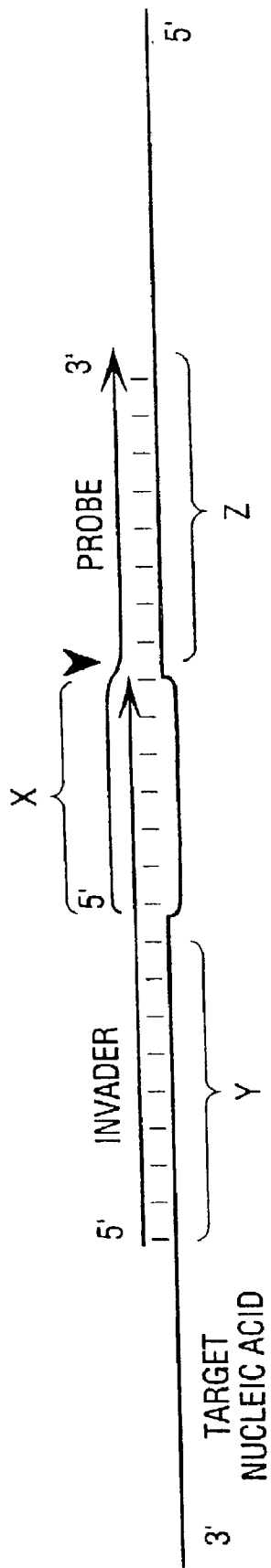


FIG. 29

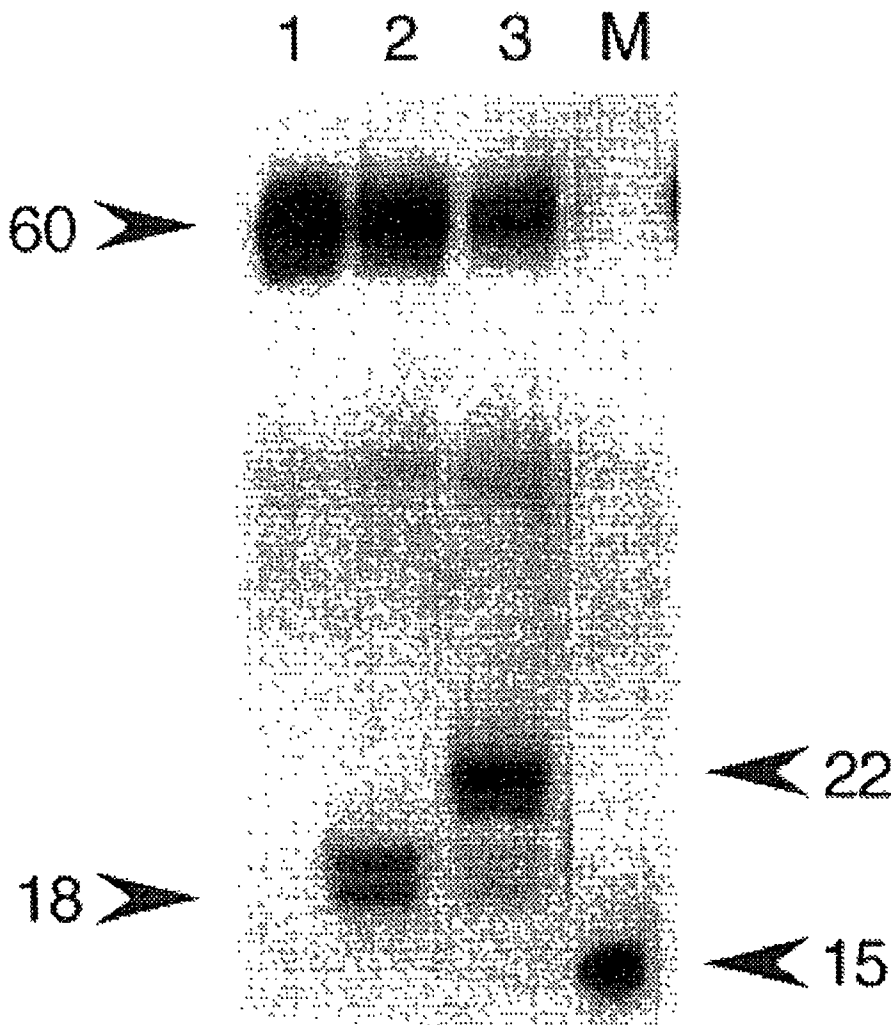


FIG. 31

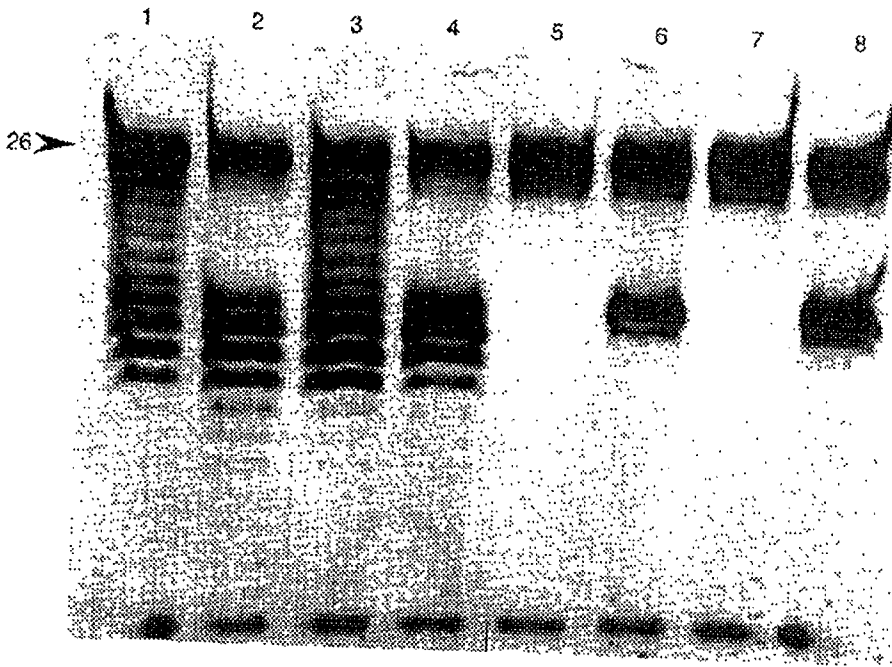


FIG. 33

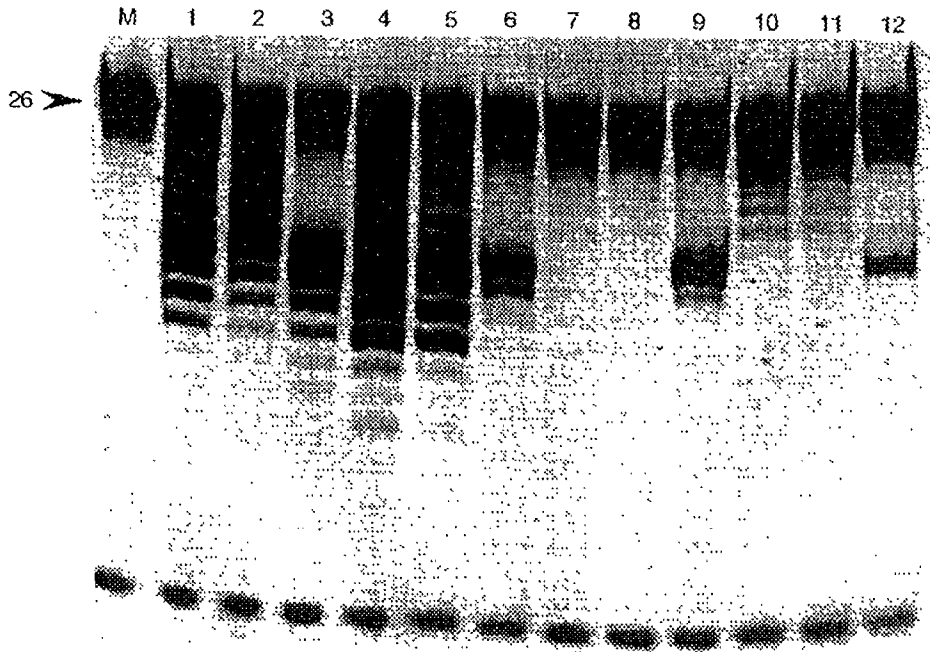


FIG. 34

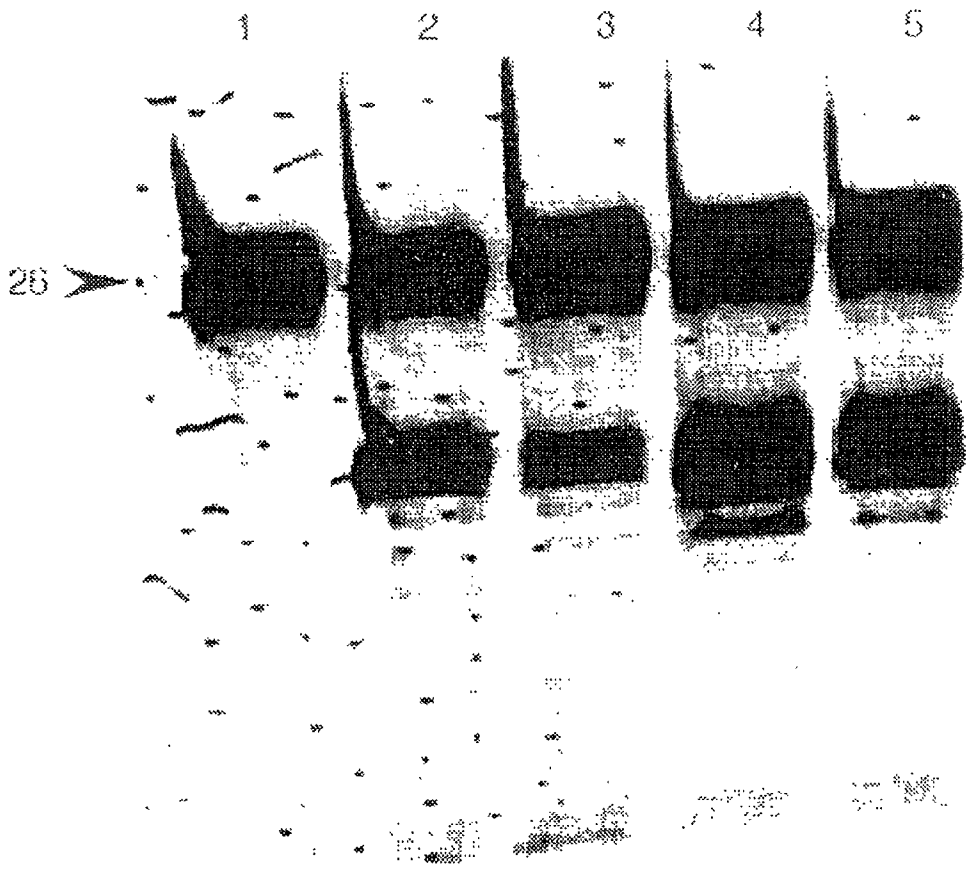


FIG. 35

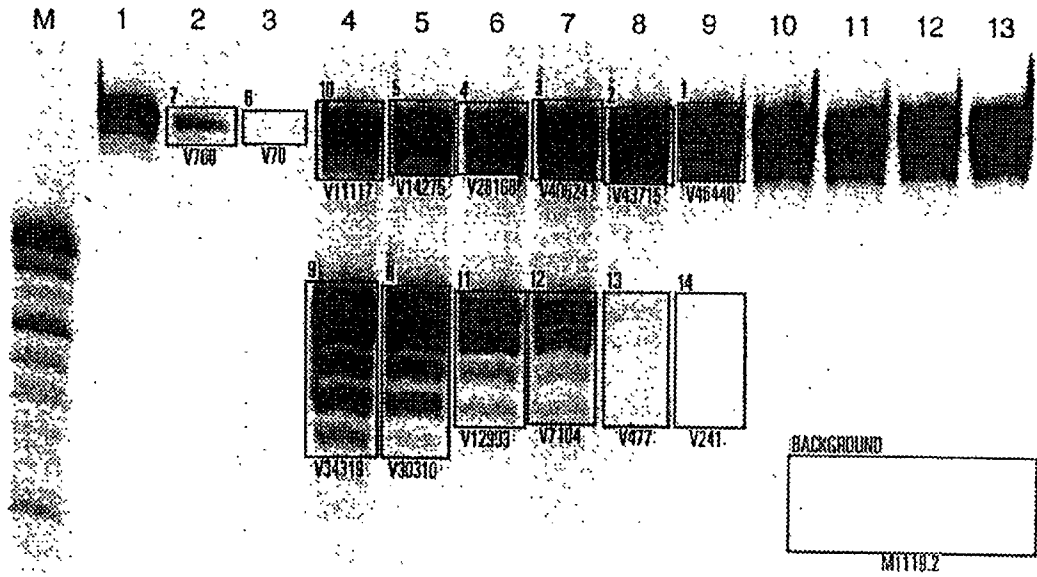


FIG. 36

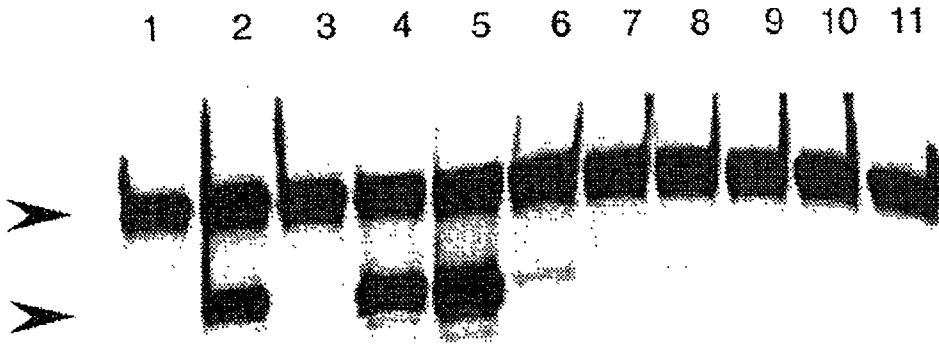


FIG. 37

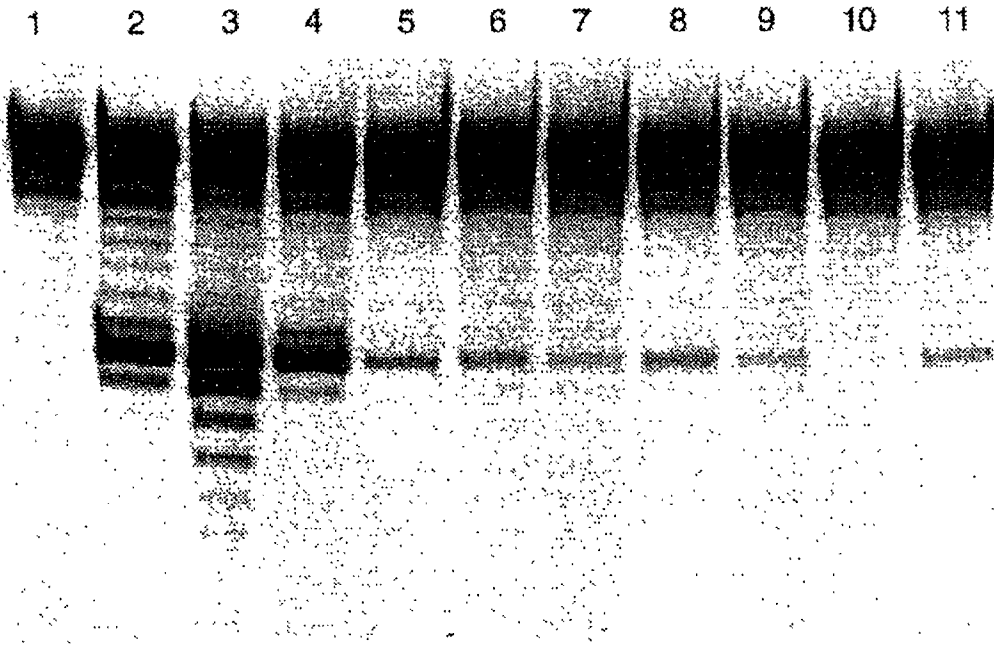


FIG. 38

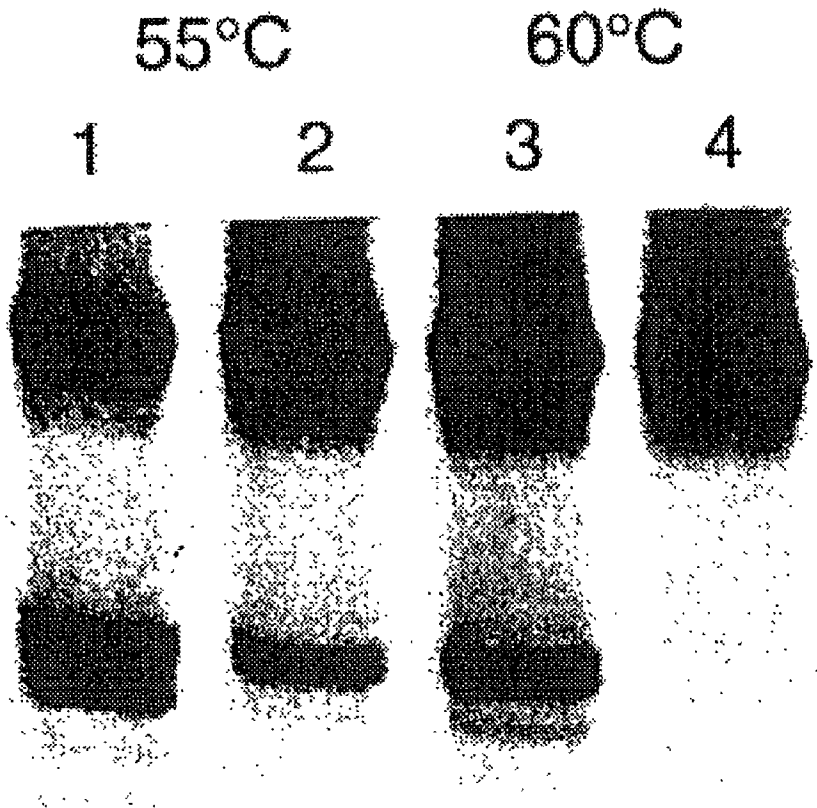


FIG. 39

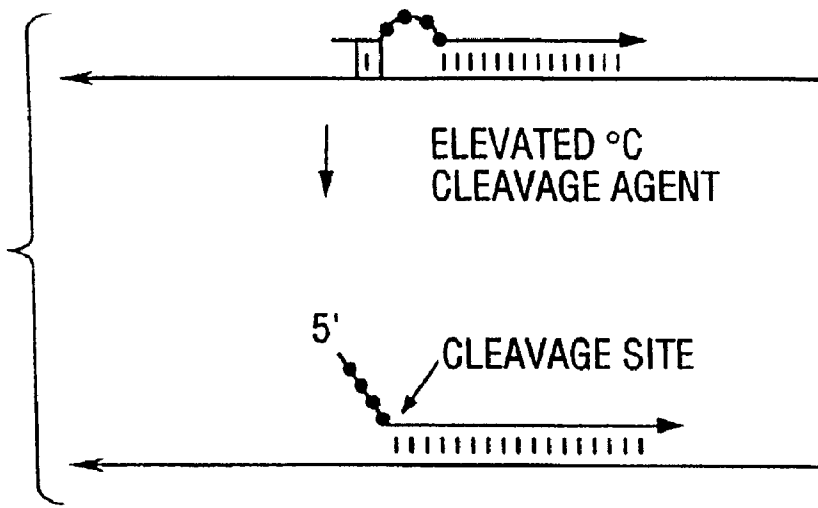


FIG. 40A

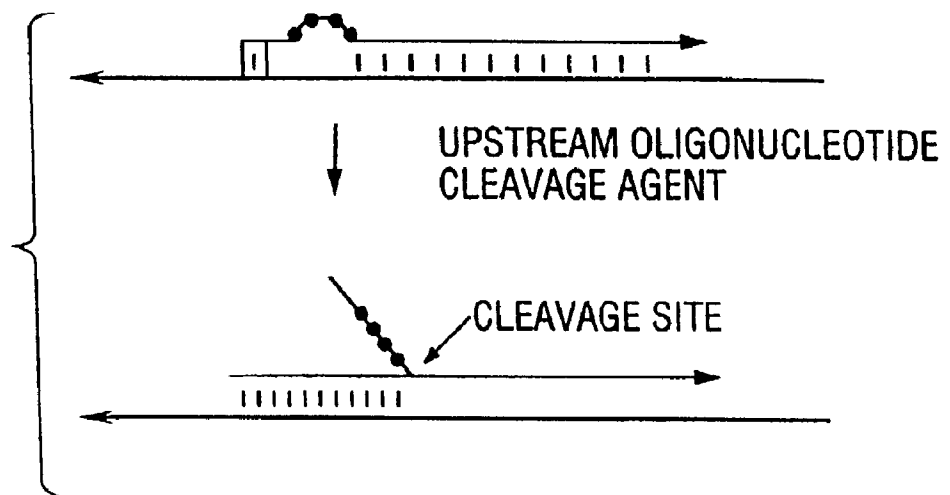


FIG. 40B

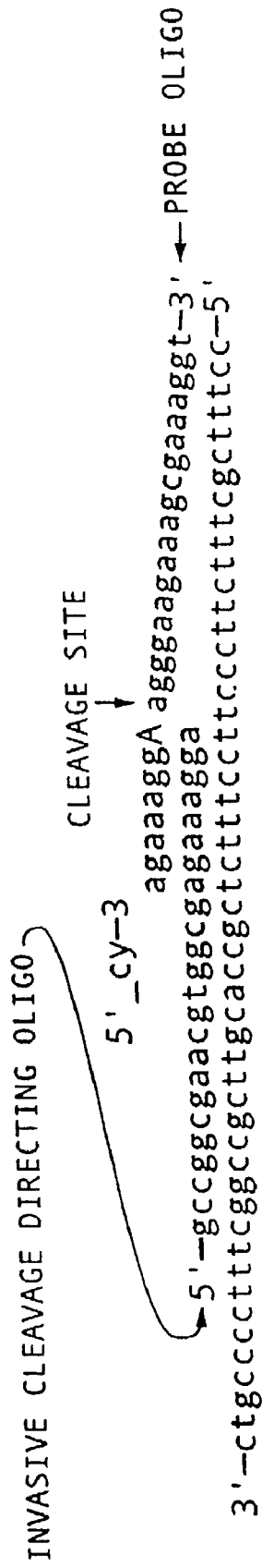


FIG. 41

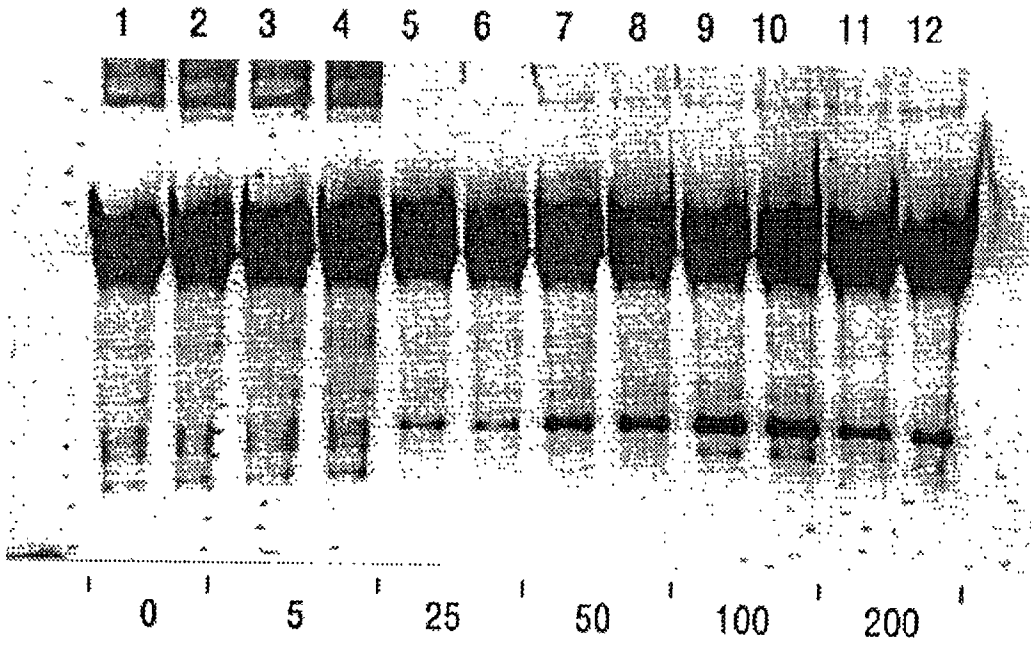


FIG. 42

1 2 3 4 5 6 7 8 9 10

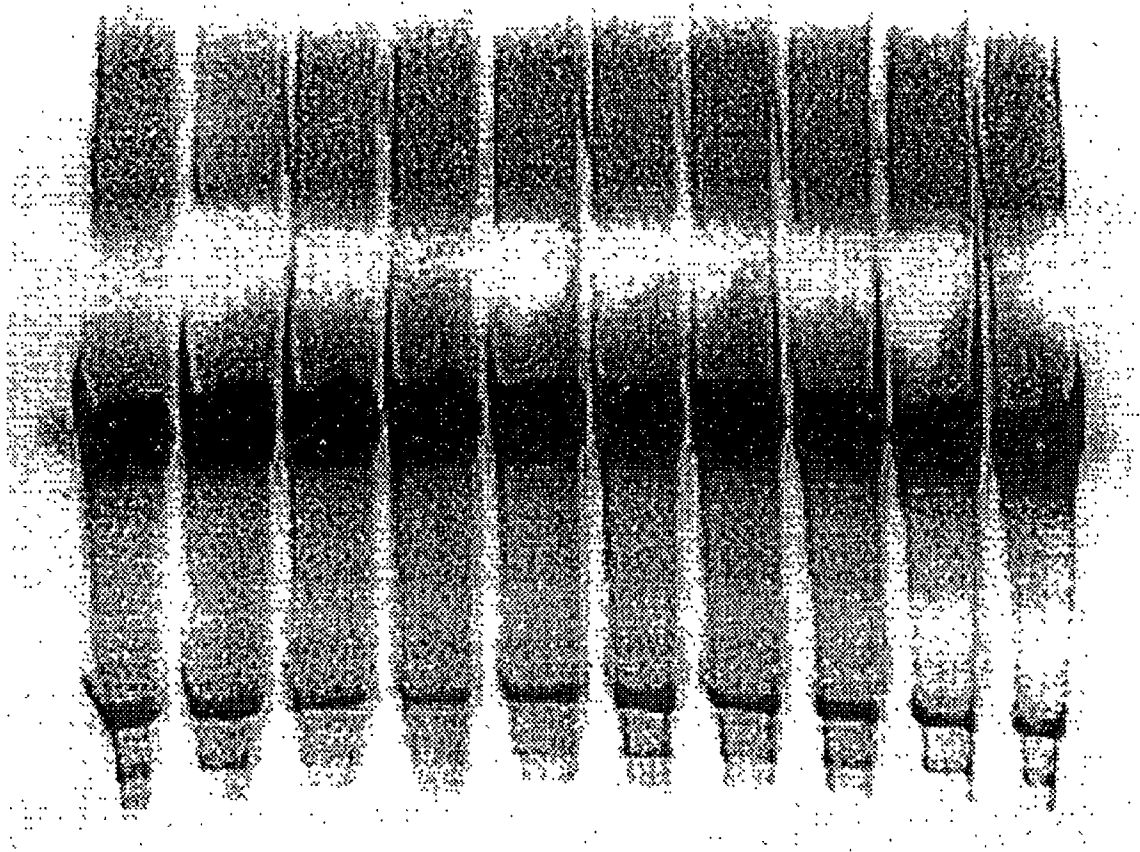


FIG. 43

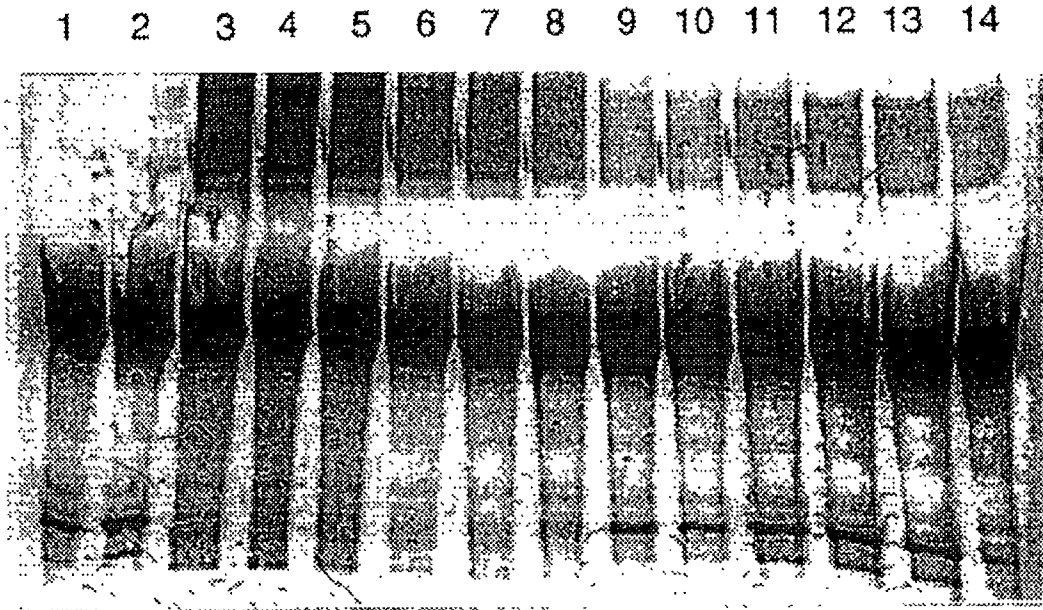


FIG. 44

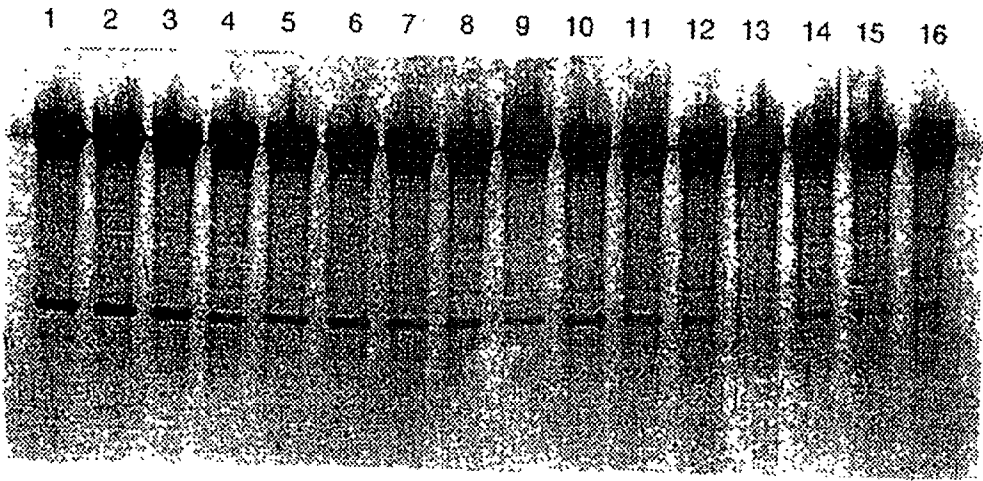


FIG. 45

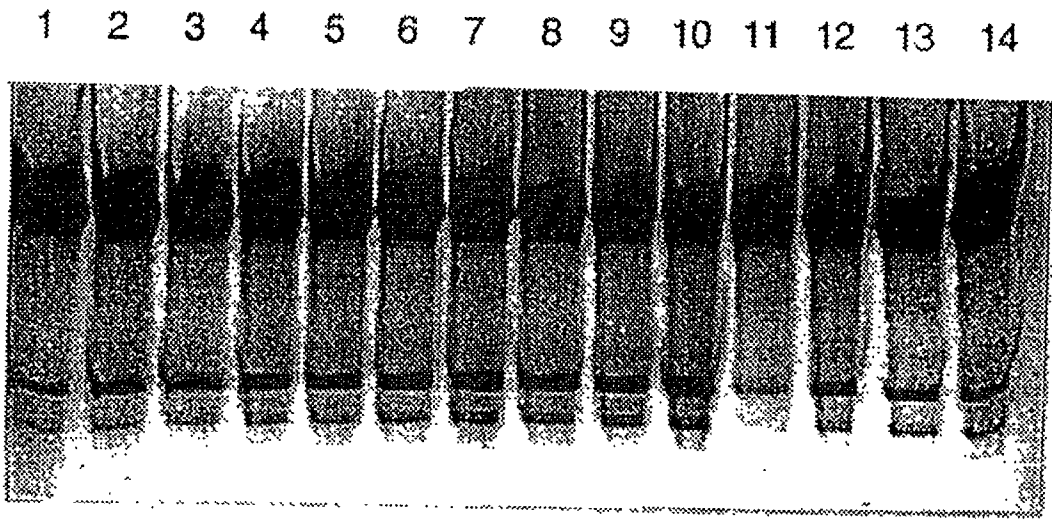


FIG. 46

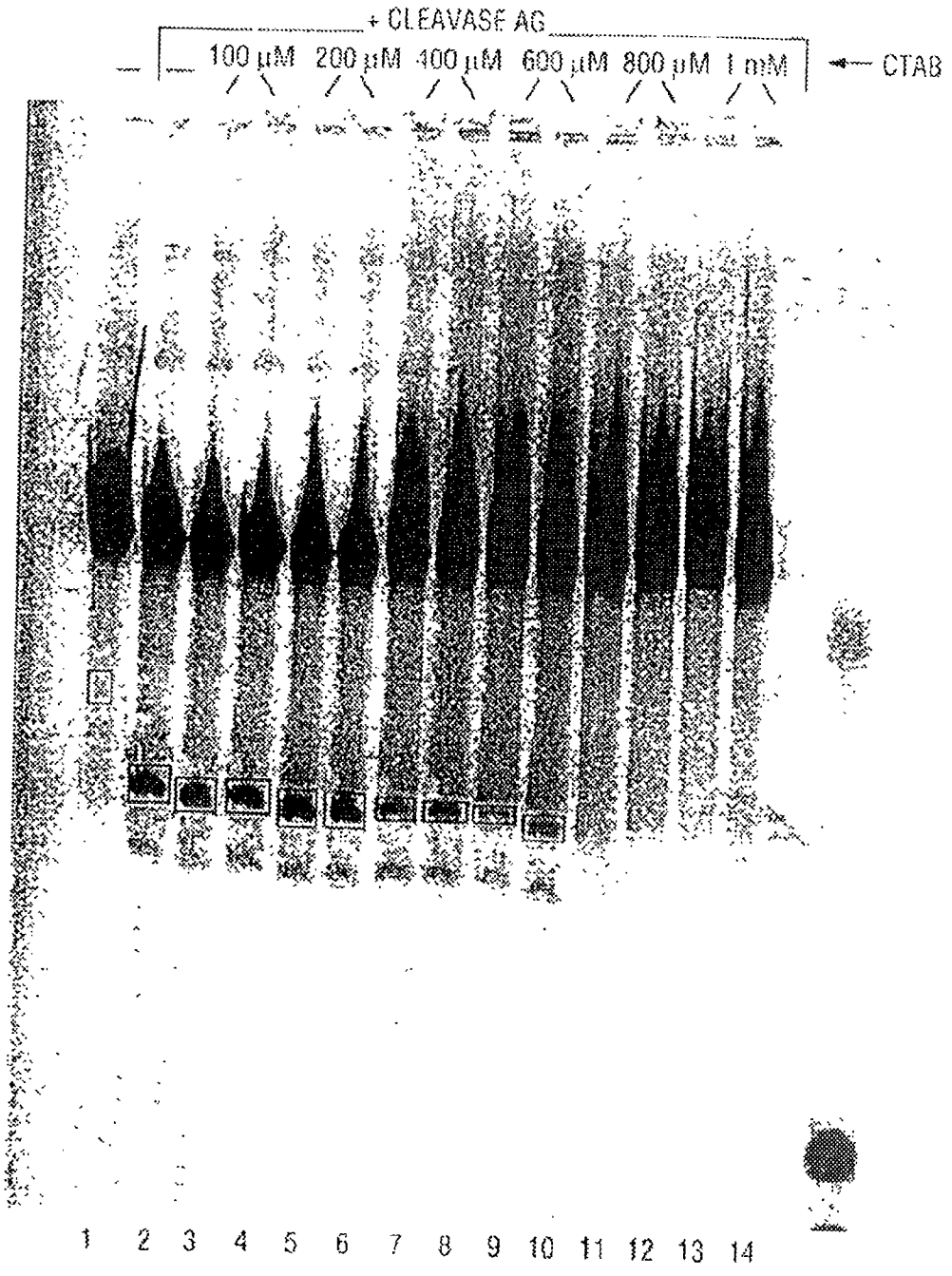


FIG. 47

1 2 3 4 5 6 7 8 9 10 11 12

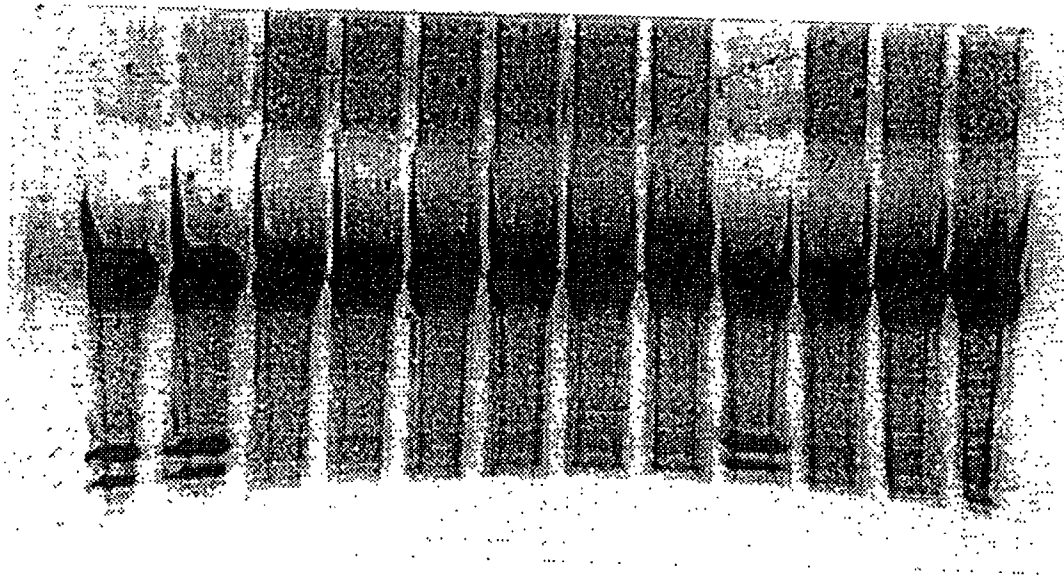


FIG. 48

1 2 3 4 5 6 7 8

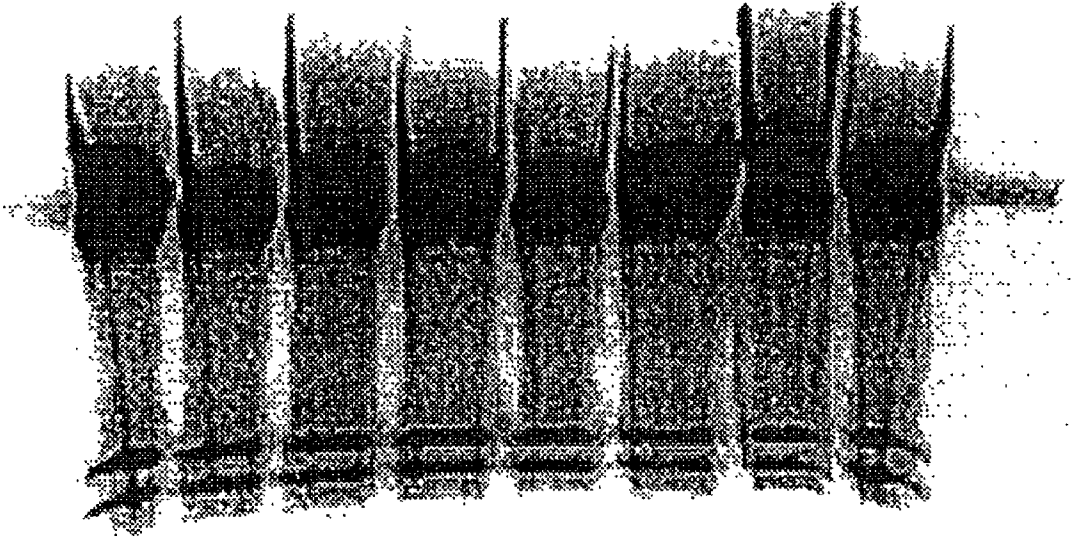


FIG. 49

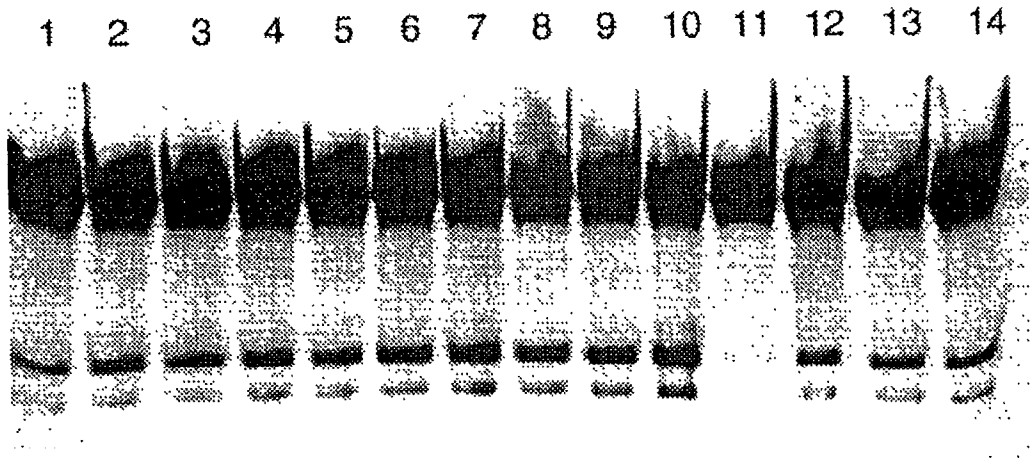


FIG. 50

1 2 3 4 5 6 7

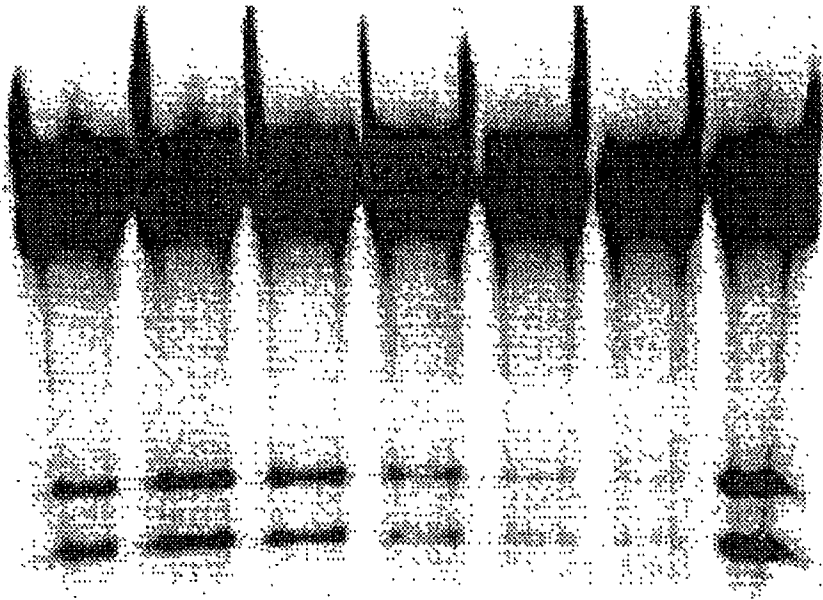


FIG. 51

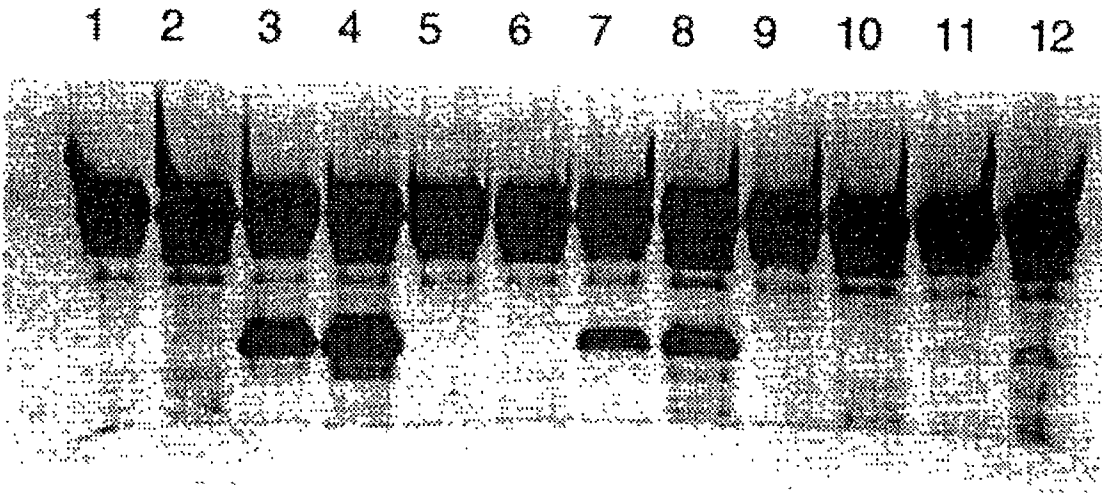


FIG. 52

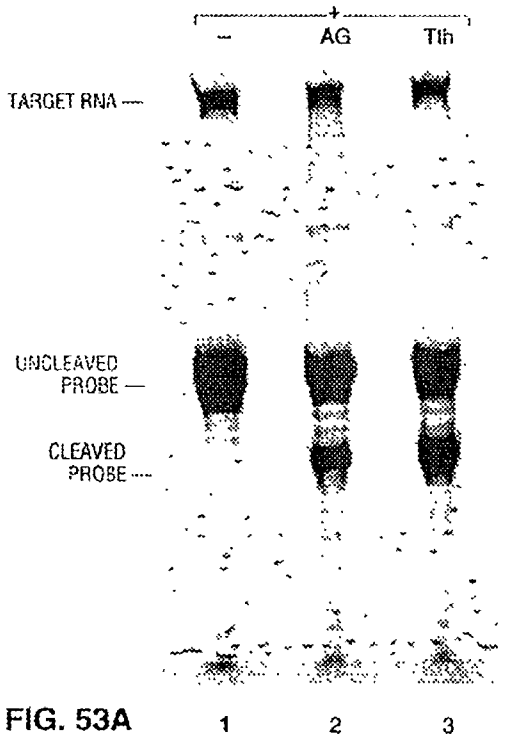


FIG. 53A

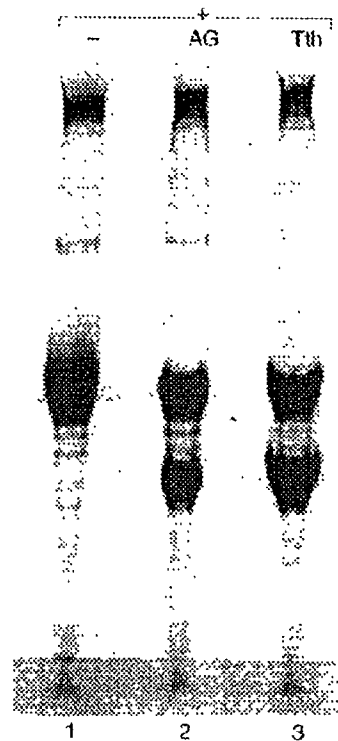


FIG. 53B

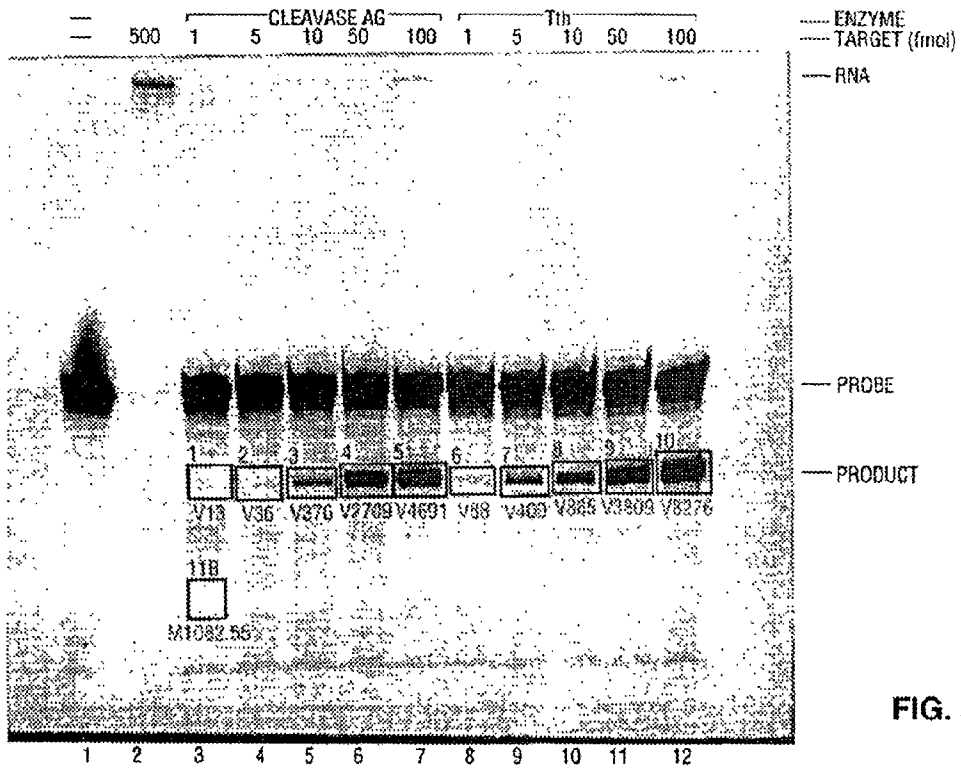


FIG. 54

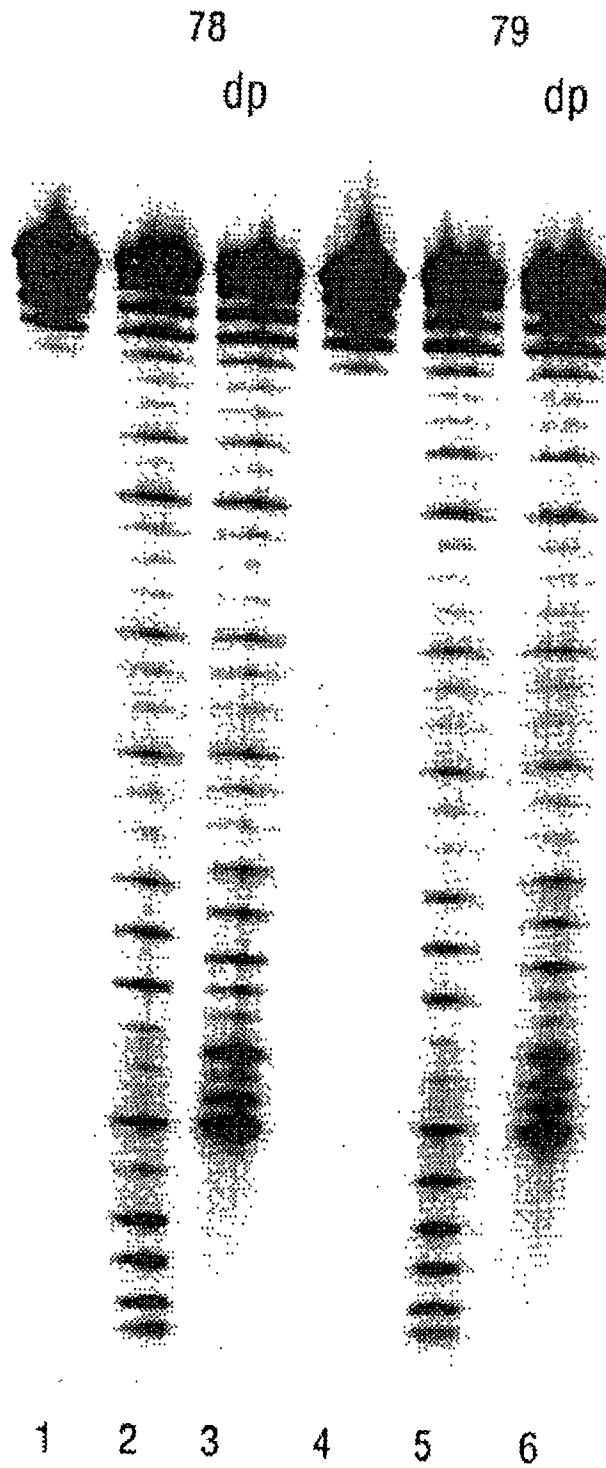


FIG. 55

70 (C10 amino T's)
74 (C6 amino T's)

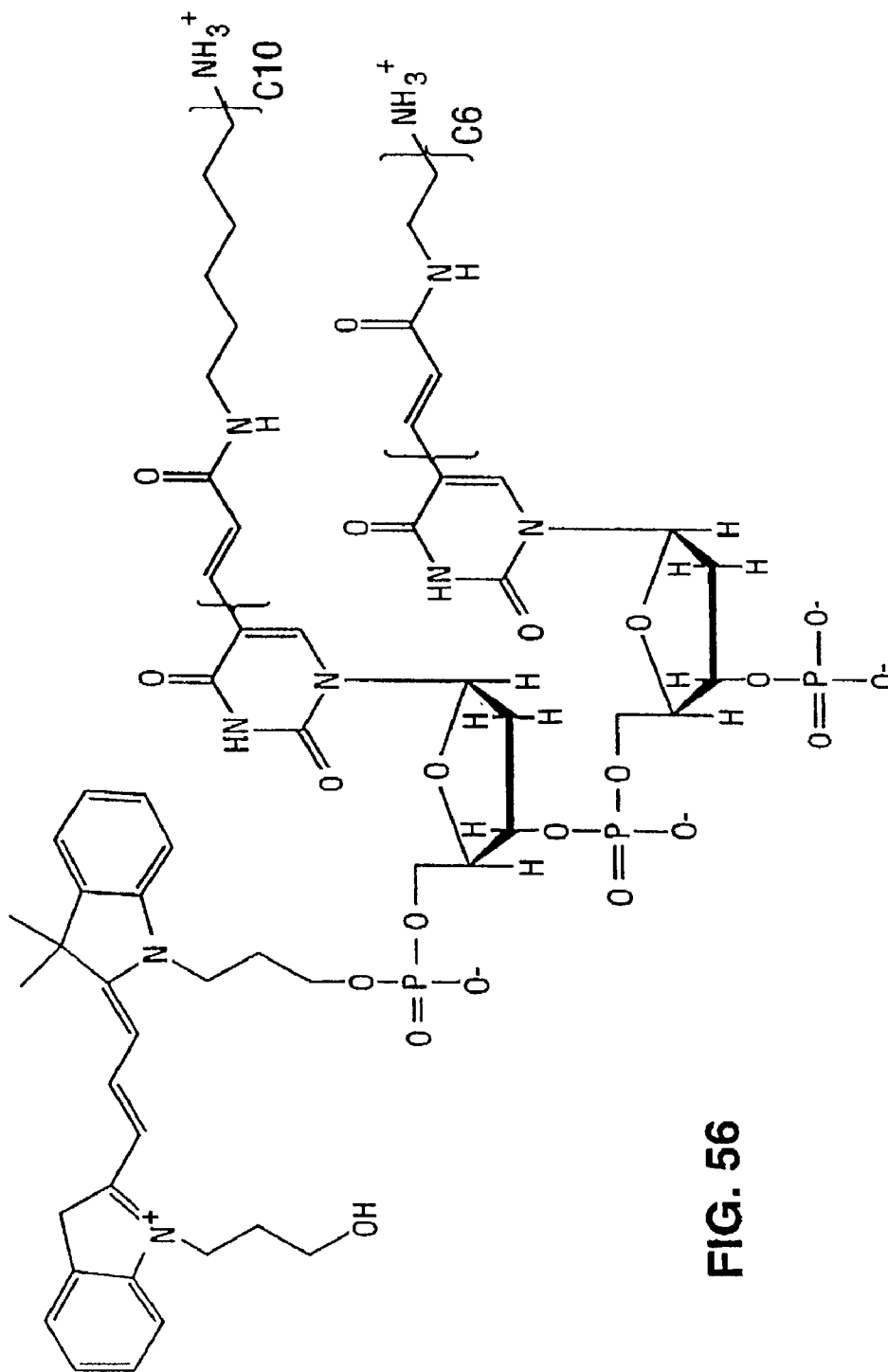


FIG. 56

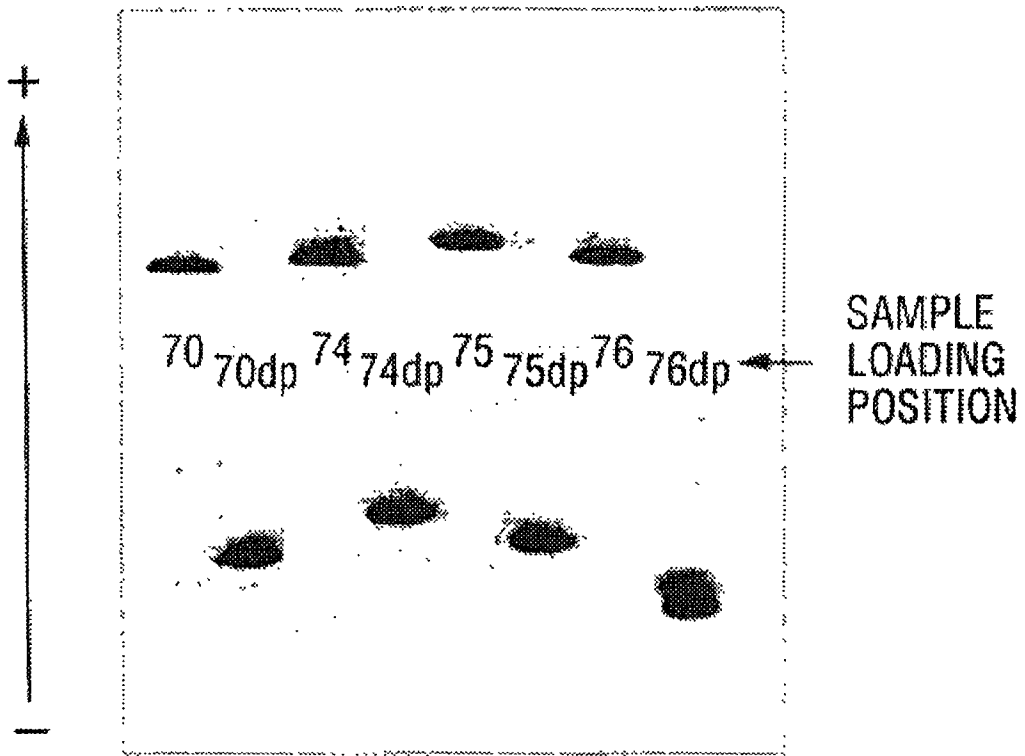


FIG. 59

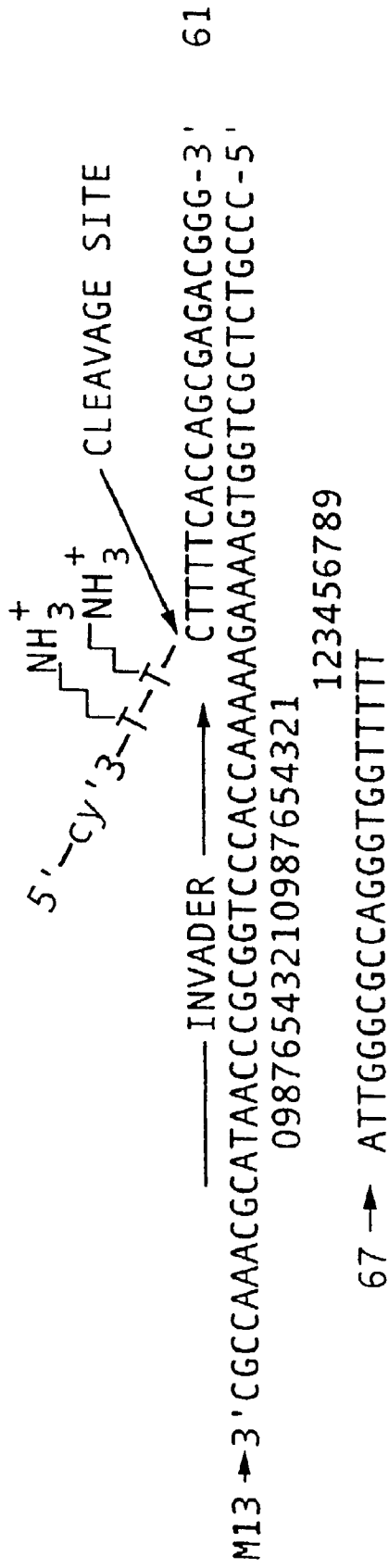


FIG. 60A

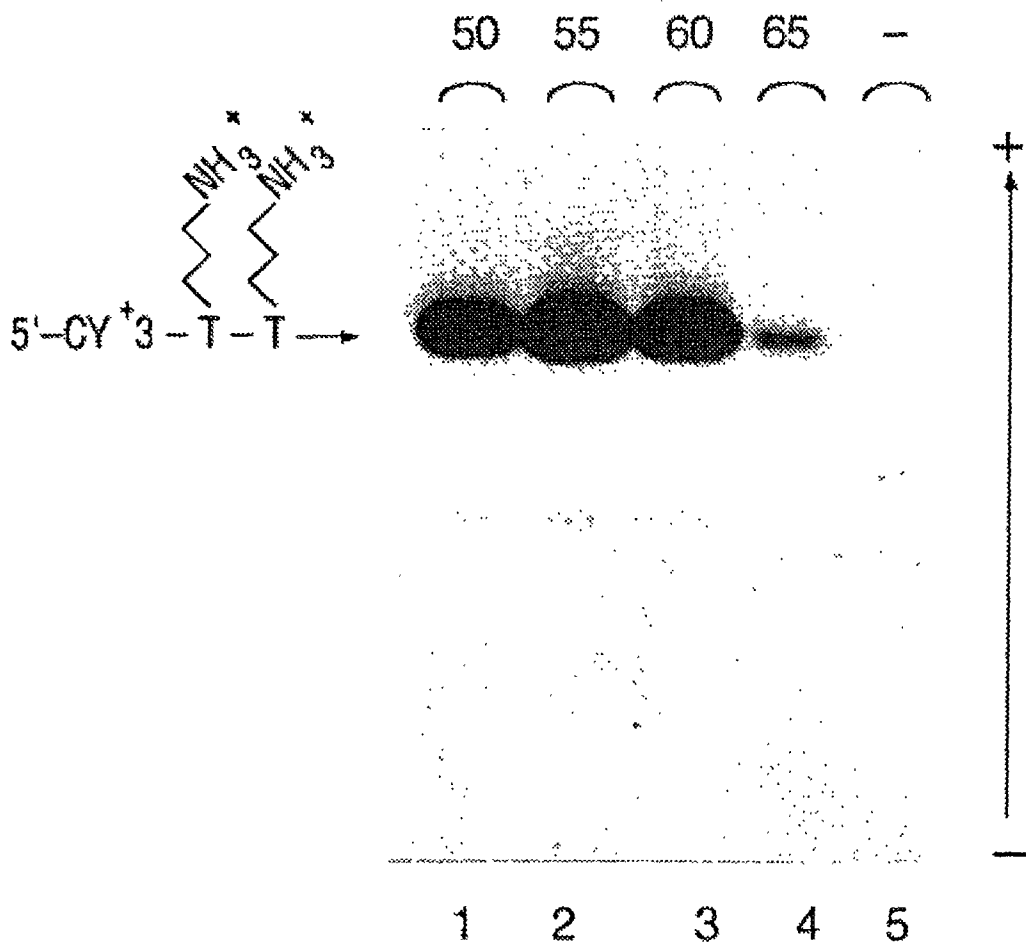


FIG. 60B

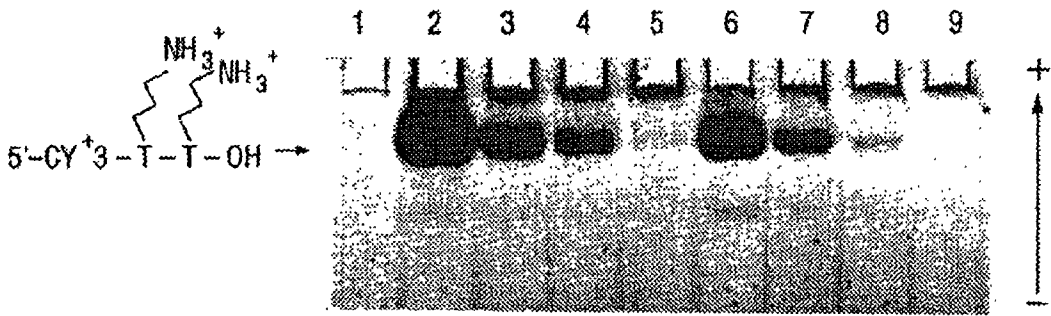


FIG. 61

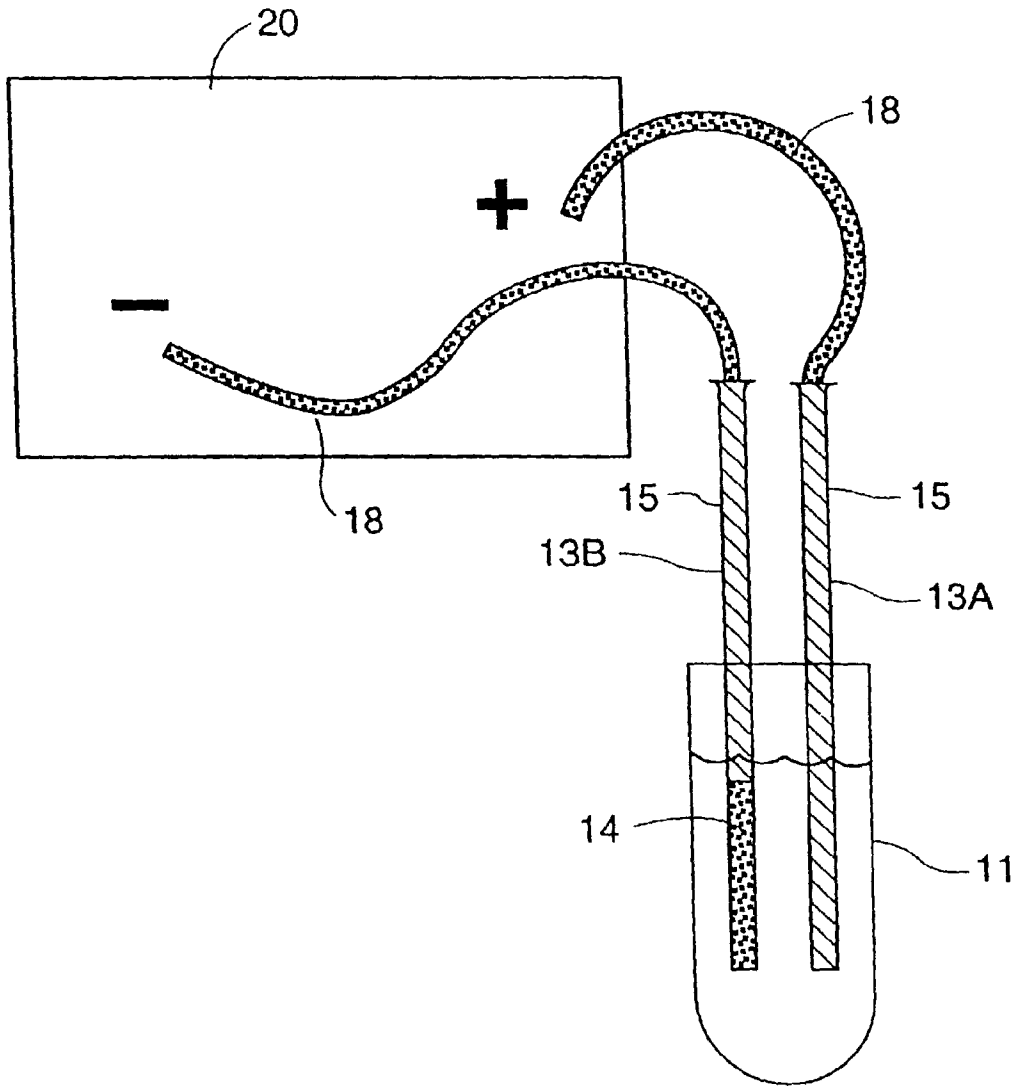


FIG. 62

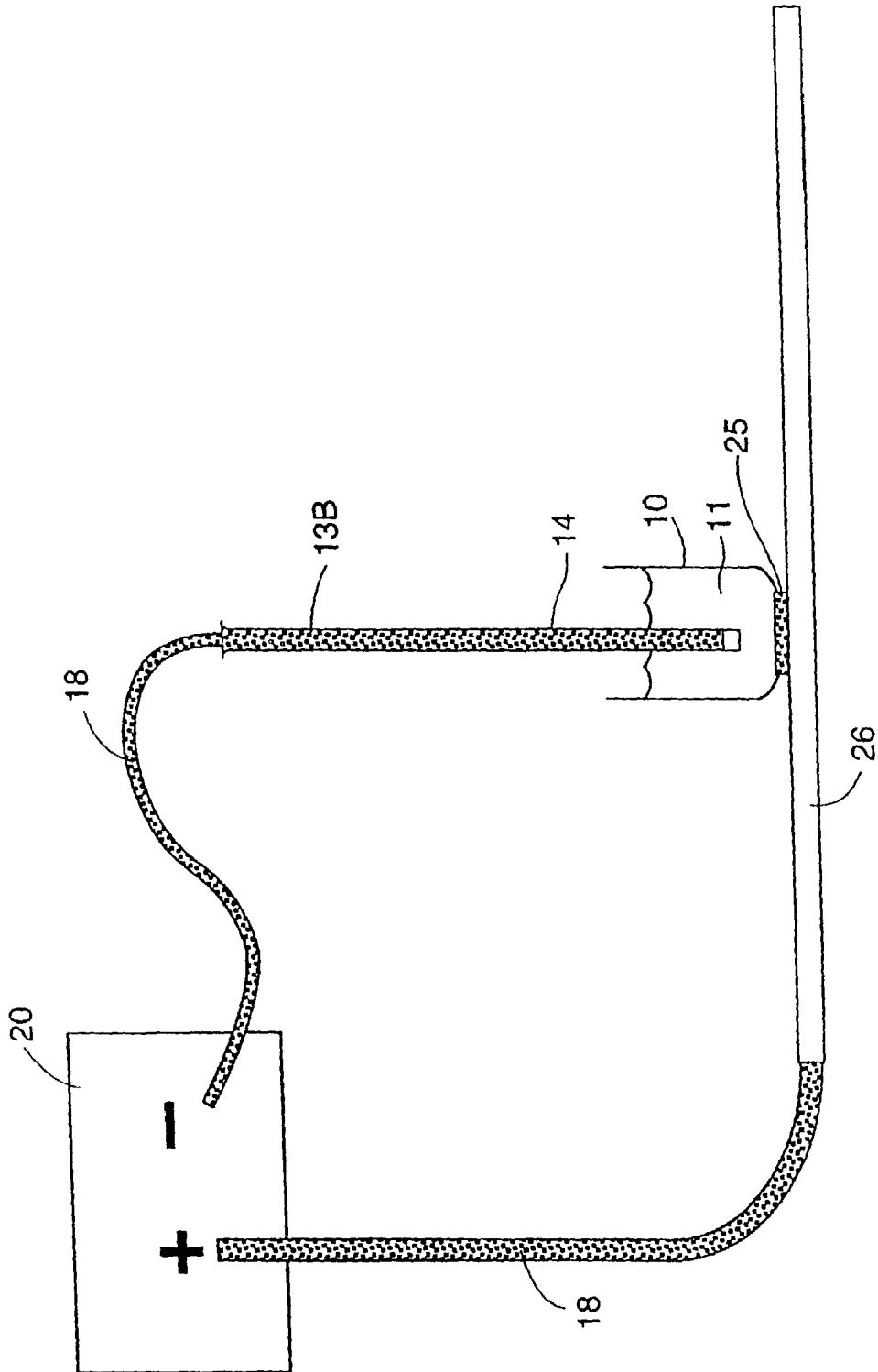


FIG. 63



FIG. 64



FIG. 65A



FIG. 65B



FIG. 65C



FIG. 65D

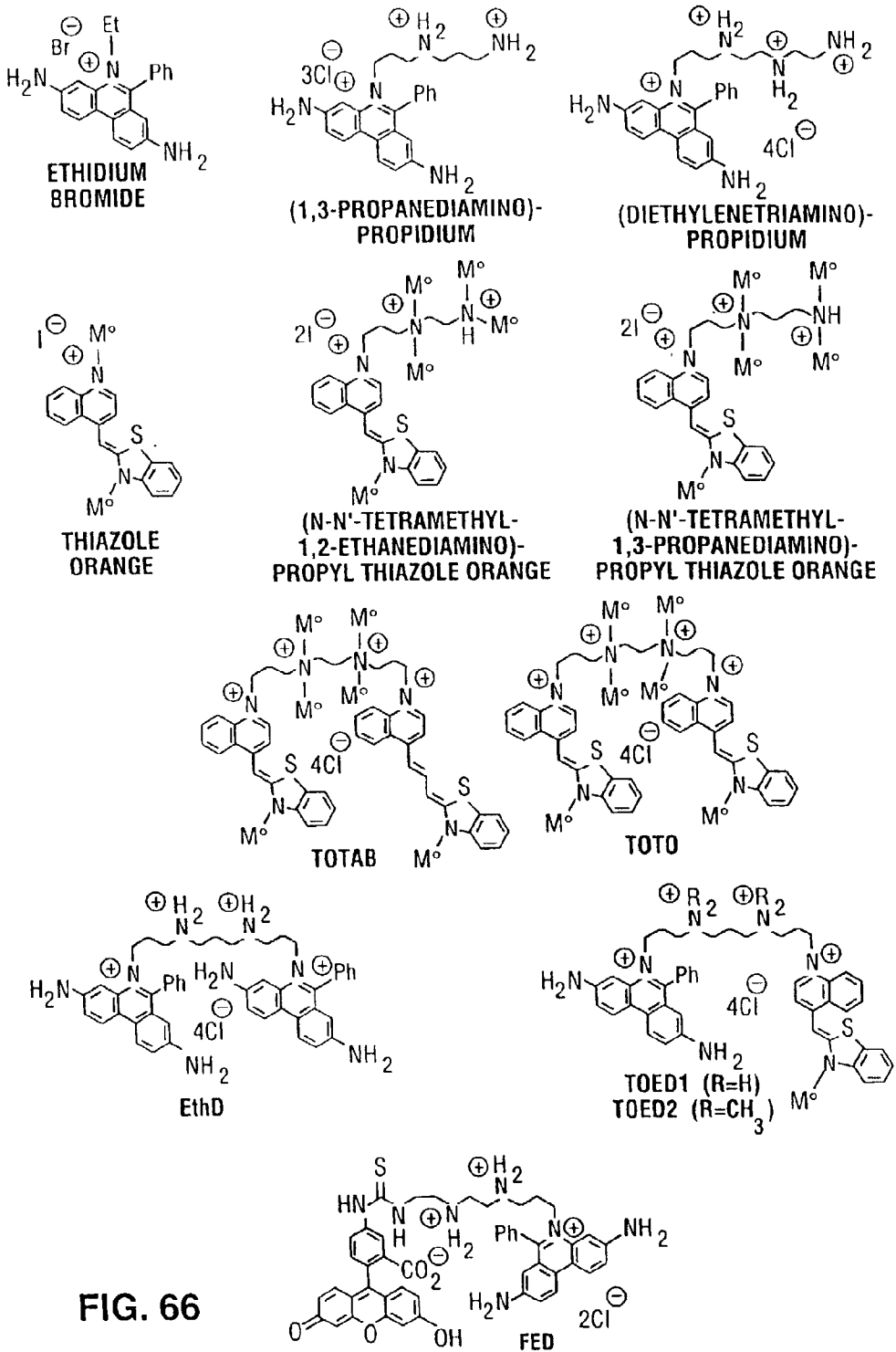


FIG. 66

NUCLEIC ACID DETECTION EMPLOYING CHARGED ADDUCTS

[0001] This is a Continuation-In-Part of co-pending application Ser. No. 08/599,491, filed on Jan. 24, 1996.

FIELD OF THE INVENTION

[0002] The present invention relates to means for the detection and characterization of nucleic acid sequences and variations in nucleic acid sequences. The present invention relates to methods for forming a nucleic acid cleavage structure on a target sequence and cleaving the nucleic acid cleavage structure in a site-specific manner. The 5' nuclease activity of a variety of enzymes is used to cleave the target-dependent cleavage structure, thereby indicating the presence of specific nucleic acid sequences or specific variations thereof. The present invention further provides novel methods and devices for the separation of nucleic acid molecules based by charge.

BACKGROUND OF THE INVENTION

[0003] The detection and characterization of specific nucleic acid sequences and sequence variations has been utilized to detect the presence of viral or bacterial nucleic acid sequences indicative of an infection, the presence of variants or alleles of mammalian genes associated with disease and cancers and the identification of the source of nucleic acids found in forensic samples, as well as in paternity determinations.

[0004] Various methods are known to the art which may be used to detect and characterize specific nucleic acid sequences and sequence variants. Nonetheless, as nucleic acid sequence data of the human genome, as well as the genomes of pathogenic organisms accumulates, the demand for fast, reliable, cost-effective and user-friendly tests for the detection of specific nucleic acid sequences continues to grow. Importantly, these tests must be able to create a detectable signal from samples which contain very few copies of the sequence of interest. The following discussion examines two levels of nucleic acid detection assays currently in use: I. Signal Amplification Technology for detection of rare sequences; and II. Direct Detection Technology for detection of higher copy number sequences.

[0005] I. Signal Amplification Technology Methods for Amplification

[0006] The "Polymerase Chain Reaction" (PCR) comprises the first generation of methods for nucleic acid amplification. However, several other methods have been developed that employ the same basis of specificity, but create signal by different amplification mechanisms. These methods include the "Ligase Chain Reaction" (LCR), "Self-Sustained Synthetic Reaction" (3SR/NASBA), and "Q β -Replicase" (Q β).

[0007] Polymerase Chain Reaction (PCR)

[0008] The polymerase chain reaction (PCR), as described in U.S. Pat. Nos. 4,683,195 and 4,683,202 to Mullis and Mullis et al. (the disclosures of which are hereby incorporated by reference), describe a method for increasing the concentration of a segment of target sequence in a mixture of genomic DNA without cloning or purification. This technology provides one approach to the problems of low

target sequence concentration. PCR can be used to directly increase the concentration of the target to an easily detectable level. This process for amplifying the target sequence involves introducing a molar excess of two oligonucleotide primers which are complementary to their respective strands of the double-stranded target sequence to the DNA mixture containing the desired target sequence. The mixture is denatured and then allowed to hybridize. Following hybridization, the primers are extended with polymerase so as to form complementary strands. The steps of denaturation, hybridization, and polymerase extension can be repeated as often as needed, in order to obtain relatively high concentrations of a segment of the desired target sequence.

[0009] The length of the segment of the desired target sequence is determined by the relative positions of the primers with respect to each other, and, therefore, this length is a controllable parameter. Because the desired segments of the target sequence become the dominant sequences (in terms of concentration) in the mixture, they are said to be "PCR-amplified."

[0010] Ligase Chain Reaction (LCR or LAR)

[0011] The ligase chain reaction (LCR; sometimes referred to as "Ligase Amplification Reaction" (LAR) described by Barany, Proc. Natl. Acad. Sci., 88:189 (1991); Barany, PCR Methods and Applic., 1:5 (1991); and Wu and Wallace, Genomics 4:560 (1989) has developed into a well-recognized alternative method for amplifying nucleic acids. In LCR, four oligonucleotides, two adjacent oligonucleotides which uniquely hybridize to one strand of target DNA, and a complementary set of adjacent oligonucleotides, which hybridize to the opposite strand are mixed and DNA ligase is added to the mixture. Provided that there is complete complementarity at the junction, ligase will covalently link each set of hybridized molecules. Importantly, in LCR, two probes are ligated together only when they base-pair with sequences in the target sample, without gaps or mismatches. Repeated cycles of denaturation, hybridization and ligation amplify a short segment of DNA. LCR has also been used in combination with PCR to achieve enhanced detection of single-base changes. Segev, PCT Public. No. WO9001069 μ l (1990). However, because the four oligonucleotides used in this assay can pair to form two short ligatable fragments, there is the potential for the generation of target-independent background signal. The use of LCR for mutant screening is limited to the examination of specific nucleic acid positions.

[0012] Self-Sustained Synthetic Reaction (3SR/NASBA)

[0013] The self-sustained sequence replication reaction (3SR) (Guatelli et al., Proc. Natl. Acad. Sci., 87:1874-1878 [1990], with an erratum at Proc. Natl. Acad. Sci., 87:7797 [1990]) is a transcription-based in vitro amplification system (Kwok et al., Proc. Natl. Acad. Sci., 86:1173-1177 [1989]) that can exponentially amplify RNA sequences at a uniform temperature. The amplified RNA can then be utilized for mutation detection (Fahy et al., PCR Meth. Appl., 1:25-33 [1991]). In this method, an oligonucleotide primer is used to add a phage RNA polymerase promoter to the 5' end of the sequence of interest. In a cocktail of enzymes and substrates that includes a second primer, reverse transcriptase, RNase H, RNA polymerase and ribo- and deoxyribonucleoside triphosphates, the target sequence undergoes repeated rounds of transcription, cDNA synthesis and second-strand

synthesis to amplify the area of interest. The use of 3SR to detect mutations is kinetically limited to screening small segments of DNA (e.g., 200-300 base pairs).

[0014] Q-Beta (Q β) Replicase

[0015] In this method, a probe which recognizes the sequence of interest is attached to the replicatable RNA template for Q β replicase. A previously identified major problem with false positives resulting from the replication of unhybridized probes has been addressed through use of a sequence-specific ligation step. However, available thermostable DNA ligases are not effective on this RNA substrate, so the ligation must be performed by T4 DNA ligase at low temperatures (37° C.). This prevents the use of high temperature as a means of achieving specificity as in the LCR, the ligation event can be used to detect a mutation at the junction site, but not elsewhere.

[0016] Table 1 below, lists some of the features desirable for systems useful in sensitive nucleic acid diagnostics, and summarizes the abilities of each of the major amplification methods (See also, Landgren, Trends in Genetics 9:199 [1993]).

[0017] A successful diagnostic method must be very specific. A straight-forward method of controlling the specificity of nucleic acid hybridization is by controlling the temperature of the reaction. While the 3SR/NASBA, and Q β systems are all able to generate a large quantity of signal, one or more of the enzymes involved in each cannot be used at high temperature (i.e., >55° C.). Therefore the reaction temperatures cannot be raised to prevent non-specific hybridization of the probes. If probes are shortened in order to make them melt more easily at low temperatures, the likelihood of having more than one perfect match in a complex genome increases. For these reasons, PCR and LCR currently dominate the research field in detection technologies.

TABLE 1

FEATURE	METHOD:				
	PCR	LCR	PCR & LCR	3SR NASBA	Q β
Amplifies Target	+	+	+	+	
Recognition of Independent Sequences Required	+	+	+	+	+
Performed at High Temp.	+	+			
Operates at Fixed Temp.				+	+
Exponential Amplification	+	+	+	+	+
Generic Signal Generation					+
Easily Automatable					

[0018] The basis of the amplification procedure in the PCR and LCR is the fact that the products of one cycle become usable templates in all subsequent cycles, consequently doubling the population with each cycle. The final yield of any such doubling system can be expressed as: $(1+X)^n=y$, where "X" is the mean efficiency (percent copied in each cycle), "n" is the number of cycles, and "y" is the overall efficiency, or yield of the reaction (Mullis, PCR Methods Applic., 1:1 [1991]). If every copy of a target DNA is utilized as a template in every cycle of a polymerase chain reaction, then the mean efficiency is 100%. If 20 cycles of PCR are performed, then the yield will be 2^{20} , or 1,048,576

copies of the starting material. If the reaction conditions reduce the mean efficiency to 85%, then the yield in those 20 cycles will be only 1.85^{20} , or 220,513 copies of the starting material. In other words, a PCR running at 85% efficiency will yield only 21% as much final product, compared to a reaction running at 100% efficiency. A reaction that is reduced to 50% mean efficiency will yield less than 1% of the possible product.

[0019] In practice, routine polymerase chain reactions rarely achieve the theoretical maximum yield, and PCRs are usually run for more than 20 cycles to compensate for the lower yield. At 50% mean efficiency, it would take 34 cycles to achieve the million-fold amplification theoretically possible in 20, and at lower efficiencies, the number of cycles required becomes prohibitive. In addition, any background products that amplify with a better mean efficiency than the intended target will become the dominant products.

[0020] Also, many variables can influence the mean efficiency of PCR, including target DNA length and secondary structure, primer length and design, primer and dNTP concentrations, and buffer composition, to name but a few. Contamination of the reaction with exogenous DNA (e.g., DNA spilled onto lab surfaces) or cross-contamination is also a major consideration. Reaction conditions must be carefully optimized for each different primer pair and target sequence, and the process can take days, even for an experienced investigator. The laboriousness of this process, including numerous technical considerations and other factors, presents a significant drawback to using PCR in the clinical setting. Indeed, PCR has yet to penetrate the clinical market in a significant way. The same concerns arise with LCR, as LCR must also be optimized to use different oligonucleotide sequences for each target sequence. In addition, both methods require expensive equipment, capable of precise temperature cycling.

[0021] Many applications of nucleic acid detection technologies, such as in studies of allelic variation, involve not only detection of a specific sequence in a complex background, but also the discrimination between sequences with few, or single, nucleotide differences. One method for the detection of allele-specific variants by PCR is based upon the fact that it is difficult for Taq polymerase to synthesize a DNA strand when there is a mismatch between the template strand and the 3' end of the primer. An allele-specific variant may be detected by the use of a primer that is perfectly matched with only one of the possible alleles; the mismatch to the other allele acts to prevent the extension of the primer, thereby preventing the amplification of that sequence. This method has a substantial limitation in that the base composition of the mismatch influences the ability to prevent extension across the mismatch, and certain mismatches do not prevent extension or have only a minimal effect (Kwok et al., Nucl. Acids Res., 18:999 [1990]).

[0022] A similar 3'-mismatch strategy is used with greater effect to prevent ligation in the LCR (Barany, PCR Meth. Applic., 1:5 [1991]). Any mismatch effectively blocks the action of the thermostable ligase, but LCR still has the drawback of target-independent background ligation products initiating the amplification. Moreover, the combination of PCR with subsequent LCR to identify the nucleotides at individual positions is also a clearly cumbersome proposition for the clinical laboratory.

[0023] II. Direct Detection Technology

[0024] When a sufficient amount of a nucleic acid to be detected is available, there are advantages to detecting that sequence directly, instead of making more copies of that target, (e.g., as in PCR and LCR). Most notably, a method that does not amplify the signal exponentially is more amenable to quantitative analysis. Even if the signal is enhanced by attaching multiple dyes to a single oligonucleotide, the correlation between the final signal intensity and amount of target is direct. Such a system has an additional advantage that the products of the reaction will not themselves promote further reaction, so contamination of lab surfaces by the products is not as much of a concern. Traditional methods of direct detection including Northern and Southern blotting and RNase protection assays usually require the use of radioactivity and are not amenable to automation. Recently devised techniques have sought to eliminate the use of radioactivity and/or improve the sensitivity in automatable formats. Two examples are the "Cycling Probe Reaction" (CPR), and "Branched DNA" (bDNA)

[0025] The cycling probe reaction (CPR) (Duck et al., *BioTech.*, 9:142 [1990]), uses a long chimeric oligonucleotide in which a central portion is made of RNA while the two termini are made of DNA. Hybridization of the probe to a target DNA and exposure to a thermostable RNase H causes the RNA portion to be digested. This destabilizes the remaining DNA portions of the duplex, releasing the remainder of the probe from the target DNA and allowing another probe molecule to repeat the process. The signal, in the form of cleaved probe molecules, accumulates at a linear rate. While the repeating process increases the signal, the RNA portion of the oligonucleotide is vulnerable to RNases that may be carried through sample preparation.

[0026] Branched DNA (bDNA), described by Urdea et al., *Gene* 61:253-264 (1987), involves oligonucleotides with branched structures that allow each individual oligonucleotide to carry 35 to 40 labels (e.g., alkaline phosphatase enzymes). While this enhances the signal from a hybridization event, signal from non-specific binding is similarly increased.

[0027] While both of these methods have the advantages of direct detection discussed above, neither the CPR or bDNA methods can make use of the specificity allowed by the requirement of independent recognition by two or more probe (oligonucleotide) sequences, as is common in the signal amplification methods described in section I. above. The requirement that two oligonucleotides must hybridize to a target nucleic acid in order for a detectable signal to be generated confers an extra measure of stringency on any detection assay. Requiring two oligonucleotides to bind to a target nucleic acid reduces the chance that false "positive" results will be produced due to the non-specific binding of a probe to the target. The further requirement that the two oligonucleotides must bind in a specific orientation relative to the target, as is required in PCR, where oligonucleotides must be oppositely but appropriately oriented such that the DNA polymerase can bridge the gap between the two oligonucleotides in both directions, further enhances specificity of the detection reaction. However, it is well known to those in the art that even though PCR utilizes two oligonucleotide probes (termed primers) "non-specific" amplifi-

cation (i.e., amplification of sequences not directed by the two primers used) is a common artifact. This is in part because the DNA polymerase used in PCR can accommodate very large distances, measured in nucleotides, between the oligonucleotides and thus there is a large window in which non-specific binding of an oligonucleotide can lead to exponential amplification of inappropriate product. The LCR, in contrast, cannot proceed unless the oligonucleotides used are bound to the target adjacent to each other and so the full benefit of the dual oligonucleotide hybridization is realized.

[0028] An ideal direct detection method would combine the advantages of the direct detection assays (e.g., easy quantification and minimal risk of carry-over contamination) with the specificity provided by a dual oligonucleotide hybridization assay.

SUMMARY OF THE INVENTION

[0029] The present invention relates to means for cleaving a nucleic acid cleavage structure in a site-specific manner. In one embodiment, the means for cleaving is a cleaving enzyme comprising 5' nucleases derived from thermostable DNA polymerases. These polymerases form the basis of a novel method of detection of specific nucleic acid sequences. The present invention contemplates use of novel detection methods for various uses, including, but not limited to clinical diagnostic purposes.

[0030] In one embodiment, the present invention contemplates a DNA sequence encoding a DNA polymerase altered in sequence (i.e., a "mutant" DNA polymerase) relative to the native sequence, such that it exhibits altered DNA synthetic activity from that of the native (i.e., "wild type") DNA polymerase. It is preferred that the encoded DNA polymerase is altered such that it exhibits reduced synthetic activity compared to that of the native DNA polymerase. In this manner, the enzymes of the invention are predominantly 5' nucleases and are capable of cleaving nucleic acids in a structure-specific manner in the absence of interfering synthetic activity.

[0031] Importantly, the 5' nucleases of the present invention are capable of cleaving linear duplex structures to create single discrete cleavage products. These linear structures are either 1) not cleaved by the wild type enzymes (to any significant degree), or 2) are cleaved by the wild type enzymes so as to create multiple products. This characteristic of the 5' nucleases has been found to be a consistent property of enzymes derived in this manner from thermostable polymerases across eubacterial thermophilic species.

[0032] It is not intended that the invention be limited by the nature of the alteration necessary to render the polymerase synthesis-deficient. Nor is it intended that the invention be limited by the extent of the deficiency. The present invention contemplates various structures, including altered structures (primary, secondary, etc.), as well as native structures, that may be inhibited by synthesis inhibitors.

[0033] Where the polymerase structure is altered, it is not intended that the invention be limited by the means by which the structure is altered. In one embodiment, the alteration of the native DNA sequence comprises a change in a single nucleotide. In another embodiment, the alteration of the native DNA sequence comprises a deletion of one or more

nucleotides. In yet another embodiment, the alteration of the native DNA sequence comprises an insertion of one or more nucleotides. It is contemplated that the change in DNA sequence may manifest itself as change in amino acid sequence.

[0034] The present invention contemplates 5' nucleases from a variety of sources, including mesophilic, psychrophilic, thermophilic, and hyperthermophilic organisms. The preferred 5' nucleases are thermostable. Thermostable 5' nucleases are contemplated as particularly useful in that they operate at temperatures where nucleic acid hybridization is extremely specific, allowing for allele-specific detection (including single-base mismatches). In one embodiment, the thermostable 5' nucleases are selected from the group consisting of altered polymerases derived from the native polymerases of *Thermus* species, including, but not limited to *Thermus aquaticus*, *Thermus flavus*, and *Thermus thermophilus*. However, the invention is not limited to the use of thermostable 5' nucleases.

[0035] As noted above, the present invention contemplates the use of altered polymerases in a detection method. In one embodiment, the present invention provides a method of detecting the presence of a target RNA by detecting non-target cleavage products comprising: a) providing: i) a cleavage means, ii) a source of target RNA, wherein the target RNA has a first region, a second region and a third region, wherein the first region is located adjacent to and downstream from the second region, and the second region is located adjacent to and downstream from the third region, iii) a first oligonucleotide having a 5' and a 3' portion, wherein the 5' portion of the first oligonucleotide contains a sequence complementary to the second region of the target RNA and wherein the 3' portion of the first oligonucleotide contains a sequence complementary to the third region of the target RNA, iv) a second oligonucleotide having a 5' and a 3' portion wherein the 5' portion of the second oligonucleotide contains a sequence complementary to the first region of the target RNA, and the 3' portion of the second oligonucleotide contains a sequence complementary to the second region of the target RNA; b) mixing the cleavage means, the target RNA, and the first and second oligonucleotides, to create a reaction mixture under reaction conditions such that at least the 3' portion of the first oligonucleotide is annealed to the target RNA, and wherein at least the 5' portion of the second oligonucleotide is annealed to the target RNA so as to create a cleavage structure, and wherein cleavage of the cleavage structure occurs to generate non-target cleavage products; and c) detecting the non-target cleavage products.

[0036] It is contemplated that the first, second and third regions of the target be located adjacent to each other. However, the invention is not limited to the use of a target in which the three regions are contiguous with each other. Thus, the present invention contemplates the use of target RNAs wherein these three regions are contiguous with each other, as well as target RNAs wherein these three regions are not contiguous. It is further contemplated that gaps of approximately 2-10 nucleotides, representing regions of non-complementarity to the oligonucleotides (e.g., the first and/or second oligonucleotides), may be present between the three regions of the target RNA.

[0037] In at least one embodiment, it is intended that mixing of step b) is conducted under conditions such that at

least the 3' portion of the first oligonucleotide is annealed to the target RNA, and wherein at least the 5' portion of the second oligonucleotide is annealed to the target RNA. In this manner a cleavage structure is created and cleavage of this cleavage structure can occur. These conditions allow for the use of various formats. In a preferred format, the conditions of mixing comprises mixing together the target RNA with the first and second oligonucleotides and the cleavage means in an aqueous solution in which a source of divalent cations is lacking. In this format, the cleavage reaction is initiated by the addition of a solution containing Mn^{2+} or Mg^{2+} ions. In another preferred format, the conditions of mixing comprises mixing together the target RNA, and the first and second oligonucleotides in an aqueous solution containing Mn^{2+} or Mg^{2+} ions, and then adding the cleavage means to the reaction mixture.

[0038] The invention is not limited by the means employed for the detection of the non-target cleavage products. For example, the products generated by the cleavage reaction (i.e., the non-target cleavage products) may be detected by their separation of the reaction products on agarose or polyacrylamide gels and staining with ethidium bromide. Other non-gel-based detection methods are provided herein.

[0039] It is contemplated that the oligonucleotides may be labelled. Thus, if the cleavage reaction employs a first oligonucleotide containing a label, detection of the non-target cleavage products may comprise detection of the label. The invention is not limited by the nature of the label chosen, including, but not limited to, labels which comprise a dye or a radionucleotide (e.g. ^{32}P), fluorescein moiety, a biotin moiety, luminogenic, fluorogenic, phosphorescent, or fluors in combination with moieties that can suppress emission by fluorescence energy transfer (FET). Numerous methods are available for the detection of nucleic acids containing any of the above-listed labels. For example, biotin-labeled oligonucleotide(s) may be detected using non-isotopic detection methods which employ streptavidin-alkaline phosphatase conjugates. Fluorescein-labelled oligonucleotide(s) may be detected using a fluorescein-imager.

[0040] It is also contemplated that labelled oligonucleotides (cleaved or uncleaved) may be separated by means other than electrophoresis. For example, biotin-labelled oligonucleotides may be separated from nucleic acid present in the reaction mixture using para-magnetic or magnetic beads, or particles which are coated with avidin (or streptavidin). In this manner, the biotinylated oligonucleotide/avidin-magnetic bead complex can be physically separated from the other components in the mixture by exposing the complexes to a magnetic field. Additionally, the signal from the cleaved oligonucleotides may be resolved from that of the uncleaved oligonucleotides without physical separation. For example, a change in size, and therefore rate of rotation in solution of fluorescent molecules can be detected by fluorescence polarization analysis.

[0041] In a preferred embodiment, the reaction conditions comprise a cleavage reaction temperature which is less than the melting temperature of the first oligonucleotide and greater than the melting temperature of the 3' portion of the first oligonucleotide. In a particularly preferred embodiment, the reaction temperature is between approximately 40-65° C. It is contemplated that the reaction temperature at

which the cleavage reaction occurs be selected with regard to the guidelines provided in the Description of the Invention.

[0042] The invention is not limited by the nature of the oligonucleotides employed. Using a target RNA, the oligonucleotides may comprise DNA, RNA or an oligonucleotide comprising a mixture of RNA and DNA.

[0043] The invention also contemplates the use of a second oligonucleotide (i.e., the upstream oligonucleotide) which comprises a functional group (e.g., a 5' peptide region) which prevents the dissociation of the 5' portion of the second oligonucleotide from the first region of the target RNA. When such a functional group is present on the second oligonucleotide, the interaction between the 3' portion of the second oligonucleotide and the first region of the target RNA may be destabilized (i.e., designed to have a lower local melting temperature) through the use of A-T (or A-U) rich sequences, base analogs that form fewer hydrogen bonds (e.g., dG-dU pairs) or through the use of phosphorothioate backbones, in order to allow the 5' region of the first oligonucleotide to compete successfully for hybridization.

[0044] In a preferred embodiment, the cleavage means comprises a thermostable 5' nuclease. The thermostable 5' nuclease may have a portion of the amino acid sequence that is homologous to a portion of the amino acid sequence of a thermostable DNA polymerase derived from a thermophilic organism. It is contemplated that thermophilic organisms will be selected from such species as those within the genus *Thermus*, including, but not limited to *Thermus aquaticus*, *Thermus flavus* and *Thermus thermophilus*. Preferred nucleases are encoded by DNA sequences selected from the group consisting of SEQ ID NOS:1-3, 9, 10, 12, 21, 30 and 31.

[0045] In one embodiment, the present invention contemplates a DNA sequence encoding a DNA polymerase altered in sequence (i.e., a "mutant" DNA polymerase) relative to the native sequence, such that it exhibits altered DNA synthetic activity from that of the native (i.e., "wild type") DNA polymerase. With regard to the polymerase, a complete absence of synthesis is not required. However, it is desired that cleavage reactions occur in the absence of polymerase activity at a level that interferes with the method. It is preferred that the encoded DNA polymerase is altered such that it exhibits reduced synthetic activity from that of the native DNA polymerase. In this manner, the enzymes of the invention are nucleases and are capable of cleaving nucleic acids in a structure-specific manner. Importantly, the nucleases of the present invention are capable of cleaving cleavage structures to create discrete cleavage products.

[0046] The present invention utilizes such enzymes in methods for detection and characterization of nucleic acid sequences and sequence changes. The present invention also relates to means for cleaving a nucleic acid cleavage structure in a site-specific manner. Nuclease activity is used to screen for known and unknown mutations, including single base changes, in nucleic acids.

[0047] The invention is not limited to use of oligonucleotides which are completely complementary to their cognate target sequences. In one embodiment, both the first and second oligonucleotides are completely complementary to

the target RNA. In another embodiment, the first oligonucleotide is partially complementary to the target RNA. In yet another embodiment, the second oligonucleotide is partially complementary to the target RNA. In yet another embodiment, both the first and the second oligonucleotide are partially complementary to the target RNA.

[0048] In a preferred embodiment, the methods of the invention employ a source of target RNA which comprises a sample selected from the group including, but not limited to blood, saliva, cerebral spinal fluid, pleural fluid, milk, lymph, sputum and semen.

[0049] In a preferred embodiment, the method employs reaction conditions which comprise providing a source of divalent cations. In a particularly preferred embodiment, the divalent cation is selected from the group comprising Mn^{2+} and Mg^{2+} ions.

[0050] The novel detection methods of the invention may be employed for the detection of target RNAs including, but not limited to, target RNAs comprising wild type and mutant alleles of genes, including genes from humans or other animals that are or may be associated with disease or cancer. In addition, the methods of the invention may be used for the detection of and/or identification of strains of microorganisms, including bacteria, fungi, protozoa, ciliates and viruses (and in particular for the detection and identification of RNA viruses, such as HCV).

[0051] The present invention further provides a method of separating nucleic acid molecules, comprising: a) providing: i) a charge-balanced oligonucleotide and ii) a reactant; b) mixing the charge-balanced oligonucleotide with the reactant to create a reaction mixture under conditions such that a charge-unbalanced oligonucleotide is produced; and c) separating the charge-unbalanced oligonucleotide from the reaction mixture.

[0052] The method of the present invention is not limited by the nature of the reactant employed. In a preferred embodiment the reactant comprises a cleavage means. In a particularly preferred embodiment, the cleavage means is an endonuclease. In another embodiment, the cleavage means is an exonuclease. In a still further embodiment, the reactant comprises a polymerization means. In another embodiment, the reactant comprises a ligation means.

[0053] In a preferred embodiment, the charge-balanced oligonucleotide comprises a label. The invention is not limited by the nature of the label chosen, including, but not limited to, labels which comprise a dye or a radionucleotide (e.g., ^{32}P), fluorescein moiety, a biotin moiety, luminogenic, fluorogenic, phosphorescent, or fluors in combination with moieties that can suppress emission by fluorescence energy transfer (FET). The label may be a charged moiety or alternatively may be a charge neutral moiety.

[0054] In another preferred embodiment, the charge-balanced oligonucleotide comprises one or more phosphonate groups. In a preferred embodiment, the phosphonate group is a methylphosphonate group.

[0055] In one embodiment, the charge-balanced oligonucleotide has a net neutral charge and the charge-unbalanced oligonucleotide has a net positive charge. Alternatively, the charge-balanced oligonucleotide has a net neutral charge and the charge-unbalanced oligonucleotide has a net

negative charge. In yet another alternative embodiment, the charge-balanced oligonucleotide has a net negative charge and the charge-unbalanced oligonucleotide has a net positive charge. In another embodiment, the charge-balanced oligonucleotide has a net negative charge and the charge-unbalanced oligonucleotide has a net neutral charge. In another preferred embodiment, the charge-balanced oligonucleotide has a net positive charge and the charge-unbalanced oligonucleotide has a net neutral charge. Still further, the charge-balanced oligonucleotide has a net positive charge and the charge-unbalanced oligonucleotide has a net negative charge.

[0056] In a preferred embodiment, the charge-balanced oligonucleotide comprises DNA containing one or more positively charged adducts. In a preferred embodiment, the charge-balanced oligonucleotide comprises DNA containing one or more positively charged adducts and the cleavage means removes one or more nucleotides from the charge-balanced oligonucleotide to produce the charge-unbalanced oligonucleotide, wherein the charge-unbalanced oligonucleotide has a net positive charge. In another preferred embodiment, the charge-balanced oligonucleotide comprises DNA containing one or more positively charged adducts and the cleavage means removes one or more nucleotides from the charge-balanced oligonucleotide to produce the charge-unbalanced oligonucleotide, wherein the charge-unbalanced oligonucleotide has a net neutral charge. Still further, the charge-balanced oligonucleotide comprises DNA containing one or more positively charged adducts and the cleavage means removes one or more nucleotides from the charge-balanced oligonucleotide to produce the charge-unbalanced oligonucleotide, wherein the charge-unbalanced oligonucleotide has a net negative charge.

[0057] In a preferred embodiment, the charge-balanced oligonucleotide comprises DNA containing one or more negatively charged adducts (e.g., negatively charged amino acids). Examples of negative charged adducts include negatively charged amino acids (e.g., aspartate and glutamate). In a preferred embodiment, the charge-balanced oligonucleotide comprises DNA containing one or more negatively charged adducts and the cleavage means removes one or more nucleotides from the charge-balanced oligonucleotide to produce the charge-unbalanced oligonucleotide, wherein the charge-unbalanced oligonucleotide has a net negative charge. In a preferred embodiment, the charge-balanced oligonucleotide comprises DNA containing one or more negatively charged adducts and the cleavage means removes one or more nucleotides from the charge-balanced oligonucleotide to produce the charge-unbalanced oligonucleotide, wherein the charge-unbalanced oligonucleotide has a net neutral charge. In a preferred embodiment, the charge-balanced oligonucleotide comprises DNA containing one or more negatively charged adducts and the cleavage means removes one or more nucleotides from the charge-balanced oligonucleotide to produce the charge-unbalanced oligonucleotide, wherein the charge-unbalanced oligonucleotide has a net negative charge.

[0058] The present invention is not limited by the nature of the positively charged adduct(s) employed. In a preferred embodiment, the positively charged adducts are selected from the group consisting of indodicarbocyanine dye amidites (e.g., Cy3 and Cy5), amino-substituted nucleotides, ethidium bromide, ethidium homodimer, (1,3-propanedi-

amino)propidium, (diethylenetriamino)propidium, thiazole orange, (N-N'-tetramethyl-1,3-propanediamino)propyl thiazole orange, (N-N'-tetramethyl-1,2-ethanediamino)propyl thiazole orange, thiazole orange-thiazole orange homodimer (TOTO), thiazole orange-thiazole blue heterodimer (TOTAB), thiazole orange-ethidium heterodimer 1 (TOED1), thiazole orange-ethidium heterodimer 2 (TOED2), florescien-ethidium heterodimer (FED) and positively charged amino acids.

[0059] In another preferred embodiment, the separating step comprises subjecting the reaction mixture to an electrical field comprising a positive pole and a negative pole under conditions such that the charge-unbalanced oligonucleotide migrates toward the positive pole (i.e., electrode). In another embodiment, the separating step comprises subjecting the reaction mixture to an electrical field comprising a positive pole and a negative pole under conditions such that the charge-unbalanced oligonucleotide migrates toward the negative pole.

[0060] In still further embodiment, the method of the present invention further comprises detecting the presence of the separated charge-unbalanced oligonucleotide. The present invention is not limited by the detection method employed; the method of detection chosen will vary depending on the nature of the label employed (if one is employed).

[0061] The present invention further comprises a method of detecting cleaved nucleic molecules, comprising: a) providing: i) a homogeneous plurality of charge-balanced oligonucleotides; ii) a sample suspected of containing a target nucleic acid having a sequence comprising a first region complementary to said charge-balanced oligonucleotide; iii) a cleavage means; and iv) a reaction vessel; b) adding to said vessel, in any order, the sample, the charge-balanced oligonucleotides and the cleavage means to create a reaction mixture under conditions such that a portion of the charge-balanced oligonucleotides binds to the complementary target nucleic acid to create a bound (i.e., annealed) population, and such that the cleavage means cleaves at least a portion of said bound population of charge-balanced oligonucleotides to produce a population of unbound, charge-unbalanced oligonucleotides; and c) separating the unbound, charge-unbalanced oligonucleotides from the reaction mixture.

[0062] In a preferred embodiment, the method further comprises providing a homogeneous plurality of oligonucleotides complementary to a second region of the target nucleic acid, wherein the oligonucleotides are capable of binding to the target nucleic acid upstream of the charge-balanced oligonucleotides. In another preferred embodiment, the first and the second region of the target nucleic acid share a region of overlap.

[0063] The invention is not limited by the nature of the cleavage means employed. In one embodiment, the cleavage means comprises a thermostable 5' nuclease. In a preferred embodiment, a portion of the amino acid sequence of the 5' nuclease is homologous to a portion of the amino acid sequence of a thermostable DNA polymerase derived from a thermophilic organism. In a preferred embodiment, the organism is selected from the group consisting of *Thermus aquaticus*, *Thermus flavus* and *Thermus thermophilus*. In another preferred embodiment, the nuclease is encoded by a DNA sequence selected from the group consisting of SEQ ID NOS:1-3, 9, 10, 12, 21, 30 and 31.

[0064] The invention is not limited by the nature of the target nucleic acid. The target nucleic acid may comprise single-stranded DNA, double-stranded DNA or RNA. In a preferred embodiment, the target nucleic acid comprises double-stranded DNA and prior to the addition of the cleavage means the reaction mixture is treated such that the double-stranded DNA is rendered substantially single-stranded preferably by increasing the temperature.

[0065] The invention further provides a method of separating nucleic acid molecules, comprising: a) modifying an oligonucleotide so as to produce a charge-balanced oligonucleotide; b) providing: i) a said charge-balanced oligonucleotide and ii) a reactant; c) mixing said charge-balanced oligonucleotide with said reactant to create a reaction mixture under conditions such that a charge-unbalanced oligonucleotide is produced; and d) separating said charge-unbalanced oligonucleotide from said reaction mixture.

[0066] The invention is not limited by the nature of the modification. In a preferred embodiment, the modifying step comprises the covalent attachment of a positively charged adduct to one or bases of the oligonucleotide. In another preferred embodiment, the modifying step comprises the covalent attachment of a negatively charged adduct to one or bases of the oligonucleotide. In a still further embodiment, the modifying comprises the incorporation of one or more amino-substituted bases during synthesis of the oligonucleotide. In another embodiment, the modifying comprises the incorporation of one or more phosphonate groups during synthesis of said oligonucleotide. In a preferred embodiment, the phosphonate group is a methylphosphonate group.

[0067] The invention further provides a method of treating a nucleic acid molecule, comprising: a) providing: i) a charge-balanced oligonucleotide and ii) a reactant; b) mixing said charge-balanced oligonucleotide with said reactant to create a reaction mixture under conditions such that a charge-unbalanced oligonucleotide is produced.

[0068] The invention further provides a method of treating a nucleic acid molecule, comprising: a) modifying an oligonucleotide so as to produce a charge-balanced oligonucleotide; b) providing: i) said charge-balanced oligonucleotide and ii) a reactant; c) mixing the charge-balanced oligonucleotide with the reactant to create a reaction mixture under conditions such that a charge-unbalanced oligonucleotide is produced.

DESCRIPTION OF THE DRAWINGS

[0069] FIG. 1A provides a schematic of one embodiment of the detection method of the present invention.

[0070] FIG. 1B provides a schematic of a second embodiment of the detection method of the present invention.

[0071] FIG. 2 is a comparison of the nucleotide structure of the DNAP genes isolated from *Thermus aquaticus* (SEQ ID NO:1), *Thermus flavus* (SEQ ID NO:2) and *Thermus thermophilus* (SEQ ID NO:3); the consensus sequence (SEQ ID NO:7) is shown at the top of each row.

[0072] FIG. 3 is a comparison of the amino acid sequence of the DNAP isolated from *Thermus aquaticus* (SEQ ID NO:4), *Thermus flavus* (SEQ ID NO:5), and *Thermus thermophilus* (SEQ ID NO:6); the consensus sequence (SEQ ID NO:8) is shown at the top of each row.

[0073] FIGS. 4A-G are a set of diagrams of wild-type and synthesis-deficient DNAP_{Taq} genes.

[0074] FIG. 5A depicts the wild-type *Thermus flavus* polymerase gene.

[0075] FIG. 5B depicts a synthesis-deficient *Thermus flavus* polymerase gene.

[0076] FIG. 6 depicts a structure which cannot be amplified using DNAP_{Taq}.

[0077] FIG. 7 is a ethidium bromide-stained gel demonstrating attempts to amplify a bifurcated duplex using either DNAP_{Taq} or DNAP_{Stf} (i.e., the Stoffel fragment of DNAP_{Taq}).

[0078] FIG. 8 is an autoradiogram of a gel analyzing the cleavage of a bifurcated duplex by DNAP_{Taq} and lack of cleavage by DNAP_{Stf}.

[0079] FIGS. 9A-B are a set of autoradiograms of gels analyzing cleavage or lack of cleavage upon addition of different reaction components and change of incubation temperature during attempts to cleave a bifurcated duplex with DNAP_{Taq}.

[0080] FIGS. 10A-B are an autoradiogram displaying timed cleavage reactions, with and without primer.

[0081] FIGS. 11A-B are a set of autoradiograms of gels demonstrating attempts to cleave a bifurcated duplex (with and without primer) with various DNAPs.

[0082] FIGS. 12A shows the substrates and oligonucleotides used to test the specific cleavage of substrate DNAs targeted by pilot oligonucleotides.

[0083] FIG. 12B shows an autoradiogram of a gel showing the results of cleavage reactions using the substrates and oligonucleotides shown FIG. 12A.

[0084] FIG. 13A shows the substrate and oligonucleotide used to test the specific cleavage of a substrate RNA targeted by a pilot oligonucleotide.

[0085] FIG. 13B shows an autoradiogram of a gel showing the results of a cleavage reaction using the substrate and oligonucleotide shown in FIG. 13A.

[0086] FIG. 14 is a diagram of vector pTTQ18.

[0087] FIG. 15 is a diagram of Vector pET-3c.

[0088] FIGS. 16A-E depicts a set of molecules which are suitable substrates for cleavage by the 5' nuclease activity of DNAPs.

[0089] FIG. 17 is an autoradiogram of a gel showing the results of a cleavage reaction run with synthesis-deficient DNAPs.

[0090] FIG. 18 is an autoradiogram of a PEI chromatogram resolving the products of an assay for synthetic activity in synthesis-deficient DNAP_{Taq} clones.

[0091] FIG. 19A depicts the substrate molecule used to test the ability of synthesis-deficient DNAPs to cleave short hairpin structures.

[0092] FIG. 19B shows an autoradiogram of a gel resolving the products of a cleavage reaction run using the substrate shown in FIG. 19A.

- [0093] FIG. 20A shows the A- and T-hairpin molecules used in the trigger/detection assay.
- [0094] FIG. 20B shows the sequence of the alpha primer used in the trigger/detection assay.
- [0095] FIG. 20C shows the structure of the cleaved A- and T-hairpin molecules.
- [0096] FIG. 20D depicts the complementarity between the A- and T-hairpin molecules.
- [0097] FIG. 21 provides the complete 206-mer duplex sequence employed as a substrate for the 5' nucleases of the present invention
- [0098] FIGS. 22A and B show the cleavage of linear nucleic acid substrates (based on the 206-mer of FIG. 21) by wild type DNAPs and 5' nucleases isolated from *Thermus aquaticus* and *Thermus flavus*.
- [0099] FIG. 23 provides a detailed schematic corresponding to the of one embodiment of the detection method of the present invention.
- [0100] FIG. 24 shows the propagation of cleavage of the linear duplex nucleic acid structures of FIG. 23 by the 5' nucleases of the present invention.
- [0101] FIG. 25A shows the "nibbling" phenomenon detected with the DNAPs of the present invention.
- [0102] FIG. 25B shows that the "nibbling" of FIG. 25A is 5' nucleolytic cleavage and not phosphatase cleavage.
- [0103] FIG. 26 demonstrates that the "nibbling" phenomenon is duplex dependent.
- [0104] FIG. 27 is a schematic showing how "nibbling" can be employed in a detection assay.
- [0105] FIG. 28 demonstrates that "nibbling" can be target directed.
- [0106] FIG. 29 provides a schematic drawing of a target nucleic acid with an invader oligonucleotide and a probe oligonucleotide annealed to the target.
- [0107] FIG. 30 provides a schematic showing the S-60 hairpin oligonucleotide (SEQ ID NO:40) with the annealed P-15 oligonucleotide (SEQ ID NO:41).
- [0108] FIG. 31 is an autoradiogram of a gel showing the results of a cleavage reaction run using the S-60 hairpin in the presence or absence of the P-15 oligonucleotide.
- [0109] FIG. 32 provides a schematic showing three different arrangements of target-specific oligonucleotides and their hybridization to a target nucleic acid which also has a probe oligonucleotide annealed thereto.
- [0110] FIG. 33 is the image generated by a fluorescence imager showing that the presence of an invader oligonucleotide causes a shift in the site of cleavage in a probe/target duplex.
- [0111] FIG. 34 is the image generated by a fluorescence imager showing the products of invader-directed cleavage assays run using the three target-specific oligonucleotides diagrammed in FIG. 32.
- [0112] FIG. 35 is the image generated by a fluorescence imager showing the products of invader-directed cleavage assays run in the presence or absence of non-target nucleic acid molecules.
- [0113] FIG. 36 is the image generated by a fluorescence imager showing the products of invader-directed cleavage assays run in the presence of decreasing amounts of target nucleic acid.
- [0114] FIG. 37 is the image generated by a fluorescence imager showing the products of invader-directed cleavage assays run in the presence or absence of saliva extract using various thermostable 5' nucleases or DNA polymerases.
- [0115] FIG. 38 is the image generated by a fluorescence imager showing the products of invader-directed cleavage assays run using various 5' nucleases.
- [0116] FIG. 39 is the image generated by a fluorescence imager showing the products of invader-directed cleavage assays run using two target nucleic acids which differ by a single basepair at two different reaction temperatures.
- [0117] FIG. 40A provides a schematic showing the effect of elevated temperature upon the annealing and cleavage of a probe oligonucleotide along a target nucleic acid wherein the probe contains a region of noncomplementarity with the target.
- [0118] FIG. 40B provides a schematic showing the effect of adding an upstream oligonucleotide upon the annealing and cleavage of a probe oligonucleotide along a target nucleic acid wherein the probe contains a region of non-complementarity with the target.
- [0119] FIG. 41 provides a schematic showing an arrangement of a target-specific invader oligonucleotide (SEQ ID NO:50) and a target-specific probe oligonucleotide (SEQ ID NO:49) bearing a 5' Cy3 label along a target nucleic acid (SEQ ID NO:42).
- [0120] FIG. 42 is the image generated by a fluorescence imager showing the products of invader-directed cleavage assays run in the presence of increasing concentrations of KCl.
- [0121] FIG. 43 is the image generated by a fluorescence imager showing the products of invader-directed cleavage assays run in the presence of increasing concentrations of NaCl.
- [0122] FIG. 44 is the image generated by a fluorescence imager showing the products of invader-directed cleavage assays run in the presence of increasing concentrations of LiCl.
- [0123] FIG. 45 is the image generated by a fluorescence imager showing the products of invader-directed cleavage assays run in the presence of increasing concentrations of KGlu.
- [0124] FIG. 46 is the image generated by a fluorescence imager showing the products of invader-directed cleavage assays run in the presence of increasing concentrations of $MnCl_2$ or $MgCl_2$.
- [0125] FIG. 47 is the image generated by a fluorescence imager showing the products of invader-directed cleavage assays run in the presence of increasing concentrations of CTAB.

[0126] FIG. 48 is the image generated by a fluorescence imager showing the products of invader-directed cleavage assays run in the presence of increasing concentrations of PEG.

[0127] FIG. 49 is the image generated by a fluorescence imager showing the products of invader-directed cleavage assays run in the presence of glycerol, Tween-20 and/or Nonidet-P40.

[0128] FIG. 50 is the image generated by a fluorescence imager showing the products of invader-directed cleavage assays run in the presence of increasing concentrations of gelatin in reactions containing or lacking KCl or LiCl.

[0129] FIG. 51 is the image generated by a fluorescence imager showing the products of invader-directed cleavage assays run in the presence of increasing amounts of genomic DNA or tRNA.

[0130] FIG. 52 is the image generated by a fluorescence imager showing the products of invader-directed cleavage assays run use a HCV RNA target.

[0131] FIG. 53 is the image generated by a fluorescence imager showing the products of invader-directed cleavage assays run using a HCV RNA target and demonstrate the stability of RNA targets under invader-directed cleavage assay conditions.

[0132] FIG. 54 is the image generated by a fluorescence imager showing the sensitivity of detection and the stability of RNA in invader-directed cleavage assays run using a HCV RNA target.

[0133] FIG. 55 is the image generated by a fluorescence imager showing thermal degradation of oligonucleotides containing or lacking a 3' phosphate group.

[0134] FIG. 56 depicts the structure of amino-modified oligonucleotides 70 and 74.

[0135] FIG. 57 depicts the structure of amino-modified oligonucleotide 75

[0136] FIG. 58 depicts the structure of amino-modified oligonucleotide 76.

[0137] FIG. 59 is the image generated by a fluorescence imager scan of an IEF gel showing the migration of substrates 70, 70dp, 74, 74dp, 75, 75dp, 76 and 76dp.

[0138] FIG. 60A provides a schematic showing an arrangement of a target-specific invader oligonucleotide (SEQ ID NO:61) and a target-specific probe oligonucleotide (SEQ ID NO:62) bearing a 5' Cy3 label along a target nucleic acid (SEQ ID NO:63).

[0139] FIG. 60B is the image generated by a fluorescence imager showing the detection of specific cleavage products generated in an invasive cleavage assay using charge reversal (i.e., charge based separation of cleavage products).

[0140] FIG. 61 is the image generated by a fluorescence imager which depicts the sensitivity of detection of specific cleavage products generated in an invasive cleavage assay using charge reversal.

[0141] FIG. 62 depicts a first embodiment of a device for the charge-based separation of oligonucleotides.

[0142] FIG. 63 depicts a second embodiment of a device for the charge-based separation of oligonucleotides.

[0143] FIG. 64 shows an autoradiogram of a gel showing the results of cleavage reactions run in the presence or absence of a primer oligonucleotide; a sequencing ladder is shown as a size marker.

[0144] FIGS. 65a-d depict four pairs of oligonucleotides; in each pair shown, the upper arrangement of a probe annealed to a target nucleic acid lacks an upstream oligonucleotide and the lower arrangement contains an upstream oligonucleotide.

[0145] FIG. 66 shows the chemical structure of several positively charged heterodimeric DNA-binding dyes.

DEFINITIONS

[0146] As used herein, the terms "complementary" or "complementarity" are used in reference to polynucleotides (i.e., a sequence of nucleotides such as an oligonucleotide or a target nucleic acid) related by the base-pairing rules. For example, for the sequence "A-G-T," is complementary to the sequence "T-C-A." Complementarity may be "partial," in which only some of the nucleic acids' bases are matched according to the base pairing rules. Or, there may be "complete" or "total" complementarity between the nucleic acids. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of hybridization between nucleic acid strands. This is of particular importance in amplification reactions, as well as detection methods which depend upon binding between nucleic acids.

[0147] The term "homology" refers to a degree of identity. There may be partial homology or complete homology. A partially identical sequence is one that is less than 100% identical to another sequence.

[0148] As used herein, the term "hybridization" is used in reference to the pairing of complementary nucleic acids. Hybridization and the strength of hybridization (i.e., the strength of the association between the nucleic acids) is impacted by such factors as the degree of complementarity between the nucleic acids, stringency of the conditions involved, the T_m of the formed hybrid, and the G:C ratio within the nucleic acids.

[0149] As used herein, the term " T_m " is used in reference to the "melting temperature." The melting temperature is the temperature at which a population of double-stranded nucleic acid molecules becomes half dissociated into single strands. The equation for calculating the T_m of nucleic acids is well known in the art. As indicated by standard references, a simple estimate of the T_m value may be calculated by the equation: $T_m = 81.5 + 0.41(\% G+C)$, when a nucleic acid is in aqueous solution at 1 M NaCl (see e.g., Anderson and Young, Quantitative Filter Hybridization, in *Nucleic Acid Hybridization* (1985). Other references include more sophisticated computations which take structural as well as sequence characteristics into account for the calculation of T_m .

[0150] As used herein the term "stringency" is used in reference to the conditions of temperature, ionic strength, and the presence of other compounds, under which nucleic acid hybridizations are conducted. With "high stringency"

conditions, nucleic acid base pairing will occur only between nucleic acid fragments that have a high frequency of complementary base sequences. Thus, conditions of "weak" or "low" stringency are often required when it is desired that nucleic acids which are not completely complementary to one another be hybridized or annealed together.

[0151] The term "gene" refers to a DNA sequence that comprises control and coding sequences necessary for the production of a polypeptide or precursor. The polypeptide can be encoded by a full length coding sequence or by any portion of the coding sequence so long as the desired enzymatic activity is retained.

[0152] The term "wild-type" refers to a gene or gene product which has the characteristics of that gene or gene product when isolated from a naturally occurring source. A wild-type gene is that which is most frequently observed in a population and is thus arbitrarily designed the "normal" or "wild-type" form of the gene. In contrast, the term "modified" or "mutant" refers to a gene or gene product which displays modifications in sequence and/or functional properties (L e., altered characteristics) when compared to the wild-type gene or gene product. It is noted that naturally-occurring mutants can be isolated; these are identified by the fact that they have altered characteristics when compared to the wild-type gene or gene product.

[0153] The term "recombinant DNA vector" as used herein refers to DNA sequences containing a desired coding sequence and appropriate DNA sequences necessary for the expression of the operably linked coding sequence in a particular host organism. DNA sequences necessary for expression in prokaryotes include a promoter, optionally an operator sequence, a ribosome binding site and possibly other sequences. Eukaryotic cells are known to utilize promoters, polyadenylation signals and enhancers.

[0154] The term "LTR" as used herein refers to the long terminal repeat found at each end of a provirus (i.e., the integrated form of a retrovirus). The LTR contains numerous regulatory signals including transcriptional control elements, polyadenylation signals and sequences needed for replication and integration of the viral genome. The viral LTR is divided into three regions called U3, R and U5.

[0155] The U3 region contains the enhancer and promoter elements. The U5 region contains the polyadenylation signals. The R (repeat) region separates the U3 and U5 regions and transcribed sequences of the R region appear at both the 5' and 3' ends of the viral RNA.

[0156] The term "oligonucleotide" as used herein is defined as a molecule comprised of two or more deoxyribonucleotides or ribonucleotides, preferably at least 5 nucleotides, more preferably at least about 10-15 nucleotides and more preferably at least about 15 to 30 nucleotides. The exact size will depend on many factors, which in turn depends on the ultimate function or use of the oligonucleotide. The oligonucleotide may be generated in any manner, including chemical synthesis, DNA replication, reverse transcription, or a combination thereof.

[0157] Because mononucleotides are reacted to make oligonucleotides in a manner such that the 5' phosphate of one mononucleotide pentose ring is attached to the 3' oxygen of its neighbor in one direction via a phosphodiester linkage, an end of an oligonucleotide is referred to as the "5' end" if its

5' phosphate is not linked to the 3' oxygen of a mononucleotide pentose ring and as the "3' end" if its 3' oxygen is not linked to a 5' phosphate of a subsequent mononucleotide pentose ring. As used herein, a nucleic acid sequence, even if internal to a larger oligonucleotide, also may be said to have 5' and 3' ends. A first region along a nucleic acid strand is said to be upstream of another region if the 3' end of the first region is before the 5' end of the second region when moving along a strand of nucleic acid in a 5' to 3' direction.

[0158] When two different, non-overlapping oligonucleotides anneal to different regions of the same linear complementary nucleic acid sequence, and the 3' end of one oligonucleotide points towards the 5' end of the other, the former may be called the "upstream" oligonucleotide and the latter the "downstream" oligonucleotide.

[0159] The term "primer" refers to an oligonucleotide which is capable of acting as a point of initiation of synthesis when placed under conditions in which primer extension is initiated. An oligonucleotide "primer" may occur naturally, as in a purified restriction digest or may be produced synthetically.

[0160] A primer is selected to be "substantially" complementary to a strand of specific sequence of the template. A primer must be sufficiently complementary to hybridize with a template strand for primer elongation to occur. A primer sequence need not reflect the exact sequence of the template. For example, a non-complementary nucleotide fragment may be attached to the 5' end of the primer, with the remainder of the primer sequence being substantially complementary to the strand. Non-complementary bases or longer sequences can be interspersed into the primer, provided that the primer sequence has sufficient complementarity with the sequence of the template to hybridize and thereby form a template primer complex for synthesis of the extension product of the primer.

[0161] "Hybridization" methods involve the annealing of a complementary sequence to the target nucleic acid (the sequence to be detected; the detection of this sequence may be by either direct or indirect means). The ability of two polymers of nucleic acid containing complementary sequences to find each other and anneal through base pairing interaction is a well-recognized phenomenon. The initial observations of the "hybridization" process by Marmur and Lane, *Proc. Natl. Acad. Sci. USA* 46:453 (1960) and Doty et al., *Proc. Natl. Acad. Sci. USA* 46:461 (1960) have been followed by the refinement of this process into an essential tool of modern biology.

[0162] With regard to complementarity, it is important for some diagnostic applications to determine whether the hybridization represents complete or partial complementarity. For example, where it is desired to detect simply the presence or absence of pathogen DNA (such as from a virus, bacterium, fungi, mycoplasma, protozoan) it is only important that the hybridization method ensures hybridization when the relevant sequence is present; conditions can be selected where both partially complementary probes and completely complementary probes will hybridize. Other diagnostic applications, however, may require that the hybridization method distinguish between partial and complete complementarity. It may be of interest to detect genetic polymorphisms. For example, human hemoglobin is composed, in part, of four polypeptide chains. Two of these

chains are identical chains of 141 amino acids (alpha chains) and two of these chains are identical chains of 146 amino acids (beta chains). The gene encoding the beta chain is known to exhibit polymorphism. The normal allele encodes a beta chain having glutamic acid at the sixth position. The mutant allele encodes a beta chain having valine at the sixth position. This difference in amino acids has a profound (most profound when the individual is homozygous for the mutant allele) physiological impact known clinically as sickle cell anemia. It is well known that the genetic basis of the amino acid change involves a single base difference between the normal allele DNA sequence and the mutant allele DNA sequence.

[0163] The complement of a nucleic acid sequence as used herein refers to an oligonucleotide which, when aligned with the nucleic acid sequence such that the 5' end of one sequence is paired with the 3' end of the other, is in "antiparallel association." Certain bases not commonly found in natural nucleic acids may be included in the nucleic acids of the present invention and include, for example, inosine and 7-deazaguanine. Complementarity need not be perfect; stable duplexes may contain mismatched base pairs or unmatched bases. Those skilled in the art of nucleic acid technology can determine duplex stability empirically considering a number of variables including, for example, the length of the oligonucleotide, base composition and sequence of the oligonucleotide, ionic strength and incidence of mismatched base pairs.

[0164] Stability of a nucleic acid duplex is measured by the melting temperature, or " T_m ." The T_m of a particular nucleic acid duplex under specified conditions is the temperature at which on average half of the base pairs have disassociated.

[0165] The term "label" as used herein refers to any atom or molecule which can be used to provide a detectable (preferably quantifiable) signal, and which can be attached to a nucleic acid or protein. Labels may provide signals detectable by fluorescence, radioactivity, colorimetry, gravimetry, X-ray diffraction or absorption, magnetism, enzymatic activity, and the like. A label may be a charged moiety (positive or negative charge) or alternatively, may be charge neutral.

[0166] The term "cleavage structure" as used herein, refers to a structure which is formed by the interaction of a probe oligonucleotide and a target nucleic acid to form a duplex, said resulting structure being cleavable by a cleavage means, including but not limited to an enzyme. The cleavage structure is a substrate for specific cleavage by said cleavage means in contrast to a nucleic acid molecule which is a substrate for non-specific cleavage by agents such as phosphodiesterases which cleave nucleic acid molecules without regard to secondary structure (i.e., no formation of a duplexed structure is required).

[0167] The term "cleavage means" as used herein refers to any means which is capable of cleaving a cleavage structure, including but not limited to enzymes. The cleavage means may include native DNAPs having 5' nuclease activity (e.g., Taq DNA polymerase, *E. coli* DNA polymerase I) and, more specifically, modified DNAPs having 5' nuclease but lacking synthetic activity. The ability of 5' nucleases to cleave naturally occurring structures in nucleic acid templates (structure-specific cleavage) is useful to detect internal

sequence differences in nucleic acids without prior knowledge of the specific sequence of the nucleic acid. In this manner, they are structure-specific enzymes. Structure-specific enzymes are enzymes which recognize specific secondary structures in a nucleic molecule and cleave these structures. The cleavage means of the invention cleave a nucleic acid molecule in response to the formation of cleavage structures; it is not necessary that the cleavage means cleave the cleavage structure at any particular location within the cleavage structure.

[0168] The cleavage means is not restricted to enzymes having solely 5' nuclease activity. The cleavage means may include nuclease activity provided from a variety of sources including the Cleavase® enzymes, Taq DNA polymerase and *E. coli* DNA polymerase I.

[0169] The term "thermostable" when used in reference to an enzyme, such as a 5' nuclease, indicates that the enzyme is functional or active (i.e., can perform catalysis) at an elevated temperature, i.e., at about 55° C. or higher.

[0170] The term "cleavage products" as used herein, refers to products generated by the reaction of a cleavage means with a cleavage structure (i.e., the treatment of a cleavage structure with a cleavage means).

[0171] The term "target nucleic acid" refers to a nucleic acid molecule which contains a sequence which has at least partial complementarity with at least a probe oligonucleotide and may also have at least partial complementarity with an invader oligonucleotide. The target nucleic acid may comprise single- or double-stranded DNA or RNA.

[0172] The term "probe oligonucleotide" refers to an oligonucleotide which interacts with a target nucleic acid to form a cleavage structure in the presence or absence of an invader oligonucleotide. When annealed to the target nucleic acid, the probe oligonucleotide and target form a cleavage structure and cleavage occurs within the probe oligonucleotide. In the presence of an invader oligonucleotide upstream of the probe oligonucleotide along the target nucleic acid will shift the site of cleavage within the probe oligonucleotide (relative to the site of cleavage in the absence of the invader).

[0173] The term "non-target cleavage product" refers to a product of a cleavage reaction which is not derived from the target nucleic acid. As discussed above, in the methods of the present invention, cleavage of the cleavage structure occurs within the probe oligonucleotide. The fragments of the probe oligonucleotide generated by this target nucleic acid-dependent cleavage are "non-target cleavage products." The term "invader oligonucleotide" refers to an oligonucleotide which contains sequences at its 3' end which are substantially the same as sequences located at the 5' end of a probe oligonucleotide; these regions will compete for hybridization to the same segment along a complementary target nucleic acid.

[0174] The term "substantially single-stranded" when used in reference to a nucleic acid substrate means that the substrate molecule exists primarily as a single strand of nucleic acid in contrast to a double-stranded substrate which exists as two strands of nucleic acid which are held together by inter-strand base pairing interactions.

[0175] The term "sequence variation" as used herein refers to differences in nucleic acid sequence between two nucleic

acids. For example, a wild-type structural gene and a mutant form of this wild-type structural gene may vary in sequence by the presence of single base substitutions and/or deletions or insertions of one or more nucleotides. These two forms of the structural gene are said to vary in sequence from one another. A second mutant form of the structural gene may exist. This second mutant form is said to vary in sequence from both the wild-type gene and the first mutant form of the gene.

[0176] The term “liberating” as used herein refers to the release of a nucleic acid fragment from a larger nucleic acid fragment, such as an oligonucleotide, by the action of a 5' nuclease such that the released fragment is no longer covalently attached to the remainder of the oligonucleotide.

[0177] The term “ K_m ” as used herein refers to the Michaelis-Menten constant for an enzyme and is defined as the concentration of the specific substrate at which a given enzyme yields one-half its maximum velocity in an enzyme catalyzed reaction.

[0178] The term “nucleotide analog” as used herein refers to modified or non-naturally occurring nucleotides such as 7-deaza purines (i.e., 7-deaza-dATP and 7-deaza-dGTP). Nucleotide analogs include base analogs and comprise modified forms of deoxyribonucleotides as well as ribonucleotides.

[0179] The term “polymorphic locus” is a locus present in a population which shows variation between members of the population (i.e., the most common allele has a frequency of less than 0.95). In contrast, a “monomorphic locus” is a genetic locus at little or no variations seen between members of the population (generally taken to be a locus at which the most common allele exceeds a frequency of 0.95 in the gene pool of the population).

[0180] The term “microorganism” as used herein means an organism too small to be observed with the unaided eye and includes, but is not limited to bacteria, virus, protozoans, fungi, and ciliates.

[0181] The term “microbial gene sequences” refers to gene sequences derived from a microorganism.

[0182] The term “bacteria” refers to any bacterial species including eubacterial and archaeobacterial species.

[0183] The term “virus” refers to obligate, ultramicroscopic, intracellular parasites incapable of autonomous replication (i.e., replication requires the use of the host cell's machinery).

[0184] The term “multi-drug resistant” or “multiple-drug resistant” refers to a microorganism which is resistant to more than one of the antibiotics or antimicrobial agents used in the treatment of said microorganism.

[0185] The term “sample” in the present specification and claims is used in its broadest sense. On the one hand it is meant to include a specimen or culture (e.g., microbiological cultures). On the other hand, it is meant to include both biological and environmental samples.

[0186] Biological samples may be animal, including human, fluid, solid (e.g., stool) or tissue, as well as liquid and solid food and feed products and ingredients such as dairy items, vegetables, meat and meat by-products, and waste. Biological samples may be obtained from all of the

various families of domestic animals, as well as feral or wild animals, including, but not limited to, such animals as ungulates, bear, fish, lagamorphs, rodents, etc.

[0187] Environmental samples include environmental material such as surface matter, soil, water and industrial samples, as well as samples obtained from food and dairy processing instruments, apparatus, equipment, utensils, disposable and non-disposable items. These examples are not to be construed as limiting the sample types applicable to the present invention.

[0188] The term “source of target nucleic acid” refers to any sample which contains nucleic acids (RNA or DNA). Particularly preferred sources of target nucleic acids are biological samples including, but not limited to blood, saliva, cerebral spinal fluid, pleural fluid, milk, lymph, sputum and semen.

[0189] An oligonucleotide is said to be present in “excess” relative to another oligonucleotide (or target nucleic acid sequence) if that oligonucleotide is present at a higher molar concentration than the other oligonucleotide (or target nucleic acid sequence). When an oligonucleotide such as a probe oligonucleotide is present in a cleavage reaction in excess relative to the concentration of the complementary target nucleic acid sequence, the reaction may be used to indicate the amount of the target nucleic acid present. Typically, when present in excess, the probe oligonucleotide will be present at least a 100-fold molar excess; typically at least 1 pmole of each probe oligonucleotide would be used when the target nucleic acid sequence was present at about 10 fmoles or less.

[0190] A sample “suspected of containing” a first and a second target nucleic acid may contain either, both or neither target nucleic acid molecule.

[0191] The term “charge-balanced” oligonucleotide refers to an oligonucleotide (the input oligonucleotide in a reaction) which has been modified such that the modified oligonucleotide bears a charge, such that when the modified oligonucleotide is either cleaved (i.e., shortened) or elongated, a resulting product bears a charge different from the input oligonucleotide (the “charge-unbalanced” oligonucleotide) thereby permitting separation of the input and reacted oligonucleotides on the basis of charge. The term “charge-balanced” does not imply that the modified or balanced oligonucleotide has a net neutral charge (although this can be the case). Charge-balancing refers to the design and modification of an oligonucleotide such that a specific reaction product generated from this input oligonucleotide can be separated on the basis of charge from the input oligonucleotide.

[0192] For example, in an invader-directed cleavage assay in which the probe oligonucleotide bears the sequence: 5'-TTCTTTTCACCAGCGAGACGGG-3' (i.e., SEQ ID NO:61 without the modified bases) and cleavage of the probe occurs between the second and third residues, one possible charge-balanced version of this oligonucleotide would be: 5'-Cy3-AminoT-Amino-TCTTTTCACCAGC-GAGAC GGG-3'. This modified oligonucleotide bears a net negative charge. After cleavage, the following oligonucleotides are generated: 5'-Cy3-AminoT-Amino-T-3' and 5'-CTTTTCACCAGCGAGACGGG-3' (residues 3-22of SEQ ID NO:61). 5'-Cy3-AminoT-Amino-T-3' bears a

detectable moiety (the positively-charged Cy3 dye) and two amino-modified bases. The amino-modified bases and the Cy3 dye contribute positive charges in excess of the negative charges contributed by the phosphate groups and thus the 5'-Cy3-AminoT-Amino-T-3' oligonucleotide has a net positive charge. The other, longer cleavage fragment, like the input probe, bears a net negative charge. Because the 5'-Cy3-AminoT-Amino-T-3' fragment is separable on the basis of charge from the input probe (the charge-balanced oligonucleotide), it is referred to as a charge-unbalanced oligonucleotide. The longer cleavage product cannot be separated on the basis of charge from the input oligonucleotide as both oligonucleotides bear a net negative charge; thus, the longer cleavage product is not a charge-unbalanced oligonucleotide.

[0193] The term "net neutral charge" when used in reference to an oligonucleotide, including modified oligonucleotides, indicates that the sum of the charges present (i.e., R—NH³⁺ groups on thymidines, the N3 nitrogen of cytosine, presence or absence of phosphate groups, etc.) under the desired reaction conditions is essentially zero. An oligonucleotide having a net neutral charge would not migrate in an electrical field.

[0194] The term "net positive charge" when used in reference to an oligonucleotide, including modified oligonucleotides, indicates that the sum of the charges present (i.e., R—NH³⁺ groups on thymidines, the N3 nitrogen of cytosine, presence or absence of phosphate groups, etc.) under the desired reaction conditions is +1 or greater. An oligonucleotide having a net positive charge would migrate toward the negative electrode in an electrical field.

[0195] The term "net negative charge" when used in reference to an oligonucleotide, including modified oligonucleotides, indicates that the sum of the charges present (i.e., R—NH³⁺ groups on thymidines, the N3 nitrogen of cytosine, presence or absence of phosphate groups, etc.) under the desired reaction conditions is -1 or lower. An oligonucleotide having a net negative charge would migrate toward the positive electrode in an electrical field.

[0196] The term "polymerization means" refers to any agent capable of facilitating the addition of nucleoside triphosphates to an oligonucleotide. Preferred polymerization means comprise DNA polymerases.

[0197] The term "ligation means" refers to any agent capable of facilitating the ligation (i.e., the formation of a phosphodiester bond between a 3'-OH and a 5'-P located at the termini of two strands of nucleic acid). Preferred ligation means comprise DNA ligases and RNA ligases.

[0198] The term "reactant" is used herein in its broadest sense. The reactant can comprise an enzymatic reactant, a chemical reactant or ultraviolet light (ultraviolet light, particularly short wavelength ultraviolet light is known to break oligonucleotide chains). Any agent capable of reacting with an oligonucleotide to either shorten (i.e., cleave) or elongate the oligonucleotide is encompassed within the term "reactant." The term "adduct" is used herein in its broadest sense to indicate any compound or element which can be added to an oligonucleotide. An adduct may be charged (positively or negatively) or may be charge neutral. An adduct may be added to the oligonucleotide via covalent or non-covalent linkages. Examples of adducts, include but are not limited to

indodicarbocyanine dye amidites, amino-substituted nucleotides, ethidium bromide, ethidium homodimer, (1,3-propanediamino)propidium, (diethylenetriamino)propidium, thiazole orange, (N-N'-tetramethyl-1,3-propanediamino)propyl thiazole orange, (N-N'-tetramethyl-1,2-ethanediamino)propyl thiazole orange, thiazole orange-thiazole orange homodimer (TOTO), thiazole orange-thiazole blue heterodimer (TOTAB), thiazole orange-ethidium heterodimer 1 (TOED1), thiazole orange-ethidium heterodimer 2 (TOED2) and florescien-ethidium heterodimer (FED), psoralens, biotin, streptavidin, avidin, etc.

[0199] Where a first oligonucleotide is complementary to a region of a target nucleic acid and a second oligonucleotide has complementary to the same region (or a portion of this region) a "region of overlap" exists along the target nucleic acid. The degree of overlap will vary depending upon the nature of the complementarity (see, e.g., region "X" in FIG. 29 and the accompanying discussion)

DESCRIPTION OF THE INVENTION

[0200] The present invention relates to methods and compositions for treating nucleic acid, and in particular, methods and compositions for detection and characterization of nucleic acid sequences and sequence changes.

[0201] The present invention relates to means for cleaving a nucleic acid cleavage structure in a site-specific manner. In particular, the present invention relates to a cleaving enzyme having 5' nuclease activity without interfering nucleic acid synthetic ability.

[0202] This invention provides 5' nucleases derived from thermostable DNA polymerases which exhibit altered DNA synthetic activity from that of native thermostable DNA polymerases. The 5' nuclease activity of the polymerase is retained while the synthetic activity is reduced or absent. Such 5' nucleases are capable of catalyzing the structure-specific cleavage of nucleic acids in the absence of interfering synthetic activity. The lack of synthetic activity during a cleavage reaction results in nucleic acid cleavage products of uniform size.

[0203] The novel properties of the polymerases of the invention form the basis of a method of detecting specific nucleic acid sequences. This method relies upon the amplification of the detection molecule rather than upon the amplification of the target sequence itself as do existing methods of detecting specific target sequences.

[0204] DNA polymerases (DNAPs), such as those isolated from *E. coli* or from thermophilic bacteria of the genus *Thermus*, are enzymes that synthesize new DNA strands. Several of the known DNAPs contain associated nuclease activities in addition to the synthetic activity of the enzyme.

[0205] Some DNAPs are known to remove nucleotides from the 5' and 3' ends of DNA chains [Kornberg, *DNA Replication*, W.H. Freeman and Co., San Francisco, pp. 127-139 (1980)]. These nuclease activities are usually referred to as 5' exonuclease and 3' exonuclease activities, respectively. For example, the 5' exonuclease activity located in the N-terminal domain of several DNAPs participates in the removal of RNA primers during lagging strand synthesis during DNA replication and the removal of damaged nucleotides during repair. Some DNAPs, such as the *E.*

coli DNA polymerase (DNAPEc1), also have a 3' exonuclease activity responsible for proof-reading during DNA synthesis (Kornberg, *supra*).

[0206] A DNAP isolated from *Thermus aquaticus*, termed Taq DNA polymerase (DNAPTaq), has a 5' exonuclease activity, but lacks a functional 3' exonucleolytic domain [Tindall and Kunkell, *Biochem. 27:6008* (1988)]. Derivatives of DNAPEc1 and DNAPTaq, respectively called the Klenow and Stoffel fragments, lack 5' exonuclease domains as a result of enzymatic or genetic manipulations [Brutlag et al., *Biochem. Biophys. Res. Commun. 37:982* (1969); Erlich et al., *Science 252:1643* (1991); Setlow and Kornberg, *J. Biol. Chem. 247:232* (1972)].

[0207] The 5' exonuclease activity of DNAPTaq was reported to require concurrent synthesis [Gelfand, *PCR Technology—Principles and Applications for DNA Amplification* (H. A. Erlich, Ed.), Stockton Press, New York, p. 19 (1989)]. Although mononucleotides predominate among the digestion products of the 5' exonucleases of DNAPTaq and DNAPEc1, short oligonucleotides (≤ 12 nucleotides) can also be observed implying that these so-called 5' exonucleases can function endonucleolytically [Setlow, *supra*; Holland et al., *Proc. Natl. Acad. Sci. USA 88:7276* (1991)].

[0208] In WO 92/06200, Gelfand et al. show that the preferred substrate of the 5' exonuclease activity of the thermostable DNA polymerases is displaced single-stranded DNA. Hydrolysis of the phosphodiester bond occurs between the displaced single-stranded DNA and the double-helical DNA with the preferred exonuclease cleavage site being a phosphodiester bond in the double helical region. Thus, the 5' exonuclease activity usually associated with DNAPs is a structure-dependent single-stranded endonuclease and is more properly referred to as a 5' nuclease. Exonucleases are enzymes which cleave nucleotide molecules from the ends of the nucleic acid molecule. Endonucleases, on the other hand, are enzymes which cleave the nucleic acid molecule at internal rather than terminal sites. The nuclease activity associated with some thermostable DNA polymerases cleaves endonucleolytically but this cleavage requires contact with the 5' end of the molecule being cleaved. Therefore, these nucleases are referred to as 5' nucleases.

[0209] When a 5' nuclease activity is associated with a eubacterial Type A DNA polymerase, it is found in the one-third N-terminal region of the protein as an independent functional domain. The C-terminal two-thirds of the molecule constitute the polymerization domain which is responsible for the synthesis of DNA. Some Type A DNA polymerases also have a 3' exonuclease activity associated with the two-third C-terminal region of the molecule.

[0210] The 5' exonuclease activity and the polymerization activity of DNAPs have been separated by proteolytic cleavage or genetic manipulation of the polymerase molecule. To date thermostable DNAPs have been modified to remove or reduce the amount of 5' nuclease activity while leaving the polymerase activity intact.

[0211] The Klenow or large proteolytic cleavage fragment of DNAPEc1 contains the polymerase and 3' exonuclease activity but lacks the 5' nuclease activity. The Stoffel fragment of DNAPTaq (DNAPStf) lacks the 5' nuclease activity due to a genetic manipulation which deleted the N-terminal

289 amino acids of the polymerase molecule [Erlich et al., *Science 252:1643* (1991)]. WO 92/06200 describes a thermostable DNAP with an altered level of 5' to 3' exonuclease. U.S. Pat. No. 5,108,892 describes a *Thermus aquaticus* DNAP without a 5' to 3' exonuclease. However, the art of molecular biology lacks a thermostable DNA polymerase with a lessened amount of synthetic activity.

[0212] The present invention provides 5' nucleases derived from thermostable Type A DNA polymerases that retain 5' nuclease activity but have reduced or absent synthetic activity. The ability to uncouple the synthetic activity of the enzyme from the 5' nuclease activity proves that the 5' nuclease activity does not require concurrent DNA synthesis as was previously reported (Gelfand, *PCR Technology, supra*).

[0213] The description of the invention is divided into: I. Detection of Specific Nucleic Acid Sequences Using 5' Nucleases; II. Generation of 5' Nucleases Derived From Thermostable DNA Polymerases; III. Detection of Specific Nucleic Acid Sequences Using 5' Nucleases in an Invader-Directed Cleavage Assay; IV. A Comparison Of Invasive Cleavage And Primer-Directed Cleavage; and V. Fractionation Of Specific Nucleic Acids By Selective Charge Reversal.

[0214] I. Detection of Specific Nucleic Acid Sequences Using 5' Nucleases

[0215] The 5' nucleases of the invention form the basis of a novel detection assay for the identification of specific nucleic acid sequences. This detection system identifies the presence of specific nucleic acid sequences by requiring the annealing of two oligonucleotide probes to two portions of the target sequence. As used herein, the term "target sequence" or "target nucleic acid sequence" refers to a specific nucleic acid sequence within a polynucleotide sequence, such as genomic DNA or RNA, which is to be either detected or cleaved or both.

[0216] FIG. 1A provides a schematic of one embodiment of the detection method of the present invention. The target sequence is recognized by two distinct oligonucleotides in the triggering or trigger reaction. It is preferred that one of these oligonucleotides is provided on a solid support. The other can be provided free. In FIG. 1A the free oligo is indicated as a "primer" and the other oligo is shown attached to a bead designated as type 1. The target nucleic acid aligns the two oligonucleotides for specific cleavage of the 5' arm (of the oligo on bead 1) by the DNAPs of the present invention (not shown in FIG. 1A).

[0217] The site of cleavage (indicated by a large solid arrowhead) is controlled by the distance between the 3' end of the "primer" and the downstream fork of the oligo on bead 1. The latter is designed with an uncleavable region (indicated by the striping). In this manner neither oligonucleotide is subject to cleavage when misaligned or when unattached to target nucleic acid.

[0218] Successful cleavage releases a single copy of what is referred to as the alpha signal oligo. This oligo may contain a detectable moiety (e.g., fluorescein). On the other hand, it may be unlabelled.

[0219] In one embodiment of the detection method, two more oligonucleotides are provided on solid supports. The

oligonucleotide shown in **FIG. 1A** on bead 2 has a region that is complementary to the alpha signal oligo (indicated as alpha prime) allowing for hybridization. This structure can be cleaved by the DNAPs of the present invention to release the beta signal oligo. The beta signal oligo can then hybridize to type 3 beads having an oligo with a complementary region (indicated as beta prime). Again, this structure can be cleaved by the DNAPs of the present invention to release a new alpha oligo.

[0220] At this point, the amplification has been linear. To increase the power of the method, it is desired that the alpha signal oligo hybridized to bead type 2 be liberated after release of the beta oligo so that it may go on to hybridize with other oligos on type 2 beads. Similarly, after release of an alpha oligo from type 3 beads, it is desired that the beta oligo be liberated.

[0221] The liberation of "captured" signal oligos can be achieved in a number of ways. First, it has been found that the DNAPs of the present invention have a true 5' exonuclease capable of "nibbling" the 5' end of the alpha (and beta) prime oligo (discussed below in more detail). Thus, under appropriate conditions, the hybridization is destabilized by nibbling of the DNAP. Second, the alpha - alpha prime (as well as the beta—beta prime) complex can be destabilized by heat (e.g., thermal cycling).

[0222] With the liberation of signal oligos by such techniques, each cleavage results in a doubling of the number of signal oligos. In this manner, detectable signal can quickly be achieved.

[0223] **FIG. 1B** provides a schematic of a second embodiment of the detection method of the present invention. Again, the target sequence is recognized by two distinct oligonucleotides in the triggering or trigger reaction and the target nucleic acid aligns the two oligonucleotides for specific cleavage of the 5' arm by the DNAPs of the present invention (not shown in **FIG. 1B**). The first oligo is completely complementary to a portion of the target sequence. The second oligonucleotide is partially complementary to the target sequence; the 3' end of the second oligonucleotide is fully complementary to the target sequence while the 5' end is non-complementary and forms a single-stranded arm. The non-complementary end of the second oligonucleotide may be a generic sequence which can be used with a set of standard hairpin structures (described below). The detection of different target sequences would require unique portions of two oligonucleotides: the entire first oligonucleotide and the 3' end of the second oligonucleotide. The 5' arm of the second oligonucleotide can be invariant or generic in sequence.

[0224] The annealing of the first and second oligonucleotides near one another along the target sequence forms a forked cleavage structure which is a substrate for the 5' nuclease of DNA polymerases. The approximate location of the cleavage site is again indicated by the large solid arrowhead in **FIG. 1B**.

[0225] The 5' nucleases of the invention are capable of cleaving this structure but are not capable of polymerizing the extension of the 3' end of the first oligonucleotide. The lack of polymerization activity is advantageous as extension of the first oligonucleotide results in displacement of the annealed region of the second oligonucleotide and results in

moving the site of cleavage along the second oligonucleotide. If polymerization is allowed to occur to any significant amount, multiple lengths of cleavage product will be generated. A single cleavage product of uniform length is desirable as this cleavage product initiates the detection reaction.

[0226] The trigger reaction may be run under conditions that allow for thermocycling. Thermocycling of the reaction allows for a logarithmic increase in the amount of the trigger oligonucleotide released in the reaction.

[0227] The second part of the detection method allows the annealing of the fragment of the second oligonucleotide liberated by the cleavage of the first cleavage structure formed in the triggering reaction (called the third or trigger oligonucleotide) to a first hairpin structure. This first hairpin structure has a single-stranded 5' arm and a single-stranded 3' arm. The third oligonucleotide triggers the cleavage of this first hairpin structure by annealing to the 3' arm of the hairpin thereby forming a substrate for cleavage by the 5' nuclease of the present invention. The cleavage of this first hairpin structure generates two reaction products: 1) the cleaved 5' arm of the hairpin called the fourth oligonucleotide, and 2) the cleaved hairpin structure which now lacks the 5' arm and is smaller in size than the uncleaved hairpin. This cleaved first hairpin may be used as a detection molecule to indicate that cleavage directed by the trigger or third oligonucleotide occurred. Thus, this indicates that the first two oligonucleotides found and annealed to the target sequence thereby indicating the presence of the target sequence in the sample.

[0228] The detection products are amplified by having the fourth oligonucleotide anneal to a second hairpin structure. This hairpin structure has a 5' single-stranded arm and a 3' single-stranded arm. The fourth oligonucleotide generated by cleavage of the first hairpin structure anneals to the 3' arm of the second hairpin structure thereby creating a third cleavage structure recognized by the 5' nuclease. The cleavage of this second hairpin structure also generates two reaction products: 1) the cleaved 5' arm of the hairpin called the fifth oligonucleotide which is similar or identical in sequence to the third nucleotide, and 2) the cleaved second hairpin structure which now lacks the 5' arm and is smaller in size than the uncleaved hairpin. This cleaved second hairpin may be as a detection molecule and amplifies the signal generated by the cleavage of the first hairpin structure. Simultaneously with the annealing of the fourth oligonucleotide, the third oligonucleotide is dissociated from the cleaved first hairpin molecule so that it is free to anneal to a new copy of the first hairpin structure. The disassociation of the oligonucleotides from the hairpin structures may be accomplished by heating or other means suitable to disrupt base-pairing interactions.

[0229] Further amplification of the detection signal is achieved by annealing the fifth oligonucleotide (similar or identical in sequence to the third oligonucleotide) to another molecule of the first hairpin structure. Cleavage is then performed and the oligonucleotide that is liberated then is annealed to another molecule of the second hairpin structure. Successive rounds of annealing and cleavage of the first and second hairpin structures, provided in excess, are performed to generate a sufficient amount of cleaved hairpin products to be detected. The temperature of the detection reaction is

cycled just below and just above the annealing temperature for the oligonucleotides used to direct cleavage of the hairpin structures, generally about 55° C. to 70° C. The number of cleavages will double in each cycle until the amount of hairpin structures remaining is below the K_m for the hairpin structures. This point is reached when the hairpin structures are substantially used up. When the detection reaction is to be used in a quantitative manner, the cycling reactions are stopped before the accumulation of the cleaved hairpin detection products reach a plateau.

[0230] Detection of the cleaved hairpin structures may be achieved in several ways. In one embodiment detection is achieved by separation on agarose or polyacrylamide gels followed by staining with ethidium bromide. In another embodiment, detection is achieved by separation of the cleaved and uncleaved hairpin structures on a gel followed by autoradiography when the hairpin structures are first labelled with a radioactive probe and separation on chromatography columns using HPLC or FPLC followed by detection of the differently sized fragments by absorption at OD₂₆₀. Other means of detection include detection of changes in fluorescence polarization when the single-stranded 5' arm is released by cleavage, the increase in fluorescence of an intercalating fluorescent indicator as the amount of primers annealed to 3' arms of the hairpin structures increases. The formation of increasing amounts of duplex DNA (between the primer and the 3' arm of the hairpin) occurs if successive rounds of cleavage occur.

[0231] The hairpin structures may be attached to a solid support, such as an agarose, styrene or magnetic bead, via the 3' end of the hairpin. A spacer molecule may be placed between the 3' end of the hairpin and the bead, if so desired. The advantage of attaching the hairpin structures to a solid support is that this prevents the hybridization of the two hairpin structures to one another over regions which are complementary. If the hairpin structures anneal to one another, this would reduce the amount of hairpins available for hybridization to the primers released during the cleavage reactions. If the hairpin structures are attached to a solid support, then additional methods of detection of the products of the cleavage reaction may be employed. These methods include, but are not limited to, the measurement of the released single-stranded 5' arm when the 5' arm contains a label at the 5' terminus. This label may be radioactive, fluorescent, biotinylated, etc. If the hairpin structure is not cleaved, the S' label will remain attached to the solid support. If cleavage occurs, the 5' label will be released from the solid support.

[0232] The 3' end of the hairpin molecule may be blocked through the use of dideoxynucleotides. A 3' terminus containing a dideoxynucleotide is unavailable to participate in reactions with certain DNA modifying enzymes, such as terminal transferase. Cleavage of the hairpin having a 3' terminal dideoxynucleotide generates a new, unblocked 3' terminus at the site of cleavage. This new 3' end has a free hydroxyl group which can interact with terminal transferase thus providing another means of detecting the cleavage products.

[0233] The hairpin structures are designed so that their self-complementary regions are very short (generally in the range of 3-8 base pairs). Thus, the hairpin structures are not stable at the high temperatures at which this reaction is

performed (generally in the range of 50-75° C.) unless the hairpin is stabilized by the presence of the annealed oligonucleotide on the 3' arm of the hairpin. This instability prevents the polymerase from cleaving the hairpin structure in the absence of an associated primer thereby preventing false positive results due to non-oligonucleotide directed cleavage.

[0234] As discussed above, the use of the 5' nucleases of the invention which have reduced polymerization activity is advantageous in this method of detecting specific nucleic acid sequences. Significant amounts of polymerization during the cleavage reaction would cause shifting of the site of cleavage in unpredictable ways resulting in the production of a series of cleaved hairpin structures of various sizes rather than a single easily quantifiable product. Additionally, the primers used in one round of cleavage could, if elongated, become unusable for the next cycle, by either forming an incorrect structure or by being too long to melt off under moderate temperature cycling conditions. In a pristine system (i.e., lacking the presence of dNTPs), one could use the unmodified polymerase, but the presence of nucleotides (dNTPs) can decrease the per cycle efficiency enough to give a false negative result. When a crude extract (genomic DNA preparations, crude cell lysates, etc.) is employed or where a sample of DNA from a PCR reaction, or any other sample that might be contaminated with dNTPs, the 5' nucleases of the present invention that were derived from thermostable polymerases are particularly useful.

[0235] II. Generation of 5' Nucleases from Thermostable DNA Polymerases

[0236] The genes encoding Type A DNA polymerases share about 85% homology to each other on the DNA sequence level. Preferred examples of thermostable polymerases include those isolated from *Thermus aquaticus*, *Thermus flavus*, and *Thermus thermophilus*. However, other thermostable Type A polymerases which have 5' nuclease activity are also suitable. FIGS. 2 and 3 compare the nucleotide and amino acid sequences of the three above mentioned polymerases. In FIGS. 2 and 3, the consensus or majority sequence derived from a comparison of the nucleotide (FIG. 2) or amino acid (FIG. 3) sequence of the three thermostable DNA polymerases is shown on the top line. A dot appears in the sequences of each of these three polymerases whenever an amino acid residue in a given sequence is identical to that contained in the consensus amino acid sequence. Dashes are used to introduce gaps in order to maximize alignment between the displayed sequences. When no consensus nucleotide or amino acid is present at a given position, an "X" is placed in the consensus sequence. SEQ ID NOS:1-3 display the nucleotide sequences and SEQ ID NOS:4-6 display the amino acid sequences of the three wild-type polymerases. SEQ ID NO:1 corresponds to the nucleic acid sequence of the wild type *Thermus aquaticus* DNA polymerase gene isolated from the YT-1 strain [Lawyer et al., *J. Biol. Chem.* 264:6427 (1989)]. SEQ ID NO:2 corresponds to the nucleic acid sequence of the wild type *Thermus flavus* DNA polymerase gene [Akhmetzjanov and Vakhitov, *Nucl. Acids Res.* 20:5839 (1992)]. SEQ ID NO:3 corresponds to the nucleic acid sequence of the wild type *Thermus thermophilus* DNA polymerase gene [Gelfand et al., WO 91/09950 (1991)]. SEQ ID NOS:7-8

depict the consensus nucleotide and amino acid sequences, respectively for the above three DNAPs (also shown on the top row in FIGS. 2 and 3).

[0237] The 5' nucleases of the invention derived from thermostable polymerases have reduced synthetic ability, but retain substantially the same 5' exonuclease activity as the native DNA polymerase. The term "substantially the same 5' nuclease activity" as used herein means that the 5' nuclease activity of the modified enzyme retains the ability to function as a structure-dependent single-stranded endonuclease but not necessarily at the same rate of cleavage as compared to the unmodified enzyme. Type A DNA polymerases may also be modified so as to produce an enzyme which has increases 5' nuclease activity while having a reduced level of synthetic activity. Modified enzymes having reduced synthetic activity and increased 5' nuclease activity are also envisioned by the present invention.

[0238] By the term "reduced synthetic activity" as used herein it is meant that the modified enzyme has less than the level of synthetic activity found in the unmodified or "native" enzyme. The modified enzyme may have no synthetic activity remaining or may have that level of synthetic activity that will not interfere with the use of the modified enzyme in the detection assay described below. The 5' nucleases of the present invention are advantageous in situations where the cleavage activity of the polymerase is desired, but the synthetic ability is not (such as in the detection assay of the invention).

[0239] As noted above, it is not intended that the invention be limited by the nature of the alteration necessary to render the polymerase synthesis deficient. The present invention contemplates a variety of methods, including but not limited to: 1) proteolysis; 2) recombinant constructs (including mutants); and 3) physical and/or chemical modification and/or inhibition.

[0240] 1. Proteolysis

[0241] Thermostable DNA polymerases having a reduced level of synthetic activity are produced by physically cleaving the unmodified enzyme with proteolytic enzymes to produce fragments of the enzyme that are deficient in synthetic activity but retain 5' nuclease activity. Following proteolytic digestion, the resulting fragments are separated by standard chromatographic techniques and assayed for the ability to synthesize DNA and to act as a 5' nuclease. The assays to determine synthetic activity and 5' nuclease activity are described below.

[0242] 2. Recombinant Constructs

[0243] The examples below describe a preferred method for creating a construct encoding a 5' nuclease derived from a thermostable DNA polymerase. As the Type A DNA polymerases are similar in DNA sequence, the cloning strategies employed for the *Thermus aquaticus* and *flavus* polymerases are applicable to other thermostable Type A polymerases. In general, a thermostable DNA polymerase is cloned by isolating genomic DNA using molecular biological methods from a bacteria containing a thermostable Type A DNA polymerase. This genomic DNA is exposed to primers which are capable of amplifying the polymerase gene by PCR.

[0244] This amplified polymerase sequence is then subjected to standard deletion processes to delete the poly-

merase portion of the gene. Suitable deletion processes are described below in the examples.

[0245] The example below discusses the strategy used to determine which portions of the DNAP_{Taq} polymerase domain could be removed without eliminating the 5' nuclease activity. Deletion of amino acids from the protein can be done either by deletion of the encoding genetic material, or by introduction of a translational stop codon by mutation or frame shift. In addition, proteolytic treatment of the protein molecule can be performed to remove segments of the protein.

[0246] In the examples below, specific alterations of the *Taq* gene were: a deletion between nucleotides 1601 and 2502 (the end of the coding region), a 4 nucleotide insertion at position 2043, and deletions between nucleotides 1614 and 1848 and between nucleotides 875 and 1778 (numbering is as in SEQ ID NO:1). These modified sequences are described below in the examples and at SEQ ID NOS:9-12.

[0247] Those skilled in the art understand that single base pair changes can be innocuous in terms of enzyme structure and function. Similarly, small additions and deletions can be present without substantially changing the exonuclease or polymerase function of these enzymes.

[0248] Other deletions are also suitable to create the 5' nucleases of the present invention. It is preferable that the deletion decrease the polymerase activity of the 5' nucleases to a level at which synthetic activity will not interfere with the use of the 5' nuclease in the detection assay of the invention. Most preferably, the synthetic ability is absent. Modified polymerases are tested for the presence of synthetic and 5' nuclease activity as in assays described below. Thoughtful consideration of these assays allows for the screening of candidate enzymes whose structure is heretofore as yet unknown. In other words, construct "X" can be evaluated according to the protocol described below to determine whether it is a member of the genus of 5' nucleases of the present invention as defined functionally, rather than structurally.

[0249] In the example below, the PCR product of the amplified *Thermus aquaticus* genomic DNA did not have the identical nucleotide structure of the native genomic DNA and did not have the same synthetic ability of the original clone. Base pair changes which result due to the infidelity of DNAP_{Taq} during PCR amplification of a polymerase gene are also a method by which the synthetic ability of a polymerase gene may be inactivated. The examples below and FIGS. 4A and 5A indicate regions in the native *Thermus aquaticus* and *flavus* DNA polymerases likely to be important for synthetic ability. There are other base pair changes and substitutions that will likely also inactivate the polymerase.

[0250] It is not necessary, however, that one start out the process of producing a 5' nuclease from a DNA polymerase with such a mutated amplified product. This is the method by which the examples below were performed to generate the synthesis-deficient DNAP_{Taq} mutants, but it is understood by those skilled in the art that a wild-type DNA polymerase sequence may be used as the starting material for the introduction of deletions, insertion and substitutions to produce a 5' nuclease. For example, to generate the synthesis-deficient DNAP_{Tfl} mutant, the primers listed in SEQ ID

NOS:13-14 were used to amplify the wild type DNA polymerase gene from *Thermus flavus* strain AT-62. The amplified polymerase gene was then subjected to restriction enzyme digestion to delete a large portion of the domain encoding the synthetic activity.

[0251] The present invention contemplates that the nucleic acid construct of the present invention be capable of expression in a suitable host. Those in the art know methods for attaching various promoters and 3' sequences to a gene structure to achieve efficient expression. The examples below disclose two suitable vectors and six suitable vector constructs. Of course, there are other promoter/vector combinations that would be suitable. It is not necessary that a host organism be used for the expression of the nucleic acid constructs of the invention. For example, expression of the protein encoded by a nucleic acid construct may be achieved through the use of a cell-free in vitro transcription/translation system. An example of such a cell-free system is the commercially available TnT™ Coupled Reticulocyte Lysate System (Promega Corporation, Madison, Wis.).

[0252] Once a suitable nucleic acid construct has been made, the 5' nuclease may be produced from the construct. The examples below and standard molecular biological teachings enable one to manipulate the construct by different suitable methods.

[0253] Once the 5' nuclease has been expressed, the polymerase is tested for both synthetic and nuclease activity as described below.

[0254] 3. Physical and/or Chemical Modification and/or Inhibition

[0255] The synthetic activity of a thermostable DNA polymerase may be reduced by chemical and/or physical means. In one embodiment, the cleavage reaction catalyzed by the 5' nuclease activity of the polymerase is run under conditions which preferentially inhibit the synthetic activity of the polymerase. The level of synthetic activity need only be reduced to that level of activity which does not interfere with cleavage reactions requiring no significant synthetic activity.

[0256] As shown in the examples below, concentrations of Mg^{++} greater than 5 mM inhibit the polymerization activity of the native DNAPtaq. The ability of the 5' nuclease to function under conditions where synthetic activity is inhibited is tested by running the assays for synthetic and 5' nuclease activity, described below, in the presence of a range of Mg^{++} concentrations (5 to 10 mM). The effect of a given concentration of Mg^{++} is determined by quantitation of the amount of synthesis and cleavage in the test reaction as compared to the standard reaction for each assay.

[0257] The inhibitory effect of other ions, polyamines, denaturants, such as urea, formamide, dimethylsulfoxide, glycerol and non-ionic detergents (Triton X-100 and Tween-20), nucleic acid binding chemicals such as, actinomycin D, ethidium bromide and psoralens, are tested by their addition to the standard reaction buffers for the synthesis and 5' nuclease assays. Those compounds having a preferential inhibitory effect on the synthetic activity of a thermostable polymerase are then used to create reaction conditions under which 5' nuclease activity (cleavage) is retained while synthetic activity is reduced or eliminated.

[0258] Physical means may be used to preferentially inhibit the synthetic activity of a polymerase. For example,

the synthetic activity of thermostable polymerases is destroyed by exposure of the polymerase to extreme heat (typically 96 to 100° C.) for extended periods of time (greater than or equal to 20 minutes). While these are minor differences with respect to the specific heat tolerance for each of the enzymes, these are readily determined. Polymerases are treated with heat for various periods of time and the effect of the heat treatment upon the synthetic and 5' nuclease activities is determined.

[0259] III. Detection of Specific Nucleic Acid Sequences Using 5' Nucleases in an Invader-Directed Cleavage Assay

[0260] The present invention provides means for forming a nucleic acid cleavage structure which is dependent upon the presence of a target nucleic acid and cleaving the nucleic acid cleavage structure so as to release distinctive cleavage products. 5' nuclease activity is used to cleave the target-dependent cleavage structure and the resulting cleavage products are indicative of the presence of specific target nucleic acid sequences in the sample.

[0261] The present invention further provides assays in which the target nucleic acid is reused or recycled during multiple rounds of hybridization with oligonucleotide probes and cleavage without the need to use temperature cycling (i.e., for periodic denaturation of target nucleic acid strands) or nucleic acid synthesis (i.e., for the displacement of target nucleic acid strands). Through the interaction of the cleavage means (e.g., a 5' nuclease) an upstream oligonucleotide, the cleavage means can be made to cleave a downstream oligonucleotide at an internal site in such a way that the resulting fragments of the downstream oligonucleotide dissociate from the target nucleic acid, thereby making that region of the target nucleic acid available for hybridization to another, uncleaved copy of the downstream oligonucleotide.

[0262] As illustrated in FIG. 29, the methods of the present invention employ at least a pair of oligonucleotides that interact with a target nucleic acid to form a cleavage structure for a structure-specific nuclease. More specifically, the cleavage structure comprises i) a target nucleic acid that may be either single-stranded or double-stranded (when a double-stranded target nucleic acid is employed, it may be rendered single stranded, e.g., by heating); ii) a first oligonucleotide, termed the "probe," which defines a first region of the target nucleic acid sequence by being the complement of that region (regions X and Z of the target as shown in FIG. 29); iii) a second oligonucleotide, termed the "invader," the 5' part of which defines a second region of the same target nucleic acid sequence (regions Y and X in FIG. 29), adjacent to and downstream of the first target region (regions X and Z), and the second part of which overlaps into the region defined by the first oligonucleotide (region X depicts the region of overlap). The resulting structure is diagrammed in FIG. 29.

[0263] While not limiting the invention or the instant discussion to any particular mechanism of action, the diagram in FIG. 29 represents the effect on the site of cleavage caused by this type of arrangement of a pair of oligonucleotides. The design of such a pair of oligonucleotides is described below in detail. In FIG. 29, the 3' ends of the nucleic acids (i.e., the target and the oligonucleotides) are indicated by the use of the arrowheads on the ends of the lines depicting the strands of the nucleic acids (and where

space permits, these ends are also labelled "3"). It is readily appreciated that the two oligonucleotides (the invader and the probe) are arranged in a parallel orientation relative to one another, while the target nucleic acid strand is arranged in an anti-parallel orientation relative to the two oligonucleotides. Further it is clear that the invader oligonucleotide is located upstream of the probe oligonucleotide and that with respect to the target nucleic acid strand, region Z is upstream of region X and region X is upstream of region Y (that is region Y is downstream of region X and region X is downstream of region Z). Regions of complementarity between the opposing strands are indicated by the short vertical lines. While not intended to indicate the precise location of the site(s) of cleavage, the area to which the site of cleavage within the probe oligonucleotide is shifted by the presence of the invader oligonucleotide is indicated by the solid vertical arrowhead. An alternative representation of the target/invader/probe cleavage structure is shown in **FIG. 32c**. Neither diagram (i.e., **FIG. 29** or **FIG. 32c**) is intended to represent the actual mechanism of action or physical arrangement of the cleavage structure and further it is not intended that the method of the present invention be limited to any particular mechanism of action.

[0264] It can be considered that the binding of these oligonucleotides divides the target nucleic acid into three distinct regions: one region that has complementarity to only the probe (shown as "Z"); one region that has complementarity only to the invader (shown as "Y"); and one region that has complementarity to both oligonucleotides (shown as "X").

[0265] Design of these oligonucleotides (i.e., the invader and the probe) is accomplished using practices which are standard in the art. For example, sequences that have self complementarity, such that the resulting oligonucleotides would either fold upon themselves, or hybridize to each other at the expense of binding to the target nucleic acid, are generally avoided.

[0266] One consideration in choosing a length for these oligonucleotides is the complexity of the sample containing the target nucleic acid. For example, the human genome is approximately 3×10^9 basepairs in length. Any 10 nucleotide sequence will appear with a frequency of 1:4¹⁰, or 1:1048, 576 in a random string of nucleotides, which would be approximately 2,861 times in 3 billion basepairs. Clearly an oligonucleotide of this length would have a poor chance of binding uniquely to a 10 nucleotide region within a target having a sequence the size of the human genome. If the target sequence were within a 3 kb plasmid, however, such an oligonucleotide might have a very reasonable chance of binding uniquely. By this same calculation it can be seen that an oligonucleotide of 16 nucleotides (i.e., a 16-mer) is the minimum length of a sequence which is mathematically likely to appear once in 3×10^9 basepairs.

[0267] A second consideration in choosing oligonucleotide length is the temperature range in which the oligonucleotides will be expected to function. A 16-mer of average base content (50% G-C basepairs) will have a calculated T_m (the temperature at which 50% of the sequence is dissociated) of about 41° C., depending on, among other things, the concentration of the oligonucleotide and its target, the salt content of the reaction and the precise order of the nucleotides. As a practical matter, longer

oligonucleotides are usually chosen to enhance the specificity of hybridization. Oligonucleotides 20 to 25 nucleotides in length are often used as they are highly likely to be specific if used in reactions conducted at temperatures which are near their T_m s (within about 5° of the T_m). In addition, with calculated T_m s in the range of 50° to 70° C., such oligonucleotides (i.e., 20 to 25-mers) are appropriately used in reactions catalyzed by thermostable enzymes, which often display optimal activity near this temperature range.

[0268] The maximum length of the oligonucleotide chosen is also based on the desired specificity. One must avoid choosing sequences that are so long that they are either at a high risk of binding stably to partial complements, or that they cannot easily be dislodged when desired (e.g., failure to disassociate from the target once cleavage has occurred).

[0269] The first step of design and selection of the oligonucleotides for the invader-directed cleavage is in accordance with these sample general principles. Considered as sequence-specific probes individually, each oligonucleotide may be selected according to the guidelines listed above. That is to say, each oligonucleotide will generally be long enough to be reasonably expected to hybridize only to the intended target sequence within a complex sample, usually in the 20 to 40 nucleotide range. Alternatively, because the invader-directed cleavage assay depends upon the concerted action of these oligonucleotides, the composite length of the 2 oligonucleotides which span/bind to the X, Y, Z regions may be selected to fall within this range, with each of the individual oligonucleotides being in approximately the 13 to 17 nucleotide range. Such a design might be employed if a non-thermostable cleavage means were employed in the reaction, requiring the reactions to be conducted at a lower temperature than that used when thermostable cleavage means are employed. In some instances, it may be desirable to have these oligonucleotides bind multiple times within a target nucleic acid (e.g., which bind to multiple variants or multiple similar sequences within a target). It is not intended that the method of the present invention be limited to any particular size of the probe or invader oligonucleotide.

[0270] The second step of designing an oligonucleotide pair for this assay is to choose the degree to which the upstream "invader" oligonucleotide sequence will overlap into the downstream "probe" oligonucleotide sequence, and consequently, the sizes into which the probe will be cleaved. A key feature of this assay is that the probe oligonucleotide can be made to "turn over," that is to say cleaved probe can be made to depart to allow the binding and cleavage of other copies of the probe molecule, without the requirements of thermal denaturation or displacement by polymerization. While in one embodiment of this assay probe turnover may be facilitated by an exonucleolytic digestion by the cleavage agent, it is central to the present invention that the turnover does not require this exonucleolytic activity.

[0271] Choosing the Amount of Overlap (Length of the X Region)

[0272] One way of accomplishing such turnover can be envisioned by considering the diagram in **FIG. 29**. It can be seen that the T_m of each oligonucleotide will be a function of the full length of that oligonucleotide: i.e., the T_m of the invader= $T_m(Y+X)$, and the T_m of the probe= $T_m(X+Y)$ for the probe. When the probe is cleaved the X region is released, leaving the Z section. If the T_m of Z is less than the

reaction temperature, and the reaction temperature is less than the $T_{m(X+Z)}$, then cleavage of the probe will lead to the departure of Z, thus allowing a new (X+Z) to hybridize. It can be seen from this example that the X region must be sufficiently long that the release of X will drop the T_m of the remaining probe section below the reaction temperature: a G-C rich X section may be much shorter than an A-T rich X section and still accomplish this stability shift.

[0273] Designing Oligonucleotides which Interact with the Y and Z Regions

[0274] If the binding of the invader oligonucleotide to the target is more stable than the binding of the probe (e.g., if it is long, or is rich in G-C basepairs in the Y region), then the copy of X associated with the invader may be favored in the competition for binding to the X region of the target, and the probe may consequently hybridize inefficiently, and the assay may give low signal. Alternatively, if the probe binding is particularly strong in the Z region, the invader will still cause internal cleavage, because this is mediated by the enzyme, but portion of the probe oligonucleotide bound to the Z region may not dissociate at the reaction temperature, turnover may be poor, and the assay may again give low signal.

[0275] It is clearly beneficial for the portions of the oligonucleotide which interact with the Y and Z regions to be similar in stability, i.e., they must have similar melting temperatures. This is not to say that these regions must be the same length. As noted above, in addition to length, the melting temperature will also be affected by the base content and the specific sequence of those bases. The specific stability designed into the invader and probe sequences will depend on the temperature at which one desires to perform the reaction.

[0276] This discussion is intended to illustrate that (within the basic guidelines for oligonucleotide specificity discussed above) it is the balance achieved between the stabilities of the probe and invader sequences and their X and Y component sequences, rather than the absolute values of these stabilities, that is the chief consideration in the selection of the probe and invader sequences.

[0277] Design of the Reaction Conditions

[0278] Target nucleic acids that may be analyzed using the methods of the present invention which employ a 5' nuclease as the cleavage means include many types of both RNA and DNA. Such nucleic acids may be obtained using standard molecular biological techniques. For example, nucleic acids (RNA or DNA) may be isolated from a tissue sample (e.g., a biopsy specimen), tissue culture cells, samples containing bacteria and/or viruses (including cultures of bacteria and/or viruses), etc. The target nucleic acid may also be transcribed in vitro from a DNA template or may be chemically synthesized or generated in a PCR. Furthermore, nucleic acids may be isolated from an organism, either as genomic material or as a plasmid or similar extrachromosomal DNA, or they may be a fragment of such material generated by treatment with a restriction endonuclease or other cleavage agents or it may be synthetic.

[0279] Assembly of the target, probe, and invader nucleic acids into the cleavage reaction of the present invention uses principles commonly used in the design of oligonucleotide base enzymatic assays, such as dideoxynucleotide sequenc-

ing and polymerase chain reaction (PCR). As is done in these assays, the oligonucleotides are provided in sufficient excess that the rate of hybridization to the target nucleic acid is very rapid. These assays are commonly performed with 50 fmoles to 2 pmoles of each oligonucleotide per μ l of reaction mixture. In the Examples described herein, amounts of oligonucleotides ranging from 250 fmoles to 5 pmoles per μ l of reaction volume were used. These values were chosen for the purpose of ease in demonstration and are not intended to limit the performance of the present invention to these concentrations. Other (e.g., lower) oligonucleotide concentrations commonly used in other molecular biological reactions are also contemplated.

[0280] It is desirable that an invader oligonucleotide be immediately available to direct the cleavage of each probe oligonucleotide that hybridizes to a target nucleic acid. For this reason, in the Examples described herein, the invader oligonucleotide is provided in excess over the probe oligonucleotide; often this excess is 10-fold. While this is an effective ratio, it is not intended that the practice of the present invention be limited to any particular ratio of invader-to-probe (a ratio of 2- to 100-fold is contemplated).

[0281] Buffer conditions must be chosen that will be compatible with both the oligonucleotide/target hybridization and with the activity of the cleavage agent. The optimal buffer conditions for nucleic acid modification enzymes, and particularly DNA modification enzymes, generally included enough mono- and di-valent salts to allow association of nucleic acid strands by base-pairing. If the method of the present invention is performed using an enzymatic cleavage agent other than those specifically described here, the reactions may generally be performed in any such buffer reported to be optimal for the nuclease function of the cleavage agent. In general, to test the utility of any cleavage agent in this method, test reactions are performed wherein the cleavage agent of interest is tested in the MOPS/MnCl₂/KCl buffer or Mg-containing buffers described herein and in whatever buffer has been reported to be suitable for use with that agent, in a manufacturer's data sheet, a journal article, or in personal communication.

[0282] The products of the invader-directed cleavage reaction are fragments generated by structure-specific cleavage of the input oligonucleotides. The resulting cleaved and/or uncleaved oligonucleotides may be analyzed and resolved by a number of methods including electrophoresis (on a variety of supports including acrylamide or agarose gels, paper, etc.), chromatography, fluorescence polarization, mass spectrometry and chip hybridization. The invention is illustrated using electrophoretic separation for the analysis of the products of the cleavage reactions. However, it is noted that the resolution of the cleavage products is not limited to electrophoresis. Electrophoresis is chosen to illustrate the method of the invention because electrophoresis is widely practiced in the art and is easily accessible to the average practitioner.

[0283] The probe and invader oligonucleotides may contain a label to aid in their detection following the cleavage reaction. The label may be a radioisotope (e.g., a ³²P or ³S-labelled nucleotide) placed at either the 5' or 3' end of the oligonucleotide or alternatively, the label may be distributed throughout the oligonucleotide (i.e., a uniformly labelled oligonucleotide). The label may be a nonisotopic detectable

moiety, such as a fluorophore, which can be detected directly, or a reactive group which permits specific recognition by a secondary agent. For example, biotinylated oligonucleotides may be detected by probing with a streptavidin molecule which is coupled to an indicator (e.g., alkaline phosphatase or a fluorophore) or a hapten such as dioxigenin may be detected using a specific antibody coupled to a similar indicator.

[0284] Optimization of Reaction Conditions

[0285] The invader-directed cleavage reaction is useful to detect the presence of specific nucleic acids. In addition to the considerations listed above for the selection and design of the invader and probe oligonucleotides, the conditions under which the reaction is to be performed may be optimized for detection of a specific target sequence.

[0286] One objective in optimizing the invader-directed cleavage assay is to allow specific detection of the fewest copies of a target nucleic acid. To achieve this end, it is desirable that the combined elements of the reaction interact with the maximum efficiency, so that the rate of the reaction (e.g., the number of cleavage events per minute) is maximized. Elements contributing to the overall efficiency of the reaction include the rate of hybridization, the rate of cleavage, and the efficiency of the release of the cleaved probe.

[0287] The rate of cleavage will be a function of the cleavage means chosen, and may be made optimal according to the manufacturer's instructions when using commercial preparations of enzymes or as described in the examples herein. The other elements (rate of hybridization, efficiency of release) depend upon the execution of the reaction, and optimization of these elements is discussed below.

[0288] Three elements of the cleavage reaction that significantly affect the rate of nucleic acid hybridization are the concentration of the nucleic acids, the temperature at which the cleavage reaction is performed and the concentration of salts and/or other charge-shielding ions in the reaction solution.

[0289] The concentrations at which oligonucleotide probes are used in assays of this type are well known in the art, and are discussed above. One example of a common approach to optimizing an oligonucleotide concentration is to choose a starting amount of oligonucleotide for pilot tests; 0.01 to 2 μ M is a concentration range used in many oligonucleotide-based assays. When initial cleavage reactions are performed, the following questions may be asked of the data: Is the reaction performed in the absence of the target nucleic acid substantially free of the cleavage product?; Is the site of cleavage specifically shifted in accordance with the design of the invader oligonucleotide?; Is the specific cleavage product easily detected in the presence of the uncleaved probe (or is the amount of uncut material overwhelming the chosen visualization method)?

[0290] A negative answer to any of these questions would suggest that the probe concentration is too high, and that a set of reactions using serial dilutions of the probe should be performed until the appropriate amount is identified. Once identified for a given target nucleic acid in a given sample type (e.g., purified genomic DNA, body fluid extract, lysed bacterial extract), it should not need to be re-optimized. The sample type is important because the complexity of the material present may influence the probe optimum.

[0291] Conversely, if the chosen initial probe concentration is too low, the reaction may be slow, due to inefficient hybridization. Tests with increasing quantities of the probe will identify the point at which the concentration exceeds the optimum. Since the hybridization will be facilitated by excess of probe, it is desirable, but not required, that the reaction be performed using probe concentrations just below this point.

[0292] The concentration of invader oligonucleotide can be chosen based on the design considerations discussed above. In a preferred embodiment, the invader oligonucleotide is in excess of the probe oligonucleotide. In a particularly preferred embodiment, the invader is approximately 10-fold more abundant than the probe.

[0293] Temperature is also an important factor in the hybridization of oligonucleotides. The range of temperature tested will depend in large part, on the design of the oligonucleotides, as discussed above. In a preferred embodiment, the reactions are performed at temperatures slightly below the T_m of the least stable oligonucleotide in the reaction. Melting temperatures for the oligonucleotides and for their component regions (X, Y and Z, **FIG. 29**), can be estimated through the use of computer software or, for a more rough approximation, by assigning the value of 2° C. per A-T basepair, and 4° C. per G-C basepair, and taking the sum across an expanse of nucleic acid. The latter method may be used for oligonucleotides of approximately 10-30 nucleotides in length. Because even computer prediction of the T_m of a nucleic acid is only an approximation, the reaction temperatures chosen for initial tests should bracket the calculated T_m . While optimizations are not limited to this, 5° C. increments are convenient test intervals in these optimization assays.

[0294] When temperatures are tested, the results can be analyzed for specificity (the first two of the questions listed above) in the same way as for the oligonucleotide concentration determinations. Non-specific cleavage (i.e., cleavage of the probe at many or all positions along its length) would indicate non-specific interactions between the probe and the sample material, and would suggest that a higher temperature should be employed. Conversely, little or no cleavage would suggest that even the intended hybridization is being prevented, and would suggest the use of lower temperatures. By testing several temperatures, it is possible to identify an approximate temperature optimum, at which the rate of specific cleavage of the probe is highest. If the oligonucleotides have been designed as described above, the T_m of the Z-region of the probe oligonucleotide should be below this temperature, so that turnover is assured.

[0295] A third determinant of hybridization efficiency is the salt concentration of the reaction. In large part, the choice of solution conditions will depend on the requirements of the cleavage agent, and for reagents obtained commercially, the manufacturer's instructions are a resource for this information. When developing an assay utilizing any particular cleavage agent, the oligonucleotide and temperature optimizations described above should be performed in the buffer conditions best suited to that cleavage agent.

[0296] A "no enzyme" control allows the assessment of the stability of the labeled oligonucleotides under particular reaction conditions, or in the presence of the sample to be tested (i.e., in assessing the sample for contaminating

nucleases). In this manner, the substrate and oligonucleotides are placed in a tube containing all reaction components, except the enzyme and treated the same as the enzyme-containing reactions. Other controls may also be included. For example, a reaction with all of the components except the target nucleic acid will serve to confirm the dependence of the cleavage on the presence of the target sequence.

[0297] Probing for Multiple Alleles

[0298] The invader-directed cleavage reaction is also useful in the detection and quantification of individual variants or alleles in a mixed sample population. By way of example, such a need exists in the analysis of tumor material for mutations in genes associated with cancers. Biopsy material from a tumor can have a significant complement of normal cells, so it is desirable to detect mutations even when present in fewer than 5% of the copies of the target nucleic acid in a sample. In this case, it is also desirable to measure what fraction of the population carries the mutation. Similar analyses may also be done to examine allelic variation in other gene systems, and it is not intended that the method of the present invention by limited to the analysis of tumors.

[0299] As demonstrated below, reactions can be performed under conditions that prevent the cleavage of probes bearing even a single-nucleotide difference mismatch within the region of the target nucleic acid termed "Z" in FIG. 29, but that permit cleavage of a similar probe that is completely complementary to the target in this region. Thus, the assay may be used to quantitate individual variants or alleles within a mixed sample.

[0300] The use of multiple, differently labelled probes in such an assay is also contemplated. To assess the representation of different variants or alleles in a sample, one would provide a mixture of probes such that each allele or variant to be detected would have a specific probe (i.e., perfectly matched to the Z region of the target sequence) with a unique label (e.g., no two variant probes with the same label would be used in a single reaction). These probes would be characterized in advance to ensure that under a single set of reaction conditions, they could be made to give the same rate of signal accumulation when mixed with their respective target nucleic acids. Assembly of a cleavage reaction comprising the mixed probe set, a corresponding invader oligonucleotide, the target nucleic acid sample, and the appropriate cleavage agent, along with performance of the cleavage reaction under conditions such that only the matched probes would cleave, would allow independent quantification of each of the species present, and would therefore indicate their relative representation in the target sample.

[0301] IV. A Comparison of Invasive Cleavage and Primer-Directed Cleavage

[0302] As discussed herein, the terms "invasive" or "invader-directed" cleavage specifically denote the use of a first, upstream oligonucleotide, as defined below, to cause specific cleavage at a site within a second, downstream sequence. To effect such a direction of cleavage to a region within a duplex, it is required that the first and second oligonucleotides overlap in sequence. That is to say, a portion of the upstream oligonucleotide, termed the "invader", has significant homology to a portion of the

downstream "probe" oligonucleotide, so that these regions would tend to basepair with the same complementary region of the target nucleic acid to be detected. While not limiting the present invention to any particular mechanism, the overlapping regions would be expected to alternate in their occupation of the shared hybridization site. When the probe oligonucleotide fully anneals to the target nucleic acid, and thus forces the 3' region of the invader to remain unpaired, the structure so formed is not a substrate for the 5' nucleases of the present invention. By contrast, when the inverse is true, the structure so formed is substrate for these enzymes, allowing cleavage and release of the portion of the probe oligonucleotide that is displaced by the invader oligonucleotide. The shifting of the cleavage site to a region the probe oligonucleotide that would otherwise be basepaired to the target sequence is one hallmark of the invasive cleavage assay (i.e., the invader-directed cleavage assay) of the present invention.

[0303] It is beneficial at this point to contrast the invasive cleavage as described above with two other forms of probe cleavage that may lead to internal cleavage of a probe oligonucleotide, but which do not comprise invasive cleavage. In the first case, a hybridized probe may be subject to duplex-dependent 5' to 3' exonuclease "nibbling," such that the oligonucleotide is shortened from the 5' end until it cannot remain bound to the target (see, e.g., Examples 6-8 and FIGS. 26-28). The site at which such nibbling stops can appear to be discrete, and, depending on the difference between the melting temperature of the full-length probe and the temperature of the reaction, this stopping point may be 1 or several nucleotides into the probe oligonucleotide sequence. Such "nibbling" is often indicated by the presence of a "ladder" of longer products ascending size up to that of the full length of the probe, but this is not always the case. While any one of the products of such a nibbling reaction may be made to match in size and cleavage site the products of an invasive cleavage reaction, the creation of these nibbling products would be highly dependent on the temperature of the reaction and the nature of the cleavage agent, but would be independent of the action of an upstream oligonucleotide, and thus could not be construed to involve invasive cleavage.

[0304] A second cleavage structure that may be considered is one in which a probe oligonucleotide has several regions of complementarity with the target nucleic acid, interspersed with one or more regions or nucleotides of noncomplementarity. These noncomplementary regions may be thought of as "bubbles" within the nucleic acid duplex. As temperature is elevated, the regions of complementarity can be expected to "melt" in the order of their stability, lowest to highest. When a region of lower stability is near the end of a segment of duplex, and the next region of complementarity along the strand has a higher melting temperature, a temperature can be found that will cause the terminal region of duplex to melt first, opening the first bubble, and thereby creating a preferred substrate structure of the cleavage by the 5' nucleases of the present invention (FIG. 40a). The site of such cleavage would be expected to be on the 5' arm, within 2 nucleotides of the junction between the single and double-stranded regions (Lyamichev et al., supra and U.S. Pat. No. 5,422,253).

[0305] An additional oligonucleotide could be introduced to basepair along the target nucleic acid would have a similar

effect of opening this bubble for subsequent cleavage of the unpaired 5' arm (**FIG. 40b** and **FIG. 6**). Note in this case, the 3' terminal nucleotides of the upstream oligonucleotide anneals along the target nucleic acid sequence in such a manner that the 3' end is located within the "bubble" region. Depending on the precise location of the 3' end of this oligonucleotide, the cleavage site may be along the newly unpaired 5' arm, or at the site expected for the thermally opened bubble structure as described above. In the former case the cleavage is not within a duplexed region, and is thus not invasive cleavage, while in the latter the oligonucleotide is merely an aide in inducing cleavage at a site that might otherwise be exposed through the use of temperature alone (i.e., in the absence of the additional oligonucleotide), and is thus not considered to be invasive cleavage.

[0306] In summary, any arrangement of oligonucleotides used for the cleavage-based detection of a target sequence can be analyzed to determine if the arrangement is an invasive cleavage structure as contemplated herein. An invasive cleavage structure supports cleavage of the probe in a region that, in the absence of an upstream oligonucleotide, would be expected to be basepaired to the target nucleic acid.

[0307] Example 26 below provides further guidance for the design and execution of a experiments which allow the determination of whether a given arrangement of a pair of upstream and downstream (i.e., the probe) oligonucleotides when annealed along a target nucleic acid would form an invasive cleavage structure.

[0308] V. Fractionation of Specific Nucleic Acids by Selective Charge Reversal

[0309] Some nucleic acid-based detection assays involve the elongation and/or shortening of oligonucleotide probes. For example, as described herein, the primer-directed, primer-independent, and invader-directed cleavage assays, as well as the "nibbling" assay all involve the cleavage (i.e., shortening) of oligonucleotides as a means for detecting the presence of a target nucleic sequence. Examples of other detection assays which involve the shortening of an oligonucleotide probe include the "TaqMan" or nick-translation PCR assay described in U.S. Pat. No. 5,210,015 to Gelfand et al. (the disclosure of which is herein incorporated by reference), the assays described in U.S. Pat. Nos. 4,775,619 and 5,118,605 to Urdea (the disclosures of which are herein incorporated by reference), the catalytic hybridization amplification assay described in U.S. Pat. No. 5,403,711 to Walder and Walder (the disclosure of which is herein incorporated by reference), and the cycling probe assay described in U.S. Pat. Nos. 4,876,187 and 5,011,769 to Duck et al. (the disclosures of which are herein incorporated by reference). Examples of detection assays which involve the elongation of an oligonucleotide probe (or primer) include the polymerase chain reaction (PCR) described in U.S. Pat. Nos. 4,683,195 and 4,683,202 to Mullis and Mullis et al. (the disclosures of which are herein incorporated by reference) and the ligase chain reaction (LCR) described in U.S. Pat. Nos. 5,427,930 and 5,494,810 to Birkenmeyer et al. and Barany et al. (the disclosures of which are herein incorporated by reference). The above examples are intended to be illustrative of nucleic acid-based detection assays that involve the elongation and/or shortening of oligonucleotide probes and do not provide an exhaustive list.

[0310] Typically, nucleic acid-based detection assays that involve the elongation and/or shortening of oligonucleotide probes require post-reaction analysis to detect the products of the reaction. It is common that, the specific reaction product(s) must be separated from the other reaction components, including the input or unreacted oligonucleotide probe. One detection technique involves the electrophoretic separation of the reacted and unreacted oligonucleotide probe. When the assay involves the cleavage or shortening of the probe, the unreacted product will be longer than the reacted or cleaved product. When the assay involves the elongation of the probe (or primer), the reaction products will be greater in length than the input. Gel-based electrophoresis of a sample containing nucleic acid molecules of different lengths separates these fragments primarily on the basis of size. This is due to the fact that in solutions having a neutral or alkaline pH, nucleic acids having widely different sizes (i.e., molecular weights) possess very similar charge-to-mass ratios and do not separate [Andrews, Electrophoresis, 2nd Edition, Oxford University Press (1986), pp. 153-154]. The gel matrix acts as a molecular sieve and allows nucleic acids to be separated on the basis of size and shape (e.g., linear, relaxed circular or covalently closed supercoiled circles).

[0311] Unmodified nucleic acids have a net negative charge due to the presence of negatively charged phosphate groups contained within the sugar-phosphate backbone of the nucleic acid. Typically, the sample is applied to gel near the negative pole and the nucleic acid fragments migrate into the gel toward the positive pole with the smallest fragments moving fastest through the gel.

[0312] The present invention provides a novel means for fractionating nucleic acid fragments on the basis of charge. This novel separation technique is related to the observation that positively charged adducts can affect the electrophoretic behavior of small oligonucleotides because the charge of the adduct is significant relative to charge of the whole complex. In addition, to the use of positively charged adducts (e.g., Cy3 and Cy5 amidite fluorescent dyes, the positively charged heterodimeric DNA-binding dyes shown in **FIG. 66**, etc.), the oligonucleotide may contain amino acids (particularly useful amino acids are the charged amino acids: lysine, arginine, aspartate, glutamate), modified bases, such as amino-modified bases, and/or a phosphonate backbone (at all or a subset of the positions). In addition as discussed further below, a neutral dye or detection moiety (e.g., biotin, streptavidin, etc.) may be employed in place of a positively charged adduct in conjunction with the use of amino-modified bases and/or a complete or partial phosphonate backbone.

[0313] This observed effect is of particular utility in assays based on the cleavage of DNA molecules. Using the assays described herein as an example, when an oligonucleotide is shortened through the action of a Cleavase® enzyme or other cleavage agent, the positive charge can be made to not only significantly reduce the net negative charge, but to actually override it, effectively "flipping" the net charge of the labeled entity. This reversal of charge allows the products of target-specific cleavage to be partitioned from uncleaved probe by extremely simple means. For example, the products of cleavage can be made to migrate towards a negative electrode placed at any point in a reaction vessel, for focused detection without gel-based electrophoresis;

Example 24 provides examples of devices suitable for focused detection without gel-based electrophoresis. When a slab gel is used, sample wells can be positioned in the center of the gel, so that the cleaved and uncleaved probes can be observed to migrate in opposite directions. Alternatively, a traditional vertical gel can be used, but with the electrodes reversed relative to usual DNA gels (i.e., the positive electrode at the top and the negative electrode at the bottom) so that the cleaved molecules enter the gel, while the uncleaved disperse into the upper reservoir of electrophoresis buffer.

[0314] An important benefit of this type of readout is the absolute nature of the partition of products from substrates, i.e., the separation is virtually 100%. This means that an abundance of uncleaved probe can be supplied to drive the hybridization step of the probe-based assay, yet the unconsumed (i.e., unreacted) probe can, in essence, be subtracted from the result to reduce background by virtue of the fact that the unreacted probe will not migrate to the same pole as the specific reaction product.

[0315] Through the use of multiple positively charged adducts, synthetic molecules can be constructed with sufficient modification that the normally negatively charged strand is made nearly neutral. When so constructed, the presence or absence of a single phosphate group can mean the difference between a net negative or a net positive charge. This observation has particular utility when one objective is to discriminate between enzymatically generated fragments of DNA, which lack a 3' phosphate, and the products of thermal degradation, which retain a 3' phosphate (and thus two additional negative charges). Examples 23 and 24 demonstrate the ability to separate positively charged reaction products from a net negatively charged substrate oligonucleotide. As discussed in these examples, oligonucleotides may be transformed from net negative to net positively charged compounds. In Example 24, the positively charged dye, Cy3 was incorporated at the 5' end of a 22-mer (SEQ ID NO:61) which also contained two amino-substituted residues at the 5' end of the oligonucleotide; this oligonucleotide probe carries a net negative charge. After cleavage, which occurred 2 nucleotides into the probe, the following labelled oligonucleotide was released: 5'-Cy3-AminoT-AminoT-3' (as well as the remaining 20 nucleotides of SEQ ID NO:61). This short fragment bears a net positive charge while the remainder of the cleaved oligonucleotide and the unreacted or input oligonucleotide bear net negative charges.

[0316] The present invention contemplates embodiments wherein the specific reaction product produced by any cleavage of any oligonucleotide can be designed to carry a net positive charge while the unreacted probe is charge neutral or carries a net negative charge. The present invention also contemplates embodiments where the released product may be designed to carry a net negative charge while the input nucleic acid carries a net positive charge. Depending on the length of the released product to be detected, positively charged dyes may be incorporated at the one end of the probe and modified bases may be placed along the oligonucleotide such that upon cleavage, the released fragment containing the positively charged dye carries a net positive charge. Amino-modified bases may be used to balance the charge of the released fragment in cases where the presence of the positively charged adduct (e.g., dye) alone is not sufficient to impart a net positive charge on

the released fragment. In addition, the phosphate backbone may be replaced with a phosphonate backbone at a level sufficient to impart a net positive charge (this is particularly useful when the sequence of the oligonucleotide is not amenable to the use of amino-substituted bases); FIGS. 56 and 57 show the structure of short oligonucleotides containing a phosphonate group on the second T residue). An oligonucleotide containing a fully phosphonate-substituted backbone would be charge neutral (absent the presence of modified charged residues bearing a charge or the presence of a charged adduct) due to the absence of the negatively charged phosphate groups. Phosphonate-containing nucleotides (e.g., methylphosphonate-containing nucleotides are readily available and can be incorporated at any position of an oligonucleotide during synthesis using techniques which are well known in the art.

[0317] In essence, the invention contemplates the use of charge-based separation to permit the separation of specific reaction products from the input oligonucleotides in nucleic acid-based detection assays. The foundation of this novel separation technique is the design and use of oligonucleotide probes (typically termed "primers" in the case of PCR) which are "charge balanced" so that upon either cleavage or elongation of the probe it becomes "charge unbalanced," and the specific reaction products may be separated from the input reactants on the basis of the net charge.

[0318] In the context of assays which involve the elongation of an oligonucleotide probe (i.e., a primer), such as is the case in PCR, the input primers are designed to carry a net positive charge. Elongation of the short oligonucleotide primer during polymerization will generate PCR products which now carry a net negative charge. The specific reaction products may then easily be separated and concentrated away from the input primers using the charge-based separation technique described herein (the electrodes will be reversed relative to the description in Example 24 as the product to be separated and concentrated after a PCR will carry a negative charge).

Experimental

[0319] The following examples serve to illustrate certain preferred embodiments and aspects of the present invention and are not to be construed as limiting the scope thereof.

[0320] In the disclosure which follows, the following abbreviations apply: ° C. (degrees Centigrade); g (gravitational field); vol (volume); w/v (weight to volume); v/v (volume to volume); BSA (bovine serum albumin); CTAB (cetyltrimethylammonium bromide); HPLC (high pressure liquid chromatography); DNA (deoxyribonucleic acid); p (plasmid); μ l (microliters); ml (milliliters); μ g (micrograms); pmoles (picomoles); mg (milligrams); M (molar); mM (milliMolar); μ M (microMolar); nm (nanometers); kdal (kilodaltons); OD (optical density); EDTA (ethylene diamine tetra-acetic acid); FITC (fluorescein isothiocyanate); SDS (sodium dodecyl sulfate); NaPO₄ (sodium phosphate); Tris (tris(hydroxymethyl)-aminomethane); PMSF (phenylmethylsulfonylfluoride); TBE (Tris-Borate-EDTA, i.e., Tris buffer titrated with boric acid rather than HCl and containing EDTA); PBS (phosphate buffered saline); PPBS (phosphate buffered saline containing 1 mM PMSF); PAGE (polyacrylamide gel electrophoresis); Tween (polyoxyethylene-sorbitan); Dynal (Dynal A.S., Oslo, Norway); Epicentre (Epicen-

tre Technologies, Madison, Wis.); MJ Research (MJ Research, Watertown, Mass.); National Biosciences (Plymouth, Minn.); New England Biolabs (Beverly, Mass.); Novagen (Novagen, Inc., Madison, Wis.); Perkin Elmer (Norwalk, Conn.); Promega Corp. (Madison, Wis.); Stratagene (Stratagene Cloning Systems, La Jolla, Calif.); USB (U.S. Biochemical, Cleveland, Ohio).

EXAMPLE 1

Characteristics of Native Thermostable DNA Polymerases

[0321] A. 5' Nuclease Activity of DNAPtaq

[0322] During the polymerase chain reaction (PCR) [Saiki et al., *Science* 239:487 (1988); Mullis and Faloona, *Methods in Enzymology* 155:335 (1987)], DNAPtaq is able to amplify many, but not all, DNA sequences. One sequence that cannot be amplified using DNAPtaq is shown in **FIG. 6** (Hairpin structure is SEQ ID NO:15, PRIMERS are SEQ ID NOS:16-17.) This DNA sequence has the distinguishing characteristic of being able to fold on itself to form a hairpin with two single-stranded arms, which correspond to the primers used in PCR.

[0323] To test whether this failure to amplify is due to the 5' nuclease activity of the enzyme, we compared the abilities of DNAPtaq and DNAPStf to amplify this DNA sequence during 30 cycles of PCR. Synthetic oligonucleotides were obtained from The Biotechnology Center at the University of Wisconsin-Madison. The DNAPtaq and DNAPStf were from Perkin Elmer (i.e., Amplitaq™ DNA polymerase and the Stoffel fragment of Amplitaq™ DNA polymerase). The substrate DNA comprised the hairpin structure shown in **FIG. 6** cloned in a double-stranded form into pUC19. The primers used in the amplification are listed as SEQ ID NOS:16-17. Primer SEQ ID NO:17 is shown annealed to the 3' arm of the hairpin structure in **FIG. 6**. Primer SEQ ID NO:16 is shown as the first 20 nucleotides in bold on the 5' arm of the hairpin in **FIG. 6**.

[0324] Polymerase chain reactions comprised 1 ng of supercoiled plasmid target DNA, 5 pmoles of each primer, 40 μM each dNTP, and 2.5 units of DNAPtaq or DNAPStf, in a 50 μl solution of 10 mM Tris-Cl pH 8.3. The DNAPtaq reactions included 50 μM KCl and 1.5 mM MgCl₂. The temperature profile was 95° C. for 30 sec., 55° C. for 11 min. and 72° C. for 1 min., through 30 cycles. Ten percent of each reaction was analyzed by gel electrophoresis through 6% polyacrylamide (cross-linked 29:1) in a buffer of 45 mM Tris.Borate, pH 8.3, 1.4 mM EDTA.

[0325] The results are shown in **FIG. 7**. The expected product was made by DNAPStf (indicated simply as "S") but not by DNAPtaq (indicated as "T"). We conclude that the 5' nuclease activity of DNAPtaq is responsible for the lack of amplification of this DNA sequence.

[0326] To test whether the 5' unpaired nucleotides in the substrate region of this structured DNA are removed by DNAPtaq, the fate of the end-labeled 5' arm during four cycles of PCR was compared using the same two polymerases (**FIG. 8**). The hairpin templates, such as the one described in **FIG. 6**, were made using DNAPStf and a ³²P-5'-end-labeled primer. The 5'-end of the DNA was released as a few large fragments by DNAPtaq but not by

DNAPStf. The sizes of these fragments (based on their mobilities) show that they contain most or all of the unpaired 5' arm of the DNA. Thus, cleavage occurs at or near the base of the bifurcated duplex. These released fragments terminate with 3' OH groups, as evidenced by direct sequence analysis, and the abilities of the fragments to be extended by terminal deoxynucleotidyl transferase.

[0327] **FIGS. 9-11** show the results of experiments designed to characterize the cleavage reaction catalyzed by DNAPtaq. Unless otherwise specified, the cleavage reactions comprised 0.01 pmoles of heat-denatured, end-labeled hairpin DNA (with the unlabeled complementary strand also present), 1 pmole primer (complementary to the 3' arm) and 0.5 units of DNAPtaq (estimated to be 0.026 pmoles) in a total volume of 10 μl of 10 mM Tris-Cl, pH 8.5, 50 mM KCl and 1.5 mM MgCl₂. As indicated, some reactions had different concentrations of KCl, and the precise times and temperatures used in each experiment are indicated in the individual figures. The reactions that included a primer used the one shown in **FIG. 6** (SEQ ID NO:17). In some instances, the primer was extended to the junction site by providing polymerase and selected nucleotides.

[0328] Reactions were initiated at the final reaction temperature by the addition of either the MgCl₂ or enzyme. Reactions were stopped at their incubation temperatures by the addition of 8 μl of 95% formamide with 20 mM EDTA and 0.05% marker dyes. The T_m calculations listed were made using the Oligo™ primer analysis software from National Biosciences, Inc. These were determined using 0.25 μM as the DNA concentration, at either 15 or 65 mM total salt (the 1.5 mM MgCl₂ in all reactions was given the value of 15 mM salt for these calculations).

[0329] **FIG. 9** is an autoradiogram containing the results of a set of experiments and conditions on the cleavage site. **FIG. 9A** is a determination of reaction components that enable cleavage. Incubation of 5'-end-labeled hairpin DNA was for 30 minutes at 55° C., with the indicated components. The products were resolved by denaturing polyacrylamide gel electrophoresis and the lengths of the products, in nucleotides, are indicated. **FIG. 9B** describes the effect of temperature on the site of cleavage in the absence of added primer. Reactions were incubated in the absence of KCl for 10 minutes at the indicated temperatures. The lengths of the products, in nucleotides, are indicated.

[0330] Surprisingly, cleavage by DNAPtaq requires neither a primer nor dNTPs (see **FIG. 9A**). Thus, the 5' nuclease activity can be uncoupled from polymerization. Nuclease activity requires magnesium ions, though manganese ions can be substituted, albeit with potential changes in specificity and activity. Neither zinc nor calcium ions support the cleavage reaction. The reaction occurs over a broad temperature range, from 25° C. to 85° C., with the rate of cleavage increasing at higher temperatures.

[0331] Still referring to **FIG. 9**, the primer is not elongated in the absence of added dNTPs. However, the primer influences both the site and the rate of cleavage of the hairpin. The change in the site of cleavage (**FIG. 9A**) apparently results from disruption of a short duplex formed between the arms of the DNA substrate. In the absence of primer, the sequences indicated by underlining in **FIG. 6** could pair, forming an extended duplex. Cleavage at the end of the extended duplex would release the 11 nucleotide fragment

seen on the **FIG. 9A** lanes with no added primer. Addition of excess primer (**FIG. 9A**, lanes 3 and 4) or incubation at an elevated temperature (**FIG. 9B**) disrupts the short extension of the duplex and results in a longer 5' arm and, hence, longer cleavage products.

[0332] The location of the 3' end of the primer can influence the precise site of cleavage. Electrophoretic analysis revealed that in the absence of primer (**FIG. 9B**), cleavage occurs at the end of the substrate duplex (either the extended or shortened form, depending on the temperature) between the first and second base pairs. When the primer extends up to the base of the duplex, cleavage also occurs one nucleotide into the duplex. However, when a gap of four or six nucleotides exists between the 3' end of the primer and the substrate duplex, the cleavage site is shifted four to six nucleotides in the 5' direction.

[0333] **FIG. 10** describes the kinetics of cleavage in the presence (**FIG. 10A**) or absence (**FIG. 10B**) of a primer oligonucleotide. The reactions were run at 55° C. with either 50 mM KCl (**FIG. 10A**) or 20 mM KCl (**FIG. 10B**). The reaction products were resolved by denaturing polyacrylamide gel electrophoresis and the lengths of the products, in nucleotides, are indicated. "M", indicating a marker, is a 5' end-labeled 19-nt oligonucleotide. Under these salt conditions, **FIGS. 10A and 10B** indicate that the reaction appears to be about twenty times faster in the presence of primer than in the absence of primer. This effect on the efficiency may be attributable to proper alignment and stabilization of the enzyme on the substrate.

[0334] The relative influence of primer on cleavage rates becomes much greater when both reactions are run in 50 mM KCl. In the presence of primer, the rate of cleavage increases with KCl concentration, up to about 50 mM. However, inhibition of this reaction in the presence of primer is apparent at 100 mM and is complete at 150 mM KCl. In contrast, in the absence of primer the rate is enhanced by concentration of KCl up to 20 mM, but it is reduced at concentrations above 30 mM. At 50 mM KCl, the reaction is almost completely inhibited. The inhibition of cleavage by KCl in the absence of primer is affected by temperature, being more pronounced at lower temperatures.

[0335] Recognition of the 5' end of the arm to be cut appears to be an important feature of substrate recognition. Substrates that lack a free 5' end, such as circular M13 DNA, cannot be cleaved under any conditions tested. Even with substrates having defined 5' arms, the rate of cleavage by DNAPtaq is influenced by the length of the arm. In the presence of primer and 50 mM KCl, cleavage of a 5' extension that is 27 nucleotides long is essentially complete within 2 minutes at 55° C. In contrast, cleavages of molecules with 5' arms of 84 and 188 nucleotides are only about 90% and 40% complete after 20 minutes. Incubation at higher temperatures reduces the inhibitory effects of long extensions indicating that secondary structure in the 5' arm or a heat-labile structure in the enzyme may inhibit the reaction. A mixing experiment, run under conditions of substrate excess, shows that the molecules with long arms do not preferentially tie up the available enzyme in non-productive complexes. These results may indicate that the 5' nuclease domain gains access to the cleavage site at the end of the bifurcated duplex by moving down the 5' arm from one end to the other. Longer 5' arms would be expected to

have more adventitious secondary structures (particularly when KCl concentrations are high), which would be likely to impede this movement.

[0336] Cleavage does not appear to be inhibited by long 3' arms of either the substrate strand target molecule or pilot nucleic acid, at least up to 2 kilobases. At the other extreme, 3' arms of the pilot nucleic acid as short as one nucleotide can support cleavage in a primer-independent reaction, albeit inefficiently. Fully paired oligonucleotides do not elicit cleavage of DNA templates during primer extension.

[0337] The ability of DNAPtaq to cleave molecules even when the complementary strand contains only one unpaired 3' nucleotide may be useful in optimizing allele-specific PCR. PCR primers that have unpaired 3' ends could act as pilot oligonucleotides to direct selective cleavage of unwanted templates during preincubation of potential template-primer complexes with DNAPtaq in the absence of nucleoside triphosphates.

[0338] B. 5' Nuclease Activities of Other DNAPs

[0339] To determine whether other 5' nucleases in other DNAPs would be suitable for the present invention, an array of enzymes, several of which were reported in the literature to be free of apparent 5' nuclease activity, were examined. The ability of these other enzymes to cleave nucleic acids in a structure-specific manner was tested using the hairpin substrate shown in **FIG. 6** under conditions reported to be optimal for synthesis by each enzyme.

[0340] DNAPEc1 and DNAP Klenow were obtained from Promega Corporation; the DNAP of *Pyrococcus furiosus* ["Pfu", Bargseid et al., *Strategies* 4:34 (1991)] was from Strategene; the DNAP of *Thermococcus litoralis* ["Tli", Vent™(exo-), Perler et al., *Proc. Natl. Acad. Sci. USA* 89:5577 (1992)] was from New England Biolabs; the DNAP of *Thermus flavus* ["Tfl", Kaledin et al., *Biokhimiya* 46:1576 (1981)] was from Epicentre Technologies; and the DNAP of *Thermus thermophilus* ["Tth", Carballeira et al., *Biotechniques* 9:276 (1990); Myers et al., *Biochem.* 30:7661 (1991)] was from U.S. Biochemicals.

[0341] 0.5 units of each DNA polymerase was assayed in a 20 μ l reaction, using either the buffers supplied by the manufacturers for the primer-dependent reactions, or 10 mM Tris.Cl, pH 8.5, 1.5 mM MgCl₂, and 20 mM KCl. Reaction mixtures were at held 72° C. before the addition of enzyme.

[0342] **FIG. 11** is an autoradiogram recording the results of these tests. **FIG. 11A** demonstrates reactions of endonucleases of DNAPs of several thermophilic bacteria. The reactions were incubated at 55° C. for 10 minutes in the presence of primer or at 72° C. for 30 minutes in the absence of primer, and the products were resolved by denaturing polyacrylamide gel electrophoresis. The lengths of the products, in nucleotides, are indicated. **FIG. 11B** demonstrates endonucleolytic cleavage by the 5' nuclease of DNAPEc1. The DNAPEc1 and DNAP Klenow reactions were incubated for 5 minutes at 37° C. Note the light band of cleavage products of 25 and 11 nucleotides in the DNAPEc1 lanes (made in the presence and absence of primer, respectively). **FIG. 7B** also demonstrates DNAPtaq reactions in the presence (+) or absence (-) of primer. These reactions were run in 50 mM and 20 mM KCl, respectively, and were incubated at 55° C. for 10 minutes.

[0343] Referring to FIG. 11A, DNAPs from the eubacteria *Thermus thermophilus* and *Thermus flavus* cleave the substrate at the same place as DNAPtaq, both in the presence and absence of primer. In contrast, DNAPs from the archaeobacteria *Pyrococcus furiosus* and *Thermococcus litoralis* are unable to cleave the substrates endonucleolytically. The DNAPs from *Pyrococcus furiosus* and *Thermococcus litoralis* share little sequence homology with eubacterial enzymes (Ito et al., *Nucl. Acids Res.* 19:4045 (1991); Mathur et al., *Nucl. Acids Res.* 19:6952 (1991); see also Perler et al.). Referring to FIG. 11B, DNAPEc1 also cleaves the substrate, but the resulting cleavage products are difficult to detect unless the 3' exonuclease is inhibited. The amino acid sequences of the 5' nuclease domains of DNAPEc1 and DNAPtaq are about 38% homologous (Gelfand, supra).

[0344] The 5' nuclease domain of DNAPtaq also shares about 19% homology with the 5' exonuclease encoded by gene 6 of bacteriophage T7 [Dunn et al., *J. Mol. Biol.* 166:477 (1983)]. This nuclease, which is not covalently attached to a DNAP polymerization domain, is also able to cleave DNA endonucleolytically, at a site similar or identical to the site that is cut by the 5' nucleases described above, in the absence of added primers.

[0345] C. Transcleavage

[0346] The ability of a 5' nuclease to be directed to cleave efficiently at any specific sequence was demonstrated in the following experiment. A partially complementary oligonucleotide termed a "pilot oligonucleotide" was hybridized to sequences at the desired point of cleavage. The non-complementary part of the pilot oligonucleotide provided a structure analogous to the 3' arm of the template (see FIG. 6), whereas the 5' region of the substrate strand became the 5' arm. A primer was provided by designing the 3' region of the pilot so that it would fold on itself creating a short hairpin with a stabilizing tetra-loop [Antao et al., *Nucl. Acids Res.* 19:5901 (1991)]. Two pilot oligonucleotides are shown in FIG. 12A. Oligonucleotides 19-12 (SEQ ID NO:18), 30-12 (SEQ ID NO:19) and 30-0 (SEQ ID NO:20) are 31, 42 or 30 nucleotides long, respectively. However, oligonucleotides 19-12 (SEQ ID NO:18) and 34-19 (SEQ ID NO:19) have only 19 and 30 nucleotides, respectively, that are complementary to different sequences in the substrate strand. The pilot oligonucleotides are calculated to melt off their complements at about 50° C. (19-12) and about 75° C. (30-12). Both pilots have 12 nucleotides at their 3' ends, which act as 3' arms with base-paired primers attached.

[0347] To demonstrate that cleavage could be directed by a pilot oligonucleotide, we incubated a single-stranded target DNA with DNAPtaq in the presence of two potential pilot oligonucleotides. The transcleavage reactions, where the target and pilot nucleic acids are not covalently linked, includes 0.01 pmoles of single end-labeled substrate DNA, 1 unit of DNAPtaq and 5 pmoles of pilot oligonucleotide in a volume of 20 μ l of the same buffers. These components were combined during a one minute incubation at 95° C., to denature the PCR-generated double-stranded substrate DNA, and the temperatures of the reactions were then reduced to their final incubation temperatures. Oligonucleotides 30-12 and 19-12 can hybridize to regions of the substrate DNAs that are 85 and 27 nucleotides from the 5' end of the targeted strand.

[0348] FIG. 21 shows the complete 206-mer sequence (SEQ ID NO:32). The 206-mer was generated by PCR. The

M13/pUC 24-mer reverse sequencing (-48) primer and the M13/pUC sequencing (-47) primer from New England Biolabs (catalogue nos. 1233 and 1224 respectively) were used (50 pmoles each) with the pGEM3z(f+) plasmid vector (Promega Corp.) as template (10 ng) containing the target sequences. The conditions for PCR were as follows: 50 μ M of each dNTP and 2.5 units of Taq DNA polymerase in 100 μ l of 20 mM Tris-Cl, pH 8.3, 1.5 mM MgCl₂, 50 mM KCl with 0.05% Tween-20 and 0.05% NP-40. Reactions were cycled 35 times through 95° C. for 45 seconds, 63° C. for 45 seconds, then 72° C. for 75 seconds. After cycling, reactions were finished off with an incubation at 72° C. for 5 minutes. The resulting fragment was purified by electrophoresis through a 6% polyacrylamide gel (29:1 cross link) in a buffer of 45 mM Tris-Borate, pH 8.3, 1.4 mM EDTA, visualized by ethidium bromide staining or autoradiography, excised from the gel, eluted by passive diffusion, and concentrated by ethanol precipitation.

[0349] Cleavage of the substrate DNA occurred in the presence of the pilot oligonucleotide 19-12 at 50° C. (FIG. 12B, lanes 1 and 7) but not at 75° C. (lanes 4 and 10). In the presence of oligonucleotide 30-12 cleavage was observed at both temperatures. Cleavage did not occur in the absence of added oligonucleotides (lanes 3, 6 and 12) or at about 80° C. even though at 50° C. adventitious structures in the substrate allowed primer-independent cleavage in the absence of KCl (FIG. 12B, lane 9). A non-specific oligonucleotide with no complementarity to the substrate DNA did not direct cleavage at 50° C., either in the absence or presence of 50 mM KCl (lanes 13 and 14). Thus, the specificity of the cleavage reactions can be controlled by the extent of complementarity to the substrate and by the conditions of incubation.

[0350] D. Cleavage of RNA

[0351] An shortened RNA version of the sequence used in the transcleavage experiments discussed above was tested for its ability to serve as a substrate in the reaction. The RNA is cleaved at the expected place, in a reaction that is dependent upon the presence of the pilot oligonucleotide. The RNA substrate, made by T7 RNA polymerase in the presence of [α -³²P]UTP, corresponds to a truncated version of the DNA substrate used in FIG. 12B. Reaction conditions were similar to those in used for the DNA substrates described above, with 50 mM KCl; incubation was for 40 minutes at 55° C. The pilot oligonucleotide used is termed 30-0 (SEQ ID NO:20) and is shown in FIG. 13A.

[0352] The results of the cleavage reaction is shown in FIG. 13B. The reaction was run either in the presence or absence of DNAPtaq or pilot oligonucleotide as indicated in FIG. 13B.

[0353] Strikingly, in the case of RNA cleavage, a 3' arm is not required for the pilot oligonucleotide. It is very unlikely that this cleavage is due to previously described RNaseH, which would be expected to cut the RNA in several places along the 30 base-pair long RNA-DNA duplex. The 5' nuclease of DNAPtaq is a structure-specific RNaseH that cleaves the RNA at a single site near the 5' end of the heteroduplexed region.

[0354] It is surprising that an oligonucleotide lacking a 3' arm is able to act as a pilot in directing efficient cleavage of an RNA target because such oligonucleotides are unable to direct efficient cleavage of DNA targets using native

DNAPs. However, some 5' nucleases of the present invention (for example, clones E, F and G of FIG. 4) can cleave DNA in the absence of a 3' arm. In other words, a non-extendable cleavage structure is not required for specific cleavage with some 5' nucleases of the present invention derived from thermostable DNA polymerases.

[0355] We tested whether cleavage of an RNA template by DNAP_{Taq} in the presence of a fully complementary primer could help explain why DNAP_{Taq} is unable to extend a DNA oligonucleotide on an RNA template, in a reaction resembling that of reverse transcriptase. Another thermophilic DNAP, DNAP_{Th}, is able to use RNA as a template, but only in the presence of Mn⁺⁺, so we predicted that this enzyme would not cleave RNA in the presence of this cation. Accordingly, we incubated an RNA molecule with an appropriate pilot oligonucleotide in the presence of DNAP_{Taq} or DNAP_{Th}, in buffer containing either Mg⁺⁺ or Mn⁺⁺. As expected, both enzymes cleaved the RNA in the presence of Mg⁺⁺. However, DNAP_{Taq}, but not DNAP_{Th}, degraded the RNA in the presence of Mn⁺⁺. We conclude that the 5' nuclease activities of many DNAPs may contribute to their inability to use RNA as templates.

EXAMPLE 2

Generation of 5' Nucleases from Thermostable DNA Polymerases

[0356] Thermostable DNA polymerases were generated which have reduced synthetic activity, an activity that is an undesirable side-reaction during DNA cleavage in the detection assay of the invention, yet have maintained thermostable nuclease activity. The result is a thermostable polymerase which cleaves nucleic acids DNA with extreme specificity.

[0357] Type A DNA polymerases from eubacteria of the genus *Thermus* share extensive protein sequence identity (90% in the polymerization domain, using the Lipman-Pearson method in the DNA analysis software from DNASTar, Wis.) and behave similarly in both polymerization and nuclease assays. Therefore, we have used the genes for the DNA polymerase of *Thermus aquaticus* (DNAP_{Taq}) and *Thermus flavus* (DNAP_{Th}) as representatives of this class. Polymerase genes from other eubacterial organisms, such as *Thermus thermophilus*, *Thermus* sp., *Thermotoga maritima*, *Thermosiphon africanus* and *Bacillus stearothermophilus* are equally suitable. The DNA polymerases from these thermophilic organisms are capable of surviving and performing at elevated temperatures, and can thus be used in reactions in which temperature is used as a selection against non-specific hybridization of nucleic acid strands.

[0358] The restriction sites used for deletion mutagenesis, described below, were chosen for convenience. Different sites situated with similar convenience are available in the *Thermus thermophilus* gene and can be used to make similar constructs with other Type A polymerase genes from related organisms.

[0359] A. Creation of 5' Nuclease Constructs

[0360] 1. Modified DNAP_{Taq} Genes

[0361] The first step was to place a modified gene for the Taq DNA polymerase on a plasmid under control of an inducible promoter. The modified Taq polymerase gene was

isolated as follows: The Taq DNA polymerase gene was amplified by polymerase chain reaction from genomic DNA from *Thermus aquaticus*, strain YT-1 (Lawyer et al., supra), using as primers the oligonucleotides described in SEQ ID NOS:13-14. The resulting fragment of DNA has a recognition sequence for the restriction endonuclease EcoRI at the 5' end of the coding sequence and a BglIII sequence at the 3' end. Cleavage with BglIII leaves a 5' overhang or "sticky end" that is compatible with the end generated by BamHI. The PCR-amplified DNA was digested with EcoRI and BamHI. The 2512 bp fragment containing the coding region for the polymerase gene was gel purified and then ligated into a plasmid which contains an inducible promoter.

[0362] In one embodiment of the invention, the pTTQ18 vector, which contains the hybrid trp-lac (tac) promoter, was used [M.J.R. Stark, *Gene* 5:255 (1987)] and shown in FIG. 14. The tac promoter is under the control of the *E. coli* lac repressor. Repression allows the synthesis of the gene product to be suppressed until the desired level of bacterial growth has been achieved, at which point repression is removed by addition of a specific inducer, isopropyl-β-D-thiogalactopyranoside (IPTG). Such a system allows the expression of foreign proteins that may slow or prevent growth of transformants.

[0363] Bacterial promoters, such as tac, may not be adequately suppressed when they are present on a multiple copy plasmid. If a highly toxic protein is placed under control of such a promoter, the small amount of expression leaking through can be harmful to the bacteria. In another embodiment of the invention, another option for repressing synthesis of a cloned gene product was used. The non-bacterial promoter, from bacteriophage T7, found in the plasmid vector series pET-3 was used to express the cloned mutant Taq polymerase genes [FIG. 15; Studier and Moffatt, *J. Mol. Biol.* 189:113 (1986)]. This promoter initiates transcription only by T7 RNA polymerase. In a suitable strain, such as BL21(DE3)pL_{YS}, the gene for this RNA polymerase is carried on the bacterial genome under control of the lac operator. This arrangement has the advantage that expression of the multiple copy gene (on the plasmid) is completely dependent on the expression of T7 RNA polymerase, which is easily suppressed because it is present in a single copy.

[0364] For ligation into the pTTQ18 vector (FIG. 14), the PCR product DNA containing the Taq polymerase coding region (mutTaq, clone 4B, SEQ ID NO:21) was digested with EcoRI and BglIII and this fragment was ligated under standard "sticky end" conditions [Sambrook et al. *Molecular Cloning*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, pp. 1.63-1.69 (1989)] into the EcoRI and BamHI sites of the plasmid vector pTTQ18. Expression of this construct yields a translational fusion product in which the first two residues of the native protein (Met-Arg) are replaced by three from the vector (Met-Asn-Ser), but the remainder of the natural protein would not change. The construct was transformed into the JM109 strain of *E. coli* and the transformants were plated under incompletely repressing conditions that do not permit growth of bacteria expressing the native protein. These plating conditions allow the isolation of genes containing pre-existing mutations, such as those that result from the infidelity of Taq polymerase during the amplification process.

[0365] Using this amplification/selection protocol, we isolated a clone (depicted in **FIG. 4B**) containing a mutated Taq polymerase gene (mutTaq, clone 4B). The mutant was first detected by its phenotype, in which temperature-stable 5' nuclease activity in a crude cell extract was normal, but polymerization activity was almost absent (approximately less than 1% of wild type Taq polymerase activity).

[0366] DNA sequence analysis of the recombinant gene showed that it had changes in the polymerase domain resulting in two amino acid substitutions: an A to G change at nucleotide position 1394 causes a Glu to Gly change at amino acid position 465 (numbered according to the natural nucleic and amino acid sequences, SEQ ID NOS:1 and 4) and another A to G change at nucleotide position 2260 causes a Gln to Arg change at amino acid position 754. Because the Gln to Gly mutation is at a nonconserved position and because the Glu to Arg mutation alters an amino acid that is conserved in virtually all of the known Type A polymerases, this latter mutation is most likely the one responsible for curtailing the synthesis activity of this protein. The nucleotide sequence for the **FIG. 4B** construct is given in SEQ ID NO:21. The enzyme encoded by this sequence is referred to as Cleavase® A/G.

[0367] Subsequent derivatives of DNAPtaq constructs were made from the mutTaq gene, thus, they all bear these amino acid substitutions in addition to their other alterations, unless these particular regions were deleted. These mutated sites are indicated by black boxes at these locations in the diagrams in **FIG. 4**. In **FIG. 4**, the designation "3' Exo" is used to indicate the location of the 3' exonuclease activity associated with Type A polymerases which is not present in DNAPtaq. All constructs except the genes shown in **FIGS. 4E, F** and **G** were made in the pTTQ18 vector.

[0368] The cloning vector used for the genes in **FIGS. 4E and F** was from the commercially available pET-3 series, described above. Though this vector series has only a BamHI site for cloning downstream of the T7 promoter, the series contains variants that allow cloning into any of the three reading frames. For cloning of the PCR product described above, the variant called pET-3c was used (**FIG. 15**). The vector was digested with BamHI, dephosphorylated with calf intestinal phosphatase, and the sticky ends were filled in using the Klenow fragment of DNAPEc1 and dNTPs. The gene for the mutant Taq DNAP shown in **FIG. 4B** (mutTaq, clone 4B) was released from pTTQ18 by digestion with EcoRI and Sall, and the "sticky ends" were filled in as was done with the vector. The fragment was ligated to the vector under standard blunt-end conditions (Sambrook et al., *Molecular Cloning*, supra), the construct was transformed into the BL21(DE3)pLYS strain of *E. coli*, and isolates were screened to identify those that were ligated with the gene in the proper orientation relative to the promoter. This construction yields another translational fusion product, in which the first two amino acids of DNAPtaq (Met-Arg) are replaced by 13 from the vector plus two from the PCR primer (Met-Ala-Ser-Met-Thr-Gly-Gly-Gln-Gln-Met-Gly-Arg-Ile-Asn-Ser) (SEQ ID NO:29).

[0369] Our goal was to generate enzymes that lacked the ability to synthesize DNA, but retained the ability to cleave nucleic acids with a 5' nuclease activity. The act of primed, templated synthesis of DNA is actually a coordinated series of events, so it is possible to disable DNA synthesis by

disrupting one event while not affecting the others. These steps include, but are not limited to, primer recognition and binding, dNTP binding and catalysis of the inter-nucleotide phosphodiester bond. Some of the amino acids in the polymerization domain of DNAPEc1 have been linked to these functions, but the precise mechanisms are as yet poorly defined.

[0370] One way of destroying the polymerizing ability of a DNA polymerase is to delete all or part of the gene segment that encodes that domain for the protein, or to otherwise render the gene incapable of making a complete polymerization domain. Individual mutant enzymes may differ from each other in stability and solubility both inside and outside cells. For instance, in contrast to the 5' nuclease domain of DNAPEc1, which can be released in an active form from the polymerization domain by gentle proteolysis [Setlow and Kornberg, *J. Biol. Chem.* 247:232 (1972)], the Thermus nuclease domain, when treated similarly, becomes less soluble and the cleavage activity is often lost.

[0371] Using the mutant gene shown in **FIG. 4B** as starting material, several deletion constructs were created. All cloning technologies were standard (Sambrook et al., supra) and are summarized briefly, as follows:

[0372] **FIG. 4C**: The mutTaq construct was digested with PstI, which cuts once within the polymerase coding region, as indicated, and cuts immediately downstream of the gene in the multiple cloning site of the vector. After release of the fragment between these two sites, the vector was re-ligated, creating an 894-nucleotide deletion, and bringing into frame a stop codon 40 nucleotides downstream of the junction. The nucleotide sequence of this 5' nuclease (clone 4C) is given in SEQ ID NO:9.

[0373] **FIG. 4D**: The mutTaq construct was digested with NheI, which cuts once in the gene at position 2047. The resulting four-nucleotide 5' overhanging ends were filled in, as described above, and the blunt ends were re-ligated. The resulting four-nucleotide insertion changes the reading frame and causes termination of translation ten amino acids downstream of the mutation. The nucleotide sequence of this 5' nuclease (clone 4D) is given in SEQ ID NO:10.

[0374] **FIG. 4E**: The entire mutTaq gene was cut from pTTQ18 using EcoRI and Sall and cloned into pET-3c, as described above. This clone was digested with BstXI and XcmI, at unique sites that are situated as shown in **FIG. 4E**. The DNA was treated with the Klenow fragment of DNAPEc1 and dNTPs, which resulted in the 3' overhangs of both sites being trimmed to blunt ends. These blunt ends were ligated together, resulting in an out-of-frame deletion of 1540 nucleotides. An in-frame termination codon occurs 18 triplets past the junction site. The nucleotide sequence of this 5' nuclease (clone 4E) is given in SEQ ID NO:11, with the appropriate leader sequence given in SEQ ID NO:30. It is also referred to as Cleavase® BX.

[0375] **FIG. 4F**: The entire mutTaq gene was cut from pTTQ18 using EcoRI and Sall and cloned into pET-3c, as described above. This clone was digested with BstXI and BamHI, at unique sites that are situated as shown in the diagram. The DNA was treated with the Klenow fragment of DNAPEc1 and dNTPs, which resulted in the 3' overhang of the BstXI site being trimmed to a blunt end, while the 5' overhang of the BamHI site was filled in to make a blunt

end. These ends were ligated together, resulting in an in-frame deletion of 903 nucleotides. The nucleotide sequence of the 5' nuclease (clone 4F) is given in SEQ ID NO:12. It is also referred to as Cleavase® BB.

[0376] FIG. 4G: This polymerase is a variant of that shown in FIG. 4E. It was cloned in the plasmid vector pET-21 (Novagen). The non-bacterial promoter from bacteriophage T7, found in this vector, initiates transcription only by T7 RNA polymerase. See Studier and Moffatt, supra. In a suitable strain, such as (DES)pLYS, the gene for this RNA polymerase is carried on the bacterial genome under control of the lac operator. This arrangement has the advantage that expression of the multiple copy gene (on the plasmid) is completely dependent on the expression of T7 RNA polymerase, which is easily suppressed because it is present in a single copy. Because the expression of these mutant genes is under this tightly controlled promoter, potential problems of toxicity of the expressed proteins to the host cells are less of a concern.

[0377] The pET-21 vector also features a "His*Tag", a stretch of six consecutive histidine residues that are added on the carboxy terminus of the expressed proteins. The resulting proteins can then be purified in a single step by metal chelation chromatography, using a commercially available (Novagen) column resin with immobilized Ni⁺⁺ ions. The 2.5 ml columns are reusable, and can bind up to 20 mg of the target protein under native or denaturing (guanidine*HCl or urea) conditions.

[0378] *E. coli* (DES)pLYS cells are transformed with the constructs described above using standard transformation techniques, and used to inoculate a standard growth medium (e.g., Luria-Bertani broth). Production of T7 RNA polymerase is induced during log phase growth by addition of IPTG and incubated for a further 12 to 17 hours. Aliquots of culture are removed both before and after induction and the proteins are examined by SDS-PAGE. Staining with Coomassie Blue allows visualization of the foreign proteins if they account for about 3-5% of the cellular protein and do not co-migrate with any of the major protein bands. Proteins that co-migrate with major host protein must be expressed as more than 10% of the total protein to be seen at this stage of analysis.

[0379] Some mutant proteins are sequestered by the cells into inclusion bodies. These are granules that form in the cytoplasm when bacteria are made to express high levels of a foreign protein, and they can be purified from a crude lysate, and analyzed by SDS-PAGE to determine their protein content. If the cloned protein is found in the inclusion bodies, it must be released to assay the cleavage and polymerase activities. Different methods of solubilization may be appropriate for different proteins, and a variety of methods are known. See e.g., Builder & Ogez, U.S. Pat. No. 4,511,502 (1985); Olson, U.S. Pat. No. 4,518,526 (1985); Olson & Pai, U.S. Pat. No. 4,511,503 (1985); Jones et al., U.S. Pat. No. 4,512,922 (1985), all of which are hereby incorporated by reference.

[0380] The solubilized protein is then purified on the Ni⁺⁺ column as described above, following the manufacturers instructions (Novagen). The washed proteins are eluted from the column by a combination of imidazole competitor (1 M) and high salt (0.5 M NaCl), and dialyzed to exchange the buffer and to allow denature proteins to refold. Typical

recoveries result in approximately 20 µg of specific protein per ml of starting culture. The DNAP mutant is referred to as Cleavase® BN and the sequence is given in SEQ ID NO:31.

[0381] 2. Modified DNAPTfl Gene

[0382] The DNA polymerase gene of *Thermus flavus* was isolated from the "*T. flavus*" AT-62 strain obtained from the American Type Tissue Collection (ATCC 33923). This strain has a different restriction map than does the *T. flavus* strain used to generate the sequence published by Akhmetzjanov and Vakhitov, supra. The published sequence is listed as SEQ ID NO:2. No sequence data has been published for the DNA polymerase gene from the AT-62 strain of *T. flavus*.

[0383] Genomic DNA from *T. flavus* was amplified using the same primers used to amplify the *T. aquaticus* DNA polymerase gene (SEQ ID NOS:13-14). The approximately 2500 base pair PCR fragment was digested with EcoRI and BamHI. The over-hanging ends were made blunt with the Klenow fragment of DNAPEc1 and dNTPs. The resulting approximately 1800 base pair fragment containing the coding region for the N-terminus was ligated into pET-3c, as described above. This construct, clone 5B, is depicted in FIG. 5B. The wild type *T. flavus* DNA polymerase gene is depicted in FIG. 5A. The 5B clone has the same leader amino acids as do the DNAPTaq clones 4E and F which were cloned into pET-3c; it is not known precisely where translation termination occurs, but the vector has a strong transcription termination signal immediately downstream of the cloning site.

[0384] B. Growth and Induction of Transformed Cells

[0385] Bacterial cells were transformed with the constructs described above using standard transformation techniques and used to inoculate 2 mls of a standard growth medium (e.g., Luria-Bertani broth). The resulting cultures were incubated as appropriate for the particular strain used, and induced if required for a particular expression system. For all of the constructs depicted in FIGS. 4 and 5, the cultures were grown to an optical density (at 600 nm wavelength) of 0.5 OD.

[0386] To induce expression of the cloned genes, the cultures were brought to a final concentration of 0.4 mM IPTG and the incubations were continued for 12 to 17 hours. 50 µl aliquots of each culture were removed both before and after induction and were combined with 20 µl of a standard gel loading buffer for sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE). Subsequent staining with Coomassie Blue (Sambrook et al., supra) allows visualization of the foreign proteins if they account for about 3-5% of the cellular protein and do not co-migrate with any of the major *E. coli* protein bands. Proteins that do co-migrate with a major host protein must be expressed as more than 10% of the total protein to be seen at this stage of analysis.

[0387] C. Heat Lysis and Fractionation

[0388] Expressed thermostable proteins, i.e., the 5' nucleases, were isolated by heating crude bacterial cell extracts to cause denaturation and precipitation of the less stable *E. coli* proteins. The precipitated *E. coli* proteins were then, along with other cell debris, removed by centrifugation. 1.7 mls of the culture were pelleted by microcentrifuga-

gation at 12,000 to 14,000 rpm for 30 to 60 seconds. After removal of the supernatant, the cells were resuspended in 400 μ l of buffer A (50 mM Tris-HCl, pH 7.9, 50 mM dextrose, 1 mM EDTA), re-centrifuged, then resuspended in 80 μ l of buffer A with 4 mg/ml lysozyme. The cells were incubated at room temperature for 15 minutes, then combined with 80 μ l of buffer B (10 mM Tris-HCl, pH 7.9, 50 mM KCl, 1 mM EDTA, 1 mM PMSF, 0.5% Tween-20, 0.5% Nonidet-P40).

[0389] This mixture was incubated at 75° C. for 1 hour to denature and precipitate the host proteins. This cell extract was centrifuged at 14,000 rpm for 15 minutes at 4° C., and the supernatant was transferred to a fresh tube. An aliquot of 0.5 to 1 μ l of this supernatant was used directly in each test reaction, and the protein content of the extract was determined by subjecting 7 μ l to electrophoretic analysis, as above. The native recombinant Taq DNA polymerase [Englke, Anal. Biochem 191:396 (1990)], and the double point mutation protein shown in FIG. 4B are both soluble and active at this point.

[0390] The foreign protein may not be detected after the heat treatments due to sequestration of the foreign protein by the cells into inclusion bodies. These are granules that form in the cytoplasm when bacteria are made to express high levels of a foreign protein, and they can be purified from a crude lysate, and analyzed SDS PAGE to determine their protein content. Many methods have been described in the literature, and one approach is described below.

[0391] D. Isolation and Solubilization of Inclusion Bodies

[0392] A small culture was grown and induced as described above. A 1.7 ml aliquot was pelleted by brief centrifugation, and the bacterial cells were resuspended in 100 μ l of Lysis buffer (50 mM Tris-HCl, pH 8.0, 1 mM EDTA, 100 mM NaCl). 2.5 μ l of 20 mM PMSF were added for a final concentration of 0.5 mM, and lysozyme was added to a concentration of 1.0 mg/ml. The cells were incubated at room temperature for 20 minutes, deoxycholic acid was added to 1 mg/ml (1 μ l of 100 mg/ml solution), and the mixture was further incubated at 37° C. for about 15 minutes or until viscous. DNase I was added to 10 μ g/ml and the mixture was incubated at room temperature for about 30 minutes or until it was no longer viscous.

[0393] From this mixture the inclusion bodies were collected by centrifugation at 14,000 rpm for 15 minutes at 4° C., and the supernatant was discarded. The pellet was resuspended in 100 μ l of lysis buffer with 10 mM EDTA (pH 8.0) and 0.5% Triton X-100. After 5 minutes at room temperature, the inclusion bodies were pelleted as before, and the supernatant was saved for later analysis. The inclusion bodies were resuspended in 50 μ l of distilled water, and 5 μ l was combined with SDS gel loading buffer (which dissolves the inclusion bodies) and analyzed electrophoretically, along with an aliquot of the supernatant.

[0394] If the cloned protein is found in the inclusion bodies, it may be released to assay the cleavage and polymerase activities and the method of solubilization must be compatible with the particular activity. Different methods of solubilization may be appropriate for different proteins, and a variety of methods are discussed in *Molecular Cloning* (Sambrook et al., supra). The following is an adaptation we have used for several of our isolates.

[0395] 20 μ l of the inclusion body-water suspension were pelleted by centrifugation at 14,000 rpm for 4 minutes at room temperature, and the supernatant was discarded. To further wash the inclusion bodies, the pellet was resuspended in 20 μ l of lysis buffer with 2M urea, and incubated at room temperature for one hour. The washed inclusion bodies were then resuspended in 2 μ l of lysis buffer with 8M urea; the solution clarified visibly as the inclusion bodies dissolved. Undissolved debris was removed by centrifugation at 14,000 rpm for 4 minutes at room temperature, and the extract supernatant was transferred to a fresh tube.

[0396] To reduce the urea concentration, the extract was diluted into KH_2PO_4 . A fresh tube was prepared containing 180 μ l of 50 mM KH_2PO_4 , pH 9.5, 1 mM EDTA and 50 mM NaCl. A 2 μ l aliquot of the extract was added and vortexed briefly to mix. This step was repeated until all of the extract had been added for a total of 10 additions. The mixture was allowed to sit at room temperature for 15 minutes, during which time some precipitate often forms. Precipitates were removed by centrifugation at 14,000 rpm, for 15 minutes at room temperature, and the supernatant was transferred to a fresh tube. To the 200 μ l of protein in the KH_2PO_4 solution, 140-200 μ l of saturated $(\text{NH}_4)_2\text{SO}_4$ were added, so that the resulting mixture was about 41% to 50% saturated $(\text{NH}_4)_2\text{SO}_4$. The mixture was chilled on ice for 30 minutes to allow the protein to precipitate, and the protein was then collected by centrifugation at 14,000 rpm, for 4 minutes at room temperature. The supernatant was discarded, and the pellet was dissolved in 20 μ l Buffer C (20 mM HEPES, pH 7.9, 1 mM EDTA, 0.5% PMSF, 25 mM KCl and 0.5% each of Tween-20 and Nonidet P 40). The protein solution was centrifuged again for 4 minutes to pellet insoluble materials, and the supernatant was removed to a fresh tube. The protein contents of extracts prepared in this manner were visualized by resolving 1-4 μ l by SDS-PAGE; 0.5 to 1 μ l of extract was tested in the cleavage and polymerization assays as described.

[0397] E. Protein Analysis for Presence of Nuclease and Synthetic Activity

[0398] The 5' nucleases described above and shown in FIGS. 4 and 5 were analyzed by the following methods.

[0399] 1. Structure Specific Nuclease Assay

[0400] A candidate modified polymerase is tested for 5' nuclease activity by examining its ability to catalyze structure-specific cleavages. By the term "cleavage structure" as used herein, is meant a nucleic acid structure which is a substrate for cleavage by the 5' nuclease activity of a DNAP.

[0401] The polymerase is exposed to test complexes that have the structures shown in FIG. 16. Testing for 5' nuclease activity involves three reactions: 1) a primer-directed cleavage (FIG. 16B) is performed because it is relatively insensitive to variations in the salt concentration of the reaction and can, therefore, be performed in whatever solute conditions the modified enzyme requires for activity; this is generally the same conditions preferred by unmodified polymerases; 2) a similar primer-directed cleavage is performed in a buffer which permits primer-independent cleavage, i.e., a low salt buffer, to demonstrate that the enzyme is viable under these conditions; and 3) a primer-independent cleavage (FIG. 16A) is performed in the same low salt buffer.

[0402] The bifurcated duplex is formed between a substrate strand and a template strand as shown in FIG. 16. By

the term "substrate strand" as used herein, is meant that strand of nucleic acid in which the cleavage mediated by the 5' nuclease activity occurs. The substrate strand is always depicted as the top strand in the bifurcated complex which serves as a substrate for 5' nuclease cleavage (**FIG. 16**). By the term "template strand" as used herein, is meant the strand of nucleic acid which is at least partially complementary to the substrate strand and which anneals to the substrate strand to form the cleavage structure. The template strand is always depicted as the bottom strand of the bifurcated cleavage structure (**FIG. 16**). If a primer (a short oligonucleotide of 19 to 30 nucleotides in length) is added to the complex, as when primer-dependent cleavage is to be tested, it is designed to anneal to the 3' arm of the template strand (**FIG. 16B**). Such a primer would be extended along the template strand if the polymerase used in the reaction has synthetic activity.

[0403] The cleavage structure may be made as a single hairpin molecule, with the 3' end of the target and the 5' end of the pilot joined as a loop as shown in **FIG. 16E**. A primer oligonucleotide complementary to the 3' arm is also required for these tests so that the enzyme's sensitivity to the presence of a primer may be tested.

[0404] Nucleic acids to be used to form test cleavage structures can be chemically synthesized, or can be generated by standard recombinant DNA techniques. By the latter method, the hairpin portion of the molecule can be created by inserting into a cloning vector duplicate copies of a short DNA segment, adjacent to each other but in opposing orientation. The double-stranded fragment encompassing this inverted repeat, and including enough flanking sequence to give short (about 20 nucleotides) unpaired 5' and 3' arms, can then be released from the vector by restriction enzyme digestion, or by PCR performed with an enzyme lacking a 5' exonuclease (e.g., the Stoffel fragment of Amplitaq™ DNA polymerase, Vent™ DNA polymerase).

[0405] The test DNA can be labeled on either end, or internally, with either a radioisotope, or with a non-isotopic tag. Whether the hairpin DNA is a synthetic single strand or a cloned double strand, the DNA is heated prior to use to melt all duplexes. When cooled on ice, the structure depicted in **FIG. 16E** is formed, and is stable for sufficient time to perform these assays.

[0406] To test for primer-directed cleavage (Reaction 1), a detectable quantity of the test molecule (typically 1-100 fmol of ³²P-labeled hairpin molecule) and a 10 to 100-fold molar excess of primer are placed in a buffer known to be compatible with the test enzyme. For Reaction 2, where primer-directed cleavage is performed under condition which allow primer-independent cleavage, the same quantities of molecules are placed in a solution that is the same as the buffer used in Reaction 1 regarding pH, enzyme stabilizers (e.g., bovine serum albumin, nonionic detergents, gelatin) and reducing agents (e.g., dithiothreitol, 2-mercaptoethanol) but that replaces any monovalent cation salt with 20 mM KCl; 20 mM KCl is the demonstrated optimum for primer-independent cleavage. Buffers for enzymes, such as DNApEcl, that usually operate in the absence of salt are not supplemented to achieve this concentration. To test for primer-independent cleavage (Reaction 3) the same quantity of the test molecule, but no primer, are combined under the same buffer conditions used for Reaction 2.

[0407] All three test reactions are then exposed to enough of the enzyme that the molar ratio of enzyme to test complex is approximately 1:1. The reactions are incubated at a range of temperatures up to, but not exceeding, the temperature allowed by either the enzyme stability or the complex stability, whichever is lower, up to 80° C. for enzymes from thermophiles, for a time sufficient to allow cleavage (10 to 60 minutes). The products of Reactions 1, 2 and 3 are resolved by denaturing polyacrylamide gel electrophoresis, and visualized by autoradiography or by a comparable method appropriate to the labeling system used. Additional labeling systems include chemiluminescence detection, silver or other stains, blotting and probing and the like. The presence of cleavage products is indicated by the presence of molecules which migrate at a lower molecular weight than does the uncleaved test structure. These cleavage products indicate that the candidate polymerase has structure-specific 5' nuclease activity.

[0408] To determine whether a modified DNA polymerase has substantially the same 5' nuclease activity as that of the native DNA polymerase, the results of the above-described tests are compared with the results obtained from these tests performed with the native DNA polymerase. By "substantially the same 5' nuclease activity" we mean that the modified polymerase and the native polymerase will both cleave test molecules in the same manner. It is not necessary that the modified polymerase cleave at the same rate as the native DNA polymerase.

[0409] Some enzymes or enzyme preparations may have other associated or contaminating activities that may be functional under the cleavage conditions described above and that may interfere with 5' nuclease detection. Reaction conditions can be modified in consideration of these other activities, to avoid destruction of the substrate, or other masking of the 5' nuclease cleavage and its products. For example, the DNA polymerase I of *E. Coli* (Pol I), in addition to its polymerase and 5' nuclease activities, has a 3' exonuclease that can degrade DNA in a 3' to 5' direction. Consequently, when the molecule in **FIG. 16E** is exposed to this polymerase under the conditions described above, the 3' exonuclease quickly removes the unpaired 3' arm, destroying the bifurcated structure required of a substrate for the 5' exonuclease cleavage and no cleavage is detected. The true ability of Pol I to cleave the structure can be revealed if the 3' exonuclease is inhibited by a change of conditions (e.g., pH), mutation, or by addition of a competitor for the activity. Addition of 500 pmoles of a single-stranded competitor oligonucleotide, unrelated to the **FIG. 16E** structure, to the cleavage reaction with Pol I effectively inhibits the digestion of the 3' arm of the **FIG. 16E** structure without interfering with the 5' exonuclease release of the 5' arm. The concentration of the competitor is not critical, but should be high enough to occupy the 3' exonuclease for the duration of the reaction.

[0410] Similar destruction of the test molecule may be caused by contaminants in the candidate polymerase preparation. Several sets of the structure specific nuclease reactions may be performed to determine the purity of the candidate nuclease and to find the window between under and over exposure of the test molecule to the polymerase preparation being investigated.

[0411] The above described modified polymerases were tested for 5' nuclease activity as follows: Reaction I was

performed in a buffer of 10 mM Tris-Cl, pH 8.5 at 20° C., 1.5 mM MgCl₂ and 50 mM KCl and in Reaction 2 the KCl concentration was reduced to 20 mM. In Reactions 1 and 2, 10 fmoles of the test substrate molecule shown in **FIG. 16E** were combined with 1 pmole of the indicated primer and 0.5 to 1.0 μ l of extract containing the modified polymerase (prepared as described above). This mixture was then incubated for 10 minutes at 55° C. For all of the mutant polymerases tested these conditions were sufficient to give complete cleavage. When the molecule shown in **FIG. 16E** was labeled at the 5' end, the released 5' fragment, 25 nucleotides long, was conveniently resolved on a 20% polyacrylamide gel (19:1 cross-linked) with 7 M urea in a buffer containing 45 mM Tris-borate pH 8.3, 1.4 mM EDTA. Clones 4C-F and 5B exhibited structure-specific cleavage comparable to that of the unmodified DNA polymerase. Additionally, clones 4E, 4F and 4G have the added ability to cleave DNA in the absence of a 3' arm as discussed above. Representative cleavage reactions are shown in **FIG. 17**.

[0412] For the reactions shown in **FIG. 17**, the mutant polymerase clones 4E (Taq mutant) and SB (Tfl mutant) were examined for their ability to cleave the hairpin substrate molecule shown in **FIG. 16E**. The substrate molecule was labeled at the 5' terminus with ³²P, 10 fmoles of heat-denatured, end-labeled substrate DNA and 0.5 units of DNAP_{Taq} (lane 1) or 0.5 μ l of 4e or 5b extract (**FIG. 17**, lanes 2-7, extract was prepared as described above) were mixed together in a buffer containing 10 mM Tris-Cl, pH 8.5, 50 mM KCl and 1.5 mM MgCl₂. The final reaction volume was 10 μ l. Reactions shown in lanes 4 and 7 contain in addition 50 μ M of each dNTP. Reactions shown in lanes 3, 4, 6 and 7 contain 0.2 μ M of the primer oligonucleotide (complementary to the 3' arm of the substrate and shown in **FIG. 16E**). Reactions were incubated at 55° C. for 4 minutes. Reactions were stopped by the addition of 8 μ l of 95% formamide containing 20 mM EDTA and 0.05% marker dyes per 10 μ l reaction volume. Samples were then applied to 12% denaturing acrylamide gels. Following electrophoresis, the gels were autoradiographed. **FIG. 17** shows that clones 4E and 5B exhibit cleavage activity similar to that of the native DNAP_{Taq}. Note that some cleavage occurs in these reactions in the absence of the primer. When long hairpin structure, such as the one used here (**FIG. 16E**), are used in cleavage reactions performed in buffers containing 50 mM KCl a low level of primer-independent cleavage is seen. Higher concentrations of KCl suppress, but do not eliminate, this primer-independent cleavage under these conditions.

[0413] 2. Assay for Synthetic Activity

[0414] The ability of the modified enzyme or proteolytic fragments is assayed by adding the modified enzyme to an assay system in which a primer is annealed to a template and DNA synthesis is catalyzed by the added enzyme. Many standard laboratory techniques employ such an assay. For example, nick translation and enzymatic sequencing involve extension of a primer along a DNA template by a polymerase molecule.

[0415] In a preferred assay for determining the synthetic activity of a modified enzyme an oligonucleotide primer is annealed to a single-stranded DNA template, e.g., bacteriophage M13 DNA, and the primer/template duplex is incubated in the presence of the modified polymerase in

question, deoxynucleoside triphosphates (dNTPs) and the buffer and salts known to be appropriate for the unmodified or native enzyme. Detection of either primer extension (by denaturing gel electrophoresis) or dNTP incorporation (by acid precipitation or chromatography) is indicative of an active polymerase. A label, either isotopic or non-isotopic, is preferably included on either the primer or as a dNTP to facilitate detection of polymerization products. Synthetic activity is quantified as the amount of free nucleotide incorporated into the growing DNA chain and is expressed as amount incorporated per unit of time under specific reaction conditions.

[0416] Representative results of an assay for synthetic activity is shown in **FIG. 18**. The synthetic activity of the mutant DNAP_{Taq} clones 4B-F was tested as follows: A master mixture of the following buffer was made: 1.2X PCR buffer (1X PCR buffer contains 50 mM KCl, 1.5 mM MgCl₂, 10 mM Tris-Cl, pH 8.5 and 0.05% each Tween 20 and Nonidet P40), 50 μ M each of dGTP, dATP and dTTP, 5 μ M dCTP and 0.125 μ M α -³²P-dCTP at 600 Ci/mmol. Before adjusting this mixture to its final volume, it was divided into two equal aliquots. One received distilled water up to a volume of 50 μ l to give the concentrations above. The other received 5 μ g of single-stranded M13mp18 DNA (approximately 2.5 pmol or 0.05 μ M final concentration) and 250 pmol of M13 sequencing primer (5 μ M final concentration) and distilled water to a final volume of 50 μ l. Each cocktail was warmed to 75° C. for 5 minutes and then cooled to room temperature. This allowed the primers to anneal to the DNA in the DNA-containing mixtures.

[0417] For each assay, 4 μ l of the cocktail with the DNA was combined with 1 μ l of the mutant polymerase, prepared as described, or 1 unit of DNAP_{Taq} (Perkin Elmer) in 1 μ l of dH₂O. A "no DNA" control was done in the presence of the DNAP_{Taq} (**FIG. 18**, lane 1), and a "no enzyme" control was done using water in place of the enzyme (lane 2). Each reaction was mixed, then incubated at room temperature (approx. 22° C.) for 5 minutes, then at 55° C. for 2 minutes, then at 72° C. for 2 minutes.

[0418] This step incubation was done to detect polymerization in any mutants that might have optimal temperatures lower than 72° C. After the final incubation, the tubes were spun briefly to collect any condensation and were placed on ice. One μ l of each reaction was spotted at an origin 1.5 cm from the bottom edge of a polyethyleneimine (PEI) cellulose thin layer chromatography plate and allowed to dry. The chromatography plate was run in 0.75 M NaH₂PO₄, pH 3.5, until the buffer front had run approximately 9 cm from the origin. The plate was dried, wrapped in plastic wrap, marked with luminescent ink, and exposed to X-ray film. Incorporation was detected as counts that stuck where originally spotted, while the unincorporated nucleotides were carried by the salt solution from the origin.

[0419] Comparison of the locations of the counts with the two control lanes confirmed the lack of polymerization activity in the mutant preparations. Among the modified DNAP_{Taq} clones, only clone 4B retains any residual synthetic activity as shown in **FIG. 18**.

EXAMPLE 3

5' Nucleases Derived from Thermostable DNA Polymerases can Cleave Short Hairpin Structures with Specificity

[0420] The ability of the 5' nucleases to cleave hairpin structures to generate a cleaved hairpin structure suitable as a detection molecule was examined. The structure and sequence of the hairpin test molecule is shown in **FIG. 19A** (SEQ ID NO:15). The oligonucleotide (labeled "primer" in **FIG. 19A**, SEQ ID NO:22) is shown annealed to its complementary sequence on the 3' arm of the hairpin test molecule. The hairpin test molecule was single-end labeled with ³²P using a labeled T7 promoter primer in a polymerase chain reaction. The label is present on the 5' arm of the hairpin test molecule and is represented by the star in **FIG. 19A**.

[0421] The cleavage reaction was performed by adding 10 fmoles of heat-denatured, end-labeled hairpin test molecule, 0.2 μ M of the primer oligonucleotide (complementary to the 3' arm of the hairpin), 50 μ M of each dNTP and 0.5 units of DNAPtaq (Perkin Elmer) or 0.5 μ l of extract containing a 5' nuclease (prepared as described above) in a total volume of 10 μ l in a buffer containing 10 mM Tris-Cl, pH 8.5, 50 mM KCl and 1.5 mM MgCl₂. Reactions shown in lanes 3, 5 and 7 were run in the absence of dNTPs.

[0422] Reactions were incubated at 55° C. for 4 minutes. Reactions were stopped at 55° C. by the addition of 8 μ l of 95% formamide with 20 mM EDTA and 0.05% marker dyes per 10 μ l reaction volume. Samples were not heated before loading onto denaturing polyacrylamide gels (10% polyacrylamide, 19:1 crosslinking, 7 M urea, 89 mM Tris-borate, pH 8.3, 2.8 mM EDTA). The samples were not heated to allow for the resolution of single-stranded and re-duplexed uncleaved hairpin molecules.

[0423] **FIG. 19B** shows that altered polymerases lacking any detectable synthetic activity cleave a hairpin structure when an oligonucleotide is annealed to the single-stranded 3' arm of the hairpin to yield a single species of cleaved product (**FIG. 19B**, lanes 3 and 4). 5' nucleases, such as clone 4D, shown in lanes 3 and 4, produce a single cleaved product even in the presence of dNTPs. 5' nucleases which retain a residual amount of synthetic activity (less than 1% of wild type activity) produce multiple cleavage products as the polymerase can extend the oligonucleotide annealed to the 3' arm of the hairpin thereby moving the site of cleavage (clone 4B, lanes 5 and 6). Native DNAPtaq produces even more species of cleavage products than do mutant polymerases retaining residual synthetic activity and additionally converts the hairpin structure to a double-stranded form in the presence of dNTPs due to the high level of synthetic activity in the native polymerase (**FIG. 19B**, lane 8).

EXAMPLE 4

Test of the Trigger/Detection Assay

[0424] To test the ability of an oligonucleotide of the type released in the trigger reaction of the trigger/detection assay to be detected in the detection reaction of the assay, the two hairpin structures shown in **FIG. 20A** were synthesized using standard techniques. The two hairpins are termed the A-hairpin (SEQ ID NO:23) and the T-hairpin (SEQ ID NO:24). The predicted sites of cleavage in the presence of

the appropriate annealed primers are indicated by the arrows. The A- and T-hairpins were designed to prevent intra-strand mis-folding by omitting most of the T residues in the A-hairpin and omitting most of the A residues in the T-hairpin. To avoid mis-priming and slippage, the hairpins were designed with local variations in the sequence motifs (e.g., spacing T residues one or two nucleotides apart or in pairs). The A- and T-hairpins can be annealed together to form a duplex which has appropriate ends for directional cloning in pUC-type vectors; restriction sites are located in the loop regions of the duplex and can be used to elongate the stem regions if desired.

[0425] The sequence of the test trigger oligonucleotide is shown in **FIG. 20B**; this oligonucleotide is termed the alpha primer (SEQ ID NO:25). The alpha primer is complementary to the 3' arm of the T-hairpin as shown in **FIG. 20A**. When the alpha primer is annealed to the T-hairpin, a cleavage structure is formed that is recognized by thermostable DNA polymerases. Cleavage of the T-hairpin liberates the 5' single-stranded arm of the T-hairpin, generating the tau primer (SEQ ID NO:26) and a cleaved T-hairpin (**FIG. 20B**; SEQ ID NO:27). The tau primer is complementary to the 3' arm of the A-hairpin as shown in **FIG. 20A**. Annealing of the tau primer to the A-hairpin generates another cleavage structure; cleavage of this second cleavage structure liberates the 5' single-stranded arm of the A-hairpin, generating another molecule of the alpha primer which then is annealed to another molecule of the T-hairpin. Thermocycling releases the primers so they can function in additional cleavage reactions. Multiple cycles of annealing and cleavage are carried out. The products of the cleavage reactions are primers and the shortened hairpin structures shown in **FIG. 20C**. The shortened or cleaved hairpin structures may be resolved from the uncleaved hairpins by electrophoresis on denaturing acrylamide gels.

[0426] The annealing and cleavage reactions are carried as follows: In a 50 μ l reaction volume containing 10 mM Tris-Cl, pH 8.5, 1.0 MgCl₂, 75 mM KCl, 1 pmole of A-hairpin, 1 pmole T-hairpin, the alpha primer is added at equimolar amount relative to the hairpin structures (1 pmole) or at dilutions ranging from 10- to 10⁶-fold and 0.5 μ l of extract containing a 5' nuclease (prepared as described above) are added. The predicted melting temperature for the alpha or trigger primer is 60° C. in the above buffer. Annealing is performed just below this predicted melting temperature at 55° C. Using a Perkin Elmer DNA Thermal Cycler, the reactions are annealed at 55° C. for 30 seconds. The temperature is then increased slowly over a five minute period to 72° C. to allow for cleavage. After cleavage, the reactions are rapidly brought to 55° C. (1° C. per second) to allow another cycle of annealing to occur. A range of cycles are performed (20, 40 and 60 cycles) and the reaction products are analyzed at each of these number of cycles. The number of cycles which indicates that the accumulation of cleaved hairpin products has not reached a plateau is then used for subsequent determinations when it is desirable to obtain a quantitative result.

[0427] Following the desired number of cycles, the reactions are stopped at 55° C. by the addition of 8 μ l of 95% formamide with 20 mM EDTA and 0.05% marker dyes per 10 μ l reaction volume. Samples are not heated before loading onto denaturing polyacrylamide gels (10% polyacrylamide, 19:1 crosslinking, 7 M urea, 89 mM tris-borate,

pH 8.3, 2.8 mM EDTA). The samples were not heated to allow for the resolution of single-stranded and re-duplexed uncleaved hairpin molecules.

[0428] The hairpin molecules may be attached to separate solid support molecules, such as agarose, styrene or magnetic beads, via the 3' end of each hairpin. A spacer molecule may be placed between the 3' end of the hairpin and the bead if so desired. The advantage of attaching the hairpins to a solid support is that this prevents the hybridization of the A- and T-hairpins to one another during the cycles of melting and annealing. The A- and T-hairpins are complementary to one another (as shown in FIG. 20D) and if allowed to anneal to one another over their entire lengths this would reduce the amount of hairpins available for hybridization to the alpha and tau primers during the detection reaction.

[0429] The 5' nucleases of the present invention are used in this assay because they lack significant synthetic activity. The lack of synthetic activity results in the production of a single cleaved hairpin product (as shown in FIG. 19B, lanes 6 and 8) or 2) the presence of primer-independent cleavage in the reaction. The presence of primer-independent cleavage is detected in the trigger/detection assay by the presence of different sized products at the fork of the cleavage structure. Primer-independent cleavage can be dampened or repressed, when present, by the use of uncleavable nucleotides in the fork region of the hairpin molecule. For example, thiolated nucleotides can be used to replace several nucleotides at the fork region to prevent primer-independent cleavage.

EXAMPLE 5

Cleavage of Linear Nucleic Acid Substrates

[0430] From the above, it should be clear that native (i.e., "wild type") thermostable DNA polymerases are capable of cleaving hairpin structures in a specific manner and that this discovery can be applied with success to a detection assay. In this example, the mutant DNAPs of the present invention are tested against three different cleavage structures shown in FIG. 22A. Structure 1 in FIG. 22A is simply single stranded 206-mer (the preparation and sequence information for which was discussed above). Structures 2 and 3 are duplexes; structure 2 is the same hairpin structure as shown in FIG. 12A (bottom), while structure 3 has the hairpin portion of structure 2 removed.

[0431] The cleavage reactions comprised 0.01 pmoles of the resulting substrate DNA, and 1 pmole of pilot oligonucleotide in a total volume of 10 μ l of 10 mM Tris-Cl, pH 8.3, 100 mM KCl, 1 mM MgCl₂. Reactions were incubated for 30 minutes at 55° C., and stopped by the addition of 8 μ l of 95% formamide with 20 mM EDTA and 0.05% marker dyes. Samples were heated to 75° C. for 2 minutes immediately before electrophoresis through a 10% polyacrylamide gel (19:1 cross link), with 7M urea, in a buffer of 45 mM Tris-Borate, pH 8.3, 1.4 mM EDTA.

[0432] The results were visualized by autoradiography and are shown in FIG. 22B with the enzymes indicated as follows: I is native Taq DNAP; II is native Tfl DNAP; III is Cleavase® BX shown in FIG. 4E; IV is Cleavase® BB

shown in FIG. 4F; V is the mutant shown in FIG. 5B; and VI is Cleavase® BN shown in FIG. 4G.

[0433] Structure 2 was used to "normalize" the comparison. For example, it was found that it took 50 ng of Taq DNAP and 300 ng of Cleavase® BN to give similar amounts of cleavage of Structure 2 in thirty (30) minutes. Under these conditions native Taq DNAP is unable to cleave Structure 3 to any significant degree. Native Tfl DNAP cleaves Structure 3 in a manner that creates multiple products.

[0434] By contrast, all of the mutants tested cleave the linear duplex of Structure 3. This finding indicates that this characteristic of the mutant DNA polymerases is consistent of thermostable polymerases across thermophilic species.

[0435] The finding described herein that the mutant DNA polymerases of the present invention are capable of cleaving linear duplex structures allows for application to a more straightforward assay design (FIG. 1A). FIG. 23 provides a more detailed schematic corresponding to the assay design of FIG. 1A.

[0436] The two 43-mers depicted in FIG. 23 were synthesized by standard methods. Each included a fluorescein on the 5' for detection purposes and a biotin on the 3' end to allow attachment to streptavidin coated paramagnetic particles (the biotin-avidin attachment is indicated by "").

[0437] Before the trityl groups were removed, the oligos were purified by HPLC to remove truncated by-products of the synthesis reaction. Aliquots of each 43-mer were bound to M-280 Dynabeads (Dynal) at a density of 100 pmoles per mg of beads. Two (2) mgs of beads (200 μ l) were washed twice in 1 \times wash/bind buffer (1 M NaCl, 5 mM Tris-Cl, pH 7.5, 0.5 mM EDTA) with 0.1% BSA, 200 μ l per wash. The beads were magnetically sedimented between washes to allow supernatant removal. After the second wash, the beads were resuspended in 200 μ l of 2 \times wash/bind buffer (2 M NaCl, 10 mM Tris-Cl, pH 7.5 with 1 mM EDTA), and divided into two 100 μ l aliquots. Each aliquot received 1 μ l of a 100 μ M solution of one of the two oligonucleotides. After mixing, the beads were incubated at room temperature for 60 minutes with occasional gentle mixing. The beads were then sedimented and analysis of the supernatants showed only trace amounts of unbound oligonucleotide, indicating successful binding. Each aliquot of beads was washed three times, 100 μ l per wash, with IX wash/bind buffer, then twice in a buffer of 10 mM Tris-Cl, pH 8.3 and 75 mM KCl. The beads were resuspended in a final volume of 100 μ l of the Tris/KCl, for a concentration of 1 pmole of oligo bound to 10 μ g of beads per μ l of suspension. The beads were stored at 4° C. between uses.

[0438] The types of beads correspond to FIG. 1A. That is to say, type 2 beads contain the oligo (SEQ ID NO:33) comprising the complementary sequence (SEQ ID NO:34) for the alpha signal oligo (SEQ ID NO:35) as well as the beta signal oligo (SEQ ID NO:36) which when liberated is a 24-mer. This oligo has no "As" and is "T" rich. Type 3 beads contain the oligo (SEQ ID NO:37) comprising the complementary sequence (SEQ ID NO:38) for the beta signal oligo (SEQ ID NO:39) as well as the alpha signal oligo (SEQ ID NO:35) which when liberated is a 20-mer. This oligo has no "Ts" and is "A" rich.

[0439] Cleavage reactions comprised 1 μ l of the indicated beads, 10 pmoles of unlabelled alpha signal oligo as "pilot"

(if indicated) and 500 ng of Cleavase® BN in 20 μ l of 75 mM KCl, 10 mM Tris-Cl, pH 8.3, 1.5 mM MgCl₂ and 10 μ M CTAB. All components except the enzyme were assembled, overlaid with light mineral oil and warmed to 53° C. The reactions were initiated by the addition of prewarmed enzyme and incubated at that temperature for 30 minutes. Reactions were stopped at temperature by the addition of 16 μ l of 95% formamide with 20 mM EDTA and 0.05% each of bromophenol blue and xylene cyanol. This addition stops the enzyme activity and, upon heating, disrupts the biotin-avidin link, releasing the majority (greater than 95%) of the oligos from the beads. Samples were heated to 75° C. for 2 minutes immediately before electrophoresis through a 10% polyacrylamide gel (19:1 cross link), with 7 M urea, in a buffer of 45 mM Tris-Borate, pH 8.3, 1.4 mM EDTA. Results were visualized by contact transfer of the resolved DNA to positively charged nylon membrane and probing of the blocked membrane with an anti-fluorescein antibody conjugated to alkaline phosphatase. After washing, the signal was developed by incubating the membrane in Western Blue (Promega) which deposits a purple precipitate where the antibody is bound.

[0440] FIG. 24 shows the propagation of cleavage of the linear duplex nucleic acid structures of FIG. 23 by the DNAP mutants of the present invention. The two center lanes contain both types of beads. As noted above, the beta signal oligo (SEQ ID NO:36) when liberated is a 24-mer and the alpha signal oligo (SEQ ID NO:35) when liberated is a 20-mer. The formation of the two lower bands corresponding to the 24-mer and 20-mer is clearly dependent on "pilot".

EXAMPLE 6

[0441] 5' Exonucleolytic Cleavage ("Nibbling") by Thermostable DNAPs

[0442] It has been found that thermostable DNAPs, including those of the present invention, have a true 5' exonuclease capable of nibbling the 5' end of a linear duplex nucleic acid structures. In this example, the 206 base pair DNA duplex substrate is again employed (see above). In this case, it was produced by the use of one ³²P labeled primer and one unlabeled primer in a polymerase chain reaction. The cleavage reactions comprised 0.01 pmoles of heat-denatured, end-labeled substrate DNA (with the unlabeled strand also present), 5 pmoles of pilot oligonucleotide (see pilot oligos in FIG. 12A) and 0.5 units of DNAPtaq or 0.5 μ l of Cleavase® BB in the *E. coli* extract (see above), in a total volume of 10 μ l of 10 mM Tris-Cl, pH 8.5, 50 mM KCl, 1.5 mM MgCl₂.

[0443] Reactions were initiated at 65° C. by the addition of pre-warmed enzyme, then shifted to the final incubation temperature for 30 minutes. The results are shown in FIG. 25A. Samples in lanes 1-4 are the results with native Taq DNAP, while lanes 5-8 shown the results with Cleavase® BB. The reactions for lanes 1, 2, 5, and 6 were performed at 65° C. and reactions for lanes 3, 4, 7, and 8 were performed at 50° C. and all were stopped at temperature by the addition of 8 μ l of 95% formamide with 20 mM EDTA and 0.05% marker dyes. Samples were heated to 75° C. for 2 minutes immediately before electrophoresis through a 10% acrylamide gel (19:1 cross-linked), with 7 M urea, in a buffer of 45 mM TrisBorate, pH 8.3, 1.4 mM EDTA. The expected product in reactions 1, 2, 5, and 6 is 85 nucleotides long; in

reactions 3 and 7, the expected product is 27 nucleotides long. Reactions 4 and 8 were performed without pilot, and should remain at 206 nucleotides. The faint band seen at 24 nucleotides is residual end-labeled primer from the PCR.

[0444] The surprising result is that Cleavase® BB under these conditions causes all of the label to appear in a very small species, suggesting the possibility that the enzyme completely hydrolyzed the substrate. To determine the composition of the fastest-migrating band seen in lanes 5-8 (reactions performed with the deletion mutant), samples of the 206 base pair duplex were treated with either T7 gene 6 exonuclease (USB) or with calf intestine alkaline phosphatase (Promega), according to manufacturers' instructions, to produce either labeled mononucleotide (lane a of FIG. 25B) or free ³²P-labeled inorganic phosphate (lane b of FIG. 25B), respectively. These products, along with the products seen in lane 7 of panel A were resolved by brief electrophoresis through a 20% acrylamide gel (19:1 cross-link), with 7 M urea, in a buffer of 45 mM Tris-Borate, pH 8.3, 1.4 mM EDTA. Cleavase® BB is thus capable of converting the substrate to mononucleotides.

EXAMPLE 7

Nibbling is Duplex Dependent

[0445] The nibbling by Cleavase® BB is duplex dependent. In this example, internally labeled, single strands of the 206-mer were produced by 15 cycles of primer extension incorporating α -³²P labeled dCTP combined with all four unlabeled dNTPs, using an unlabeled 206-bp fragment as a template. Single and double stranded products were resolved by electrophoresis through a non-denaturing 6% polyacrylamide gel (29:1 cross-link) in a buffer of 45 mM TrisBorate, pH 8.3, 1.4 mM EDTA, visualized by autoradiography, excised from the gel, eluted by passive diffusion, and concentrated by ethanol precipitation.

[0446] The cleavage reactions comprised 0.04 pmoles of substrate DNA, and 2 μ l of Cleavase® BB (in an *E. coli* extract as described above) in a total volume of 40 μ l of 10 mM Tris-Cl, pH 8.5, 50 mM KCl, 1.5 mM MgCl₂. Reactions were initiated by the addition of pre-warmed enzyme; 10 μ l aliquots were removed at 5, 10, 20, and 30 minutes, and transferred to prepared tubes containing 8 μ l of 95% formamide with 30 mM EDTA and 0.05% marker dyes. Samples were heated to 75° C. for 2 minutes immediately before electrophoresis through a 10% acrylamide gel (19:1 cross-linked), with 7 M urea, in a buffer of 45 mM Tris-Borate, pH 8.3, 1.4 mM EDTA. Results were visualized by autoradiography as shown in FIG. 26. Clearly, the cleavage by Cleavase® BB depends on a duplex structure; no cleavage of the single strand structure is detected whereas cleavage of the 206-mer duplex is complete.

EXAMPLE 8

Nibbling can be Target Directed

[0447] The nibbling activity of the DNAPs of the present invention can be employed with success in a detection assay. One embodiment of such an assay is shown in FIG. 27. In this assay, a labelled oligo is employed that is specific for a target sequence. The oligo is in excess of the target so that hybridization is rapid. In this embodiment, the oligo contains two fluorescein labels whose proximity on the oligo

causes their emission to be quenched. When the DNAP is permitted to nibble the oligo the labels separate and are detectable. The shortened duplex is destabilized and dissociates. Importantly, the target is now free to react with an intact labelled oligo.

[0448] The reaction can continue until the desired level of detection is achieved. An analogous, although different, type of cycling assay has been described employing lambda exonuclease. See C. G. Copley and C. Boot, *BioTechniques* 13:888 (1992).

[0449] The success of such an assay depends on specificity. In other words, the oligo must hybridize to the specific target. It is also preferred that the assay be sensitive; the oligo ideally should be able to detect small amounts of target. FIG. 28A shows a 5'-end ³²P-labelled primer bound to a plasmid target sequence. In this case, the plasmid was pUC19 (commercially available) which was heat denatured by boiling two (2) minutes and then quick chilling. The primer is a 21-mer (SEQ ID NO:39). The enzyme employed was Cleavase® BX (a dilution equivalent to 5×10⁻³ μl extract) in 100 mM KCl, 10 mM Tris-Cl, pH 8.3, 2 mM MnCl₂. The reaction was performed at 55° C. for sixteen (16) hours with or without genomic background DNA (from chicken blood). The reaction was stopped by the addition of 8 μl of 95% formamide with 20 mM EDTA and marker dyes.

[0450] The products of the reaction were resolved by PAGE (10% polyacrylamide, 19:1 cross link, 1× TBE) as seen in FIG. 28B. Lane "M" contains the labelled 21-mer. Lanes 1-3 contain no specific target, although Lanes 2 and 3 contain 100 ng and 200 ng of genomic DNA, respectively. Lanes 4, 5 and 6 all contain specific target with either 0 ng, 100 ng or 200 ng of genomic DNA, respectively. It is clear that conversion to mononucleotides occurs in Lanes 4, 5 and 6 regardless of the presence or amount of background DNA. Thus, the nibbling can be target directed and specific.

EXAMPLE 9

Cleavage Purification

[0451] As noted above, expressed thermostable proteins, i.e., the 5' nucleases, were isolated by crude bacterial cell extracts. The precipitated *E. coli* proteins were then, along with other cell debris, removed by centrifugation. In this example, cells expressing the BN clone were cultured and collected (500 grams). For each gram (wet weight) of *E. coli*, 3 ml of lysis buffer (50 mM Tris-HCl, pH 8.0, 1 mM EDTA, 100 μM NaCl) was added. The cells were lysed with 200 μg/ml lysozyme at room temperature for 20 minutes. Thereafter deoxycholic acid was added to make a 0.2% final concentration and the mixture was incubated 15 minutes at room temperature.

[0452] The lysate was sonicated for approximately 6-8 minutes at 0° C. The precipitate was removed by centrifugation (39,000 g for 20 minutes). Polyethyleneimine was added (0.5%) to the supernatant and the mixture was incubated on ice for 15 minutes. The mixture was centrifuged (5,000 g for 15 minutes) and the supernatant was retained. This was heated for 30 minutes at 60° C. and then centrifuged again (5,000 g for 15 minutes) and the supernatant was again retained.

[0453] The supernatant was precipitated with 35% ammonium sulfate at 4° C. for 15 minutes. The mixture was then

centrifuged (5,000 g for 15 minutes) and the supernatant was removed. The precipitate was then dissolved in 0.25 M KCl, 20 Tris pH 7.6, 0.2% Tween and 0.1 EDTA) and then dialyzed against Binding Buffer (8× Binding Buffer comprises: 40 mM imidazole, 4M NaCl, 160 mM Tris-HCl, pH 7.9).

[0454] The solubilized protein is then purified on the Ni⁺⁺ column (Novagen). The Binding Buffer is allowed to drain to the top of the column bed and load the column with the prepared extract. A flow rate of about 10 column volumes per hour is optimal for efficient purification. If the flow rate is too fast, more impurities will contaminate the eluted fraction.

[0455] The column is washed with 25 ml (10 volumes) of 1× Binding Buffer and then washed with 15 ml (6 volumes) of 1× Wash Buffer (8× Wash Buffer comprises: 480 mM imidazole, 4M NaCl, 160 mM Tris-HCl, pH 7.9). The bound protein was eluted with 15 ml (6 volumes) of 1× Elute Buffer (4× Elute Buffer comprises: 4 mM imidazole, 2 M NaCl, 80 mM Tris-HCl, pH 7.9). Protein is then reprecipitated with 35% Ammonium Sulfate as above. The precipitate was then dissolved and dialyzed against: 20 mM Tris, 100 mM KCl, 1 mM EDTA). The solution was brought up to 0.1% each of Tween 20 and NP-40 and stored at 4° C.

EXAMPLE 10

The Use of Various Divalent Cations in the Cleavage Reaction Influences the Nature of the Resulting Cleavage Products

[0456] In comparing the 5' nucleases generated by the modification and/or deletion of the C-terminal polymerization domain of *Thermus aquaticus* DNA polymerase (DNAPtaq), as diagrammed in FIGS. 4B-G, significant differences in the strength of the interactions of these proteins with the 3' end of primers located upstream of the cleavage site (as depicted in FIG. 6) were noted. In describing the cleavage of these structures by Pol I-type DNA polymerases [Example 1 and Lyamichev et al. (1993) *Science* 260:778], it was observed that in the absence of a primer, the location of the junction between the double-stranded region and the single-stranded 5' and 3' arms determined the site of cleavage, but in the presence of a primer, the location of the 3' end of the primer became the determining factor for the site of cleavage. It was postulated that this affinity for the 3' end was in accord with the synthesizing function of the DNA polymerase.

[0457] Structure 2, shown in FIG. 22A, was used to test the effects of a 3' end proximal to the cleavage site in cleavage reactions comprising several different solutions [e.g., solutions containing different salts (KCl or NaCl), different divalent cations (Mn²⁺ or Mg²⁺), etc.] as well as the use of different temperatures for the cleavage reaction. When the reaction conditions were such that the binding of the enzyme (e.g., a DNAP comprising a 5' nuclease, a modified DNAP or a 5' nuclease) to the 3' end (of the pilot oligonucleotide) near the cleavage site was strong, the structure shown is cleaved at the site indicated in FIG. 22A. This cleavage releases the unpaired 5' arm and leaves a nick between the remaining portion of the target nucleic acid and the folded 3' end of the pilot oligonucleotide. In contrast, when the reaction conditions are such that the binding of the

DNAP (comprising a 5' nuclease) to the 3' end was weak, the initial cleavage was as described above, but after the release of the 5' arm, the remaining duplex is digested by the exonuclease function of the DNAP.

[0458] One way of weakening the binding of the DNAP to the 3' end is to remove all or part of the domain to which at least some of this function has been attributed. Some of 5' nucleases created by deletion of the polymerization domain of DNAPtaq have enhanced true exonuclease function, as demonstrated in Example 6.

[0459] The affinity of these types of enzymes (i.e., 5' nucleases associated with or derived from DNAPs) for recessed 3' ends may also be affected by the identity of the divalent cation present in the cleavage reaction. It was demonstrated by Longley et al. [Nucl. Acids Res. 18:7317 (1990)] that the use of $MnCl_2$ in a reaction with DNAPtaq enabled the polymerase to remove nucleotides from the 5' end of a primer annealed to a template, albeit inefficiently. Similarly, by examination of the cleavage products generated using Structure 2 from FIG. 22A, as described above, in a reaction containing either DNAPtaq or the Cleavase® BB nuclease, it was observed that the substitution of $MnCl_2$ for $MgCl_2$ in the cleavage reaction resulted in the exonucleolytic "nibbling" of the duplex downstream of the initial cleavage site. While not limiting the invention to any particular mechanism, it is thought that the substitution of $MnCl_2$ for $MgCl_2$ in the cleavage reaction lessens the affinity of these enzymes for recessed 3' ends.

[0460] In all cases, the use of $MnCl_2$ enhances the 5' nuclease function, and in the case of the Cleavase® BB nuclease, a 50- to 100-fold stimulation of the 5' nuclease function is seen. Thus, while the exonuclease activity of these enzymes was demonstrated above in the presence of $MgCl_2$, the assays described below show a comparable amount of exonuclease activity using 50 to 100-fold less enzyme when $MnCl_2$ is used in place of $MgCl_2$. When these reduced amounts of enzyme are used in a reaction mixture containing $MgCl_2$, the nibbling or exonuclease activity is much less apparent than that seen in Examples 6-8.

[0461] Similar effects are observed in the performance of the nucleic acid detection assay described in Examples 11-18 below when reactions performed in the presence of either $MgCl_2$ or $MnCl_2$ are compared. In the presence of either divalent cation, the presence of the invader oligonucleotide (described below) forces the site of cleavage into the probe duplex, but in the presence of $MnCl_2$ the probe duplex can be further nibbled producing a ladder of products that are visible when a 3' end label is present on the probe oligonucleotide. When the invader oligonucleotide is omitted from a reaction containing Mn^{2+} , the probe is nibbled from the 5' end. Mg^{2+} -based reactions display minimal nibbling of the probe oligonucleotide. In any of these cases, the digestion of the probe is dependent upon the presence of the target nucleic acid. In the examples below, the ladder produced by the enhanced nibbling activity observed in the presence of Mn^{2+} is used as a positive indicator that the probe oligonucleotide has hybridized to the target sequence.

EXAMPLE 11

Invasive 5' Endonucleolytic Cleavage by Thermostable 5' Nucleases in the Absence of Polymerization

[0462] As described in the examples above, 5' nucleases cleave near the junction between single-stranded and base-paired regions in a bifurcated duplex, usually about one base pair into the base-paired region. In this example, it is shown that thermostable 5' nucleases, including those of the present invention (e.g., Cleavase® BN nuclease, Cleavase® A/G nuclease), have the ability to cleave a greater distance into the base paired region when provided with an upstream oligonucleotide bearing a 3' region that is homologous to a 5' region of the subject duplex, as shown in FIG. 30.

[0463] FIG. 30 shows a synthetic oligonucleotide which was designed to fold upon itself which consists of the following sequence: 5'-GTTCTCTGCTCTCTGGTTCGCTGTCTCGCTTGTGAAACAAGCGAGA-CAGCGTGGTCTCTCG-3' (SEQ ID NO:40). This oligonucleotide is referred to as the "S-60 Hairpin." The 15 basepair hairpin formed by this oligonucleotide is further stabilized by a "tri-loop" sequence in the loop end (i.e., three nucleotides form the loop portion of the hairpin) [Hiraro, I. et al. (1994) Nucleic Acids Res. 22(4):576]. FIG. 30 also shows the sequence of the P-15 oligonucleotide and the location of the region of complementarity shared by the P-15 and S-60 hairpin oligonucleotides. The sequence of the P-15 oligonucleotide is 5'-CGAGAGACCACGCTG-3' (SEQ ID NO:41). As discussed in detail below, the solid black arrowheads shown in FIG. 29 indicate the sites of cleavage of the S-60 hairpin in the absence of the P-15 oligonucleotide and the hollow arrow heads indicate the sites of cleavage in the presence of the P-15 oligonucleotide. The size of the arrow head indicates the relative utilization of a particular site.

[0464] The S-60 hairpin molecule was labeled on its 5' end with biotin for subsequent detection. The S-60 hairpin was incubated in the presence of a thermostable 5' nuclease in the presence or the absence of the P-15 oligonucleotide. The presence of the full duplex which can be formed by the S-60 hairpin is demonstrated by cleavage with the Cleavase® BN 5' nuclease, in a primer-independent fashion (i.e., in the absence of the P-15 oligonucleotide). The release of 18 and 19-nucleotide fragments from the 5' end of the S-60 hairpin molecule showed that the cleavage occurred near the junction between the single and double stranded regions when nothing is hybridized to the 3' arm of the S-60 hairpin (FIG. 31, lane 2).

[0465] The reactions shown in FIG. 31 were conducted as follows. Twenty fmole of the 5' biotin-labeled hairpin DNA (SEQ ID NO:40) was combined with 0.1 ng of Cleavase® BN enzyme and 1 μ l of 100 mM MOPS (pH 7.5) containing 0.5% each of Tween-20 and NP-40 in a total volume of 9 μ l. In the reaction shown in lane 1, the enzyme was omitted and the volume was made up by addition of distilled water (this served as the uncut or no enzyme control). The reaction shown in lane 3 of FIG. 31 also included 0.5 pmole of the P15 oligonucleotide (SEQ ID NO:41), which can hybridize to the unpaired 3' arm of the S-60 hairpin (SEQ ID NO:40), as diagrammed in FIG. 30.

[0466] The reactions were overlaid with a drop of mineral oil, heated to 95° C. for 15 seconds, then cooled to 37° C.,

and the reaction was started by the addition of 1 μ l of 10 mM $MnCl_2$ to each tube. After 5 minutes, the reactions were stopped by the addition of 6 μ l of 95% formamide containing 20 mM EDTA and 0.05% marker dyes. Samples were heated to 75° C. for 2 minutes immediately before electrophoresis through a 15% acrylamide gel (19:1 cross-linked), with 7 M urea, in a buffer of 45 mM Tris-Borate, pH 8.3, 1.4 mM EDTA.

[0467] After electrophoresis, the gel plates were separated allowing the gel to remain flat on one plate. A 0.2 mm-pore positively-charged nylon membrane (NYTRAN, Schleicher and Schuell, Keene, N.H.), pre-wetted in H_2O , was laid on top of the exposed gel. All air bubbles were removed. Two pieces of 3MM filter paper (Whatman) were then placed on top of the membrane, the other glass plate was replaced, and the sandwich was clamped with binder clips. Transfer was allowed to proceed overnight. After transfer, the membrane was carefully peeled from the gel and allowed to air dry. After complete drying, the membrane was washed in 1.2 \times Sequenase Images Blocking Buffer (United States Biochemical) using 0.3 ml of buffer/cm² of membrane. The wash was performed for 30 minutes at room temperature. A streptavidin-alkaline phosphatase conjugate (SAAP, United States Biochemical) was added to a 1:4000 dilution directly to the blocking solution, and agitated for 15 minutes. The membrane was rinsed briefly with H_2O and then washed three times for 5 minutes per wash using 0.5 ml/cm² of 1 \times SAAP buffer (100 mM Tris-HCl, pH 10, 50 mM NaCl) with 0.1% sodium dodecyl sulfate (SDS). The membrane was rinsed briefly with H_2O between each wash. The membrane was then washed once in 1 \times SAAP buffer containing 1 mM $MgCl_2$ without SDS, drained thoroughly and placed in a plastic heat-sealable bag. Using a sterile pipet, 5 mls of CDP-Star[™] (Tropix, Bedford, Mass.) chemiluminescent substrate for alkaline phosphatase were added to the bag and distributed over the entire membrane for 2-3 minutes. The CDP-Star[™]-treated membrane was exposed to XRP X-ray film (Kodak) for an initial exposure of 10 minutes.

[0468] The resulting autoradiograph is shown in FIG. 31. In FIG. 31, the lane labelled "M" contains the biotinylated P-15 oligonucleotide which served as a marker. The sizes (in nucleotides) of the uncleaved S-60 hairpin (60 nuc; lane 1), the marker (15 nuc; lane "M") and the cleavage products generated by cleavage of the S-60 hairpin in the presence (lane 3) or absence (lane 2) of the P-15 oligonucleotide are indicated.

[0469] Because the complementary regions of the S-60 hairpin are located on the same molecule, essentially no lag time should be needed to allow hybridization (i.e., to form the duplex region of the hairpin). This hairpin structure would be expected to form long before the enzyme could locate and cleave the molecule. As expected, cleavage in the absence of the primer oligonucleotide was at or near the junction between the duplex and single-stranded regions, releasing the unpaired 5' arm (FIG. 31, lane 2). The resulting cleavage products were 18 and 19 nucleotides in length.

[0470] It was expected that stability of the S-60 hairpin with the tri-loop would prevent the P-15 oligonucleotide from promoting cleavage in the "primer-directed" manner described in Example 1 above, because the 3' end of the "primer" would remain unpaired. Surprisingly, it was found that the enzyme seemed to mediate an "invasion" by the

P-15 primer into the duplex region of the S-60 hairpin, as evidenced by the shifting of the cleavage site 3 to 4 basepairs further into the duplex region, releasing the larger products (22 and 21 nuc.) observed in lane 3 of FIG. 31.

[0471] The precise sites of cleavage of the S-60 hairpin are diagrammed on the structure in FIG. 30, with the solid black arrowheads indicating the sites of cleavage in the absence of the P-15 oligonucleotide and the hollow arrow heads indicating the sites of cleavage in the presence of P-15.

[0472] These data show that the presence on the 3' arm of an oligonucleotide having some sequence homology with the first several bases of the similarly oriented strand of the downstream duplex can be a dominant factor in determining the site of cleavage by 5' nucleases. Because the oligonucleotide which shares some sequence homology with the first several bases of the similarly oriented strand of the downstream duplex appears to invade the duplex region of the hairpin, it is referred to as an "invader" oligonucleotide. As shown in the examples below, an invader oligonucleotide appears to invade (or displace) a region of duplexed nucleic acid regardless of whether the duplex region is present on the same molecule (i.e., a hairpin) or whether the duplex is formed between two separate nucleic acid strands.

EXAMPLE 12

The Invader Oligonucleotide Shifts the Site of Cleavage in a Pre-Formed Probe/Target Duplex

[0473] In Example 11 it was demonstrated that an invader oligonucleotide could shift the site at which a 5' nuclease cleaves a duplex region present on a hairpin molecule. In this example, the ability of an invader oligonucleotide to shift the site of cleavage within a duplex region formed between two separate strands of nucleic acid molecules was examined.

[0474] A single-stranded target DNA comprising the single-stranded circular M13mp19 molecule and a labeled (fluorescein) probe oligonucleotide were mixed in the presence of the reaction buffer containing salt (KCl) and divalent cations (Mg^{2+} or Mn^{2+}) to promote duplex formation. The probe oligonucleotide refers to a labelled oligonucleotide which is complementary to a region along the target molecule (e.g., M13mp19). A second oligonucleotide (unlabelled) was added to the reaction after the probe and target had been allowed to anneal. The second oligonucleotide binds to a region of the target which is located downstream of the region to which the probe oligonucleotide binds. This second oligonucleotide contains sequences which are complementary to a second region of the target molecule. If the second oligonucleotide contains a region which is complementary to a portion of the sequences along the target to which the probe oligonucleotide also binds, this second oligonucleotide is referred to as an invader oligonucleotide (see FIG. 32c).

[0475] FIG. 32 depicts the annealing of two oligonucleotides to regions along the M13mp19 target molecule (bottom strand in all three structures shown). In FIG. 32 only a 52 nucleotide portion of the M13mp19 molecule is shown; this 52 nucleotide sequence is listed in SEQ ID NO:42. The probe oligonucleotide contains a fluorescein label at the 3' end; the sequence of the probe is 5'-AGAAAGGAAGG-GAAGAAAGC GAAAGG-3' (SEQ ID NO:43). In FIG. 32,

sequences comprising the second oligonucleotide, including the invader oligonucleotide are underlined. In **FIG. 32a**, the second oligonucleotide, which has the sequence 5'-GACGGGAAAGCCGGCGA ACG-3' (SEQ ID NO:44), is complementary to a different and downstream region of the target molecule than is the probe oligonucleotide (labeled with fluorescein or "Fluor"); there is a gap between the second, upstream oligonucleotide and the probe for the structure shown in **FIG. 32a**. In **FIG. 32b**, the second, upstream oligonucleotide, which has the sequence 5'-GAAAGCCGGCGAACGTGGCG-3' (SEQ ID NO:45), is complementary to a different region of the target molecule than is the probe oligonucleotide, but in this case, the second oligonucleotide and the probe oligonucleotide are adjacent to one another (that is the 3' end of the second, upstream oligonucleotide is immediately adjacent to the 5' end of the probe such that no gap exists between these two oligonucleotides). In **FIG. 32c**, the second, upstream oligonucleotide [5'-GGCGAACGTGGCGAGAAAGGA-3' (SEQ ID NO:46)] and the probe oligonucleotide share a region of complementarity with the target molecule. Thus, the upstream oligonucleotide has a 3' arm which has a sequence identical to the first several bases of the downstream probe. In this situation, the upstream oligonucleotide is referred to as an "invader" oligonucleotide.

[0476] The effect of the presence of an invader oligonucleotide upon the pattern of cleavage in a probe/target duplex formed prior to the addition of the invader was examined. The invader oligonucleotide and the enzyme were added after the probe was allowed to anneal to the target and the position and extent of cleavage of the probe were examined to determine a) if the invader was able to shift the cleavage site to a specific internal region of the probe, and b), if the reaction could accumulate specific cleavage products over time, even in the absence of thermal cycling, polymerization, or exonuclease removal of the probe sequence.

[0477] The reactions were carried out as follows. Twenty μ l each of two enzyme mixtures were prepared, containing 2 μ l of Cleavase® A/G nuclease extract (prepared as described in Example 2), with or without 50 pmole of the invader oligonucleotide (SEQ ID NO:46), as indicated, per 4 μ l of the mixture. For each of the eight reactions shown in **FIG. 33**, 150 fmole of M13mp19 single-stranded DNA (available from Life Technologies, Inc.) was combined with 5 pmoles of fluorescein labeled probe (SEQ ID NO:43), to create the structure shown in **FIG. 31c**, but without the invader oligonucleotide present (the probe/target mixture). One half (4 tubes) of the probe/target mixtures were combined with 1 μ l of 100 mM MOPS, pH 7.5 with 0.5% each of Tween-20 and NP-40, 0.5 μ l of 1 M KCl and 0.25 μ l of 80 mM MnCl₂, and distilled water to a volume of 6 μ l. The second set of probe/target mixtures were combined with 1 μ l of 100 mM MOPS, pH 7.5 with 0.5% each of Tween-20 and NP-40, 0.5 μ l of 1 M KCl and 0.25 μ l of 80 mM MgCl₂. The second set of mixtures therefore contained MgCl₂ in place of the MnCl₂ present in the first set of mixtures.

[0478] The mixtures (containing the probe/target with buffer, KCl and divalent cation) were covered with a drop of ChillOut® evaporation barrier (MJ Research) and were brought to 60° C. for 5 minutes to allow annealing. Four μ l of the above enzyme mixtures without the invader oligonucleotide was added to reactions whose products are shown in lanes 1, 3, 5 and 7 of **FIG. 33**. Reactions whose products

are shown lanes 2, 4, 6, and 8 of **FIG. 33** received the same amount of enzyme mixed with the invader oligonucleotide (SEQ ID NO:46). Reactions 1, 2, 5 and 6 were incubated for 5 minutes at 60° C. and reactions 3, 4, 7 and 8 were incubated for 15 minutes at 60° C.

[0479] All reactions were stopped by the addition of 8 μ l of 95% formamide with 20 mM EDTA and 0.05% marker dyes. Samples were heated to 90° C. for 1 minute immediately before electrophoresis through a 20% acrylamide gel (19:1 cross-linked), containing 7 M urea, in a buffer of 45 mM Tris-Borate, pH 8.3, 1.4 mM EDTA. Following electrophoresis, the reaction products were visualized by the use of an Hitachi FMBIO fluorescence imager, the output of which is seen in **FIG. 33**. The very low molecular weight fluorescent material seen in all lanes at or near the salt front in **FIG. 33** and other fluoro-imager figures is observed when fluorescently-labeled oligonucleotides are electrophoresed and imaged on a fluoro-imager. This material is not a product of the cleavage reaction.

[0480] The use of MnCl₂ in these reactions (lanes 1-4) stimulates the true exonuclease or "nibbling" activity of the Cleavase® enzyme, as described in Example 7, as is clearly seen in lanes 1 and 3 of **FIG. 33**. This nibbling of the probe oligonucleotide (SEQ ID NO:43) in the absence of invader oligonucleotide (SEQ ID NO:46) confirms that the probe oligonucleotide is forming a duplex with the target sequence. The ladder-like products produced by this nibbling reaction may be difficult to differentiate from degradation of the probe by nucleases that might be present in a clinical specimen. In contrast, introduction of the invader oligonucleotide (SEQ ID NO:46) caused a distinctive shift in the cleavage of the probe, pushing the site of cleavage 6 to 7 bases into the probe, confirming the annealing of both oligonucleotides. In presence of MnCl₂, the exonuclease "nibbling" may occur after the invader-directed cleavage event, until the residual duplex is destabilized and falls apart.

[0481] In a magnesium based cleavage reaction (lanes 5-8), the nibbling or true exonuclease function of the Cleavase® A/G is enzyme suppressed (but the endonucleolytic function of the enzyme is essentially unaltered), so the probe oligonucleotide is not degraded in the absence of the invader (**FIG. 33**, lanes 5 and 7). When the invader is added, it is clear that the invader oligonucleotide can promote a shift in the site of the endonucleolytic cleavage of the annealed probe. Comparison of the products of the 5 and 15 minute reactions with invader (lanes 6 and 8 in **FIG. 33**) shows that additional probe hybridizes to the target and is cleaved. The calculated melting temperature (T_m) of the portion of probe that is not invaded (i.e., nucleotides 9-26 of SEQ ID NO:43) is 56° C., so the observed turnover (as evidenced by the accumulation of cleavage products with increasing reaction time) suggests that the full length of the probe molecule, with a calculated T_m of 76° C., is must be involved in the subsequent probe annealing events in this 60° C. reaction.

EXAMPLE 13

The Overlap of the 3' Invader Oligonucleotide Sequence with the 5' Region of the Probe Causes a Shift in the Site of Cleavage

[0482] In Example 12, the ability of an invader oligonucleotide to cause a shift in the site of cleavage of a probe

annealed to a target molecule was demonstrated. In this example, experiments were conducted to examine whether the presence of an oligonucleotide upstream from the probe was sufficient to cause a shift in the cleavage site(s) along the probe or whether the presence of nucleotides on the 3' end of the invader oligonucleotide which have the same sequence as the first several nucleotides at the 5' end of the probe oligonucleotide were required to promote the shift in cleavage.

[0483] To examine this point, the products of cleavage obtained from three different arrangements of target-specific oligonucleotides are compared. A diagram of these oligonucleotides and the way in which they hybridize to a test nucleic acid, M13mp19, is shown in FIG. 32. In FIG. 32a, the 3' end of the upstream oligonucleotide (SEQ ID NO:45) is located upstream of the 5' end of the downstream "probe" oligonucleotide (SEQ ID NO:43) such that a region of the M13 target which is not paired to either oligonucleotide is present. In FIG. 32b, the sequence of the upstream oligonucleotide (SEQ ID NO:45) is immediately upstream of the probe (SEQ ID NO:43), having neither a gap nor an overlap between the sequences. FIG. 32c diagrams the arrangement of the substrates used in the assay of the present invention, showing that the upstream "invader" oligonucleotide (SEQ ID NO:46) has the same sequence on a portion of its 3' region as that present in the 5' region of the downstream probe (SEQ ID NO:43). That is to say, these regions will compete to hybridize to the same segment of the M13 target nucleic acid.

[0484] In these experiments, four enzyme mixtures were prepared as follows (planning 5 μ l per digest): Mixture 1 contained 2.25 μ l of Cleavase® A/G nuclease extract (prepared as described in Example 2) per 5 μ l of mixture, in 20 mM MOPS, pH 7.5 with 0.1% each of Tween 20 and NP-40, 4 mM MnCl₂ and 100 mM KCl. Mixture 2 contained 11.25 units of Taq DNA polymerase (Promega Corp., Madison, WI) per 5 μ l of mixture in 20 mM MOPS, pH 7.5 with 0.1% each of Tween 20 and NP-40, 4 mM MnCl₂ and 100 mM KCl. Mixture 3 contained 2.25 μ l of Cleavase® A/G nuclease extract per 5 μ l of mixture in 20 mM Tris-HCl, pH 8.5, 4 mM MgCl₂ and 100 mM KCl. Mixture 4 contained 11.25 units of Taq DNA polymerase per 5 μ l of mixture in 20 mM Tris-HCl, pH 8.5, 4 mM MgCl₂ and 100 mM KCl.

[0485] For each reaction, 50 fmole of M13mp19 single-stranded DNA (the target nucleic acid) was combined with 5 pmole of the probe oligonucleotide (SEQ ID NO:43 which contained a fluorescein label at the 3' end) and 50 pmole of one of the three upstream oligonucleotides diagrammed in FIG. 32 (i.e., one of SEQ ID NOS:44-46), in a total volume of 5 μ l of distilled water. The reactions were overlaid with a drop of ChillOut™ evaporation barrier (MJ Research) and warmed to 62° C. The cleavage reactions were started by the addition of 5 μ l of an enzyme mixture to each tube, and the reactions were incubated at 62° C. for 30 min. The reactions shown in lanes 1-3 of FIG. 34 received Mixture 1; reactions 4-6 received Mixture 2; reactions 7-9 received Mixture 3 and reactions 10-12 received Mixture 4.

[0486] After 30 minutes at 62° C., the reactions were stopped by the addition of 8 μ l of 95% formamide with 20 mM EDTA and 0.05% marker dyes. Samples were heated to 75° C. for 2 minutes immediately before electrophoresis

through a 20% acrylamide gel (19:1 cross-linked), with 7 M urea, in a buffer of 45 mM Tris-Borate, pH 8.3, 1.4 mM EDTA.

[0487] Following electrophoresis, the products of the reactions were visualized by the use of an Hitachi FMBIO fluorescence imager, the output of which is seen in FIG. 34. The reaction products shown in lanes 1, 4, 7 and 10 of FIG. 34 were from reactions which contained SEQ ID NO:44 as the upstream oligonucleotide (see FIG. 32a). The reaction products shown in lanes 2, 5, 8 and 11 of FIG. 34 were from reactions which contained SEQ ID NO:45 as the upstream oligonucleotide (see FIG. 32b). The reaction products shown in lanes 3, 6, 9 and 12 of FIG. 34 were from reactions which contained SEQ ID NO:46, the invader oligonucleotide, as the upstream oligonucleotide (see FIG. 32c).

[0488] Examination of the Mn²⁺ based reactions using either Cleavase® A/G nuclease or DNAPtaq as the cleavage agent (lanes 1 through 3 and 4 through 6, respectively) shows that both enzymes have active exonuclease function in these buffer conditions. The use of a 3' label on the probe oligonucleotide allows the products of the nibbling activity to remain labeled, and therefore visible in this assay. The ladders seen in lanes 1, 2, 4 and 5 confirm that the probe hybridize to the target DNA as intended. These lanes also show that the location of the non-invasive oligonucleotides have little effect on the products generated. The uniform ladder created by these digests would be difficult to distinguish from a ladder caused by a contaminating nuclease, as one might find in a clinical specimen. In contrast, the products displayed in lanes 3 and 6, where an invader oligonucleotide was provided to direct the cleavage, show a very distinctive shift, so that the primary cleavage product is smaller than those seen in the non-invasive cleavage. This product is then subject to further nibbling in these conditions, as indicated by the shorter products in these lanes. These invader-directed cleavage products would be easily distinguished from a background of non-specific degradation of the probe oligonucleotide.

[0489] When Mg²⁺ is used as the divalent cation the results are even more distinctive. In lanes 7, 8, 10 and 11 of FIG. 34, where the upstream oligonucleotides were not invasive, minimal nibbling is observed. The products in the DNAPtaq reactions show some accumulation of probe that has been shortened on the 5' end by one or two nucleotides consistent with previous examination of the action of this enzyme on nicked substrates (Longley et al., supra). When the upstream oligonucleotide is invasive, however, the appearance of the distinctively shifted probe band is seen. These data clearly indicated that it is the invasive 3' portion of the upstream oligonucleotide that is responsible for fixing the site of cleavage of the downstream probe.

[0490] Thus, the above results demonstrate that it is the presence of the free or initially non-annealed nucleotides at the 3' end of the invader oligonucleotide which mediate the shift in the cleavage site, not just the presence of an oligonucleotide annealed upstream of the probe. Nucleic acid detection assays which employ the use of an invader oligonucleotide are termed "invader-directed cleavage" assays.

EXAMPLE 14

Invader-Directed Cleavage Recognizes Single and Double Stranded Target Molecules in a Background of Non-Target DNA Molecules

[0491] For a nucleic acid detection method to be broadly useful, it must be able to detect a specific target in a sample that may contain large amounts of other DNA, e.g., bacterial or human chromosomal DNA. The ability of the invader directed cleavage assay to recognize and cleave either single- or double-stranded target molecules in the presence of large amounts of non-target DNA was examined. In these experiments a model target nucleic acid, M13, in either single or double stranded form (single-stranded M13mp18 is available from Life Technologies, Inc and double-stranded M13mp19 is available from New England Biolabs), was combined with human genomic DNA (Novagen, Madison, Wis.) and then utilized in invader-directed cleavage reactions. Before the start of the cleavage reaction, the DNAs were heated to 95° C. for 15 minutes to completely denature the samples, as is standard practice in assays, such as polymerase chain reaction or enzymatic DNA sequencing, which involve solution hybridization of oligonucleotides to double-stranded target molecules.

[0492] For each of the reactions shown in lanes 2-5 of FIG. 35, the target DNA (25 fmole of the ss DNA or 1 pmole of the ds DNA) was combined with 50 pmole of the invader oligonucleotide (SEQ ID NO:46); for the reaction shown in lane 1 the target DNA was omitted. Reactions 1, 3 and 5 also contained 470 ng of human genomic DNA. These mixtures were brought to a volume of 10 μ l with distilled water, overlaid with a drop of ChillOut™ evaporation barrier (MJ Research), and brought to 95° C. for 15 minutes. After this incubation period, and still at 95° C., each tube received 10 μ l of a mixture comprising 2.25 μ l of Cleavase® A/G nuclease extract (prepared as described in Example 2) and 5 pmole of the probe oligonucleotide (SEQ ID NO:43), in 20 mM MOPS, pH 7.5 with 0.1% each of Tween 20 and NP-40, 4 mM MnCl₂ and 100 mM KCl. The reactions were brought to 62° C. for 15 minutes and stopped by the addition of 12 μ l of 95% formamide with 20 mM EDTA and 0.05% marker dyes. Samples were heated to 75° C. for 2 minutes immediately before electrophoresis through a 20% acrylamide gel (19:1 cross-linked), with 7 M urea, in a buffer of 45 mM Tris-Borate, pH 8.3, 1.4 mM EDTA. The products of the reactions were visualized by the use of an Hitachi FMBIO fluorescence imager. The results are displayed in FIG. 35.

[0493] In FIG. 35, lane 1 contains the products of the reaction containing the probe (SEQ ID NO:43), the invader oligonucleotide (SEQ ID NO:46) and human genomic DNA. Examination of lane 1 shows that the probe and invader oligonucleotides are specific for the target sequence, and that the presence of genomic DNA does not cause any significant background cleavage.

[0494] In FIG. 35, lanes 2 and 3 contain reaction products from reactions containing the single-stranded target DNA (M13mp18), the probe (SEQ ID NO:43) and the invader oligonucleotide (SEQ ID NO:46) in the absence or presence of human genomic DNA, respectively. Examination of lanes 2 and 3 demonstrate that the invader detection assay may be used to detect the presence of a specific sequence on a single-stranded target molecule in the presence or absence of a large excess of competitor DNA (human genomic DNA).

[0495] In FIG. 35, lanes 4 and 5 contain reaction products from reactions containing the double-stranded target DNA (M13mp19), the probe (SEQ ID NO:43) and the invader oligonucleotide (SEQ ID NO:46) in the absence or presence of human genomic DNA, respectively. Examination of lanes 4 and 5 show that double stranded target molecules are eminently suitable for invader-directed detection reactions. The success of this reaction using a short duplexed molecule, M13mp19, as the target in a background of a large excess of genomic DNA is especially noteworthy as it would be anticipated that the shorter and less complex M13 DNA strands would be expected to find their complementary strand more easily than would the strands of the more complex human genomic DNA. If the M13 DNA reannealed before the probe and/or invader oligonucleotides could bind to the target sequences along the M13 DNA, the cleavage reaction would be prevented. In addition, because the denatured genomic DNA would potentially contain regions complementary to the probe and/or invader oligonucleotides it was possible that the presence of the genomic DNA would inhibit the reaction by binding these oligonucleotides thereby preventing their hybridization to the M13 target. The above results demonstrate that these theoretical concerns are not a problem under the reaction conditions employed above.

[0496] In addition to demonstrating that the invader detection assay may be used to detect sequences present in a double-stranded target, these data also show that the presence of a large amount of non-target DNA (470 ng/20 μ l reaction) does not lessen the specificity of the cleavage. While this amount of DNA does show some impact on the rate of product accumulation, probably by binding a portion of the enzyme, the nature of the target sequence, whether single- or double-stranded nucleic acid, does not limit the application of this assay.

EXAMPLE 15

Signal Accumulation in the Invader-Directed Cleavage Assay as a Function of Target Concentration

[0497] To investigate whether the invader-directed cleavage assay could be used to indicate the amount of target nucleic acid in a sample, the following experiment was performed. Cleavage reactions were assembled which contained an invader oligonucleotide (SEQ ID NO:46), a labelled probe (SEQ ID NO:43) and a target nucleic acid, M13mp19. A series of reactions, which contained smaller and smaller amounts of the M13 target DNA, was employed in order to examine whether the cleavage products would accumulate in a manner that reflected the amount of target DNA present in the reaction.

[0498] The reactions were conducted as follows. A master mix containing enzyme and buffer was assembled. Each 5 μ l of the master mixture contained 25 ng of Cleavase® BN nuclease in 20 mM MOPS (pH 7.5) with 0.1% each of Tween 20 and NP-40, 4 mM MnCl₂ and 100 mM KCl. For each of the cleavage reactions shown in lanes 4-13 of FIG. 36, a DNA mixture was generated which contained 5 pmoles of the fluorescein-labelled probe oligonucleotide (SEQ ID NO:43), 50 pmoles of the invader oligonucleotide (SEQ ID NO:46) and 100, 50, 10, 5, 1, 0.5, 0.1, 0.05, 0.01 or 0.005 fmole of single-stranded M13mp19, respectively, for every

5 μ l of the DNA mixture. The DNA solutions were covered with a drop of ChillOut® evaporation barrier (MJ Research) and brought to 61° C. The cleavage reactions were started by the addition of 5 μ l of the enzyme mixture to each of tubes (final reaction volume was 10 μ l). After 30 minutes at 61° C., the reactions were terminated by the addition of 8 μ l of 95% formamide with 20 mM EDTA and 0.05% marker dyes. Samples were heated to 90° C. for 1 minutes immediately before electrophoresis through a 20% denaturing acrylamide gel (19:1 cross-linked) with 7 M urea, in a buffer containing 45 mM Tris-Borate (pH 8.3), 1.4 mM EDTA. To provide reference (i.e., standards), 1.0, 0.1 and 0.01 pmole aliquots of fluorescein-labelled probe oligonucleotide (SEQ ID NO:43) were diluted with the above formamide solution to a final volume of 18 μ l. These reference markers were loaded into lanes 1-3, respectively of the gel. The products of the cleavage reactions (as well as the reference standards) were visualized following electrophoresis by the use of a Hitachi FM BIO fluorescence imager. The results are displayed in FIG. 36.

[0499] In FIG. 36, boxes appear around fluorescein-containing nucleic acid (i.e., the cleaved and uncleaved probe molecules) and the amount of fluorescein contained within each box is indicated under the box. The background fluorescence of the gel (see box labelled "background") was subtracted by the fluoro-imager to generate each value displayed under a box containing cleaved or uncleaved probe products (the boxes are numbered 1-14 at top left with a V followed by a number below the box). The lane marked "M" contains fluoresceinated oligonucleotides which served as markers.

[0500] The results shown in FIG. 36, demonstrate that the accumulation of cleaved probe molecules in a fixed-length incubation period reflects the amount of target DNA present in the reaction. The results also demonstrate that the cleaved probe products accumulate in excess of the copy number of the target. This is clearly demonstrated by comparing the results shown in lane 3, in which 10 fmole (0.01 pmole) of uncut probe are displayed with the results shown in 5, where the products which accumulated in response to the presence of 10 fmole of target DNA are displayed. These results show that the reaction can cleave hundreds of probe oligonucleotide molecules for each target molecule present, dramatically amplifying the target-specific signal generated in the invader-directed cleavage reaction.

EXAMPLE 16

Effect of Saliva Extract on the Invader-Directed Cleavage Assay

[0501] For a nucleic acid detection method to be useful in a medical (i.e., a diagnostic) setting, it must not be inhibited by materials and contaminants likely to be found in a typical clinical specimen. To test the susceptibility of the invader-directed cleavage assay to various materials, including but not limited to nucleic acids, glycoproteins and carbohydrates, likely to be found in a clinical sample, a sample of human saliva was prepared in a manner consistent with practices in the clinical laboratory and the resulting saliva extract was added to the invader-directed cleavage assay. The effect of the saliva extract upon the inhibition of cleavage and upon the specificity of the cleavage reaction was examined.

[0502] One and one-half milliliters of human saliva were collected and extracted once with an equal volume of a mixture containing phenol:chloroform:isoamyl alcohol (25:24:1). The resulting mixture was centrifuged in a micro-centrifuge to separate the aqueous and organic phases. The upper, aqueous phase was transferred to a fresh tube. One-tenth volumes of 3 M NaOAc were added and the contents of the tube were mixed. Two volumes of 100% ethyl alcohol were added to the mixture and the sample was mixed and incubated at room temperature for 15 minutes to allow a precipitate to form. The sample was centrifuged in a micro-centrifuge at 13,000 rpm for 5 minutes and the supernatant was removed and discarded. A milky pellet was easily visible. The pellet was rinsed once with 70% ethanol, dried under vacuum and dissolved in 200 μ l of 10 mM Tris-HCl, pH 8.0, 0.1 mM EDTA (this constitutes the saliva extract). Each μ l of the saliva extract was equivalent to 7.5 μ l of saliva. Analysis of the saliva extract by scanning ultraviolet spectrophotometry showed a peak absorbance at about 260 nm and indicated the presence of approximately 45 ng of total nucleic acid per μ l of extract.

[0503] The effect of the presence of saliva extract upon the following enzymes was examined: Cleavase® BN nuclease, Cleavase® A/G nuclease and three different lots of DNAPtaq: AmpliTaq® (Perkin Elmer; a recombinant form of DNAPtaq), AmpliTaq® LD (Perkin-Elmer; a recombinant DNAPtaq preparation containing very low levels of DNA) and Taq DNA polymerase (Fischer). For each enzyme tested, an enzyme/probe mixture was made comprising the chosen amount of enzyme with 5 pmole of the probe oligonucleotide (SEQ ID NO:43) in 10 μ l of 20 mM MOPS (pH 7.5) containing 0.1% each of Tween 20 and NP-40, 4 mM MnCl₂, 100 mM KCl and 100 μ g/ml BSA. The following amounts of enzyme were used: 25 ng of Cleavase® BN prepared as described in Example 9; 2 μ l of Cleavase® A/G nuclease extract prepared as described in Example 2; 2.25 μ l (11.25 polymerase units) the following DNA polymerases: AmpliTaq® DNA polymerase (Perkin Elmer); AmpliTaq® DNA polymerase LD (low DNA; from Perkin Elmer); Taq DNA polymerase (Fisher Scientific).

[0504] For each of the reactions shown in FIG. 37, except for that shown in lane 1, the target DNA (50 fmoles of single-stranded M13mp19 DNA) was combined with 50 pmole of the invader oligonucleotide (SEQ ID NO:46) and 5 pmole of the probe oligonucleotide (SEQ ID NO:43); target DNA was omitted in reaction I (lane 1). Reactions 1, 3, 5, 7, 9 and 11 included 1.5 l of saliva extract. These mixtures were brought to a volume of 5 μ l with distilled water, overlaid with a drop of ChillOut® evaporation barrier (MJ Research) and brought to 95° C. for 10 minutes. The cleavage reactions were then started by the addition of 5 μ l of the desired enzyme/probe mixture; reactions 1, 4 and 5 received Cleavase® A/G nuclease. Reactions 2 and 3 received Cleavase® BN; reactions 6 and 7 received AmpliTaq®; reactions 8 and 9 received AmoliTaq® LD; and reactions 10 and 11 received Taq DNA Polymerase from Fisher Scientific.

[0505] The reactions were incubated at 63° C. for 30 minutes and were stopped by the addition of 6 μ l of 95% formamide with 20 mM EDTA and 0.05% marker dyes. Samples were heated to 75° C. for 2 minutes immediately before electrophoresis through a 20% acrylamide gel (19:1 cross-linked), with 7 M urea, in a buffer of 45 mM Tris-

Borate, pH 8.3, 1.4 mM EDTA. The products of the reactions were visualized by the use of an Hitachi FMBIO fluorescence imager, and the results are displayed in FIG. 37.

[0506] A pairwise comparison of the lanes shown in FIG. 37 without and with the saliva extract, treated with each of the enzymes, shows that the saliva extract has different effects on each of the enzymes. While the Cleavase® BN nuclease and the AmpliTaq® are significantly inhibited from cleaving in these conditions, the Cleavase® A/G nuclease and AmpliTaq® LD display little difference in the yield of cleaved probe. The preparation of Taq DNA polymerase from Fisher Scientific shows an intermediate response, with a partial reduction in the yield of cleaved product. From the standpoint of polymerization, the three DNAPtaq variants should be equivalent; these should be the same protein with the same amount of synthetic activity. It is possible that the differences observed could be due to variations in the amount of nuclease activity present in each preparation caused by different handling during purification, or by different purification protocols. In any case, quality control assays designed to assess polymerization activity in commercial DNAP preparations would be unlikely to reveal variation in the amount of nuclease activity present. If preparations of DNAPtaq were screened for full 5' nuclease activity (i.e., if the 5' nuclease activity was specifically quantitated), it is likely that the preparations would display sensitivities (to saliva extract) more in line with that observed using Cleavase® A/G nuclease, from which DNAPtaq differs by a very few amino acids.

[0507] It is worthy of note that even in the slowed reactions of Cleavase® BN and the DNAPtaq variants there is no noticeable increase in non-specific cleavage of the probe oligonucleotide due to inappropriate hybridization or saliva-borne nucleases.

EXAMPLE 17

Comparison of Additional 5' Nucleases in the Invader-Directed Cleavage Assay

[0508] A number of eubacterial Type A DNA polymerases (i.e., Pol I type DNA polymerases) have been shown to function as structure specific endonucleases (Example 1 and Lyamichev et al., supra). In this example, it was demonstrated that the enzymes of this class can also be made to catalyze the invader-directed cleavage of the present invention, albeit not as efficiently as the Cleavase® enzymes.

[0509] Cleavase® BN nuclease and Cleavase® A/G nuclease were tested along side three different thermostable DNA polymerases: *Thermus aquaticus* DNA polymerase (Promega), *Thermus thermophilus* and *Thermus flavus* DNA polymerases (Epicentre). The enzyme mixtures used in the reactions shown in lanes 1-11 of FIG. 38 contained the following, each in a volume of 5 μ l: Lane 1: 20 mM MOPS (pH 7.5) with 0.1% each of Tween 20 and NP-40, 4 mM MnCl₂, 100 mM KCl; Lane 2: 25 ng of Cleavase® BN nuclease in the same solution described for lane 1; Lane 3: 2.25 μ l of Cleavase® A/G nuclease extract (prepared as described in Example 2), in the same solution described for lane 1; Lane 4: 2.25 μ l of Cleavase® A/G nuclease extract in 20 mM Tris-Cl, (pH 8.5), 4 mM MgCl₂ and 100 mM KCl; Lane 5: 11.25 polymerase units of Taq DNA polymerase in

the same buffer described for lane 4; Lane 6: 11.25 polymerase units of Tth DNA polymerase in the same buffer described for lane 1; Lane 7: 11.25 polymerase units of Tth DNA polymerase in a 2 \times concentration of the buffer supplied by the manufacturer, supplemented with 4 mM MnCl₂; Lane 8: 11.25 polymerase units of Tth DNA polymerase in a 2 \times concentration of the buffer supplied by the manufacturer, supplemented with 4 mM MgCl₂; Lane 9: 2.25 polymerase units of Tfl DNA polymerase in the same buffer described for lane 1; Lane 10: 2.25 polymerase units of Tfl polymerase in a 2 \times concentration of the buffer supplied by the manufacturer, supplemented with 4 mM MnCl₂; Lane 11: 2.25 polymerase units of Tfl DNA polymerase in a 2 \times concentration of the buffer supplied by the manufacturer, supplemented with 4 mM MgCl₂.

[0510] Sufficient target DNA, probe and invader for all 11 reactions was combined into a master mix. This mix contained 550 fmoles of single-stranded M13mp19 target DNA, 550 pmoles of the invader oligonucleotide (SEQ ID NO:46) and 55 pmoles of the probe oligonucleotide (SEQ ID NO:43), each as depicted in FIG. 32c, in 55 μ l of distilled water. Five μ l of the DNA mixture was dispensed into each of 11 labeled tubes and overlaid with a drop of ChillOut® evaporation barrier (MJ Research). The reactions were brought to 63° C. and cleavage was started by the addition of 5 μ l of the appropriate enzyme mixture. The reaction mixtures were then incubated at 63° C. temperature for 15 minutes. The reactions were stopped by the addition of 8 μ l of 95% formamide with 20 mM EDTA and 0.05% marker dyes. Samples were heated to 90° C. for 1 minute immediately before electrophoresis through a 20% acrylamide gel (19:1 cross-linked), with 7 M urea, in a buffer of 45 mM Tris-Borate (pH 8.3), 1.4 mM EDTA. Following electrophoresis, the products of the reactions were visualized by the use of an Hitachi FMBIO fluorescence imager, and the results are displayed in FIG. 38. Examination of the results shown in FIG. 38 demonstrates that all of the 5' nucleases tested have the ability to catalyze invader-directed cleavage in at least one of the buffer systems tested. Although not optimized here, these cleavage agents are suitable for use in the methods of the present invention.

EXAMPLE 18

The Invader-Directed Cleavage Assay can Detect Single Base Differences in Target Nucleic Acid Sequences

[0511] The ability of the invader-directed cleavage assay to detect single base mismatch mutations was examined. Two target nucleic acid sequences containing Cleavase® enzyme-resistant phosphorothioate backbones were chemically synthesized and purified by polyacrylamide gel electrophoresis. Targets comprising phosphorothioate backbones were used to prevent exonucleolytic nibbling of the target when duplexed with an oligonucleotide. A target oligonucleotide, which provides a target sequence that is completely complementary to the invader oligonucleotide (SEQ ID NO:46) and the probe oligonucleotide (SEQ ID NO:43), contained the following sequence: 5'-CCTTTCGCTTTCTTCCTTC-CITTCTCGCCACGTTCCGCCGGC-3' (SEQ ID NO:47). A second target sequence containing a single base change relative to SEQ ID NO:47 was synthesized:

5'-CCTTTCGCTCTCTTCCCTTCCTTCTCGCC ACGT-TCGCCGGC-3 (SEQ ID NO:48; the single base change relative to SEQ ID NO:47 is shown using bold and underlined type). The consequent mismatch occurs within the "Z" region of the target as represented in **FIG. 29**.

[0512] To discriminate between two target sequences which differ by the presence of a single mismatch), invader-directed cleavage reactions were conducted using two different reaction temperatures (55° C. and 60° C.). Mixtures containing 200 fmoles of either SEQ ID NO:47 or SEQ ID NO:48, 3 pmoles of fluorescein-labelled probe oligonucleotide (SEQ ID NO:43), 7.7 pmoles of invader oligonucleotide (SEQ ID NO:46) and 2 μ l of Cleavase® A/G nuclease extract (prepared as described in Example 2) in 9 μ l of 10 mM MOPS (pH 7.4) with 50 mM KCl were assembled, 0 covered with a drop of ChillOut® evaporation barrier (MJ Research) and brought to the appropriate reaction temperature. The cleavage reactions were initiated by the addition of 1 μ l of 20 mM MgCl₂. After 30 minutes at either 55° C. or 60° C., 10 μ l of 95% formamide with 20 mM EDTA and 0.05% marker dyes was added to stop the reactions. The reaction mixtures were then heated to 90° C. for one minute prior to loading 4 μ l onto 20% denaturing polyacrylamide gels. The resolved reaction products were visualized using a Hitachi FMBIO fluorescence imager. The resulting image is shown in **FIG. 39**.

[0513] In **FIG. 39**, lanes 1 and 2 show the products from reactions conducted at 55° C.; lanes 3 and 4 show the products from reactions conducted at 60° C. Lanes 1 and 3 contained products from reactions containing SEQ ID NO:47 (perfect match to probe) as the target. Lanes 2 and 4 contained products from reactions containing SEQ ID NO:48 (single base mis-match with probe) as the target. The target that does not have a perfect hybridization match (i.e., complete complementarity) with the probe will not bind as strongly, i.e., the T_m of that duplex will be lower than the T_m of the same region if perfectly matched. The results presented here show that reaction conditions can be varied to either accommodate the mis-match (e.g., by lowering the temperature of the reaction) or to exclude the binding of the mismatched sequence (e.g., by raising the reaction temperature).

[0514] The results shown in **FIG. 39** demonstrate that the specific cleavage event which occurs in invader-directed cleavage reactions can be eliminated by the presence of a single base mis-match between the probe oligonucleotide and the target sequence. Thus, reaction conditions can be chosen so as to exclude the hybridization of mis-matched invader-directed cleavage probes thereby diminishing or even eliminating the cleavage of the probe. In an extension of this assay system, multiple cleavage probes, each possessing a separate reporter molecule (i.e., a unique label), could also be used in a single cleavage reaction, to simultaneously probe for two or more variants in the same target region. The products of such a reaction would allow not only the detection of mutations which exist within a target molecule, but would also allow a determination of the relative concentrations of each sequence (i.e., mutant and wild type or multiple different mutants) present within samples containing a mixture of target sequences. When provided in equal amounts, but in a vast excess (e.g., at least a 100-fold molar excess; typically at least 1 pmole of each probe oligonucleotide would be used when the target

sequence was present at about 10 fmoles or less) over the target and used in optimized conditions. As discussed above, any differences in the relative amounts of the target variants will not affect the kinetics of hybridization, so the amounts of cleavage of each probe will reflect the relative amounts of each variant present in the reaction.

[0515] The results shown in the example clearly demonstrate that the invader-directed cleavage reaction can be used to detect single base difference between target nucleic acids.

EXAMPLE 19

The Invader-Directed Cleavage Reaction is Insensitive to Large Changes in Reaction Conditions

[0516] The results shown above demonstrated that the invader-directed cleavage reaction can be used for the detection of target nucleic acid sequences and that this assay can be used to detect single base difference between target nucleic acids. These results demonstrated that 5' nucleases (e.g., Cleavase®BN, Cleavase® A/G, DNAPtaq, DNAPTth, DNAPTfl) could be used in conjunction with a pair of overlapping oligonucleotides as an efficient way to recognize nucleic acid targets. In the experiments below it is demonstrated that invasive cleavage reaction is relatively insensitive to large changes in conditions thereby making the method suitable for practice in clinical laboratories.

[0517] The effects of varying the conditions of the cleavage reaction were examined for their effect(s) on the specificity of the invasive cleavage and the on the amount of signal accumulated in the course of the reaction. To compare variations in the cleavage reaction a "standard" invader cleavage reaction was first defined. In each instance, unless specifically stated to be otherwise, the indicated parameter of the reaction was varied, while the invariant aspects of a particular test were those of this standard reaction. The results of these tests are shown in **FIGS. 42-51**.

[0518] a) The Standard Invader-Directed Cleavage Reaction

[0519] The standard reaction was defined as comprising 1 fmole of M13mp18 single-stranded target DNA (New England Biolabs), 5 pmoles of the labeled probe oligonucleotide (SEQ ID NO:49), 10 pmole of the upstream invader oligonucleotide (SEQ ID NO:50) and 2 units of Cleavase® A/G in 10 μ l of 10 mM MOPS, pH 7.5 with 100 mM KCl, 4 mM MnCl₂, and 0.05% each Tween-20 and Nonidet-P40. For each reaction, the buffers, salts and enzyme were combined in a volume of 5 μ l; the DNAs (target and two oligonucleotides) were combined in 5 μ l of dH₂O and overlaid with a drop of ChillOut® evaporation barrier (MJ Research). When multiple reactions were performed with the same reaction constituents, these formulations were expanded proportionally.

[0520] Unless otherwise stated, the sample tubes with the DNA mixtures were warmed to 61° C., and the reactions were started by the addition of 5 μ l of the enzyme mixture. After 20 minutes at this temperature, the reactions were stopped by the addition of 8 μ l of 95% formamide with 20 mM EDTA and 0.05% marker dyes. Samples were heated to 75° C. for 2 minutes immediately before electrophoresis through a 20% acrylamide gel (19:1 cross-linked), with 7 M

urea, in a buffer of 45 mM Tris-Borate, pH 8.3, 1.4 mM EDTA. The products of the reactions were visualized by the use of an Hitachi FMBIO fluorescence imager. In each case, the uncut probe material was visible as an intense black band or blob, usually in the top half of the panel, while the desired products of invader specific cleavage were visible as one or two narrower black bands, usually in the bottom half of the panel. Under some reaction conditions, particularly those with elevated salt concentrations, a secondary cleavage product is also visible (thus generating a doublet). Ladders of lighter grey bands generally indicate either exonuclease nibbling of the probe oligonucleotide or heat-induced, non-specific breakage of the probe.

[0521] FIG. 41 depicts the annealing of the probe and invader oligonucleotides to regions along the M13mp18 target molecule (the bottom strand). In FIG. 41 only a 52 nucleotide portion of the M13mp18 molecule is shown; this 52 nucleotide sequence is listed in SEQ ID NO:42 (this sequence is identical in both M13mp18 and M13mp19). The probe oligonucleotide (top strand) contains a Cy3 amidite label at the 5' end; the sequence of the probe is 5'-AGAAAGGAAGGGAAGAAAGCGAAA GGT-3' (SEQ ID NO:49). The bold type indicates the presence of a modified base (2'-O—CH₃). Cy3 amidite (Pharmacia) is an indodicarbocyanine dye amidite which can be incorporated at any position during the synthesis of oligonucleotides; Cy3 fluoresces in the yellow region (excitation and emission maximum of 554 and 568 nm, respectively). The invader oligonucleotide (middle strand) has the following sequence: 5'-GCCGCGAACGTGGCGAGAAAGGA-3' (SEQ ID NO:50).

[0522] b) KCl Titration

[0523] FIG. 42 shows the results of varying the KCl concentration in combination with the use of 2 mM MnCl₂, in an otherwise standard reaction. The reactions were performed in duplicate for confirmation of observations; the reactions shown in lanes 1 and 2 contained no added KCl, lanes 3 and 4 contained KCl at 5 mM, lanes 5 and 6 contained 25 mM KCl, lanes 7 and 8 contained 50 mM KCl, lanes 9 and 10 contained 100 mM KCl and lanes 11 and 12 contained 200 mM KCl. These results show that the inclusion of KCl allows the generation of a specific cleavage product. While the strongest signal is observed at the 100 mM KCl concentration, the specificity of signal in the other reactions with KCl at or above 25 mM indicates that concentrations in the full range (i.e., 25-200 mM) may be chosen if it is so desirable for any particular reaction conditions.

[0524] As shown in FIG. 42, the invader-directed cleavage reaction requires the presence of salt (e.g., KCl) for effective cleavage to occur. In other reactions, it has been found that KCl can inhibit the activity of certain Cleavase® enzymes when present at concentrations above about 25 mM (For example, in cleavage reactions using the S-60 oligonucleotide shown in FIG. 30, in the absence of primer, the Cleavase® BN enzyme loses approximately 50% of its activity in 50 mM KCl). Therefore, the use of alternative salts in the invader-directed cleavage reaction was examined. In these experiments, the potassium ion was replaced with either Na⁺ or Li⁺ or the chloride ion was replaced with glutamic acid. The replacement of KCl with alternative salts is described below in sections c-e.

[0525] c) NaCl Titration

[0526] FIG. 43 shows the results of using various concentrations of NaCl in place of KCl (lanes 3-10) in combination with the use 2 mM MnCl₂, in an otherwise standard reaction, in comparison to the effects seen with 100 mM KCl (lanes 1 and 2). The reactions analyzed in lanes 3 and 4 contained NaCl at 75 mM, lanes 5 and 6 contained 100 mM, lanes 7 and 8 contained 150 mM and lanes 9 and 10 contained 200 mM. These results show that NaCl can be used as a replacement for KCl in the invader-directed cleavage reaction (i.e., the presence of NaCl, like KCl, enhances product accumulation).

[0527] d) LiCl Titration

[0528] FIG. 44 shows the results of using various concentrations of LiCl in place of KCl (lanes 3-14) in otherwise standard reactions, compared to the effects seen with 100 mM KCl (lanes 1 and 2). The reactions analyzed in lanes 3 and 4 contained LiCl at 25 mM, lanes 5 and 6 contained 50 mM, lanes 7 and 8 contained 75 mM, lanes 9 and 10 contained 100 mM, lanes 11 and 12 contained 150 mM and lanes 13 and 14 contained 200 mM. These results demonstrate that LiCl can be used as a suitable replacement for KCl in the invader-directed cleavage reaction (i.e., the presence of LiCl, like KCl, enhances product accumulation).

[0529] e) KGlu Titration

[0530] FIG. 45 shows the results of using a glutamate salt of potassium (KGlu) in place of the more commonly used chloride salt (KCl) in reactions performed over a range of temperatures. KGlu has been shown to be a highly effective salt source for some enzymatic reactions, showing a broader range of concentrations which permit maximum enzymatic activity [Leirmo et al. (1987) *Biochem.* 26:2095]. The ability of KGlu to facilitate the annealing of the probe and invader oligonucleotides to the target nucleic acid was compared to that of LiCl. In these experiments, the reactions were run for 15 minutes, rather than the standard 20 minutes. The reaction analyzed in lane 1 contained 150 mM LiCl and was run at 65° C.; the reactions analyzed in lanes 2-4 contained 200 mM, 300 mM and 400 mM KGlu, respectively and were run at 65° C. The reactions analyzed in lanes 5-8 repeated the array of salt concentrations used in lanes 1-4, but were performed at 67° C.; lanes 9-12 show the same array run at 69° C. and lanes 13-16 show the same array run at 71° C. The results shown in FIG. 45 demonstrate that KGlu was very effective as a salt in the invasive cleavage reactions. In addition, these data show that the range of allowable KGlu concentrations was much greater than that of LiCl, with full activity apparent even at 400 mM KGlu.

[0531] f) MnCl₂ and MgCl₂ Titration and Ability to Replace MnCl₂ with MgCl₂

[0532] In some instances it may be desirable to perform the invasive cleavage reaction in the presence of Mg²⁺, either in addition to, or in place of Mn²⁺ as the necessary divalent cation required for activity of the enzyme employed. For example, some common methods of preparing DNA from bacterial cultures or tissues use MgCl₂ in solutions which are used to facilitate the collection of DNA by precipitation. In addition, elevated concentrations (i.e., greater than 5 mM) of divalent cation can be used to facilitate hybridization of nucleic acids, in the same way that the monovalent salts were used above, thereby enhancing

the invasive cleavage reaction. In this experiment, the tolerance of the invasive cleavage reaction was examined for 1) the substitution of $MgCl_2$ for $MnCl_2$ and for the ability to produce specific product in the presence of increasing concentrations of $MgCl_2$ and $MnCl_2$.

[0533] FIG. 46 shows the results of either varying the concentration of $MnCl_2$ from 2 mM to 8 mM, replacing the $MnCl_2$ with $MgCl_2$ at 2 to 4 mM, or of using these components in combination in an otherwise standard reaction. The reactions analyzed in lanes 1 and 2 contained 2 mM each $MnCl_2$ and $MgCl_2$, lanes 3 and 4 contained 2 mM $MnCl_2$ only, lanes 5 and 6 contained 3 mM $MnCl_2$, lanes 7 and 8 contained 4 mM $MnCl_2$, lanes 9 and 10 contained 8 mM $MnCl_2$. The reactions analyzed in lanes 11 and 12 contained 2 mM $MgCl_2$ and lanes 13 and 14 contained 4 mM $MgCl_2$. These results show that both $MnCl_2$ and $MgCl_2$ can be used as the necessary divalent cation to enable the cleavage activity of the Cleavase® A/G enzyme in these reactions and that the invasive cleavage reaction can tolerate a broad range of concentrations of these components.

[0534] In addition to examining the effects of the salt environment on the rate of product accumulation in the invasive cleavage reaction, the use of reaction constituents shown to be effective in enhancing nucleic acid hybridization in either standard hybridization assays (e.g., blot hybridization) or in ligation reactions was examined. These components may act as volume excluders, increasing the effective concentration of the nucleic acids of interest and thereby enhancing hybridization, or they may act as charge-shielding agents to minimize repulsion between the highly charged backbones of the nucleic acids strands. The results of these experiments are described in sections g and h below.

[0535] g) Effect of CTAB Addition

[0536] The polycationic detergent cetyltrimethylammonium bromide (CTAB) has been shown to dramatically enhance hybridization of nucleic acids [Pontius and Berg (1991) Proc. Natl. Acad. Sci. USA 88:8237]. The data shown in FIG. 47 depicts the results of adding the detergent CTAB to invasive cleavage reactions in which 150 mM LiCl was used in place of the KCl in otherwise standard reactions. Lane 1 shows unreacted (i.e., uncut) probe, and the reaction shown in lane 1 is the LiCl-modified standard reaction without CTAB. The reactions analyzed in lanes 3 and 4 contained 100 μM CTAB, lanes 5 and 6 contained 200 μM CTAB, lanes 7 and 8 contained 400 μM CTAB, lanes 9 and 10 contained 600 μM CTAB, lanes 11 and 12 contained 800 μM CTAB and lanes 13 and 14 contained 1 mM CTAB. These results showed that the lower amounts of CTAB may have a very moderate enhancing effect under these reaction conditions, and the presence of CTAB in excess of about 500 μM was inhibitory to the accumulation of specific cleavage product.

[0537] h) Effect of PEG Addition

[0538] FIG. 48 shows the effect of adding polyethylene glycol (PEG) at various percentage (w/v) concentrations to otherwise standard reactions. The effects of increasing the reaction temperature of the PEG-containing reactions was also examined. The reactions assayed in lanes 1 and 2 were the standard conditions without PEG, lanes 3 and 4 contained 4% PEG, lanes 5 and 6 contained 8% PEG and lanes 7 and 8 contained 12% PEG. Each of the aforementioned

reactions was performed at 61° C. The reactions analyzed in lanes 9, 10, 11 and 12 were performed at 65° C., and contained 0%, 4%, 8% and 12% PEG, respectively. These results show that at all percentages tested, and at both temperatures tested, the inclusion of PEG substantially eliminated the production of specific cleavage product.

[0539] In addition to the data presented above (i.e., effect of CTAB and PEG addition), the presence of 1× Denhardt's in the reaction mixture was found to have no adverse effect upon the cleavage reaction [SOX Denhardt's contains per 500 ml: 5 g Ficoll, 5 g polyvinylpyrrolidone, 5 g BSA]. In addition, the presence of each component of Denhardt's was examined individually (i.e., Ficoll alone, polyvinylpyrrolidone alone, BSA alone) for the effect upon the invader-directed cleavage reaction; no adverse effect was observed.

[0540] i) Effect of the Addition of Stabilizing Agents

[0541] Another approach to enhancing the output of the invasive cleavage reaction is to enhance the activity of the enzyme employed, either by increasing its stability in the reaction environment or by increasing its turnover rate. Without regard to the precise mechanism by which various agents operate in the invasive cleavage reaction, a number of agents commonly used to stabilize enzymes during prolonged storage were tested for the ability to enhance the accumulation of specific cleavage product in the invasive cleavage reaction.

[0542] FIG. 49 shows the effects of adding glycerol at 15% and of adding the detergents Tween-20 and Nonidet-P40 at 1.5%, alone or in combination, in otherwise standard reactions. The reaction analyzed in lane 1 was a standard reaction. The reaction analyzed in lane 2 contained 1.5% NP-40, lane 3 contained 1.5% Tween 20, lane 4 contained 15% glycerol. The reaction analyzed in lane 5 contained both Tween-20 and NP-40 added at the above concentrations, lane 6 contained both glycerol and NP-40, lane 7 contained both glycerol and Tween-20, and lane 8 contained all three agents. The results shown in FIG. 49 demonstrate that under these conditions these adducts had little or no effect on the accumulation of specific cleavage product.

[0543] FIG. 50 shows the effects of adding gelatin to reactions in which the salt identity and concentration were varied from the standard reaction. In addition, all of these reactions were performed at 65° C., instead of 61° C. The reactions assayed in lanes 1-4 lacked added KCl, and included 0.02%, 0.05%, 0.1% or 0.2% gelatin, respectively. Lanes 5, 6, 7 and 8 contained the same titration of gelatin, respectively, and included 100 mM KCl. Lanes 9, 10, 11 and 12, also had the same titration of gelatin, and additionally included 150 mM LiCl in place of KCl. Lanes 13 and 14 show reactions that did not include gelatin, but which contained either 100 mM KCl or 150 mM LiCl, respectively. The results shown in FIG. 50 demonstrated that in the absence of salt the gelatin had a moderately enhancing effect on the accumulation of specific cleavage product, but when either salt (KCl or LiCl) was added to reactions performed under these conditions, increasing amounts of gelatin reduced the product accumulation.

[0544] j) Effect of Adding Large Amounts of Non-Target Nucleic Acid

[0545] In detecting specific nucleic acid sequences within samples, it is important to determine if the presence of

additional genetic material (i.e., non-target nucleic acids) will have a negative effect on the specificity of the assay. In this experiment, the effect of including large amounts of non-target nucleic acid, either DNA or RNA, on the specificity of the invasive cleavage reaction was examined. The data was examined for either an alteration in the expected site of cleavage, or for an increase in the nonspecific degradation of the probe oligonucleotide.

[0546] FIG. 51 shows the effects of adding non-target nucleic acid (e.g., genomic DNA or tRNA) to an invasive cleavage reaction performed at 65° C., with 150 mM LiCl in place of the KCl in the standard reaction. The reactions assayed in lanes 1 and 2 contained 235 and 470 ng of genomic DNA, respectively. The reactions analyzed in lanes 3, 4, 5 and 6 contained 100 ng, 200 ng, 500 ng and 1 µg of tRNA, respectively. Lane 7 represents a control reaction which contained no added nucleic acid beyond the amounts used in the standard reaction. The results shown in FIG. 51 demonstrate that the inclusion of non-target nucleic acid in large amounts could visibly slow the accumulation of specific cleavage product (while not limiting the invention to any particular mechanism, it is thought that the additional nucleic acid competes for binding of the enzyme with the specific reaction components). In additional experiments it was found that the effect of adding large amounts of non-target nucleic acid can be compensated for by increasing the enzyme in the reaction. The data shown in FIG. 51 also demonstrate that a key feature of the invasive cleavage reaction, the specificity of the detection, was not compromised by the presence of large amounts of non-target nucleic acid.

[0547] In addition to the data presented above, invasive cleavage reactions were run with succinate buffer at pH 5.9 in place of the MOPS buffer used in the "standard" reaction; no adverse effects were observed.

[0548] The data shown in FIGS. 42-51 and described above demonstrate that the invasive cleavage reaction can be performed using a wide variety of reaction conditions and is therefore suitable for practice in clinical laboratories.

EXAMPLE 20

Detection of RNA Targets by Invader-Directed Cleavage

[0549] In addition to the clinical need to detect specific DNA sequences for infectious and genetic diseases, there is a need for technologies that can quantitatively detect target nucleic acids that are composed of RNA. For example, a number of viral agents, such as hepatitis C virus (HCV) and human immunodeficiency virus (HIV) have RNA genomic material, the quantitative detection of which can be used as a measure of viral load in a patient sample. Such information can be of critical diagnostic or prognostic value.

[0550] Hepatitis C virus (HCV) infection is the predominant cause of post-transfusion non-A, non-B (NANB) hepatitis around the world. In addition, HCV is the major etiologic agent of hepatocellular carcinoma (HCC) and chronic liver disease world wide. The genome of HCV is a small (9.4 kb) RNA molecule. In studies of transmission of HCV by blood transfusion it has been found the presence of HCV antibody, as measured in standard immunological tests, does not always correlate with the infectivity of the

sample, while the presence of HCV RNA in a blood sample strongly correlates with infectivity. Conversely, serological tests may remain negative in immunosuppressed infected individuals, while HCV RNA may be easily detected [J. A. Cuthbert (1994) *Clin. Microbiol. Rev.* 7:505].

[0551] The need for and the value of developing a probe-based assay for the detection the HCV RNA is clear. The polymerase chain reaction has been used to detect HCV in clinical samples, but the problems associated with carry-over contamination of samples has been a concern. Direct detection of the viral RNA without the need to perform either reverse transcription or amplification would allow the elimination of several of the points at which existing assays may fail.

[0552] The genome of the positive-stranded RNA hepatitis C virus comprises several regions including 5' and 3' non-coding regions (i.e., 5' and 3' untranslated regions) and a polyprotein coding region which encodes the core protein (C), two envelope glycoproteins (E1 and E2/NS1) and six nonstructural glycoproteins (NS2-NS5b). Molecular biological analysis of the HCV genome has showed that some regions of the genome are very highly conserved between isolates, while other regions are fairly rapidly changeable. The 5' noncoding region (NCR) is the most highly conserved region in the HCV. These analyses have allowed these viruses to be divided into six basic genotype groups, and then further classified into over a dozen sub-types [the nomenclature and division of HCV genotypes is evolving; see Altamirano et al., *J. Infect. Dis.* 171:1034 (1995) for a recent classification scheme].

[0553] In order to develop a rapid and accurate method of detecting HCV present in infected individuals, the ability of the invader-directed cleavage reaction to detect HCV RNA was examined. Plasmids containing DNA derived from the conserved 5'-untranslated region of six different HCV RNA isolates were used to generate templates for in vitro transcription. The HCV sequences contained within these six plasmids represent genotypes 1 (four sub-types represented; 1a, 1b, 1c, and Δ1c), 2, and 3. The nomenclature of the HCV genotypes used herein is that of Simmonds et al. [as described in Altamirano et al., supra]. The Δ1c subtype was used in the model detection reaction described below.

[0554] a) Generation of Plasmids Containing HCV Sequences

[0555] Six DNA fragments derived from HCV were generated by RT-PCR using RNA extracted from serum samples of blood donors; these PCR fragments were a gift of Dr. M. Altamirano (University of British Columbia, Vancouver). These PCR fragments represent HCV sequences derived from HCV genotypes 1a, 1b, 1c, Δ1c, 2c and 3a.

[0556] The RNA extraction, reverse transcription and PCR were performed using standard techniques (Altamirano et al., supra). Briefly, RNA was extracted from 100 µl of serum using guanidine isothiocyanate, sodium lauryl sarkosate and phenol-chloroform [Inchauspe et al., *Hepatology* 14:595 (1991)]. Reverse transcription was performed according to the manufacturer's instructions using a GeneAmp rTh reverse transcriptase RNA PCR kit (Perkin-Elmer) in the presence of an external antisense primer, HCV342. The sequence of the HCV342 primer is 5'-GGTTTTTCTTTGAGG TTTAG-3' (SEQ ID NO:51).

Following termination of the RT reaction, the sense primer HCV7 [5'-GCGACACTCCACCATAGAT-3' (SEQ ID NO:52)] and magnesium were added and a first PCR was performed. Aliquots of the first PCR products were used in a second (nested) PCR in the presence of primers HCV46 [5'-CTGTCTTCACGCAGAAAGC-3' (SEQ ID NO:53)] and HCV308 [5'-GCACGGT CTACGAGACCTC-3' (SEQ ID NO:54)]. The PCRs produced a 281 bp product which corresponds to a conserved 5' noncoding region (NCR) region of HCV between positions -284 and -4 of the HCV genome (Altramirano et al., supra).

[0557] The six 281 bp PCR fragments were used directly for cloning or they were subjected to an additional amplification step using a 50 μ l PCR comprising approximately 100 fmoles of DNA, the HCV46 and HCV308 primers at 0.1 μ M, 100 μ M of all four dNTPs and 2.5 units of Taq DNA polymerase in a buffer containing 10 mM Tris-HCl, pH 8.3, 50 mM KCl, 1.5 mM MgCl₂ and 0.1% Tween 20. The PCRs were cycled 25 times at 96° C. for 45 sec., 55° C. for 45 sec. and 72° C. for 1 min. Two microliters of either the original DNA samples or the reamplified PCR products were used for cloning in the linear pT7Blue T-vector (Novagen, Madison, Wis.) according to manufacturer's protocol. After the PCR products were ligated to the pT7Blue T-vector, the ligation reaction mixture was used to transform competent JM109 cells (Promega). Clones containing the pT7Blue T-vector with an insert were selected by the presence of colonies having a white color on LB plates containing 40 μ g/ml X-Gal, 40 μ g/ml IPTG and 50 μ g/ml ampicillin. Four colonies for each PCR sample were picked and grown overnight in 2 ml LB media containing 50 μ g/ml carbenicillin. Plasmid DNA was isolated using the following alkaline miniprep protocol. Cells from 1.5 ml of the overnight culture were collected by centrifugation for 2 min. in a microcentrifuge (14K rpm), the supernatant was discarded and the cell pellet was resuspended in 50 μ l TE buffer with 10 μ g/ml RNase A (Pharmacia). One hundred microliters of a solution containing 0.2 N NaOH, 1% SDS was added and the cells were lysed for 2 min. The lysate was gently mixed with 100 μ l of 1.32 M potassium acetate, pH 4.8, and the mixture was centrifuged for 4 min. in a microcentrifuge (14K rpm); the pellet comprising cell debris was discarded. Plasmid DNA was precipitated from the supernatant with 200 μ l ethanol and pelleted by centrifugation a microcentrifuge (14K rpm). The DNA pellet was air dried for 15 min. and was then redissolved in 50 μ l TE buffer (10 mM Tris-HCl, pH 7.8, 1 mM EDTA).

[0558] b) Reamplification of HCV Clones to Add the Phage T7 Promoter for Subsequent *In Vitro* Transcription

[0559] To ensure that the RNA product of transcription had a discrete 3' end it was necessary to create linear transcription templates which stopped at the end of the HCV sequence. These fragments were conveniently produced using the PCR to reamplify the segment of the plasmid containing the phage promoter sequence and the HCV insert. For these studies, the clone of HCV type Δ 1c was reamplified using a primer that hybridizes to the T7 promoter sequence: 5'-TAATACGACTCACTATAGGG-3' (SEQ ID NO:55; "the T7 promoter primer") (Novagen) in combination with the 3' terminal HCV-specific primer HCV308 (SEQ ID NO:54). For these reactions, 1 μ l of plasmid DNA (approximately 10 to 100 ng) was reamplified in a 200 μ l PCR using the T7 and HCV308 primers as described above

with the exception that 30 cycles of amplification were employed. The resulting amplicon was 354 bp in length. After amplification the PCR mixture was transferred to a fresh 1.5 ml microcentrifuge tube, the mixture was brought to a final concentration of 2 M NH₄OAc, and the products were precipitated by the addition of one volume of 100% isopropanol. Following a 10 min. incubation at room temperature, the precipitates were collected by centrifugation, washed once with 80% ethanol and dried under vacuum. The collected material was dissolved in 100 μ l nuclease-free distilled water (Promega).

[0560] Segments of RNA were produced from this amplicon by *in vitro* transcription using the RiboMAX™ Large Scale RNA Production System (Promega) in accordance with the manufacturer's instructions, using 5.3 μ g of the amplicon described above in a 100 μ l reaction. The transcription reaction was incubated for 3.75 hours, after which the DNA template was destroyed by the addition of 5-6 μ l of RQ1 RNase-free DNase (1 unit/ μ l) according to the RiboMAX™ kit instructions. The reaction was extracted twice with phenol/chloroform/isoamyl alcohol (50:48:2) and the aqueous phase was transferred to a fresh microcentrifuge tube. The RNA was then collected by the addition of 10 μ l of 3M NH₄OAc, pH 5.2 and 110 μ l of 100% isopropanol. Following a 5 min. incubation at 4° C., the precipitate was collected by centrifugation, washed once with 80% ethanol and dried under vacuum. The sequence of the resulting RNA transcript (HCV1.1 transcript) is listed in SEQ ID NO:56.

[0561] c) Detection of the HCV1.1 Transcript in the Invader-Directed Cleavage Assay

[0562] Detection of the HCV1.1 transcript was tested in the invader-directed cleavage assay using an HCV-specific probe oligonucleotide [5'-CCGGTCGTCCTGGCAATXCC-3' (SEQ ID NO:57); X indicates the presence of a fluorescein dye on an abasic linker] and an HCV-specific invader oligonucleotide [5'-GTTTATCCAAGAAAGGACC CGGTCC-3' (SEQ ID NO:58)] that causes a 6-nucleotide invasive cleavage of the probe.

[0563] Each 10 μ l of reaction mixture comprised 5 pmole of the probe oligonucleotide (SEQ ID NO:57) and 10 pmole of the invader oligonucleotide (SEQ ID NO:58) in a buffer of 10 mM MOPS, pH 7.5 with 50 mM KCl, 4 mM MnCl₂, 0.05% each Tween-20 and Nonidet-P40 and 7.8 units RNasin® ribonuclease inhibitor (Promega). The cleavage agents employed were Cleavase® A/G (used at 5.3 ng/10 μ l reaction) or DNAPTth (used at 5 polymerase units/10 μ l reaction). The amount of RNA target was varied as indicated below. When RNase treatment is indicated, the target RNAs were pre-treated with 10 μ g of RNase A (Sigma) at 37° C. for 30 min. to demonstrate that the detection was specific for the RNA in the reaction and not due to the presence of any residual DNA template from the transcription reaction. RNase-treated aliquots of the HCV RNA were used directly without intervening purification.

[0564] For each reaction, the target RNAs were suspended in the reaction solutions as described above, but lacking the cleavage agent and the MnCl₂ for a final volume of 10 μ l, with the invader and probe at the concentrations listed above. The reactions were warmed to 46° C. and the reactions were started by the addition of a mixture of the appropriate enzyme with MnCl₂. After incubation for 30 min. at 46° C., the reactions were stopped by the addition of

8 μ l of 95% formamide, 10 mM EDTA and 0.02% methyl violet (methyl violet loading buffer). Samples were then resolved by electrophoresis through a 15% denaturing polyacrylamide gel (19:1 cross-linked), containing 7 M urea, in a buffer of 45 mM Tris-Borate, pH 8.3, 1.4 mM EDTA. Following electrophoresis, the labeled reaction products were visualized using the FMBIO-100 Image Analyzer (Hitachi), with the resulting imager scan shown in FIG. 52.

[0565] In FIG. 52, the samples analyzed in lanes 1-4 contained 1 pmole of the RNA target, the reactions shown in lanes 5-8 contained 100 fmole of the RNA target and the reactions shown in lanes 9-12 contained 10 fmole of the RNA target. All odd-numbered lanes depict reactions performed using Cleavase® A/G enzyme and all even-numbered lanes depict reactions performed using DNAPTth. The reactions analyzed in lanes 1, 2, 5, 6, 9 and 10 contained RNA that had been pre-digested with RNase A. These data demonstrate that the invasive cleavage reaction efficiently detects RNA targets and further, the absence of any specific cleavage signal in the RNase-treated samples confirms that the specific cleavage product seen in the other lanes is dependent upon the presence of input RNA.

EXAMPLE 21

The Fate of the Target RNA in the Invader-Directed Cleavage Reaction

[0566] In this example, the fate of the RNA target in the invader-directed cleavage reaction was examined. As shown above in Example 19, when RNAs are hybridized to DNA oligonucleotides, the 5' nucleases associated with DNA polymerases can be used to cleave the RNAs; such cleavage can be suppressed when the 5' arm is long or when it is highly structured [Lyamichev et al. (1993) *Science* 260:778 and U.S. Pat. No. 5,422,253, the disclosure of which is herein incorporated by reference]. In this experiment, the extent to which the RNA target would be cleaved by the cleavage agents when hybridized to the detection oligonucleotides (i.e., the probe and invader oligonucleotides) was examined using reactions similar to those described in Example 20, performed using fluorescein-labeled RNA as a target.

[0567] Transcription reactions were performed as described in Example 20 with the exception that 2% of the UTP in the reaction was replaced with fluorescein-12-UTP (Boehringer Mannheim) and 5.3 μ g of the amplicon was used in a 100 μ l reaction. The transcription reaction was incubated for 2.5 hours, after which the DNA template was destroyed by the addition of 5-6 μ l of RQ1 RNase-free DNase (1 unit/l) according to the RiboMAX™ kit instructions. The organic extraction was omitted and the RNA was collected by the addition of 10 μ l of 3M NaOAc, pH 5.2 and 110 μ l of 100% isopropanol. Following a 5 min. incubation at 4° C., the precipitate was collected by centrifugation, washed once with 80% ethanol and dried under vacuum. The resulting RNA was dissolved in 100 μ l of nuclease-free water. 50% of the sample was purified by electrophoresis through a 8% denaturing polyacrylamide gel (19:1 cross-linked), containing 7 M urea, in a buffer of 45 mM Tris-Borate, pH 8.3, 1.4 mM EDTA. The gel slice containing the full-length material was excised and the RNA was eluted by soaking the slice overnight at 4° C. in 200 μ l of 10 mM Tris-Cl, pH 8.0, 0.1 mM EDTA and 0.3 M NaOAc. The RNA

was then precipitated by the addition of 2.5 volumes of 100% ethanol. After incubation at -20° C. for 30 min., the precipitates were recovered by centrifugation, washed once with 80% ethanol and dried under vacuum. The RNA was dissolved in 25 μ l of nuclease-free water and then quantitated by UV absorbance at 260 nm.

[0568] Samples of the purified RNA target were incubated for 5 or 30 min. in reactions that duplicated the Cleavase® A/G and DNAPTth invader reactions described in Example 20 with the exception that the reactions lacked probe and invader oligonucleotides. Subsequent analysis of the products showed that the RNA was very stable, with a very slight background of non-specific degradation, appearing as a gray background in the gel lane. The background was not dependent on the presence of enzyme in the reaction.

[0569] Invader detection reactions using the purified RNA target were performed using the probe/invader pair described in Example 20 (SEQ ID NOS:57 and 58). Each reaction included 500 fmole of the target RNA, 5 pmoles of the fluorescein-labeled probe and 10 pmoles of the invader oligonucleotide in a buffer of 10 mM MOPS, pH 7.5 with 150 mM LiCl, 4 mM MnCl₂, 0.05% each Tween-20 and Nonidet-P40 and 39 units RNAsin® (Promega). These components were combined and warmed to 50° C. and the reactions were started by the addition of either 53 ng of Cleavase® A/G or 5 polymerase units of DNAPTth. The final reaction volume was 10 μ l. After 5 min at 50° C., 5 μ l aliquots of each reaction were removed to tubes containing 4 μ l of 95% formamide, 10 mM EDTA and 0.02% methyl violet. The remaining aliquot received a drop of ChillOut® evaporation barrier and was incubated for an additional 25 min. These reactions were then stopped by the addition of 4 μ l of the above formamide solution. The products of these reactions were resolved by electrophoresis through separate 20% denaturing polyacrylamide gels (19:1 cross-linked), containing 7 M urea, in a buffer of 45 mM Tris-Borate, pH 8.3, 1.4 mM EDTA. Following electrophoresis, the labeled reaction products were visualized using the FMBIO-100 Image Analyzer (Hitachi), with the resulting imager scans shown in FIGS. 53A (5 min reactions) and 53B (30 min. reactions).

[0570] In FIG. 53 the target RNA is seen very near the top of each lane, while the labeled probe and its cleavage products are seen just below the middle of each panel. The FMBIO-100 Image Analyzer was used to quantitate the fluorescence signal in the probe bands. In each panel, lane 1 contains products from reactions performed in the absence of a cleavage agent, lane 2 contains products from reactions performed using Cleavase® A/G and lane 3 contains products from reactions performed using DNAPTth.

[0571] Quantitation of the fluorescence signal in the probe bands revealed that after a 5 min. incubation, 12% or 300 fmole of the probe was cleaved by the Cleavase® A/G and 29% or 700 fmole was cleaved by the DNAPTth. After a 30 min. incubation, Cleavase® A/G had cleaved 32% of the probe molecules and DNAPTth had cleaved 70% of the probe molecules. (The images shown in FIGS. 53A and 53B were printed with the intensity adjusted to show the small amount of background from the RNA degradation, so the bands containing strong signals are saturated and therefore these images do not accurately reflect the differences in measured fluorescence) The data shown in FIG. 53 clearly

shows that, under invasive cleavage conditions, RNA molecules are sufficiently stable to be detected as a target and that each RNA molecule can support many rounds of probe cleavage.

EXAMPLE 22

Titration of Target RNA in the Invader-Directed Cleavage Assay

[0572] One of the primary benefits of the invader-directed cleavage assay as a means for detection of the presence of specific target nucleic acids is the correlation between the amount of cleavage product generated in a set amount of time and the quantity of the nucleic acid of interest present in the reaction. The benefits of quantitative detection of RNA sequences was discussed in Example 20. In this example, we demonstrate the quantitative nature of the detection assay through the use of various amounts of target starting material. In addition to demonstrating the correlation between the amounts of input target and output cleavage product, these data graphically show the degree to which the RNA target can be recycled in this assay

[0573] The RNA target used in these reactions was the fluorescein-labeled material described in Example 21 (i.e., SEQ ID NO:56). Because the efficiency of incorporation of the fluorescein-12-UTP by the T7 RNA polymerase was not known, the concentration of the RNA was determined by measurement of absorbance at 260 nm, not by fluorescence intensity. Each reaction comprised 5 pmoles of the fluorescein-labeled probe (SEQ ID NO:57) and 10 pmoles of the invader oligonucleotide (SEQ ID NO:58) in a buffer of 10 mM MOPS, pH 7.5 with 150 mM LiCl, 4 mM MnCl₂, 0.05% each Tween-20 and Nonidet-P40 and 39 units of RNAsin® (Promega). The amount of target RNA was varied from 1 to 100 fmoles, as indicated below. These components were combined, overlaid with ChillOut® evaporation barrier (MJ Research) and warmed to 50° C.; the reactions were started by the addition of either 53 ng of Cleavase® A/G or 5 polymerase units of DNAPT_h, to a final reaction volume of 10 μ l. After 30 minutes at 50° C., reactions were stopped by the addition of 8 μ l of 95% formamide, 10 mM EDTA and 0.02% methyl violet. The unreacted markers in lanes 1 and 2 were diluted in the same total volume (18 μ l). The samples were heated to 90° C. for 1 minute and 2.5 μ l of each of these reactions were resolved by electrophoresis through a 20% denaturing polyacrylamide gel (19:1 cross link) with 7M urea in a buffer of 45 mM Tris-Borate, pH 8.3, 1.4 mM EDTA, and the labeled reaction products were visualized using the FMBIO-100 Image Analyzer (Hitachi), with the resulting imager scans shown in FIG. 54.

[0574] In FIG. 54, lanes 1 and 2 show 5 pmoles of uncut probe and 500 fmoles of untreated RNA, respectively. The probe is the very dark signal near the middle of the panel, while the RNA is the thin line near the top of the panel. These RNAs were transcribed with a 2% substitution of fluorescein-12-UTP for natural UTP in the transcription reaction. The resulting transcript contains 74 U residues, which would give an average of 1.5 fluorescein labels per molecule. With one tenth the molar amount of RNA loaded in lane 2, the signal in lane 2 should be approximately one seventh (0.15 \times) the fluorescence intensity of the probe in lane 1. Measurements indicated that the intensity was closer to one fortieth, indicating an efficiency of label incorporation

of approximately 17%. Because the RNA concentration was verified by A260 measurement this does not alter the experimental observations below, but it should be noted that the signal from the RNA and the probes does not accurately reflect the relative amounts in the reactions.

[0575] The reactions analyzed in lanes 3 through 7 contained 1, 5, 10, 50 and 100 fmoles of target, respectively, with cleavage of the probe accomplished by Cleavase® A/G. The reactions analyzed in lanes 8 through 12 repeated the same array of target amounts, with cleavage of the probe accomplished by DNAPT_h. The boxes seen surrounding the product bands show the area of the scan in which the fluorescence was measured for each reaction. The number of fluorescence units detected within each box is indicated below each box; background fluorescence was also measured.

[0576] It can be seen by comparing the detected fluorescence in each lane that the amount of product formed in these 30 minute reactions can be correlated to the amount of target material. The accumulation of product under these conditions is slightly enhanced when DNAPT_h is used as the cleavage agent, but the correlation with the amount of target present remains. This demonstrates that the invader assay can be used as a means of measuring the amount of target RNA within a sample.

[0577] Comparison of the fluorescence intensity of the input RNA with that of the cleaved product shows that the invader-directed cleavage assay creates signal in excess of the amount of target, so that the signal visible as cleaved probe is far more intense than that representing the target RNA. This further confirms the results described in Example >>, in which it was demonstrated that each RNA molecule could be used many times.

EXAMPLE 23

Detection of DNA by Charge Reversal

[0578] The detection of specific targets is achieved in the invader-directed cleavage assay by the cleavage of the probe oligonucleotide. In addition to the methods described in the preceding examples, the cleaved probe may be separated from the uncleaved probe using the charge reversal technique described below. This novel separation technique is related to the observation that positively charged adducts can affect the electrophoretic behavior of small oligonucleotides because the charge of the adduct is significant relative to charge of the whole complex. Observations of aberrant mobility due to charged adducts have been reported in the literature, but in all cases found, the applications pursued by other scientists have involved making oligonucleotides larger by enzymatic extension. As the negatively charged nucleotides are added on, the positive influence of the adduct is reduced to insignificance. As a result, the effects of positively charged adducts have been dismissed and have received infinitesimal notice in the existing literature.

[0579] This observed effect is of particular utility in assays based on the cleavage of DNA molecules. When an oligonucleotide is shortened through the action of a Cleavase® enzyme or other cleavage agent, the positive charge can be made to not only significantly reduce the net negative charge, but to actually override it, effectively "flipping" the net charge of the labeled entity. This reversal of charge allows the products of target-specific cleavage to be parti-

tioned from uncleaved probe by extremely simple means. For example, the products of cleavage can be made to migrate towards a negative electrode placed at any point in a reaction vessel, for focused detection without gel-based electrophoresis. When a slab gel is used, sample wells can be positioned in the center of the gel, so that the cleaved and uncleaved probes can be observed to migrate in opposite directions. Alternatively, a traditional vertical gel can be used, but with the electrodes reversed relative to usual DNA gels (i.e., the positive electrode at the top and the negative electrode at the bottom) so that the cleaved molecules enter the gel, while the uncleaved disperse into the upper reservoir of electrophoresis buffer.

[0580] An additional benefit of this type of readout is that the absolute nature of the partition of products from substrates means that an abundance of uncleaved probe can be supplied to drive the hybridization step of the probe-based assay, yet the unconsumed probe can be subtracted from the result to reduce background.

[0581] Through the use of multiple positively charged adducts, synthetic molecules can be constructed with sufficient modification that the normally negatively charged strand is made nearly neutral. When so constructed, the presence or absence of a single phosphate group can mean the difference between a net negative or a net positive charge. This observation has particular utility when one objective is to discriminate between enzymatically generated fragments of DNA, which lack a 3' phosphate, and the products of thermal degradation, which retain a 3' phosphate (and thus two additional negative charges).

[0582] a) Characterization of the Products of Thermal Breakage of DNA Oligonucleotides

[0583] Thermal degradation of DNA probes results in high background which can obscure signals generated by specific enzymatic cleavage, decreasing the signal-to-noise ratio. To better understand the nature of DNA thermal degradation products, we incubated the 5' tetrachloro-fluorescein (TET)-labeled oligonucleotides 78 (SEQ ID NO:59) and 79 (SEQ ID NO:60) (100 pmole each) in 50 μ l 10 mM NaCO₃ (pH 10.6), 50 mM NaCl at 90° C. for 4 hours. To prevent evaporation of the samples, the reaction mixture was overlaid with 50 μ l of ChillOut® 14 liquid wax (MJ Research). The reactions were then divided in two equal aliquots (A and B). Aliquot A was mixed with 25 μ l of methyl violet loading buffer and Aliquot B was dephosphorylated by addition of 2.5 μ l of 100 mM MgCl₂ and 1 μ l of 1 unit/ μ l Calf Intestinal Alkaline Phosphatase (CIAP) (Promega), with incubation at 37° C. for 30 min. after which 25 μ l of methyl violet loading buffer was added. One microliter of each sample was resolved by electrophoresis through a 12% polyacrylamide denaturing gel and imaged as described in Example 21; a 585 nm filter was used with the FMBIO Image Analyzer. The resulting imager scan is shown in FIG. 55. In FIG. 55, lanes 1-3 contain the TET-labeled oligonucleotide 78 and lanes 4-6 contain the TET-labeled oligonucleotide 79. Lanes 1 and 4 contain products of reactions which were not heat treated. Lanes 2 and 5 contain products from reactions which were heat treated and lanes 3 and 6 contain products from reactions which were heat treated and subjected to phosphatase treatment.

[0584] As shown in FIG. 55, heat treatment causes significant breakdown of the 5'-TET-labeled DNA, generating

a ladder of degradation products (FIG. 55, lanes 2, 3, 5 and 6). Band intensities correlate with purine and pyrimidine base positioning in the oligonucleotide sequences, indicating that backbone hydrolysis may occur through formation of abasic intermediate products that have faster rates for purines than for pyrimidines [Lindahl and Karlstrom (1973) Biochem. 12:5151].

[0585] Dephosphorylation decreases the mobility of all products generated by the thermal degradation process, with the most pronounced effect observed for the shorter products (FIG. 55, lanes 3 and 6). This demonstrates that thermally degraded products possess a 3' end terminal phosphoryl group which can be removed by dephosphorylation with CIAP. Removal of the phosphoryl group decreases the overall negative charge by 2. Therefore, shorter products which have a small number of negative charges are influenced to a greater degree upon the removal of two charges. This leads to a larger mobility shift in the shorter products than that observed for the larger species.

[0586] The fact that the majority of thermally degraded DNA products contain 3' end phosphate groups and Cleavage® enzyme-generated products do not allowed the development of simple isolation methods for products generated in the invader-directed cleavage assay. The extra two charges found in thermal breakdown products do not exist in the specific cleavage products. Therefore, if one designs assays that produce specific products which contain a net positive charge of one or two, then similar thermal breakdown products will either be negative or neutral. The difference can be used to isolate specific products by reverse charge methods as shown below.

[0587] b) Dephosphorylation of Short Amino-Modified Oligonucleotides can Reverse the Net Charge of the Labeled Product

[0588] To demonstrate how oligonucleotides can be transformed from net negative to net positively charged compounds, the four short amino-modified oligonucleotides labeled 70, 74, 75 and 76 and shown in FIGS. 56-58 were synthesized (FIG. 56 shows both oligonucleotides 70 and 74). All four modified oligonucleotides possess Cy-3 dyes positioned at the 5'-end which individually are positively charged under reaction and isolation conditions described in this example. Compounds 70 and 74 contain two amino modified thymidines that, under reaction conditions, display positively charged R-NH₃⁺ groups attached at the C5 position through a C₁₀ or C₆ linker, respectively. Because compounds 70 and 74 are 3'-end phosphorylated, they consist of four negative charges and three positive charges. Compound 75 differs from 74 in that the internal C₆ amino modified thymidine phosphate in 74 is replaced by a thymidine methyl phosphonate. The phosphonate backbone is uncharged and so there are a total of three negative charges on compound 75. This gives compound 75 a net negative one charge. Compound 76 differs from 70 in that the internal amino modified thymidine is replaced by an internal cytosine phosphonate. The pK_a of the N3 nitrogen of cytosine can be from 4 to 7. Thus, the net charges of this compound, can be from -1 to 0 depending on the pH of the solution. For the simplicity of analysis, each group is assigned a whole number of charges, although it is realized that, depending on the pK_a of each chemical group and ambient pH, a real charge may differ from the whole number

assigned. It is assumed that this difference is not significant over the range of pHs used in the enzymatic reactions studied here.

[0589] Dephosphorylation of these compounds, or the removal of the 3' end terminal phosphoryl group, results in elimination of two negative charges and generates products that have a net positive charge of one. In this experiment, the method of isoelectric focusing (IEF) was used to demonstrate a change from one negative to one positive net charge for the described substrates during dephosphorylation.

[0590] Substrates 70, 74, 75 and 76 were synthesized by standard phosphoramidite chemistries and deprotected for 24 hours at 22° C. in 14 M aqueous ammonium hydroxide solution, after which the solvent was removed in vacuo. The dried powders were resuspended in 200 μ l of H₂O and filtered through 0.2 μ m filters. The concentration of the stock solutions was estimated by UV-absorbance at 261 nm of samples diluted 200-fold in H₂O using a spectrophotometer (Spectronic Genesys 2, Milton Roy, Rochester, N.Y.).

[0591] Dephosphorylation of compounds 70 and 74, 75 and 76 was accomplished by treating 10 μ l of the crude stock solutions (ranging in concentration from approximately 0.5 to 2 mM) with 2 units of CIAP in 100 μ l of CIAP buffer (Promega) at 37° C. for 1 hour. The reactions were then heated to 75° C. for 15 min. in order to inactivate the CIAP. For clarity, dephosphorylated compounds are designated 'dp'. For example, after dephosphorylation, substrate 70 becomes 70dp.

[0592] To prepare samples for IEF experiments, the concentration of the stock solutions of substrate and dephosphorylated product were adjusted to a uniform absorbance of 8.5×10^{-3} at 532 nm by dilution with water. Two microliters of each sample were analyzed by IEF using a PhastSystem electrophoresis unit (Pharmacia) and PhastGel IEF 3-9 media (Pharmacia) according to the manufacturer's protocol. Separation was performed at 15° C. with the following program: pre-run; 2,000 V, 2.5 mA, 3.5 W, 75 Vh; load; 200 V, 2.5 mA, 3.5 W, 15 Vh; Vh; 2,000 V; 2.5 mA; 3.5 W, 130 Vh. After separation, samples were visualized by using the FMBIO Image Analyzer (Hitachi) fitted with a 585 nm filter. The resulting imager scan is shown in FIG. 59.

[0593] FIG. 59 shows results of IEF separation of substrates 70, 74, 75 and 76 and their dephosphorylated products. The arrow labeled "Sample Loading Position" indicates a loading line, the '+' sign shows the position of the positive electrode and the '-' sign indicates the position of the negative electrode.

[0594] The results shown in FIG. 59 demonstrate that substrates 70, 74, 75 and 76 migrated toward the positive electrode, while the dephosphorylated products 70dp, 74dp, 75dp and 76dp migrated toward negative electrode. The observed differences in mobility direction was in accord with predicted net charge of the substrates (minus one) and the products (plus one). Small perturbations in the mobilities of the phosphorylated compounds indicate that the overall pIs vary. This was also true for the dephosphorylated compounds. The presence of the cytosine in 76dp, for instance, moved this compound further toward the negative electrode which was indicative of a higher overall pI relative to the other dephosphorylated compounds. It is important to note that additional positive charges can be obtained by using a

combination of natural amino modified bases (70dp and 74dp) along with uncharged methylphosphonate bridges (products 75dp and 76dp).

[0595] The results shown above demonstrate that the removal of a single phosphate group can flip the net charge of an oligonucleotide to cause reversal in an electric field, allowing easy separation of products, and that the precise base composition of the oligonucleotides affect absolute mobility but not the charge-flipping effect.

EXAMPLE 23

Detection of Specific Cleavage Products in the Invader-Directed Cleavage Reaction by Charge Reversal

[0596] In this example the ability to isolate products generated in the invader-directed cleavage assay from all other nucleic acids present in the reaction cocktail was demonstrated using charge reversal. This experiment utilized the following Cy3-labeled oligonucleotide: 5'-Cy3-AminoT-AminoT-CTTTTCACCAGCGAGACGGG-3' (SEQ ID NO:61; termed "oligo 61"). Oligo 61 was designed to release upon cleavage a net positively charged labeled product. To test whether or not a net positively charged 5'-end labeled product would be recognized by the Cleavase® enzymes in the invader-directed cleavage assay format, probe oligo 61 (SEQ ID NO:61) and invading oligonucleotide 67 (SEQ ID NO:62) were chemically synthesized on a DNA synthesizer (ABI 391) using standard phosphoramidite chemistries and reagents obtained from Glen Research (Sterling, Va.).

[0597] Each assay reaction comprised 100 fmoles of M13mp18 single stranded DNA, 10 pmoles each of the probe (SEQ ID NO:61) and invader (SEQ ID NO:62) oligonucleotides, and 20 units of Cleavase® A/G in a 10 μ l solution of 10 mM MOPS, pH 7.4 with 100 mM KCl. Samples were overlaid with mineral oil to prevent evaporation. The samples were brought to either 50° C., 55° C., 60° C., or 65° C. and cleavage was initiated by the addition of 1 μ l of 40 mM MnCl₂. Reactions were allowed to proceed for 25 minutes and then were terminated by the addition of 10 μ l of 95% formamide containing 20 mM EDTA and 0.02% methyl violet. The negative control experiment lacked the target M13mp18 and was run at 60° C. Five microliters of each reaction were loaded into separate wells of a 20% denaturing polyacrylamide gel (cross-linked 29:1) with 8 M urea in a buffer containing 45 mM Tris-Borate (pH 8.3) and 1.4 mM EDTA. An electric field of 20 watts was applied for 30 minutes, with the electrodes oriented as indicated in FIG. 60B (i.e., in reverse orientation). The products of these reactions were visualized using the FMBIO fluorescence imager and the resulting imager scan is shown in FIG. 60B.

[0598] FIG. 60A provides a schematic illustration showing an alignment of the invader (SEQ ID NO:61) and probe (SEQ ID NO:62) along the target M13mp18 DNA; only 53 bases of the M13mp18 sequence is shown (SEQ ID NO:63). The sequence of the invader oligonucleotide is displayed under the M13mp18 target and an arrow is used above the M13mp18 sequence to indicate the position of the invader relative to the probe and target. As shown in FIG. 60A, the invader and probe oligonucleotides share a 2 base region of overlap.

[0599] In FIG. 60B, lanes 1-6 contain reactions performed at 50° C., 55° C., 60° C., and 65° C., respectively; lane 5 contained the control reaction (lacking target). In FIG. 60B, the products of cleavage are seen as dark bands in the upper half of the panel; the faint lower band seen appears in proportion to the amount of primary product produced and, while not limiting the invention to a particular mechanism, may represent cleavage one nucleotide into the duplex. The uncleaved probe does not enter the gel and is thus not visible. The control lane showed no detectable signal over background (lane 5). As expected in an invasive cleavage reaction, the rate of accumulation of specific cleavage product was temperature-dependent. Using these particular oligonucleotides and target, the fastest rate of accumulation of product was observed at 55° C. (lane 2) and very little product observed at 65° C. (lane 4).

[0600] When incubated for extended periods at high temperature, DNA probes can break non-specifically (i.e., suffer thermal degradation) and the resulting fragments contribute an interfering background to the analysis. The products of such thermal breakdown are distributed from single-nucleotides up to the full length probe. In this experiment, the ability of charge based separation of cleavage products (i.e., charge reversal) would allow the sensitive separation of the specific products of target-dependent cleavage from probe fragments generated by thermal degradation was examined.

[0601] To test the sensitivity limit of this detection method, the target M13mp18 DNA was serially diluted ten fold over than range of 1 fmole to 1 amole. The invader and probe oligonucleotides were those described above (i.e., SEQ ID NOS:61 and 62). The invasive cleavage reactions were run as described above with the following modifications: the reactions were performed at 55° C., 250 mM or 100 mM KGLu was used in place of the 100 mM KCl and only 1 pmole of the invader oligonucleotide was added. The reactions were initiated as described above and allowed to progress for 12.5 hours. A negative control reaction which lacked added M13mp18 target DNA was also run. The reactions were terminated by the addition of 10 μ l of 95% formamide containing 20 mM EDTA and 0.02% methyl violet, and 5 μ l of these mixtures were electrophoresed and visualized as described above. The resulting imager scan is shown in FIG. 61.

[0602] In FIG. 61, lane 1 contains the regative control; lanes 2-5 contain reactions performed using 100 mM KGLu; lanes 6-9 contain reactions performed using 250 mM KGLu. The reactions resolved in lanes 2 and 6 contained 1 fmole of target DNA; those in lanes 3 and 7 contained 100 amole of target; those in lanes 4 and 8 contained 10 amole of target and those in lanes 5 and 9 contained 1 amole of target. The results shown in FIG. 61 demonstrate that the detection limit using charge reversal to detect the production of specific cleavage products in an invasive cleavage reaction is at or below 1 attomole or approximately 6.02×10^5 target molecules. No detectable signal was observed in the control lane, which indicates that non-specific hydrolysis or other breakdown products do not migrate in the same direction as enzyme-specific cleavage products. The excitation and emission maxima for Cy3 are 554 and 568, respectively, while the FMBIO Imager Analyzer excites at 532 and detects at 585. Therefore, the limit of detection of specific cleavage products can be improved by the use of more closely matched excitation source and detection filters.

EXAMPLE 24

Devices and Methods for the Separation and Detection of Charged Reaction Products

[0603] This example is directed at methods and devices for isolating and concentrating specific reaction products produced by enzymatic reactions conducted in solution whereby the reactions generate charged products from either a charge neutral substrate or a substrate bearing the opposite charge borne by the specific reaction product. The methods and devices of this example allow isolation of, for example, the products generated by the invader-directed cleavage assay of the present invention.

[0604] The methods and devices of this example are based on the principle that when an electric field is applied to a solution of charged molecules, the migration of the molecules toward the electrode of the opposite charge occurs very rapidly. If a matrix or other inhibitory material is introduced between the charged molecules and the electrode of opposite charge such that this rapid migration is dramatically slowed, the first molecules to reach the matrix will be nearly stopped, thus allowing the lagging molecules to catch up. In this way a dispersed population of charged molecules in solution can be effectively concentrated into a smaller volume. By tagging the molecules with a detectable moiety (e.g., a fluorescent dye), detection is facilitated by both the concentration and the localization of the analytes. This example illustrates two embodiments of devices contemplated by the present invention; of course, variations of these devices will be apparent to those skilled in the art and are within the spirit and scope of the present invention.

[0605] FIG. 62 depicts one embodiment of a device for concentrating the positively-charged products generated using the methods of the present invention. As shown in FIG. 62, the device comprises a reaction tube (10) which contains the reaction solution (11). One end of each of two thin capillaries (or other tubes with a hollow core) (13A and 13B) are submerged in the reaction solution (11). The capillaries (13A and 13B) may be suspended in the reaction solution (11) such that they are not in contact with the reaction tube itself; one appropriate method of suspending the capillaries is to hold them in place with clamps (not shown). Alternatively, the capillaries may be suspended in the reaction solution (11) such that they are in contact with the reaction tube itself. Suitable capillaries include glass capillary tubes commonly available from scientific supply companies (e.g., Fisher Scientific or VWR Scientific) or from medical supply houses that carry materials for blood drawing and analysis. Though the present invention is not limited to capillaries of any particular inner diameter, tubes with inner diameters of up to about $\frac{1}{8}$ inch (approximately 3 mm) are particularly preferred for use with the present invention; for example Kimble No. 73811-99 tubes (VWR Scientific) have an inner diameter of 1.1 mm and are a suitable type of capillary tube. Although the capillaries of the device are commonly composed of glass, any nonconductive tubular material, either rigid or flexible, that can contain either a conductive material or a trapping material is suitable for use in the present invention. One example of a suitable flexible tube is Tygon® clear plastic tubing (Part No. R3603; inner diameter= $\frac{1}{16}$ inch; outer diameter= $\frac{1}{8}$ inch).

[0606] As illustrated in FIG. 62, capillary 13A is connected to the positive electrode of a power supply (20) (e.g.,

a controllable power supply available through the laboratory suppliers listed above or through electronics supply houses like Radio Shack) and capillary **13B** is connected to the negative electrode of the power supply (**20**). Capillary **13B** is filled with a trapping material (**14**) capable of trapping the positively-charged reaction products by allowing minimal migration of products that have entered the trapping material (**14**). Suitable trapping materials include, but are not limited to, high percentage (e.g., about 20%) acrylamide polymerized in a high salt buffer (0.5 M or higher sodium acetate or similar salt); such a high percentage polyacrylamide matrix dramatically slows the migration of the positively-charged reaction products. Alternatively, the trapping material may comprise a solid, negatively-charged matrix, such as negatively-charged latex beads, that can bind the incoming positively-charged products. It should be noted that any amount of trapping material (**14**) capable of inhibiting any concentrating the positively-charged reaction products may be used. Thus, while the capillary **13B** in FIG. 62 only contains trapping material in the lower, submerged portion of the tube, the trapping material (**14**) can be present in the entire capillary (**13B**); similarly, less trapping material (**14**) could be present than that shown in FIG. 62 because the positively-charged reaction products generally accumulate within a very small portion of the bottom of the capillary (**13B**). The amount of trapping material need only be sufficient to make contact with the reaction solution (**11**) and have the capacity to collect the reaction products. When capillary **13B** is not completely filled with the trapping material, the remaining space is filled with any conductive material (**15**); suitable conductive materials are discussed below.

[0607] By comparison, the capillary (**13A**) connected to the positive electrode of the power supply **20** may be filled with any conductive material (**15**; indicated by the hatched lines in FIG. 62). This may be the sample reaction buffer (e.g., 10 mM MOPS, pH 7.5 with 150 mM LiCl, 4 mM MnCl₂), a standard electrophoresis buffer (e.g., 45 mM Tris-Borate, pH 8.3, 1.4 mM EDTA), or the reaction solution (**11**) itself. The conductive material (**15**) is frequently a liquid, but a semi-solid material (e.g., a gel) or other suitable material might be easier to use and is within the scope of the present invention. Moreover, that trapping material used in the other capillary (i.e., capillary **13B**) may also be used as the conductive material. Conversely, it should be noted that the same conductive material used in the capillary (**13A**) attached to the positive electrode may also be used in capillary **13B** to fill the space above the region containing the trapping material (**14**) (see FIG. 62).

[0608] The top end of each of the capillaries (**13A** and **13B**) is connected to the appropriate electrode of the power supply (**20**) by electrode wire (**18**) or other suitable material. Fine platinum wire (e.g., 0.1 to 0.4 mm, Aesar Johnson Matthey, Ward Hill, Mass.) is commonly used as conductive wire because it does not corrode under electrophoresis conditions. The electrode wire (**18**) can be attached to the capillaries (**13A** and **13B**) by a nonconductive adhesive (not shown), such as the silicone adhesives that are commonly sold in hardware stores for sealing plumbing fixtures. If the capillaries are constructed of a flexible material, the electrode wire (**18**) can be secured with a small hose clamp or constricting wire (not shown) to compress the opening of the capillaries around the electrode wire. If the conducting

material (**15**) is a gel, an electrode wire (**18**) can be embedded directly in the gel within the capillary.

[0609] The cleavage reaction is assembled in the reaction tube (**10**) and allowed to proceed therein as described in preceding examples (e.g., Examples 22-23). Though not limited to any particular volume of reaction solution (**11**), a preferred volume is less than 10 ml and more preferably less than 0.1 ml. The volume need only be sufficient to permit contact with both capillaries. After the cleavage reaction is completed, an electric field is applied to the capillaries by turning on the power source (**20**). As a result, the positively-charged products generated in the course of the invader-directed cleavage reaction which employs an oligonucleotide, which when cleaved, generates a positively charged fragment (described in Ex. 23) but when uncleaved bears a net negative charge, migrate to the negative capillary, where their migration is slowed or stopped by the trapping material (**14**), and the negatively-charged uncut and thermally degraded probe molecules migrate toward the positive electrode. Through the use of this or a similar device, the positively-charged products of the invasive cleavage reaction are separated from the other material (i.e., uncut and thermally degraded probe) and concentrated from a large volume. Concentration of the product in a small amount of trapping material (**14**) allows for simplicity of detection, with a much higher signal-to-noise ratio than possible with detection in the original reaction volume. Because the concentrated product is labelled with a detectable moiety like a fluorescent dye, a commercially-available fluorescent plate reader (not shown) can be used to ascertain the amount of product. Suitable plate readers include both top and bottom laser readers. Capillary **13B** can be positioned with the reaction tube (**10**) at any desired position so as to accommodate use with either a top or a bottom plate reading device.

[0610] In the alternative embodiment of the present invention depicted in FIG. 63, the procedure described above is accomplished by utilizing only a single capillary (**13B**). The capillary (**13B**) contains the trapping material (**14**) described above and is connected to an electrode wire (**18**), which in turn is attached to the negative electrode of a power supply (**20**). The reaction tube (**10**) has an electrode (**25**) embedded into its surface such that one surface of the electrode is exposed to the interior of the reaction tube (**10**) and another surface is exposed to the exterior of the reaction tube. The surface of the electrode (**25**) on the exterior of the reaction tube is in contact with a conductive surface (**26**) connected to the positive electrode of the power supply (**20**) through an electrode wire (**18**). Variations of the arrangement depicted in FIG. 63 are also contemplated by the present invention. For example, the electrode (**25**) may be in contact with the reaction solution (**11**) through the use of a small hole in the reaction tube (**10**); furthermore, the electrode wire (**18**) can be directly attached to the electrode wire (**18**), thereby eliminating the conductive surface (**26**).

[0611] As indicated in FIG. 63, the electrode (**25**) is embedded in the bottom of a reaction tube (**10**) such that one or more reaction tubes may be set on the conductive surface (**26**). This conductive surface could serve as a negative electrode for multiple reaction tubes; such a surface with appropriate contacts could be applied through the use of metal foils (e.g., copper or platinum, Aesar Johnson Matthey, Ward Hill, Mass.) in much the same way contacts are

applied to circuit boards. Because such a surface contact would not be exposed to the reaction sample directly, less expensive metals, such as the copper could be used to make the electrical connections.

[0612] The above devices and methods are not limited to separation and concentration of positively charged oligonucleotides. As will be apparent to those skilled in the art, negatively charged reaction products may be separated from neutral or positively charged reactants using the above device and methods with the exception that capillary 13B is attached to the positive electrode of the power supply (20) and capillary 13A or alternatively, electrode 25, is attached to the negative electrode of the power supply (20).

EXAMPLE 25

Primer-Directed and Primer Independent Cleavage Occur at the Same Site when the Primer Extends to the 3' Side of a Mismatched "Bubble" in the Downstream Duplex

[0613] As discussed above in Example 1, the presence of a primer upstream of a bifurcated duplex can influence the site of cleavage, and the existence of a gap between the 3' end of the primer and the base of the duplex can cause a shift of the cleavage site up the unpaired 5' arm of the structure (see also Lyamichev et al., supra and U.S. Pat. No. 5,422,253). The resulting non-invasive shift of the cleavage site in response to a primer is demonstrated in FIGS. 9, 10 and 11, in which the primer used left a 4-nucleotide gap (relative to the base of the duplex). In FIGS. 9-11, all of the "primer-directed" cleavage reactions yielded a 21 nucleotide product, while the primer-independent cleavage reactions yielded a 25 nucleotide product. The site of cleavage obtained when the primer was extended to the base of the duplex, leaving no gap was examined. The results are shown in FIG. 64 (FIG. 64 is a reproduction of FIG. 2C in Lyamichev et al. These data were derived from the cleavage of the structure shown in FIG. 6, as described in Example 1. Unless otherwise specified, the cleavage reactions comprised 0.01 pmoles of heat-denatured, end-labeled hairpin DNA (with the unlabeled complementary strand also present), 1 pmole primer [complementary to the 3' arm shown in FIG. 6 and having the sequence: 5'-GAATTCGATTAGGTGACACTATAGAATACA (SEQ ID NO:64)] and 0.5 units of DNAPtaq (estimated to be 0.026 pmoles) in a total volume of 10 μ l of 10 mM Tris-Cl, pH 8.5, and 1.5 mM MgCl₂ and 50 mM KCl. The primer was omitted from the reaction shown in the first lane of FIG. 64 and included in lane 2. These reactions were incubated at 55° C. for 10 minutes. Reactions were initiated at the final reaction temperature by the addition of either the MgCl₂ or enzyme. Reactions were stopped at their incubation temperatures by the addition of 8 μ l of 95% formamide with 20 mM EDTA and 0.05% marker dyes.

[0614] FIG. 64 is an autoradiogram that indicates the effects on the site of cleavage of a bifurcated duplex structure in the presence of a primer that extends to the base of the hairpin duplex. The size of the released cleavage product is shown to the left (i.e., 25 nucleotides). A dideoxynucleotide sequencing ladder of the cleavage substrate is shown on the right as a marker (lanes 3-6).

[0615] These data show that the presence of a primer that is adjacent to a downstream duplex (lane 2) produces

cleavage at the same site as seen in reactions performed in the absence of the primer (lane 1) (see FIGS. 9A and B, 10B and 11A for additional comparisons). When the 3' terminal nucleotides of the upstream oligonucleotide can base pair to the template strand but are not homologous to the displaced strand in the region immediately upstream of the cleavage site (i.e., when the upstream oligonucleotide is opening up a "bubble" in the duplex), the site to which cleavage is apparently shifted is not wholly dependent on the presence of an upstream oligonucleotide.

[0616] As discussed above in the Background section and in Table 1, the requirement that two independent sequences be recognized in an assay provides a highly desirable level of specificity. In the invasive cleavage reactions of the present invention, the invader and probe oligonucleotides must hybridize to the target nucleic acid with the correct orientation and spacing to enable the production of the correct cleavage product. When the distinctive pattern of cleavage is not dependent on the successful alignment of both oligonucleotides in the detection system these advantages of independent recognition are lost.

EXAMPLE 26

Invasive Cleavage and Primer-Directed Cleavage when there is Only Partial Homology in the "X" Overlap Region

[0617] While not limiting the present invention to any particular mechanism, invasive cleavage occurs when the site of cleavage is shifted to a site within the duplex formed between the probe and the target nucleic acid in a manner that is dependent on the presence of an upstream oligonucleotide which shares a region of overlap with the downstream probe oligonucleotide. In some instances, the 5' region of the downstream oligonucleotide may not be completely complementary to the target nucleic acid. In these instances, cleavage of the probe may occur at an internal site within the probe even in the absence of an upstream oligonucleotide (in contrast to the base-by-base nibbling seen when a fully paired probe is used without an invader). Invasive cleavage is characterized by an apparent shifting of cleavage to a site within a downstream duplex that is dependent on the presence of the invader oligonucleotide.

[0618] A comparison between invasive cleavage and primer-directed cleavage may be illustrated by comparing the expected cleavage sites of a set of probe oligonucleotides having decreasing degrees of complementarity to the target strand in the 5' region of the probe (i.e., the region that overlaps with the invader). A simple test, similar to that performed on the hairpin substrate above (Ex. 25), can be performed to compare invasive cleavage with the non-invasive primer-directed cleavage described above. Such a set of test oligonucleotides is diagrammed in FIG. 65. The structures shown in FIG. 65 are grouped in pairs, labeled "a", "b", "c", and "d". Each pair has the same probe sequence annealed to the target strand (SEQ ID NO:65), but the top structure of each pair is drawn without an upstream oligonucleotide, while the bottom structure includes this oligonucleotide (SEQ ID NO:66). The sequences of the probes shown in FIGS. 64a-64d are listed in SEQ ID NOS:43, 67, 68 and 69, respectively. Probable sites of cleavage are indicated by the black arrowheads. (It is noted that the precise site of cleavage on each of these structures

may vary depending on the choice of cleavage agent and other experimental variables. These particular sites are provided for illustrative purposes only.) To conduct this test, the site of cleavage of each probe is determined both in the presence and the absence of the upstream oligonucleotide, in reaction conditions such as those described in Example 19. The products of each pair of reactions are then be compared to determine whether the fragment released from the 5' end of the probe increases in size when the upstream oligonucleotide is included in the reaction.

[0619] The arrangement shown in FIG. 65a, in which the probe molecule is completely complementary to the target strand, is similar to that shown in FIG. 32. Treatment of the top structure with the 5' nuclease of a DNA polymerase would cause exonucleolytic nibbling of the probe (i.e., in the absence of the upstream oligonucleotide). In contrast, inclusion of an invader oligonucleotide would cause a distinctive cleavage shift similar, to those observed in FIG. 33.

[0620] The arrangements shown in FIGS. 65b and 65c have some amount of unpaired sequence at the 5' terminus of the probe (3 and 5 bases, respectively). These small 5' arms are suitable cleavage substrate for the 5' nucleases and would be cleaved within 2 nucleotide's of the junction between the single stranded region and the duplex. In these arrangements, the 3' end of the upstream oligonucleotide shares identity with a portion of the 5' region of the probe which is complementary to the target sequence (that is the 3' end of the invader has to compete for binding to the target with a portion of the 5' end of the probe). Therefore, when the upstream oligonucleotide is included it is thought to mediate a shift in the site of cleavage into the downstream duplex (although the present invention is not limited to any

particular mechanism of action), and this would, therefore, constitute invasive cleavage. If the extreme 5' nucleotides of the unpaired region of the probe were able to hybridize to the target strand, the cleavage site in the absence of the invader might change but the addition of the invader oligonucleotide would still shift the cleavage site to the proper position.

[0621] Finally, in the arrangement shown in FIG. 65d, the probe and upstream oligonucleotides share no significant regions of homology, and the presence of the upstream oligonucleotide would not compete for binding to the target with the probe. Cleavage of the structures shown in FIG. 64d would occur at the same site with or without the upstream oligonucleotide, and is thus would not constitute invasive cleavage.

[0622] By examining any upstream oligonucleotide/probe pair in this way, it can easily be determined whether the resulting cleavage is invasive or merely primer-directed. Such analysis is particularly useful when the probe is not fully complementary to the target nucleic acid, so that the expected result may not be obvious by simple inspection of the sequences.

[0623] From the above it is clear that the invention provides reagents and methods to permit the detection and characterization of nucleic acid sequences and variations in nucleic acid sequences. The invader-directed cleavage reaction of the present invention provides an ideal direct detection method that combines the advantages of the direct detection assays (e.g., easy quantification and minimal risk of carry-over contamination) with the specificity provided by a dual oligonucleotide hybridization assay.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 48

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGAGGGGGA TGCTGCCCT CTTTGAGCCC AAGGGCCGGG TCCTCTGGT GGACGGCCAC	60
CACCTGGCCT ACCGCACCTT CCACGCCCTG AAGGGCTCA CCACCAGCCG GGGGAGCCG	120
GTGCAGCGG TCTACGGCTT CGCCAAGAGC CTCTCAAGG CCCTCAAGGA GGACGGGGAC	180
GCGGTGATCG TGGTCTTTGA CGCCAAGGCC CCCTCCTTCC GCCACGAGGC CTACGGGGGG	240
TACAAGGCGG GCCGGGCCCC CACGCCGGAG GACTTTCCCC GGCAACTCGC CCTCATCAAG	300
GAGCTGGTGG ACCTCCTGGG GCTGGCGCGC CTCGAGGTCC CGGGCTACGA GGCGGACGAC	360
GTCTGGCCA GCCTGGCCAA GAAGGCGGAA AAGGAGGGCT ACGAGGTCCG CATCCTCACC	420

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GCCGACAAAG	ACCTTTACCA	GCTCCTTTCC	GACCGCATCC	ACGTCCTCCA	CCCCGAGGGG	480
TACCTCATCA	CCCCGGCCTG	GCTTTGGGAA	AAGTACGGCC	TGAGGCCCGA	CCAGTGGGCC	540
GACTACCGGG	CCCTGACCGG	GGACGAGTCC	GACAACCTTC	CCGGGGTCAA	GGGCATCGGG	600
GAGAAGACGG	CGAGGAAGCT	TCTGGAGGAG	TGGGGGAGCC	TGGAAGCCCT	CCTCAAGAAC	660
CTGGACCGGC	TGAAGCCCGC	CATCCGGGAG	AAGATCCTGG	CCCACATGGA	CGATCTGAAG	720
CTCTCCTGGG	ACCTGGCCAA	GGTGCGCACC	GACCTGCCCC	TGGAGGTGGA	CTTCGCCAAA	780
AGGCGGGAGC	CCGACCGGGA	GAGGCTTAGG	GCCTTCTTGG	AGAGGCTTGA	GTTTGGCAGC	840
CTCCTCCACG	AGTTCGGCCT	TCTGGAAAGC	CCCAAGGCC	TGGAGGAGGC	CCCCTGGCCC	900
CCGCCGGAAG	GGGCCTTCGT	GGGCTTTGTG	CTTCCCGCA	AGGAGCCCAT	GTGGCCGAT	960
CTTCTGGCCC	TGGCCGCCCG	CAGGGGGGGC	CGGGTCCACC	GGGCCCCCGA	GCCTTATAAA	1020
GCCCTCAGGG	ACCTGAAGGA	GGCGCGGGGG	CTTCTCGCCA	AAGACCTGAG	CGTCTTGCC	1080
CTGAGGGAAG	GCCTTGGCCT	CCCGCCCGGC	GACGACCCCA	TGCTCCTCGC	CTACCTCCTG	1140
GACCCTTCCA	ACACCACCCC	CGAGGGGGTG	GCCCGCGCCT	ACGGCGGGGA	GTGGACGGAG	1200
GAGGCGGGGG	AGCGGGCCCG	CCTTCCGAG	AGGCTCTTCG	CCAACCTGTG	GGGAGGCTT	1260
GAGGGGGAGG	AGAGGCTCCT	TTGGCTTTAC	CGGGAGGTGG	AGAGGCCCTT	TCCGCTGTC	1320
CTGGCCACA	TGGAGGCCAC	GGGGTGC	CTGGACGTGG	CCTATCTCAG	GGCCTTGTC	1380
CTGGAGGTGG	CCGAGGAGAT	CGCCCGCCTC	GAGGCCGAGG	TCTTCCGCTT	GGCGGCCAC	1440
CCCTTCAACC	TCAACTCCCG	GGACCAGCTG	GAAAGGGTCC	TCTTTGACGA	GCTAGGGCTT	1500
CCCGCCATCG	GCAAGACGGA	GAAGACCGGC	AAGCGCTCCA	CCAGCGCCGC	CGTCTGGAG	1560
GCCCTCCGCG	AGGCCCAACC	CATCGTGGAG	AAGATCCTGC	AGTACCGGGA	GCTCACCAAG	1620
CTGAAGAGCA	CCTACATTGA	CCCCTTGCCG	GACCTCATCC	ACCCAGGAC	GGGCCGCCTC	1680
CACACCCGCT	TCAACCAGAC	GGCCACGGCC	ACGGGCAGGC	TAAGTAGCTC	CGATCCCAAC	1740
CTCCAGAACA	TCCCCGTCCG	CACCCCGCTT	GGGCAGAGGA	TCCCGCCGGC	CTTCATCGCC	1800
GAGGAGGGGT	GGCTATTGGT	GGCCCTGGAC	TATAGCCAGA	TAGAGCTCAG	GGTGCTGGCC	1860
CACCTCTCCG	GCGACGAGAA	CCTGATCCGG	GTCCTCCAGG	AGGGCGGGGA	CATCCACACG	1920
GAGACCGCCA	GCTGGATGTT	CGGCGTCCCG	CGGGAGGCCG	TGACCCCTT	GATGCGCCGG	1980
GCGGCCAAGA	CCATCAACTT	CGGGTCCCTC	TACGGCATGT	CGGCCACCG	CCTCTCCAG	2040
GAGCTAGCCA	TCCCTTACGA	GGAGGCCAG	GCCCTCATTG	AGCGCTACTT	TCAGAGCTTC	2100
CCCAAGGTGC	GGGCCTGGAT	TGAGAAGACC	CTGGAGGAGG	GCAGGAGCG	GGGTACGTG	2160
GAGACCTCT	TCGGCCCGCG	CCGCTACGTG	CCAGACCTAG	AGGCCCGGGT	GAAGAGCGTG	2220
CGGGAGGCGG	CCGAGCGCAT	GGCCTTCAAC	ATGCCCGTCC	AGGCACCGC	CGCCGACCTC	2280
ATGAAGCTGG	CTATGGTGAA	GCTCTTCCCC	AGGCTGGAGG	AAATGGGGGC	CAGGATGCTC	2340
CTTCAGGTCC	ACGACGAGCT	GGTCTCGAG	GCCCCAAAAG	AGAGGGCGGA	GGCCGTGGCC	2400
CGGCTGGCCA	AGGAGGTTCAT	GGAGGGGGTG	TATCCCCTGG	CCGTGCCCCCT	GGAGGTGGAG	2460
GTGGGGATAG	GGGAGGACTG	GCTCTCCGCC	AAGGAGTGAT	ACCACC		2506

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2496 base pairs

(B) TYPE: nucleic acid

-continued

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATGGCGATGC	TTCCCCCTTT	TGAGCCCAAA	GGCCGCGTGC	TCCTGGTGGG	CGGCCACCAC	60
CTGGCCTACC	GCACCTTCTT	TGCCCTCAAG	GGCCTCACCA	CCAGCCGCGG	CGAACCCGTT	120
CAGGCGGTCT	ACGGCTTCGC	CAAAGCCCTC	CTCAAGGCC	TGAAGGAGGA	CGGGGACGTG	180
GTGGTGGTGG	TCTTTGACGC	CAAGGCCCCC	TCCTTCCGCC	ACGAGGCCCTA	CGAGGCCTAC	240
AAGGCGGGCC	GGGCCCCCAC	CCCGGAGGAC	TTTCCCCGGC	AGCTGGCCCT	CATCAAGGAG	300
TTGGTGGACC	TCCTAGGCCT	TGTGCGGCTG	GAGGTTCCCG	GCTTTGAGGC	GGACGACGTG	360
CTGGCCACCC	TGGCCAAGCG	GGCGGAAAAG	GAGGGGTACG	AGGTGCGCAT	CCTCACTGCC	420
GACCGCGACC	TCTACCAGCT	CCTTTCGGAG	CGCATCGCCA	TCCTCCACCC	TGAGGGGTAC	480
CTGATCACCC	CGGCGTGGCT	TTACGAGAAG	TACGGCCTGC	GCCCGGAGCA	GTGGGTGGAC	540
TACCGGGCCC	TGGCGGGGGA	CCCCTCGGAT	AACATCCCCG	GGGTGAAGGG	CATCGGGGAG	600
AAGACCGCCC	AGAGGCTCAT	CCGCGAGTGG	GGGAGCCTGG	AAAACCTCTT	CCAGCACCTG	660
GACCAGGTGA	AGCCCTCCTT	GCGGGAGAAG	CTCCAGGCGG	GCATGGAGGC	CCTGGCCCTT	720
TCCCGGAAGC	TTTCCCAGGT	GCACACTGAC	CTGCCCTTGG	AGGTGGACTT	CGGGAGGCGC	780
CGCACACCCA	ACCTGGAGGG	TCTGCGGGCT	TTTTTGGAGC	GGTGGAGTT	TGGAAGCCTC	840
CTCCACGAGT	TCGGCTCCTT	GGAGGGGCCG	AAGGCGGCG	AGGAGGCCCC	CTGGCCCTT	900
CCGGAAGGGG	CTTTTTTGGG	CTTTTCTTTT	TCCCGTCCCG	AGCCCATGTG	GGCCGAGCTT	960
CTGGCCCTGG	CTGGGGCGTG	GGAGGGGCGC	CTCCATCGGG	CACAAGACCC	CCTTAGGGGC	1020
CTGAGGGACC	TTAAGGGGTT	GCGGGGAATC	CTGGCCAAGG	ACCTGGCGGT	TTTGGCCCTG	1080
CGGGAGGGCC	TGGACCTCTT	CCCAGAGGAC	GACCCCATGC	TCCTGGCCTA	CCTTCTGGAC	1140
CCCTCCAACA	CCACCCCTGA	GGGGGTGGCC	CGGCGTTACG	GGGGGGAGTG	GACGGAGGAT	1200
GCGGGGAGA	GGGCCCTCCT	GGCCGAGCGC	CTCTTCCAGA	CCCTAAAGGA	GCGCCTTAAG	1260
GGAGAAGAAC	GCCTGCTTTG	GCTTTACGAG	GAGGTGGAGA	AGCCGCTTTC	CGGGTGTGTTG	1320
GCCCGGATGG	AGGCCACGGG	GGTCCGGCTG	GACGTGGCCT	ACCTCCAGGC	CCTCTCCCTG	1380
GAGGTGGAGG	CGGAGGTGCG	CCAGCTGGAG	GAGGAGGTCT	TCCGCCTGGC	CGGCCACCCC	1440
TTCAACCTCA	ACTCCCAGCA	CCAGCTGGAG	CGGGTGCTCT	TTGACGAGCT	GGCCCTGCCT	1500
GCCATCGGCA	AGACGGAGAA	GACGGGGA	CGCTCCACCA	GCGCTGCCGT	GCTGGAGGCC	1560
CTGCGAGAGG	CCCACCCCAT	CGTGGACCGC	ATCCTGCAGT	ACCGGGAGCT	CACCAAGCTC	1620
AAGAACACCT	ACATAGACCC	CCTGCCCGCC	CTGGTCCACC	CCAAGACCGG	CGGCCTCCAC	1680
ACCCGCTTCA	ACCAGACGGC	CACCGCCACG	GGCAGGCTTT	CCAGCTCCGA	CCCCAACCTG	1740
CAGAACATCC	CCGTGCGCAC	CCCTCTGGGC	CAGCGCATCC	GCCGAGCCTT	CGTGGCCGAG	1800
GAGGCTGGG	TGCTGGTGGT	CTTGGACTAC	AGCCAGATTG	AGCTTCGGGT	CCTGGCCCAC	1860
CTCTCCGGGG	ACGAGAACCT	GATCCGGGTC	TTTCAGGAGG	GGAGGGACAT	CCACACCCAG	1920
ACCGCCAGCT	GGATGTTCCG	CGTTTCCCCC	GAAGGGGTAG	ACCCTCTGAT	GCGCCGGGCG	1980
GCCAAGACCA	TCAACTTCGG	GGTGCTCTAC	GGCATGTCCG	CCCACCGCCT	CTCCGGGGAG	2040
CTTTCCATCC	CCTACGAGGA	GGCGGTGGCC	TTCATTGAGC	GCTACTTCCA	GAGCTACCCC	2100

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AAGGTGCGGG	CCTGGATTGA	GGGACCCTC	GAGGAGGCC	GCCGGCGGG	GTATGTGGAG	2160
ACCTCTTCG	GCCGCCGGC	CTATGTGCC	GACCTCAACG	CCCGGTGAA	GAGCGTGCC	2220
GAGGCGGGC	AGCGCATGC	CTCAACATG	CCGGTCCAGG	GCACCGCCG	CGACCTCATG	2280
AAGCTGGCCA	TGGTGCGGCT	TTTCCCCCG	CTTCAGGAAC	TGGGGGCGAG	GATGCTTTTG	2340
CAGGTGCACG	ACGAGCTGGT	CCTCGAGGCC	CCCAAGGACC	GGGCGGAGAG	GGTAGCCGCT	2400
TTGGCCAAGG	AGGTCATGGA	GGGGTCTGG	CCCCTGCAGG	TGCCCTGGA	GGTGGAGGTG	2460
GGCCTGGGGG	AGGACTGGCT	CTCCGCCAAG	GAGTAG			2496

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATGGAGGCGA	TGCTTCCGCT	CTTTGAACCC	AAAGGCCGGG	TCCTCCTGGT	GGACGGCCAC	60
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GTGCAGGCGG	TCTACGGCTT	CGCCAAGAGC	CTCCTCAAGG	CCCTGAAGGA	GGACGGGTAC	180
AAGGCCGTCT	TCGTGGTCTT	TGACGCCAAG	GCCCCCTCCT	TCCGCCACGA	GGCCTACGAG	240
GCCTACAAGG	CGGGAGGGG	CCCGACCCC	GAGGACTTCC	CCCGGCAGCT	CGCCCTCATC	300
AAGGAGCTGG	TGGACCTCCT	GGGGTTTACC	CGCCTCGAGG	TCCCCGGCTA	CGAGGCGGAC	360
GACGTTCTCG	CCACCTTGGC	CAAGAAGGCG	GAAAAGGAGG	GGTACGAGGT	GCGCATCCTC	420
ACCGCCGACC	GCGACCTCTA	CCAACCTGTC	TCCGACCGCG	TCGCCCTCCT	CCACCCGAG	480
GGCCACCTCA	TCACCCCGGA	GTGGCTTTGG	GAGAAGTACG	GCCTCAGGCC	GGAGCAGTGG	540
GTGGACTTCC	GCGCCCTCGT	GGGGGACCCC	TCCGACAACC	TCCCCGGGGT	CAAGGGCATC	600
GGGGAGAAGA	CCGCCCTCAA	GCTCCTCAAG	GAGTGGGGAA	GCCTGGAAAA	CCTCCTCAAG	660
AACCTGGACC	GGGTAAAGCC	AGAAAACGTC	CGGGAGAAGA	TCAAGGCCCA	CCTGGAAGAC	720
CTCAGGCTCT	CCTTGGAGCT	CTCCCGGGTG	CGCACCGACC	TCCCCCTGGA	GGTGGACCTC	780
GCCCAGGGGC	GGGAGCCGA	CGGGAGGGG	CTTAGGGCCT	TCCTGGAGAG	GCTGGAGTTC	840
GGCAGCCTCC	TCCACGAGTT	CGCCCTCCTG	GAGGCCCCCG	CCCCCTGGA	GGAGGCCCCC	900
TGGCCCCCGC	CGGAAGGGGC	CTTCGTGGGC	TTCGTCCTCT	CCCGCCCCGA	GCCCATGTGG	960
GCGGAGCTTA	AAGCCCTGGC	CGCCTGCAGG	GACGGCCGGG	TGCACCGGGC	AGCAGACCCC	1020
TTGGCGGGG	TAAAGGACCT	CAAGGAGGTC	CGGGCCCTCC	TCGCCAAGGA	CCTCGCCGTC	1080
TTGGCCTCGA	GGGAGGGGCT	AGACCTCGTG	CCCGGGGACG	ACCCCATGCT	CCTCGCCTAC	1140
CTCCTGGACC	CCTCCAACAC	CACCCCGGAG	GGGGTGGCGC	GGCGCTACGG	GGGGAGTGG	1200
ACGGAGGACG	CCGCCACCG	GGCCCTCCTC	TCGGAGAGGC	TCCATCGGAA	CCTCCTTAAG	1260
CGCCTCGAGG	GGGAGGAGAA	GCTCCTTTGG	CTCTACCACG	AGGTGGAAAA	GCCCCCTCTC	1320
CGGGTCCTGG	CCCACATGGA	GGCCACCGGG	GTACGGCTGG	ACGTGGCCTA	CCTTCAGGCC	1380
CTTTCCTTGG	AGCTTGC	GGAGATCCGC	CGCCTCGAGG	AGGAGGTCTT	CCGCTTGGCG	1440

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GGCCACCCCT TCAACCTCAA CTCCCAGGAC CAGCTGGAAA GGGTGCTCTT TGACGAGCTT 1500
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CTGGAGGCC TACGGGAGGC CCACCCATC GTGAGAAGA TCCTCCAGCA CCGGAGGCTC 1620
ACCAAGCTCA AGAACACCTA CGTGGACCCC CTCCAAGCC TCGTCCACCC GAGGACGGGC 1680
CGCCTCCACA CCCGCTTCAA CCAGACGGCC ACGGCCACGG GGAGGCTTAG TAGCTCCGAC 1740
CCCAACCTGC AGAACATCCC CGTCCGCACC CCCTTGGGCC AGAGGATCCG CCGGGCCTTC 1800
GTGGCCGAGG CGGGTTGGGC GTTGTGGGCC CTGGACTATA GCCAGATAGA GCTCCGCGTC 1860
CTCGCCACC TCTCCGGGGA CGAAAACCTG ATCAGGGTCT TCCAGGAGGG GAAGGACATC 1920
CACACCCAGA CCGCAAGCTG GATGTTCCGC GTCCCCCGG AGGCCGTGGA CCCCTGATG 1980
CGCCGGGCGG CCAAGACGGT GAACTTCGGC GTCCTCTACG GCATGTCCGC CCATAGGCTC 2040
TCCCAGGAGC TTGCCATCCC CTACGAGGAG GCGGTGGCCT TTATAGAGGC TACTTCCAAA 2100
GCTTCCCAA GGTGCGGGCC TGGATAGAAA AGACCCCTGA GGAGGGGAGG AAGCGGGGCT 2160
ACGTGGAAC CCTCTTCGGA AGAAGCGCT ACGTGCCCGA CCTCAACGCC CGGGTGAAGA 2220
GCGTCAGGGA GGCCGCGGAG CGCATGGCCT TCAACATGCC CGTCCAGGGC ACCGCCGCGG 2280
ACCTCATGAA GCTCGCCATG GTGAAGCTCT TCCCCGCCT CCGGGAGATG GGGGCCCGCA 2340
TGCTCTCCA GGTCCACGAC GAGCTCTCC TGGAGGCCCC CCAAGCGCGG GCCGAGGAGG 2400
TGGCGGCTTT GGCCAAGGAG GCCATGGAGA AGGCCTATCC CCTCGCCGTG CCCCTGAGG 2460
TGGAGGTGGG GATGGGGGAG GACTGGCTTT CCGCCAAGGG TTAG 2504

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(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 832 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
1           5           10           15
Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly
20          25          30
Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
35          40          45
Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val
50          55          60
Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly
65          70          75          80
Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
85          90          95
Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu
100         105         110
Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys
115        120        125
Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp
130        135        140

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Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly
 145 150 155 160
 Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
 165 170 175
 Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn
 180 185 190
 Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu
 195 200 205
 Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu
 210 215 220
 Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys
 225 230 235 240
 Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val
 245 250 255
 Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe
 260 265 270
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
 275 280 285
 Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
 290 295 300
 Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp
 305 310 315 320
 Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro
 325 330 335
 Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu
 340 345 350
 Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro
 355 360 365
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400
 Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu
 405 410 415
 Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu
 420 425 430
 Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445
 Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala
 450 455 460
 Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His
 465 470 475 480
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
 485 490 495
 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg
 500 505 510
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525
 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr
 530 535 540
 Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu

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50					55					60					
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu	Ala	Tyr
65					70					75					80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala
				85					90					95	
Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Val	Arg	Leu	Glu	Val
			100						105					110	
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Arg	Ala
		115					120						125		
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu
		130					135					140			
Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ala	Ile	Leu	His	Pro	Glu	Gly	Tyr
145					150					155					160
Leu	Ile	Thr	Pro	Ala	Trp	Leu	Tyr	Glu	Lys	Tyr	Gly	Leu	Arg	Pro	Glu
				165					170						175
Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn	Ile
			180						185					190	
Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Gln	Arg	Leu	Ile	Arg
		195					200						205		
Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Phe	Gln	His	Leu	Asp	Gln	Val	Lys
		210					215					220			
Pro	Ser	Leu	Arg	Glu	Lys	Leu	Gln	Ala	Gly	Met	Glu	Ala	Leu	Ala	Leu
225					230					235					240
Ser	Arg	Lys	Leu	Ser	Gln	Val	His	Thr	Asp	Leu	Pro	Leu	Glu	Val	Asp
				245					250						255
Phe	Gly	Arg	Arg	Arg	Thr	Pro	Asn	Leu	Glu	Gly	Leu	Arg	Ala	Phe	Leu
				260					265					270	
Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu	Glu
		275							280				285		
Gly	Pro	Lys	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	Ala
		290					295						300		
Phe	Leu	Gly	Phe	Ser	Phe	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu	Leu
305					310					315					320
Leu	Ala	Leu	Ala	Gly	Ala	Trp	Glu	Gly	Arg	Leu	His	Arg	Ala	Gln	Asp
				325					330						335
Pro	Leu	Arg	Gly	Leu	Arg	Asp	Leu	Lys	Gly	Val	Arg	Gly	Ile	Leu	Ala
			340						345					350	
Lys	Asp	Leu	Ala	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Asp	Leu	Phe	Pro
		355						360				365			
Glu	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn	Thr
		370					375					380			
Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu	Asp
385					390					395					400
Ala	Gly	Glu	Arg	Ala	Leu	Leu	Ala	Glu	Arg	Leu	Phe	Gln	Thr	Leu	Lys
				405					410						415
Glu	Arg	Leu	Lys	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Glu	Glu	Val
			420						425					430	
Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	Arg	Met	Glu	Ala	Thr	Gly	Val
		435						440					445		
Arg	Leu	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu	Val	Glu	Ala
		450					455					460			

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Glu Val Arg Gln Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro
 465 470 475 480
 Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu
 485 490 495
 Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser
 500 505 510
 Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val
 515 520 525
 Asp Arg Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr
 530 535 540
 Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Gly Arg Leu His
 545 550 555 560
 Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser
 565 570 575
 Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg
 580 585 590
 Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Val Leu Val Val Leu
 595 600 605
 Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp
 610 615 620
 Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Gln
 625 630 635 640
 Thr Ala Ser Trp Met Phe Gly Val Ser Pro Glu Gly Val Asp Pro Leu
 645 650 655
 Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met
 660 665 670
 Ser Ala His Arg Leu Ser Gly Glu Leu Ser Ile Pro Tyr Glu Glu Ala
 675 680 685
 Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg Ala
 690 695 700
 Trp Ile Glu Gly Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu
 705 710 715 720
 Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val
 725 730 735
 Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val
 740 745 750
 Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Arg Leu Phe
 755 760 765
 Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His Asp
 770 775 780
 Glu Leu Val Leu Glu Ala Pro Lys Asp Arg Ala Glu Arg Val Ala Ala
 785 790 795 800
 Leu Ala Lys Glu Val Met Glu Gly Val Trp Pro Leu Gln Val Pro Leu
 805 810 815
 Glu Val Glu Val Gly Leu Gly Glu Asp Trp Leu Ser Ala Lys Glu
 820 825 830

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 834 amino acids
 (B) TYPE: amino acid

-continued

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

Met Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
1      5      10      15
Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly
20      25      30
Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
35      40      45
Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe
50      55      60
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
65      70      75      80
Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85      90      95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
100     105     110
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys
115     120     125
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg
130     135     140
Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His Pro Glu
145     150     155     160
Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165     170     175
Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp
180     185     190
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu
195     200     205
Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg
210     215     220
Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu Glu Asp
225     230     235     240
Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu
245     250     255
Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Arg
260     265     270
Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
275     280     285
Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro
290     295     300
Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp
305     310     315     320
Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val His Arg
325     330     335
Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
340     345     350
Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
355     360     365

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Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 410 415
 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
 420 425 430
 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445
 Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
 450 455 460
 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
 465 470 475 480
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys Thr Gly
 500 505 510
 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
 515 520 525
 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
 530 535 540
 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
 545 550 555 560
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590
 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
 595 600 605
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln

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CTTCCC GCCA TCGGCAAGAC GGAGAAGACN GGCAAGCGCT CCACCAGCGC CGCCGTGCTG 1560
GAGGCCCTNC GNGAGGCCCA CCCCATCGTG GAGAAGATCC TGCAGTACCG GGAGCTCACC 1620
AAGCTCAAGA ACACCTACAT NGACCCCTG CCNGNCCTCG TCCACCCAG GACGGGCCGC 1680
CTCCACACCC GCTTCAACCA GACGGCCACG GCCACGGCA GGCTTAGTAG CTCCGACCCC 1740
AACCTGCAGA ACATCCCCGT CCGCACCCCN CTGGGCCAGA GGATCCGCCG GGCCTTCGTG 1800
GCCGAGGAGG GNTGGGTGTT GGTGGCCCTG GACTATAGCC AGATAGAGCT CCGGGTCCTG 1860
GCCCACCTCT CCGGGGACGA GAACCTGATC CGGTCTTCC AGGAGGGGAG GGACATCCAC 1920
ACCCAGACCG CCAGCTGGAT GTTCGGCGTC CCCCAGGAG CCGTGGACCC CCTGATGCGC 1980
CGGGCGGCCA AGACCATCAA CTTCGGGGTC CTCTACGGCA TGTCCGCCCA CCGCCTCTCC 2040
CAGGAGCTTG CCATCCCTA CGAGGAGCG GTGGCCTTCA TTGAGCGCTA CTTCAGAGC 2100
TTCCCCAAGG TCGGGGCTG GATTGAGAAG ACCCTGGAGG AGGGCAGGAG GCGGGGTAC 2160
GTGGAGACCC TCTTCGGCCG CCGGCGCTAC GTGCCCGACC TCAACGCCCG GGTGAAGAGC 2220
GTGCGGGAGG CGGCGGAGCG CATGGCCTTC AACATGCCCG TCCAGGGCAC CGCCGCCGAC 2280
CTCATGAAGC TGGCCATGTT GAAGCTCTTC CCCCAGCTNC AGGAAATGGG GGCCAGGATG 2340
CTCCTNCAGG TCCACGACGA GCTGGTCTC GAGGCCCCCA AAGAGCGGGC GGAGGNGGTG 2400
GCCGCTTTGG CCAAGGAGGT CATGGAGGG GTCTATCCCC TGGCCGTGCC CCTGGAGGTG 2460
GAGGTGGGGA TGGGGGAGGA CTGGCTCTCC GCCAAGGAGT AG 2502

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(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

Met Xaa Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
1      5      10      15
Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly
      20      25      30
Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
      35      40      45
Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Xaa Val
      50      55      60
Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala
      65      70      75      80
Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
      85      90      95
Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Xaa Arg Leu Glu
      100     105     110
Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys
      115     120     125
Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp
      130     135     140
Leu Tyr Gln Leu Leu Ser Asp Arg Ile Ala Val Leu His Pro Glu Gly
      145     150     155     160

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Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
 165 170 175
 Glu Gln Trp Val Asp Tyr Arg Ala Leu Xaa Gly Asp Pro Ser Asp Asn
 180 185 190
 Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Xaa Lys Leu Leu
 195 200 205
 Xaa Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg Val
 210 215 220
 Lys Pro Xaa Xaa Arg Glu Lys Ile Xaa Ala His Met Glu Asp Leu Xaa
 225 230 235 240
 Leu Ser Xaa Xaa Leu Ser Xaa Val Arg Thr Asp Leu Pro Leu Glu Val
 245 250 255
 Asp Phe Ala Xaa Arg Arg Glu Pro Asp Arg Glu Gly Leu Arg Ala Phe
 260 265 270
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
 275 280 285
 Glu Xaa Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Glu Gly
 290 295 300
 Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
 305 310 315 320
 Leu Leu Ala Leu Ala Ala Arg Xaa Gly Arg Val His Arg Ala Xaa
 325 330 335
 Asp Pro Leu Xaa Gly Leu Arg Asp Leu Lys Glu Val Arg Gly Leu Leu
 340 345 350
 Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Xaa
 355 360 365
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400
 Asp Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Phe Xaa Asn Leu
 405 410 415
 Xaa Xaa Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Xaa Glu
 420 425 430
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445
 Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Val Ala
 450 455 460
 Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
 465 470 475 480
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
 485 490 495
 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg
 500 505 510
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525
 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr
 530 535 540
 Tyr Ile Asp Pro Leu Pro Xaa Leu Val His Pro Arg Thr Gly Arg Leu
 545 550 555 560

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AAGGAGCTGG	TGGACCTCCT	GGGGCTGGCG	CGCCTCGAGG	TCCCGGGCTA	CGAGGCGGAC	360
GACGTCCTGG	CCAGCCTGGC	CAAGAAGGCG	GAAAAGGAGG	GCTACGAGGT	CCGCATCCTC	420
ACCGCCGACA	AAGACCTTTA	CCAGCTCCTT	TCCGACC GCA	TCCACGTCCT	CCACCCCGAG	480
GGGTACCTCA	TCACCCCGGC	CTGGCTTTGG	GAAAAGTACG	GCCTGAGGCC	CGACCAGTGG	540
GCCGACTACC	GGGCCCTGAC	CGGGGACGAG	TCCGACAACC	TTCCCGGGGT	CAAGGGCATC	600
GGGGAGAAGA	CGGCAGGAA	GCTTCTGGAG	GAGTGGGGGA	GCCTGGAAGC	CCTCCTCAAG	660
AACCTGGACC	GGCTGAAGCC	CGCCATCCGG	GAGAAGATCC	TGGCCACAT	GGACGATCTG	720
AAGCTCTCCT	GGGACCTGGC	CAAGGTGCGC	ACCGACCTGC	CCCTGGAGGT	GGACTTCGCC	780
AAAAGGCGGG	AGCCCGACCG	GGAGAGGCTT	AGGGCCTTTC	TGGAGAGGCT	TGAGTTTGGC	840
AGCTTCCTCC	ACGAGTTCGG	CCTTCTGGAA	AGCCCAAGG	CCCTGGAGGA	GGCCCCCTGG	900
CCCCCGCCGG	AAGGGGCTTT	CGTGGGCTTT	GTGCTTTCCC	GCAAGGAGCC	CATGTGGGCC	960
GATCTTCTGG	CCCTGGCCGC	CGCCAGGGGG	GGCCGGGTCC	ACCGGGCCCC	CGAGCCTTAT	1020
AAAGCCCTCA	GGGACCTGAA	GGAGGCGCGG	GGGCTTCTCG	CCAAAGACCT	GAGCGTTCTG	1080
GCCCTGAGGG	AAGGCTTGG	CCTCCCGCCC	GGCGACGACC	CCATGCTCCT	CGCCTACCTC	1140
CTGGACCCTT	CCAACACCAC	CCCCGAGGGG	GTGGCCCGGC	GCTACGGCGG	GGAGTGGACG	1200
GAGGAGGCGG	GGGAGCGGGC	CGCCCTTTCC	GAGAGGCTCT	TCGCCAACCT	GTGGGGGAGG	1260
CTTGAGGGGG	AGGAGAGGCT	CCTTTGGCTT	TACCGGGAGG	TGGAGAGGCC	CCTTCCGCT	1320
GTCCTGGCCC	ACATGGAGGC	CACGGGGGTG	CGCCTGGACG	TGGCCTATCT	CAGGGCCTTG	1380
TCCCTGGAGG	TGGCCGGGGA	GATCGCCCGC	CTCGAGGCCG	AGGTCTTCCG	CCTGGCCGGC	1440
CACCCCTTCA	ACCTCAACTC	CCGGGACCAG	CTGAAAAGGG	TCCTCTTTGA	CGAGCTAGGG	1500
CTTCCCGCCA	TCGGCAAGAC	GGAGAAGACC	GGCAAGCGCT	CCACCAGCGC	CGCCGTCCTG	1560
GAGGCCCTCC	GCGAGGCCCA	CCCCATCGTG	GAGAAGATCC	TGCAGGCATG	CAAGCTTGGC	1620
ACTGGCCGTC	GTTTTACAAC	GTCGTGA				1647

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2088 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

ATGAATTCGG	GGATGCTGCC	CCTCTTTGAG	CCCAAGGGCC	GGGTCCTCCT	GGTGGACGGC	60
CACCACCTGG	CCTACCGCAC	CTTCCACGCC	CTGAAGGGCC	TCACCACCAG	CCGGGGGAG	120
CCGGTGCAGG	CGGTCTACGG	CTTCGCCAAG	AGCCTCCTCA	AGGCCCTCAA	GGAGGACGGG	180
GACGCGGTGA	TCGTGGTCTT	TGACGCCAAG	GCCCCCTCCT	TCCGCCACGA	GGCCTACGGG	240
GGGTACAAGG	CGGGCCGGGC	CCCCACGCCG	GAGGACTTTC	CCCGCAACT	CGCCCTCATC	300
AAGGAGCTGG	TGGACCTCCT	GGGGCTGGCG	CGCCTCGAGG	TCCCGGGCTA	CGAGGCGGAC	360
GACGTCCTGG	CCAGCCTGGC	CAAGAAGGCG	GAAAAGGAGG	GCTACGAGGT	CCGCATCCTC	420
ACCGCCGACA	AAGACCTTTA	CCAGCTCCTT	TCCGACC GCA	TCCACGTCCT	CCACCCCGAG	480
GGGTACCTCA	TCACCCCGGC	CTGGCTTTGG	GAAAAGTACG	GCCTGAGGCC	CGACCAGTGG	540

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GCCGACTACC	GGGCCCTGAC	CGGGGACGAG	TCCGACAACC	TTCCCGGGGT	CAAGGGCATC	600
GGGGAGAAGA	CGCGAGGAA	GCTTCTGGAG	GAGTGGGGGA	GCCTGGAAGC	CCTCCTCAAG	660
AACCTGGACC	GGCTGAAGCC	CGCCATCCGG	GAGAAGATCC	TGGCCACAT	GGACGATCTG	720
AAGCTCTCCT	GGGACCTGGC	CAAGGTGCGC	ACCGACCTGC	CCCTGGAGGT	GGACTTCGCC	780
AAAAGCGGG	AGCCCGACCG	GGAGAGGCTT	AGGGCCTTTC	TGGAGAGGCT	TGAGTTGGC	840
AGCCTCCTCC	ACGAGTTCGG	CCTTCTGGAA	AGCCCCAAGG	CCCTGGAGGA	GGCCCCCTGG	900
CCCCCGCCGG	AAGGGGCCTT	CGTGGGCTTT	GTGCTTTCCC	GCAAGGAGCC	CATGTGGGCC	960
GATCTTCTGG	CCCTGGCCCG	CGCCAGGGGG	GGCCGGGTCC	ACCGGGCCCC	CGAGCCTTAT	1020
AAAGCCCTCA	GGGACCTGAA	GGAGGCGCGG	GGGCTTCTCG	CCAAAGACCT	GAGCGTTCTG	1080
GCCCTGAGGG	AAGGCCTTGG	CCTCCCGCCC	GGCGACGACC	CCATGCTCCT	CGCCTACCTC	1140
CTGGACCCTT	CCAACACCAC	CCCCGAGGGG	GTGGCCCGGC	GCTACGGCGG	GGAGTGGACG	1200
GAGGAGCGCG	GGGAGCGGGC	CGCCCTTTCC	GAGAGGCTCT	TCGCCAACCT	GTGGGGGAGG	1260
CTTGAGGGGG	AGGAGAGGCT	CCTTTGGCTT	TACCGGGAGG	TGGAGAGGCC	CCTTTCCGCT	1320
GTCTGGCCC	ACATGGAGGC	CACGGGGGTG	CGCCTGGACG	TGGCCTATCT	CAGGGCCTTG	1380
TCCTTGAGG	TGGCCGGGA	GATCGCCCGC	CTCGAGGCCG	AGGTCTTCCG	CCTGGCCGGC	1440
CACCCCTTCA	ACCTCAACTC	CCGGGACCAG	CTGGAAAGGG	TCCTCTTTGA	CGAGCTAGGG	1500
CTTCCCGCCA	TCGGCAAGAC	GGAGAAGACC	GGCAAGCGCT	CCACCAGCGC	CGCCGTCTCG	1560
GAGGCCCTCC	GCGAGGCCCA	CCCCATCGTG	GAGAAGATCC	TGCAGTACCG	GGAGCTCACC	1620
AAGCTGAAGA	GCACCTACAT	TGACCCCTTG	CCGGACCTCA	TCCACCCAG	GACGGGCCGC	1680
CTCCACACCC	GCTTCAACCA	GACGGCCACG	GCCACGGGCA	GGCTAAGTAG	CTCCGATCCC	1740
AACCTCCAGA	ACATCCCCGT	CCGCACCCCG	CTTGGGCAGA	GGATCCCGCG	GGCCTTCATC	1800
GCCGAGGAGG	GGTGGCTATT	GGTGGCCCTG	GACTATAGCC	AGATAGAGCT	CAGGGTGCTG	1860
GCCCACCTCT	CCGGCGACGA	GAACCTGATC	CGGGTCTTCC	AGGAGGGGCG	GGACATCCAC	1920
ACGGAGACCG	CCAGCTGGAT	GTTCGGCGTC	CCCCGGGAGG	CCGTGGACCC	CCTGATGCGC	1980
CGGGCGGCCA	AGACCATCAA	CTTCGGGGTC	CTCTACGGCA	TGTCGGCCCA	CGCCTCTCC	2040
CAGGAGCTAG	CTAGCCATCC	CTTACGAGGA	GGCCAGGCC	TTCATTGA		2088

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 962 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATGAATTCGG	GGATGCTGCC	CCTCTTTGAG	CCCAAGGGCC	GGGTCTCCT	GGTGGACGGC	60
CACCACCTGG	CCTACCGCAC	CTTCCACGCC	CTGAAGGGCC	TCACCACCAG	CCGGGGGGAG	120
CCGGTGCAGG	CGGTCTACGG	CTTCGCCAAG	AGCCTCTCA	AGGCCCTCAA	GGAGGACGGG	180
GACGCGGTGA	TCGTGGTCTT	TGACGCCAAG	GCCCCCTCCT	TCCGCCACGA	GGCCTACGGG	240
GGGTACAAGG	CGGGCCGGGC	CCCCACGCCG	GAGGACTTTC	CCCCGCAACT	CGCCCTCATC	300

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AAGGAGCTGG	TGGACCTCCT	GGGGCTGGCG	CGCCTCGAGG	TCCCGGGCTA	CGAGGCGGAC	360
GACGTCCTGG	CCAGCCTGGC	CAAGAAGGCG	GAAAAGGAGG	GCTACGAGGT	CCGCATCCTC	420
ACCGCCGACA	AAGACCTTTA	CCAGCTTCTT	TCCGACCGCA	TCCACGTCCT	CCACCCCGAG	480
GGGTACCTCA	TCACCCCGGC	CTGGCTTTGG	GAAAAGTACG	GCCTGAGGCC	CGACCAGTGG	540
GCCGACTACC	GGGCCCTGAC	CGGGGACGAG	TCCGACAACC	TTCCCGGGGT	CAAGGGCATC	600
GGGGAGAAGA	CGGCGAGGAA	GCTTCTGGAG	GAGTGGGGGA	GCCTGGAAGC	CCTCCTCAAG	660
AACCTGGACC	GGCTGAAGCC	CGCCATCCGG	GAGAAGATCC	TGGCCACAT	GGACGATCTG	720
AAGCTCTCCT	GGGACCTGGC	CAAGGTGCGC	ACCGACCTGC	CCCTGGAGGT	GGACTTCGCC	780
AAAAGGCGGG	AGCCCGACCG	GGAGAGGCTT	AGGGCCTTTC	TGGAGAGGCT	TGAGTTTGGC	840
AGCTCCTCC	ACGAGTTCGG	CCTTCTGGAA	AGCCCAAGT	CATGGAGGGG	GTGTATCCCC	900
TGGCCGTGCC	CCTGGAGGTG	GAGGTGGGGA	TAGGGGAGGA	CTGGCTCTCC	GCCAAGGAGT	960
GA						962

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1600 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

ATGGAATTTCG	GGGATGCTGC	CCCTCTTTGA	GCCCAAGGGC	CGGGTCTCTC	TGGTGGACGG	60
CCACCACCTG	GCCTACCSCA	CCTTCCACGC	CCTGAAGGGC	CTCACCACCA	GCCGGGGGGA	120
GCCGCTGACG	GCGGTCTACG	GCTTCGCCAA	GAGCCTCCTC	AAGGCCCTCA	AGGAGGACGG	180
GGACGCGGTG	ATCGTGGTCT	TTGACGCCAA	GGCCCCCTCC	TTCCGCCACG	AGGCCTACGG	240
GGGGTACAAG	GCGGGCCGGG	CCCCACGCC	GGAGGACTTT	CCCCGGCAAC	TCGCCCTCAT	300
CAAGGAGCTG	GTGGACCTCC	TGGGGCTGGC	GCGCCTCGAG	GTCCCGGGCT	ACGAGGCGGA	360
CGACGTCCTG	GCCAGCCTGG	CCAAGAAGGC	GGAAAAGGAG	GGCTACGAGG	TCCGCATCCT	420
CACCGCCGAC	AAAGACCTTT	ACCAGCTCCT	TTCCGACCGC	ATCCACGTCC	TCCACCCCGA	480
GGGGTACCTC	ATCACCCCGG	CCTGGCTTTG	GGAAAAGTAC	GGCCTGAGGC	CCGACCAGTG	540
GGCCGACTAC	CGGGCCCTGA	CGGGGACGGA	GTCCGACAAC	CTTCCCGGGG	TCAAGGGCAT	600
CGGGGAGAAG	ACGGCGAGGA	AGCTTCTGGA	GGAGTGGGGG	AGCCTGGAAG	CCCTCCTCAA	660
GAACTTGAGC	CGGTGAAGC	CCGCCATCCG	GGAGAAGATC	CTGGCCACAC	TGGACGATCT	720
GAAGCTCTCC	TGGACCTGG	CCAAGGTGCG	CACCGACCTG	CCCCTGGAGG	TGGACTTCGC	780
CAAAAGGCGG	GAGCCCGACC	GGGAGAGGCT	TAGGGCCTTT	CTGGAGAGGC	TTGAGTTTGG	840
CAGCTCCTC	CACGAGTTCC	GCCTTCTGGA	AAGCCCCAAG	ATCCCGCGGG	CCTTCATCGC	900
CGAGGAGGGG	TGGCTATTGG	TGGCCCTGGA	CTATAGCCAG	ATAGAGCTCA	GGGTGCTGGC	960
CCACCTCTCC	GGGACGAGA	ACCTGATCCG	GGTCTTCCAG	GAGGGGCGGG	ACATCCACAC	1020
GGAGACCGCC	AGCTGGATGT	TCGGCTTCCC	CCGGGAGGCC	GTGACCCCC	TGATGCGCCG	1080
GGCGCCAAG	ACCATCAACT	TCGGGTCTCT	CTACGGCATG	TCGGCCACC	GCCTCTCCCA	1140
GGAGCTAGCC	ATCCCTTACG	AGGAGGCCCA	GGCCTTCATT	GAGCGCTACT	TTCAGAGCTT	1200

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CCCCAAGGTG CGGGCCTGGA TTGAGAAGAC CCTGGAGGAG GGCAGGAGGC GGGGGTACGT 1260
 GGAGACCCTC TTCGGCCGCC GCCGCTACGT GCCAGACCTA GAGGCCCGGG TGAAGAGCGT 1320
 GCGGGAGGCG GCCGAGCGCA TGGCCTTCAA CATGCCCGTC CGGGGCACCG CCGCCGACCT 1380
 CATGAAGCTG GCTATGGTGA AGCTCTTCCC CAGGCTGGAG GAAATGGGGG CCAGGATGCT 1440
 CCTTCAGGTC CACGACGAGC TGGTCTCGA GGCCCCAAAA GAGAGGGCGG AGGCCGTGGC 1500
 CCGGCTGGCC AAGGAGGTCA TGGAGGGGT GTATCCCCTG GCCGTGCCCC TGGAGGTGGA 1560
 GGTGGGGATA GGGGAGGACT GGCTCTCCGC CAAGGAGTGA 1600

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CACGAATTCG GGGATGCTGC CCCTCTTTGA GCCCAA 36

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GTGAGATCTA TCACTCCTTG GCGGAGAGCC AGTC 34

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 91 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TAATACGACT CACTATAGGG AGACCGGAAT TCGAGCTCGC CCGGGCGAGC TCGAATTCCG 60

TGTATTCTAT AGTGTACCT AAATCGAATT C 91

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TAATACGACT CACTATAGGG 20

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(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GAATTCGATT TAGGTGACAC TATAGAA

27

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GTAATCATGG TCATAGCTGG TAGCTTGCTA C

31

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GGATCCTCTA GAGTCGACCT GCAGGCATGC CTACCTTGGT AG

42

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GGATCCTCTA GAGTCGACCT GCAGGCATGC

30

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ATGAATTCGG GGATGCTGCC CCTCTTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC

60

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CACCACCTGG	CCTACCGCAC	CTTCCACGCC	CTGAAGGGCC	TCACCACCAG	CGGGGGGAG	120
CCGGTGCAGG	CGGTCTACGG	CTTCGCCAAG	AGCCTCCTCA	AGGCCCTCAA	GGAGGACGGG	180
GACGCGGTGA	TCGTGGTCTT	TGACGCCAAG	GCCCCCTCCT	TCCGCCACGA	GGCCTACGGG	240
GGGTACAAGG	CGGGCCGGGG	CCCCACGCCG	GAGGACTTTC	CCCGGCAACT	CGCCCTCATC	300
AAGGAGCTGG	TGGACCTCCT	GGGGCTGGCG	CGCCTCGAGG	TCCCGGGCTA	CGAGGCGGAC	360
GACGTCCTGG	CCAGCCTGGC	CAAGAAGGCG	GAAAAGGAGG	GCTACGAGGT	CCGCATCCTC	420
ACCGCCGACA	AAGACCTTTA	CCAGTCCCTT	TCCGACCACA	TCCACGTCTT	CCACCCGAG	480
GGGTACCTCA	TCACCCCGGC	CTGGCTTTGG	GAAAAGTACG	GCCTGAGGCC	CGACCAGTGG	540
GCCGACTACC	GGGCCCTGAC	CGGGGACGAG	TCCGACAACC	TTCCCGGGGT	CAAGGGCATC	600
GGGAGAAGA	CGGCAGGAA	GCTTCTGGAG	GAGTGGGGGA	GCCTGGAAGC	CCTCCTCAAG	660
AACCTGGACC	GGCTGAAGCC	CGCCATCCGG	GAGAAGATCC	TGGCCACAT	GGACGATCTG	720
AAGCTCTCCT	GGGACCTGGC	CAAGGTGCGC	ACCGACCTGC	CCCTGGAGGT	GGACTTCGCC	780
AAAAGCGGG	AGCCCGACCG	GGAGAGGCTT	AGGGCCTTTC	TGGAGAGGCT	TGAGTTTGGC	840
AGCCTCCTCC	ACGAGTTCGG	CCTTCTGGAA	AGCCCCAAGG	CCCTGGAGGA	GGCCCCCTGG	900
CCCCCGCCGG	AAGGGGCCTT	CGTGGGCTTT	GTGCTTTCCC	GCAAGGAGCC	CATGTGGGCC	960
GATCTTCTGG	CCCTGGCCCG	CGCCAGGGGG	GGCCGGGTCC	ACCGGGCCCC	CGAGCCTTAT	1020
AAAGCCCTCA	GGGACCTGAA	GGAGGCGCGG	GGGCTTCTCG	CCAAAGACCT	GAGCGTTCTG	1080
GCCCTGAGGG	AAGGCTTGG	CCTCCCGCCC	GGCGACGACC	CCATGCTCCT	CGCCTACCTC	1140
CTGGACCCTT	CCAACACCAC	CCCCGAGGGG	GTGGCCCGGC	GCTACGGCGG	GGAGTGACG	1200
GAGGAGCGCG	GGGAGCGGGC	CGCCCTTTCC	GAGAGGCTCT	TCGCCAACCT	GTGGGGGAGG	1260
CTTGAGGGGG	AGGAGAGGCT	CCTTTGGCTT	TACCGGGAGG	TGGAGAGGCC	CCTTTCCGCT	1320
GTCTGGCCC	ACATGGAGGC	CACGGGGGTG	CGCCTGGACG	TGGCCTATCT	CAGGGCCTTG	1380
TCCCTGGAGG	TGGCCGGGGA	GATCGCCCGC	CTCGAGGCCG	AGGTCTTCCG	CCTGGCCGGC	1440
CACCCCTTCA	ACCTCAACTC	CCGGGACCAG	CTGGAAAGGG	TCCTCTTTGA	CGAGCTAGGG	1500
CTTCCCGCCA	TCGGCAAGAC	GGAGAAGACC	GGCAAGCGCT	CCACCAGCGC	CGCCGTCCCTG	1560
GAGGCCCTCC	GCGAGGCCCA	CCCCATCGTG	GAGAAGATCC	TGCAGTACCG	GGAGCTCACC	1620
AAGCTGAAGA	GCACCTACAT	TGACCCCTTG	CCGGACCTCA	TCCACCCAG	GACGGGCCGC	1680
CTCCACACCC	GCTTCAACCA	GACGGCCACG	GCCACGGGCA	GGCTAAGTAG	CTCCGATCCC	1740
AACCTCCAGA	ACATCCCCGT	CCGCACCCCG	CTTGGGCAGA	GGATCCCGCG	GGCCTTCATC	1800
GCCGAGGAGG	GGTGGCTATT	GGTGGCCCTG	GACTATAGCC	AGATAGAGCT	CAGGGTGCTG	1860
GCCCACCTCT	CCGGCGACGA	GAACCTGATC	CGGGTCTTCC	AGGAGGGGCG	GGACATCCAC	1920
ACGGAGACCG	CCAGCTGGAT	GTTCGGCGTC	CCCCGGGAGG	CCGTGGACCC	CCTGATGCGC	1980
CGGGCGGCCA	AGACCATCAA	CTTCGGGGTC	CTCTACGGCA	TGTCGGCCCA	CGCCTCTCC	2040
CAGGAGCTAG	CCATCCCTTA	CGAGGAGGCC	CAGGCCTTCA	TTGAGCGCTA	CTTTCAGAGC	2100
TTCCCCAAGG	TGCGGGCCTG	GATTGAGAAG	ACCTTGGAGG	AGGGCAGGAG	GCGGGGGTAC	2160
GTGAGACCC	TCTTCGGCCG	CGGCCCTAC	GTGCCAGACC	TAGAGGCCCG	GGTGAAGAGC	2220
GTGCGGGAGG	CGGCCGAGCG	CATGGCCTTC	AACATGCCCG	TCCGGGGCAC	CGCCGCCGAC	2280
CTCATGAAGC	TGGCTATGGT	GAAGCTCTTC	CCCAGGCTGG	AGGAAATGGG	GGCCAGGATG	2340

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CTCCTTCAGG TCCACGACGA GCTGGTCCTC GAGGCCCAA AAGAGAGGGC GGAGGCCGTG	2400
GCCCGGCTGG CCAAGGAGGT CATGGAGGGG GTGTATCCCC TGGCCGTGCC CCTGGAGGTG	2460
GAGGTGGGGA TAGGGGAGGA CTGGCTCTCC GCCAAGGAGT GA	2502

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GATTTAGGTG AACTATAG	19
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(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CGGACGAACA AGCGAGACAG CGACACAGGT ACCACATGGT ACAAGAGGCA AGAGAGACGA	60
CACAGCAGAA AC	72

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GTTTCTGCTG TGTCGTCTCT CTGCTCTT GTACCATGTG GTACCTGTGT CGCTGTCTCG	60
CTTGTTCTGTC	70

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GACGAACAAG CGAGACAGCG	20
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(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GTTTCTGCTG TGTCGTCTCT CTTG 24

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CCTCTTGTCAT CATGTGGTAC CTGTGTCGCT GTCTCGCTTG TTCGTC 46

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

ACACAGGTAC CACATGGTAC AAGAGGCAAG AGAGACGACA CAGCAGAAAC 50

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 969 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

ATGGCTAGCA TGACTGGTGG ACAGCAAATG GGTCCGATCA ATTCGGGGAT GCTGCCCTC 60
TTTGAGCCCA AGGGCCGGGT CCTCCTGGTG GACGGCCACC ACCTGGCCTA CCGCACCTTC 120
CACGCCCTGA AGGGCCTCAC CACCAGCCGG GGGGAGCCGG TGCAGGCGGT CTACGGCTTC 180
GCCAAGAGCC TCCTCAAGGC CCTCAAGGAG GACGGGGACG CGGTGATCGT GGTCTTTGAC 240

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GCCAAGGCC	CCTCCTCCG	CCACGAGCC	TACGGGGGT	ACAAGCGGG	CCGGCCCCC	300
ACGCCGAGG	ACTTTCCTCG	GCAACTCGCC	CTCATCAAGG	AGCTGGTGA	CCTCCTGGG	360
CTGGCGGCC	TCGAGGTCC	GGGCTACGAG	GCGGACGACG	TCCTGGCCAG	CCTGGCCAAG	420
AAGCGGAAA	AGGAGGGCTA	CGAGGTCCGC	ATCCTCACCG	CCGACAAAGA	CCTTTACCAG	480
CTTCTTTCCG	ACCGCATCCA	CGTCTCCAC	CCCGAGGGT	ACCTCATCAC	CCCGCCTGG	540
CTTTGGGAAA	AGTACGGCCT	GAGGCCCGAC	CAGTGGGCCG	ACTACCGGGC	CCTGACCGGG	600
GACGAGTCCG	ACAACCTTCC	CGGGTCAAG	GGCATCGGGG	AGAAGACGGC	GAGGAAGCTT	660
CTGGAGGAGT	GGGGAGCCT	GGAAGCCCTC	CTCAAGAACC	TGGACCGGCT	GAAGCCCGCC	720
ATCCGGGAGA	AGATCCTGGC	CCACATGGAC	GATCTGAAGC	TCTCCTGGGA	CCTGGCCAAG	780
GTGCGCACCG	ACCTGCCCTC	GGAGGTGGAC	TTCGCCAAAA	GGCGGGAGCC	CGACCGGGAG	840
AGGCTTAGGG	CCTTCTTGA	GAGGCTTGAG	TTTGGCAGCC	TCCTCCACGA	GTTCCGCCTT	900
CTGGAAAGCC	CCAAGTCATG	GAGGGGGTGT	ATCCCTGGC	CGTGCCCTG	GAGGTGGAGG	960
TGGGGATAG						969

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 948 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATGGTAGCA	TGACTGGTG	ACAGCAAATG	GGTCGGATCA	ATTGGGGAT	GCTGCCCTC	60
TTTGTAGCCA	AGGGCCGGT	CCTCCTGGTG	GACGGCCACC	ACCTGGCCTA	CCGCACCTTC	120
CACGCCCTGA	AGGGCTCAC	CACCAGCCGG	GGGAGCCGG	TGCAGGCGGT	CTACGGCTTC	180
GCCAAGAGCC	TCCTCAAGGC	CCTCAAGGAG	GACGGGACG	CGGTGATCGT	GGTCTTTGAC	240
GCCAAGGCC	CCTCCTCCG	CCACGAGCC	TACGGGGGT	ACAAGCGGG	CCGGCCCCC	300
ACGCCGAGG	ACTTTCCTCG	GCAACTCGCC	CTCATCAAGG	AGCTGGTGA	CCTCCTGGG	360
CTGGCGGCC	TCGAGGTCC	GGGCTACGAG	GCGGACGACG	TCCTGGCCAG	CCTGGCCAAG	420
AAGCGGAAA	AGGAGGGCTA	CGAGGTCCGC	ATCCTCACCG	CCGACAAAGA	CCTTTACCAG	480
CTTCTTTCCG	ACCGCATCCA	CGTCTCCAC	CCCGAGGGT	ACCTCATCAC	CCCGCCTGG	540
CTTTGGGAAA	AGTACGGCCT	GAGGCCCGAC	CAGTGGGCCG	ACTACCGGGC	CCTGACCGGG	600
GACGAGTCCG	ACAACCTTCC	CGGGTCAAG	GGCATCGGGG	AGAAGACGGC	GAGGAAGCTT	660
CTGGAGGAGT	GGGGAGCCT	GGAAGCCCTC	CTCAAGAACC	TGGACCGGCT	GAAGCCCGCC	720
ATCCGGGAGA	AGATCCTGGC	CCACATGGAC	GATCTGAAGC	TCTCCTGGGA	CCTGGCCAAG	780
GTGCGCACCG	ACCTGCCCTC	GGAGGTGGAC	TTCGCCAAAA	GGCGGGAGCC	CGACCGGGAG	840
AGGCTTAGGG	CCTTCTTGA	GAGGCTTGAG	TTTGGCAGCC	TCCTCCACGA	GTTCCGCCTT	900
CTGGAAAGCC	CCAAGGCCG	ACTCGAGCAC	CACCACCACC	ACCACTGA		948

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 206 base pairs

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(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

CGCCAGGGTT TTCCCAGTCA CGACGTTGTA AAACGACGGC CAGTGAATTG TAATACGACT 60
 CACTATAGGG CGAATTCGAG CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTGCAGGCAT 120
 GCAAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG 180
 TTCCTGTGT GAAATTGTTA TCCGCT 206

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TTCTGGGTTT TCTGCTCTCT GTCGCTGTC TCGCTTGTTT GTC 43

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

GCTGTCTCGC TTGTTCGTC 19

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GACGAACAAG CGAGACAGCG 20

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

TTCTGGGTTT TCTGCTCTCT GGTC 24

-continued

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

GACGAACAAG CGAGACAGCG ACCAGAGAGC AGAGAACCCA GAA

43

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

ACCAGAGAGC AGAGAACCCA GAA

23

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

AACAGCTATG ACCATGATTA C

21

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

GTTCTCTGCT CTCTGGTCGC TGTCTCGCTT GTGAAACAAG CGAGACAGCG TGGTCTCTCG

60

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

CGAGAGACCA CGCTG

15

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(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CCTTTCGCTT TCTTCCCTTC CTTTCTCGCC ACGTTCGCCG GCTTTCCTCCG TC 52

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

AGAAAGGAAG GGAAGAAAGC GAAAGG 26

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GACGGGGAAA GCCGGCGAAC G 21

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

GAAAGCCGGC GAACGTGGCG 20

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GGCGAACGTG GCGAGAAAGG A 21

(2) INFORMATION FOR SEQ ID NO: 47:

-continued

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

CCTTTCGCTT TCTTCCCTTC CTTTCTCGCC ACGTTCGCC GC

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(2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

CCTTTCGCTC TCTTCCCTTC CTTTCTCGCC ACGTTCGCC GC

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We claim:

1. A method of detecting the presence of a target RNA molecule by detecting non-target cleavage products comprising:

a) providing:

- i) a cleavage means,
- ii) a source of target RNA, said target RNA having a first region, a second region and a third region, wherein said first region is located adjacent to and downstream from said second region and wherein said second region is located adjacent to and downstream from said third region;
- iii) a first oligonucleotide having a 5' and a 3' portion wherein said 5' portion of said first oligonucleotide contains a sequence complementary to said second region of said target RNA and wherein said 3' portion of said first oligonucleotide contains a sequence complementary to said third region of said target RNA;
- iv) a second oligonucleotide having a 5' and a 3' portion wherein said 5' portion of said second oligonucleotide contains a sequence complementary to said first region of said target RNA and wherein said 3' portion of said second oligonucleotide contains a sequence complementary to said second region of said target nucleic acid;

b) mixing said cleavage means, said target RNA, said first oligonucleotide and said second oligonucleotide to create a reaction mixture under reaction conditions such that at least said 3' portion of said first oligonucleotide is annealed to said target RNA and wherein at least said 5' portion of said second oligonucleotide is annealed to said target RNA so as to create a cleavage structure and wherein cleavage of said cleavage structure occurs to generate non-target cleavage products; and

c) detecting said non-target cleavage products.

2. The method of claim 1 wherein said reaction conditions comprise a cleavage reaction temperature which is less than the melting temperature of said first oligonucleotide when annealed to said target RNA and greater than the melting temperature of said 3' portion of said first oligonucleotide.

3. The method of claim 1 wherein said reaction temperature is between approximately 40 and 65 degrees centigrade.

4. The method of claim 1 wherein said first and second oligonucleotides comprise DNA.

5. The method of claim 1 wherein said cleavage means comprises a thermostable 5' nuclease.

6. The method of claim 5 wherein a portion of the amino acid sequence of said nuclease is homologous to a portion of the amino acid sequence of a thermostable DNA polymerase derived from a thermophilic organism.

7. The method of claim 6 wherein said organism is selected from the group consisting of *Thermus aquaticus*, *Thermus flavus* and *Thermus thermophilus*.

8. The method of claim 7 wherein said nuclease is encoded by a DNA sequence selected from the group consisting of SEQ ID NOS:1-3, 9, 10, 12, 21, 30 and 31.

9. The method of claim 1 wherein said first oligonucleotide is completely complementary to said target RNA and wherein said second oligonucleotide is completely complementary to said target RNA.

10. The method of claim 1 wherein said first oligonucleotide is partially complementary to said target RNA.

11. The method of claim 1 wherein said second oligonucleotide is partially complementary to said target RNA.

12. The method of claim 1 wherein said detection of said non-target cleavage products comprises electrophoretic separation of the products of said reaction followed by visualization of said separated non-target cleavage products.

13. The method of claim 1 wherein said source of target RNA comprises a sample selected from the group comprising blood, saliva, cerebral spinal fluid, pleural fluid, milk, lymph, sputum and semen.

14. The method of claim 1 wherein said reaction conditions comprise providing a source of divalent cations.

15. The method of claim 14 wherein said divalent cation is selected from the group comprising Mn^{2+} and Mg^{2+} ions.

16. A method of separating nucleic acid molecules, comprising:

a) providing:

i) a charge-balanced oligonucleotide and

ii) a reactant;

b) mixing said charge-balanced oligonucleotide with said reactant to create a reaction mixture under conditions such that a charge-unbalanced oligonucleotide is produced; and

c) separating said charge-unbalanced oligonucleotide from said reaction mixture.

17. The method of claim 16, wherein said reactant comprises a cleavage means.

18. The method of claim 17, wherein said cleavage means is an endonuclease.

19. The method of claim 17, wherein said cleavage means is an exonuclease.

20. The method of claim 16, wherein said reactant comprises a polymerization means.

21. The method of claim 16, wherein said reactant comprises a ligation means.

22. The method of claim 16, wherein said charge-balanced oligonucleotide comprises a label.

23. The method of claim 16, wherein said charge-balanced oligonucleotide comprises one or more phosphonate groups.

24. The method of claim 16, wherein said charge-balanced oligonucleotide has a net neutral charge and said charge-unbalanced oligonucleotide has a net positive charge.

25. The method of claim 16, wherein said charge-balanced oligonucleotide has a net neutral charge and said charge-unbalanced oligonucleotide has a net negative charge.

26. The method of claim 16, wherein said charge-balanced oligonucleotide has a net negative charge and said charge-unbalanced oligonucleotide has a net positive charge.

27. The method of claim 16, wherein said charge-balanced oligonucleotide has a net negative charge and said charge-unbalanced oligonucleotide has a net neutral charge.

28. The method of claim 16, wherein said charge-balanced oligonucleotide has a net positive charge and said charge-unbalanced oligonucleotide has a net neutral charge.

29. The method of claim 16, wherein said charge-balanced oligonucleotide has a net positive charge and said charge-unbalanced oligonucleotide has a net negative charge.

30. The method of claim 17, wherein said charge-balanced oligonucleotide comprises DNA containing one or more positively charged adducts.

31. The method of claim 30, wherein said cleavage means removes one or more nucleotides from said charge-balanced

oligonucleotide to produce said charge-unbalanced oligonucleotide, wherein said charge-unbalanced oligonucleotide has a net positive charge.

32. The method of claim 30, wherein said cleavage means removes one or more nucleotides from said charge-balanced oligonucleotide to produce said charge-unbalanced oligonucleotide, wherein said charge-unbalanced oligonucleotide has a net neutral charge.

33. The method of claim 30, wherein said cleavage means removes one or more nucleotides from said charge-balanced oligonucleotide to produce said charge-unbalanced oligonucleotide, wherein said charge-unbalanced oligonucleotide has a net negative charge.

34. The method of claim 17, wherein said charge-balanced oligonucleotide comprises DNA containing one or more negatively charged adducts.

35. The method of claim 34, wherein said cleavage means removes one or more nucleotides from said charge-balanced oligonucleotide to produce said charge-unbalanced oligonucleotide, wherein said charge-unbalanced oligonucleotide has a net negative charge.

36. The method of claim 34, wherein said cleavage means removes one or more nucleotides from said charge-balanced oligonucleotide to produce said charge-unbalanced oligonucleotide, wherein said charge-unbalanced oligonucleotide has a net neutral charge.

37. The method of claim 34, wherein said cleavage means removes one or more nucleotides from said charge-balanced oligonucleotide to produce said charge-unbalanced oligonucleotide, wherein said charge-unbalanced oligonucleotide has a net negative charge.

38. The method of claim 30, wherein said one or more positively charged adducts are selected from the group consisting of indodicarbocyanine dye amidites, amino-substituted nucleotides, ethidium bromide, ethidium homodimer, (1,3-propanediamino)propidium, (diethylenetriamino)propidium, thiazole orange, (N-N'-tetramethyl-1,3-propanediamino)propyl thiazole orange, (N-N'-tetramethyl-1,2-ethanediamino)propyl thiazole orange, thiazole orange-thiazole orange homodimer (TOTO), thiazole orange-thiazole blue heterodimer (TOTAB), thiazole orange-ethidium heterodimer 1 (TOED1), thiazole orange-ethidium heterodimer 2 (TOED2) and florescien-ethidium heterodimer (FED).

39. The method of claim 16, wherein said separating comprises subjecting said reaction mixture to an electrical field comprising a positive pole and a negative pole under conditions such that said charge-unbalanced oligonucleotide migrates toward said positive pole.

40. The method of claim 16, wherein said separating comprises subjecting said reaction mixture to an electrical field comprising a positive pole and a negative pole under conditions such that said charge-unbalanced oligonucleotide migrates toward said negative pole.

41. The method of claim 39 further comprising detecting the presence of said separated charge-unbalanced oligonucleotide.

42. A method of detecting cleaved nucleic molecules, comprising:

a) providing:

i) a homogeneous plurality of charge-balanced oligonucleotides;

- ii) a sample suspected of containing a target nucleic acid having a sequence comprising a first region complementary to said charge-balanced oligonucleotide;
 - iii) a cleavage means; and
 - iv) a reaction vessel;
- b) adding to said vessel, in any order, said sample, said charge-balanced oligonucleotides and said cleavage means to create a reaction mixture under conditions such that a portion of said charge-balanced oligonucleotides binds to said complementary target nucleic acid to create a bound population, and such that said cleavage means cleaves at least a portion of said bound population of charge-balanced oligonucleotides to produce a population of unbound, charge-unbalanced oligonucleotides; and
- c) separating said unbound, charge-unbalanced oligonucleotides from said reaction mixture.
- 43.** The method of claim 42 further comprising providing a homogeneous plurality of oligonucleotides complementary to a second region of said target nucleic acid, wherein said oligonucleotides are capable of binding to said target nucleic acid upstream of said charge-balanced oligonucleotides.
- 44.** The method of claim 43, wherein said first and said second region of said target nucleic acid share a region of overlap.
- 45.** The method of claim 42, wherein said cleavage means comprises a thermostable 5' nuclease.
- 46.** The method of claim 45 wherein a portion of the amino acid sequence of said nuclease is homologous to a portion of the amino acid sequence of a thermostable DNA polymerase derived from a thermophilic organism.
- 47.** The method of claim 46 wherein said organism is selected from the group consisting of *Thermus aquaticus*, *Thermus flavus* and *Thermus thermophilus*.
- 48.** The method of claim 47 wherein said nuclease is encoded by a DNA sequence selected from the group consisting of SEQ ID NOS:1-3, 9, 10, 12, 21, 30 and 31.
- 49.** The method of claim 42, wherein said target nucleic acid comprises single-stranded DNA.
- 50.** The method of claim 42 wherein said target nucleic acid comprises double-stranded DNA and prior to the addition of said cleavage means said reaction mixture is treated such that said double-stranded DNA is rendered substantially single-stranded.
- 51.** The method of claim 50 wherein said treatment to render said double-stranded DNA is rendered substantially single-stranded by increasing the temperature.
- 52.** The method of claim 42 wherein said target nucleic acid comprises RNA.

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