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- (73) Patenthaver: **Indena S.p.A., Viale Ortles, 12, 20139 Milano, Italien**
- (72) Opfinder: **LONGO, Valeria, c/o INDENA S.p.A., Viale Ortles, 12, 20139 MILANO, Italien**  
**BERLANDA, Davide, c/o INDENA S.p.A., Viale Ortles, 12, 20139 MILANO, Italien**
- (74) Fuldmægtig i Danmark: **Zacco Denmark A/S, Arne Jacobsens Allé 15, 2300 København S, Danmark**
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**LAURA JAAKOLA ET AL: "Novel approaches based on DNA barcoding and high-resolution melting of amplicons for authenticity analyses of berry species", FOOD CHEMISTRY, vol. 123, no. 2, 1 November 2010 (2010-11-01), pages 494-500, XP055040634, ISSN: 0308-8146, DOI: 10.1016/j.foodchem.2010.04.069**  
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# DESCRIPTION

[0001] The present invention provides a method for the identification of *Vaccinium myrtillus* in a botanical composition, which is based on the detection of specific genomic fragments using PCR amplification. The invention further provides a kit specifically designed for implementing the method of invention.

## Background of the invention

[0002] Plant extracts are widely used in the medical, nutraceutical, cosmetic and food industry. One of the main issues encountered when dealing with plant extracts is that of determining not only their chemical composition, but also their botanical origin, in order to exclude the risk of counterfeit.

[0003] Genetic-based methods for determining the botanical origin of plant materials are known in the art (Parker, J., et al., Field-based species identification of closely-related plants using real-time nanopore sequencing. *Sci Rep*, 2017. 7(1): p. 8345; Group, C.P.W., A DNA barcode for land plants. *Proc Natl Acad Sci USA*, 2009. 106(31): p. 12794-7; Fazekas, A.J., et al., DNA barcoding methods for land plants. *Methods Mol Biol*, 2012. 858: p. 223). Such methods are based on the comparison of the DNA present in the plant material with known DNA sequences present in publicly available databases. For example, WO 2006/020147 (The Regents of the University of California) discloses a method for identifying individual biological genetic components present in a botanical mixture, said method being based on a combination of genomic-locus specific PCR, single strand conformation polymorphyspm (SSCP), and sequence analysis. The method is said to be able to provide information on the biologic components of the composition without requiring prior knowledge as to which botanicals may be present and to detect and identify unknown biologic components that may be present in the mixture.

[0004] Methods for the genetic identification of plants from botanical samples are also disclosed in CN102146477, CN106119394, CN1372005, CN107142329, CN107653330, CN105624291, CN105603107, ES2176066, CN104673930, CN102222969, CN102732513, CN105063203, JP2007282626. In some cases, the methods for the identification of botanical species are based on the detection, by PCR amplification, of specific sequences located within the nuclear ribosomal RNA-encoding locus containing the internal transcribed spacer (ITS) regions ITS-1 and/or ITS-2. In certain cases (CN1052429, CN105603107, ES2176066), the methods are aimed at identifying adulterations in commercialised products containing plant materials.

[0005] Jaakola L et al., *Food Chemistry* vol. 123, no. 2 (2010) pp. 494-500, discloses the identification of commercially important berry species by means of a combined approach of DNA barcoding and HRM (High Resolution Melting) analysis, using designed primer pairs

which enable the species-specific identification of wild berries. *Vaccinium myrtillus* is identified through HRM analysis of an amplicon located in the ITS (Internal Transcribed Spacer) region obtained with primers ITSVm2f and ITSVm2r.

[0006] CN108642207 discloses the construction of an allelic map of the bilberry plant, and a method for the identification of blueberry varieties and related species using primerspecific PCR-amplification.

[0007] Marieschi M. et al, Food Chemistry vol. 202 (2016) pp. 438-444 discloses a method based on Sequence Characterized Amplified Regions (SCARs) to detect the presence of *V. myrtillus* and adulterating species useful for multiple batches analysis.

[0008] Koskima Ki JJ et al., European Journal of Plant Pathology, Kluwer Academic Publishers - vol. 125 no. 4 (2009) pp. 629-640 discloses the relative expression of bilberry genes quantified by Real-Time PCR with SYBR-green as the fluorescent reporter.

[0009] When plant materials are processed and, in particular, when they are subjected to extraction procedures, the DNA degrades giving rise to fragments of variable size and amount according to the extraction method and which cannot be directly compared with known DNA sequences, thereby making it difficult, if not practically impossible, to apply to extracts the genomic identification methods that can be applied on the starting materials.

[0010] *Vaccinium myrtillus* extracts are largely used in pharmaceutical, cosmetic, nutraceutical and dietary products due to their known health-beneficial properties. The clinical benefits of *V. myrtillus* as both a dietary supplement and a therapeutic have been attributed to the presence of abundant amounts of flavonoids and anthocyanins. For extract manufacturers, it is important to guarantee that *V. myrtillus* extracts have the required specifications in terms of chemical components and the declared pure botanical origin. It would therefore be desirable to provide a method that allows to identify *V. myrtillus* in a botanical composition, e.g. in a plant extract, securing high levels of accuracy and species-specificity particularly when *V. myrtillus* is in admixture with closely related contaminant species.

### **Description of invention**

[0011] These objectives are achieved by the present invention, which is defined in the appended claims, and which provides a method for the specific and accurate identification of *Vaccinium myrtillus* in a botanical composition through detection of a nucleic acid fragment which is contained in the residual DNA of *V. myrtillus* extracts.

[0012] Specifically, the method of invention comprises detecting, in a sample of botanical composition, a *V. myrtillus*-specific nucleic acid fragment located within the internal transcribed spacer 1, 5.8S ribosomal RNA gene and the internal transcribed spacer 2, wherein said nucleic acid fragment consists of either SEQ ID NO:1 or a sequence comprising SEQ ID NO: 1 which is

selected from the group of SEQ ID NOs:2, 3 and 4.

**[0013]** According to the present invention, the primers used for PCR-amplification are selected from the following pairs:

1. (i) SEQ ID NO:5 and SEQ ID NO:6;
2. (ii) SEQ ID NO:7 and SEQ ID NO:8;
3. (iii) SEQ ID NO:9 and SEQ ID NO: 10;
4. (iv) SEQ ID NO: 11 and SEQ ID NO: 12;

**[0014]** According to the present invention, the PCR is a real-time PCR (rtPCR) and the method of invention comprises the following steps:

1. (a) isolating nucleic acids from a sample of botanical composition;
2. (b) conducting a rt-PCR on the isolated nucleic acids, using:
  - a pair of primers selected from the group consisting of:
    1. (i) SEQ ID NO:5 and SEQ ID NO:6;
    2. (ii) SEQ ID NO:7 and SEQ ID NO:8;
    3. (iii) SEQ ID NO:9 and SEQ ID NO: 10;
    4. (iv) SEQ ID NO: 11 and SEQ ID NO: 12;and
  - a probe annealing within the nucleic acid region amplified by the primers, said probe having sequence SEQ ID NO: 13;
3. (c) determining the presence of the amplification product,

whereby detection of the amplification product is indicative of the presence of *Vaccinium myrtillus* in the botanical composition.

**[0015]** According to the invention, the botanical composition is a mixture of plants or parts thereof, e.g. leaves, fruits, bark, roots, including plant extracts and particularly fruit extracts, which are intended for consumption or therapeutic use. In a preferred embodiment, the botanical composition is a product containing an extract of fruits of *Vaccinium myrtillus*, alone or in combination with related species such as *Empetrum nigrum*, *Sambucus nigra*, *Vaccinium oxycoccos*, *Vaccinium corymbosum* and *Vaccinium macrocarpon*.

**[0016]** The isolation of nucleic acids involves their separation and purification from other components of the plant mixture or extract and it can be conducted with conventional techniques using commercially available kits. In particular, the genomic DNA may be isolated using extraction-precipitation protocols, silica-membrane- or anion-exchangebased procedures.

**[0017]** Real-time PCR technology is known in the art and it combines the polymerase chain reaction chemistry with the use of fluorescent reporter molecules in order to monitor the

production of amplification products during each cycle of the PCR reaction. The amplification of the target DNA is obtained by repeated cycles of denaturation followed by primer- and probe-annealing and by DNA polymerase-catalyzed primer extension. DNA amplification is monitored at each cycle of PCR by measuring a fluorescent signal which is produced for instance by non-specific fluorescent dyes that intercalate with double-stranded DNA or by sequence specific DNA probes consisting of oligonucleotides labelled with a fluorescent reporter which allows for detection after probe hybridization with its complementary DNA target. Suitable intercalating dyes include SYBR<sup>®</sup> (Green I, Green II, Gold), LCGreen<sup>®</sup>, SYTO-(9, 13, 16, 60, 62, 64, 82), BOBO-3, LCGreen<sup>®</sup>, POPO-3, BEBO, TO-PRO3, PicoGreen<sup>®</sup>, SYTOX Orange and similar commercially available fluorescent dyes (fluorophores).

**[0018]** The oligonucleotide probe is labeled with a fluorescent reporter (fluorophore) at one end and a quencher of fluorescence at the opposite end of the probe. The 5' exonuclease activity of the polymerase cleaves the probe releasing the reporter molecule resulting in an increase of the fluorescence intensity. Examples of fluorophores include 5- or 6-carboxyfluorescein (5- or 6-FAM), tetrachlorofluorescein (TET), hexachloro-6-carboxyfluorescein (HEX), 6-carboxy-4',5'-dichloro-2',7'-dimethoxyfluorescein succinimidyl ester (JOE), tetramethylrhodamine (TAMRA), 5-carboxytetramethylrhodamine (TAMRASE), carboxy-X-rhodamine (ROX), 4-(dimethylaminoazo)benzene-4-carboxylic acid (DABCYL). Examples of quenchers include those of the BHQ (Black Hole Quencher<sup>®</sup>) family, NFQ-MGB (non-fluorescent quencher and minor groove binder), QSY 7 or 21 carboxylic acid succinimidyl ester.

**[0019]** The parameters and conditions of the rtPCR, such as the temperature and the length of each cycle of denaturation and annealing, can be adjusted depending on the nucleic acid fragment to be amplified, on the set of primers used in the amplification and on other variables, as known to anyone skilled in the art. In a preferred embodiment of the invention, the nucleic acid fragments herein disclosed are amplified with primers (i) through (iv) applying the following conditions:

- initial denaturation step at 95°C for 180 sec
- 2-step cycles of 15 sec at 95°C (1<sup>st</sup> step) and 15 sec at 62-68.5°C (2<sup>nd</sup> step) repeated forty (40) to fifty (50) times.

**[0020]** The specific combinations of primers and probe according to the invention allows for the specific identification of *Vaccinium myrtillus* in botanical compositions containing closely related species such as *Empetrum nigrum*, *Sambucus nigra*, *Vaccinium oxycoccos*, *Vaccinium corymbosum* and *Vaccinium macrocarpon*. As reported in the experimental section, the use of a probe different from the *Vaccinium myrtillus*-specific probe SEQ ID NO:13 and likewise annealing with fragments SEQ ID NOs:1-4, abolishes the system ability to identify *Vaccinium myrtillus* in admixture with *Empetrum* using the same primers and rt-PCR conditions disclosed above. This denotes the specificity of the selected combination of primers, probe and the

effectiveness of the rtPCR conditions according to the invention.

**[0021]** Another aspect of the invention regards a kit for the identification of *Vaccinium myrtillus* in a botanical composition. The kit of invention comprises at least one pair of primers selected from (i) through (iv) and the probe as above defined. In addition the kit may comprise, in separate containers, reagents needed for running the (rt)PCR, particularly the deoxynucleotides and the DNA polymerase, and reagents for isolating, purifying and optionally quantifying DNA. The kit may also contain DNA of *Vaccinium myrtillus* as positive control and nuclease-free water or buffer as negative control, as well as a leaflet with the instructions for performing the PCR assay.

**[0022]** In a preferred embodiment of invention the kit contains:

- one tube or vial containing all reagents necessary to perform the analysis (DNA Polymerase, dNTPs, Buffer, Probe chemistry, Primers and Probe)
- one tube or vial containing the positive control (DNA of *Vaccinium myrtillus*)
- one tube or vial containing the negative control DNA (Nuclease-free water) The kit can be used with all commercially available Real-time PCR System.

### **Description of the figures**

**[0023]**

**Figure 1:** rt-PCR amplification protocol.

**Figure 2:** rt-PCR amplification results (a) and melt curve analysis (b) of genomic DNA isolated from *Vaccinium myrtillus* frozen fruit.

**Figure 3:** Standard curve analysis for *Vaccinium myrtillus*.

**Figure 4:** Probe-based rt-PCR amplification with M-FAM probe specific for *V. myrtillus* NTC: negative control.

**Figure 5:** (a) Probe-based rt-PCR amplification with M-FAM probe specific for *V. myrtillus* in a mixed samples with a ratio reported in the legend. NTC: negative control; (b) Probe-based rt-PCR amplification with E-HEX probe specific for *E. nigrum* in a mixed samples with a ratio reported in the legend. NTC: negative control.

**Figure 6:** Correlation between Cq Mean and percentage of target species for *V. myrtillus*.

**Figure 7:** Experimental scheme used for rt-PCR analysis of dry extract samples.

**Figure 8:** rt-PCR amplification of residual DNAs isolated from *Vaccinium myrtillus* dry-extract samples. The positive control is the gDNA extracted from *Vaccinium myrtillus* frozen fruit. a)

Primer set L; b) Primer set S.

**Figure 9:** Agarose gel analysis of rt-PCR amplicons.

**Figure 10:** Alignment analysis of sequenced amplicons (top) and relative sequence identity matrix (bottom).

**Figure 11:** rt-PCR of *Vaccinium myrtillus* E. ET. 36%. Amplification and melt curves.

**Figure 12:** rt-PCR of *Vaccinium myrtillus* E. ET. 36% with probe-based method. PTC: positive control (gDNA extracted from frozen fruit of *V. myrtillus*); NTC: negative control.

## **EXPERIMENTAL SECTION - general procedures**

### **Extraction of genomic DNA (gDNA)**

**[0024]** The DNA extraction was performed by using the NucleoSpin<sup>®</sup> plant II protocol as described by the supplier (Macherey nagel. Cat. 740770.250 - July 2014/Rev.09).

### **Purification of residual DNA from the dry extract.**

**[0025]** The first purification was done by using the kit NucleoSpin<sup>®</sup> plant II Maxi protocol as described by the supplier (Macherey nagel. Cat. 740770.250 - July 2014/Rev.09), with some modification reported below.

- Weigh 3-5 g of dry extract in a 50 ml conical tube
- Add 3 ml of distilled water
- Add 9 ml of lysis buffer
- Vortex for 30 sec
- Transfer the sample to a NucleoSpin<sup>®</sup> Filter Maxi
- Centrifuge 5 min at 4500 x g, collect the clear flow-through and discard the NucleoSpin Filter Maxi
- Add 20 ml binding buffer
- Vortex for 30 sec.
- Load sample on a NucleoSpin<sup>®</sup> Plant II Maxi Column
- Centrifuge for 3 min at 4500 x g and discard the flow-through.
- Repeat the loading for all the resting sample
- Add 4 ml wash buffer (PW1) to the NucleoSpin<sup>®</sup> Plant II Maxi Column
- Centrifuge for 3 min at 4500 x g and discard the flow-through.

- Add 10 ml wash buffer (PW2) to the NucleoSpin® Plant II Maxi Column
- Centrifuge for 3 min at 4500 x g and discard the flow-through.
- Add 2 ml wash buffer (PW2) to the NucleoSpin® Plant II Maxi Column
- Centrifuge for 12 min at 4500 x g and discard the flow-through.
- Place the NucleoSpin® Plant II Maxi Column into a new collection tube (50 ml)
- Pipette 1000 µl elution buffer (PE) (65°C) onto the membrane.
- Incubate the NucleoSpin® Plant II Maxi Column for 5 min at 65°C
- Centrifuge for 3 min at 4500 x g to elute the DNA

[0026] The second purification was done by using the kit ReliaPrep™ DNA Clean-UP and Concentration System protocol as described by the supplier (Promega. Cat. A2893).

### Quantification of DNA

[0027] The DNA was quantified through the NanoQuant Plate™ instrument. The quantification was performed by using the UV-method. The 260 nm absorbance was used to quantify the DNA as 1 OD at 260 nm correspond to 50 µg/µl of DNA. The 260 nm/280 nm absorbance ratio was determined for the assessment of DNA purity.

### rt-PCR and Melt curve analysis

[0028] The rt-PCR amplification was performed by using the SYBR Green or probe based chemistry as described by the supplier (SsoAdvanced™ Universal SYBR® Green Supermix, BioRad Cat. N. 1725272; SsoAdvanced™ Universal Probes Supermix, BioRad Cat. N. 1725281), with 3-step based amplification protocol, as reported in [Figure 1](#).

### Real-time PCR

[0029] Prepare the mix as follos, final volume 20 µl:

Probe Mastermix (BioRad or equivalent) 2X	10 µl
Primer F 10 µM	0.5 µl
Primer R 10 µM	0.5 µl
Probe M-FAM 10 µM	0.5 µl
DNA 0.5 - 30 ng/ µl	2 µl
Nuclease-free water	6.5 µl

[0030] Load the sample in a real-time instrument (BioRad or equivalent) and set the following method:

95°C	180 sec	
95°C	15 sec	50 X
62 C - 68.5°C	15 sec	

[0031] Acquisition after the second step of cycling.

### DNA sequencing

[0032] The amplified DNA was purified on agarose gel and the purified fragment was sequenced through the generation of two sequences for each sample: one is generated by using forward primer and the other one by using reverse primer. Each sequencing tube was prepared by mixing the purified DNA and TRIS-HCl 5 mM pH 8.0 in order to obtain the concentration requested for the sequencing (depending on the length of the sequence, 2-5 ng/µL).

[0033] The sequences were analysed by using BioEdit or BLAST software in order to compare and identify the sequences.

### EXAMPLES

#### Example 1 - Method validation

[0034] The gDNA was purified and quantified (**Table 1**) for the *Vaccinium myrtillus* frozen fruit and its contaminant/related species hereafter reported:

**Table 1.** Quantification of gDNA extracted for all species tested in the present report.

	Ref. QdL	DNA (ng/µl)	Ratio (260/280)
<i>Vaccinium myrtillus</i>	1072/10/12	7.9	1.61
<i>Empetrum nigrum</i>	1072/10/6	29	2.07
<i>Sambucus nigra</i>	1072/10/4	12	2
<i>Vaccinium macrocarpon</i>	1072/10/7	3.4	2.83
<i>Vaccinium oxycoccos</i>	1072/10/1	6.9	1.25
<i>Vaccinium corymbosum</i>	1072/10/3	10.2	1.23

[0035] The set-up of rt-PCR reaction parameters, in terms of Cq (quantification cycle) and Tm (melt temperature) peak, were initially evaluated by using the gDNA extracted from *Vaccinium myrtillus* frozen fruit (Figure 2). The rt-PCR results showed that the designed primers allow the amplification of a single DNA region for all primer set (Tables 2 and 3).

Table 2

Region	Name	Sequence (5'→3')	Tm (°C)	Amplicon (bp)
Large sequence (L)	Vac-ex_LF	CCATCGAGTCTTTGAACGCA	57.3	275
	Vac-ex_LR	CACTTCAGGGTCAAATGGGC	59.4	
Small sequence (S)	Vac-ex_sF	GCATTGCGTCACCCACTC	58.2	131
	Vac-ex_sR	ACTTGTCGTTGAATGTCCGT CA	57.3	
Large sequence 2 (L2)	Frw_Large 2	TTGCAGAATCCCGTGAACCA	57.3	230
	Rev_Small 2	TTTAGCAACCACCACTTGTC GT	58.4	
Small sequence 2 (S2)	Frw Small 2	TGAAGGCACGTCTGCCTG	58.2	170
	Rev_Small 2	TTTAGCAACCACCACTTGTC GT	58.4	

Table 3

Primer set	Sample	Cq	Cq Mean	Cq Std. Dev
L2	1072/10/12	25.61	25.37	0.212
		25.28		
		25.21		
S2	1072/10/12	26.17	25.89	0.247
		25.70		
		25.80		
L	1072/10/12	24.88	25.11	0.203
		25.20		
		25.25		
S	1072/10/12	25.97	26.15	0.166
		26.19		
		26.29		

[0036] The rt-PCR was also performed with DNA isolated from *V. myrtillus* contaminant/related species and the results showed that it is possible to distinguish the different DNA by using the primer sets and particularly the small 2 primers (Table 4).

**Table 4 - melt curve peak results**

Sample	Large2	Small2	Large	Small
<i>V. myrtillus</i>	90.50	90.50	90.50	89.50
<i>E. nigrum</i>	88.50	88.00	90.50	89.00/89.50
<i>S. nigra</i>	88.50	87.50	89.50	87.50
<i>V. oxycoccos</i>	91.00	91.00	91.00	89.50/90.00
<i>V. corymbosum</i>	89.00	89.00	89.00	88.00
<i>V. macrocarpon</i>	91.50	91.50	91.00	90.50

[0037] The linearity of the amplification curve was also evaluated with the standard curve generation for *Vaccinium myrtillus* by using the small 2 primer set (Figure 3). It is possible to see that the linearity has been ensured in the tested range of concentration (almost 0.0625 - 8.00 ng/μl).

[0038] In order to improve the method capability to distinguish between *Vaccinium myrtillus* and contaminant/related species, the rtPCR was conducted with the Minor Groove Binding-Probe (M-FAM -SEQ ID NO: 13) specifically designed to enable the amplification of *V. myrtillus* sequences.

[0039] In a comparative experiment, the rtPCR was conducted with simultaneous use of the Minor Groove Binding-Probes SEQ ID NO: 13 (M-FAM) and SEQ ID NO: 14 (E-HEX).

[0040] To test the probe-based method different subsets of experiments have been carried out, summarized in the table below.

**Table 5**

Probe	Sample	Expected result	Result
M-FAM	<i>V. myrtillus</i>	Amplification of <i>V. myrtillus</i>	Figure 4
	<i>E. nigrum</i>		
	<i>S. nigra</i>		
	<i>V. oxycoccos</i>		
	<i>V. corymbosum</i>		
	<i>V. macrocarpon</i>		
M-FAM	<i>V. myrtillus</i>	No Amplification	Figure

Probe	Sample	Expected result	Result
	100%		5(a)
	<i>E. nigrum</i> 100%	Amplification	
	<i>V. myrtillus</i> 95%	Proportional amplification with the percentage of <i>V. myrtillus</i>	
	<i>E. nigrum</i> 5%		
	<i>V. myrtillus</i> 98%		
	<i>E. nigrum</i> 2%		
	<i>V. myrtillus</i> 99%		
	<i>E. nigrum</i> 1%		
E- HEX	<i>V. myrtillus</i> 100%		No Amplification
	<i>E. nigrum</i> 100%	Amplification	
	<i>V. myrtillus</i> 95%	Proportional amplification with the percentage of <i>E. nigrum</i>	
	<i>E. nigrum</i> 5%		
	<i>V. myrtillus</i> 98%		
	<i>E. nigrum</i> 2%		
	<i>V. myrtillus</i> 99%		
	<i>E. nigrum</i> 1%		

[0041] The amplification results were proportional to the content of the target species (Figure 6).

#### Example 2 - *Vaccinium myrtillus* dry-extract residual DNA identification

[0042] For each sample, two independent isolations of residual DNA were performed (biological replicates) and for each extracted DNA three technical replicates were tested, Figure 7.

[0043] The whole procedure was initially performed on four samples: 32549/H76, 32549/H80, 32549/H83, 32549/H84. After the residual DNA isolation and quantification (Table 6), these samples were analysed for their rt-PCR amplification characteristics (Cq and Tm) compared

with that of positive control (Figure 8 and Table 7).

**Table 6 - Residual DNA quantification**

Sample	Biological replicate	DNA (ng / $\mu$ L)	Ratio (260 / 280)
32549/H76	1	0	3.5
	2	1	1.25
32549/H80	1	0	0
	2	1.1	0.55
32549/H83	1	0.7	1.4
	2	0	2
32549/H84	1	10.3	1.41
	2	10.3	1.38

**Table 7 - rt-PCR Summary results**

Sample	DNA (ng/ $\mu$ L)	Cq. Mean	Cq. Std. Dev	Melt Temp
32549/H76_2	1.0	32.05	0.180	89.50
32549/H83_1	0.7	35.26	0.181	89.00
32549/H84_1	10.3	28.96	0.119	89.50
32549/H84_2	10.6	28.44	0.092	89.50
Negative ctrl	0.0	None	None	None
Positive ctrl	24.8	23.60	0.040	89.50

**[0044]** The results of rt-PCR amplification with all samples showed that:

- the DNA was amplified for the positive control as well as for all tested samples;
- the negative control (no DNA) showed no amplification signal;
- positive control and samples showed equal values for T<sub>m</sub> peaks.

**[0045]** This result indicates that the amplicons have the same characteristics in terms of length and/or nucleotide bases composition.

**[0046]** Moreover the Cq results are correlated with the DNA amount tested, meaning that the amplification is specific for the selected target.

**[0047]** To verify if the generated amplicons have the same sequence of the positive control, all amplified sequences were purified on agarose gel (Figure 9) and the purified fragments were sequenced (Figure 10).

**[0048]** The agarose gel analysis confirmed the differences of the amplicons length: the fragment generated with primer set S shows a length of about 130 bp, while the fragment

generated with primer set L shows a length of about 270 bp. Moreover, from gel agarose analysis it is possible to see also the presence of unspecific rt-PCR products, as in **Figure 9**, lane 4 for the sample 32549/H83\_1 where two bands are visible, in good accord with  $T_m$  peak results (**Figure 8, b**).

**[0049]** All generated sequences were aligned by considering only the portion with high quality sequencing parameters. The sequencing results (**Figure 10**) showed that all amplicon sequences (small and large) are identical to the sequence of the *Vaccinium myrtillus* standard reference.

### **Example 3 - *Vaccinium myrtillus* 36% dry ethanolic extract (E. ET.) residual DNA identification**

**[0050]** The residual DNA analysis was also performed on samples with Indena code 9042202, MIRTILLO (*V. MYRTILLUS*) E. ET. 36% after the dry-powder mixing phase, 32788/M1, 32786/M2, 32788/M2. The previous samples 32549/H76, 32549/H80 and 32549/H83 were tested again as control samples.

**[0051]** In order to optimize the purification procedure, after the first step of DNA purification the isolated residual DNA was processed with ReliaPrep™ Kit (Promega). The results in terms of DNA quantity (ng/  $\mu$ L) and quality (260/280 ratio) on the two purification steps (**Table 8**) revealed that the concentration as well as the purification are better introducing the second step.

**Table 8 - Residual DNA quantification - E. ET. 36%**

Sample	I purification		II purification	
	DNA (ng/ $\mu$ L)	Ratio (260/280)	DNA (ng/ $\mu$ L)	Ratio (260/280)
32549/H76	0	-	2.3	1.77
32549/H80	0	2	0.2	0.5
32549/H83	0	0.84	2.1	1.75
32788/M1	1.2	0.71	3.4	1.55
32786/M2	0	-	2.5	1.67
32788/M2	0.3	0.75	3.6	1.5

**[0052]** The rt-PCR analysis was performed by using SYBR green (**Figure 11**) and probe-based methods (**Figure 12**), according to the protocols described above.

**[0053]** The results indicate that:

(a) all tested samples showed the same  $T_m$  peak of the positive control (**Figure 11** and **Table 9**) when analysed with SYBR green method:

**Table 9 - rt-PCR Summary results, SYBR green method - E. ET. 36%**

Sample	DNA (ng/ $\mu$ L)	Cq. Mean	Cq. Std. Dev	Melt Temp
32549/H76	2.3	31.59	0.099	89.50
32549/H80	0.2	31.87	0.107	89.50
32549/H83	2.1	33.61	0.276	89.50
32788/M1	3.4	31.85	0.286	89.50
32786/M2	2.5	31.88	0.011	89.50
32788/M2	3.6	31.36	0.144	89.50
Negative ctrl	0	0	0	None
Positive ctrl	24.8	23.75	0.016	89.50

(b) all tested samples were detected with the probe specific for the sequence of *V. myrtillus* (**Figure 12** and **Table 10**) when analysed with probe-based method.

**Table 10 - rt-PCR Summary results, Probe-based method - E. ET. 36%**

Sample	DNA (ng/ $\mu$ L)	Cq. Mean	Cq. Std. Dev
32549/H76	2.3	31.52	0.306
32549/H80	0.2	31.38	0.073
32549/H83	2.1	33.44	0.326
32788/M1	3.4	31.10	0.098
32786/M2	2.5	31.52	0.156
32788/M2	3.6	30.53	0.197
Negative ctrl	0	0	0
Positive ctrl	7.45	24.84	0.177

#### Example 4 - Kit for the analysis

**[0054]** The kit is composed by:

- One 1.5 ml tube containing all reagents necessary to perform the analysis (DNA Polymerase, dNTPs, Buffer, Probe chemistry, Primers and Probe)
- One 1.5 ml tube containing the positive control (DNA of *Vaccinium myrtillus*)
- One 1.5 ml tube containing the negative control DNA (Nuclease-free water)

**[0055]** The kit can be used with all commercially available Real-time PCR System (es: BioRad CFX96™, BioRad CFX96™, bCube®, Roche LightCycler® 480, etc)

**List of sequences****[0056]****Nucleic acid fragments**

GCATTGCGTCACCCACTCCCCCGTGCCCCAAGCGGGCACGTCGGAGCGTGG  
 GCGGATATTGGCCCCCGTTTCGCATCCGTGCGCGGTTCGGCCTAAAAAACGGG  
 TCCCAATGACGGACATCACGACAAGT (SEQ ID NO:1)

TGAAGGCACGTCTGCCTGGGCGTCACGCATTGCGTCACCCACTCCCCCGTGC  
 CCCAAGCGGGCACGTCGGAGCGTGGGCGGATATTGGCCCCCGTTTCGCATCC  
 GTGCGCGGTTCGGCCTAAAAAACGGGTCCCAATGACGGACATCACGACAAGT  
 GGTGGTTGCTAAA (SEQ ID NO:2)

TTGCAGAATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCGCCTGAAGCC  
 ATTAGGTTGAAGGCACGTCTGCCTGGGCGTCACGCATTGCGTCACCCACTCCC  
 CCCGTGCCCCAAGCGGGCACGTCGGAGCGTGGGCGGATATTGGCCCCCGTT  
 CGCATCCGTGCGCGGTTCGGCCTAAAAAACGGGTCCCAATGACGGACATCAC  
 GACAAGTGGTGGTTGCTAAA (SEQ ID NO:3)

CCATCGAGTCTTTGAACGCAAGTTGCGCCTGAAGCCATTAGGTTGAAGGCAC  
 GTCTGCCTGGGCGTCACGCATTGCGTCACCCACTCCCCCGTGCCCCAAGCGG  
 GCACGTCGGAGCGTGGGCGGATATTGGCCCCCGTTTCGCATCCGTGCGCGGT  
 CGGCCTAAAAAACGGGTCCCAATGACGGACATCACGACAAGTGGTGGTTGCT  
 TAAACCGTCGCGTCACGTCGTGCATGCCATCGTTTGTGCGGGTTGGCCATT  
 TGACCCTGAAGTG (SEQ ID NO:4)

**Primers****"S"**

F	GCATTGCGTCACCCACTC	(SEQ ID NO:5)
R	ACTTGTCGTGATGTCCGTCA	(SEQ ID NO:6)

**"S2"**

F	TGAAGGCACGTCTGCCTG	(SEQ ID NO:7)
R	TTTAGCAACCACCACTTGTCGT	(SEQ ID NO:8)

**"L2"**

F	TTGCAGAATCCCGTGAACCA	(SEQ ID NO:9)
R	TTTAGCAACCACCACTTGTCGT	(SEQ ID NO:10)

"L"

F	CCATCGAGTCTTTGAACGCA	(SEQ ID NO:11)
R	CACTTCAGGGTCAAATGGGC	(SEQ ID NO: 12)

**Probes**

M-FAM

ACGTCGGAGCGTGGGC (SEQ ID NO:13)

E-HEX

TAGGGCGGGTAAGTGAGT (SEQ ID NO:14)

**REFERENCES CITED IN THE DESCRIPTION**

## Cited references

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- [CN107653330 \[0004\]](#)
- [CN105624291 \[0004\]](#)
- [CN105603107 \[0004\] \[0004\]](#)
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- [CN104673930 \[0004\]](#)

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## **Patentkrav**

- 5 **1.** Fremgangsmåde til identifikation af *Vaccinium myrtillus* i en botanisk sammensætning, som omfatter påvisning fra en prøve deraf ved hjælp af PCR-amplifikation af et *V. myrtillus*-nukleinsyrefragment placeret inden for den interne transskriberede spacer 1, den 5.8S ribosomale RNA-genomiske region og den interne transskriberede spacer 2, hvilken fremgangsmåde omfatter følgende trin:
- 10 (a) isolering af nukleinsyrer fra prøven;
- (b) udførelse af en realtids-PCR på den isolerede nukleinsyre ved hjælp af:
- et sæt primere, der er udvalgt fra gruppen bestående af:
    - (i) SEQ ID NO:5 og SEQ ID NO:6;
    - (ii) SEQ ID NO:7 og SEQ ID NO:8;
    - (iii) SEQ ID NO:9 og SEQ ID NO: 10;
    - 15 (iv) SEQ ID NO: 11 og SEQ ID NO: 12;
- og
- en probe, der hærdes i nukleinsyreregionen, der er amplificeret af primerne, hvilken probe består af sekvensen SEQ ID NO: 13;
- 20 (c) bestemmelse af tilstedeværelsen af amplifikationsproduktet, hvor påvisningen af amplifikationsproduktet er indikativ for tilstedeværelsen af *Vaccinium myrtillus* i den botaniske sammensætning.
- 2.** Fremgangsmåde ifølge krav 1, hvor sættet af primere (i) anvendes i trin (b).
- 25 **3.** Fremgangsmåde ifølge krav 1-2, hvor rt-PCR udføres under følgende betingelser:
- indledende denatureringstrin ved 95°C i 180 sekunder;
  - 2-trins cyklusser på 15 sek. ved 95°C (1. trin) og 15 sek. ved 62-68,5°C (2. trin) gentaget 40 til 50 gange.

4. Fremgangsmåde ifølge krav 1-3, hvor den botaniske sammensætning er et planteekstrakt.
- 5 5. Kit til identifikation af *Vaccinium myrtillus* i en botanisk sammensætning, omfattende et sæt primere og en sonde som defineret i krav 1.
6. Kit ifølge krav 5, yderligere omfattende en DNA-polymerase, en blanding af deoxynukleotider (dNTP) og bufferopløsninger.
- 10 7. Kit ifølge krav 5-6, yderligere omfattende, i separate beholdere, en prøve af *Vaccinium myrtillus*-nukleinsyre til anvendelse som positiv kontrol og nukle-asefri vand eller bufferopløsning som negativ kontrol.

# DRAWINGS

Figure 1

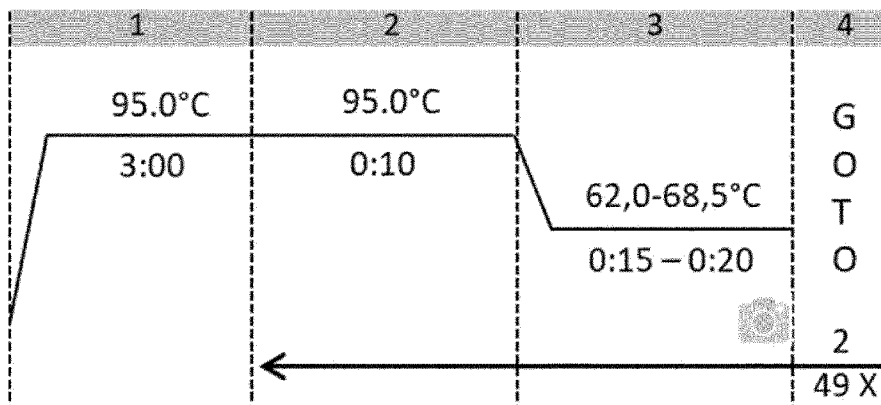
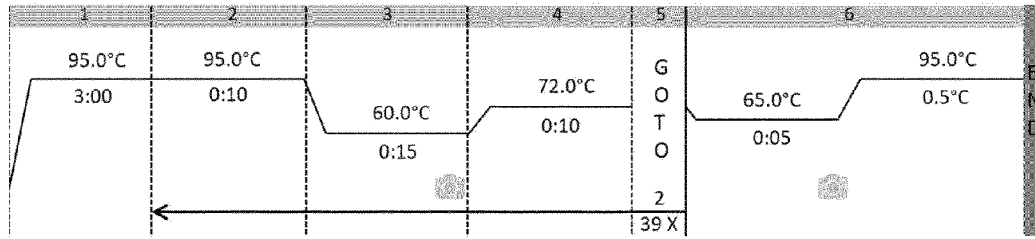


Figure 2

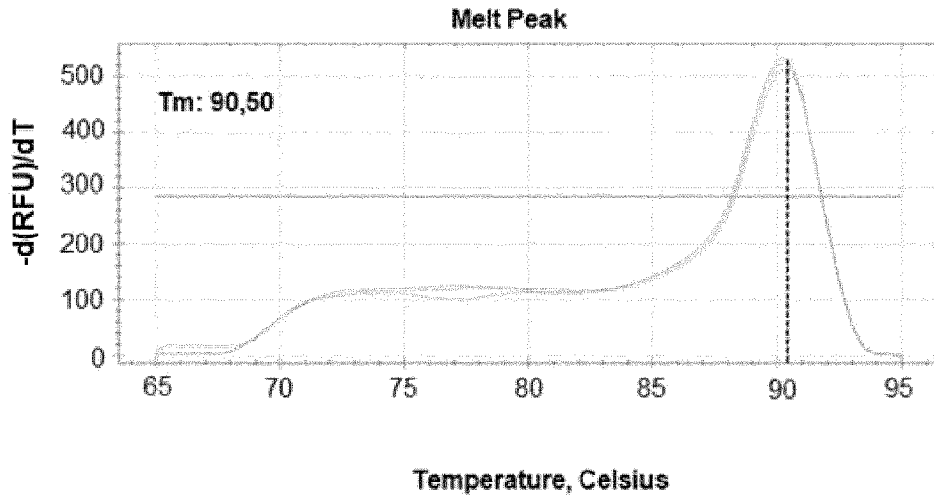
a)

Primer set	Sample	Cq	Cq Mean	Cq Std. Dev
L2	1072/10/12	25.61	25.37	0.212
		25.28		
		25.21		
S2	1072/10/12	26.17	25.89	0.247
		25.70		
		25.80		
L	1072/10/12	24.88	25.11	0.203
		25.20		
		25.25		
S	1072/10/12	25.97	26.15	0.166
		26.19		
		26.29		

Figure 2 (continued)

b)

Primer set L2



Primer set L

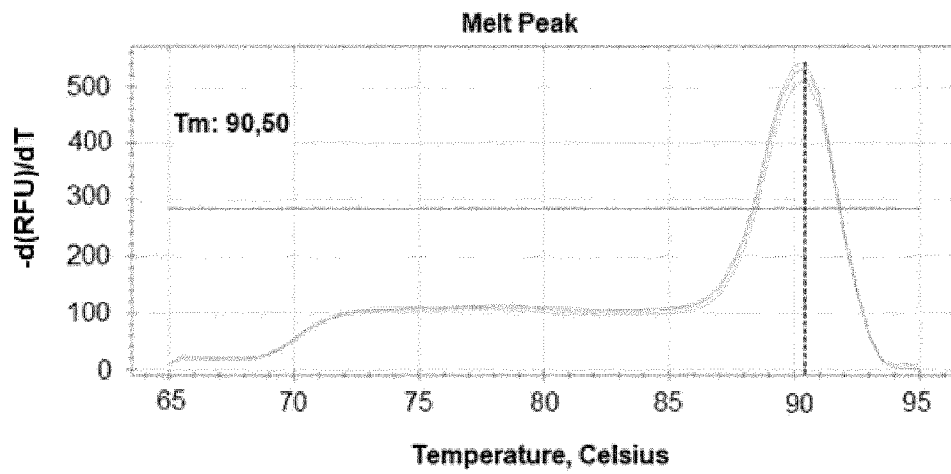
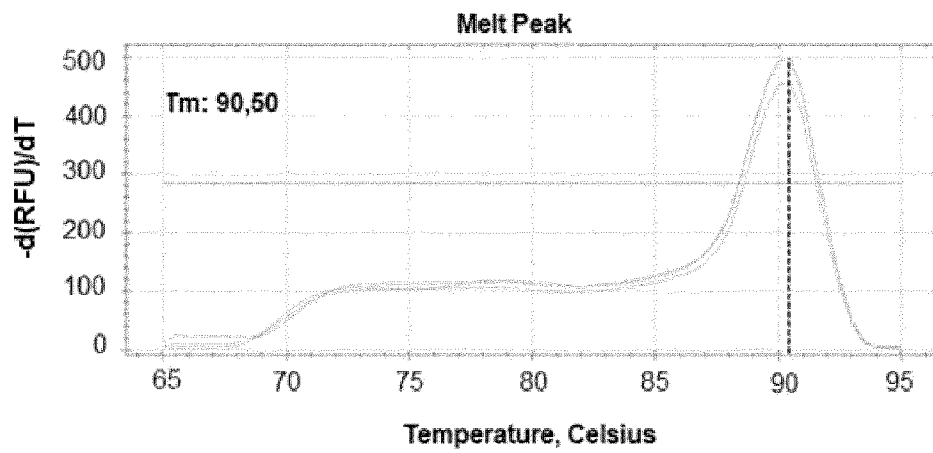


Figure 2 (continued)

Primer set S2



Primer set S

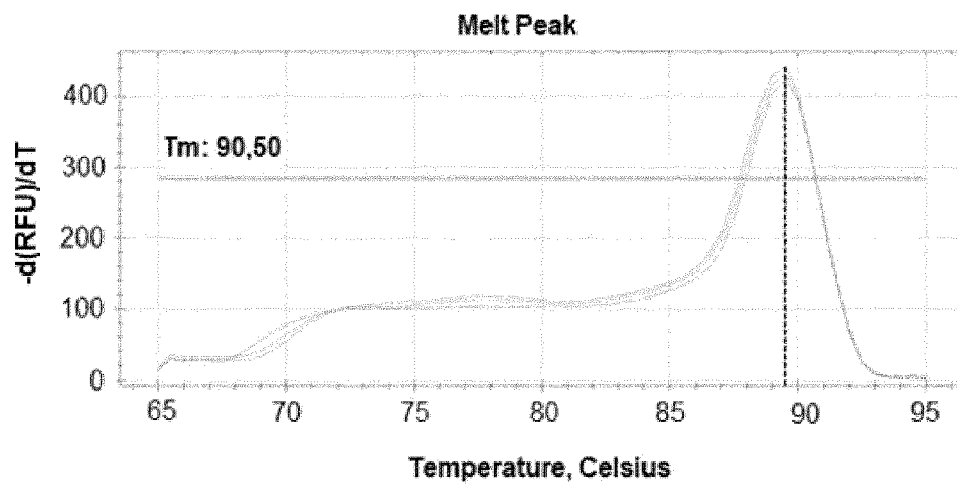
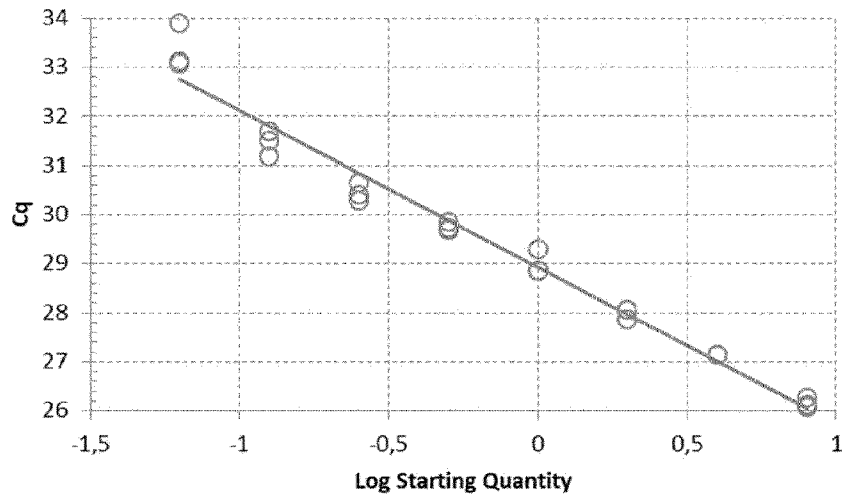


Figure 3



○ Standard

— SYBR

E=106,1% R<sup>2</sup>=0,975 Slope=-3,183 y-int=28,931

Figure 4

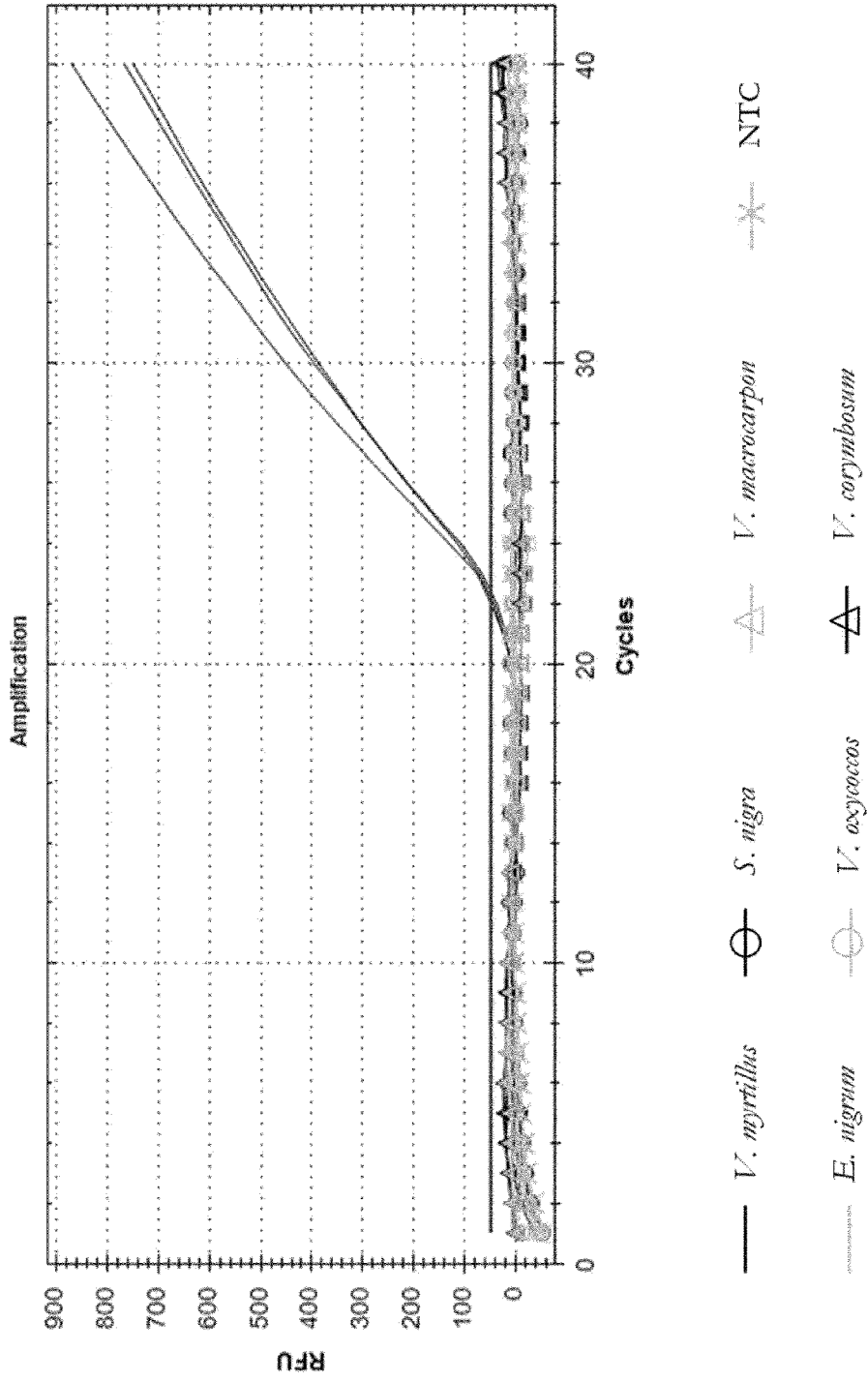


Figure 5

(a)

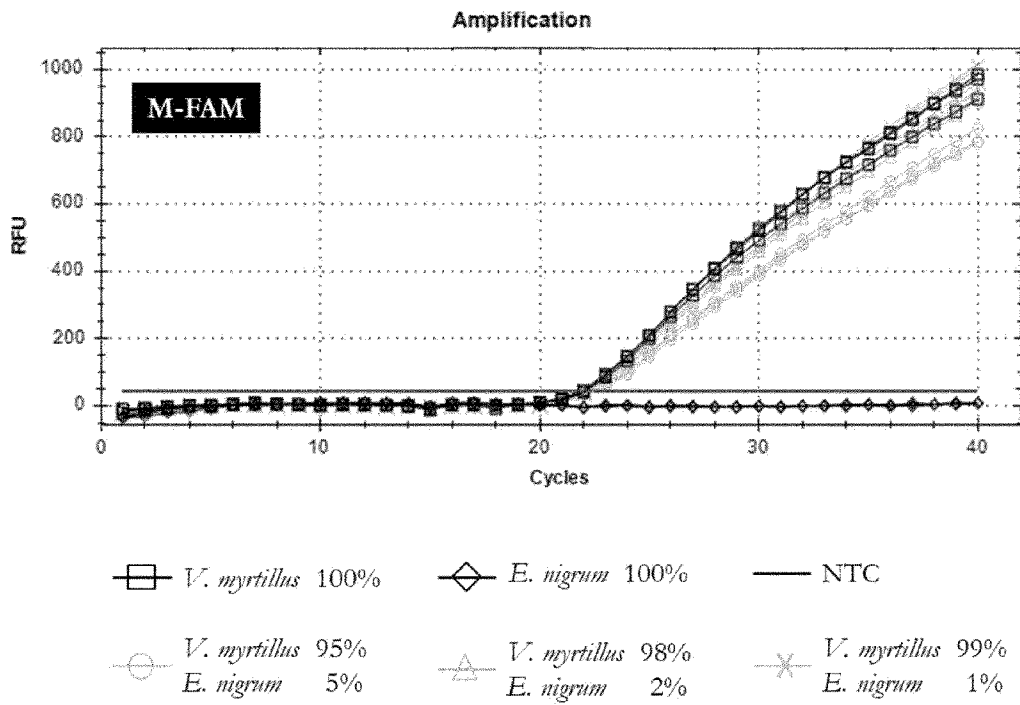


Figure 5 (continued)

(b)

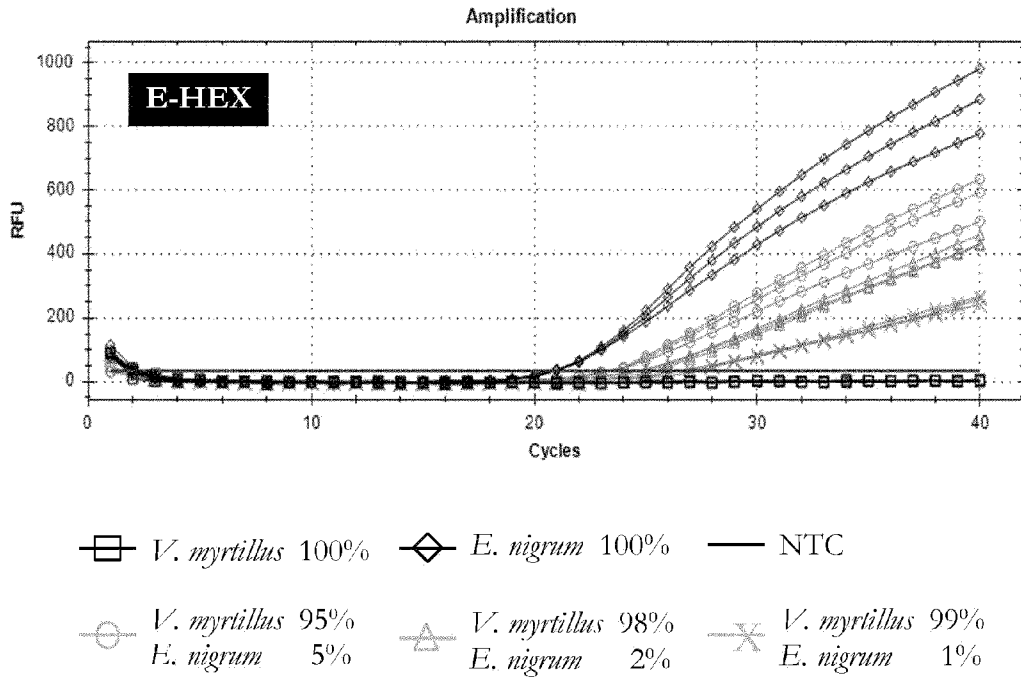


Figure 6

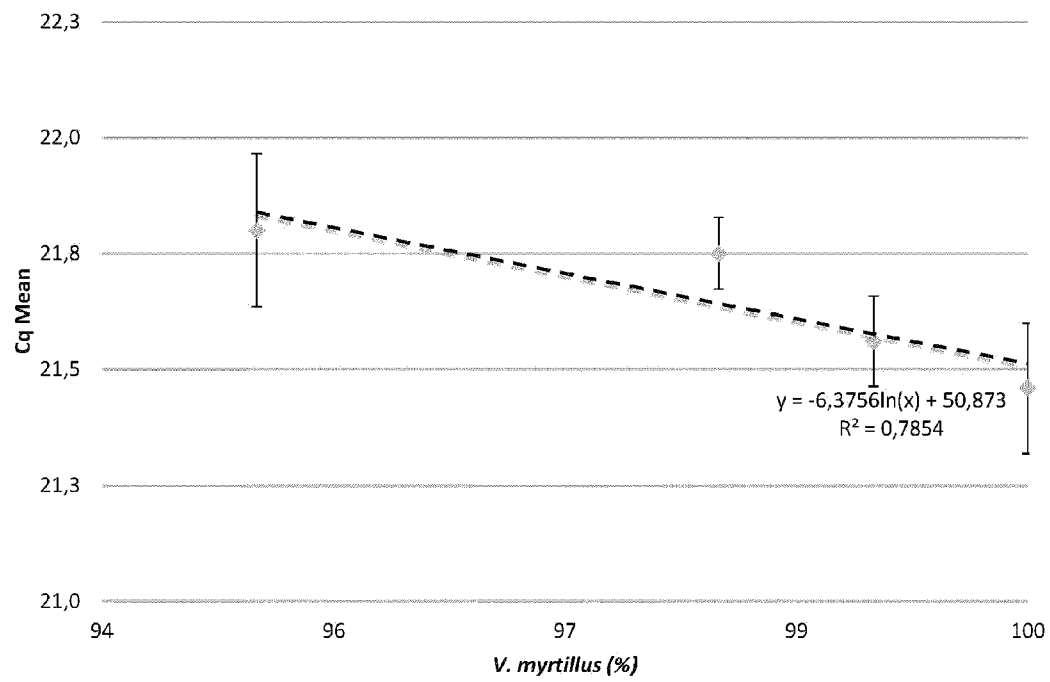


Figure 7

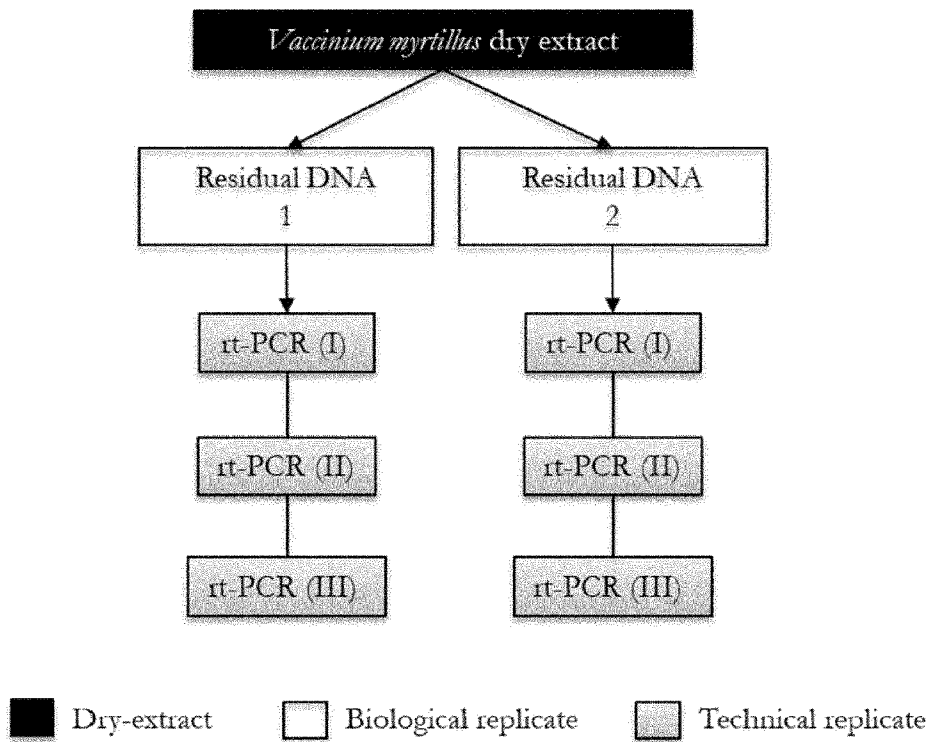
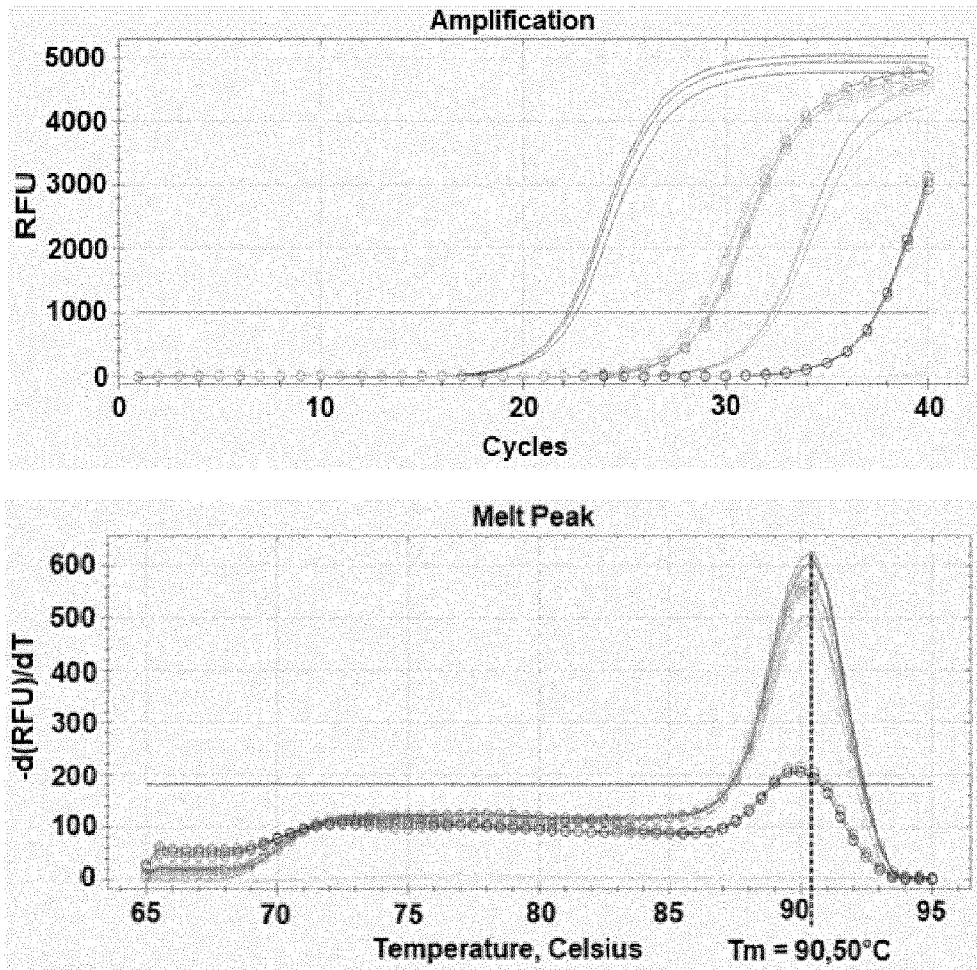


Figure 8

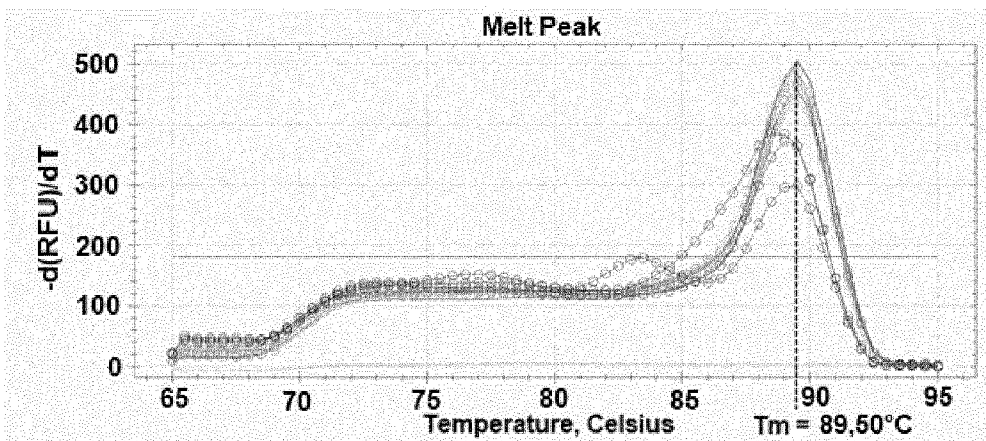
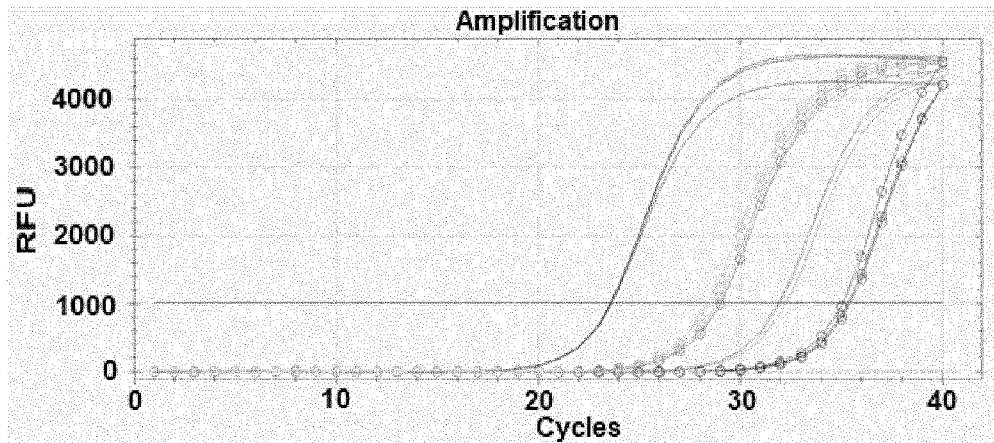
a)



- |       |                                  |   |             |
|-------|----------------------------------|---|-------------|
| —     | <i>V. myrtillus</i> fruit sample | ⊖ | 32549/H83_1 |
| - - - | Negative control                 | ⊖ | 32549/H84_1 |
| ⋯     | 32549/H76_2                      | ⊖ | 32549/H84_2 |

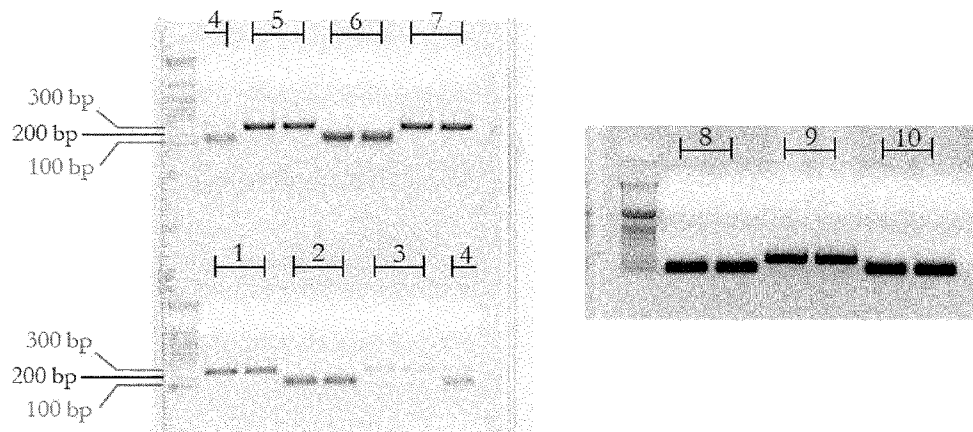
Figure 8 (continued)

b)



- |                                    |               |
|------------------------------------|---------------|
| — <i>V. myrtillus</i> fruit sample | ⊙ 32549/H83_1 |
| - - - Negative control             | ⊙ 32549/H84_1 |
| — 32549/H76_2                      | ⊙ 32549/H84_2 |

Figure 9



- |    |                   |     |                        |
|----|-------------------|-----|------------------------|
| 1. | 32549/H76_2 Large | 6.  | 32549/H84_1 Small      |
| 2. | 32549/H76_2 Small | 7.  | 32549/H84_2 Large      |
| 3. | 32549/H83_1 Large | 8.  | 32549/H84_2 Small      |
| 4. | 32549/H83_1 Small | 9.  | Positive control Large |
| 5. | 32549/H84_1 Large | 10. | Positive control Small |



Figure 11

32549/H76

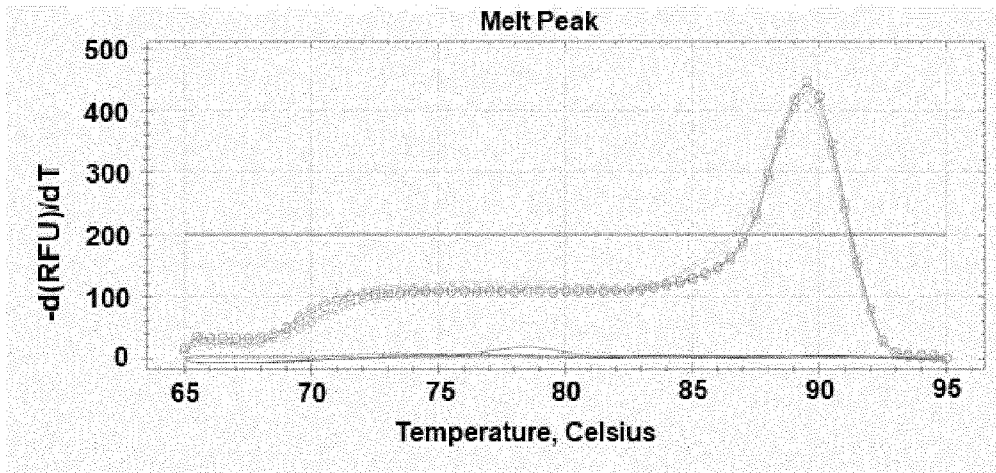
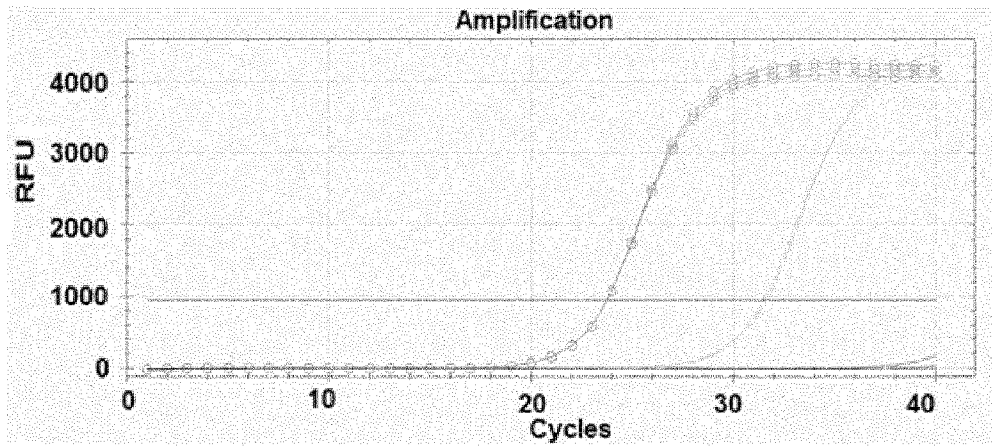


Figure 11 (continued)

32549/H180

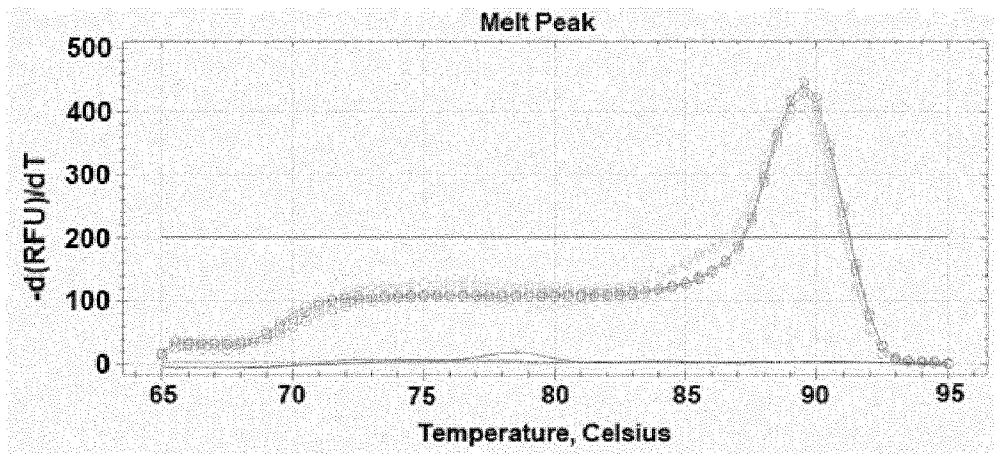
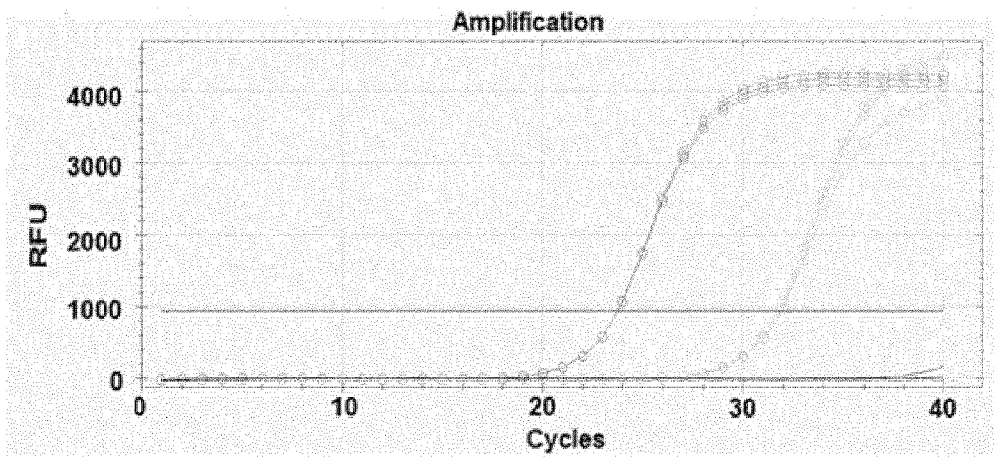


Figure 11 (continued)

32549/H83

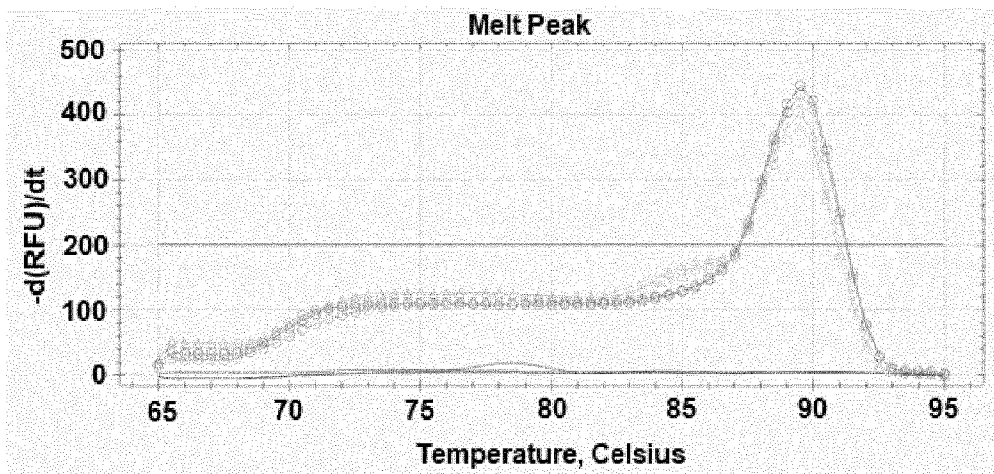
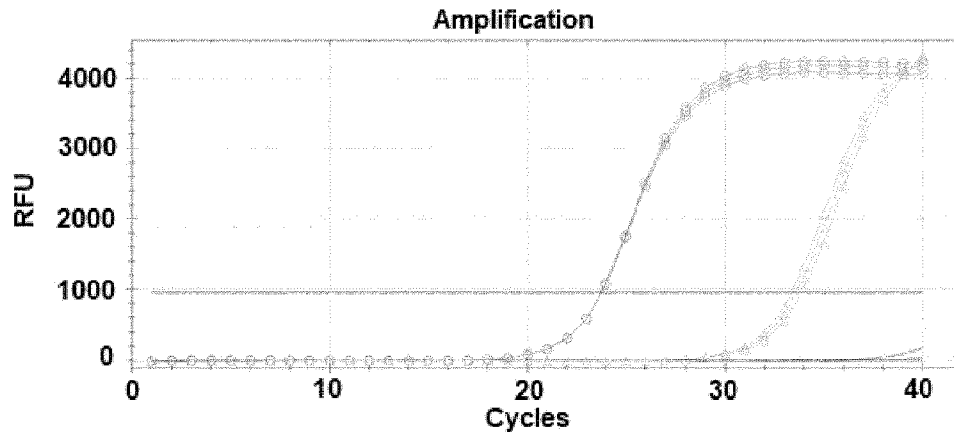


Figure 11 (continued)

32788/M1

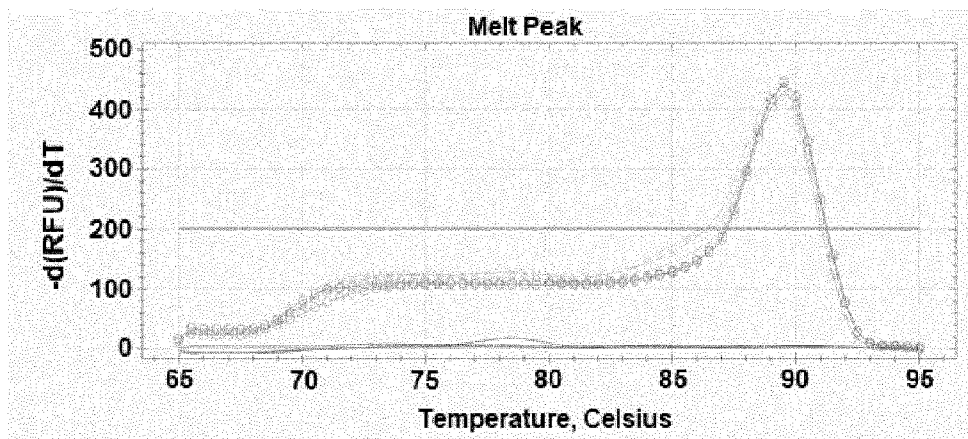
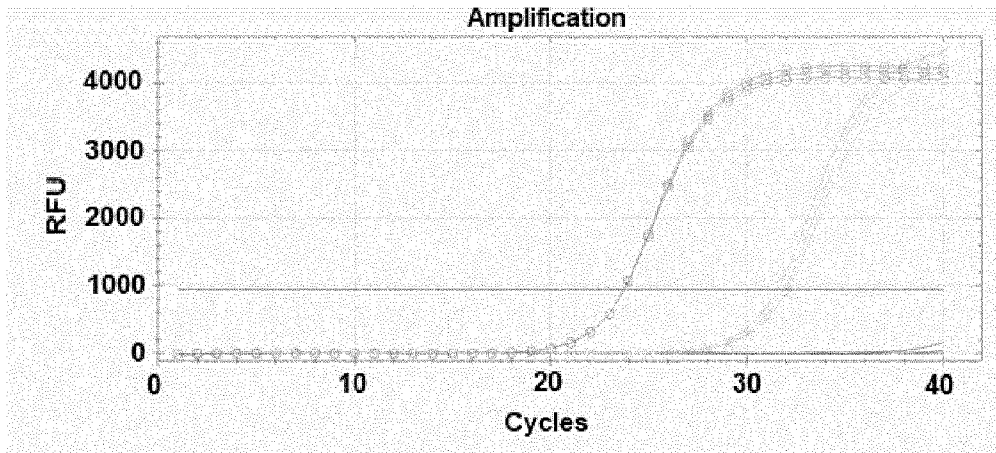


Figure 11 (continued)

32786/M2

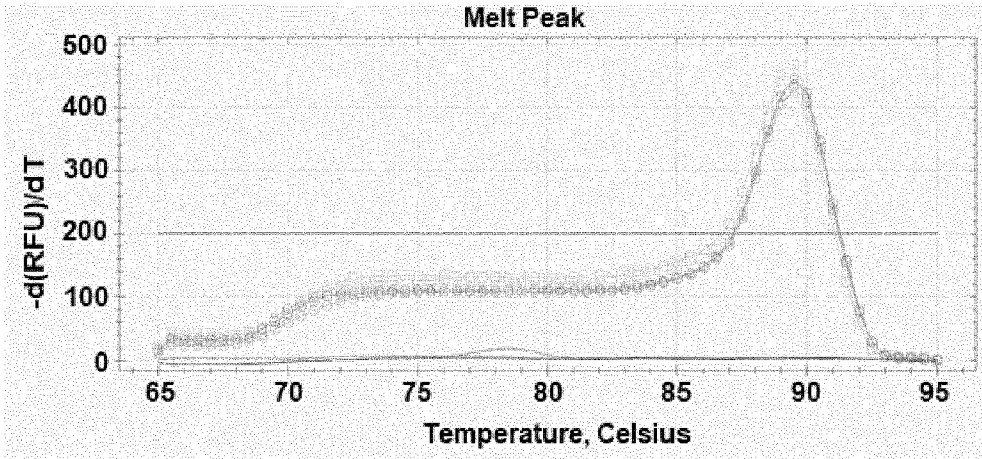
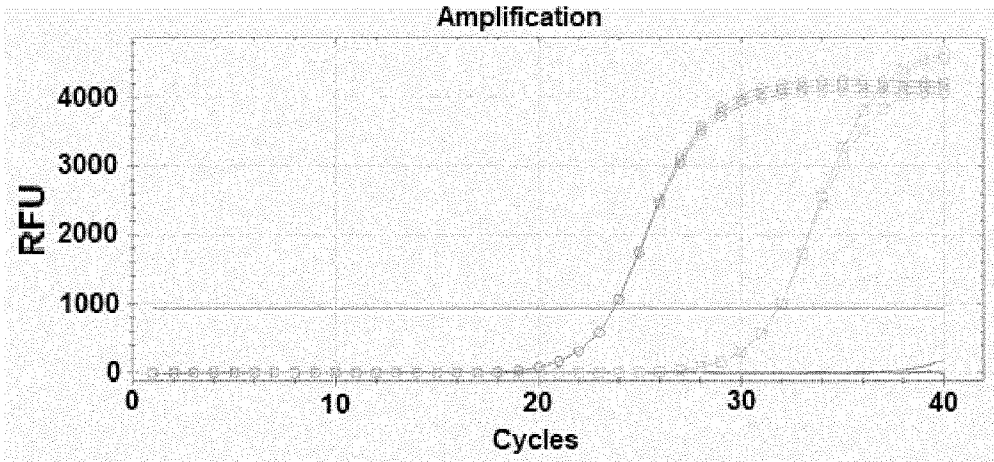


Figure 11 (continued)

32788/M2

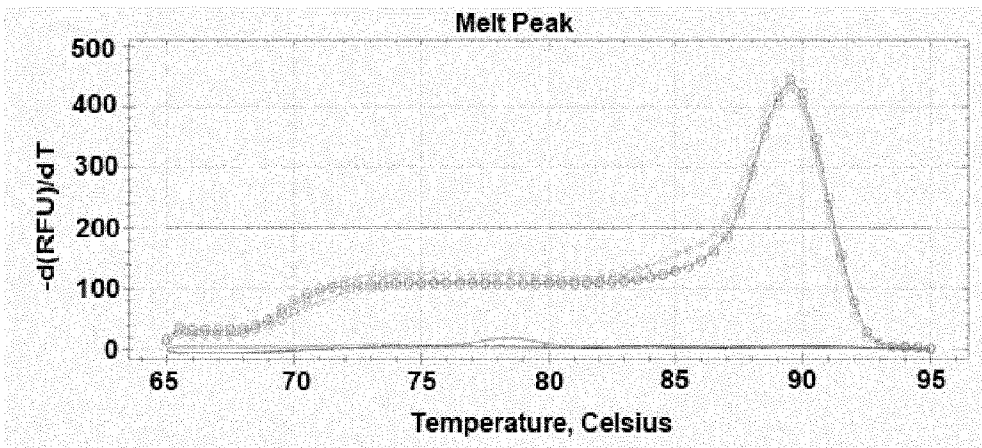
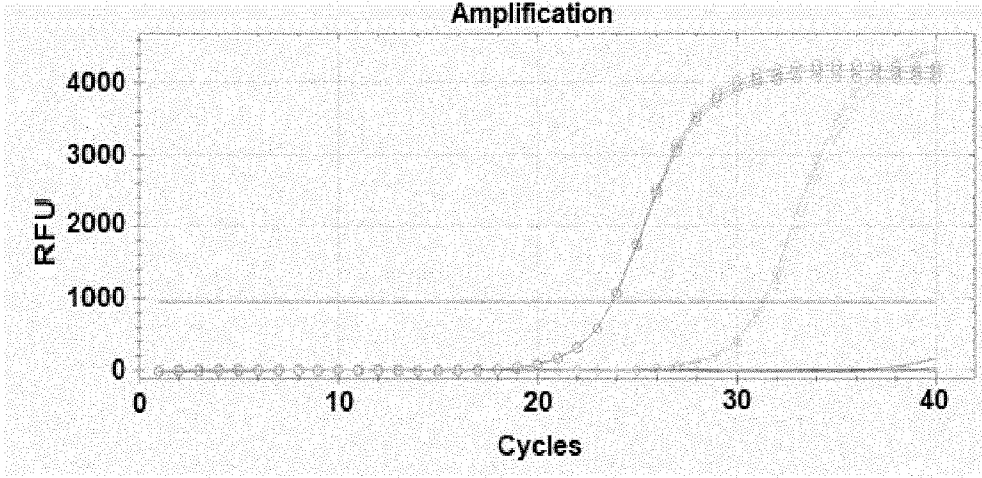
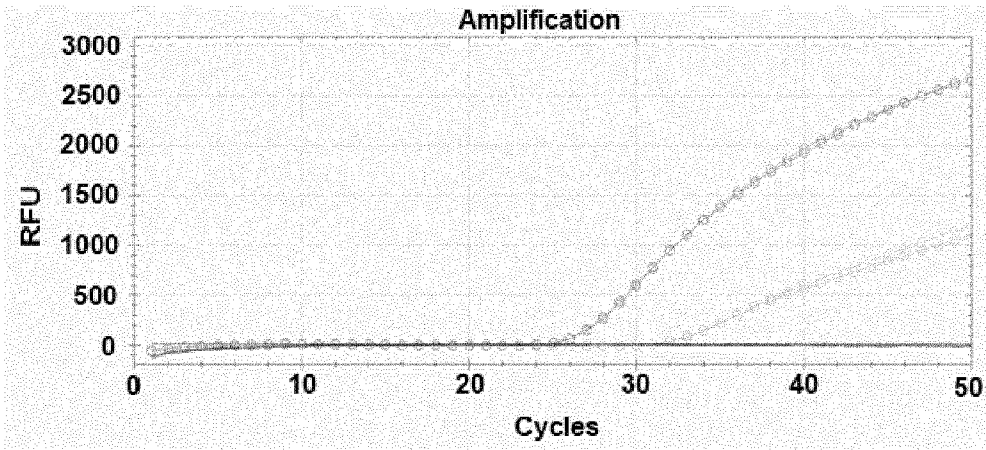
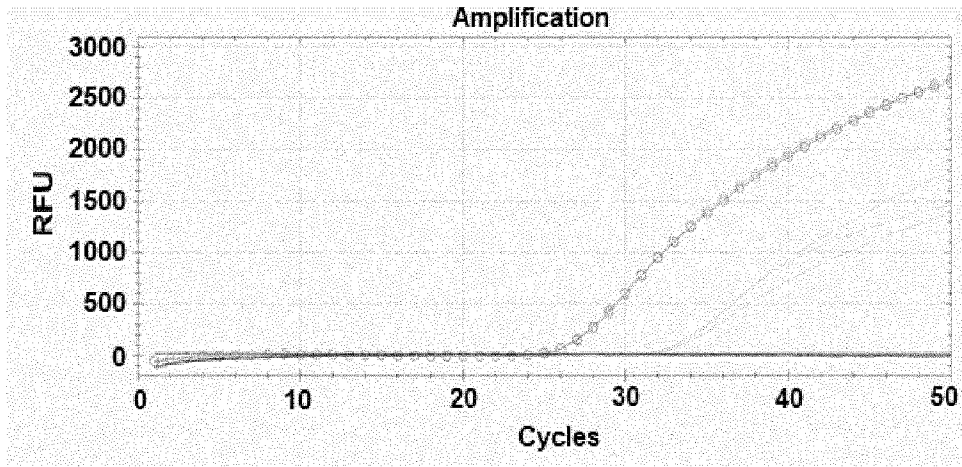
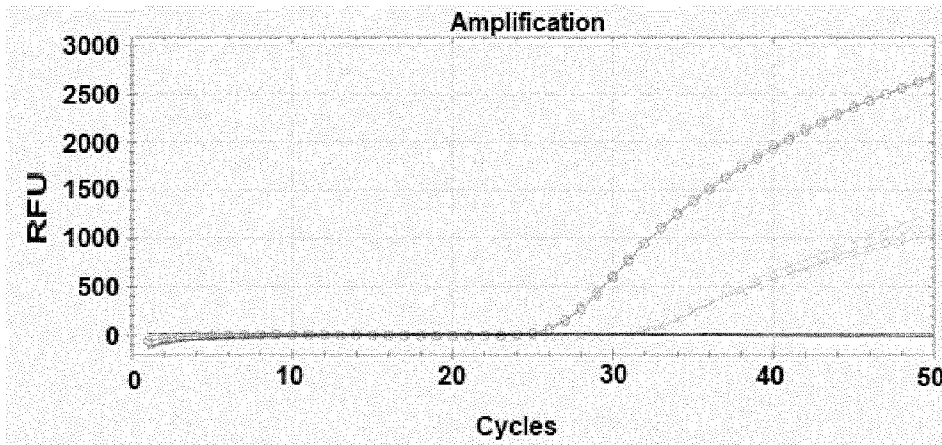
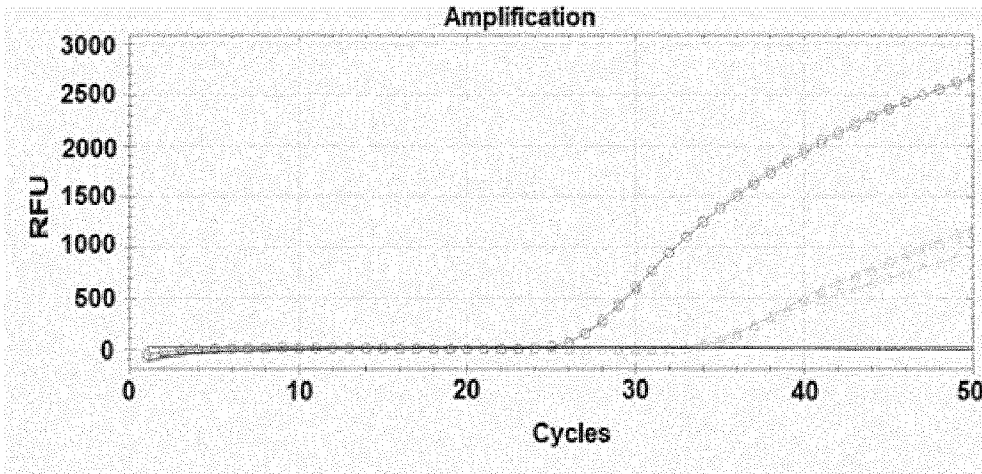


Figure 12



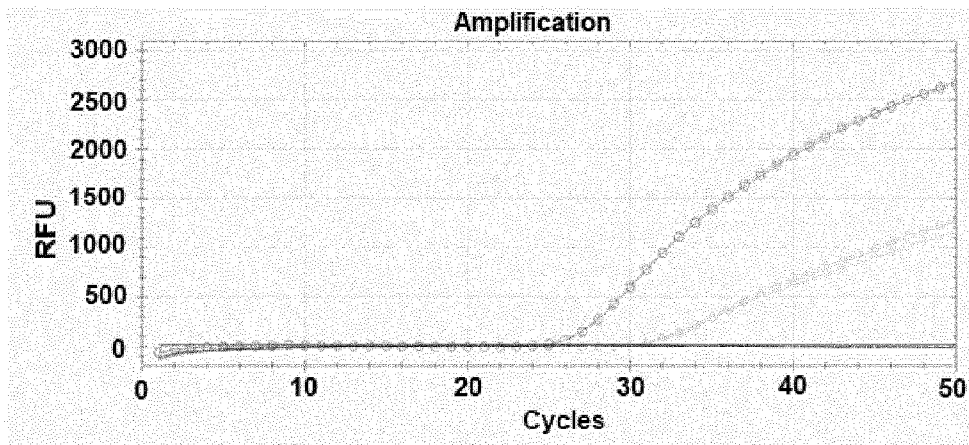
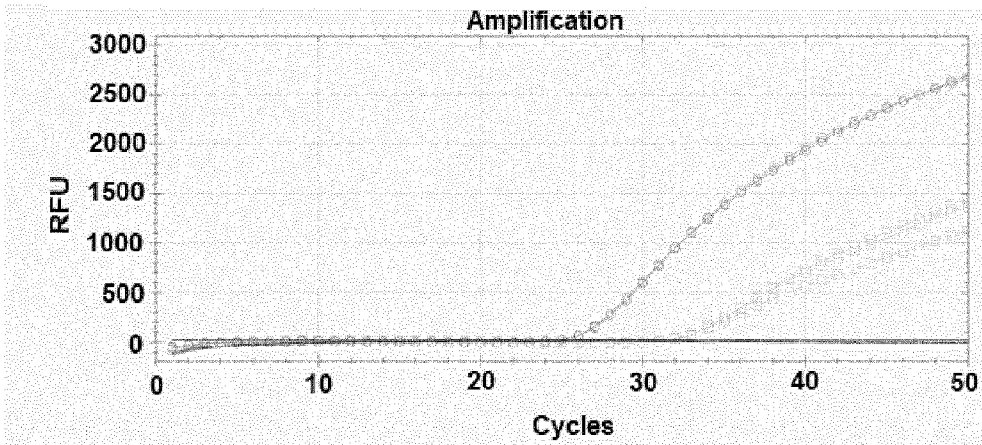
- |             |             |             |       |
|-------------|-------------|-------------|-------|
| — 32549/H76 | ○ 32549/H80 | △ 32549/H83 | ⊖ PTC |
| ✱ 32788/M1  | □ 32786/M2  | ◇ 32788/M2  | — NTC |

Figure 12 (continued)



- |        |           |        |           |        |           |        |     |
|--------|-----------|--------|-----------|--------|-----------|--------|-----|
| -----  | 32549/H76 | ○----- | 32549/H80 | △----- | 32549/H83 | ○----- | PTC |
| ×----- | 32788/M1  | □----- | 32786/M2  | ◇----- | 32788/M2  | —      | NTC |

Figure 12 (continued)



- |                 |             |             |       |
|-----------------|-------------|-------------|-------|
| ----- 32549/H76 | ○ 32549/H80 | △ 32549/H83 | ⊖ PTC |
| * 32788/M1      | □ 32786/M2  | ◇ 32788/M2  | — NTC |

SEKVENSLISTE

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