

FILED

10 DEC 27 PM 4:06

CLERK, U.S. DISTRICT COURT
SOUTHERN DISTRICT OF CALIFORNIA

MTD
DEPUTY

1 Kurtis D. MacFerrin, California Bar No. 178006
2 Adam M. Tschop, California Bar No. 209767
3 Rip J. Finst, California Bar No. 234478
4 Life Technologies Corporation
5 5791 Van Allen Way
6 Carlsbad, California 92008
7 Telephone: (760)603-7200
8 Facsimile: (760)602-6500

6 Attorneys for Plaintiff
7 Life Technologies Corporation

8 UNITED STATES DISTRICT COURT
9 SOUTHERN DISTRICT OF CALIFORNIA

BY FAX

11 LIFE TECHNOLOGIES CORPORATION,
12 Plaintiff,
13 vs.
14 BIOSEARCH TECHNOLOGIES INC.,
15 Defendant

Case No.:

10 CV 2665 DMS

WVG

COMPLAINT

JURY TRIAL DEMANDED

18 Plaintiff Life Technologies Corporation ("Life Technologies") files this complaint
19 against Defendant Biosearch Technologies, Inc. ("Biosearch").

20 JURISDICTION AND VENUE

21 1. This is an action for patent infringement arising under the Patent Laws of the United
22 States, 35 U.S.C §§ 100, *et seq.* This court has subject matter jurisdiction over this action under
23 28 U.S.C. §§ 1331, 1332 and 1338(a). The Court has personal jurisdiction over the Defendant in
24 that it is a California corporation with a principal place of business within this state. In addition,
25
26
27
28

CR

1 Defendant regularly conducts business in this state and has committed acts in this judicial district
2 which give rise to this action.

3 2. Venue is proper in this judicial district pursuant to 28 U.S.C §§ 1391(b), (c) and 1400(b).
4 Plaintiff believes and based thereon alleges that Biosearch resides in this judicial district within
5 the meaning of 28 U.S.C §1391(c), and further, that Biosearch has committed, contributed to,
6 and/or induced acts of patent infringement in this judicial district and provides goods or services
7 and does business in this judicial district.
8

9 **PARTIES**

10 3. Life Technologies is a Delaware corporation, with a principal place of business at 5791
11 Van Allen Way, Carlsbad, California 92008.

12 4. Life Technologies is the assignee of U.S. Patent No. 7,160,997 (“the ‘997 Patent”),
13 entitled “Methods of using FET labeled oligonucleotides that include a 3’→5’ exonuclease
14 resistant quencher domain and compositions for practicing the same.”
15

16 5. Upon information and belief, Biosearch is a California corporation, with its principal
17 place of business at 81 Digital Drive, Novato, California 94949-5754.
18

19 6. Upon information and belief, Biosearch manufactures, offers for sale and sells
20 fluorescent-labeled probes for DNA analysis, including Defendant’s “BHQplus” probes.
21

22 **FIRST CLAIM FOR RELIEF**

23 **INFRINGEMENT OF UNITED STATES PATENT NO. 7,160,997**

24 7. Plaintiff realleges and incorporates by reference the allegations of paragraphs 1 through
25 6.

26 8. The ‘997 Patent issued on January 9, 2007. A true and correct copy of the ‘997 Patent is
27 attached hereto as Exhibit A.
28

1 9. Upon information and belief, Biosearch has directly infringed, contributorily infringed,
2 and/or actively induced infringement of one or more claims of the '997 Patent, and Biosearch is
3 continuing such infringement by practicing or causing others to practice one or more of the
4 inventions claimed in the '997 Patent. For example, Biosearch makes, uses, sells and/or offers
5 for sale fluorescent-labeled probes for DNA analysis, including Defendant's "BHQplus" probes,
6 that infringe one or more claims of the '997 Patent in this district and elsewhere in the United
7 States.
8

9 10. Plaintiff has suffered damages as a result of Biosearch's infringement and will continue
10 to suffer damages as a result of Biosearch's continued infringement.
11

12 11. Biosearch's infringement has caused and will, until enjoined, continue to cause
13 irreparable injury to Plaintiff for which there is no adequate remedy at law.

14 **DEMAND FOR JURY TRIAL**

15 12. Pursuant to Federal Rule of Civil Procedure 38, Plaintiff demands a jury trial on all issues
16 triable of right by a jury.
17

18 **PRAYER FOR RELIEF**

19 WHEREFORE, Plaintiff prays for judgment as follows:

- 20 a. that Biosearch be adjudged to have infringed the '997 Patent;
- 21 b. that an injunction be issued against further infringement of the '997 Patent by
22 Biosearch and its officers, agents, servants, employees and all persons in active
23 concert or participation with them;
- 24 c. that Biosearch account and pay actual damages, but no less than a reasonable royalty,
25 to Plaintiff to compensate it for Biosearch's infringement of the '997 Patent as
26 provided by 35 U.S.C. § 284;
27
28

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28

- d. that Biosearch pay interest and costs to Plaintiff as provided for by 35 U.S.C. § 284;
- e. the Plaintiff be granted such other and further relief as the Court deems just and equitable.

DATED: December 27, 2010

Respectfully submitted,

/s/Kurtis D. MacFerrin
KURTIS D. MACFERRIN

Attorneys for Plaintiff
Life Technologies Corporation

Exhibit A
'997 Patent



US007160997B2

(12) **United States Patent**
Chou et al.

(10) **Patent No.:** **US 7,160,997 B2**
(45) **Date of Patent:** **Jan. 9, 2007**

(54) **METHODS OF USING FET LABELED OLIGONUCLEOTIDES THAT INCLUDE A 3'→5' EXONUCLEASE RESISTANT QUENCHER DOMAIN AND COMPOSITIONS FOR PRACTICING THE SAME**

6,072,046 A * 6/2000 Reed et al. 536/23.1
6,117,635 A 9/2000 Nazarenko et al.
6,248,526 B1 6/2001 Weimer
6,660,845 B1 * 12/2003 Gall et al. 536/23.1

FOREIGN PATENT DOCUMENTS

(76) **Inventors:** **Qun Chou**, 4635 Via Aciando, Camarillo, CA (US) 93012; **Dragan Spasic**, 1310 Skyline Dr., Daly City, CA (US) 94015

EP 1275735 1/2003
WO WO 01/42505 5/2001
WO WO01/86001 6/2001
WO WO 200186001 A1 * 11/2001

OTHER PUBLICATIONS

(*) **Notice:** Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 146 days.

Chou, Q. et al. "Use of Dark-Quenched FRET probes in Real-Time PCR", *American Biotechnology Laboratory*, 19(8):34 (2001).

(21) **Appl. No.:** **10/222,943**

Kreuzer, K-A, et al. "Simultaneous Absolute Quantification of Target and Control Templates by Real-Time Fluorescence Reverse Transcription-PCR Using 4-(4-Dimethylaminophenylazo)benzoic Acid as a Dark Quencher Dye" *Clinical Chemistry*, 47(3):488-490 (2001).

(22) **Filed:** **Aug. 15, 2002**

EPO Supplemental Search Report, Mailed Mar. 14, 2006.

(65) **Prior Publication Data**

US 2003/0165920 A1 Sep. 4, 2003

* cited by examiner

Related U.S. Application Data

(63) Continuation-in-part of application No. 10/087,229, filed on Feb. 27, 2002, now Pat. No. 6,818,420.

Primary Examiner—Kenneth R. Horlick

Assistant Examiner—Young J. Kim

(74) *Attorney, Agent, or Firm*—Todd B. Buck; Castellano Malm Ferrario & Buck

(51) **Int. Cl.**

C07H 21/04 (2006.01)
C12Q 1/68 (2006.01)
C12P 19/34 (2006.01)

(57) **ABSTRACT**

(52) **U.S. Cl.** **536/24.3**; 435/6; 435/91.1; 435/91.2; 536/23.1; 536/24.3; 536/24.33

Methods and compositions are provided for detecting a primer extension product in a reaction mixture. In the subject methods, a primer extension reaction is conducted in the presence of a polymerase having 3'→5' exonuclease activity and at least one FET labeled oligonucleotide probe that includes a 3'→5' exonuclease resistant quencher domain. Also provided are systems and kits for practicing the subject methods. The subject invention finds use in a variety of different applications, and are particularly suited for use in high fidelity PCR based reactions, including SNP detection applications, allelic variation detection applications, and the like.

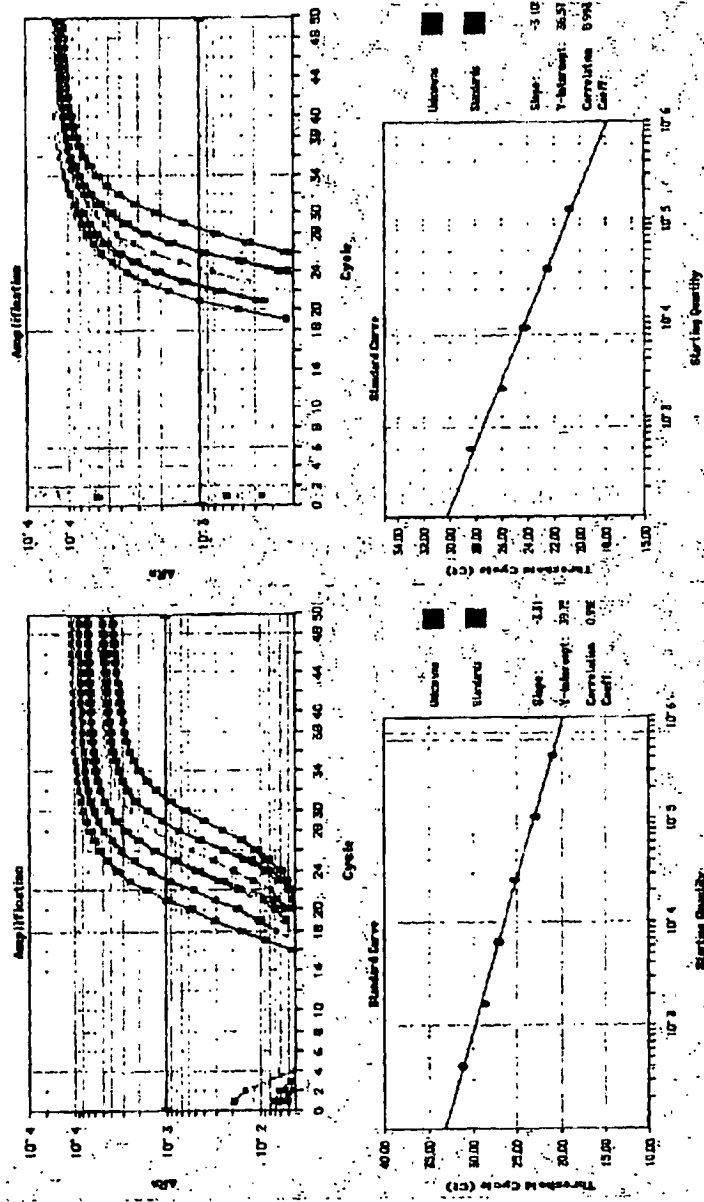
(58) **Field of Classification Search** 435/6, 435/91.1, 91.2; 536/23.1, 24.3, 24.33
See application file for complete search history.

(56) **References Cited**

U.S. PATENT DOCUMENTS

4,794,073 A * 12/1988 Dattagupta et al. 435/6
5,177,196 A * 1/1993 Meyer et al. 536/22.1
5,538,848 A * 7/1996 Livak et al. 435/6
5,840,493 A * 11/1998 Davis et al. 435/6

19 Claims, 9 Drawing Sheets



ACT-P1 Probe (TET/BHQ1): Real Time PCR using Taq + Pwo DNA Polymerase
Real Time PCR using Taq DNA Polymerase

Figure 1A

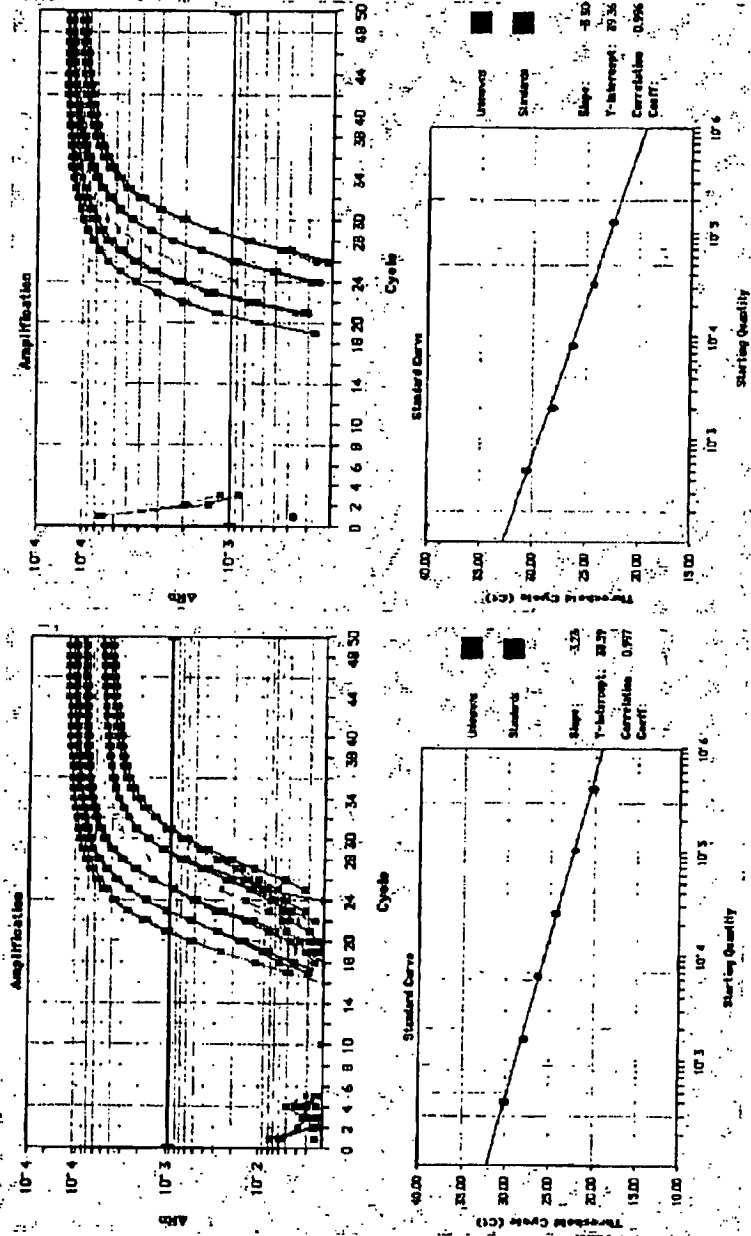
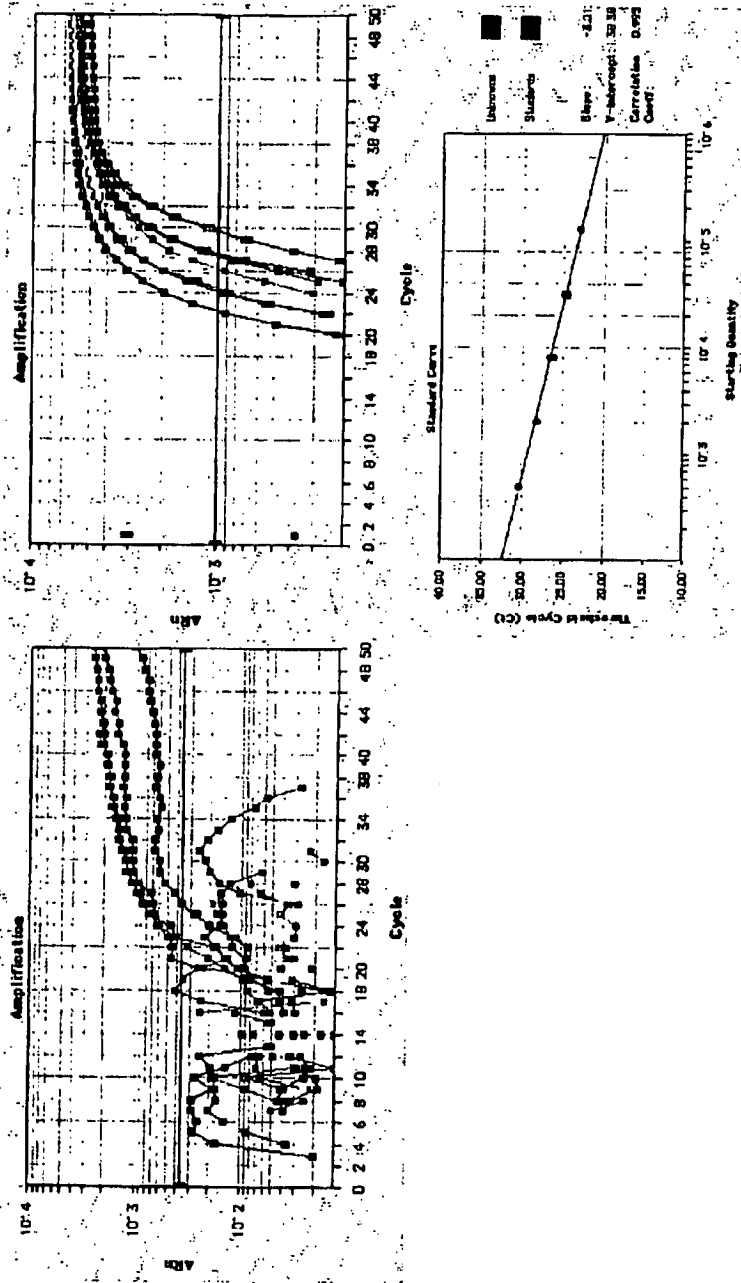


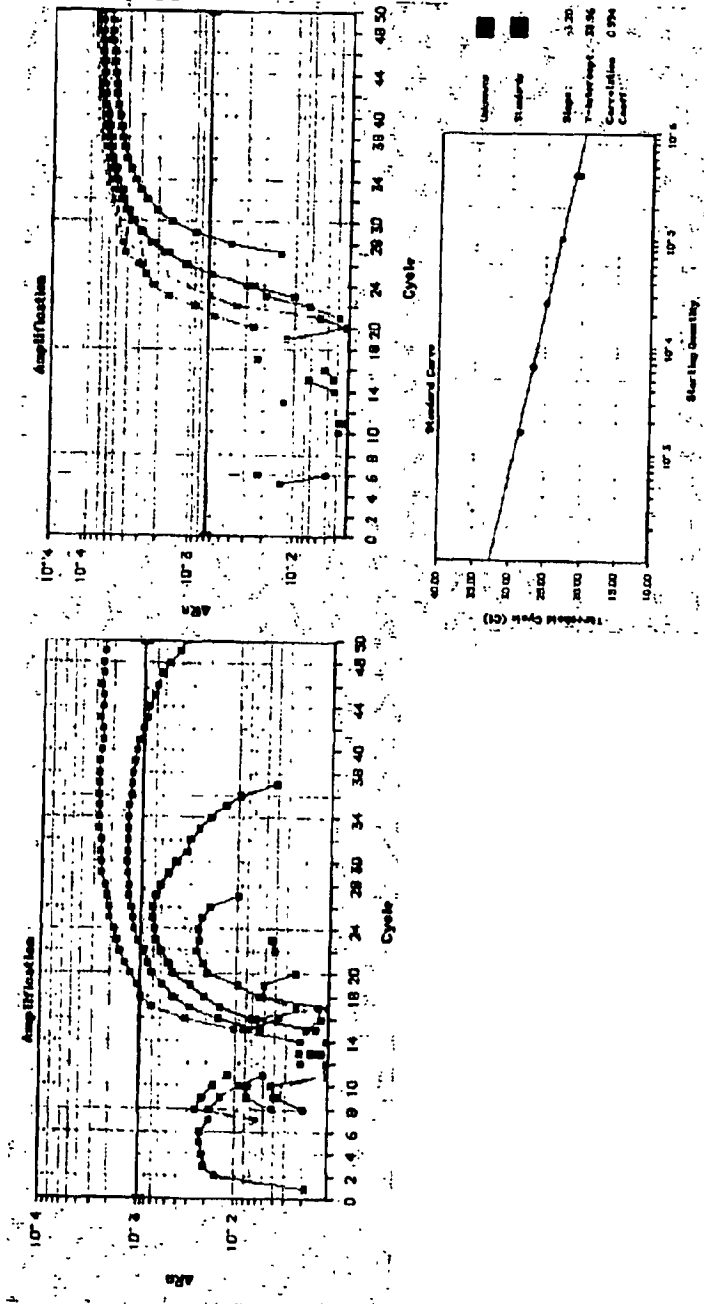
Figure 1B



ACT-P3 Probe (TET/Dabcyl):
Real Time PCR using Taq + Pwo DNA Polymerase

Real Time PCR using Taq DNA Polymerase

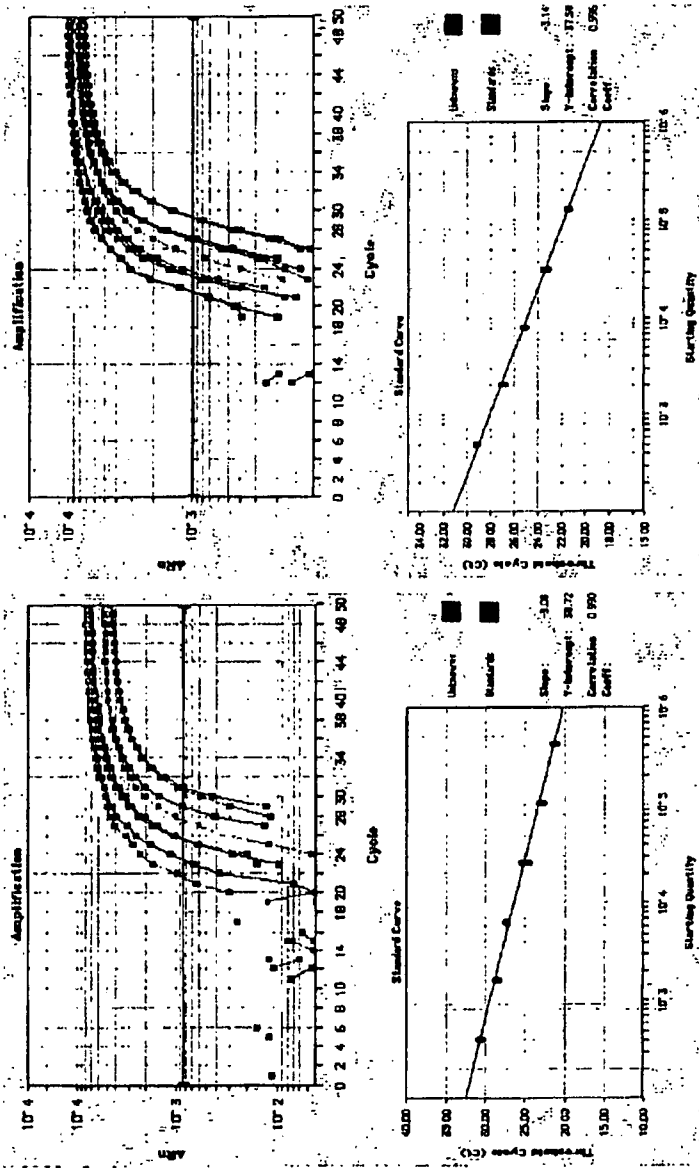
Figure 1C



ACT-P4 Probe (TET/TAMRA):
Real Time PCR using Taq + Pwo DNA Polymerase

Real Time PCR using Taq DNA Polymerase

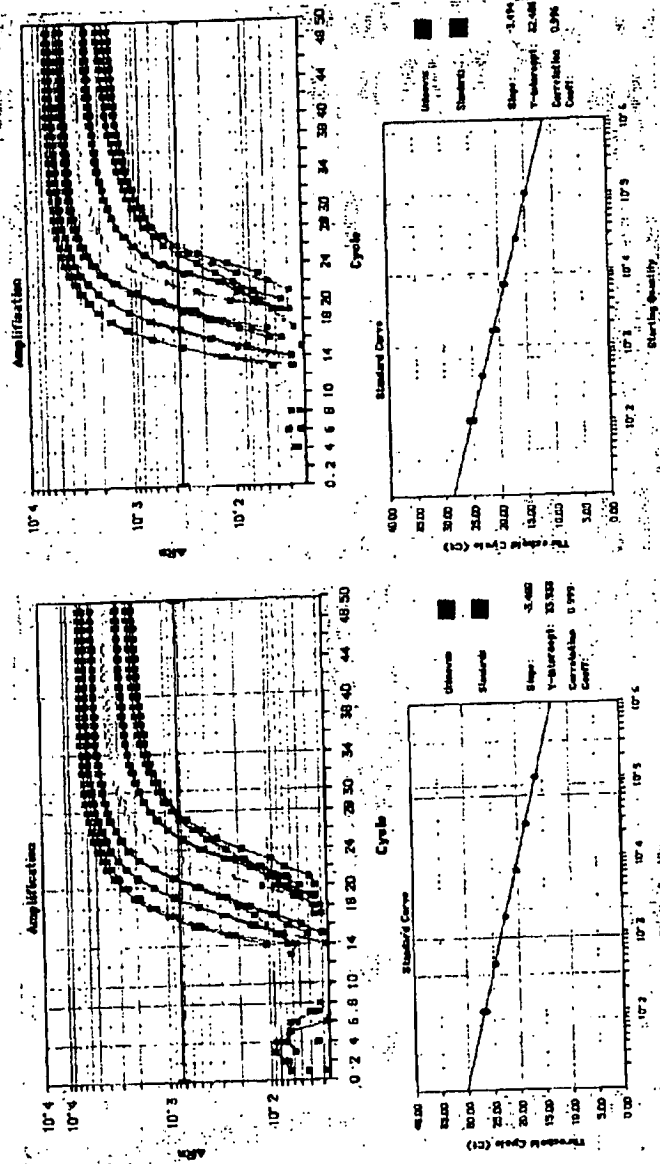
Figure 1D



ACT-PS Probe (1'ET/TAMRA S-oligo):
Real Time PCR using Taq + Pwo DNA Polymerase

Real Time PCR using Taq DNA Polymerase

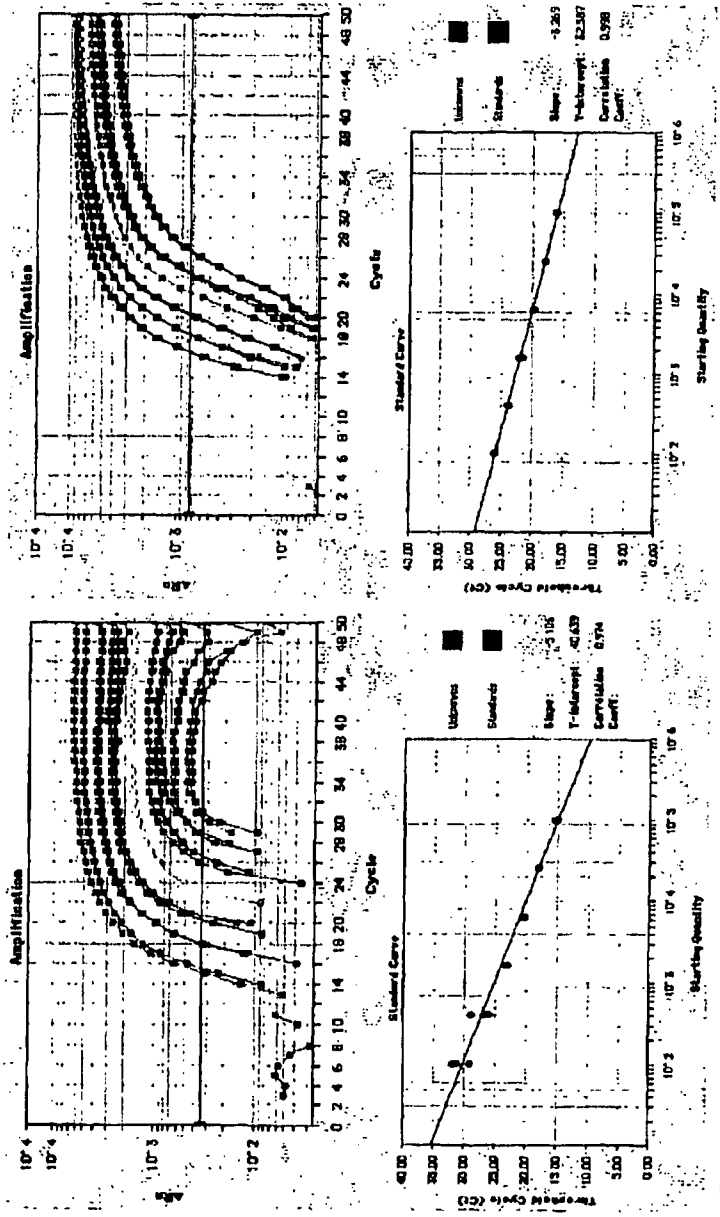
Figure 1E



Real Time PCR using Taq DNA Polymerase

BCL-2 Probe (FAM/BHQ1):
Real Time PCR using Taq + Pwo DNA Polymerase

Figure 2A



Real Time PCR using Taq DNA Polymerase

BCL-P4 Probe (FAM/TAMRA):
Real Time PCR using Taq + Pwo DNA Polymerase

Figure 2B

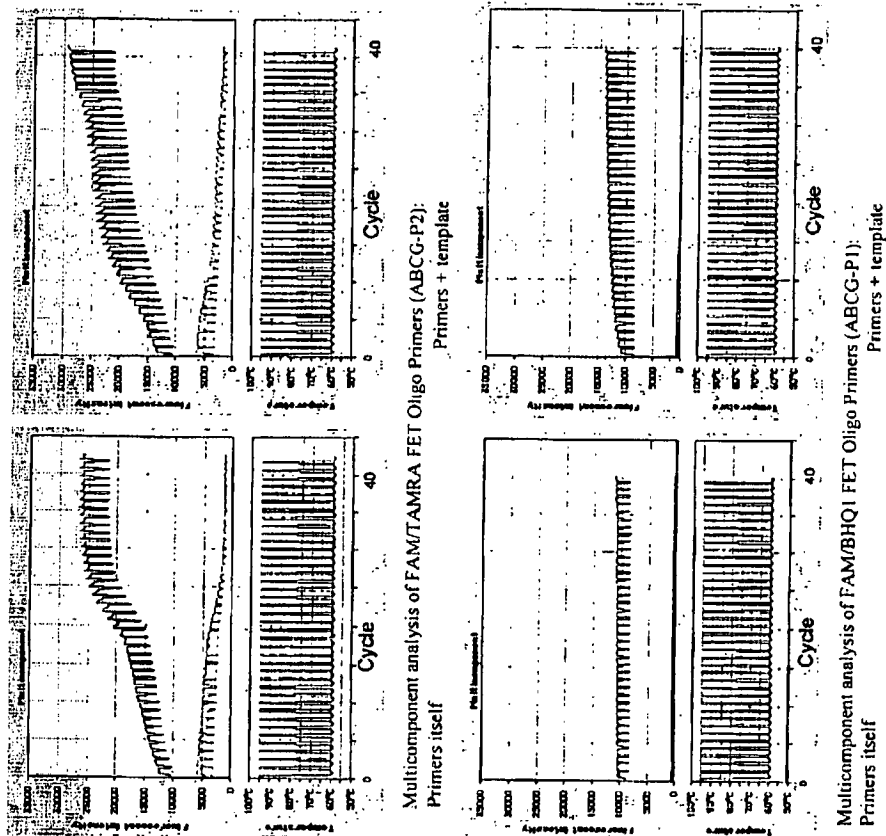


Figure 3

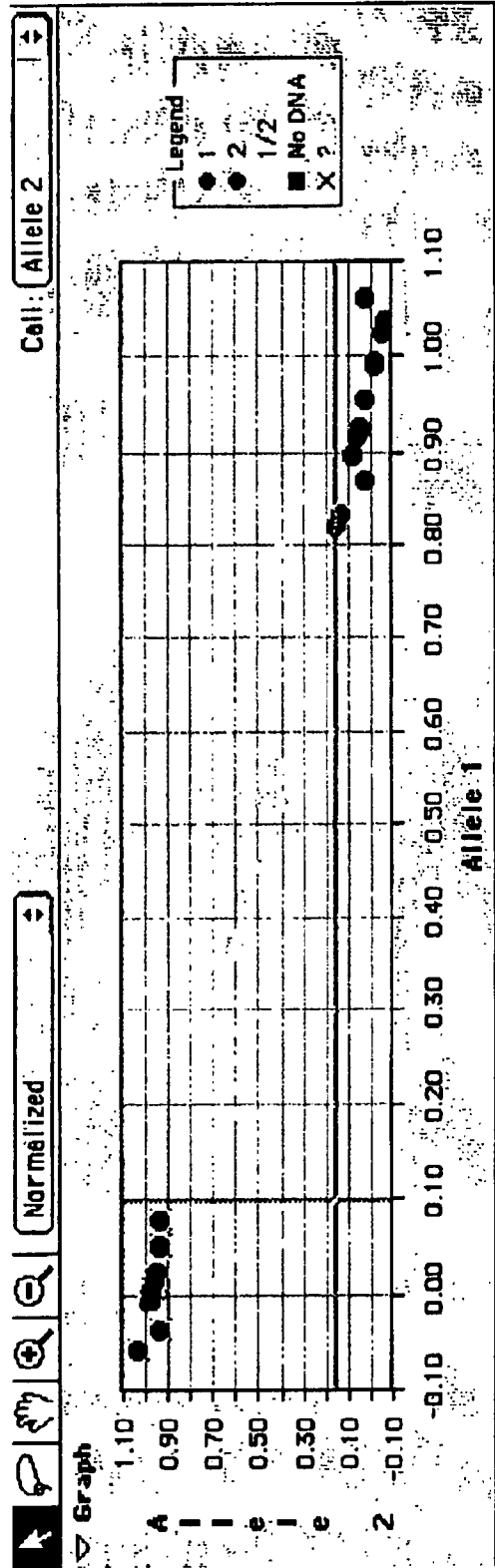


Figure 4

US 7,160,997 B2

1

**METHODS OF USING FET LABELED
OLIGONUCLEOTIDES THAT INCLUDE A
3'→5' EXONUCLEASE RESISTANT
QUENCHER DOMAIN AND COMPOSITIONS
FOR PRACTICING THE SAME**

**CROSS-REFERENCE TO RELATED
APPLICATIONS**

This application is a continuation-in-part of application Ser. No. 10/087,229 filed on Feb. 27, 2002 now U.S. Pat. No. 6,818,420, the disclosure of which is herein incorporated by reference.

INTRODUCTION

1. Technical Field

The technical field of this invention is the polymerase chain reaction (PCR); and particularly high fidelity real-time PCR.

2. Background of the Invention

The polymerase chain reaction (PCR) is a powerful method for the rapid and exponential amplification of target nucleic acid sequences. PCR has facilitated the development of gene characterization and molecular cloning techniques including the direct sequencing of PCR amplified DNA, the determination of allelic variation, and the detection of infectious and genetic disease disorders. PCR is performed by repeated cycles of heat denaturation of a DNA template containing the target sequence, annealing of opposing primers to the complementary DNA strands, and extension of the annealed primers with a DNA polymerase. Multiple PCR cycles result in the exponential amplification of the nucleotide sequence delineated by the flanking amplification primers.

An important modification of the original PCR technique was the substitution of *Thermus aquaticus* (Taq) DNA polymerase in place of the Klenow fragment of *E. coli* DNA pol I (Saiki, et al. Science, 230:1350-1354 (1988)). The incorporation of a thermostable DNA polymerase into the PCR protocol obviates the need for repeated enzyme additions and permits elevated annealing and primer extension temperatures which enhance the specificity of primer:template associations. Taq DNA polymerase thus serves to increase the specificity and simplicity of PCR.

Although Taq DNA polymerase is used in the vast majority of PCR performed today, it has a fundamental drawback: purified Taq DNA polymerase enzyme is devoid of 3' to 5' exonuclease activity and thus cannot excise misinserted nucleotides (Tindall, et al., Biochemistry, 29:5226-5231 (1990)). Consistent with these findings, the observed error rate (mutations per nucleotide per cycle) of Taq polymerase is relatively high; estimates range from 2×10^{-4} during PCR (Saiki et al., Science, 239:487-491 (1988); Keohavaong et al. Proc. Natl. Acad. Sci. USA, 86:9253-9257 (1989)) to 2×10^{-5} for base substitution errors produced during a single round of DNA synthesis of the lacZ gene (Eckert et al., Nucl. Acids Res. 18:3739-3744 (1990)).

Polymerase induced mutations incurred during PCR increase arithmetically as a function of cycle number. For example, if an average of two mutations occur during one cycle of amplification, 20 mutations will occur after 10 cycles and 40 will occur after 20 cycles. Each mutant and wild type template DNA molecule will be amplified exponentially during PCR and thus a large percentage of the resulting amplification products will contain mutations. Mutations introduced by Taq DNA polymerase during DNA

2

amplification have hindered PCR applications that require high fidelity DNA synthesis. Several independent studies suggest that 3' to 5' exonuclease-dependent proofreading enhances the fidelity of DNA synthesis (Reyland et al, J. Biol. Chem., 263:6518-6524, 1988; Kunkel et al, J. Biol. Chem., 261:13610-13616, 1986; Bernad et al, Cell, 58:219-228, 1989). As such, it is desirable, where possible, to include a 3' to 5' exonuclease-dependent proofreading activity in PCR based reactions. For example, if Taq DNA Polymerase (error rate 2×10^{-4}) is used to amplify a 100 bp sequence for 40 cycles by PCR, about 55% of the amplification products will contain one or more errors. In contrast, if a Pwo DNA Polymerase having proof-reading activities is used for the amplification, only 10% of the products will contain an error under the same conditions. The error rate produced by a mixture of Taq DNA Polymerase and a proofreading DNA Polymerase between these two values (Cline et al, Nucleic Acids Res., 24(18):3546-51, 1996).

In many PCR based reactions, a signal producing system is employed, e.g., to detect the production of amplified product. One type of signal producing system that is attractive for use in PCR based reactions is the fluorescence energy transfer (FET) system, in which a nucleic acid detector includes fluorescence donor and acceptor groups. FET label systems include a number of advantages over other labeling systems, including the ability to perform homogeneous assays in which a separation step of bound vs. unbound labeled nucleic acid detector is not required.

In such real time detection systems using a FET labeled nucleic acid detector, high fidelity amplification is critical. Any error in sequences where a FET labeled nucleic acid detector binds can cause probes not to bind or wrong probes to bind in the case of allele discrimination, resulting in weak signal or the wrong signal being produced. For example, if a 30 bp PCR fragment which is the target of a FET labeled probe is amplified using Taq DNA Polymerase for 40 cycles, about 22% of the amplification fragments will contain one or more errors. In contrast, if a Pwo DNA Polymerase having proof-reading activities is used for the amplification, only 3% of the amplification fragments will contain an error under the same conditions. Therefore, the standard low fidelity amplification can cause a decrease in sensitivity or mis-typing in the case of allele discrimination.

However, as discovered by the current invention a disadvantage of currently available FET labeled nucleic acids having TAMRA or Dabcyl as a quencher is that such nucleic acids are subject to 3'→5' exonuclease degradation. Accordingly, such FET labeled nucleic acids are not suitable for use in high fidelity PCR applications, where 3'→5' exonuclease activity, i.e., proofreading activity, is present.

As such, there is significant interest in the identification and development of FET labeled nucleic acids that can be used in high fidelity PCR applications.

Relevant Literature

U.S. Patents of interest include: U.S. Pat. Nos. 5,538,848 and 6,248,526. Also of interest are: WO 01/86001 and WO 01/42505.

SUMMARY OF THE INVENTION

Methods and compositions are provided for detecting a primer extension product in a reaction mixture. In certain embodiments of the subject methods, a primer extension reaction is conducted in the presence of a polymerase having 3'→5' exonuclease activity and at least one FET labeled oligonucleotide probe that includes a 3'→5' exonuclease resistant quencher domain. In certain embodiments a nucleic

US 7,160,997 B2

3

acid intercalator is covalently bonded to the FET labeled oligonucleotide. In certain embodiments, a minor groove binder is employed in the reaction. In these latter two embodiments, the polymerase may or may not include a 3'→5' exonuclease activity. Also provided are systems and kits for practicing the subject methods. The subject invention finds use in a variety of different applications, and is particularly suited for use in high fidelity PCR based reactions, including SNP detection applications, allelic variation detection applications, and the like.

Definitions

As used herein, "nucleic acid" means either DNA, RNA, single-stranded or double-stranded, and any chemical modifications thereof. Modifications include, but are not limited to, those which provide other chemical groups that incorporate additional charge, polarizability, hydrogen bonding, electrostatic interaction, and functionality to the nucleic acid. Such modifications include, but are not limited to, 2'-position sugar modifications, 5-position pyrimidine modifications, 8-position purine modifications, modifications at exocyclic amines, substitution of 4-thiouridine, substitution of 5-bromo or 5-iodo-uracil; backbone modifications, methylations, unusual base-pairing combinations such as the isobases isocytidine and isoguanidine and the like. Modifications can also include 3' and 5' modifications such as capping.

As used herein, "fluorescent group" refers to a molecule that, when excited with light having a selected wavelength, emits light of a different wavelength. Fluorescent groups may also be referred to as "fluorophores".

As used herein, "fluorescence-modifying group" refers to a molecule that can alter in any way the fluorescence emission from a fluorescent group. A fluorescence-modifying group generally accomplishes this through an energy transfer mechanism. Depending on the identity of the fluorescence-modifying group, the fluorescence emission can undergo a number of alterations, including, but not limited to, attenuation, complete quenching, enhancement, a shift in wavelength, a shift in polarity, a change in fluorescence lifetime. One example of a fluorescence-modifying group is a quenching group.

As used herein, "energy transfer" refers to the process by which the fluorescence emission of a fluorescent group is altered by a fluorescence-modifying group. If the fluorescence-modifying group is a quenching group, then the fluorescence emission from the fluorescent group is attenuated (quenched). Energy transfer can occur through fluorescence resonance energy transfer, or through direct energy transfer. The exact energy transfer mechanisms in these two cases are different. It is to be understood that any reference to energy transferee in the instant application encompasses all of these mechanistically-distinct phenomena. Energy transfer is also referred to herein as fluorescent energy transfer or FET.

As used herein, "energy transfer pair" refers to any two, molecules that participate in energy transfer. Typically, one of the molecules acts as a fluorescent group, and the other acts as a fluorescence-modifying group. The preferred energy transfer pair of the instant invention comprises a fluorescent group and a quenching group. In some cases, the distinction between the fluorescent group and the fluorescence-modifying group may be blurred. For example, under certain circumstances, two adjacent fluorescein groups can quench one another's fluorescence emission via direct energy transfer. For this reason, there is no limitation on the identity of the individual members of the energy transfer pair in this application. All that is required is that the

4

spectroscopic properties of the energy transfer pair as a whole change in some measurable way if the distance between the individual members is altered by some critical amount.

"Energy transfer pair" is used to refer to a group of molecules that form a single complex within which energy transfer occurs. Such complexes may comprise, for example, two fluorescent groups which may be different from one another and one quenching group, two quenching groups and one fluorescent group, or multiple fluorescent groups and multiple quenching groups. In cases where there are multiple fluorescent groups and/or multiple quenching groups, the individual groups may be different from one another.

As used herein, "quenching group" refers to any fluorescence-modifying group that can attenuate at least partly the light emitted by a fluorescent group. We refer herein to this attenuation as "quenching". Hence, illumination of the fluorescent group in the presence of the quenching group leads to an emission signal that is less intense than expected, or even completely absent. Quenching occurs through energy transfer between the fluorescent group and the quenching group.

As used herein, "fluorescence resonance energy transfer" or "FRET" refers to an energy transfer phenomenon in which the light emitted by the excited fluorescent group is absorbed at least partially by a fluorescence-modifying group. If the fluorescence-modifying group is a quenching group, then that group can either radiate the absorbed light as light of a different wavelength, or it can dissipate it as heat. FRET depends on an overlap between the emission spectrum of the fluorescent group and the absorption spectrum of the quenching group. FRET also depends on the distance between the quenching group and the fluorescent group. Above a certain critical distance, the quenching group is unable to absorb the light emitted by the fluorescent group, or can do so only poorly.

As used herein "direct energy transfer" refers to an energy transfer mechanism in which passage of a photon between the fluorescent group and the fluorescence-modifying group does not occur. Without being bound by a single mechanism, it is believed that in direct energy transfer, the fluorescent group and the fluorescence-modifying group interfere with each others electronic structure. If the fluorescence-modifying group is a quenching group, this will result in the quenching group preventing the fluorescent group from even emitting light.

In general, quenching by direct energy transfer is more efficient than quenching by FRET. Indeed, some quenching groups that do not quench particular fluorescent groups by FRET (because they do not have the necessary spectral overlap with the fluorescent group) can do so efficiently by direct energy transfer. Furthermore, some fluorescent groups can act as quenching groups themselves if they are close enough to other fluorescent groups to cause direct energy transfer. For example, under these conditions, two adjacent fluorescein groups can quench one another's fluorescence effectively. For these reasons, there is no limitation on the nature of the fluorescent groups and quenching groups useful for the practice of this invention.

An example of "stringent hybridization conditions" is hybridization at 50° C. or higher and 6.0xSSC (900 mM NaCl/90 mM sodium citrate). Another example of stringent hybridization conditions is overnight incubation at 42° C. or higher in a solution: 50% formamide, 6xSSC (900 mM NaCl, 90 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 10% dextran sulfate, and 20 µg/ml denatured,

US 7,160,997 B2

5

sheared salmon sperm DNA. Stringent hybridization conditions are hybridization conditions that are at least as stringent as the above representative conditions, where conditions are considered to be at least as stringent if they are at least about 80% as stringent typically at least about 90% as stringent as the above specific stringent conditions. Other stringent hybridization conditions are known in the art and, may also be employed.

As used herein, the term "nucleic acid intercalator" refers to a molecule that binds to a nucleic acid by inserting itself in between base pairs of adjacent nucleotides without unwinding and without extension of the nucleic acid helix. In general, nucleic acid intercalators are aromatic compounds having a flat configuration, and are preferably polycyclic.

As used herein, the term "minor groove binder" refers to a molecule that binds to a nucleic acid by inserting itself into the minor groove of a DNA helix. In general, minor groove binders are capable of binding within the minor groove of a DNA helix with an association constant of $10^3 M^{-1}$ or greater. In addition, minor groove binders generally have crescent shaped three-dimensional structures.

As used herein, "3' end" means at any location on the oligonucleotide from and including the 3' terminus to the center of the oligonucleotide, usually at any location from and including the 3' terminus to about 10 bp from the 3' terminus, and more usually at any location from and including the 3' terminus to about 5 bp from the 3' terminus.

As used herein, "5' end" means at any location on the oligonucleotide from and including the 5' terminus to the center of the oligonucleotide, usually at any location from and including the 5' terminus to about 10 bp from the 5' terminus, and more usually at any location from and including the 5' terminus to about 5 bp from the 5' terminus.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGS. 1A to 1E provide graphical results of assays comparing the function of various TET labeled FET probes under high fidelity and standard PCR conditions.

FIGS. 2A to 2B provide graphical results of assays comparing the function of FAM/BHQ1 FET probe and FAM/TAMRA FET probe under high fidelity and standard PCR conditions.

FIG. 3 provides graphical results of a multicomponent analysis of a FAM/TAMRA FET oligo primer and a FAM/BHQ1 FET oligo primer.

FIG. 4 provides graphical results of assays for allele discrimination using FAM and TET labeled FET probes under high fidelity PCR conditions.

DESCRIPTION OF THE SPECIFIC EMBODIMENTS

Methods and compositions are provided for detecting a primer extension product in a reaction mixture. In certain embodiments of subject methods, a primer extension reaction is conducted in the presence of a polymerase having 3'→5' exonuclease activity and at least one FET labeled oligonucleotide probe that includes a 3'→5' exonuclease resistant quencher domain. In certain embodiments, a nucleic acid intercalator covalently bonded to said FET labeled oligonucleotide. In certain embodiments, a minor groove binder is employed in the reaction. In these latter two embodiments, the polymerase employed may or may not have 3'→5' exonuclease activity. Also provided are systems and kits for practicing the subject methods. The subject invention finds use in a variety of different applications, and

6

is particularly suited for use in high fidelity PCR based reactions, including SNP detection applications, allelic variation detection applications, and the like.

Before the subject invention is described further, it is to be understood that the invention is not limited to the particular embodiments of the invention described below, as variations of the particular embodiments may be made and still fall within the scope of the appended claims. It is also to be understood that the terminology employed is for the purpose of describing particular embodiments, and is not intended to be limiting. Instead, the scope of the present invention will be established by the appended claims.

In this specification and the appended claims, the singular forms "a," "an" and "the" include plural reference unless the context clearly dictates otherwise. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs.

Where a range of values is provided, it is understood that each intervening value, to the tenth of the unit of the lower limit unless the context clearly dictates otherwise, between the upper and lower limit of that range, and any other stated or intervening value in that stated range, is encompassed within the invention. The upper and lower limits of these smaller ranges may independently be included in the smaller ranges, and are also encompassed within the invention, subject to any specifically excluded limit in the stated range. Where the stated range includes one or both of the limits, ranges excluding either or both of those included limits are also included in the invention.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs. Although any methods, devices and materials similar or equivalent to those described herein can be used in the practice or testing of the invention, the preferred methods, devices and materials are now described.

All publications mentioned herein are incorporated herein by reference for the purpose of describing and disclosing those components that are described in the publications that might be used in connection with the presently described invention.

As summarized above, the subject invention provides methods of detecting the production of a primer extension product in a primer extension reaction mixture by using a FET labeled oligonucleotide probe. In further describing the subject invention, the methods are described first in greater detail, followed by a review of representative specific applications in which the methods finds use, as well as systems and kits that find use in practicing the subject methods.

Methods

As summarized above, the subject invention provides methods for detecting the production of primer extension products in a primer extension reaction mixture. In other words, the subject invention provides methods of determining whether primer extension products are produced in a primer extension reaction. By primer extension product is meant a nucleic acid molecule that results from a template dependent primer extension reaction. Template dependent primer extension reactions are those reactions in which a polymerase extends a nucleic acid primer molecule that is hybridized to a template nucleic acid molecule, where the sequence of bases that is added to the terminus of the primer nucleic acid molecule is determined by the sequence of bases in the template strand. Template dependent primer extension reactions include both amplification and non-

US 7,160,997 B2

7

amplification primer extension reactions. In many embodiments of the subject invention, the template dependent primer extension reaction in which the production of primer extension products is detected is an amplification reaction, e.g., a polymerase chain reaction (PCR).

A feature of certain embodiments of the subject methods is that the template dependent primer extension reaction in which the production of primer extension products is detected is a "high fidelity" reaction. By "high fidelity" reaction is meant that the reaction has a low error rate, i.e., a low rate of wrong nucleotide incorporation. As such, the error rate of the subject reactions is typically less than about 2×10^{-4} , usually less than about 1×10^{-5} and more usually less than about 1×10^{-6} . In other embodiments, the reaction mixture is not a high fidelity reaction mixture.

Preparation of High Fidelity Reaction Mixture

In practicing the subject methods of these embodiments, the first step is to produce a "high fidelity" primer extension mixture, e.g., a composition of matter that includes, all of the elements necessary for a high fidelity primer extension reaction to occur, where the primer extension mixture further includes at least one FET, labeled oligonucleotide that includes a 3'→5' exonuclease resistant quencher domain.

FET occurs when a suitable fluorescent energy donor and an energy acceptor moiety are in close proximity to one another. The excitation energy absorbed by the donor is transferred to the acceptor which can then further dissipate this energy either by fluorescent emission if a fluorophore, or by non-fluorescent means if a quencher. A donor-acceptor pair comprises two fluorophores having overlapping spectra, where the donor emission overlaps the acceptor absorption, so that there is energy transfer from the excited fluorophore to the other member of the pair. It is not essential that the excited fluorophore actually fluoresce, it being sufficient that the excited fluorophore be able to efficiently absorb the excitation energy and efficiently transfer it to the emitting fluorophore.

As such, the FET labeled oligonucleotides employed in the subject methods are nucleic acid detectors that include a fluorophore domain where the fluorescent energy donor, i.e., donor, is positioned and an acceptor domain where the fluorescent energy acceptor, i.e., acceptor, is positioned. As mentioned above, the donor domain includes the donor fluorophore. The donor fluorophore may be positioned anywhere in the nucleic acid detector, but is typically present at the 5' terminus of the detector.

The acceptor domain includes the fluorescence energy acceptor. The acceptor may be positioned anywhere in the acceptor domain, but is typically present at the 3' terminus of the nucleic acid detector.

In addition to the fluorophore and acceptor domains, the FET labeled oligonucleotides also include a target nucleic acid binding domain, which binds to a target nucleic acid sequence, e.g., under stringent hybridization conditions (as defined above). This target binding domain typically ranges in length from about 10 to about 60 nt, usually from about 15 to about 30 nt. Depending on the nature of the oligonucleotide and the assay itself, the target binding domain may hybridize to a region of the template nucleic acid or a region of the primer extension product. For example, where the assay is a 5' nuclease assay, e.g., in which a Taqman type oligonucleotide probe is employed, the target binding domain hybridizes under stringent conditions to a target binding site of the template nucleic acid, which is downstream or 3' of the primer binding site. In alternative embodiments, e.g., in molecular beacon type assays, the target binding domain hybridizes to a domain of a primer extension product.

8

The overall length of the FET labeled oligonucleotides, which includes all three domains mentioned above, typically ranges from about 10 to about 60 nt, usually from about 15 to about 30 nt.

The donor fluorophore of the subject probes is typically one that is excited efficiently by a single light source of narrow bandwidth, particularly a laser source. The emitting or accepting fluorophores are selected to be able to receive the energy from the donor fluorophore and emit light. Usually the donor fluorophores will absorb in the range of about 350–800 nm, more usually in the range of about 350–600 nm or 500–750 nm. The transfer of the optical excitation from the donor to the acceptor depends on the distance between the two fluorophores. Thus, the distance must be chosen to provide efficient energy transfer from the donor to the acceptor. The distance between the donor and acceptor moieties on the FET oligonucleotides employed in the subject invention, at least in certain configurations (such as upon intramolecular association) typically ranges from about 10 to about 100 angstroms

The fluorophores for FET pairs may be selected so as to be from a similar chemical family or a different one, such as cyanine dyes, xanthenes or the like. Fluorophores of interest include, but are not limited to: fluorescein dyes (e.g., 5-carboxyfluorescein (5-FAM), 6-carboxyfluorescein (6-FAM), 2',4',1,4,-tetrachlorofluorescein (TET), 2',4', 5',7', 1,4-hexachlorofluorescein (HEX), and 2',7'-dimethoxy-4', 5'-dichloro-6-carboxyfluorescein (JOE)), cyanine dyes such as Cy5, dansyl derivatives, rhodamine dyes (e.g., tetramethyl-6-carboxyrhodamine (TAMRA), and tetrapropano-6-carboxyrhodamine (ROX)), DABSYL, DABCYL, cyanine, such as Cy3, anthraquinone, nitrothiazole, and nitroimidazole compounds, and the like. Fluorophores of interest are further described in WO 01/42505 and WO 01/86001, as well as the priority U.S. Applications of these documents the disclosures of the latter of which are herein incorporated by reference.

A feature of the subject FET labeled oligonucleotides is that they are 3'→5' exonuclease resistant. As such, they are not degraded by 3'→5' exonucleases, i.e., enzymes having 3'→5' exonuclease activity. The 3'→5' exonuclease resistance of the subject FET labeled oligonucleotides may arise from the presence of the acceptor moiety present in the acceptor domain of the FET labeled oligonucleotide. In many, though not all embodiments, the acceptor moiety is present at the 3' terminus of the acceptor domain, and in many embodiments at the 3' terminus of the FET labeled oligonucleotide as a whole.

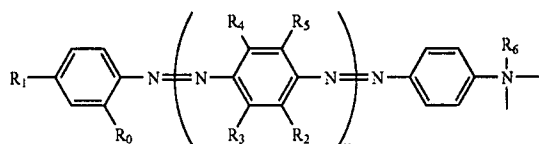
Any acceptor or donor that imparts 3'→5' exonuclease resistance onto the FET labeled oligonucleotides may be employed. In many embodiments, the acceptor moiety is a quencher molecule, e.g., a molecule that absorbs transferred energy but does not emit fluorescence, e.g., a dark quencher. In many embodiments, the dark quencher has maximum absorbance of between about 400 and about 700 nm, and often between about 500 and about 600 nm.

In certain embodiments, the dark quencher comprises a substituted 4-(phenyldiazenyl)phenylamine structure, often comprising at least two residues selected from aryl, substituted aryl, heteroaryl, substituted heteroaryl and combination thereof, wherein at least two of said residues are covalently linked via an exocyclic diazo bond.

US 7,160,997 B2

9

In certain embodiments, the dark quencher is described by the following formula:



wherein:

$R_0, R_1, R_2, R_3, R_4, R_5$ are independently: —H, halogen, — $O(CH_2)_nCH_3$, — $(CH_2)_nCH_3$, — NO_2 , SO_3 , — $N[(CH_2)_nCH_3]_2$ wherein $n=0$ to 5 or —CN; R_6 is —H or — $(CH_2)_nCH_3$ where $n=0$ to 5; and v is a number from 0 to 10.

Dark quenchers of interest are further described in WO 01/42505 and WO 01/86001, as well as the priority U.S. Applications of these documents, the disclosures of the latter of which are herein incorporated by reference.

The FET labeled oligonucleotide may be structured in a variety of different ways, so long as it includes the above-described donor, acceptor and target nucleic acid binding domains. Typically, the FET labeled oligonucleotide is structured such that energy transfer occurs between the fluorophore and acceptor of the FET labeled oligonucleotide probe upon fluorophore excitation when the FET labeled oligonucleotide is not hybridized to target nucleic acid.

In certain embodiments, the oligonucleotide is a single stranded molecule that does not form intramolecular structures and in which energy transfer occurs because the spacing of the donor and acceptor provides for energy transfer in the single stranded linear format. In these embodiments, energy transfer also occurs between the fluorophore and acceptor of FET labeled oligonucleotide probe upon fluorophore excitation when the FET labeled oligonucleotide probe is hybridized to a target nucleic acid. Specific examples of such FET labeled oligonucleotide probes include the Taqman™ type probes, as described in U.S. Pat. No. 6,248,526, the disclosure of which is herein incorporated by reference (as well as Held et al., *Genome Res.* (1996) 6:986–994; Holland et al., *Proc. Nat'l Acad. Sci. USA* (1991) 88:7276–7280; and Lee et al., *Nuc. Acids Res.* (1993) 21:3761–3766 (1993)). In many of these embodiments, the target nucleic acid binding domain is one that hybridizes to, i.e., is complementary to, a sequence of the template nucleic acid, i.e., the target nucleic acid of the target nucleic acid binding domain is a sequence present in the template nucleic acid.

In other embodiments, the probe oligonucleotides are structured such that energy transfer does not occur between the fluorophore and acceptor of said FET labeled oligonucleotide probe upon fluorophore excitation when the FET labeled oligonucleotide probe is hybridized to a target nucleic acid. Examples of these types of probe structures include: Scorpion probes (as described in Whitcombe et al., *Nature Biotechnology* (1999) 17:804–807; U.S. Pat. of which is herein incorporated by reference), Sunrise probes (as described in Nazarenko et al., *Nuc. Acids Res.* (1997) 25:2516–2521; U.S. Pat. No. 6,117,635, the disclosure of which is herein incorporated by reference), Molecular Beacons (Tyagi et al., *Nature Biotechnology* (1996) 14:303–308; U.S. Pat. No. 5,989,823, the disclosure of which is incorporated herein by reference), and conformationally assisted probes (as described in provisional application Ser. No. 60/138,376, the disclosure of which is herein

10

incorporated by reference). In many of these embodiments, the target binding sequence or domain comprises a hybridization domain complementary to a sequence of the primer extension product.

Since the primer extension reaction mixture produced in the initial step of the subject methods of these particular embodiments is a high fidelity primer extension reaction mixture, it further includes an enzyme having 3'→5' exonuclease activity. In many embodiments, the 3'→5' exonuclease is a polymerase that has 3'→5' exonuclease activity. In many embodiments, the high fidelity nature of the reaction mixture is provided by the presence of a combination of two or more polymerases, at least one of which includes a 3'→5' exonuclease. In certain embodiments, e.g., in 5' nuclease applications, care is taken to ensure that a polymerase having 5'→3' nuclease activity is also included. In many embodiments, the polymerase combination employed includes at least one Family A polymerase and, in many embodiments, a Family A polymerase and a Family B polymerase, where the terms "Family A" and "Family B" correspond to the classification scheme reported in Braithwaite & Ito, *Nucleic Acids Res.* (1993) 21:787–802. Family A polymerases of interest include *Thermus aquaticus* polymerases, including the naturally occurring polymerase (Taq) and derivatives and homologues thereof, such as KlenTaq (as described in *Proc. Natl. Acad. Sci. USA* (1994) 91:2216–2220); *Thermus thermoophilus* polymerases, including the naturally occurring polymerase (Tth) and derivatives and homologues thereof, and the like. Family B polymerases of interest include *Thermococcus litoralis* DNA polymerase (Vent) as described in Perler et al., *Proc. Natl. Acad. Sci. USA* (1992) 89:5577; *Pyrococcus* species GB-D (Deep Vent); *Pyrococcus furiosus* DNA polymerase (Pfu) as described in Lundberg et al., *Gene* (1991) 108:1–6, *Pyrococcus woesei* (Pwo) and the like. Of the two types of polymerases employed, the Family A polymerase will typically be present in the reaction mixture in an amount greater than the Family B polymerase, where the difference in activity will usually be at least 10-fold, and more usually at least about 100-fold. Accordingly, the reaction mixture typically comprise from about 0.1 U/μl to 1 U/μl Family A polymerase, usually from about 0.2 to 0.5 U/μl Family A polymerase, while the amount of Family B polymerase will typically range from about 0.01 mU/μl to 10 mU/μl, usually from about 0.05 to 1 mU/μl and more usually from about 0.1 to 0.5 mU/μl, where "U" corresponds to incorporation of 10 nmoles dNTP into acid-insoluble material in 30 min at 74° C.

In certain embodiments, a nucleic acid intercalator is present in the reaction mixture. In certain of these embodiments, the nucleic acid intercalator is bonded to the FET probe, such that it is stably associated with the FET probe under the conditions of use. In many of these embodiments, the FET probes employed in the subject invention include a nucleic acid intercalator covalently bonded to the FET labeled oligonucleotide.

The nucleic acid intercalators of interest function to stabilize the nucleic acid helix formed from the FET labeled oligonucleotide. Covalent binding of nucleic acid intercalators of interest also serve to increase hybrid stability by providing additional binding energy. Furthermore, nucleic acid intercalators of interest provide the FET labeled oligonucleotide greater affinity for its complementary sequence. In addition, nucleic acid intercalators provides exonuclease activity resistance when added to the 3' end of said FET labeled oligonucleotide. The nucleic acid intercalator component of the FET probes of this embodiment may be

US 7,160,997 B2

11

located at any location of the FET probe, e.g., at the 3' end or the 5' end of said FET labeled oligonucleotide, where in many embodiments the intercalator is covalently bonded to the 3' end, e.g., within at least about 10, such as within about 5 nt residues of the 3' end.

In general, nucleic acid intercalators of interest are aromatic compounds having a flat configuration. They may be cyclic, or polycyclic, particularly polycyclic aromatic having at least two rings, usually at least three rings and not more than about six rings, more usually not more than about five rings, where at least two of the rings are fused, usually at least three of the rings are fused, and usually not more than four of the rings being fused. The aromatic compound may be carbocyclic or heterocyclic, particularly having from one to three, more usually one to two nitrogen atoms as heteroannular atoms. Other heteroannular atoms may include oxygen and sulfur (chalcogen). The rings may be substituted by a wide variety of substituents, which substituents may include alkyl groups of from one to four carbon atoms, usually from one to two carbon atoms, oxy, which includes hydroxy, alkoxy and carboxy ester, generally of from one to four carbon atoms, amino, including mono- and disubstituted amino, particularly mono- and dialkyl amino, of from 0 to 8, usually 0 to 6 carbon atoms, thio, particularly alkylthio from 1 to 4, usually 1 to 2 carbon atoms, cyano, non-oxo-carbonyl, such as carboxy and derivatives thereof, particularly carboxamide or carboxyalkyl, of from 1 to 8 or 1 to 6 carbon atoms, usually 2 to 6 carbon atoms and more usually 2 to 4 carbon atoms, oxo-carbonyl or acyl, generally from 1 to 4 carbon atoms, halo, particularly of atomic number 9 to 35, etc.

Polycyclic compounds which find use as nucleic acid intercalators include acridines, phenanthridines, porphyrins, phenylindoles, and bisbenzamides.

The intercalator may be covalently bonded to the FET labeled oligonucleotide using any convenient protocol, which may or may not employ a linker group, where representative protocols include those protocols provided herein for covalent bonding of the fluorescer/quencher moieties to the FET labeled probes.

DNA intercalators are further described in U.S. Pat. No. 6,280,933; the disclosure of which is herein incorporated by reference.

In certain embodiments, another component of the reaction mixture produced in the first step of the subject methods is a minor groove binder. Minor groove binders of interest are those capable of binding isohelically into the minor groove of double stranded DNA by fitting edge-on into the minor groove, replacing the spine of hydration and following the natural curvature of the DNA. This type of molecular recognition is at least partially driven by formation of hydrogen bonds between the minor groove binder and the DNA. The minor groove binders of interest form bifurcated hydrogen bonds with nucleotide base pairs, and numerous van der Waals contacts with various atoms in the nucleotide backbone. These atomic interactions stabilize the DNA-minor groove binder structure and, in turn, effectively strengthen the interaction of the two DNA strands of the helix.

In general, minor groove binders of interest are those capable of binding within the minor groove of a DNA helix with an association constant of $10^3 M^{-1}$ or greater, as determined by using the assay described in Taquet et al., *Biochemistry* 1998 Jun. 23;37(25):9119-26. The minor groove binders have a strong preference for A-T (adenine and thymine) rich regions of double stranded DNA. However,

12

minor groove binders which show preference to C-G (cytosine and guanine) rich regions are also of interest. Generally, minor groove binders of interest stabilize A-T hydrogen bonds more than C-G bonds, (thus stabilizing weaker sequences). Minor groove binders form extremely stable duplexes

The minor groove binders may be free in the aqueous buffer medium of the primer extension mixture, or bound to the FET labeled oligonucleotide (covalently or non-covalently). The minor groove binder may be linked to a covalent structure or chain of atoms that attaches the minor groove binder to the oligonucleotide. This linking chain can and sometimes is considered as part of the minor groove binder, and does not adversely affect the minor groove binding properties. Furthermore, the minor groove binders may be attached to either the 3' end or the 5' end of the FET labeled oligonucleotide.

In general, minor groove binders have crescent shaped three-dimensional structures, and generally have a molecular weight of between approximately 150 to approximately 2000 Daltons. Examples of minor groove binders include netropsin, distamycin, distamycin A, lexitropsin, mithramycin, chromomycin A₃, olivomycin, anthramycin, sibiromycin, pentamidine, stilbamidine, berenil, CC-1065, Hoechst 33258, 4'-6-diamidino-2-phenylindole (DAPI), and derivatives thereof. Typically, the minor groove binder is a N-methylpyrrole peptide such as netropsin and distamycin A. Minor groove binders are further described in U.S. Pat. Nos. 5,801,155 and 5,955,590; the disclosures of which are herein incorporated by reference.

In those embodiments where the minor groove binder is present in the reaction mixture, the amount of minor groove binder present in the reaction mixture typically ranges from about 0.02 μM to about 1.5 μM , usually from about 0.1 μM to about 0.75 μM and more usually from about 0.2 μM to about 0.5 μM .

Another component of the reaction mixture produced in the first step of the subject methods is the template nucleic acid. The nucleic acid that serves as template may be single stranded or double stranded, where the nucleic acid is typically deoxyribonucleic acid (DNA). The length of the template nucleic acid may be as short as 50 bp, but usually be at least about 100 bp long, and more usually at least about 150 bp long, and may be as long as 10,000 bp or longer, e.g., 50,000 bp in length or longer, including a genomic DNA extract, or digest thereof, etc. The nucleic acid may be free in solution, flanked at one or both ends with non-template nucleic acid, present in a vector, e.g. plasmid and the like, with the only criteria being that the nucleic acid be available for participation in the primer extension reaction. The template nucleic acid may be present in purified form, or in a complex mixture with other non-template nucleic acids, e.g., in cellular DNA preparation, etc.

The template nucleic acid may be derived from a variety of different sources, depending on the application for which the PCR is being performed, where such sources include organisms that comprise nucleic acids, i.e. viruses; prokaryotes, e.g. bacteria, archaea and cyanobacteria; and eukaryotes, e.g. members of the kingdom protista, such as flagellates, amoebas and their relatives, amoeboid parasites, ciliates and the like; members of the kingdom fungi, such as slime molds, acellular slime molds, cellular slime molds, water molds; true molds, conjugating fungi, sac fungi, club fungi, imperfect fungi and the like, plants, such as algae, mosses, liverworts, hornworts, club mosses, horsetails, ferns, gymnosperms and flowering plants, both monocots and dicots, and animals, including sponges, members of the

US 7,160,997 B2

13

phylum cnidaria, e.g. jelly fish, corals and the like, combjellies, worms, rotifers, roundworms, annelids, molluscs, arthropods, echinoderms, acorn worms, and vertebrates, including reptiles, fishes, birds, snakes, and mammals, e.g. rodents, primates, including humans, and the like. The template nucleic acid may be used directly from its naturally occurring source and/or preprocessed in a number of different ways, as is known in the art. In some embodiments, the template nucleic acid may be from a synthetic source.

The next component of the reaction mixture produced in the first step of the subject methods is the primers employed in the primer extension reaction, e.g., the PCR primers (such as forward and reverse primers employed in geometric amplification or a single primer employed in a linear amplification). The oligonucleotide primers with which the template nucleic acid (hereinafter referred to as template DNA for convenience) is contacted will be of sufficient length to provide for hybridization to complementary template DNA under annealing conditions (described in greater detail below) but will be of insufficient length to form stable hybrids with template DNA under polymerization conditions. The primers will generally be at least 10 bp in length, usually at least 15 bp in length and more usually at least 16 bp in length and may be as long as 30 bp in length or longer, where the length of the primers will generally range from 18 to 50 bp in length, usually from about 20 to 35 bp in length. The template DNA may be contacted with a single primer or a set of two primers (forward and reverse primers), depending on whether primer extension, linear or exponential amplification of the template DNA is desired. Where a single primer is employed, the primer will typically be complementary to one of the 3' ends of the template DNA and when two primers are employed, the primers will typically be complementary to the two 3' ends of the double stranded template DNA.

In addition to the above components, the reaction mixture produced in the subject methods includes deoxyribonucleoside triphosphates (dNTPs). Usually the reaction mixture will comprise four different types of dNTPs corresponding to the four naturally occurring bases are present, i.e. dATP, dTTP, dCTP and dGTP. In the subject methods, each dNTP will typically be present in an amount ranging from about 10 to 5000 μM , usually from about 20 to 1000 μM .

The reaction mixture prepared in the first step of the subject methods further includes an aqueous buffer medium that includes a source of monovalent ions, a source of divalent cations and a buffering agent. Any convenient source of monovalent ions, such as KCl, K-acetate, NH_4 -acetate, K-glutamate, NH_4Cl , ammonium sulfate, and the like may be employed. The divalent cation may be magnesium, manganese, zinc and the like, where the cation will typically be magnesium. Any convenient source of magnesium cation may be employed, including MgCl_2 , Mg-acetate, and the like. The amount of Mg^{2+} present in the buffer may range from 0.5 to 10 mM, but will preferably range from about 3 to 6 mM, and will ideally be at about 5 mM. Representative buffering agents or salts that may be present in the buffer include Tris, Tricine, HEPES, MOPS and the like, where the amount of buffering agent will typically range from about 5 to 150 mM, usually from about 10 to 100 mM, and more usually from about 20 to 50 mM, where in certain preferred embodiments the buffering agent will be present in an amount sufficient to provide a pH ranging from about 6.0 to 9.5, where most preferred is pH 7.3 at 72° C. Other agents which may be present in the buffer medium include chelating agents, such as EDTA, EGTA and the like.

14

In preparing the reaction mixture, the various constituent components may be combined in any convenient order. For example, the buffer may be combined with primer, polymerase and then template DNA, or all of the various constituent components may be combined at the same time to produce the reaction mixture.

Preparation of Non-High Fidelity Reaction Mixture

As indicated above, in certain embodiments, e.g., where a DNA intercalator and/or a minor groove binder is present, the reaction mixture need not be a high fidelity reaction mixture. In these embodiments, the reaction mixture is prepared as described above, but the polymerase having 3'→5' exonuclease activity, e.g., the Family B polymerases reviewed above, is not included in the reaction mixture.

Subjecting the Primer Extension Mixture to Primer Extension Reaction Conditions

Following preparation of the reaction mixture, the reaction mixture is subjected to primer extension reaction conditions, i.e., to conditions that permit for polymerase mediated primer extension by addition of nucleotides to the end of the primer molecule using the template strand as a template. In many embodiments, the primer extension reaction conditions are amplification conditions, which conditions include a plurality of reaction cycles, where each reaction cycle comprises: (1) a denaturation step, (2) an annealing step, and (3) a polymerization step. The number of reaction cycles will vary depending on the application being performed, but will usually be at least 15, more usually at least 20 and may be as high as 60 or higher, where the number of different cycles will typically range from about 20 to 40. For methods where more than about 25, usually more than about 30 cycles are performed, it may be convenient or desirable to introduce additional polymerase into the reaction mixture such that conditions suitable for enzymatic primer extension are maintained.

The denaturation step comprises heating the reaction mixture to an elevated temperature and maintaining the mixture at the elevated temperature for a period of time sufficient for any double stranded or hybridized nucleic acid present in the reaction mixture to dissociate. For denaturation, the temperature of the reaction mixture will usually be raised to, and maintained at, a temperature ranging from about 85 to 100, usually from about 90 to 98 and more usually from about 93 to 96° C. for a period of time ranging from about 3 to 120 sec, usually from about 5 to 30 sec.

Following denaturation, the reaction mixture will be subjected to conditions sufficient for primer annealing to template DNA present in the mixture. The temperature to which the reaction mixture is lowered to achieve these conditions will usually be chosen to provide optimal efficiency and specificity and will generally range from about 50 to 75, usually from about 55 to 70 and more usually from about 60 to 68° C. Annealing conditions will be maintained for a period of time ranging from about -15 sec to 30 min, usually from about 30 sec to 5 min.

Following annealing of primer to template DNA or during annealing of primer to template DNA, the reaction mixture will be subjected to conditions sufficient to provide for polymerization of nucleotides to the primer ends in manner such that the primer is extended in a 5' to 3' direction using the DNA to which it is hybridized as a template, i.e., conditions sufficient for enzymatic production of primer extension product. To achieve polymerization conditions, the temperature of the reaction mixture will typically be raised to or maintained at a temperature ranging from about 65 to 75, usually from about 67 to 73° C. and maintained for

US 7,160,997 B2

15

a period of time ranging from about 15 sec to 20 min, usually from about 30 sec to 5 min.

The above cycles of denaturation, annealing and polymerization may be performed using an automated device, typically known as a thermal cycler. Thermal cyclers that may be employed are described in U.S. Pat. Nos. 5,612,473; 5,602,756; 5,538,871; and 5,475,610, the disclosures of which are herein incorporated by reference.

Signal Detection

The next step in the subject methods is signal detection, i.e., detecting a change in a fluorescent signal from the FET labeled oligonucleotide probe present in the reaction mixture to obtain an assay result. In other words, the next step in the subject methods is to detect any modulation in the fluorescent signal generated by the FET labeled oligonucleotide present in the reaction mixture. The change may be an increase or decrease in fluorescence, depending on the nature of the label employed, but in many embodiments is an increase in fluorescence. The sample may be screened for an increase in fluorescence using any convenient means, e.g., a suitable fluorimeter, such as a thermostable-cuvette or plate-reader fluorimeter. Fluorescence is suitably monitored using a known fluorimeter. The signals from these devices, for instance in the form of photo-multiplier voltages, are sent to a data processor board and converted into a spectrum associated with each sample tube. Multiple tubes, for example 96 tubes, can be assessed at the same time. Data may be collected in this way at frequent intervals, for example once every 10 ms, throughout the reaction. By monitoring the fluorescence of the reactive molecule from the sample during each cycle, the progress of the amplification reaction can be monitored in various ways. For example, the data provided by melting peaks can be analyzed, for example by calculating the area under the melting peaks and this data plotted against the number of cycles.

The spectra generated in this way can be resolved, for example, using "fits" of pre-selected fluorescent moieties such as dyes, to form peaks representative of each signaling moiety (i.e. fluorophore). The areas under the peaks can be determined which represents the intensity value for each signal, and if required, expressed as quotients of each other. The differential of signal intensities and/or ratios will allow changes in FET to be recorded through the reaction or at different reaction conditions, such as temperatures. The changes are related to the binding phenomenon between the oligonucleotide probe and the target sequence or degradation of the oligonucleotide probe bound to the target sequence. The integral of the area under the differential peaks will allow intensity values for the FET effects to be calculated.

Screening the mixture for a change in fluorescence provides one or more assay results, depending on whether the sample is screened once at the end of the primer extension reaction, or multiple times, e.g., after each cycle, of an amplification reaction (e.g., as is done in real time PCR monitoring).

Employing Said Assay Result to Determine Whether a Primer Extension Product is Present in Said Mixture

The data generated as described above can be interpreted in various ways. In its simplest form, an increase or decrease in fluorescence from the sample in the course of or at the end of the amplification reaction is indicative of an increase in the amount of the target sequence present, i.e., primer extension product present, suggestive of the fact that the amplification reaction has proceeded and therefore the target sequence was in fact present in the sample. Quantitation is

16

also possible by monitoring the amplification reaction throughout the amplification process.

In this manner, a reaction mixture is readily screened for the presence of primer extension products. The methods are suitable for detection of a single primer extension product as well as multiplex analyses, in which two or more different FET labeled oligonucleotide probes are employed to screen for two or more different primer extension products. In these latter multiplex situations, the number of different types of probes that may be employed typically ranges from about 2 to about 20 or higher, usually from about 2 to about 15.

The above described methods of detecting the presence of one or more types of primer extension reaction products in a primer extension reaction mixture finds use in a variety of different applications, representative ones of which are now reviewed in greater detail.

Utility

The above-described inventive methods find use in a variety of different applications. In general, the subject oligonucleotide probes and methods of using the same find use in any high fidelity primer extension reaction in which a FET probe and proofreading polymerase are employed.

One type of representative application is in monitoring the progress of nucleic acid amplification reactions, such as polymerase chain reaction applications, including both linear and geometric PCR applications. As used herein, the term monitoring includes a single evaluation at the end of a series of reaction cycles as well as multiple evaluations, e.g., after each reaction cycle, such that the methods can be employed to determine whether a particular amplification reaction series has resulted in the production of primer extension product, e.g., a non-real time evaluation, as well as in a real time evaluation of the progress of the amplification reaction.

The subject methods find use in both 5' nuclease methods of monitoring a PCR amplification reaction (e.g., where a Taqman type probe is employed), and non-5' nuclease methods of monitoring a PCR amplification reaction (e.g., where a molecular beacon type probe is employed). Again, the subject methods find use in evaluating the progress of an amplification reaction at a single time (e.g., non-real time monitoring) and in real-time monitoring.

Monitoring a PCR reaction according to the subject methods finds use in a variety of specific applications. Representative applications of interest include, but are not limited to: (1) detection of allelic polymorphism; (2) SNP detection; (3) detection of rare mutations; (4) detection of allelic stage of single cells; (5) detection of single or low copy number DNA analyte molecules in a sample; etc. For example, in detection of allelic polymorphism, a nucleic acid sample to be screened, e.g., a genomic DNA cellular extract, is employed as template nucleic acid in the preparation of a primer extension reaction mixture, as described above, where the reaction mixture includes a different and distinguishable FET labeled oligonucleotide probe that is specific for each different allelic sequence to be identified, if present. The assay is then carried out as described above, where the sample is screened for a change in signal from each different oligonucleotide probe. A change in signal from a given probe is indicative of the presence of the allelic variant to which that probe is specific in the sample. Likewise, an absence of change in signal is indicative of the absence of the allelic variant in the sample. In this manner, the sample is readily screened for the presence of one or more allelic variants. A similar approach can be used for SNP detection, where a different FET labeled oligonucleotide for each SNP of interest to be screened in a nucleic acid sample is employed.

A significant benefit of employing the subject methods in PCR screening applications is that the PCR conditions may be "high fidelity," i.e., they may include a proof reading activity, such that the results obtained from the assays performed according to the subject methods are highly reliable.

Kits

Also provided are kits for practicing the subject methods. The kits according to the present invention will comprise at least: (a) a FET labeled oligonucleotide, where the kits may include two or more distinguishable FET labeled oligonucleotides, e.g., that hybridize to different target nucleic acids, e.g., two or more different SNPs; and (b) instructions for using the provide FET labeled oligonucleotide(s) in a high fidelity amplification, e.g., PCR, reaction.

The subject kits may further comprise additional reagents which are required for or convenient and/or desirable to include in the reaction mixture prepared during the subject methods, where such reagents include: one or more polymerases, including a polymerase mix, where the one or more polymerases at least include a polymerase that exhibits proofreading, i.e., 3'→5' exonuclease activity in certain embodiments; an aqueous buffer medium (either prepared or present in its constituent components, where one or more of the components may be premixed or all of the components may be separate), and the like.

The various reagent components of the kits may be present in separate containers, or may all be precombined into a reagent mixture for combination with template DNA. For example, the kit may include an intercalator-FET probe and a minor groove binder, where these two components may be present separately or combined into a single composition for use.

In addition to the above components, the subject kits will further include instructions for practicing the subject methods. These instructions may be present in the subject kits in a variety of forms, one or more of which may be present in the kit. One form in which these instructions may be present is as printed information on a suitable medium or substrate,

e.g., a piece or pieces of paper on which the information is printed, in the packaging of the kit, in a package insert, etc. Yet another means would be a computer readable medium, e.g., diskette, CD, etc., on which the information has been recorded. Yet another means that may be present is a website address which may be used via the internet to access the information at a removed site. Any convenient means may be present in the kits.

Systems

Also provided are systems for use in practicing the subject methods. The subject systems at least include one or more FET labeled oligonucleotides and a proofreading activity, as well as any other requisite components for preparing a primer extension reaction mixture, as described above. In addition, the subject systems may include any required devices for practicing the subject methods, e.g., thermal cyclers, fluorimeters, etc.

The following examples are offered by way of illustration and not by way of limitation.

Experimental Procedures

A. General

The oligonucleotides shown in Table 1 were used for the following example. Standard DNA phosphoramidites, including 6-carboxy-fluorescein (6-FAM) phosphoramidite, 5'-Tetrachloro-Fluorescein (TET) phosphoramidite, and 6-carboxytetramethyl-rhodamine (TAMRA) CPG, 3'-Dabcyl CPG, were obtained from Glen Research. Black Hole Quenchers (BHQ1, BHQ2, BHQ3) CPG were obtained from Biosearch Technology. Eclipse Dark Quencher (eDQ) CPG was obtained from Epoch Bioscience. All primers were purified using Oligo Purification Cartridges (Biosearch Technology). Doubly labeled FET probes were synthesized using CPGs with various quenchers as indicated in Table 1 and with either 6FAM-labeled or TET-labeled phosphoramidites at the 5'end. The doubly labeled FET probes were purified by preparative HPLC and PAGE using standard protocols. Phosphorothioate modification was prepared by standard procedure.

TABLE 1

Sequence Listing			
Name	SEQ ID NO	Type	Sequence
BCL-F1	1	Primer	5' GGT GGT GGA GGA GCT CTT CAG 3'
BCL-R1	2	Primer	5' CCA GCC TCC GTT ATC CTG GA 3'
BCL-P1	3	Probe	5' FAM-CCT GTG GAT GAC TGA GTA GGT GAA CCG-BHQ1-3'
BCL-P2	4	Probe	5' FAM-CCT GTG GAT GAC TGA GTA CCT GAA CCG-eDQ-3'
BCL-P3	5	Probe	5' FAM-GGT GTG GAT GAG TGA GTA CCT GAA CCG-DABCYL-3'
BCL-P4	6	Probe	5' FAM-OCT GTG GAT GAG TGA GTA GGT GAA CCG-TAMRA-3'
BCL-P5	7	S-oligo Probe	5' FAM-GGT GTG GAT GAG TGA GTA GGT GAA*G*G-TAMRA-3'
ACT-F1	8	Primer	5' GAG CTA CGA GCT GCC TGA C 3'
ACT-R1	9	Primer	5' GAC TCC ATG CCC AGG AAG 3'
ACT-P1	10	Probe	5' TET-CAT CAC CAT TGG CAA TGA GCG-BHQ1-3'
ACT-P2	11	Probe	5' TET-CAT CAC CAT TGG CAA TGA GCG-eDQ-3'
ACT-P3	12	Probe	5' TET-CAT CAC CAT TGG GAA TGA GCG-DABCYL-3'
ACT-P4	13	Probe	5' TET-CAT CAC CAT TGG GAA TGA GCG-TAMRA-3'
ACT-P5	14	S-oligo Probe	5' TET-CAT CAC CAT TGG GAA TGA *G*G-TAMRA 3'
ABCG-R1	15	Primer	5' CCC AAA AAT TCA TTA TGC TGC AA 3'
ABCG-P1	16	Primer	5' FAM-CAG CAT TCC ACG ATA TGG ATT TAC GGC -BHQ1-3

TABLE 1-continued

Sequence Listing		
Name	Type	Sequence
ABCG-P2 SEQ ID NO: 17	Primer	5' FAM-CAG CAT TCC ACG ATA TGG ATT TAC GGC -TAMRA-3'
ABCG-T1 SEQ ID NO: 18	Template	5' ATC AGC ATT CCA CGA TAT GGA TTT ACG GCA TCA GTT GCA GCA TAA TGA ATT TTT GGG A 3'
MTHFR-F1 SEQ ID NO: 19	Primer	5' GGA AGA ATG TGT CAG CCT CAA AG 3'
MTHFR-R1 SEQ ID NO: 20	Primer	5' CTG ACC TGA AGC ACT TGA AGG AG 3'
MTHFR-P1 SEQ ID NO: 21	Wt Probe	5' TET-TGA AAT CGG CTC CCG CA-BHQ1-3'
MTHFR-P2 SEQ ID NO: 22	Mut Probe	5' FAM-TGA AAT CGA CTC CCG CAG A-BHQ1-3'

*: phosphorothioate internucleotide linkage

EXAMPLE 1

Properties and use of TET Labeled FET Probes with Various Quenchers

Real Time amplifications and detection were performed in ABI PRISM 7700 (Applied Biosystems) using 30 µl reactions that contained 20 mM Tris-HCl (pH 8.3), 60 mM KCl, 5.3 mM MgCl₂, 0.2 mM dATP, 0.2 mM dTTP, 0.2 mM dGTP, 0.2 mM dCTP, 0.5 µM of each primer, 0.2 µM FET probe, 4-fold series dilute of Jurkat cDNAs, either 0.6 units Taq Polymerase (Fisher) or a mix of Taq and Pwo DNA Polymerase (Roche Molecular Biochemicals) at unit ratio of 5 to 1.

A 99 basepair segment of the human beta actin gene was amplified using primers ACT-F1 and ACT-R1 listed in Table 1. Thermal profile was 95° C. 15 sec; 50 cycles of 95° C. 15 sec, 60° C. 30 sec, 72° C. 45 sec. After amplification, fluorescent intensity at each well was measured by post PCR reading.

Five types of TET labeled FET probes (ACT-P1, ACT-P2, ACT-P3, ACT-P4 and ACT-P5 as shown in Table 1) were tested in Real Time amplification. Post PCR reading result is shown in Table 2. The emission intensity of donor under condition with template is divided by the emission intensity of donor under condition without template to give +/- signal ratio, which indicates whether the probes are degraded or not. For TET labeled FET probes having TAMRA or Dabcyl as quencher, 3'→5' exonuclease addition caused a dramatic decrease in +/- signal ratio due to cleavage of FET probes.

TABLE 2

donor/quencher	Fluorescent changes in various TET labeled FET probe during PCR					
	PCR using Taq pol.			PCR using Taq + Pwo pol.		
	no template	Template	+/- signal ratio	no template	template	+/- signal ratio
TET/BHQ1	4500.0	20250.0	4.5	4500.0	20000.0	4.4
TET/eDQ	4000.0	20000.0	5.0	4000.0	20000.0	5.0
TET/Dabcyl	6000.0	19000.0	3.2	16000.0	24000.0	1.5
TET/TAMRA	3900.0	19000.0	4.9	12000.0	18000.0	1.5
TET/TAMRA S-oligo	4000.0	20000.0	5.0	3900.0	19000.0	4.9

Real Time amplification plot is shown in FIGS. 1A-E. TET labeled FET probes having either BHQ1 or Eclipse Dark Quencher at 3'-end are resistant to 3'→5' exonuclease, and are therefore suitable for use in high fidelity PCR (FIGS.

15

20

25

30

35

40

1A and 1B). By contrast, TET labeled FET probes having either TAMRA or Dabcyl Quencher at 3'-end are degraded by 3'→5' exonuclease, and no proper real time PCR results can be obtained (FIGS. 1C and 1D). The TET labeled FET probes having TAMRA Quencher at 3'-end can also be resistant to 3'→5' exonuclease if three phosphorothioate internucleotide linkages at 3'-end are added (FIG. 1E), which confirms the reliability of this whole experiment.

EXAMPLE 2

Properties and use of FAM Labeled FET Probes with Various Quenchers

Real Time amplifications and detection were performed in ABI PRISM 7700 using 30 µl reactions that contained 20 mM Tris-HCl (pH 8.3), 60 mM KCl, 5.3 mM MgCl₂, 0.2 mM dATP, 0.2 mM dTTP, 0.2 mM dGTP, 0.2 mM dCTP, 0.5 µM of each primers, 0.2 µM FET probe, various copies of a cDNA clone of human bcl-2 gene or Jurkat cDNAs, 0.6 units Taq DNA Polymerase (Fisher Scientific) or a mix of Taq and Pwo DNA Polymerase (Roche Molecular Biochemicals) at unit ratio of 10 to 1.

A 190 basepair segment of the human bcl-2 gene was amplified using primers BCL-F1 and BCL-R1 listed in Table 1. Thermal profile was 95° C. 15 sec; 50 cycles of 95° C. 15 sec, 60° C. 30 sec, 72° C. 45 sec. After amplification, fluorescent intensity at each well was measured by post PCR reading.

Five types of FAM-labeled FET probes (BCL-P1, BCL-P2, BCL-P3, BCL-P4 and BCL-P5 as shown in Table 1)

were tested in Real Time amplification. Post PCR reading result is shown in Table 3. For FAM labeled FET probes having TAMRA or Dabcyl as quencher, 3'→5' exonuclease addition caused a dramatic decrease in +/- signal ratio due to cleavage of FET probes.

65

US 7,160,997 B2

TABLE 3

Fluorescent changes in various FAM labeled FET probe during PCR

donor/quencher	PCR using Taq pol.			PDR using Tan-i-Pwo [Po]		
	no template	template	+/- signal ratio	no template	template	+/- signal ratio
FAM/BHQ1	5000.0	20000.0	4.0	5000.0	20000.0	4.0
FAM/eDQ	5000.0	20000.0	4.0	5000.0	19000.0	3.8
FAM/Dabcy1	7000.0	20000.0	2.9	18000.0	25000.0	1.4
FAM/TAMRA	5000.0	22500.0	4.5	20000.0	30000.0	1.5
FAM/TAMRA S-oligo	10000.0	30000.0	3.0	10000.0	29000.0	2.9

Representative Real Time amplification plot is shown in FIGS. 2A-2B. FAM labeled FET probes having either BHQ1 or Eclipse Dark Quencher at 3'-end are resistant to 3'→5' exonuclease, and are therefore suitable for use in high fidelity PCR (FIG. 2A). By contrast, FAM, labeled FET probes having either TAMRA or Dabcy1 Quencher at 3'-end are degraded by 3'→5' exonuclease, and no proper real time PCR results can be obtained (FIG. 2B). Thus, similar results as Example 1 are repeated in a different system.

EXAMPLE 3

Properties of FET Oligo as Primers

PCR amplifications were performed in ABI PRISM 7700 using 30 μl reactions that contained 10 mM Tris-HCl (pH 8.85), 25 mM KCl, 5 mM (NH₄)₂SO₄, 5 mM MgCl₂, 0.2 mM dATP, 0.2 mM dTTP, 0.2 mM dGTP, 0.2 mM dCTP, 0.5 μM of each primer, 0.2 μM of each primer (ABCG-R1 and ABCG-P1 or ABCG-P2), 1 million copies of template (ABCG-T1) or just TE buffer in no template control (NTC), 0.6 units of Pwo DNA Polymerase (Roche Molecular Biochemicals). Thermal profile was 95° C. 10 sec; 40 cycles of 95° C. 15 sec, 60° C. 60 sec.

Two types of FET primers (ABCG-P1 and ABCG-P2) and a template (ABCG-T1) as listed in Table 1 were tested in Real Time Amplification of human ABC transporter ABCG2. Multicomponent analysis is shown in FIG. 3. Thus, the subject FET labeled nucleic acid detectors having a BHQ1 at 3'-end are resistant to 3'→5' exonuclease activity when used as a primer. By contrast, the FET labeled nucleic acid detectors having a TAMRA at 3'-end are degraded by 3'→5' exonuclease activity. Similar results were obtained using FET primers having mismatch at 3'-end.

EXAMPLE 4

Allele Discrimination Under High Fidelity PCR

An 89 basepair segment of the human methylenetetrahydrofolate reductase (MTHFR) gene was amplified using primers MTHFR-F1 and MTHFR-R1 listed in Table 1. Real Time amplifications and detection were performed in ABI PRISM 7700 using 30 μl reactions that contained 20 mM Tris-HCl (pH 8.3), 60 mM KCl, 5.3 mM, MgCl₂, 0.2 mM dATP, 0.2 mM dTTP, 0.2 mM dGTP, 0.2 mM dCTP, 0.1 μM of primer MTHFR-F1 and 1 μM of primer MTHFR-R1, 0.2 μM each of FET probes MTHFR-P1 and MTHFR-P2, templates containing varies number of MTHFR wild type or mutant or both as listed in table 4, a mix of Taq and Pwo DNA Polymerase (Roche Molecular Biochemicals) at unit ratio of 5 to 1. Thermal profile was 95° C. 15 sec; 50 cycles of 95° C. 15 sec, 55° C. 40 sec, 70° C. 40 sec. After amplification, fluorescent intensity at each well was measured by post PCR reading and analyzed by allele discrimi-

nation software in ABI PRISM 7700. Graphical result is shown in FIG. 4 and further summarized in Table 4.

TABLE 4

Summary of template types and allele call by PRISM 7700

Template types (copy num)	Call by PRISM 7700
mut: 10 ⁶	Allele 2
mut: 10 ⁶	Allele 2
mut: 10 ⁶	Allele 2
mut: 10 ⁶	Allele 2
wt: 10 ⁵	
mut: 10 ⁶	Allele 2
wt: 10 ⁵	
mut: 10 ⁶	Allele 2
wt: 10 ⁵	
mut: 2 × 10 ⁵	Allele ½
wt: 10 ⁵	
mut: 2 × 10 ⁵	Allele ½
wt: 10 ⁵	
mut: 2 × 10 ⁵	Allele ½
wt: 10 ⁵	
mut: 2 × 10 ⁵	Allele ½
wt: 10 ⁵	
mut: 4 × 10 ⁴	Allele ½
wt: 10 ⁵	
mut: 4 × 10 ⁴	Allele ½
wt: 10 ⁵	
mut: 4 × 10 ⁴	Allele ½
wt: 10 ⁵	
mut: 8 × 10 ³	Allele 1
wt: 10 ⁵	
mut: 8 × 10 ³	Allele 1
wt: 10 ⁵	
mut: 8 × 10 ³	Allele 1
wt: 10 ⁵	
mut: 8 × 10 ³	Allele 1
wt: 10 ⁵	
mut: 8 × 10 ³	Allele 1
wt: 10 ⁵	
mut: 8 × 10 ³	Allele 1
wt: 10 ⁵	
mut: 8 × 10 ³	Allele 1
wt: 10 ⁵	
Wt: 10 ⁶	Allele 1
Wt: 10 ⁶	Allele 1
Wt: 10 ⁶	Allele 1
Wt: 10 ⁶	Allele 1

TABLE 4-continued

Summary of template types and allele call by PRISM 7700	
Template types (copy num)	Call by PRISM 7700
No template	No amp
No template	No amp
No template	No amp
No template	No amp

Allele 1 = wild type (TET labeled probe)
 Allele 2 = mutant type (FAM labeled probe)

The call by ABI PRISM 7700 matches well with types of template used (Table 4). No template controls give no amplification signal. Thus, two different allele sequences can be detected and distinguished using FAM and TET labeled FET probes under highfidelity PCR.

B. General

The oligonucleotides shown in Table 5 were used for the following example. Standard DNA phosphoramidites, including 6-carboxy-fluorescein (6-FAM) phosphoramidite, 5'-Tetrachloro-Fluorescein (TET) phosphoramidite, Acridine (ACR) phosphoramidite and 6-carboxytetramethylrhodamine (TAMRA) CPG, 3'-Dabcyl CPG, were obtained from Glen Research. Black Hole Quenchers (BHQ1) CPG were obtained from Biosearch Technology. Eclipse Dark Quencher (eDQ) CPG was obtained from Epoch Bioscience. All primers were purified using Oligo Purification Cartridges (Biosearch Technology). Doubly labeled FET probes were synthesized using CPGs with various quenchers as indicated in Table 5 and with either 6-FAM-labeled or TET-labeled phosphoramidites at the 5'end. The doubly labeled FET probes were purified by preparative HPLC and PAGE using standard protocols. Phosphorothioate modification was prepared by standard procedure. Minor groove binder netropsin and distamycin A were purchased from Sigma.

TABLE 5

(continue)		
Name	Type	Sequence
MTHFR-P1	SEQ ID NO: 21 Wt Probe	5' TET-TGA AAT CGG CTC CCG CA-BHQ1-3'
MTHFR-P2	SEQ ID NO: 22 Mut Probe	5' FAM-TGA AAT CGA CTC CCG CAG A-BHQ1-3'
MTHFR-P13	SEQ ID NO: 23 Wt Probe	5' TET-TGA AAT CGG CTC CCG C-ACR-BHQ1-3'
MTHFR-P14	SEQ ID NO: 24 Wt Probe	5' TET-ACR TGA AAT CGG CTC CCG C-BHQ1-3'
MTHFR-P3	SEQ ID NO: 25 Mut Probe	5' FAM-TGA AAT CGA CTC CCG CAG-ACR-BHQ1-3'

Allele Discrimination using Acridine-Labeled FET Probes Under High Fidelity PCR

An 89 basepair segment of the human methylenetetrahydrofolate reductase (MTHFR) gene was amplified using primers MTHFR-F1 and MTHFR-R1 listed in Table 1. Real Time amplifications and detection were performed in ABI PRISM 7700 using 30 µl reactions that contained 20 mM Tris-HCl (pH 8.3), 60 mM KCl, 5.3 mM MgCl₂, 0.2 mM dATP, 0.2 mM dTTP, 0.2 mM dGTP, 0.2 mM dCTP, 0.15 µM of reference dye ROX, 0.5 µM each of primers MTHFR-F1 and MTHFR-R1, 0.2 µM each of FET probes, templates containing varies number of MTHFR wild type or mutant or both as listed in Table 6, a mix of Taq and Pwo DNA Polymerase (Roche Molecular Biochemicals) at unit ratio of 5 to 1. Five types of FET probes (MTHFR-P1, MTHFR-P2, MTHFR-P3, MTHFR-P13 and MTHFR-P14 as shown in Table 5) were tested in Real Time amplification. Thermal profile was 95° C. 15 sec; 50 cycles of 95° C. 15 sec, 57° C. 40 sec, 70° C. 40 sec.

Fluorescent intensity at each well was analyzed using real time data and software in ABI PRISM 7700 and summarized in Table 6. There was considerable cross-reactivity (or noise) between dyes FAM and TET (32% and 46% respectively) when normal FET probes were used. Such cross-reactivity was reduced to 2% and 4% when 3'-ACR labeled FET probes were used. However, 5'-ACR labeled FET probes did not show much difference to normal FET probes.

TABLE 6

Probe Types		Template types (copy num)		
		TET ΔRn	FAM ΔRn	% noise
5' FAM-TGA AAT CGA CTC CCG CAG -ACR-BHQ1-3'	SEQ. ID No. 25	0.1	4.1	2%
5' FAM-TGA AAT CGA CTC CCG CAG A -BHQ1-3'	SEQ. ID No. 22	1.4	4.4	32%
5' TET-TGA AAT CGG CTC CCG C -ACR-BHQ1-3'	SEQ. ID No. 23	4.5	0.2	4%
5' TET-ACR-TGA AAT CGG CTC CCG C -BHQ1-3'	SEQ. ID No. 24	2.7	0.8	30%
5' TET-TGA AAT CGG CTC CCG CA-BHQ1-3'	SEQ. ID No. 21	5.4	2.5	46%

Real Time amplifications and detection were further performed under the same conditions as above in ABI PRISM 7700 using 0.2 μM each of either normal or 3'-ACR-labeled FET probes as shown in Table 7 for allele discrimination. Real Time thermal profile was 95° C. 15 sec; 50 cycles of 95° C. 15 sec, 57° C. 40 sec, 70° C. 40 sec.

Fluorescent intensity of each dye at each well was analyzed using real time data and software in ABI PRISM 7700 and summarized in Table 6. There was considerable cross-reactivity (or noise) between dyes FAM and TET when normal FET probes were used. Such cross-reactivity was reduced to ~2% when 3'-ACR labeled FET probes were used. Because of much less cross-reactivity (or noise) between wt (TET) and mut (FAM) probes when using 3'-ACR-labeled FET probes, allelic analysis using 3'ACR-labeled probes was much closer to the theoretical prediction, therefore more accurate than using normal FET probe.

primers MTHFR-F1 and MTHFR-R1 listed in Table 1. Real Time amplifications and detection were performed in ABI PRISM 7700 using 30 μl reactions that contained 20 mM Tris-HCl (pH 8.3), 60 mM KCl, 5.3 mM MgCl₂, 0.2 mM dATP, 0.2 mM dTTP, 0.2 mM dGTP, 0.2 mM dCTP, 0.15 μM of reference dye ROX, 0.5 μM each of primers MTHFR-F1 and MTHFR-R1, FET probes, plus or minus templates containing varies number of MTHFR wild type or mutant or both as listed in table 7, a mix of Taq and Pwo DNA Polymerase (Roche Molecular Biochemicals) at unit ratio of 5 to 1. In this test 0.2 μM each of either normal or 3'-ACR-labeled FET probes as shown in Table 7, plus or minus 0.4 μM free netropsin or distamycin A, were used for allele discrimination. Thermal profile was 95° C. 15 sec; 50 cycles of 95° C. 15 sec, 63° C. 40 sec, 70° C. 40 sec., or 95° C. 15 sec; 50 cycles of 95° C. 15 sec, 57° C. 40 sec, 70° C. 40 sec.

TABLE 7

Probe Types		Template types (copy num)				
		wt: 10 ⁶	mut: 10 ⁶	wt: 10 ⁶ + mut: 10 ⁶	wt: 10 ⁶ + mut: 10 ⁵	wt: 10 ⁶ + mut: 10 ⁶
5' FAM-TGA AAT CGA CTC CCG CAG A-BHQ1-3'	FAM ΔRn	0.7	5.4	3.8	1.4	5.3
(SEQ ID NO: 22) +						
5' TET-TGA AAT CGG CTC CCG CA-BHQ1-3'	TET ΔRn	5.3	0.4	3.2	5.2	1.3
(SEQ ID NO: 21)						
% of dominant allele ΔRn to total ΔRn		88%	93%	54%	79%	80%
Theoretical %		100%	100%	50%	91%	91%
5' FAM-TGA AAT CGA CTC CCG CAG-ACR-BHQ1-3'	FAM ΔRn	0.1	4.9	3.1	0.9	5.3
(SEQ ID NO:25) +						
5' TET-TGA AAT CGG CTC CCG C-ACR-BHQ1-3'	TET ΔRn	5.2	0.1	2.9	5.6	0.8
SEQ ID NO:23						
% of dominant allele ΔRn to total ΔRn		98%	98%	52%	86%	87%
Theoretical %		100%	100%	50%	91%	91%

The above results and discussion demonstrate that 3'-ACR labeled FET nucleic acid detectors suitable for use in high fidelity PCR for allele discrimination are provided by the subject invention. As such, the subject methods represent a significant contribution to the art.

Example 7

Allele Discrimination Using Free MGB Under High Fidelity Real Time PCR

An 89 basepair segment of the human methylenetetrahydrofolate reductase (MTHFR) gene was amplified using

55

Similar results as Table 7 can be obtained at 63° C. anneal only when either free netropsin or distamycin A was included in PCR reaction mixture. There was no significant amplification when using normal PCR condition and 63° C. anneal. Similar results as Table 7 were also obtained at 57° C. anneal with or without netropsin or distamycin A. The netropsin or distamycin A acted primarily to enhance oligo's T_m, especially of AT rich sequences, so that shorter oligos/probes can be used in real time PCR to enhance allele discrimination. Such features shall help primers/probes design for AT rich sequences.

60

The above results and discussion demonstrate that the inclusion of free netropsin or distamycin A in PCR mixture

65

US 7,160,997 B2

27

suitable for use in a variety of different high fidelity PCR applications are provided by the subject invention. As such, the subject methods represent a significant contribution to the art.

The above results and discussion demonstrate that FET labeled nucleic acid detectors suitable for use in a variety of different high fidelity PCR applications are provide by the subject invention. As such, the subject methods represent a significant contribution to the art.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically

28

and individually indicated to be incorporated by reference. The citation of any publication is for its disclosure prior to the filing date and should not be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it is readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 25

<210> SEQ ID NO 1

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: human

<400> SEQUENCE: 1

ggtggtggag gagctcttca g

21

<210> SEQ ID NO 2

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: human

<400> SEQUENCE: 2

ccagcctccg ttatcctgga

20

<210> SEQ ID NO 3

<211> LENGTH: 27

<212> TYPE: DNA

<213> ORGANISM: human

<400> SEQUENCE: 3

cctgtgatg actgagtacc tgaaccg

27

<210> SEQ ID NO 4

<211> LENGTH: 27

<212> TYPE: DNA

<213> ORGANISM: human

<400> SEQUENCE: 4

cctgtgatg actgagtacc tgaaccg

27

<210> SEQ ID NO 5

<211> LENGTH: 27

<212> TYPE: DNA

<213> ORGANISM: human

<400> SEQUENCE: 5

cctgtgatg actgagtacc tgaaccg

27

<210> SEQ ID NO 6

<211> LENGTH: 27

<212> TYPE: DNA

<213> ORGANISM: human

<400> SEQUENCE: 6

US 7,160,997 B2

29

30

-continued

cctgtggatg actgagtacc tgaaccg	27
<210> SEQ ID NO 7 <211> LENGTH: 27 <212> TYPE: DNA <213> ORGANISM: human <400> SEQUENCE: 7	
cctgtggatg actgagtacc tgaaccg	27
<210> SEQ ID NO 8 <211> LENGTH: 19 <212> TYPE: DNA <213> ORGANISM: human <400> SEQUENCE: 8	
gagctacgag ctgcctgac	19
<210> SEQ ID NO 9 <211> LENGTH: 18 <212> TYPE: DNA <213> ORGANISM: human <400> SEQUENCE: 9	
gactccatgc ccaggaag	18
<210> SEQ ID NO 10 <211> LENGTH: 21 <212> TYPE: DNA <213> ORGANISM: human <400> SEQUENCE: 10	
catcaccatt ggcaatgagc g	21
<210> SEQ ID NO 11 <211> LENGTH: 21 <212> TYPE: DNA <213> ORGANISM: human <400> SEQUENCE: 11	
catcaccatt ggcaatgagc g	21
<210> SEQ ID NO 12 <211> LENGTH: 21 <212> TYPE: DNA <213> ORGANISM: human <400> SEQUENCE: 12	
catcaccatt ggcaatgagc g	21
<210> SEQ ID NO 13 <211> LENGTH: 21 <212> TYPE: DNA <213> ORGANISM: human <400> SEQUENCE: 13	
catcaccatt ggcaatgagc g	21
<210> SEQ ID NO 14 <211> LENGTH: 21 <212> TYPE: DNA <213> ORGANISM: human <400> SEQUENCE: 14	

US 7,160,997 B2

31

32

-continued

catcaccatt ggcaatgagc g 21

<210> SEQ ID NO 15
 <211> LENGTH: 23
 <212> TYPE: DNA
 <213> ORGANISM: human
 <400> SEQUENCE: 15

cccaaaaatt cattatgctg caa 23

<210> SEQ ID NO 16
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: human
 <400> SEQUENCE: 16

cagcattcca cgatatggat ttacggc 27

<210> SEQ ID NO 17
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: human
 <400> SEQUENCE: 17

cagcattcca cgatatggat ttacggc 27

<210> SEQ ID NO 18
 <211> LENGTH: 58
 <212> TYPE: DNA
 <213> ORGANISM: human
 <400> SEQUENCE: 18

atcagcattc cacgatatgg atttacggca tcagttgcag cataatgaat ttttggga 58

<210> SEQ ID NO 19
 <211> LENGTH: 23
 <212> TYPE: DNA
 <213> ORGANISM: human
 <400> SEQUENCE: 19

ggaagaatgt gtcagcctca aag 23

<210> SEQ ID NO 20
 <211> LENGTH: 23
 <212> TYPE: DNA
 <213> ORGANISM: human
 <400> SEQUENCE: 20

ctgacctgaa gcacttgaag gag 23

<210> SEQ ID NO 21
 <211> LENGTH: 17
 <212> TYPE: DNA
 <213> ORGANISM: human
 <400> SEQUENCE: 21

tgaaatcggc tcccgca 17

<210> SEQ ID NO 22
 <211> LENGTH: 19
 <212> TYPE: DNA
 <213> ORGANISM: human

-continued

```

<400> SEQUENCE: 22
tgaaatcgac tcccgcaga                               19

<210> SEQ ID NO 23
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: human

<400> SEQUENCE: 23
tgaaatcggc tcccgc                               16

<210> SEQ ID NO 24
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: human

<400> SEQUENCE: 24
tgaaatcggc tcccgc                               16

<210> SEQ ID NO 25
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: human

<400> SEQUENCE: 25
tgaaatcgac tcccgcag                             18
    
```

What is claimed is:

1. A FET labeled probe comprising a nucleic acid intercalator bonded to a FET labeled oligonucleotide, wherein said nucleic acid intercalator is covalently bonded to the 3' end of said FET labeled oligonucleotide.
2. The FET labeled probe according to claim 1, wherein said nucleic acid intercalator provides increased stability to the hybrid formed from said FET labeled oligonucleotide.
3. The FET labeled probe according to claim 1, wherein said nucleic acid intercalator provides exonuclease activity resistance to said FET labeled oligonucleotide.
4. The FET labeled probe according to claim 1, wherein said nucleic acid intercalator comprises a polycyclic compound.
5. The FET labeled probe according to claim 4, wherein said polycyclic compound comprises an aromatic ring.
6. The FET labeled probe according to claim 4, wherein said polycyclic compound comprises at least three rings and not more than six rings.
7. The FET labeled probe according to claim 4, wherein said polycyclic compound comprises at least three rings, wherein at least two of said rings are fused.
8. The FET labeled probe according to claim 7, wherein said polycyclic compound is an acridine.
9. The FET labeled probe according to claim 1, wherein said FET labeled oligonucleotide is a nucleic acid detector molecule that includes a single-stranded target binding sequence linked to fluorophore and dark quencher.
10. The FET labeled probe according to claim 9, wherein said FET labeled oligonucleotide is a probe selected from the group consisting of: Taqman probes, scorpion probes, sunrise probes, molecular beacons, conformationally assisted probes, and in situ hybridization probes.
11. A kit for use in detecting the production of a primer extension product in a primer extension reaction mixture, said kit comprising:

- (a) a FET labeled oligonucleotide that includes a 3'→5' exonuclease resistant quencher domain and a nucleic acid intercalator covalently bonded to its 3' end; and
- (b) a minor groove binder; and
- (c) a polymerase.
12. The kit according to claim 11, wherein said intercalator, said FET labeled oligonucleotide and said minor groove binder are present as a single composition.
13. A kit for use in detecting the production of a primer extension product in a primer extension reaction mixture, said kit comprising:
 - (a) a FET labeled oligonucleotide that includes a 3'→5' exonuclease resistant quencher domain and a nucleic acid intercalator covalently bonded to its 3' end; and
 - (b) a minor groove binder.
14. The kit according to claim 13, wherein said minor groove binder provides increased stability to the hybrid formed from said FET labeled oligonucleotide.
15. The kit according to claim 13, wherein said minor groove binder comprises a compound capable of binding within the minor groove of double stranded DNA.
16. The kit according to claim 13, wherein said minor groove binder comprises a compound capable of binding within the minor groove of double stranded DNA with an association constant of at least $10^3 M^{-1}$.
17. The kit according to claim 13, wherein said minor groove binder is a compound selected from the group consisting of netropsin, distamycin, lexitropsin, mithramycin, chromomycin A₃, olivomycin, anthramycin, sibiromycin, pentamidine, stilbamidine, berenil, CC-1065,

US 7,160,997 B2

35

Hoechst 33258, 4'-6-diamidino-2-phenylindole (DAPI), and derivatives thereof.

18. A kit for use in detecting the production of a primer extension product in a primer extension reaction mixture, said kit comprising:

36

(a) a FET labeled oligonucleotide that includes a 3'→5' exonuclease resistant quencher domain and a nucleic acid intercalator covalently bonded to its 3' end.

19. The kit according to claim 18, wherein said kit further comprises a polymerase.

* * * * *

JS 44 (Rev. 12/07)

CIVIL COVER SHEET

The JS 44 civil cover sheet and the information contained herein neither replace nor supplement the filing and service of pleadings or other papers as required by law, except as provided by local rules of court. This form, approved by the Judicial Conference of the United States in September 1974, is required for the use of the Clerk of Court for the purpose of initiating the civil docket sheet. (SEE INSTRUCTIONS ON THE REVERSE OF THE FORM.)

FILED
 10 DEC 27 PM 4:05

I. (a) PLAINTIFFS
 LIFE TECHNOLOGIES CORPORATION

(b) County of Residence of First Listed Plaintiff SAN DIEGO, CA
 (EXCEPT IN U.S. PLAINTIFF CASES)

(c) Attorney's (Firm Name, Address, and Telephone Number)
 KURTIS D. MACFERRIN, 5791 VAN ALLEN WAY, CARLSBAD,
 CA 92008; TEL. NO.: (760) 603-7200

DEFENDANTS
 BIOSEARCH TECHNOLOGIES INC.

County of Residence of First Listed Defendant MARIN, CA
 (IN U.S. PLAINTIFF CASES ONLY)

NOTE: IN LAND CONDEMNATION CASES, USE THE LOCATION OF THE LAND INVOLVED.

Attorneys (If Known)
10 CV 2665 DMS **WVG**

II. BASIS OF JURISDICTION (Place an "X" in One Box Only)

1 U.S. Government Plaintiff

3 Federal Question (U.S. Government Not a Party)

2 U.S. Government Defendant

4 Diversity (Indicate Citizenship of Parties in Item III)

III. CITIZENSHIP OF PRINCIPAL PARTIES (Place an "X" in One Box for Plaintiff and One Box for Defendant)

	PTF	DEF		PTF	DEF
Citizen of This State	<input type="checkbox"/> 1	<input type="checkbox"/> 1	Incorporated or Principal Place of Business In This State	<input type="checkbox"/> 4	<input type="checkbox"/> 4
Citizen of Another State	<input type="checkbox"/> 2	<input type="checkbox"/> 2	Incorporated and Principal Place of Business In Another State	<input type="checkbox"/> 5	<input type="checkbox"/> 5
Citizen or Subject of a Foreign Country	<input type="checkbox"/> 3	<input type="checkbox"/> 3	Foreign Nation	<input type="checkbox"/> 6	<input type="checkbox"/> 6

IV. NATURE OF SUIT (Place an "X" in One Box Only)

CONTRACT	TORTS	FORFEITURE/PENALTY	BANKRUPTCY	OTHER STATUTES	
<input type="checkbox"/> 110 Insurance <input type="checkbox"/> 120 Marine <input type="checkbox"/> 130 Miller Act <input type="checkbox"/> 140 Negotiable Instrument <input type="checkbox"/> 150 Recovery of Overpayment & Enforcement of Judgment <input type="checkbox"/> 151 Medicare Act <input type="checkbox"/> 152 Recovery of Defaulted Student Loans (Excl. Veterans) <input type="checkbox"/> 153 Recovery of Overpayment of Veteran's Benefits <input type="checkbox"/> 160 Stockholders' Suits <input type="checkbox"/> 190 Other Contract <input type="checkbox"/> 195 Contract Product Liability <input type="checkbox"/> 196 Franchise	PERSONAL INJURY <input type="checkbox"/> 310 Airplane <input type="checkbox"/> 315 Airplane Product Liability <input type="checkbox"/> 320 Assault, Libel & Slander <input type="checkbox"/> 330 Federal Employers' Liability <input type="checkbox"/> 340 Marine <input type="checkbox"/> 345 Marine Product Liability <input type="checkbox"/> 350 Motor Vehicle <input type="checkbox"/> 355 Motor Vehicle Product Liability <input type="checkbox"/> 360 Other Personal Injury	PERSONAL INJURY <input type="checkbox"/> 362 Personal Injury - Med. Malpractice <input type="checkbox"/> 365 Personal Injury - Product Liability <input type="checkbox"/> 368 Asbestos Personal Injury Product Liability PERSONAL PROPERTY <input type="checkbox"/> 370 Other Fraud <input type="checkbox"/> 371 Truth in Lending <input type="checkbox"/> 380 Other Personal Property Damage <input type="checkbox"/> 385 Property Damage Product Liability	<input type="checkbox"/> 610 Agriculture <input type="checkbox"/> 620 Other Food & Drug <input type="checkbox"/> 625 Drug Related Seizure of Property 21 USC 881 <input type="checkbox"/> 630 Liquor Laws <input type="checkbox"/> 640 R.R. & Truck <input type="checkbox"/> 650 Airline Regs. <input type="checkbox"/> 660 Occupational Safety/Health <input type="checkbox"/> 690 Other	<input type="checkbox"/> 422 Appeal 28 USC 158 <input type="checkbox"/> 423 Withdrawal 28 USC 157 PROPERTY RIGHTS <input type="checkbox"/> 820 Copyrights <input checked="" type="checkbox"/> 830 Patent <input type="checkbox"/> 840 Trademark	<input type="checkbox"/> 400 State Reapportionment <input type="checkbox"/> 410 Antitrust <input type="checkbox"/> 430 Banks and Banking <input type="checkbox"/> 450 Commerce <input type="checkbox"/> 460 Deportation <input type="checkbox"/> 470 Racketeer Influenced and Corrupt Organizations <input type="checkbox"/> 480 Consumer Credit <input type="checkbox"/> 490 Cable/Sat TV <input type="checkbox"/> 810 Selective Service <input type="checkbox"/> 850 Securities/Commodities/Exchange <input type="checkbox"/> 875 Customer Challenge 12 USC 3410 <input type="checkbox"/> 890 Other Statutory Actions <input type="checkbox"/> 891 Agricultural Acts <input type="checkbox"/> 892 Economic Stabilization Act <input type="checkbox"/> 893 Environmental Matters <input type="checkbox"/> 894 Energy Allocation Act <input type="checkbox"/> 895 Freedom of Information Act <input type="checkbox"/> 900 Appeal of Fee Determination Under Equal Access to Justice <input type="checkbox"/> 950 Constitutionality of State Statutes
REAL PROPERTY <input type="checkbox"/> 210 Land Condemnation <input type="checkbox"/> 220 Foreclosure <input type="checkbox"/> 230 Rent Lease & Ejectment <input type="checkbox"/> 240 Torts to Land <input type="checkbox"/> 245 Tort Product Liability <input type="checkbox"/> 290 All Other Real Property	CIVIL RIGHTS <input type="checkbox"/> 441 Voting <input type="checkbox"/> 442 Employment <input type="checkbox"/> 443 Housing/Accommodations <input type="checkbox"/> 444 Welfare <input type="checkbox"/> 445 Amer. w/Disabilities - Employment <input type="checkbox"/> 446 Amer. w/Disabilities - Other <input type="checkbox"/> 440 Other Civil Rights	PRISONER PETITIONS <input type="checkbox"/> 510 Motions to Vacate Sentence Habeas Corpus: <input type="checkbox"/> 530 General <input type="checkbox"/> 535 Death Penalty <input type="checkbox"/> 540 Mandamus & Other <input type="checkbox"/> 550 Civil Rights <input type="checkbox"/> 555 Prison Condition	LABOR <input type="checkbox"/> 710 Fair Labor Standards Act <input type="checkbox"/> 720 Labor/Mgmt. Relations <input type="checkbox"/> 730 Labor/Mgmt. Reporting & Disclosure Act <input type="checkbox"/> 740 Railway Labor Act <input type="checkbox"/> 790 Other Labor Litigation <input type="checkbox"/> 791 Empl. Ret. Inc. Security Act	SOCIAL SECURITY <input type="checkbox"/> 861 HIA (1395ff) <input type="checkbox"/> 862 Black Lung (923) <input type="checkbox"/> 863 DIWC/DIWW (405(g)) <input type="checkbox"/> 864 SSID Title XVI <input type="checkbox"/> 865 RSI (405(g))	
			IMMIGRATION <input type="checkbox"/> 462 Naturalization Application <input type="checkbox"/> 463 Habeas Corpus - Alien Detainee <input type="checkbox"/> 465 Other Immigration Actions	FEDERAL TAX SUITS <input type="checkbox"/> 870 Taxes (U.S. Plaintiff or Defendant) <input type="checkbox"/> 871 IRS—Third Party 26 USC 7609	

V. ORIGIN (Place an "X" in One Box Only)

1 Original Proceeding

2 Removed from State Court

3 Remanded from Appellate Court

4 Reinstated or Reopened

5 Transferred from another district (specify)

6 Multidistrict Litigation

7 Appeal to District Judge from Magistrate Judgment

VI. CAUSE OF ACTION

Cite the U.S. Civil Statute under which you are filing (Do not cite jurisdictional statutes unless diversity):
35 U.S.C. §§ 100, et seq 35:145 et seq

Brief description of cause:
COMPLAINT FOR PATENT INFRINGEMENT

VII. REQUESTED IN COMPLAINT:

CHECK IF THIS IS A CLASS ACTION UNDER F.R.C.P. 23

DEMAND \$

CHECK YES only if demanded in complaint:
JURY DEMAND: Yes No

VIII. RELATED CASE(S) IF ANY

(See instructions): JUDGE _____ DOCKET NUMBER _____

DATE: 12/27/2010

SIGNATURE OF ATTORNEY OF RECORD: /s/Kurtis D. MacFerrin

FOR OFFICE USE ONLY

RECEIPT # 21583 AMOUNT \$350.00 APPLYING IFP NS JUDGE _____ MAG. JUDGE _____

12-27-10

CR

Court Name: USDC California Southern
Division: 3
Receipt Number: CAS021583
Cashier ID: nsiefken
Transaction Date: 12/27/2010
Payer Name: PRO-COURIER, INC

CIVIL FILING FEE
For: LIFE TECH V BIOSEARCH TECH
Case/Party: D-CAS-3-10-CV-002665-001
Amount: \$350.00

CHECK
Check/Money Order Num: 13122
Amt Tendered: \$350.00

Total Due: \$350.00
Total Tendered: \$350.00
Change Amt: \$0.00

There will be a fee of \$45.00
charged for any returned check.