Kit for Cancer Detection

Technical Field

The present invention relates to a kit for cancer detection; more specifically, a detection kit having a primer set or probe targeting a V384D mutation.

Description of Related Art

Cancer has been the leading cause of death for a long time in human history. Numberless researches are conducted focusing on the detection and treatment of cancers. Unfortunately, most of the treatments of cancer used clinically in nowadays still are not reliable for eliminating the threat of cancer. Nevertheless, researches and clinical experience have showed that the earlier the treatment begins, the higher the survival rate is for cancer patients. These evidences give the importance of the cancer detection especially at the early stage of carcinogenesis.

Typically, the detection of carcinogenesis is made by determining biomarkers specifically existing in cancer patients. The biomarkers might be the substances specifically released by cancer cells, the cell surface markers specifically expressed by cancer cells, the gene silence or overexpression specifically happened in cancer cells, or the gene mutation specifically existing in cancer cells.

The missense mutation in the DNA mismatch repair gene hMLH1 has been reported recently as a biomarker in several kinds of cancers. The missense mutation of V384D in hMLH1 was first observed in colorectal cancer and the occurrence thereof was showed to be specific in Chinese patients in comparison with German patients (Yaping Wang, et al, 1997). Subsequent studies had confirmed the aforesaid discovery and a further study in 2004 by Chang et al. even highlighted the missense mutation of hMLH1 V384D in four kinds of cancers including colorectal cancer, gastric cancer, breast cancer, and esophageal cancer and another study in 2003 by Xianzhe Shi et al also showed the existence in lung cancer.

The aforesaid studies indicated that the missense mutation of V384D in hMLH1 could be a promising candidate for cancer detection. Moreover, the research did by the team of the instant invention further proves that the missense mutation of V384D in hMLH1 is related to the drug resistance in the EGFR-TKIs treatment of lung cancer (data showed in the following paragraphs).

In light of the foregoing, the well-designed detection tools targeting the aforesaid V384D mutation shall be helpful and valuable medical industry and clinical use. Although several researches have presented some primers and probes for the aforesaid purpose, the goal of the present invention is to provide a primer set and/or a probe being more specific and sensitive than the conventional ones.

SUMMARY

In light of the foregoing, one of the objective of the present invention is to provide a kit for cancer detection by using a promising biomarker.

Another objective of the present invention is to provide a kit for evaluating the efficacy of an EGFR-TKI treatment and/or the progression-free survival of a subject after the same so that the follow-up treating strategies can be set up as soon as possible after an EGFR-TKI treatment.

In order to achieve the above-mentioned objective, the present invention provides a kit for identifying a V384 alteration of a *MLH1* gene encoded protein of a subject, comprising:

a first primer comprising SEQ ID NO 06; and a second primer comprising SEQ ID NO 07; and/or

a first primer comprising SEQ ID NO 08; and a second primer comprising SEQ ID NO 09.

Preferably, said kit further comprises a third primer comprising SEQ ID NO 05.

Preferably, said kit of claim 1, further comprising a DNA polymerase.

Preferably, said kit further comprises a double stranded DNA binding dye.

Preferably, said double stranded DNA binding dye is SYBR® Green I, SYBR® Green II, SYBR® Gold, Oxazole Yellow, Thiazole Orange, PicoGreen, EvaGreen®, a combination thereof.

The present invention also provides a kit for identifying a V384 alteration of a *MLH1* gene encoded protein of a subject, comprising:

a first primer comprising SEQ ID NO 08; and

a second primer comprising SEQ ID NO 09.

The present invention also provides kit for identifying a V384 alteration of a *MLH1* gene encoded protein of a subject, comprising:

at least one mutation probe comprising SEQ

ID NO 10; wherein said probe is conjugated with a fluorophore; and/or

at least one wild-type probe comprising SEQ ID NO 11; wherein said probe is conjugated with a fluorophore.

Preferably, said at least one mutation probe and/or said at least one wild-type probe is further conjugated with a quencher. Preferably, said fluorophore is conjugated at the 5' end of said probe and said quencher is conjugated at the 3' end of said probe. Preferably, said at least one mutation probe comprises SEQ ID NO.17. Preferably, said at least one wild-type probe comprises SEQ ID NO.16.

Preferably, said at least one mutation probe and/or at said at least one wild-type probe comprises at least one nucleotide thereof being modified with a bridge connecting the 2' oxygen and 4' carbon thereof. Preferably, said mutation probe comprises SEQ ID NO 19 having the following sequence:

5'-CACCAGATGGATCGTACA-3'.

Preferably, said mutation probe has the 5th, 8th, 11th, and 14th nucleotides thereof counted from 5' to 3' being modified with a bridge connecting the 2' oxygen and 4' carbon.

Preferably, said wild-type probe comprises SEQ ID NO 18 having the following sequence:

5'- CACCAGATGGTTCGTACA -3'.

Preferably, said mutation probe has the 5th, 8th, 11th, and 14th nucleotides thereof counted from 5' to 3' being modified with a bridge connecting the 2' oxygen and 4' carbon.

Preferably, said kit further comprises an anchor probe conjugated with a donor fluorophore. Preferably, said at least one mutation probe comprises SEQ ID NO.21 and is conjugated with a receptor fluorophore. Preferably, said at least one wild-type probe comprises SEQ ID NO.20 and is conjugated with a receptor fluorophore. Preferably, said anchor probe comprises SEQ ID NO. 22

Preferably, said kit further comprises a primer set for amplifying at least a part of said *MLH1* gene to obtain an amplicon; wherein said amplicon comprises a site corresponding to said V384 alteration.

Preferably, said primer set is:

a forward primer comprising SEQ ID NO 12, and a reverse primer comprising SEQ ID NO 13; and/or

a forward primer comprising SEQ ID NO 14, and a reverse primer comprising SEQ ID NO 15.

Preferably, said kit further comprises a DNA polymerase.

To sum up, the present invention provides a novel primer set or a probe for identifying a V384 alteration of a *MLH1* gene and a kit having the same. By using the primer set and/or the kit of the present invention, the identification of the V384 alteration can be performed more specifically and sensitively than the conventional tools.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure. 1 shows the results of the Real-time polymerase chain reaction of the Example 1 of the instant specification (n=2); wherein the results of primer set of **SEQ ID NO 07** and **SEQ ID NO 05** were marked as curve (1), the results of primer set of **SEQ ID NO 07** and **SEQ ID NO 06** were marked as curve (2), and the results of negative control were marked as curve (3). (A) Genomic DNA of a subject without V384D mutation. (B) Genomic DNA of a subject with V384D mutation (heterozygote). (C) Artificial plasmid constructed with a partial sequence of a wild-type *MLH1* gene (homozygote). (D) Artificial plasmid constructed with a partial sequence of a *MLH1* gene with the T1151A mutation (homozygote).

Figure 2 showed the result of the HRM assay in Example 2 (n=2). (A) Standard stage; (B) Melt curve stage. Curve 1: Artificial plasmid constructed with a partial sequence of a wild-type *MLH1* gene (homozygote). Curve 2: Artificial plasmid constructed with a partial sequence of a *MLH1* gene with the T1151A mutation (homozygote).

Figure 3 showed the result of the TaqMan assay in Example 3 (n=2). (A): Artificial plasmid constructed with a partial sequence of a wild-type *MLH1* gene (homozygote). (B) Artificial plasmid constructed with a partial sequence of a *MLH1* gene with the T1151A mutation (homozygote). Curve (1): wild-type probe (negative probe, ML-TP-Wt, **SEQ ID NO 16**); curve (2): mutation probe (positive probe, ML-TP-Mt, **SEQ ID NO 17**); curve (3): control (no template used).

Figure 4 showed the result of the LNA assay in Example 4 (n=3). (A): Artificial plasmid constructed with a partial sequence of a wild-type *MLH1* gene (homozygote). (B) Artificial plasmid constructed with a partial sequence of a *MLH1* gene with the T1151A mutation (homozygote). Curve (1): wild-type probe (negative probe, ML-TP-Wt, **SEQ ID NO 18**); curve (2): mutation probe (positive probe, ML-TP-Mt, **SEQ ID NO 19**); curve (3): control (no template used).

Figure 5 showed the result of the FRET assay in Example 5 (n=2). (A)(B): probes of

ML-sensor-Wt (**SEQ ID NO 20**) and ML-anchor (**SEQ ID NO 22**) were used; (C)(D): probes of ML-sensor-Mt (**SEQ ID NO 21**) and ML-anchor (**SEQ ID NO 22**) were used. Curve (1): Artificial plasmid constructed with a partial sequence of a wild-type *MLH1* gene (homozygote). Curve (2): Artificial plasmid constructed with a partial sequence of a *MLH1* gene with the T1151A mutation (homozygote). Curve (3): control (no template used). Curve (4): VP13_0052 (heterozygote). Curve (5): VP13_0055 (wild-type; homozygote).

DETAILED DESCRIPTION

In this study, we provided a primer set and/or a probe suitable for analyzing a sequence of a *MLH1* DNA, a *MLH1* mRNA, and/or a cDNA sequence derived from said *MLH1* mRNA of a subject to identify a V384 alteration of a *MLH1* gene encoded protein.

The identification of said alteration could provide a promised possibility that the subject to be detected has already had cancer, such as colorectal cancer, gastric cancer, breast cancer, esophageal cancer, lung cancer, or a combination thereof. Moreover, in terms of a lung cancer therapy, the identification of said alteration in a subject could also provide information for evaluating efficacy of an EGFR-TKI treatment and/or for evaluating progression-free survival of said subject after an EGFR-TKI treatment.

The term of "EGFR-TKI therapy" or "EGFR-TKI treatment" used herein is referred to as a targeted therapy or targeted treatment adopting the fact that a fair amount of non-small cell lung cancer patients share a somatic mutation in the tyrosine kinase domain of epidermal growth factor receptor of tumor cells. Specifically, the "EGFR-TKI therapy" or "EGFR-TKI treatment" is conducted by using an EGFR tyrosine kinase inhibitor targeting the somatic mutation in the tyrosine kinase domain of epidermal growth factor receptor of tumor cells.

The term of "efficacy of an EGFR-TKI treatment" used herein is referred to as the effect of an EGFR-TKI treatment on the progress of tumors. If tumors keep progressing within 3 months from the initiation of an EGFR-TKI treatment, the treatment is considered as clinically ineffective. On the other hand, if the tumors are at least 30% reduced in size (based on the initial size there of before treatment), the EGFR-TKI treatment is determined as having efficacy to the subject.

The term of "progression-free survival" used herein is referred to as the time period between the initial date of a treatment and the time point that the tumor concerned begins to progress again. In other words, it is the length of time that the tumors, during this time

period, have no progress or are reduced in size.

The term of "analyzing" or "analyze" used herein is referred to as evaluating or examining a property of a subject of interest by at least of technical means. Said technical means include but not limited to polymerase chain reaction, Southern blot, and Western blot.

The description of "V384 alteration of a *MLH1* gene encoded protein" recited herein is referred to as an alternation existing in the sequence of said *MLH1* gene that results in an alteration at V384 position of a *MLH1* gene encoded protein. In an alternative embodiment of the present invention, said V384 alteration is a V384D mutation of a protein encoded by said *MLH1* gene. In an alternative embodiment, said V384D mutation can be identified as a T1151A mutation of a cDNA of said *MLH1* gene, or a T1349A mutation of a RNA of said *MLH1* gene. The term of "wild-type" is a comparative term for describing a gene and/or a protein without the aforesaid mutation/alternation.

The term of "V384" used herein is referred to as the 384th amino acid of the amino acid sequences of a *MLH1* protein (that is, a protein encoded by said *MLH1* gene); wherein "V" is the one-letter abbreviation of Valine (Val). The term of "V384 alteration" used herein is referred to as the 384th amino acid of Valine is altered to another amino acid other than Valine. The term of "V384D mutation" used herein is referred to as the 384th amino acid of Valine is altered to Aspartic acid; wherein "D" is the one-letter abbreviation of Aspartic acid (Asp). See also **SEQ ID NO 01** for the amino acid sequence having the aforesaid mutation and **SEQ ID NO 02** for the DNA sequence having the aforesaid mutation.

The term of "U1349" used herein is referred to as the 1349th nucleotide of the nucleotide sequence of a mRNA encoding a *MLH1* protein; "U" is an abbreviation of uracil. The term of "U1349 mutation" used herein is referred to as the 1349th nucleotide of thymine is altered/mutated to another nucleotide other than uracil. The term of "U1349A mutation" used herein is referred to as the 1349th nucleotide of uracil is altered to adenine; wherein "A" is an abbreviation of adenine. See also **SEQ ID NO 03** for the mRNA sequence having the aforesaid mutation.

The term of "T1151" used herein is referred to as the 1151th nucleotide of the nucleotide sequence of a cDNA; wherein said cDNA is from a mRNA of said *MLH1* gene; "T" is an abbreviation of thymine. The term of "T1151 mutation" used herein is referred to as the 1151th nucleotide of thymine is altered/mutated to another nucleotide other than

thymine. The term of "T1151A mutation" used herein is referred to as the 1151th nucleotide of thymine is altered to adenine; wherein "A" is an abbreviation of adenine. See also **SEQ ID NO 04** for the cDNA sequence having the aforesaid mutation.

Primer Sets, Probes, and Kits Using the Same

First Aspect

In the first aspect of the present invention, the V384 alteration of a *MLH1* gene encoded protein is detected by using a primer set. Said "V384 alteration of a *MLH1* gene encoded protein" is defined as set forth in the preceded paragraphs. Preferably, the detection is conducted by real-time PCR with said primer set.

In the first aspect of the present invention, a kit for identifying a V384 alteration of a *MLH1* gene encoded protein of a subject is provided. Said kit comprises a primer set, which is designed for analyzing a sequence of a *MLH1* DNA, a *MLH1* mRNA, and/or a cDNA sequence derived from said *MLH1* mRNA of a subject to identify a V384 alteration of a *MLH1* gene encoded protein.

In a preferable embodiment, said primer set comprises a first primer and a second primer. Said first primer is designed to comprise a sequence that is capable of hybridizing with a *MLH1* gene having said V384 alteration at V384 site. Said second primer is designed to comprise a sequence that is capable of hybridizing with a conserved region of said *MLH1* gene. The PCR product of said first primer and said second primer is detected representing the existence of the V384 alteration.

The term of "capable of hybridizing with a *MLH1* gene having said V384 alteration at V384 site" means said sequence is capable of base-pairing with at least one nucleotide of the codon encoding said V384 alteration in said *MLH1* gene. It is known that a codon contains three nucleotides. In a preferable embodiment, said sequence is capable of forming base-pairs with at least two nucleotides of the codon encoding said V384 alteration in said *MLH1* gene.

The term of "a conserved region of said *MLH1* gene" used herein is referred to a sequence of said *MLH1* gene that is conserved or unchanged between a wild-type *MLH1* gene and a *MLH1* gene having the aforesaid V384 alteration. The term of "wild-type" is a relative description to describe a subject without the aforesaid V384 alteration.

In an alternative embodiment, said kit further comprises a third primer. Said third primer is designed to comprise a sequence that is capable of hybridizing with a wild-type

MLH1 gene at the site of V384. The term "capable of hybridizing" is defined as preceded paragraphs.

In a practical embodiment, said kit comprises a first primer of **SEQ ID NO 06**, a second primer of **SEQ ID NO 07**, and a third primer of **SEQ ID NO 05**. This embodiment is used for a SYBR-green assay. The detection of the PCR product of said first primer and said second primer represents the existence of said V384 alteration while in this case the PCR product of said third primer and said second primer of **SEQ ID NO 07** is a control.

In another practical embodiment, said kit comprises a first primer of **SEQ ID NO 08** and a second primer of **SEQ ID NO 09**. This embodiment is used for a High Resolution Melting (HRM) assay. In a HRM assay, the DNA binding dye will bind to the PCR product at standard stage and the fluorescence can be detected. While in the melting stage, the PCT product is melted and a decay of the fluorescence signal of the DNA binding dye can be detected. By comparing the decay pattern of a sample with a wild-type control or a mutation control, the V384 alteration can be identified.

In a preferable embodiment, said kit further comprises a DNA polymerase, and/or a DNA binding dye. Preferably, said DNA polymerase is, but not limited to, Pfu DNA polymerase, Taq DNA polymerase or a combination thereof. Preferably, said DNA binding dye is, but not limited to, SYBR® Green I, SYBR® Green II, SYBR® Gold, Oxazole Yellow, Thiazole Orange, PicoGreen, EvaGreen®, or a combination thereof.

Second Aspect

In the second aspect of the present invention, the V384 alteration of a *MLH1* gene encoded protein is detected by using a probe. Said "V384 alteration of a *MLH1* gene encoded protein" is defined as set forth in the preceded paragraphs.

In the second aspect of the present invention, a kit for identifying a V384 alteration of a *MLH1* gene encoded protein of a subject is provided.

In a preferable embodiment, said kit comprises a probe, which is designed for analyzing a sequence of a *MLH1* DNA, a *MLH1* mRNA, and/or a cDNA sequence derived from said *MLH1* mRNA of a subject to *positively or negatively* identify a V384 alteration of a *MLH1* gene encoded protein.

In a *positive* scenario of identifying V384 alteration, said probe (*mutation* probe) is designed to hybridize with a segment of a genomic DNA, a mRNA and/or a cDNA of said *MLH1* gene; wherein said segment has a sequence corresponding to said V384 alternation

of a protein encoded by said *MLH1* gene. For example, said segment may have the T1349A mutation of said mRNA or the T1151A mutation of said cDNA. Through examining the result of hybridization, the aforesaid V384 alteration can be identified. In this positive scenario, the detection of the signal of hybridization between said probe and the target represents the existence of the V384 alteration. In a preferable embodiment, said mutation probe comprises **SEQ ID NO 10**.

In a *negative* scenario of identifying V384 alteration, said probe (*wild-type* probe) is designed to hybridize with a segment of a *wild-type* genomic DNA, a mRNA and/or a cDNA of said *MLH1* gene. In this negative scenario, the inexistence of the signal of hybridization between said probe and the target represents the inexistence of wild-type *MLH1* gene, giving possibility of the existence of the V384 alteration. In a preferable embodiment, said wild-type probe comprises **SEQ ID NO 11**.

Nevertheless, those having skill in the art can realize that there is a possibility that the subject be tested may have a heterozygous genotype of *MLH1* gene. That is, an allele of the *MLH1* gene the subject has is wild-type while the other allele thereof is of a V384 alteration. In that circumstance, it is preferable to use a mutation probe or use both of the mutation probe and wild-type probe for detection.

Preferably, said probe (mutation probe and wild-type probe) is modified to fulfill the purpose of targeting the V384 alternation of said *MLH1* gene. In an embodiment of the present invention, said probe is conjugated with a fluorophore and/or isotope. In a preferable embodiment, said probe is conjugated with a fluorophore and a quencher. In an alternative embodiment, said probe is further modified with a bridge connecting the 2' oxygen and 4' carbon thereof.

Preferably, said fluorophore is conjugated at the 5' end of said probe and said quencher is conjugated at the 3' end of said probe. Said fluorophore includes, but not limited to 6-carboxyfluorescein, tetrachlorofluorescein, FAM, VIC, LC640, or a combination thereof Said quencher includes, but not limited to tetramethylrhodamine, BHQ1, or a combination thereof.

In a preferable embodiment, said kit is designed for a PCR-based **TaqMan assay**. Said kit comprises a mutation probe comprising **SEQ ID NO. 17**, and/or a wild-type probe comprising **SEQ ID NO. 16**. Both of said probe are conjugated with a fluorophore and a quencher respectively at both ends of said probe.

In a preferable embodiment, said kit is designed for a PCR-based LNA assay (locked nucleic acid). Said kit comprises a mutation probe comprising **SEQ ID NO. 19**, and/or a wild-type probe comprising **SEQ ID NO. 18**. Both of said probe are conjugated with a fluorophore and a quencher respectively at both ends of said probe.

Preferably, said probe of **SEQ ID NO. 19** or **SEQ ID NO. 18** has at least one nucleotide being modified with a bridge connecting the 2' oxygen and 4' carbon thereof to form a locked nucleic acid. For instance, the 5^{th}, 8^{th}, 11^{th}, and 14^{th} nucleotides of said probe (counted from 5' to 3') are modified with a bridge connecting the 2' oxygen and 4' carbon thereof.

In an alternative embodiment, said kit is designed for a PCR-based FRET assay (Fluorescence resonance energy transfer). In a practically embodiment, said kit comprises a mutation probe and/or a wild-type probe, and an anchor probe. Said mutation probe or wild-type probe is conjugated with a first fluorophore as a receptor and said anchor is conjugated with a second fluorophore as a donor. Preferably, said mutation probe comprises **SEQ ID NO.21**, said wild-type probe comprises **SEQ ID NO.20**, and said anchor probe comprises **SEQ ID NO.22**. In a preferable embodiment, said kit comprises said mutation probe, said wild-type probe, and said anchor probe.

In a preferable embodiment, said first fluorophore is FAM, HEX, LC Red 640, Cy5, or a combination thereof. In a preferable embodiment, said second fluorophore is fluorescein or a combination thereof.

In an alternative embodiment, said kit further comprises a DNA polymerase. Preferably, said DNA polymerase has exonuclease activity.

In a preferably embodiment, said kit further comprises a primer set for amplifying a part of said *MLH1* gene to obtain an amplicon; wherein said amplicon comprises a site corresponding to said V384. Said primer set may be:

- a first primer of **SEQ ID NO 12** and a second primer of **SEQ ID NO 13**; and/or
- a first primer of **SEQ ID NO 14** and a second primer of **SEQ ID NO 15**.

The following Table 1 lists the afore-mentioned primer sets and probes of the present invention together with the technology method therefor.

Table 1: Primer sets and Probes of the present invention listed correspondingly with the technology methods

Methods	Primer name	Primer sequence	SEQ ID NO	Probe name	Probe sequence	SEQ ID NO
SYBR green I	SB-WT-sF3	GGTCTATGCCCACCAGATTGT	05	N/A	N/A	
	SB-MT-sF3	GGTCTATGCCCACCAGATTGA	06			
	SB-sR3	GTTCAAGCATCTCCTCATCTG	07			
HRM	HR-1-F	TTCTGGAAGTAGTGATAAGGT CTATGCC	08	N/A	N/A	
	HR-1-R	GGTTTGCTCAGAGGCTGCA	09			
TaqMan	TP-2-F	GGAAGTAGTGATAAGGTCTA	12	ML-TP-Wt	CCACCAGATGGTTCGTACAG ATT	16
	TP-1-R	CTGTCTTATCCTCTGTGA	13	ML-TP-Mt	CCACCAGATGGATCGTACAG ATT	17
LNA	TP-2-F	GGAAGTAGTGATAAGGTCTA	12	ML-LNA-Wt	CACCAGATGGTTCGTACA	18
	TP-1-R	CTGTCTTATCCTCTGTGA	13	ML-LNA-Mt	CACCAGATGGATCGTACA	19
FRET	FR-1-F	TAAATCCACAACAAGTCT	14	ML-sensor-Wt	ACCAGATGGTTCGTACAGAT	20
	FR-1-R	TAGAAATATCTGTCTTATCCT	15	ML-sensor-Mt	ACCAGATGGATCGTACAGAT	21
				ML-anchor	CTTCTGGAAGTAGTGATAAG GTCTATGCC	22

Example 1: Verification of the Primer Set Designed in the Present Invention (SYBR Green assay).

In this example, the primers of SB-MT-sF3 (**SEQ ID NO 06**), SB-sR3 (**SEQ ID NO 07**), and SB-WT-sF3 (**SEQ ID NO 05**) were used for a Real-time polymerase chain reaction in order to verify their capability in identifying the V384D mutation.

For the experiments, four templates were prepared including a genomic DNA extracted from a subject without V384D mutation, a genomic DNA extracted from a subject with V384D mutation (heterozygote), an artificial plasmid constructed with a partial sequence of a wild-type *MLH1* gene (homozygote), and an artificial plasmid constructed with a partial sequence of a *MLH1* gene with the T1151A mutation (homozygote). The templates and the primer set used in this example were listed in the following Table 2.

Table 2

Template	Primer Set		
	Curve (1), Fig. 1	Curve (2), Fig. 1	Curve (3), Fig. 1
Genomic DNA Subject w/o mutation	SEQ ID NO 05 SEQ ID NO 07	SEQ ID NO 06 SEQ ID NO 07	None (Ngative control)
Genomic DNA Subject w/ mutation	SEQ ID NO 05 SEQ ID NO 07	SEQ ID NO 06 SEQ ID NO 07	None (Negartive control)
Plasmid wild-type *MLH 1*	SEQ ID NO 05 SEQ ID NO 07	SEQ ID NO 06 SEQ ID NO 07	None (Negartive control)
Plasmid mutated *MLH 1*	SEQ ID NO 05 SEQ ID NO 07	SEQ ID NO 06 SEQ ID NO 07	None (Negartive control)

The experiments were conducted according to the product manual of the EZtime™ Real Time PCR premix (Yeastern Biotech Co., Ltd.). The PCR mixture contained: 1.0 μl of template (2.5μg/μl for genomic DNA template; 1μg/μl for plasmid template), 12.5μl of 2X EZtime Real-time PCR Premix, 1.0μl of forward primer (5μM), 1.0μl of reverse primer (5μM), and 9.5μl of ddH_2O was prepared. The reaction condition was: 95℃ denaturation for 10 min; 95℃ denaturation 20sec, 66℃ anneal/extension 1 min, 40 cycles; then melt curve stage: 95℃ 15 sec, 60℃ 1 min, 95℃ 30 sec, 60℃ 15 sec. The Real-time PCR instrument used was 7500 Fast (Applied Biosystem) equipped with Open 7500 Software v2.0.6.

The results were showed in Figure 1 (A) to (D); wherein the results of primer set of **SEQ ID NO 05** and **SEQ ID NO 07** were marked as curve (1), the results of primer set of **SEQ ID NO 06** and **SEQ ID NO 07** were marked as curve (2), and the results of negative control were marked as curve (3).

According to the results, the wild-type primer set (**SEQ ID NO 05** and **SEQ ID NO 07**) could only amplify the wild-type *MLH1* sequence (Figure 1A, 1B, and 1C) and the mutant primer set (**SEQ ID NO 06** and **SEQ ID NO 07**) could only amplify the *MLH1* sequence with V384D mutation (Figure 1B and 1D). The amplification plot of Figure 1A only showed curve (1) representing that it was indeed a homozygous wild-type sample. On the other hand, the amplification plot of Figure 1B showed both curve (1) and curve (2) representing that it was a heterozygous sample. Figure 1C and 1D of artificial plasmids respectively showed curve (1) and curve (2) indicating that both of them were homozygotes.

The data showed that the present mutant primer set can specifically identify the V384D mutation of a *MLH1* gene and the present wild-type primer set can specifically identify a *MLH1* gene without the V384D mutation. The results proved that the primer set of the present invention could clearly identify the V384D mutation of a sample with excellent specificity and sensitivity.

Example 2: Verification of the Primer Set Designed in the Present Invention (HRM assay).

In this example, the primers of HR-1-F (**SEQ ID NO 08**) and HR-1-R (**SEQ ID NO 09**) were used for a Real-time polymerase chain reaction in order to verify their capability in identifying the V384D mutation.

For the experiments, two templates were respectively an artificial plasmid constructed with a partial sequence of a wild-type *MLH1* gene (homozygote) and an artificial plasmid constructed with a partial sequence of a *MLH1* gene with the T1151A mutation (homozygote).

The experiments were conducted according to the product manual. Briefly, the PCR mixture contained: template 20 ng, Brilliant HRM Ultra-Fast Loci Master Mix, forward primer (HR-1-F) 0.5 uM, and reverse primer (HR-1-R) 0.5 uM. Reaction conditions: 95℃ pre-incubation for 3 min; 95℃ denaturation 5 sec, 60℃ anneal/extension 10 sec, 40 cycles; then melt curve stage: 95℃ 30 sec, 65℃ 30 sec, 95℃ 30 sec. Real-time PCR instrument is Agilent Mx3000p (Applied Biosystem). Open Applied Biosystem Software, and set the conditions in accordance with the above parameters.

Figure 2 showed the result of the HRM assay of this example. It was noted that the primer set (HR-1-F and HR-1-R) was able to amplify both of the wild-type *MLH1*

sequence and the *MLH1* sequence of V384D mutation (Figure 2(A)). In the melting stage, mutant type had a mismatch nucleotide so it may have different dissociated curve from wild type. The decay of the signal shown as curve 2 represented the mutant existing (Figure 2(B)). The result verified that the present primer set indeed recognized the V384 mutation.

Example 3: Verification of the Probe Designed in the Present Invention (TaqMan assay).

In this example, the primers of TP-2-F (**SEQ ID NO 12**) and TP-1-R (**SEQ ID NO 13**) were used for a Real-time polymerase chain reaction. Also, a mutation probe (ML-TP-Mt; labeled with VIC and TAMRA) of **SEQ ID NO 17** and a wild-type probe (ML-TP-Wt; labeled with FAM and TAMRA) of **SEQ ID NO 16** were used to verify their capability in identifying the V384D mutation.

For the experiments, two templates were respectively an artificial plasmid constructed with a partial sequence of a wild-type *MLH1* gene (homozygote) and an artificial plasmid constructed with a partial sequence of a *MLH1* gene with the T1151A mutation (homozygote).

The experiments were conducted according to the product manual. Briefly, the PCR mixture contained: template 2.0 ul (25 ng/ul), 2X Brilliant III Ultra-Fast QPCR Master Mix with Low ROX 10.0 ul, 1.0 ul forward primer (10 uM), 1.0 ul reverse primer (10 uM), 0.5 ul ML-TP-Wt (10 uM), 0.5 ul ML-TP-Mt (10 uM), ddH_2O 5.0 ul. Reaction conditions: 95℃ denaturation for 3 min; 95℃ denaturation 12 sec, 55℃ anneal 30 sec, 72℃ extension 1 min, 40 cycles. Real-time PCR instrument is 7500 Fast (Applied Biosystem). Open 7500 Software v2.0.6, and set the conditions in accordance with the above parameters.

The results were shown in Figure 3. The wild-type *MLH1* sequence could specifically detect by ML-TP-Wt probe (Figure 3(A)), and the mutant MLH1 sequence could specifically detect by ML-TP-Mt probe (Figure 3(B)). The result verified that the present probes have great specificity in detecting the V384 mutation.

Example 4: Verification of the Probe Designed in the Present Invention (LNA assay).

In this example, the primers of TP-2-F (**SEQ ID NO 12**) and TP-1-R (**SEQ ID NO 13**) were used for a Real-time polymerase chain reaction. Also, a mutation probe (ML-LNA-Mt; labeled with VIC and BHQ1) of **SEQ ID NO 19** and a wild-type probe

(ML-LNS-Wt; labeled with FAM and BHQ1) of **SEQ ID NO 18** were used to verify their capability in identifying the V384D mutation.

For the experiments, two templates were respectively an artificial plasmid constructed with a partial sequence of a wild-type *MLH1* gene (homozygote), and an artificial plasmid constructed with a partial sequence of a *MLH1* gene with the T1151A mutation (homozygote).

The experiments were conducted according to the product manual. Briefly, the PCR mixture contained: template 5.0 ul (2.5 ng/ul) or control plasmid DNA 5.0 ul (2.5 ng/ul), 2X EZtime Real-time PCR Premix 12.5 ul, 1.0 ul forward primer (10 uM), 1.0 ul reverse primer (10 uM), 0.5 ul ML-LNA-Wt (10 uM), 0.5 ul ML-LNA-Mt (10 uM), ddH_2O 4.5 ul. Reaction conditions: 95℃ denaturation for 10 min; 95℃ denaturation 15 sec, 50℃ anneal, 72℃ extension 1 min, 40 cycles; then melt curve stage: 95℃ 15 sec, 60℃ 1 min, 95℃ 30 sec, 60℃ 15 sec. Real-time PCR instrument is 7500 Fast (Applied Biosystem). Open 7500 Software v2.0.6, and set the conditions in accordance with the above parameters.

The results were shown in Figure 4. The wild-type *MLH1* sequence could specifically detect by ML-LNA-Wt probe (Figure 4(A)), and the mutant *MLH1* sequence could specifically detect by ML-LNA-Mt probe (Figure 4(B)). The result verified that the present probes have great specificity in detecting the V384 mutation.

Example 5: Verification of the Probe Designed in the Present Invention (FRET assay).

In this example, the primers of FR-1-F (**SEQ ID NO 14**) and FR-1-R (**SEQ ID NO 15**) were used for a Real-time polymerase chain reaction. Also, a mutation probe (ML-sensor-Mt; labeled with LC640) of **SEQ ID NO 21**, a wild-type probe (ML-sensor-Wt; labeled with LC640) of **SEQ ID NO 20**, and an anchor probe (ML-anchor; labeled with fluorescein) of **SEQ ID NO 22** were used to verify their capability in identifying the V384D mutation.

For the experiments, two templates were respectively an artificial plasmid constructed with a partial sequence of a wild-type *MLH1* gene (homozygote) and an artificial plasmid constructed with a partial sequence of a *MLH1* gene with the T1151A mutation (homozygote). Furthermore, two clinical samples (VP13_0055 and VP13_0052) were also used. VP13_0055 is a homozygous wild-type and VP13_0052 is a heterozygous

mutant confirmed by our previous data using next-generation sequencer (Ion PGM System; data not shown).

The experiments were conducted according to the product manual. Briefly, the PCR mixture contained: template 5.0 ul (2.5 ng/ul), 10X LightCycler FastStart DNA Master HybProbe 2.0 ul, 1.0 ul forward primer (10 uM; **SEQ ID NO 14**), 1.0 ul reverse primer (10 uM; **SEQ ID NO 15**), 0.4 ul ML-sensor-Wt (10 uM), 0.4 ul ML-sensor-Mt (10 uM), 0.4 ul ML-anchor (10uM), ddH_2O 8.6 ul. Reaction conditions: 95℃ denaturation for 10 min; 95℃ denaturation for 10 sec, 55℃ anneal for 10 sec, 72℃ extension for 30 sec, 45 cycles; then melt curve stage: 95℃ 1 min, 40℃ 2 min, 95℃ 1 min. Real-time PCR instrument is LightCycler 480 Real-Time PCR System (Roche). Open LightCycler 480 software 1.5, and set the conditions in accordance with the above parameters.

The results were shown in Figure 5. The wild-type *MLH1* sequence was detected by ML-sensor-Wt and ML-anchor, and the mutant *MLH1* sequence was detected by ML-sensor-Mt and ML-anchor. When ML-sensor-Wt and ML-anchor were used, it was noted that both of the wild-type plasmid (curve 1) and VP13_0055 (curve 5) showed melting curve (Figure 5 (A) and (B)). When ML-sensor-Mt and ML-anchor were used, it was noted that both of the mutation plasmid (curve 2) showed melting curve (Figure 5 (C) and (D)). Moreover, VP13_0052 (curve 4), as being a heterozygote, showed melting curve no matter ML-sensor-Wt and ML-anchor or ML-sensor-Mt and ML-anchor were used (Figure 5 (A) and (C)). The result verified that the present probes have great specificity in detecting the V384 mutation.

CLAIMS

1. A kit for identifying a V384 alteration of a *MLH1* gene encoded protein of a subject, comprising:

a first primer comprising a sequence of SEQ ID NO 06; and

a second primer comprising a sequence of SEQ ID NO 07.

2. The kit of claim 1, further comprising a third primer comprising a sequence of SEQ ID NO 05.

3. The kit of claim 1, further comprising a DNA polymerase.

4. The kit of claim 1, further comprising a double stranded DNA binding dye.

5. The kit of claim 4, wherein said double stranded DNA binding dye is SYBR® Green I, SYBR® Green II, SYBR® Gold, Oxazole Yellow, Thiazole Orange, or PicoGreen.

6. A kit for identifying a V384 alteration of a *MLH1* gene encoded protein of a subject, comprising:

a first primer comprising a sequence of SEQ ID NO 08; and

a second primer comprising a sequence of SEQ ID NO 09.

7. The kit of claim 6, further comprising a DNA polymerase.

8. The kit of claim 6, further comprising a double stranded DNA binding dye.

9. The kit of claim 6, wherein said double stranded DNA binding dye is EvaGreen®, or a combination thereof.