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(54) Title: METHODS FOR MULTIPLEX DETECTION OF ALLELES ASSOCIATED WITH CORNEAL DYSTROPHY

Figure 1A.

(57) Abstract: The present disclosure provides a method for detecting corneal dystrophy in a subject, comprising a reaction mixture, the reaction mixture comprising one or more labeled probes comprising a mutant TGFBI nucleotide sequence; the reaction mixture further comprises at least one amplification primer pair for amplifying a TGFBI gene sequence from a biological sample from the subject; and detecting one, two, three, four, five or six mutations selected from the group consisting of G623D, M502V, R124S, A546D, H572R, and H626R mutations in TGFBI gene, wherein the detecting comprises detecting the one or more mutations using the labeled detection probes. Further provided is a reaction kit comprising the reaction mixture.

[Continued on next page]

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METHODS FOR MULTIPLEX DETECTION OF ALLELES ASSOCIATED WITH CORNEAL DYSTROPHY

FIELD OF THE APPLICATION

[0001] This application generally relates to probes for detecting or diagnosing corneal dystrophy, and methods of detecting or diagnosing corneal dystrophy.

BACKGROUND

[0002] Real-time PCR can be used to detect differences between nucleic acid sequences having substantially identical sequences. Through the use of differentially labeled fluorescent nucleic acid probes, for example one that binds to a wild type sequence and one that binds to a mutant sequence, single nucleotide changes in the human genome can be quickly and reliably detected. This resolving power has been applied to medical diagnostics, where single nucleotide polymorphisms (SNPs), *i.e.*, single base changes found within the coding and/or non-coding sequence of a protein, are correlated to human disease.

[0003] However, real-time PCR analysis is highly dependent upon the collection and isolation of high quality samples. Poor sample collection and/or isolation require the use of longer assay conditions and greater amounts of real-time PCR reagents, both of which result in increased costs and reduced productivity. Furthermore, failure of a real-time PCR single nucleotide polymorphism detection assay can result in the need to collect additional samples, causing even greater loss in time and resources.

[0004] Accordingly, methods resulting in improved sample collection and isolation, which improve the overall success rate of the assay, reduce the reagents required for the assay, and reduce the need to collect additional samples at later time are highly desirable. Furthermore, methods for performing real-time PCR SNP detection assays with lower amounts of sample material will also reduce the challenges associated with the collection and isolation of high quality samples.

[0005] The cornea is an avascular transparent tissue at the front of the eye that begins the process of focusing light onto the retina and accounts for around two-thirds of the eye's optical power. A number of heritable conditions affect corneal clarity, and they are categorized by the affected corneal layer as posterior, stromal or superficial. Autosomal

dominant (AD), X-linked recessive (XR), and autosomal recessive (AR) inheritance patterns have all been observed, and in many cases, the disease locus has been mapped and the causative gene has been identified. The most studied corneal dystrophies are those caused by autosomal dominant missense mutations in the transforming growth factor beta-induced gene (*TGFBI*) located on chromosome 5q31.1, which encodes an extracellular matrix protein thought to play pivotal roles in physiologic and pathologic responses by mediating cell adhesion, migration, proliferation and differentiation. To date, 62 *TGFBI* mutations are reported in the Human Gene Mutation Database (HGMD) to cause a spectrum of different epithelial-stromal corneal dystrophies with corneal amyloid and non-amyloid deposits, including granular corneal dystrophy type 1 (GCD1) and type 2 (GCD2, previously designated as Avellino Corneal Dystrophy), epithelial basement membrane dystrophy (EBMD), lattice corneal dystrophy (LCD), Reis-Bücklers corneal dystrophy (RBCD) and Thiel-Behnke corneal dystrophy (TBCD). Different *TGFBI* mutations can cause specific corneal dystrophies, and a genotype-phenotype correlation has been demonstrated at two mutation hotspots, R124 and R555.

[0006] Laser in situ keratomileusis (LASIK) is a surgical procedure that provides vision correction for myopia (nearsightedness), hyperopia (farsightedness), and astigmatism. A thin flap in the corneal epithelium is cut and folded, and the exposed stromal layer is reshaped by laser to change its corneal focusing power. Small incision lenticule extraction (SMILE) is a less invasive surgery for the correction of myopia. A tiny incision is made by the laser in the epithelium layer, and a small piece of stroma (lenticule) is removed to reshape the stroma. Photorefractive keratectomy (PRK) and phototherapeutic keratectomy (PTK) surgery affect vision correction or treat various ocular disorders by removing superficial opacities and surface irregularities from the cornea. These invasive corneal surgeries induce a wound in the stromal layer, which causes the expression of *TGFBI* to be upregulated, resulting in corneal amyloid deposition within the corneas of individuals who carry the *TGFBI* mutations leading to pathology associated with corneal dystrophy. LASIK is contraindicated in individuals with granular corneal dystrophy (GCD). A commercially available genetic test, can detect within the *TGFBI* gene the five most common mutations which are linked to the five more common types of corneal dystrophy: R124H for granular corneal dystrophy type 2, R124C for lattice corneal dystrophy type 1, R124L for Reis-Buckler corneal dystrophy, R555W for granular corneal dystrophy type 1, and R555Q for Thiel-Behnke corneal dystrophy. This five mutation genetic test was originally designed for the Korean and Japanese population, where

a majority of the *TGFBI* corneal dystrophy cases are diagnosed as GCD2 caused by the R124H mutation. Within Korea and Japan, the test is used primarily as a screening tool prior to refractive surgery. However, in the US and Europe, the test is used both to screen refractive surgery candidates and as a confirmatory test for clinical diagnosis of corneal dystrophy disease.

[0007] Given the above background, what is needed in the art is to review the prevalence of different *TGFBI* mutations in various populations and geographic locations to improve the genetic test for use in different populations worldwide.

SUMMARY

[0008] In one aspect, the present disclosure provides a reaction mixture for detecting corneal dystrophy in a subject, the reaction mixture comprising a labeled probe comprising a mutant nucleotide sequence selected from the group consisting of SEQ ID NO: 25-30, 36 and 54. The reaction mixture may further comprise a corresponding labeled probe comprising a normal nucleotide sequence selected from the group consisting of SEQ ID NO: 19-24, 33 and 50. In some embodiments, the labeled probe consists of the mutant nucleotide sequence selected from the group consisting of SEQ ID NO: 25-30, 36 and 54; and/or the corresponding labeled probe consists of the normal nucleotide sequence selected from the group consisting of SEQ ID NO: 19-24, 33 and 50. In additional embodiments, the reaction mixture comprises a labeled TGFBI G623D probe comprising the nucleotide sequence of SEQ ID NO: 33 or 36; and a labeled TGFBI M502V probe comprising the nucleotide sequence of SEQ ID NO: 24 or 30. In yet further embodiments, the labeled TGFBI G623D probe comprising the nucleotide sequence of SEQ ID NO: 36; and labeled TGFBI M502V probe comprising the nucleotide sequence of SEQ ID NO: 30.

[0009] In some embodiments, the labeled probes are fluorescently labeled. In additional embodiments, each of the labeled probes comprises a different probe. In further embodiments, each of the labeled probes is independently labeled with VIC, FAM, ABY, or JUN.

[0010] In some embodiments, the reaction mixture further comprises at least one amplification primer pair for amplifying a TGFBI gene sequence from a biological sample from the subject. In additional embodiments, the reaction mixture comprises (a) a corresponding forward primer comprising a nucleotide sequence selected from the group

consisting of SEQ ID NO: 7-12 and 41; and (b) a corresponding reverse primer comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 13-18 and 47. When the reaction mixture comprises a labeled TGFBI G623D probe comprising the nucleotide sequence of SEQ ID NO: 33 or 36; and a labeled TGFBI M502V probe comprising the nucleotide sequence of SEQ ID NO: 24 or 30, the reaction mixture may further comprise (a) corresponding forward primers comprising SEQ ID NO: 10 and 12; and (b) corresponding reverse primers comprising SEQ ID NO: 16 and 18.

[0011] In one aspect, the present disclosure provides a reaction kit comprising the reaction mixture described herein. In one aspect, the reaction kit comprises a reaction mixture comprising detection probes for G623D and M502V mutations in TGBI gene. In some embodiments, the reaction kit further comprises one or more detection probes for R124S, A546D, H572R, and H626R mutations in TGBI gene. In one aspect, the present disclosure provides a reaction kit comprising the reaction mixture described herein, and one or more labeled probes for one or more TGFBI mutations selected from the group consisting of R124S, A546D, H572R, and H626R. In some embodiments, the one or more labeled probes are separate from the reaction mixture. In additional embodiments, the one or more labeled probes are selected from the group consisting of labeled probes comprising or consisting of nucleotide sequences of SEQ ID NO: 19, 25, 20, 26, 21, 27, 23, 29, 50 and 54. In yet additional embodiments, the reaction kit comprises a labeled TGFBI R124S probe comprising the nucleotide sequence of SEQ ID NO: 19 or 25. In yet additional embodiments, the reaction kit comprises a labeled TGFBI A546D probe comprising the nucleotide sequence of SEQ ID NO: 20 or 26. In yet additional embodiments, the reaction kit comprises a labeled TGFBI H572R probe comprising the nucleotide sequence of SEQ ID NO: 21 or 27. In yet additional embodiments, the reaction kit comprises a labeled TGFBI H626R probe comprising the nucleotide sequence of SEQ ID NO: 23, 29, 50 or 54. In further embodiments, the reaction kit further comprises an additional amplification primer set. In yet further embodiments, the reaction kit further comprises a third amplification primer set to amplify a TGFBI gene comprising R124S mutation, a fourth amplification primer set to amplify a TGFBI gene comprising A546D mutation, a fifth amplification primer set to amplify a TGFBI gene comprising H572R mutation, and/or a sixth amplification primer set to amplify a TGFBI gene comprising H626R mutation.

[0012] In one aspect, the present disclosure provides a method for detecting corneal dystrophy comprising detecting one, two, three, four, five or six mutations selected from the

group consisting of G623D, M502V, R124S, A546D, H572R, and H626R mutations in TGFBI gene. In some embodiments, the detecting comprises sequencing the TGFBI gene. In additional embodiments, the detecting comprises detecting the mutation using a labeled detection probe.

[0013] In one aspect, the present disclosure provides a method for detecting corneal dystrophy comprising: (A-1) amplifying a first TGFBI gene sequence from a biological sample from a subject using a reaction mixture comprising at least a first amplification primer pair and a set of at least two detection probes; (B-1) hybridizing first and second detection probes of the set of at least two detection probes to a first TGFBI gene sequence having G623D mutation and a second TGFBI gene sequence having M502V mutation, respectively; and (C-1) detecting one, two or more mutations in the TGFBI gene sequence based on the hybridization of the first and second detection probes to the first and second TGFBI gene sequences, respectively. In some embodiments, the method further comprises (A-2) amplifying a third TGFBI gene sequence from the biological sample, wherein the reaction mixture further comprises a third labeled probe for a third TGFBI mutation selected from the group consisting of R124S, A546D, H572R, and H626R; (B-2) hybridizing the third labeled probe to the third TGFBI gene sequence; and (C-2) detecting a mutation in the third TGFBI gene sequence based on the hybridization of the third detection probe to the third TGFBI gene sequence.

BRIEF DESCRIPTION OF THE DRAWINGS

[0014] **Figure 1A** illustrates world map of reported cases with various TGFBI mutations. Each bubble placed over a region or country contains the reported case information, such as ethnicities, mutations and case numbers. The map illustrates that TGFBI mutations cases are reported all over the world, except for in regions with limited research capacity or language difficulties for publication. Very few cases were reported from South America, and no case reports were identified from Africa or Russia. **Figure 1B** illustrates a red arrow pointing at England as an example of the information contained in the bubble. The legend on the left shows the reported mutations, ethnicity and total case numbers for each reported mutation.

[0015] **Figure 2** provides comparison by geographic region. The original genetic test with five mutations, the six additional mutations and the proposed expanded 11 mutation panel

were modeled in over 1,600 reported cases. The detection rate of the available genetic test with five mutations was very close between Europe and Asia.

[0016] **Figure 3** provides a table ranking the five most common mutations within reported cases from highest to lowest. In addition, it lists the case numbers from high to low for the six additional mutations.

[0017] **Figure 4** provides a table indicating the theoretical results for the available genetic test for R124C, R555W, R124H, R555Q, and R124L. This test would detect 90% of the 68 *TGFBI* CD cohort identified by the Moorfield's Corneal Dystrophy Study. The table also shows the results using the six additional mutations identified through literature research. They increase the detection rate by 7%, which brings the overall detection rate in the UK to 97%.

[0018] **Figures 5A-5C** provide exemplary sequences for targets, primers and probes used in examples.

[0019] **Figure 6A and 6B** show discrimination plot results from Example 4 using M502V and G623D TGFBI probes.

DETAILED DESCRIPTION

I. Introduction

[0020] The present disclosure is based at least in part on the discovery of a reaction mixture, reaction kit to improve the detection of corneal dystrophy.

[0021] The reported prevalence of *TGFBI* corneal dystrophies in Asia is 1 in 870 in Korea and 1 in 416 in China. Asia has a high myopia rate, and a study conducted by Holden et al. predicted that by 2050, the Asian-Pacific population will have the highest myopia prevalence rate among all populations at 66.4% compared to the global prevalence of 49.8%. With the high prevalence of myopia in these Asian populations, the use of LASIK vision correction surgery is consistently increasing and is predicted to continue to rise. With the known prevalence of *TGFBI* mutations in the Asian population and the high myopia rate, mutation testing is important in this region; subsequently, the five-mutation genetic test was initially introduced in Asian-Pacific populations.

[0022] Since the first description by Folberg et al., in 1988 of *TGFBI* mutations as the cause of granular corneal dystrophy, our awareness and understanding of this disease has increased steadily. The most common R124 and R555 mutations are well documented, and additional mutations are being examined more closely to understand the next tier of common variants. The disclosure provides the review of reports in the literature on various *TGFBI* corneal dystrophies to understand the prevalence of this disease. The worldwide prevalence of this disease is unknown; however, the disease outcome is debilitating. The ultimate treatment is corneal transplant, and the recurrent nature of the disease often requires subsequent corneal transplants, which is traumatic and costly to both the patients and the ophthalmologist. Therefore, prevention and prescreening with molecular diagnostic testing to detect mutations is key.

[0023] In some embodiments, one object is to provide enhanced testing capability in the prescreening test prior to refractive surgery. Another objective is to close the gap between the detection rate resulting from genetic testing and clinical diagnosis.

II. Select Definitions

[0024] The term "invention" or "present invention" as used herein is not meant to be limiting to any one specific embodiment of the invention but applies generally to any and all embodiments of the invention as described in the claims and specification.

[0025] As used herein, the singular forms "a", "an", and "the" include plural references unless the context clearly dictates otherwise. Thus, for example, references to "the method" includes one or more methods, and/or steps of the type described herein which will become apparent to those persons skilled in the art upon reading this disclosure.

[0026] As used herein, the term "polymorphism" and variants thereof refers to the occurrence of two or more alternative genomic sequences or alleles between or among different genomes or individuals. The terms "genetic mutation" or "genetic variation" and variants thereof include polymorphisms.

[0027] As used herein the term "single nucleotide polymorphism" ("SNP") and variants thereof refers to a site of one nucleotide that varies between alleles. A single nucleotide polymorphism (SNP) is a single base change or point mutation but also includes the so-called "indel" mutations (insertions or deletions of a nucleotide), resulting in genetic variation between individuals. SNPs, which make up about 90% of all human genetic variation, occur

every 100 to 300 bases along the 3-billion-base human genome. SNPs can occur in coding or non-coding regions of the genome. A SNP in the coding region may or may not change the amino acid sequence of a protein product. A SNP in a non-coding region can alter promoters or processing sites and may affect gene transcription and/or processing. Knowledge of whether an individual has particular SNPs in a genomic region of interest may provide sufficient information to develop diagnostic, preventive and therapeutic applications for a variety of diseases. In some embodiments, the present disclosure relates to the detection of SNPs in coding regions that alter the amino acid sequences resulting in mutations in amino acid sequences of a product from TGBI gene. For example, the present disclosure relates to the detection of SNPs causing G623D, M502V, R124S, A546D, H572R, H626R, G623D, R124S, H403Q, R124C and/or R124H mutations in TGFBI gene.

[0028] The term "primer" and variants thereof refers to an oligonucleotide that acts as a point of initiation of DNA synthesis in a PCR reaction. A primer is usually about 15 to about 35 nucleotides in length and hybridizes to a region complementary to the target sequence.

[0029] The term "probe" and variants thereof (*e.g.*, detection probe) refers to an oligonucleotide that hybridizes to a target nucleic acid in a PCR reaction. Target sequence refers to a region of nucleic acid that is to be analyzed and comprises the polymorphic site of interest.

[0030] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by those of ordinary skill in the art to which the invention pertains. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, various embodiments of methods and materials are specifically described herein.

III. Reaction Mixture

[0031] In one aspect, the present disclosure provides a reaction mixture for detecting corneal dystrophy in a subject, the reaction mixture comprising a detection probe to detect a mutation in TGBI. In some embodiments, the detection probes detect SNPs causing the amino acid mutations described herein. In one aspect, the present disclosure provides a reaction mixture for detecting corneal dystrophy in a subject, the reaction mixture comprising a mutant nucleotide sequence selected from the group consisting of SEQ ID NO: 25-30, 36 and 54. The reaction mixture may further comprise a corresponding labeled probe comprising a normal nucleotide sequence selected from the group consisting of SEQ ID NO: 19-24, 33 and

50. In some embodiments, the labeled probe consists of the mutant nucleotide sequence selected from the group consisting of SEQ ID NO: 25-30, 36 and 54; and/or the corresponding labeled probe consists of the normal nucleotide sequence selected from the group consisting of SEQ ID NO: 19-24, 33 and 50. In additional embodiments, the reaction mixture comprises a labeled TGFBI G623D probe comprising the nucleotide sequence of SEQ ID NO: 33 or 36; and a labeled TGFBI M502V probe comprising the nucleotide sequence of SEQ ID NO: 24 or 30. In yet further embodiments, the labeled TGFBI G623D probe comprising the nucleotide sequence of SEQ ID NO: 36; and labeled TGFBI M502V probe comprising the nucleotide sequence of SEQ ID NO: 30.

[0032] In some embodiments, the reaction mixture further comprises at least one amplification primer pair for amplifying a TGFBI gene sequence from a biological sample from the subject. In additional embodiments, the reaction mixture comprises (a) a corresponding forward primer comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 7-12 and 41; and (b) a corresponding reverse primer comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 13-18 and 47. When the reaction mixture comprises a labeled TGFBI G623D probe comprising the nucleotide sequence of SEQ ID NO: 33 or 36; and a labeled TGFBI M502V probe comprising the nucleotide sequence of SEQ ID NO: 24 or 30, the reaction mixture may further comprise (a) corresponding forward primers comprising SEQ ID NO: 10 and 12; and (b) corresponding reverse primers comprising SEQ ID NO: 16 and 18.

[0033] In some embodiments, the labeled probes are fluorescently labeled. In additional embodiments, each of the labeled probes comprises a different probe. In further embodiments, each of the labeled probes is independently labeled with VIC, FAM, ABY, or JUN.

IV. Diagnostic Kits

[0034] In one aspect, any or all of the reagents described herein are packaged into a diagnostic kit. Such kits include any and/or all of the primers, probes, buffers and/or other reagents described herein in any combination.

[0035] In one aspect, the present disclosure provides a reaction kit comprising primer sets, detection probes and/or reagents to detect R124S, A546D, H572R, H626R, G623D and M502V mutations in TGBI gene. In one aspect, the present disclosure provides a reaction kit comprising primer sets, detection probes and/or reagents to detect G623D and M502V

mutations in TGBI gene with a single reaction mixture comprising the combination of primer sets, probes and/or reagents to detect G623D and M502V. In some embodiments, the reaction kit further comprises one, two, three or four primer sets, detection probes and/or reagents to detect one, two, three or four TGFBI mutations selected from the group consisting of R124S, A546D, H572R, and H626R. In additional embodiments, the reaction kit further comprises one, two, three, four or five primer sets, detection probes and/or reagents to detect one, two, three, four or five TGFBI mutations selected from the group consisting of G623D, R124S, H403Q, R124C and R124H.

[0036] In one aspect, the present disclosure provides a reaction kit comprising the reaction mixture described above and one or more additional reagents. In some embodiments, the reaction kit further comprises one, two, three or four primer sets, labeled probes and/or reagents to detect one, two, three or four TGFBI mutations selected from the group consisting of R124S, A546D, H572R, and H626R. In some embodiments, the one, two, three or four primer sets, labeled probes and/or reagents to detect one, two, three or four TGFBI mutations selected from the group consisting of R124S, A546D, H572R, and H626R are separate from the reaction mixture in the kit. In additional embodiments, the reaction kit comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16 or 17 labeled probes selected from the group consisting of labeled probes comprising nucleotide sequences of SEQ ID NO: 19-24, 33, 50, 25-30, 36 and 54. In yet additional embodiments, the reaction kit comprises a labeled TGFBI R124S normal probe comprising the nucleotide sequence of SEQ ID NO: 19 and/or a labeled TGFBI R124S mutant probe comprising the nucleotide sequence of SEQ ID NO: 25. In yet additional embodiments, the reaction kit comprises a labeled TGFBI A546D normal probe comprising the nucleotide sequence of SEQ ID NO: 20 and/or a labeled TGFBI A546D mutant probe comprising the nucleotide sequence of SEQ ID NO: 26. In yet additional embodiments, the reaction kit comprises a labeled TGFBI H572R normal probe comprising the nucleotide sequence of SEQ ID NO: 21, and/or a labeled TGFBI H572R mutant probe comprising the nucleotide sequence of SEQ ID NO: 27. In yet additional embodiments, the reaction kit comprises a labeled TGFBI H626R normal probe comprising the nucleotide sequence of SEQ ID NO: 23 or 50, and/or a labeled TGFBI H626R mutant probe comprising the nucleotide sequence of SEQ ID NO: 29 or 54. In yet additional embodiments, the reaction kit excludes a kit wherein a TGFBI G623D probe is kept separately or not mixed with a TGBI M502V probe. In further embodiments, the reaction kit further comprises an additional amplification primer set. In yet further embodiments, the reaction kit further

comprises a third amplification primer set to amplify a TGFBI gene comprising the R124S mutation, a fourth amplification primer set to amplify a TGFBI gene comprising A546D mutation, a fifth amplification primer set to amplify a TGFBI gene comprising H572R mutation, and/or a sixth amplification primer set to amplify a TGFBI gene comprising H626R mutation. Herein, a TGFBI gene comprising the R124S mutation may refer to a TGFBI gene comprising a SNP causing the R124S mutation in TGBI protein product.

[0037] In additional embodiments, the reaction kit further comprises one, two, three, four or five primer sets, detection probes and/or reagents to detect one, two, three, four or five TGFBI mutations selected from the group consisting of G623D, R124S, H403Q, R124C and R124H.

[0038] In some embodiments, the reagents in the kit are included as lyophilized powders. In some embodiments, the reagents in the kit are included as lyophilized powders with instructions for reconstitution. In some embodiments, the reagents in the kit are included as liquids. In some embodiments, the reagents are included in plastic and/or glass vials or other appropriate containers. In some embodiments the primers and probes are all contained in individual containers in the kit. In some embodiments, the primers are packaged together in one container, and the probes are packaged together in another container. In some embodiments, the primers and probes are packaged together in a single container.

[0039] In some embodiments, the kit further includes control gDNA and/or DNA samples. In some embodiments the control DNA sample included is TGFBI sample having G623 normal sequence and/or TGFBI sample having M502 normal sequences. In some embodiments the control DNA sample included corresponds to the mutation being detected, including R124S, A546D, H572R, and H626R. In some embodiments, a control DNA sample corresponding to TGFBI R124 normal and a mutant DNA sample corresponding to R124C, R124H, R124L, R555W, R555Q and/or H626P are included. In some embodiments, a control DNA sample corresponding to TGFBI R124 normal and a mutant DNA sample corresponding to R124C, R124H, R124L, R555W and/or R555Q are included. In some embodiments, a control DNA sample corresponding to TGFBI R124 normal and a mutant DNA sample corresponding to R124C, R124H and/or R124L are included. In some embodiments, a control DNA sample corresponding to TGFBI R124 normal and a mutant DNA sample corresponding to R555W and/or R555Q are included. In some embodiments, a control DNA sample corresponding to TGFBI R124 normal and a mutant DNA sample

corresponding to R124C are included. In some embodiments, a control DNA sample corresponding to TGFBI R124 normal DNA and a mutant DNA sample corresponding to R124H are included. In some embodiments, a control DNA sample corresponding to TGFBI R124 normal and a mutant DNA sample corresponding to R124L are included. In some embodiments, a control DNA sample corresponding to TGFBI R124 normal DNA and a mutant DNA sample corresponding to R555W are included. In some embodiments, a control DNA sample corresponding to TGFBI R124 normal and mutant DNA sample corresponding to R555Q are included. In some embodiments, a control DNA sample corresponding to TGFBI R124 normal and mutant DNA sample corresponding to H626P are included.

[0040] In some embodiments, the concentration of the control DNA sample is 5 ng/μL, 10 ng/μL, 20 ng/μL, 30 ng/μL, 40 ng/μL, 50 ng/μL, 60 ng/μL, 70 ng/μL, 80 ng/μL, 90 ng/μL, 100 ng/μL, 110 ng/μL, 120 ng/μL, 130 ng/μL, 140 ng/μL, 150 ng/μL, 160 ng/μL, 170 ng/μL, 180 ng/μL, 190 ng/μL or 200 ng/μL. In some embodiments, the concentration of the control DNA sample is 50 ng/μL, 100 ng/μL, 150 ng/μL or 200 ng/μL. In some embodiments, the concentration of the control DNA sample is 100 ng/μL. In some embodiments, the control DNA samples have the same concentration. In some embodiments, the control DNA samples have different concentrations.

[0041] In some embodiments, the kit can further include buffers, for example, GTXpress TAQMAN® reagent mixture, or any equivalent buffer. In some embodiments, the buffer incldues any buffer described herein.

[0042] In some embodiments, the kit can further include reagents for use in cloning, such as vectors (including, *e.g.*, M13 vector).

[0043] In some embodiments, the kit further includes reagents for use in purification of DNA.

[0044] In some embodiments, the kit further includes instructions for using the kit for the detection of corneal dystrophy in a subject. In some embodiments, these instructions include various aspects of the protocols described herein.

V. Nucleic Acid Analyses

[0045] In one aspect, the present disclosure provides a method for detecting corneal dystrophy comprising detecting one, two, three, four, five or six TGFBI mutations selected from the group consisting of G623D, M502V, R124S, A546D, H572R, and H626R mutations

in TGFBI gene. In some embodiments, the method may further comprise detecting one, two, three, four, or five TGFBI mutations selected from the group consisting of G623D, R124S, H403Q, R124C and R124H.

[0046] In some embodiments, the detecting comprises sequencing the TGFBI gene. In additional embodiments, the detecting comprises detecting the mutation using a labeled detection probe.

[0047] In one aspect, the present disclosure provides a method for detecting corneal dystrophy comprising: (A-1) amplifying a first TGFBI gene sequence from a biological sample from a subject using a reaction mixture comprising at least a first amplification primer pair and a set of at least two detection probes; (B-1) hybridizing first and second detection probes of the set of at least two detection probes to a first TGFBI gene sequence having G623D mutation and a second TGFBI gene sequence having M502V mutation, respectively; and (C-1) detecting one, two or more mutations in the TGFBI gene sequence based on the hybridization of the first and second detection probes to the first and second TGFBI gene sequences, respectively. In some embodiments, the method further comprises (A-2) amplifying a third TGFBI gene sequence from the biological sample, wherein the reaction mixture further comprises a third labeled probe for a third TGFBI mutation selected from the group consisting of R124S, A546D, H572R, and H626R; (B-2) hybridizing the third labeled probe to the third TGFBI gene sequence; and (C-2) detecting a mutation in the third TGFBI gene sequence based on the hybridization of the third detection probe to the third TGFBI gene sequence.

[0048] In some embodiments, the methods herein further comprises isolating a genomic samples. In some embodiments, the method includes providing a sample of cells from a subject. In additional embodiments, the subject may be human. In some embodiments, the cells are collected by contacting a cellular surface of a patient with a substrate capable of reversibly immobilizing the cells onto a substrate.

[0049] The disclosed methods are applicable to a variety of cell types obtained from a variety of samples. In some embodiments, the cell type for use with the disclosed methods include but is not limited to epithelial cells, endothelial cells, connective tissue cells, skeletal muscle cells, endocrine cells, cardiac cells, urinary cells, melanocytes, keratinocytes, blood cells, white blood cells, buffy coat, hair cells (including, *e.g.*, hair root cells) and/or salival cells. In some embodiments, the cells are epithelial cells. In some embodiments, the cells are

subcapsular-perivascular (epithelial type 1); pale (epithelial type 2); intermediate (epithelial type 3); dark (epithelial type 4); undifferentiated (epithelial type 5); and large-medullary (epithelial type 6). In some embodiments, the cells are buccal epithelial cells (e.g., epithelial cells collected using a buccal swap). In some embodiments, the sample of cells used in the disclosed methods include any combination of the above identified cell types. In some embodiments, the cells provided are buccal epithelial cells.

[0050] In some embodiments, the sample is advantageously collected in a non-invasive manner and as such sample collection is accomplished anywhere and by almost anyone. For example, in some embodiments the sample is collected at a physician's office, at a subject's home, or at a facility where LASIK surgery is performed or to be performed. In some embodiments the patient, the patient's doctor, nurses or a physician's assistant or other clinical personnel collects the sample.

[0051] A variety of methods for analyzing the SNPs in a sample including, for example but not limited to genomic DNA (gDNA) sample, are known in the art and may include PCR methods, such as real-time PCR analysis, microarray analysis, hybridization analysis and nucleic acid sequence analysis, as well as a variety of other methods where nucleic acid compositions are analyzed and which are known to those of skill in the art. *See, for example,* Molecular Cloning (three volume set, Cold Spring Harbor Laboratory Press, 2012) and Current Protocols (Genetics and Genomics; Molecular Biology; 2003-2013).

a. Real-Time PCR

[0052] For the design of Real-Time PCR assays, several parts are coordinated, including the DNA fragment that is flanked by the two primers and subsequently amplified, often referred to as the amplicon, the two primers and the detection probe or probes to be used.

[0053] Real-time PCR relies on the visual emission of fluorescent dyes conjugated to short polynucleotides (termed "detection probes") that associate with genomic alleles in a sequence-specific fashion. Real-time PCR probes differing by a single nucleotide can be differentiated in a real-time PCR assay by the conjugation and detection of probes that fluoresce at different wavelengths. Real-Time PCR finds use in detection applications (diagnostic applications), quantification applications and genotyping applications.

[0054] Several related methods for performing real-time PCR are disclosed in the art, including assays that rely on TAQMAN® probes (U.S. Pat. Nos. 5,210,015 and 5,487,972,

and Lee et al., *Nucleic Acids Res.* 21:3761-6, 1993), molecular beacon probes (U.S. Pat. Nos. 5,925,517 and 6,103,476, and Tyagi and Kramer, *Nat. Biotechnol.* 14:303-8, 1996), self-probing amplicons (scorpions) (U.S. Pat. No. 6,326,145, and Whitcombe et al., *Nat. Biotechnol.* 17:804-7, 1999), Amplisensor (Chen *et al.*, *Appl. Environ. Microbiol.* 64:4210-6, 1998), Amplifluor (U.S. Pat. No. 6,117,635, and Nazarenko et al., *Nucleic Acids Res.* 25:2516-21, 1997, displacement hybridization probes (Li et al., *Nucleic Acids Res.* 30:E5, 2002), DzyNA-PCR (Todd et al., *Clin. Chem.* 46:625-30, 2000), fluorescent restriction enzyme detection (Cairns et al., *Biochem. Biophys. Res. Commun.* 318:684-90, 2004) and adjacent hybridization probes (U.S. Pat. No. 6,174,670 and Wittwer et al., *Biotechniques* 22:130-1, 134-8, 1997).

[0055] In one aspect, the present disclosure relates to the detection of SNPs causing G623D, M502V, R124S, A546D, H572R, H626R, G623D, R124S, H403Q, R124C and/or R124H mutations in TGFBI gene. In some instances, real-time PCR can result in detection of a variety of gene mutations, including for example but not limited to SNPs. In some embodiments, detection of SNPs in specific gene candidates is performed using real-time PCR, based on the use of intramolecular quenching of a fluorescent molecule by use of a tethered quenching moiety. Thus, according to exemplary embodiments, real-time PCR methods also include the use of molecular beacon technology. The molecular beacon technology utilizes hairpin-shaped molecules with an internally-quenched fluorophore whose fluorescence is restored by binding to a DNA target of interest (See, *e.g.*, Kramer, R. et al. *Nat. Biotechnol.* 14:303-308, 1996). In some embodiments, increased binding of the molecular beacon probe to the accumulating PCR product is used to specifically detect SNPs present in genomic DNA.

[0056] One of the many suitable genotyping procedures is the TAQMAN® allelic discrimination assay. In some instances of this assay, an oligonucleotide probe labeled with a fluorescent reporter dye at the 5' end of the probe and a quencher dye at the 3' end of the probe is utilized. The proximity of the quencher to the intact probe maintains a low fluorescence for the reporter. During the PCR reaction, the 5' nuclease activity of DNA polymerase cleaves the probe, and separates the dye and quencher. This results in an increase in fluorescence of the reporter. Accumulation of PCR product is detected directly by monitoring the increase in fluorescence of the reporter dye. The 5' nuclease activity of DNA polymerase cleaves the probe between the reporter and the quencher only if the probe hybridizes to the target and is amplified during PCR. The probe is designed to straddle a

target SNP position and hybridize to the nucleic acid molecule only if a particular SNP allele is present.

[0057] By way of example, to amplify the Avellino corneal dystrophy associated SNP located in exon 4 of the TGFBI gene, forward and reverse PCR primer pairs were constructed as described in U.S. Patent Publication No. 2012/0077200, the disclosure of which is incorporated by reference herein.

b. Real-Time PCR Cycles

[0058] Real-time PCR methods include a variety of steps or cycles as part of the methods for amplification. These cycles include denaturing double-stranded nucleic acids, annealing a forward primer, a reverse primer and a detection probe to the target genomic DNA sequence and synthesizing (*i.e.*, replicating) second-strand DNA from the annealed forward primer and the reverse primer. This three step process is referred to herein as a cycle.

[0059] In some embodiments, about 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, or 60 cycles are employed. In some embodiments, about 10 to about 60 cycles, about 20 to about 50 or about 30 to about 40 cycles are employed. In some embodiments, 40 cycles are employed.

[0060] In some embodiments, the denaturing double-stranded nucleic acids step occurs at a temperature of about 80°C to 100°C, about 85°C to about 99°C, about 90°C to about 95°C for about 1 second to about 5 seconds, about 2 seconds to about 5 seconds, or about 3 seconds to about 4 seconds. In some embodiments, the denaturing double-stranded nucleic acids step occurs at a temperature of 95°C for about 3 seconds.

[0061] In some embodiments, the annealing a forward primer, a reverse primer and a detection probe to the target genomic DNA sequence step occurs at about 40°C to about 80°C, about 50°C to about 70°C, about 55°C to about 65°C for about 15 seconds to about 45 seconds, about 20 seconds to about 40 seconds, about 25 seconds to about 35 seconds. In some embodiments, the annealing a forward primer, a reverse primer and a detection probe to the target genomic DNA sequence step occurs at about 60°C for about 30 seconds.

[0062] In some embodiments, the synthesizing (*i.e.*, replicating) second-strand DNA from the annealed forward primer and the reverse primer occurs at about 40°C to about 80°C, about 50°C to about 70°C, about 55°C to about 65°C for about 15 seconds to about 45 seconds, about 20 seconds to about 40 seconds, about 25 seconds to about 35 seconds. In some

embodiments, the annealing a forward primer, a reverse primer and a detection probe to the target genomic DNA sequence step occurs at about 60°C for about 30 seconds.

[0063] In some embodiments, it was found that about 1 µL, about 2 µL, about 3 µL, about 4 µL or about 5 µL of a genomic DNA sample prepared according to the present methods described herein, are combined with only about 0.05 µL, about 0.10 µL about 0.15 µL, about 0.20 µL, about 0.25 µL or about 0.25 µL of a 30X, 35X, 40X, 45X, 50X or 100X real-time PCR assay mix and distilled water to form the PCR master mix. In some embodiments, the PCR master mix has a final volume of about 1.5 µL, about 2.5 µL, about 5 µL, about 6 µL, about 7 µL, about 8 µL, about 9 µL, about 0 µL, about 11 µL, about 12 µL, about 13 µL, about 14 µL, about 15 µL, about 16 µL, about 17 µL, about 18 µL, about 19 µL or about 20 µL or more. In some embodiments, it was found that 2 µL of a genomic DNA sample prepared as described above, are combined with only about 0.15 µL of a 40X real-time PCR assay mix and 2.85 µL of distilled water in order to form the PCR master mix.

[0064] While exemplary reactions are described herein, one of skill would understand how to modify the temperatures and times based on the probe design. Moreover, the present methods contemplate any combination of the above times and temperatures.

c. PCR Primers and Primer Design

[0065] In some embodiments, primers are tested and designed in a laboratory setting. In some embodiments, primers are designed by computer based *in silico* methods. Primer sequences are based on the sequence of the amplicon or target nucleic acid sequence that is to be amplified. Shorter amplicons typically replicate more efficiently and lead to more efficient amplification as compared to longer amplicons.

[0066] In designing primers, one of skill would understand the need to take into account melting temperature (T_m; the temperature at which half of the primer-target duplex is dissociated and becomes single stranded and is an indication of duplex stability; increased T_m indicates increased stability) based on GC and AT content of the primers being designed as well as secondary structure considerations (increased GC content can lead to increased secondary structure). T_M's can be calculated using a variety of methods known in the art and those of skill would readily understand such various methods for calculating T_M; such methods include for example but are not limited to those available in online tools such as the T_M calculators available on the World Wide Web at promega.com/techserv/tools/biomath/calc11.htm. Primer specificity is defined by its

complete sequence in combination with the 3' end sequence, which is the portion elongated by Taq polymerase. In some embodiments, the 3' end should have at least 5 to 7 unique nucleotides not found anywhere else in the target sequence, in order to help reduce false-priming and creation of incorrect amplification products. Forward and reverse primers typically bind with similar efficiency to the target. In some instances, tools such as NCBI BLAST (located on the World Wide Web at ncbi.nlm.nih.gov) are employed to performed alignments and assist in primer design.

[0067] An additional aspect of primer design is primer complexity or linguistic sequence complexity (*see,* Kalendar R, et al. (*Genomics*, 98(2): 137-144 (2011)). Primers with greater linguistic sequence complexity (*e.g.*, nucleotide arrangement and composition) are typically more efficient. In some embodiments, the linguistic sequence complexity calculation method is used to search for conserved regions between compared sequences for the detection of low-complexity regions including simple sequence repeats, imperfect direct or inverted repeats, polypurine and polypyrimidine triple-stranded cDNA structures, and four-stranded structures (such as G-quadruplexes). In some embodiments, linguistic complexity (LC) measurements are performed using the alphabet-capacity L-gram method (*see,* A. Gabrielian, A. Bolshoy, *Computer & Chemistry* 23:263–274 (1999) and Y.L. Orlov, V.N. Potapov, Complexity: an internet resource for analysis of DNA sequence complexity, *Nucleic Acids Res.* 32: W628–W633(2004)) along the whole sequence length and calculated as the sum of the observed range (xi) from 1 to L size words in the sequence divided by the sum of the expected (E) value for this sequence length. Some G-rich (and C-rich) nucleic acid sequences fold into four-stranded DNA structures that contain stacks of G-quartets (*see,* the World Wide Web at quadruplex.org). In some instances, these quadruplexes are formed by the intermolecular association of two or four DNA molecules, dimerization of sequences that contain two G-bases, or by the intermolecular folding of a single strand containing four blocks of guanines (*see,* P.S. Ho, *PNAS,* 91:9549–9553 (1994); I.A. Il'icheva, V.L. Florent'ev, *Russian Journal of Molecular Biology* 26:512–531(1992); D. Sen, W. Gilbert, *Methods Enzymol.* 211:191–199 (1992); P.A. Rachwal, K.R. Fox, *Meth*ods 43:291–301 (2007); S. Burge, G.N. Parkinson, P. Hazel, A.K. Todd, K. Neidle, *Nucleic Acids Res.* 34:5402–5415 (2006); A. Guédin, J. Gros, P. Alberti, J. Mergny, *Nucleic Acids Res.* 38:7858–7868 (2010); O. Stegle, L. Payet, J.L. Mergny, D.J. MacKay, J.H. Leon, *Bioinformatics* 25:i374–i382 (2009); in some instances, these are eliminated from primer design because of their low linguistic complexity, LC=32% for $(TTAGGG)_4$.

[0068] These methods include various bioinformatics tools for pattern analysis in sequences having GC skew, (G−C)/(G+C), AT skew, (A−T)/(A+T), CG−AT skew, (S−W)/(S+W), or purine–pyrimidine (R−Y)/(R+Y) skew regarding CG content and melting temperature and provide tools for determining linguistic sequence complexity profiles. For example the GC skew in a sliding window of n, where n is a positive integer, bases is calculated with a step of one base, according to the formula, (G−C)/(G+C), in which G is the total number of guanines and C is the total number of cytosines for all sequences in the windows (Y. Benita, et al., *Nucleic Acids Res.* 31:e99 (2003)). Positive GC-skew values indicated an overabundance of G bases, whereas negative GC-skew values represented an overabundance of C bases. Similarly, other skews are calculated in the sequence. Such methods, as well as others, are employed to determine primer complexity in some embodiments.

[0069] According to non-limiting example embodiments, real-time PCR is performed using exonuclease primers (TAQMAN® probes). In such embodiments, the primers utilize the 5' exonuclease activity of thermostable polymerases such as Taq to cleave dual-labeled probes present in the amplification reaction (*See*, *e.g.*, Wittwer, C. et al. Biotechniques 22:130-138, 1997). While complementary to the PCR product, the primer probes used in this assay are distinct from the PCR primer and are dually-labeled with both a molecule capable of fluorescence and a molecule capable of quenching fluorescence. When the probes are intact, intramolecular quenching of the fluorescent signal within the DNA probe leads to little signal. When the fluorescent molecule is liberated by the exonuclease activity of Taq during amplification, the quenching is greatly reduced leading to increased fluorescent signal. Non-limiting examples of fluorescent probes include the 6-carboxy-floruescein moiety and the like. Exemplary quenchers include Black Hole Quencher 1 moiety and the like.

[0070] Exemplary primers include but are not limited to those described herein. Primers for use in the disclosed methods are also found in U.S. Patent Publication No. 20120077200, which is hereby incorporated by reference for all purposes. In some embodiments, the PCR primers for use in the methods of the present diclosure include but are not limited to the following listed in Table of Figures 5B and 5C, and find use in the detection of the TGFBI gene. Biophysical parameters for each primer may be calculated using the World Wide Web at primerdigital.com/tools/PrimerAnalyser.html.

[0071] In some embodiments, the real-time PCR primers for use with the disclosed methods have a linguistic sequence complexity of at least 70%, at least 72%, at least 75%, at least

77%, at least 80%, at least 82%, at least 85%, at least 88%, at least 90%, at least 92%, at least 95%, at least 97% or at least 99%.

d. Detection Probe Design and Detection Probes

[0072] Detection probes commonly employed by those of skill in the art include but are not limited to hydrolysis probes (also known as TAQMAN® probes, 5' nuclease probes or dual-labeled probes), hybridization probes, and Scorpion primers (which combine primer and detection probe in one molecule). In some embodiments, probes are designed to have higher Tm's than the primers in order to promote efficient signal production. T_m's are calculated using any of a variety of methods known in the art and those of skill would readily understand such various methods for calculating Tm; such methods include for example those available in online tools such as the calculators available on the World Wide Web at promega.com/techserv/tools/biomath/calc11.htm.

[0073] In some embodiments, detection probes contain various modifications. In some embodiments, detection probes include modified nucleic acid residues, such as but not limited to 2'-O-methyl ribonucleotide modifications, phosphorothioate backbone modifications, phosphorodithioate backbone modifications, phosphoramidate backbone modifications, methylphosphonate backbone modifications, 3' terminal phosphate modifications and/or 3' alkyl substitutions.

[0074] In some embodiments, the detection probe has increased affinity for a target sequence due to modifications. Such detection probes include detection probes with increased length, as well as detection probes containing chemical modifications. Such modifications include but are not limited to 2'-fluoro (2'-deoxy-2'-fluoro-nucleosides) modifications, LNAs (locked nucleic acids), PNAs (peptide nucleic acids), ZNAs (zip nucleic acids), morpholinos, methylphosphonates, phosphoramidates, polycationic conjugates and 2'-pyrene modifications. In some embodiments, the detector probes contains one or more modifications including 2' fluoro modifications (aka, 2'-Deoxy-2'-fluoro-nucleosides), LNAs (locked nucleic acids), PNAs (peptide nucleic acids), ZNAs (zip nucleic acids), morpholinos, methylphosphonates, phosphoramidates, and/or polycationic conjugates.

[0075] In some embodiments, the detection probes contain detectable moieties, such as those described herein as well as any detectable moieties known to those of skill in the art. Such detectable moieties include for example but are not limited to fluorescent labels and

chemiluminescent labels. Examples of such detectable moieties can also include members of FRET pairs. In some embodiments, the detection probe contains a detectable entity.

[0076] Examples of fluorescent labels include but are not limited to ABY, JUN, AMCA, DEAC (7-Diethylaminocoumarin-3-carboxylic acid); 7-Hydroxy-4-methylcoumarin-3; 7-Hydroxycoumarin-3; MCA (7-Methoxycoumarin-4-acetic acid); 7-Methoxycoumarin-3; AMF (4'-(Aminomethyl)fluorescein); 5-DTAF (5-(4,6-Dichlorotriazinyl)aminofluorescein); 6-DTAF (6-(4,6-Dichlorotriazinyl)aminofluorescein); 6-FAM (6-Carboxyfluorescein; aka FAM; including TAQMAN® FAM™); TAQMAN VIC®; 5(6)-FAM cadaverine; 5-FAM cadaverine; 5(6)-FAM ethylenediamme; 5-FAM ethylenediamme; 5-FITC (FITC Isomer I; fluorescein-5-isothiocyanate); 5-FITC cadaverin; Fluorescein-5-maleimide; 5-IAF (5-Iodoacetamidofluorescein); 6-JOE (6-Carboxy-4',5'-dichloro-2',7'-dimethoxyfluorescein); 5-CRl lO (5-Carboxyrhodamine 110); 6-CRl lO (6-Carboxyrhodamine 110); 5-CR6G (5-Carboxyrhodamine 6G); 6-CR6G (6-Carboxyrhodamine 6G); 5(6)-Caroxyrhodamine 6G cadaverine; 5(6)-Caroxyrhodamine 6G ethylenediamme; 5-ROX (5-Carboxy-X-rhodamine); 6-ROX (6-Carboxy-X-rhodamine); 5-TAMRA (5-Carboxytetramethylrhodamine); 6-TAMRA (6-Carboxytetramethylrhodamine); 5-TAMRA cadaverine; 6-TAMRA cadaverine; 5-TAMRA ethylenediamme; 6-TAMRA ethylenediamme; 5-TMR C6 maleimide; 6-TMR C6 maleimide; TR C2 maleimide; TR cadaverine; 5-TRITC; G isomer (Tetramethylrhodamine-5-isothiocyanate); 6-TRITC; R isomer (Tetramethylrhodamine-6-isothiocyanate); Dansyl cadaverine (5-Dimethylaminonaphthalene-l-(N-(5-aminopentyl))sulfonamide); EDANS C2 maleimide; fluorescamine; NBD; and pyrromethene and derivatives thereof.

[0077] Examples of chemiluminescent labels include but are not limited to those labels used with Southern Blot and Western Blot protocols (see, for *e.g.*, Sambrook and Russell, Molecular Cloning: A Laboratory Manual, (3rd ed.) (2001); incorporated by reference herein in its entirety). Examples include but are not limited to -(2'-spiroadamantane)-4-methoxy-4-(3"-phosphoryloxy)phenyl-1,2-dioxetane (AMPPD); acridinium esters and adamantyl-stabilized 1 ,2-dioxetanes, and derivatives thereof.

[0078] In some embodiments, the labeled probes are used to hybridize within the amplified region during amplification. The probes may be modified so as to avoid them from acting as primers for amplification. The detection probe may be labeled with two fluorescent dyes, one capable of quenching the fluorescence of the other dye. One dye is attached to the 5'

terminus of the probe and the other is attached to an internal site, so that quenching occurs when the probe is in a non-hybridized state.

[0079] Typically, real-time PCR probes consist of a pair of dyes (a reporter dye and an acceptor dye) that are involved in fluorescence resonance energy transfer (FRET), whereby the acceptor dye quenches the emission of the reporter dye. In general, the fluorescence-labeled probes increase the specificity of amplicon quantification.

[0080] Real-time PCR that are used in some embodiments of the disclosed methods also include the use of one or more hybridization probes (i.e., detection probes), as determined by those skilled in the art, in view of this disclosure. By way of non-limiting example, such hybridization probes include but are not limited to one or more of those provided in the described methods. Exemplary probes, such as the HEX channel and/or FAM channel probes, are understood by one skilled in the art.

[0081] According to example embodiments, detection probes and primers are conveniently selected *e.g.*, using an in silico analysis using primer design software and cross-referencing against the available nucleotide database of genes and genomes deposited at the National Center for Biotechnology Information (NCBI). Some additional guidelines may be used for selection of primers and/or probes in some embodiments. For example, in some embodiments, the primers and probes are selected such that they are close together, but not overlapping. In some embodiments, the primers may have the same (or close T_M) (*e.g.*, between about 58 °C and about 60 °C). In some embodiments, the T_M of the probe is approximately 10 °C higher than that selected for the T_M of the primers. In some embodiments, the length of the probes and primers is selected to be between about 17 and 39 base pairs, etc. These and other guidelines are used in some instances by those skilled in the art in selecting appropriate primers and/or probes.

[0082] Probes for use in the methods of the present invention include but are not limited to the following exemplary probes listed in Figures 5B and 5C.

Examples

[0083] Example 1: Worldwide Literature Search

[0084] The HGMD database was interrogated and 62 different *TGFBI* mutations were found. The HGMD database was used to identify the papers in which these mutations were

described in order to build up a picture of a worldwide distribution (Figure 1A and 1B). Each flag in the world map contains a summary of the mutations reported in a specific region or a country. The summary includes ethnicities, mutations and the total number of cases reported for each mutation (Figure 1A). The mutations are spread with no significant differences in distribution in specific populations or geographical regions. Very few cases were reported from South America, and there were no case reports from Africa or Russia. The map can be used to extract country-specific information e.g. London indicated by a red arrow in Figure 1B.

[0085] Globally, 75% of the *TGFBI* mutations reported in the over 1,600 cases consisted of one of the five mutations currently detected by the available genetic test. While reports of novel *TGFBI* mutations are likely to be published, the most common *TGFBI* mutations, found at codons R124 and R555, are conversely under-reported. Therefore, it is difficult to obtain an accurate estimation of the true worldwide detection rate of *TGFBI* dystrophies within the literature.

[0086] Based on the ranking of the highest reported case numbers from our study, the effect on *TGFBI* mutation detection rates by adding six mutations to the available genetic test panel was evaluated. The reported number of cases for each of the five most common mutations and the six additional mutations proposed for the expanded test are shown in the table of Figure 3. It is noteworthy that the H626R is the fourth most prevalent mutation after R124L. This finding supports the inclusion of this mutation in an expanded panel for the diagnosis of *TGFBI* corneal dystrophy. Although only four cases of *TGFBI* corneal dystrophy associated with M502V have been reported within the literature (Supplementary Material), heterozygous mutation for M502V was detected in one sample. Therefore, it was included in the expanded panel.

[0087] From the cases reported in the literature, the addition of the six new mutations to the existing panel may increase the worldwide detection rate from 75% to 90% (Figure 2). The addition of the additional mutations to the available genetic test would theoretically increase the detection rate by 32% in South America and 30% in North America. Europe and Asia, both with a 13% increase in detection rates would also benefit from the proposed eleven mutation panel (Figure 2).

[0088] Example 2: Global Available Genetic Test Data Analysis

[0089] Since 2008, more than 600,000 samples worldwide were tested by the available genetic test; most of the samples were from Korea and Japan, where the test is used for pre-refractive surgery screening. An analysis of the global testing data demonstrated that the detection rate in Korea is approximately 15 in 10,000 people, which closely matches the reported prevalence of 1 in 870 people.[10] The detection rate of *TGFBI* mutations in Japan (3 in 10,000) was lower than that in Korea. In Korea, the test is administered as a general screening for all refractive surgery candidates, whereas in Japan, patients are first subjected to a rigorous clinical examination and only those patients who have no detected corneal abnormalities have samples submitted for the genetic test.

[0090] The clinics/hospitals in Korea and Japan use the genetic test for screening purposes as it forms part of the practice guidelines for refractive surgery. In the US, some clinics/hospitals use the test for screening during the pre-operative examination for vision corrective surgery, whereas others use it as a confirmation for clinical diagnosis or to exclude *TGFBI* mutations if the surgeon has any doubt about the imperfections noted in the patient's cornea. European clinics utilize the test mostly for this type of clinical confirmation.

[0091] Example 3: Assessment of an Expanded Panel with Six Additional Mutations

[0092] Few population studies like the 2016 UCL, Moorfield's Corneal Dystrophy Study have conducted Sanger sequencing on the entire *TGFBI* gene. This study provided us with a set of data on which to evaluate the addition of six new mutations sites to enhance the pick-up rate in a given population. In brief, the study consisted of 91 unrelated *TGFBI* corneal dystrophy cases in which 68 had a diagnosis of epithelial-stromal *TGFBI* associated dystrophy (RBCD, TBCD, LCD and GCD) and 23 had a diagnosis of bilateral epithelial basement membrane dystrophy (EBMD)[4]. For the UK population, a set of six *TGFBI* mutations were evaluated to determine whether these mutations in combination with the five mutations genetic test were appropriate. The data showed that the detection rate in the UK cohort would increase from 90% to 97% (Table in Figure 4). Other candidate mutations may be considered, such as V625D and A620D from the table of Figure 4, in order to increase the detection rate to almost 100%. This finding demonstrates that the inclusion of six additional mutations to the available genetic test, while improving the pick-up rate, will still miss some important mutations found in the UK population.

[0093] 16 of the 19 samples with clinical indications that tested negative with the original genetic test were still negative (84.2% of the total), while three tested positive (15.7% of the

total) with the expanded panel. The WES results of a mother and son pair with a clinical diagnosis of late-onset of LCD were positive for a heterozygous *TGFBI* H626R mutation. Parallel real-time PCR testing showed the same heterozygous H626R mutation. The third sample was discovered to be heterozygous for M502V. The result was confirmed with Sanger sequencing Subsequent patient history revealed that the patient had very small corneal scarring on the left cornea. There was no family history of corneal dystrophy or opacity.

[0094] Based on the evidence in the literature, adding six mutations to the available genetic test would increase the detection rate by 15%. This coincides with the 15.7% percent increase in detection for our sample cohort (3 of 19 samples). Geographic or population differences were not deteted; therefore, the newly proposed six additional mutations are appropriate for worldwide use as an enhancement of the present genetic test. The new mutations would considerably improve the mutation detection rate.

[0095] The testing of 19 samples for the presence of the six additional mutations in the expanded panel proved that the expanded genetic test will have increased detectability of TGFBI mutations.

[0096] Example 4: Multiplexing detection of mutations

[0097] First, for each of mutations as shown in Figure 5B, version 1 (V1) primers, a VIC labeled probe with a normal sequence, and a FAM labeled probe with a mutant sequence were combined to detect the mutation. Detection for each of R124S, A546D, H572R, G623D, H626R and M502V was successful. Second, for each of A546D, H572R, and G623D mutations as shown in Figure 5B, V1 primers, a ABY labeled probe with a normal sequence, and a JUN labeled probe with a mutant sequence were combined to detect the mutation. Only the detection of G623D mutation was successful. Third, for each of R124S, H626R, and M502V mutations as shown in Figure 5C, version 2 (V2) primers, a VIC labeled probe with a normal sequence, and a FAM labeled probe with a mutant sequence were combined to detect the mutation. Detection for only H626R was successful. Fourth, for each of A546D, H572R, and G623D mutations as shown in Figure 5C, V2 primers, a ABY labeled probe with a normal sequence, and a JUN labeled probe with a mutant sequence were combined to detect the mutation. None of the mutations were detected properly. Fifth, in a single reaction mixture, primers and probes to detect different combinations of mutations were mixed.

[0098] The following PCR master mix volume calculation and PCT conditions were used:

TaqPath ProAmp Master Mix volume; 2.5 uL per test

M502V V1 primer forward and reverse primer, and VIC and FAM probe mix volume; 0.05 uL per test

G623D 20 pM V1 primer forward and reverse primer volume: 0.05 uL per test

G623D 50 pM V1 ABY probe volume: 0.025 uL per test

G623D 50 pM V1 JUN probe volume: 0.025 uL per test

Water volume: 2.35 uL per test

PCR fluorescent detection amplification cycling number and condition:

Cycle number: 40 cycles

Cycling conditions;

Pre-PCR Read (Holding State): 60.0 ˚C – 01:00 minute

Holding Stage: 95.0 ˚C – 00:20 minute

Cycling State: 40 cycles, 95.0 ˚C – 00:30 minute

Post-PCR Read (Holding Stage): 60.0 ˚C – 01:00 minute

[0099] Out of the primers and probes for different combitions of mutations in a single reaction mixture, only the V1 M502V primers and VIC and FAM probes with the V1 G623D primers and ABY and JUN probes successfully detected both mutations in a single reaction mixture as shown in Figures 6A and 6B. The combination of reagents for R124S and A546D, H626R and H572R failed to detect the mutations properly.

[00100] The following shows GRCh38.p7 Homo sapiens transforming growth factor beta induced (TGFBI), RefSeqGene on chromosome 5, NCBI Reference Sequence: NG_012646.1 (SEQ ID NO: 61).

```
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40201 ccagcatggt gatcccctgc ctgtgtgctg gacttttgag tcctcagcac caacctgtga
40261 agtggttgcc agcataatcc cattatgcag atgaggagac caaggcccag ggaagggaga
40321 accaccagca gcacgtaaaa tagctgagct gggactggaa ctcacacctc ctgactctca
40381 gtgaccacca ctgacaacag cataagtcca ggttttccag gcccatcccc tctgtgccaa
40441 cccacattca gattccttcc ccggctcccg taatctctgg catctagaat atcctcagga
40501 ctctgagagg tgatatcatg tggttgtggt gccattgccc cctacctgtg tggcctgggg
40561 ccagtcatgt gacctcccag ggtctcctct tctgtaatag ggagatgacc gtcacatcta
40621 cttcatgggt ccatcgtgag gatgaaatga gatgatctat ataaaatgct tggtacaaca
40681 ttaggtggcc ttatttttat cctgccgtct gggactgctc aggatcaatg cgccagagag
40741 cctttatttg tgtctttccc acaggtgggc tggcccactt tcctagagaa tgggacagac
40801 ctccttccca cccacaccca tctctgccaa ggctgattca ctccagcagg cggagctcat
40861 ttcacttcat ggaaccaatg acccaaagat atatccccag cactactgct ggtcagtcca
40921 ctgctgctgg gaatacagca atggtagtgg cagacagagg ccctctctta aatagcttcc
40981 agtctgagga aagagagata tgacatcaat ccattaaaat cattcatcca ttggttccac
41041 aaatatttgt tgagggctac ctatgtgcac ccccatgtta gaccctgggg aatagacatg
41101 tcattctcat gaggcttctc tactgatggg ggggaagaga attgtcaacc agataatggc
41161 actacagcct gtgtgttctt agtgactctg aggatagcac tgtggttctg tgacagataa
41221 tgaaggattt ggaagcagga atgcccagga gctcccagaa gtgggaagag atgagaggaa
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41461 tcatgctggg tatcctatgc tatgcttcac tttgagcacc taaaatacac acactgcact

```
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41581 tttaaagtaa aaatcactac aggatccatt ataaatgcca aacactaaga tgtgtgtttc
41641 cagttctccc cttcatttgt ccctgccact ccctgccctg actttgcccc acccccctagt
41701 aatgtgggct ccactctatg ctccaaactc tccctggaga gaaatcctcc ctgtggttga
41761 ggacaaggcg cagccttccc ctcccaccaa agaaggtcag attccctttt ttggttccta
41821 accatccata ccccttcttt tctcatgaag actcgggcta agcattcatt agggctgcca
41881 tctggaggat ggacccttag agctgagggg ccagcactgt gtgt
```

[00101] The following shows TGFBI gene protein product (βIG-H3 protein sequence; NCBI Reference number NG_012646.1) (SEQ ID NO: 62).

```
MALFVRLLALALALALGPAATLAGPAKSPYQLVLQHSRLRGRQHGPNVCAVQKVIGTNRKYFTNCKQW
YQRKICGKSTVISYECCPGYEKVPGEKGCPAALPLSNLYETLGVVGSTTTQLYTDRTEKLRPEMEGPG
SFTIFAPSNEAWASLPAEVLDSLVSNVNIELLNALRYHMVGRRVLTDELKHGMTLTSMYQNSNIQIHH
YPNGIVTVNCARLLKADHHATNGVVHLIDKVISTITNNIQQIIEIEDTFETLRAAVAASGLNTMLEGN
GQYTLLAPTNEAFEKIPSETLNRILGDPEALRDLLNNHILKSAMCAEAIVAGLSVETLEGTTLEVGCS
GDMLTINGKAIISNKDILATNGVIHYIDELLIPDSAKTLFELAAESDVSTAIDLFRQAGLGNHLSGSE
RLTLLAPLNSVFKDGTPPIDAHTRNLLRNHIIKDQLASKYLYHGQTLETLGGKKLRVFVYRNSLCIEN
SCIAAHDKRGRYGTLFTMDRVLTPPMGTVMDVLKGDNRFSMLVAAIQSAGLTETLNREGVYTVFAPTN
EAFRALPPRERSRLLGDAKELANILKYHIGDEILVSGGIGALVRLKSLQGDKLEVSLKNNVVSVNKEP
VAEPDIMATNGVVHVITNVLQPPANRPQERGDELADSALEIFKQASAFSRASQRSVRLAPVYQKLLER
MKH
```

[00102] All headings and section designations are used for clarity and reference purposes only and are not to be considered limiting in any way. For example, those of skill in the art will appreciate the usefulness of combining various aspects from different headings as appropriate according to the spirit and scope of the invention described herein.

[00103] All references cited herein are hereby incorporated by reference herein in their entireties and for all purposes to the same extent as if each individual publication or patent or patent application was specifically and individually indicated to be incorporated by reference in its entirety for all purposes.

[00104] Many modifications and variations of this application can be made without departing from its spirit and scope, as will be apparent to those skilled in the art. The specific embodiments and examples described herein are offered by way of example only, and the application is to be limited only by the terms of the appended claims, along with the full scope of equivalents to which the claims are entitled.

WHAT IS CLAIMED:

1. A reaction mixture for detecting corneal dystrophy in a subject, the reaction mixture comprising a labeled probe comprising a mutant nucleotide sequence selected from the group consisting of SEQ ID NO: 25-30, 36 and 54.

2. The reaction mixture according to claim 1, further comprising a corresponding labeled probe comprising a normal nucleotide sequence selected from the group consisting of SEQ ID NO: 19-24, 33 and 50.

3. The reaction mixture according to claim 2, wherein the labeled probe consists of the mutant nucleotide sequence selected from the group consisting of SEQ ID NO: 25-30, 36 and 54; and/or the corresponding labeled probe consists of the normal nucleotide sequence selected from the group consisting of SEQ ID NO: 19-24, 33 and 50.

4. The reaction mixture according to any one of claims 1-3, wherein the reaction mixture comprises a labeled TGFBI G623D probe comprising the nucleotide sequence of SEQ ID NO: 36; and a labeled TGFBI M502V probe comprising the nucleotide sequence of SEQ ID NO: 30.

5. The reaction mixture according to any one of claims 1-4, wherein the labeled probes are fluorescently labeled.

6. The reaction mixture according to any one of claims 1-5, wherein each of the labeled probes comprises a different probe and is independently labeled with VIC, FAM, ABY, or JUN.

7. The reaction mixture according to any one of claims 1-6, further comprising at least one amplification primer pair for amplifying a TGFBI gene sequence from a biological sample from the subject.

8. The reaction mixture according to any one of claims 1-7, further comprising

(a) a corresponding forward primer comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 7-12 and 41; and

(b) a corresponding reverse primer comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 13-18 and 47.

9. A reaction kit comprising (a) the reaction mixture according to any one of claims 4-8, and (b) separately from the reaction mixture, one or more labeled probes for one or more TGFBI mutations selected from the group consisting of R124S, A546D, H572R, and H626R.

10. The reaction kit according to claim 9, wherein the one or more labeled probes are selected from the group consisting of labeled probes comprising nucleotide sequences of SEQ ID NO: 19, 25, 20, 26, 21, 27, 23, 29, 50 and 54.

11. The reaction kit according to claim 9, wherein the reaction kit comprises a labeled TGFBI R124S probe comprising the nucleotide sequence of SEQ ID NO: 19 or 25.

12. The reaction kit according to claim 9, wherein the reaction kit comprises a labeled TGFBI A546D probe comprising the nucleotide sequence of SEQ ID NO: 20 or 26.

13. The reaction kit according to claim 9, wherein the reaction kit comprises a labeled TGFBI H572R probe comprising the nucleotide sequence of SEQ ID NO: 21 or 27.

14. The reaction kit according to claim 9, wherein the reaction kit comprises a labeled TGFBI H626R probe comprising the nucleotide sequence of SEQ ID NO: 23, 29, 50 or 54.

15. The reaction kit according to claim 8, further comprising a third amplification primer set.

16. A method for detecting corneal dystrophy comprising:

(A-1) amplifying a first TGFBI gene sequence from a biological sample from a subject using a reaction mixture comprising at least a first amplification primer pair and a set of at least two detection probes;

(B-1) hybridizing first and second detection probes of the set of at least two detection probes to a first TGFBI gene sequence having G623D mutation and a second TGFBI gene sequence having M502V mutation, respectively; and

(C-1) detecting one, two or more mutations in the TGFBI gene sequence based on the hybridization of the first and second detection probes to the first and second TGFBI gene sequences, respectively.

17. The method according to claim 16, wherein the reaction mixture comprises a reaction mixture of any one of claims 1-8.

18. The method according to claim 16 or 17, further comprising:

(A-2) amplifying a third TGFBI gene sequence from the biological sample, wherein the reaction mixture further comprises a third labeled probe for a third TGFBI mutation selected from the group consisting of R124S, A546D, H572R, and H626R;

(B-2) hybridizing the third labeled probe to the third TGFBI gene sequence; and

(C-2) detecting a mutation in the third TGFBI gene sequence based on the hybridization of the third detection probe to the third TGFBI gene sequence.

19. The method according to any one of claim 18, wherein the amplifying the first TGFBI gene sequence (A-1) and the amplifying the second TGFBI gene sequence (A-2) are performed separately.

20. The method according to claim 18, wherein the hybridizing (B-1) and the hybridizing (B-2) are performed separately.

21. The method according to any one of claims 18-20, wherein the detecting (C-1) and the detecting (C-2) are performed separately.

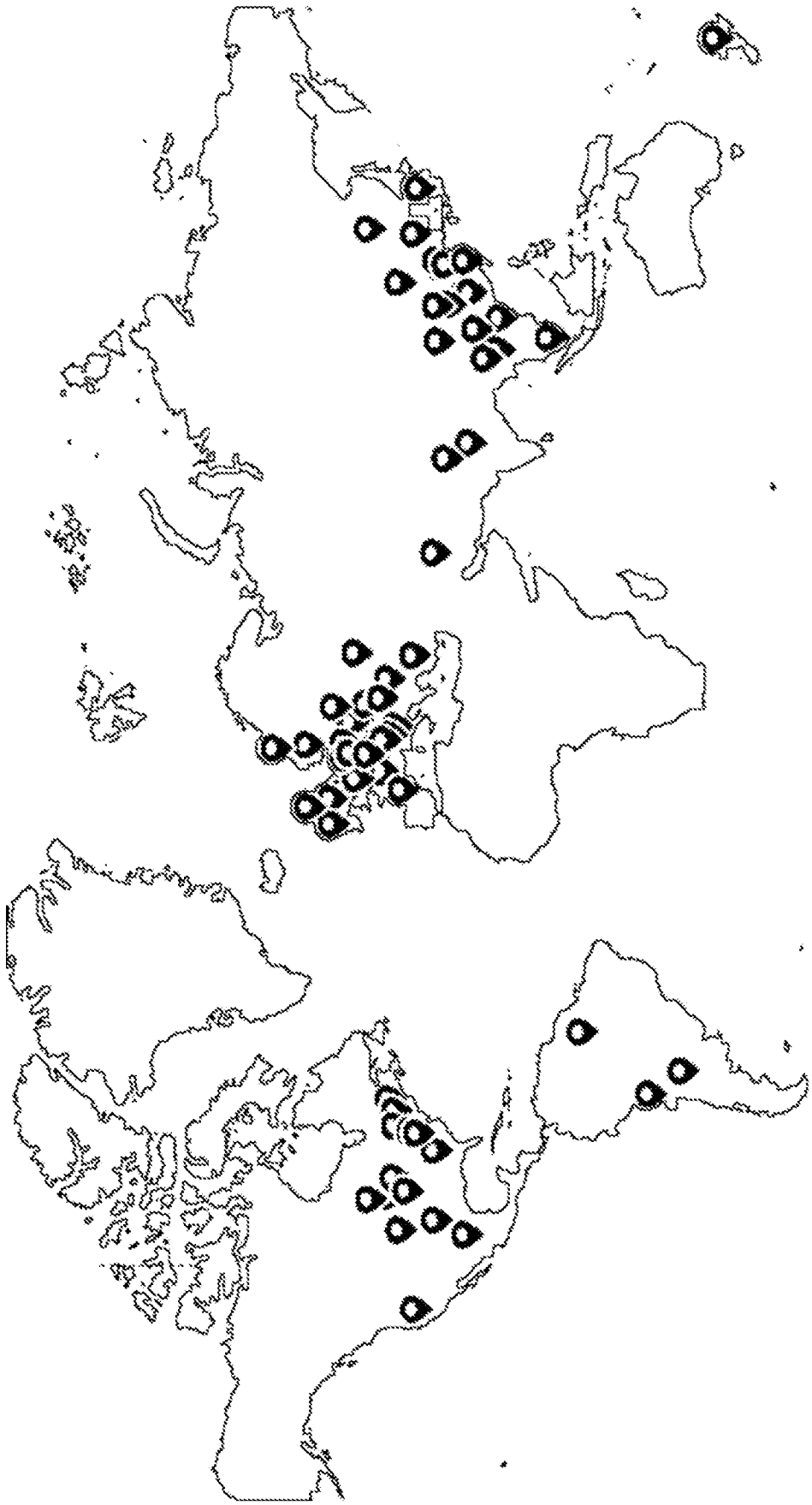


Figure 1A.

← England: G6234D; R124S; H40..
name
England: G623D; R124S; H403Q; R124C; R124H;
GCD;
description
Ethnicity: English; Iranian (H403Q); Bangladeshi
(R124C)
G623D: 5
R124S: 6
H403Q: 1 (Keratoconus)
R124C: 3
R124H: 6
GCD: 1

Figure 1B.

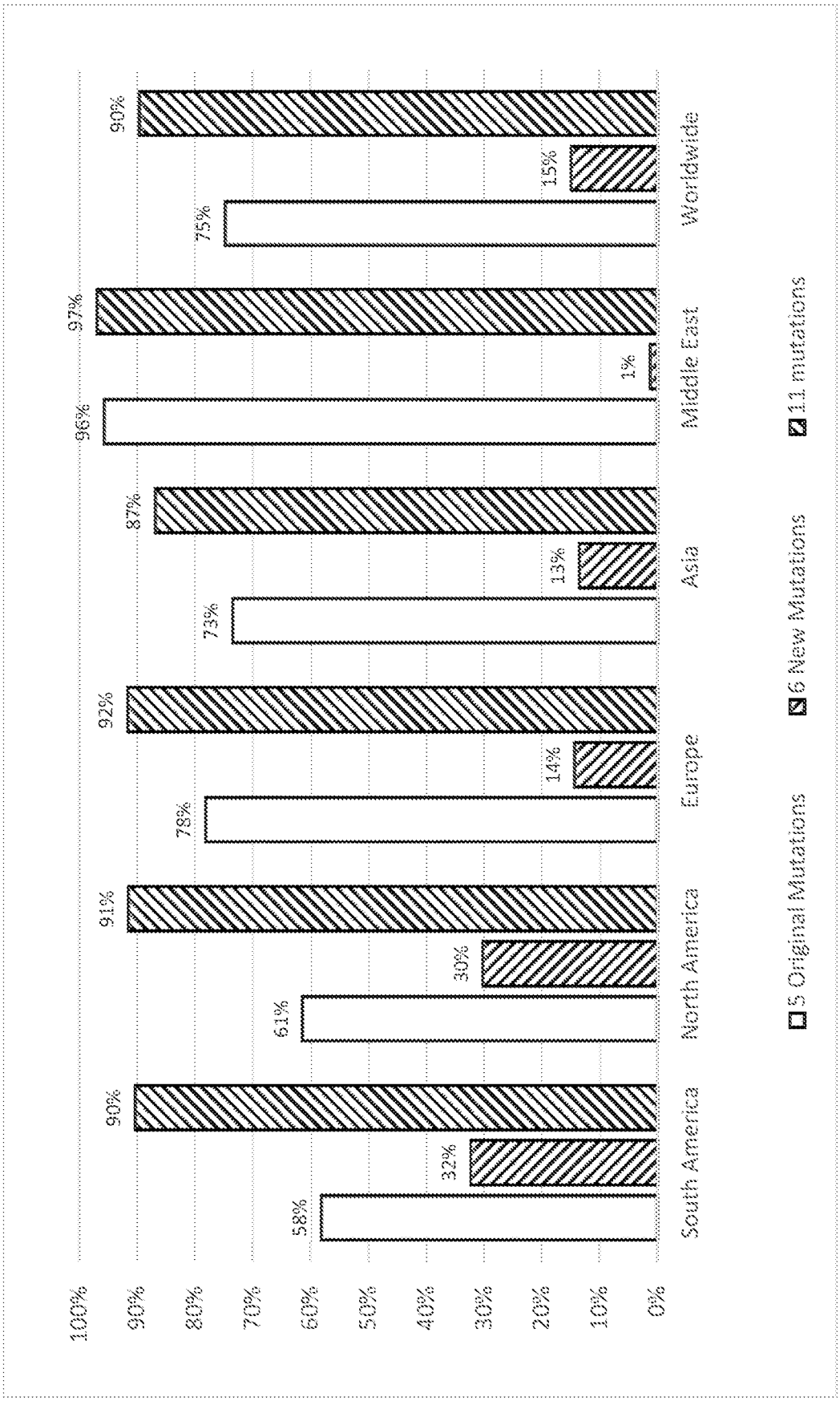

100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
South America
North America
Europe
Asia
Middle East
Worldwide
90%
58%
32%
91%
61%
30%
92%
78%
14%
87%
73%
13%
97%
96%
1%
90%
75%
15%
5 Original Mutations
6 New Mutations
11 mutations

Figure 2.

Figure 3.

Mutations	Reported Case Numbers
Five most common mutations in the current genetic test panel	
R124C Lattice Corneal Dystrophy type 1	372
R555W Granular Corneal Dystrophy type 1	338
R124H Granular Corneal Dystrophy type 2	325
R124L Reis-Buckler corneal dystrophy	110
R555Q Thiel-Behnke corneal dystrophy	75
Six additional mutations in the expended test panel	
H626R Lattice Corneal Dystrophy subtype I/IIIA	117
A546D Variant Lattice Corneal Dystrophy	48
H572R Lattice Corneal Dystrophy subtype 1	34
G623D Variant Reis-Buckler Corneal Dystrophy	26
R124S Subtype Granular Corneal Dystrophy type 1	18
M502V Variant Corneal Dystrophy and Variant Thiel-Behnke Corneal Dystrophy	4

Figure 4.

UCL/Moorfields % detection of 91 UK ethnically diverse cohort with 68 TGFBI CDs					
Clinical Diagnosis	Case #	Case %	TGFBI Mutation	Mutation #	Mutation %	Comments
Lattice Corneal Dystrophy	24	35%	R124C	19	28%	
			V625D	1	1%	Asian
			H626R*	2	3%	
			A620D	1	1%	Asian
			G623D*	1	1%	
Granular Corneal Dystrophy 1	21	31%	R555W	13	19%	
Granular Corneal Dystrophy 2			R124H	8	12%	
TB/RB CD	23	34$	R555Q	20	29%	
			R124L	1	1%	
			G623D*	2	3%	
Total TGFBI CD	68		Universal Test	61	90%	
			Additional 6 SNPs*	5	7%	
			Total 11 SNPs	66	97%	

Figure 5A.

Codon number	Position	dbSNP (19 total)	LT Assay ID	Target sequence
R124S	135382095	rs121909210	ANMFXKJ	ACGAGACCCTGGAGTCGTTGGATCCACCACCACTCAGCTGTACAC GGAC(C/A)GCACGGAGAAGCTGAGGCCTGAGATGGAGGGGCCC GGCAGCTTCACCATC SEQ ID NO: 1
A546D	135392443	rs2676077109	ANNKR6G	GACCCTCAAC CGGG AAG GAGTCTACACAGTC TTT GCT CCC ACAAATGAAG(C/A)CTTCCGAGCCCTGCCACCAAGAGAACGGAG CAG ACT CTT GGGTAAAGACC SEQ ID NO: 2
H572R	135394815	no	ANPRKRE	CTTGCCAACATCCTGAAATACC CCAAGGAACTTGCCAACATCCTGAAATACC(A/G)CATTGGTGATG AAATCCTGGTTAGCGGAGGCAT CGG GGC CCTGGTGCGGCTA SEQ ID NO: 3
G623D	135396587	rs121909215	ANRWFCC	GAGTGTCAACAAGGAGCCTGTTGCCGAGCCTGACATCATGGCCA CAAATG(G/A)CGTGGTCCATGTCATCACCAATGTTCTGCA GCC TCC AGG TAAGTGTCGCA SEQ ID NO: 4
H626R	135396596	no	ANTZ9V9	(AAGGAGCCTGTTGCCGAGC) CTGACATCATGGCCACAAATGGCGTGGTCC(A/G)TGTCATCACCA ATGTTCTGCAGCCTCC AGG TAA GTG TCGCATCCCCACTGA SEQ ID NO: 5
M502V	135391462	rs188677757	ANRWFF6	CACGACAAGAGGGGGAGGTACGGGACCCTGTTCACGATGGACC GGGTGCTGACCCCCCCCA(A/G)TGGGGACTGTCATGGATGTCCTGA AGGGAGACA ATC GCT T TAGGTAATTA GTTCCATCCC SEQ ID NO: 6

Figure 5B. Version 1 (V1)

Codon number	Primer Fwd	Primer Rev	VIC Probe (Norm)	FAM Probe (Mut)	ABY Probe (Norm) - NN complement	JUN Probe (Mut) HH compliment
R124S	CCACCACCACTCAGCTGTA C SEQ ID NO: 7 (Ver.1 Working with V1 VIC/FAM probes)	TCCATCTCAGGCCTCAGC T SEQ ID NO: 13 (Ver.1 Working with V1 VIC/FAM probes)	CTCCGTGCGGTCCGT SEQ ID NO: 19 (Ver.1 Working with V1 primers)	TCTCCGTGCTGTCCGT SEQ ID NO: 25 (Ver.1 Working with V1 primers)		
A546D	TCT ACA CAG TCT TTG CTC CCA CA SEQ ID NO: 8 (Ver.1 Working with V1 VIC/FAM probes)	CTC CGT TCT CTT GGT GGC A SEQ ID NO: 14 (Ver.1 Working with V1 VIC/FAM probes)	CTC GGA AGG CTT CAT T SEQ ID NO: 20 (Ver.1 Working with V1 primers)	CTC GGA AG**T** CTT CAT T SEQ ID NO: 26 Ver.1 (Working with V1 primers)	CTT GGT GGC AGG GCT CGG AAG **G**CT TCA TTT GT SEQ ID NO: 31 (Ver.1 Not Working)	CTT GGT GGC AGG GCT CGG AAG **T**CT TCA TTT GT SEQ ID NO: 34 (Ver.1 Not Working with any primers)
H572R	CCA AGG AAC TTG CCA ACA T SEQ ID NO: 9 (Ver.1 Working with V1 VIC/FAM probes)	CCT CCG CTA ACC AGG ATT TCA TC SEQ ID NO: 15 (Ver.1 Working with V1 VIC/FAM probes)	CCT GAA ATA CC**A** CAT TGG SEQ ID NO: 21 (Ver.1 Working with V1 primers)	CCT GAA ATA CC**G** CAT TGG SEQ ID NO: 27 (Ver.1 Working with V1 primers)	C TTG CCA ACA TCC TGA AAT ACC ACA TTG GTG AT SEQ ID NO: 32 (Ver.1 Not Working with any primers)	C TTG CCA ACA TCC TGA AAT ACC GCA TTG GTG AT SEQ ID NO: 35 (Ver.1 Not Working with any primers)
G623D	TTG CCG AGC CTG ACA TCA SEQ ID NO: 10 (Ver.1 Working with V1 VIC/FAM probes and ABY/JUN probes)	TGC AGA ACA TTG GTG ATG ACA TG SEQ ID NO: 16 (Ver.1 Working with V1 VIC/FAM probes and ABY/JUN probes)	CACAAATGGCGTGGT C SEQ ID NO: 22 (Ver.1 Working with V1 primers)	CCACAAATGACGTGGT C SEQ ID NO: 28 (Ver.1 Working with V1 primers)	CA TCA TGG CCA CAA ATG **G**CG TGG TCC ATG TC SEQ ID NO: 33 (Ver.1 Working with V1 primers)	CA TCA TGG CCA CAA ATG **A**CG TGG TCC ATG TC SEQ ID NO: 36 (Ver.1 Working with V1 primers)

Figure 5B continued

Codon number	Primer Fwd	Primer Rev	VIC Probe (Norm)	FAM Probe (Mut)	ABY Probe (Norm) - NN complement	JUN Probe (Mut) HH compliment
H626R	CTGACATCATGGCCACAAATGG SEQ ID NO: 11 (Ver.1 Working only with V1 VIC/FAM probes)	GGAGGCTGCAGAACATTGGT SEQ ID NO: 17 (Ver.1 Working only with V1 VIC/FAM probes)	CGTGGTCCATGTCATC SEQ ID NO: 23 (Ver.1 Working only with V1 primers)	TGGTCCGTGTCATC SEQ ID NO: 29 (Ver.1 Working only with V1 primers)		
M502V	GGACCGG GTG CTG ACC SEQ ID NO: 12 (Ver.1 Working only with V1 VIC/FAM probes)	CTCCCTTCAGGACATCCA SEQ ID NO: 18 (Ver.1 Working only with V1 VIC/FAM probes)	TGACAGTCCCCATTGGG SEQ ID NO: 24 (Ver.1 Working only with V1 primers) – used in multiplexing experiments with G623D	TGACAGTCCCCACTGGG SEQ ID NO: 30 (Ver. 1 Working only with V1 primers) - used in multiplexing experiments with G623D		

Figure 5C. Version 2 (V2)

Codon number	Primer Fwd	Primer Rev	VIC Probe (Norm)	FAM Probe (Mut)	ABY Probe (Norm) - NN complement	JUN Probe (Mut) HH compliment
R124S	GACCCTGGAGTCGTTGGAT C SEQ ID NO: 37 (Ver. 2 Not Working with V2 VIC/FAM probes)	CCCGGCAGCTTCACCATC SEQ ID NO: 43 (Ver. 2 Not Working with V2 VIC/FAM probes)	CGACTTCTCCGTGCGGT CCGT GTACAG SEQ ID NO: 49 (Ver. 2 Not Working)	CGACTTCGACTT TCTCCGTGCTGTC CGT GTACAG GTACAG SEQ ID NO: 53 (Ver. 2 Not Working)		
A546D	CGGGAAGGAGTCTACACAG TCTTT SEQ ID NO: 38 (Ver. 2 Not Working with V1 or V2 ABY/JUN probes)	AAGAGTCTGCTCCGTTCTCT T SEQ ID NO: 44 (Ver. 2 Not Working with V1 or V2 ABY/JUN probes)			AGGGCTCGGAAG**G**CTTC ATT SEQ ID NO: 56 (Ver. 2 Not Working with V1 Primers)	AGGGCTCGGAAG**T**CTTC ATT SEQ ID NO: 59 (Ver. 2 Not Working with V1 primers)
H572R	TGAAATACCCCAAGGAACT TG SEQ ID NO: 39 (Ver. 2 Not Working with V1 probes)	GCCCCGATGCCTCCGCTAAC CAGG SEQ ID NO: 45 (Ver. 2 Not Working with V1 probes)			ACATCCTGAAATACCACA TTGG SEQ ID NO: 57 (Ver. 2 Working with V2 primers)	ACATCCTGAAATACCGCA TTGG SEQ ID NO: 60 (Ver. 2 Working with V2 primers)
G623D	AGGAGCCTGTTGCCGAGC SEQ ID NO: 40 (Ver. 2 Not Working with V1 or V2 probes)	CCTGGAGGCTGCAGAACAT TGGTG SEQ ID NO: 46 (Ver. 2 Not Working with V1 or V2 probes)			CACAAATG **G**CGTGGTC SEQ ID NO: 58 (Ver. 2 Not Working with V1 or V2 primers)	CACAAATG**A**CGTGGTC SEQ ID NO: 61 (Ver. 2 Not Working with V1 or V2 primers)

Figure 5C continued

Codon number	Primer Fwd	Primer Rev	VIC Probe (Norm)	FAM Probe (Mut)	ABY Probe (Norm) - NN complement	JUN Probe (Mut) HH compliment
H626R	TTGCCGAGCCTGACATCATGGC SEQ ID NO: 41 (Ver. 2 Working with V2 probes)	CACTTACCTGGAGGCGCAGA SEQ ID NO: 47 (Ver. 2 Working with V2 probes)	TGGCGTGGTCCATGTC SEQ ID NO: 50 (Ver. 2 Working with V2 primers)	TGGCGTGGTCCGTGTC SEQ ID NO: 54 (Ver. 2 Working with V2 primers)		
M502V	GTTCACGATGGACCGG SEQ ID NO: 42 (Ver. 2 Not Working with V2 probes)	AGCGATTGTCTCCCTTCA SEQ ID NO: 48 (Ver. 2 Not Working with V2 probes)	TCCCCATTGGGGGGGGT SEQ ID NO: 52 (Ver. 2 Not Working with V2 primers)	TCCCCACTGGGGGGGGT SEQ ID NO: 55 (Ver. 2 Not Working with V2 primers)		

Figure 6A. G623D discrimination plot from the multiplexing experiment from Example 4.

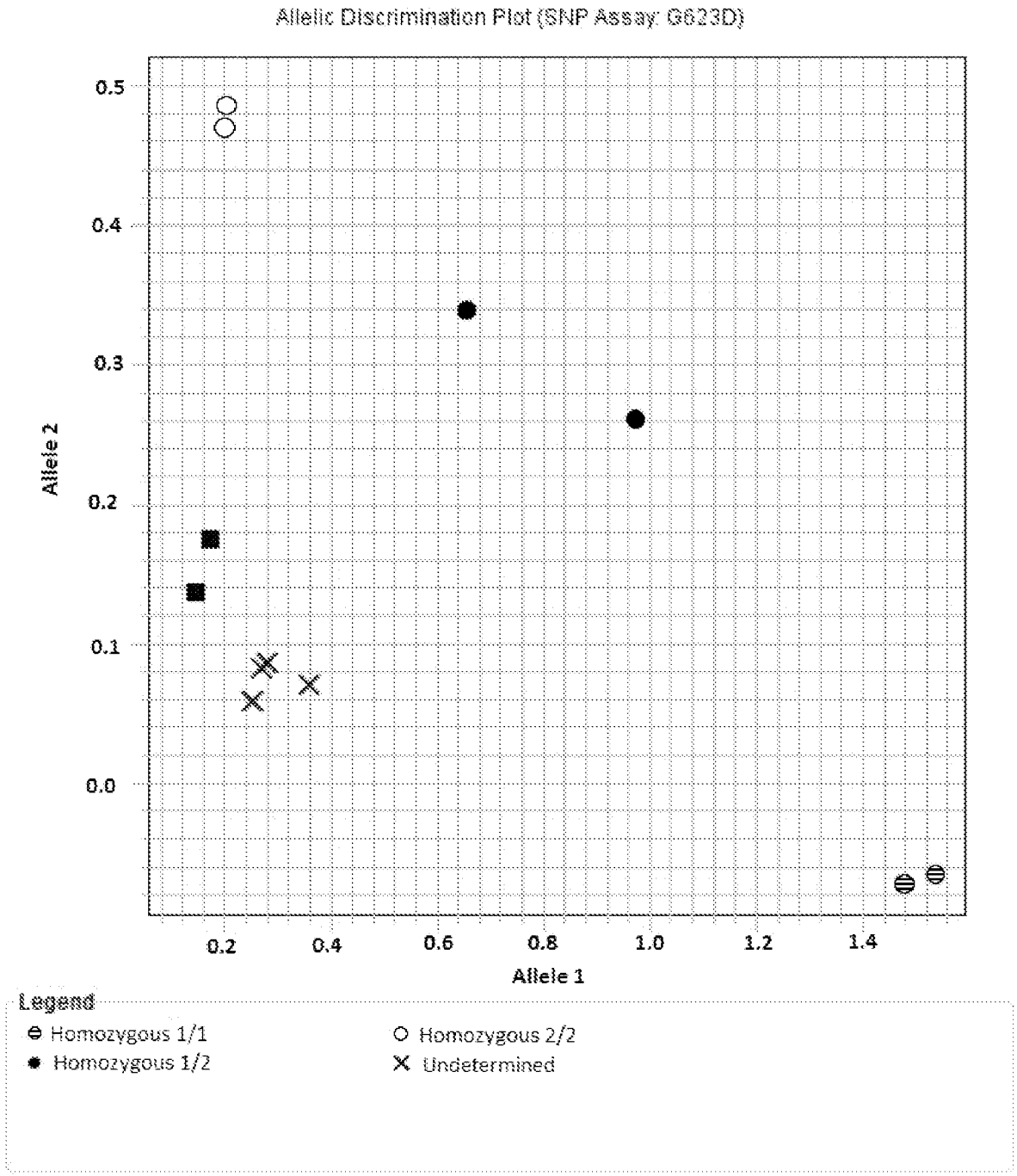
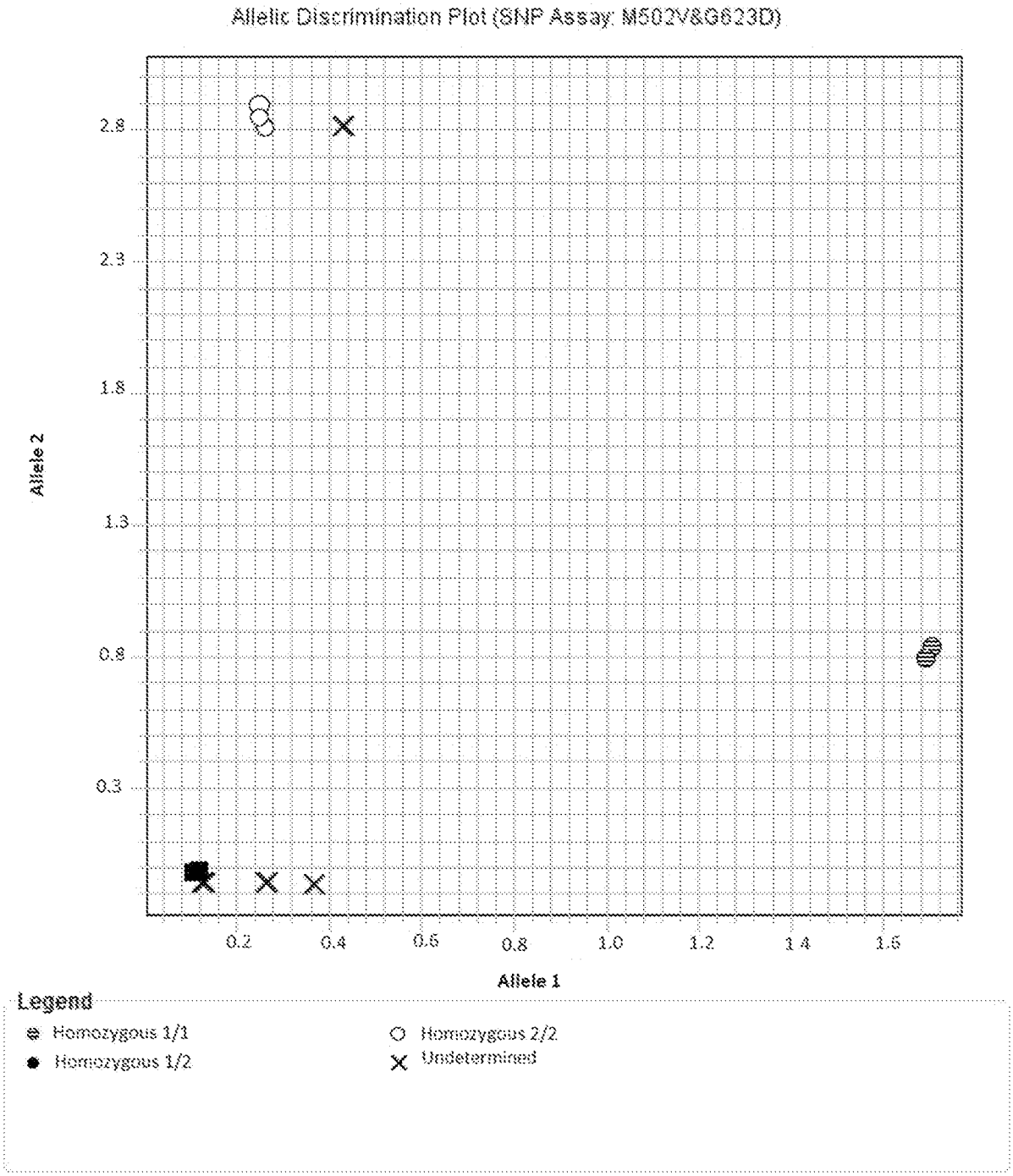


Figure 6B. M502V discrimination plot from the multiplexing experiment from Example 4.



INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2018/026962

A. CLASSIFICATION OF SUBJECT MATTER

IPC(8) - C12N 15/11; C12P 19/34; C12Q 1/68 (2018.01)

CPC - C12Q 1/6876; C12Q 1/6883; C12Q 2600/156; C12Q 2600/158; G01N 2800/16 (2018.05)

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

See Search History document

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

USPC - 435/6; 435/91.2; 536/23.1; 536/24.33; 536/24.3; 536/24.31 (keyword delimited)

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

See Search History document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2009/0305394 A1 (LEE et al) 10 December 2009 (10.12.2009) entire document	1
A	EVANS et al. "Genotype-Phenotype Correlation for TGFBI Corneal Dystrophies Identifies p.(G623D) as a Novel Cause of Epithelial Basement Membrane Dystrophy," Invest Ophthalmol Vis Sci, 01 October 2016 (01.10.2016), Vol. 57, Pgs. 5407-5414. entire document	1-4, 16
A	US 2012/0208196 A1 (HIRAI et al) 16 August 2012 (16.08.2012) entire document	1-4, 16
A	US 2014/0243222 A1 (LEE et al) 28 August 2014 (28.08.2014) entire document	1-4, 16
A	US 5,962,332 A (SINGER et al) 05 October 1999 (05.10.1999) entire document	1-4, 16
A	ZENG et al. "TGFBI Gene Mutation Analysis of Clinically Diagnosed Granular Corneal Dystrophy Patients Prior to PTK: A Pilot Study from Eastern China," Sci Rep, 04 April 2017 (04.04.2017), Vol. 7:596, Pgs. 1-5. entire document	1-4, 16

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
15 June 2018	11 JUL 2018
Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, VA 22313-1450 Facsimile No. 571-273-8300	Authorized officer Blaine R. Copenheaver PCT Helpdesk: 571-272-4300 PCT OSP: 571-272-7774

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2018/026962

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:

   a. ☒ forming part of the international application as filed:

      ☒ in the form of an Annex C/ST.25 text file.

      ☐ on paper or in the form of an image file.

   b. ☐ furnished together with the international application under PCT Rule 13*ter*.1(a) for the purposes of international search only in the form of an Annex C/ST.25 text file.

   c. ☐ furnished subsequent to the international filing date for the purposes of international search only:

      ☐ in the form of an Annex C/ST.25 text file (Rule 13*ter*.1(a)).

      ☐ on paper or in the form of an image file (Rule 13*ter*.1(b) and Administrative Instructions, Section 713).

2. ☐ In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that forming part of the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

SEQ ID NOs: 19-30, 33, 36, 50, and 54 were searched.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2018/026962

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☒ Claims Nos.: 5-15, 17-21
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.