

WHAT IS CLAIMED IS:

1. A method of determining whether twins are fraternal twins, comprising following steps:

genotyping at least one polymorphic site of fetuses of the twins, to obtain polymorphism type of the fetuses;

comparing the polymorphism type of the fetuses with corresponding polymorphic site of parents thereof; and

determining whether the twins are the fraternal twins based on a comparing result.

2. The method of claim 1, wherein the step of genotyping at least one polymorphic site of the fetuses of the twins further comprises:

extracting a nucleic acid sample of the fetuses from a pregnant sample;

constructing a sequencing library for the nucleic acid sample of the fetuses;

subjecting the sequencing library to sequencing, to obtain a sequencing result; and

determining the polymorphism type of the fetuses based on the sequencing result.

3. The method of claim 2, wherein the pregnant sample is selected from a group consisting of peripheral blood, pregnant woman urine and breast milk.

4. The method of claim 3, wherein the pregnant sample is peripheral blood.

5. The method of claim 2, prior to the step of constructing the sequencing library, further comprising:

subjecting the nucleic acid sample of the fetuses to amplifying, to obtain an amplification product containing the polymorphic site, for constructing the sequencing library.

6. The method of claim 5, wherein the amplification product has a length of 150 bp or less.

7. The method of claim 2, wherein the polymorphism is selected from a group

consisting of STR, VNTR, RFLP, STS, SSCP, CAPS and SNP.

8. The method of claim 7, wherein the polymorphic site is an STR polymorphic site being at least one selected from a group consisting of vWA, TPOX, D3S1358, D16S539, D5S818, CSF1PO, D11S2368, D2S1338, D8S1179, D13S317, D21S1437, D16S3391, Penta E, D12S1064, D12S391, D6S1043 and D19S433.

9. The method of claim 8, wherein the nucleic acid sample of the fetuses is subjected to amplifying by PCR, and

for vWA, oligonucleotides shown as SEQ ID NO: 1 and SEQ ID NO: 2 are used as PCR primers;

for TPOX, oligonucleotides shown as SEQ ID NO: 3 and SEQ ID NO: 4 are used as PCR primers;

for D3S1358, oligonucleotides shown as SEQ ID NO: 5 and SEQ ID NO: 6 are used as PCR primers;

for D16S539, oligonucleotides shown as SEQ ID NO: 7 and SEQ ID NO: 8 are used as PCR primers;

for D5S818, oligonucleotides shown as SEQ ID NO: 9 and SEQ ID NO: 10 are used as PCR primers;

for CSF1PO, oligonucleotides shown as SEQ ID NO: 11 and SEQ ID NO: 12 are used as PCR primers;

for D11S2368, oligonucleotides shown as SEQ ID NO: 13 and SEQ ID NO: 14 are used as PCR primers;

for D2S1338, oligonucleotides shown as SEQ ID NO: 15 and SEQ ID NO: 16 are used as PCR primers;

for D8S1179, oligonucleotides shown as SEQ ID NO: 17 and SEQ ID NO: 18 are used as PCR primers;

for D13S317, oligonucleotides shown as SEQ ID NO: 19 and SEQ ID NO: 20 are used as PCR primers;

for D21S1437, oligonucleotides shown as SEQ ID NO: 21 and SEQ ID NO: 22 are used as PCR primers;

for D16S3391, oligonucleotides shown as SEQ ID NO: 23 and SEQ ID NO: 24 are

used as PCR primers;

for Penta E, oligonucleotides shown as SEQ ID NO: 25 and SEQ ID NO: 26 are used as PCR primers;

for D12S1064, oligonucleotides shown as SEQ ID NO: 27 and SEQ ID NO: 28 are used as PCR primers;

for D12S391, oligonucleotides shown as SEQ ID NO: 29 and SEQ ID NO: 30 are used as PCR primers;

for D6S1043, oligonucleotides shown as SEQ ID NO: 31 and SEQ ID NO: 32 are used as PCR primers;

for D19S433, oligonucleotides shown as SEQ ID NO: 33 and SEQ ID NO: 34 are used as PCR primers.

10. A system for determining whether twins are fraternal twins, comprising:  
a genotyping apparatus, for subjecting at least one polymorphic site of fetuses of the twins to genotyping, to obtain polymorphism type of the fetuses;  
an analyzing apparatus, connected with the genotyping apparatus, and suitable for comparing the polymorphism type of the fetuses with corresponding polymorphic site of parents thereof; and determining whether the twins are the fraternal twins based on a comparing result.

11. The system of claim 10, wherein the genotyping apparatus further comprises:  
a nucleic acid extracting unit, for extracting a nucleic acid sample of the fetuses from a pregnant sample;  
a library constructing unit, connected to the nucleic acid extracting unit, and suitable for constructing a sequencing library for the nucleic acid sample of the fetuses;  
a sequencing unit, connected to the library constructing unit, and suitable for subjecting the sequencing library sequencing, to obtain a sequencing result; and  
a genotype determining unit, connected to the sequencing unit, and suitable for determining the polymorphism type of the fetuses.

12. The system of claim 10, wherein the genotyping apparatus further comprises:  
an amplifying unit, connected to the nucleic acid extracting unit and library

constructing unit respectively, and suitable for subjecting the nucleic acid sample of the fetuses to amplifying, to obtain an amplification product containing the polymorphic site, for constructing the sequencing library.

13. The system of claim 12, wherein the polymorphism is selected from a group consisting of STR, VNTR, RFLP, STS, SSCP, CAPS and SNP.

14. The system of claim 13, wherein the polymorphic site is an STR polymorphic site being at least one selected from a group consisting of vWA, TPOX, D3S1358, D16S539, D5S818, CSF1PO, D11S2368, D2S1338, D8S1179, D13S317, D21S1437, D16S3391, Penta E, D12S1064, D12S391, D6S1043 and D19S433.

15. The system of claim 14, wherein the amplifying unit is equipped with the primers, for subjecting the nucleic acid sample of the fetuses to amplifying by PCR, and

for vWA, oligonucleotides shown as SEQ ID NO: 1 and SEQ ID NO: 2 are used as PCR primers;

for TPOX, oligonucleotides shown as SEQ ID NO: 3 and SEQ ID NO: 4 are used as PCR primers;

for D3S1358, oligonucleotides shown as SEQ ID NO: 5 and SEQ ID NO: 6 are used as PCR primers;

for D16S539, oligonucleotides shown as SEQ ID NO: 7 and SEQ ID NO: 8 are used as PCR primers;

for D5S818, oligonucleotides shown as SEQ ID NO: 9 and SEQ ID NO: 10 are used as PCR primers;

for CSF1PO, oligonucleotides shown as SEQ ID NO: 11 and SEQ ID NO: 12 are used as PCR primers;

for D11S2368, oligonucleotides shown as SEQ ID NO: 13 and SEQ ID NO: 14 are used as PCR primers;

for D2S1338, oligonucleotides shown as SEQ ID NO: 15 and SEQ ID NO: 16 are used as PCR primers;

for D8S1179, oligonucleotides shown as SEQ ID NO: 17 and SEQ ID NO: 18 are used as PCR primers;

for D13S317, oligonucleotides shown as SEQ ID NO: 19 and SEQ ID NO: 20 are used as PCR primers;

for D21S1437, oligonucleotides shown as SEQ ID NO: 21 and SEQ ID NO: 22 are used as PCR primers;

for D16S3391, oligonucleotides shown as SEQ ID NO: 23 and SEQ ID NO: 24 are used as PCR primers;

for Penta E, oligonucleotides shown as SEQ ID NO: 25 and SEQ ID NO: 26 are used as PCR primers;

for D12S1064, oligonucleotides shown as SEQ ID NO: 27 and SEQ ID NO: 28 are used as PCR primers;

for D12S391, oligonucleotides shown as SEQ ID NO: 29 and SEQ ID NO: 30 are used as PCR primers;

for D6S1043, oligonucleotides shown as SEQ ID NO: 31 and SEQ ID NO: 32 are used as PCR primers;

for D19S433, oligonucleotides shown as SEQ ID NO: 33 and SEQ ID NO: 34 are used as PCR primers.

WHAT IS CLAIMED IS:

1. A method of determining whether twins are fraternal twins, comprising following steps:  
extracting a nucleic acids sample including maternal nucleic acids and fetal nucleic acids  
from a pregnant sample;

subjecting the nucleic acid sample to amplification by PCR, to obtain an amplification  
product containing an STR polymorphic site, wherein

for vWA, oligonucleotides shown as SEQ ID NO: 1 and SEQ ID NO: 2 are used as  
PCR primers;

for TPOX, oligonucleotides shown as SEQ ID NO: 3 and SEQ ID NO: 4 are used as  
PCR primers;

for D3S1358, oligonucleotides shown as SEQ ID NO: 5 and SEQ ID NO: 6 are used  
as PCR primers;

for D16S539, oligonucleotides shown as SEQ ID NO: 7 and SEQ ID NO: 8 are used  
as PCR primers;

for D5S818, oligonucleotides shown as SEQ ID NO: 9 and SEQ ID NO: 10 are used  
as PCR primers;

for CSF1PO, oligonucleotides shown as SEQ ID NO: 11 and SEQ ID NO: 12 are  
used as PCR primers;

for D11S2368, oligonucleotides shown as SEQ ID NO: 13 and SEQ ID NO: 14 are  
used as PCR primers;

for D2S1338, oligonucleotides shown as SEQ ID NO: 15 and SEQ ID NO: 16 are  
used as PCR primers;

for D8S1179, oligonucleotides shown as SEQ ID NO: 17 and SEQ ID NO: 18 are  
used as PCR primers;

for D13S317, oligonucleotides shown as SEQ ID NO: 19 and SEQ ID NO: 20 are  
used as PCR primers;

for D21S1437, oligonucleotides shown as SEQ ID NO: 21 and SEQ ID NO: 22 are  
used as PCR primers;

for D16S3391, oligonucleotides shown as SEQ ID NO: 23 and SEQ ID NO: 24 are  
used as PCR primers;

for Penta E, oligonucleotides shown as SEQ ID NO: 25 and SEQ ID NO: 26 are used as PCR primers;

for D12S1064, oligonucleotides shown as SEQ ID NO: 27 and SEQ ID NO: 28 are used as PCR primers;

for D12S391, oligonucleotides shown as SEQ ID NO: 29 and SEQ ID NO: 30 are used as PCR primers;

for D6S1043, oligonucleotides shown as SEQ ID NO: 31 and SEQ ID NO: 32 are used as PCR primers;

for D19S433, oligonucleotides shown as SEQ ID NO: 33 and SEQ ID NO: 34 are used as PCR primers,

constructing a sequencing library for the nucleic acids sample;

subjecting the sequencing library to sequencing, to obtain a sequencing result;

determining a polymorphism type based on the sequencing result for the STR polymorphic site consisting of vWA, TPOX, D3S1358, D16S539, D5S818, CSF1PO, D11S2368, D2S1338, D8S1179, D13S317, D21S1437, D16S3391, Penta E, D12S1064, D12S391, D6S1043 and D19S433;

comparing the polymorphism type with corresponding polymorphic site of parents thereof; and

determining whether the twins are the fraternal twins based on a comparing result, wherein it is determined that the twins are the fraternal twins in the case that for at least one of STR polymorphic sites, it is heterozygous in paternal genome and its allele have two copy numbers both different from that in pregnant genome which is detectable in the nucleic acids sample.

2. The method of claim 1, wherein the pregnant sample is selected from a group consisting of peripheral blood, pregnant woman urine and breast milk.

3. The method of claim 2, wherein the pregnant sample is peripheral blood.

4. The method of claim 1, wherein the amplification product has a length of 150 bp or less.

5. A system for determining whether twins are fraternal twins, comprising:

a genotyping apparatus, for subjecting a polymorphic site of fetuses of the twins to genotyping, to obtain polymorphism type of the fetuses, wherein the genotyping apparatus further comprises:

a nucleic acid extracting unit, for extracting a nucleic acid sample of the fetuses from a pregnant sample;

an amplifying unit, connected to the nucleic acid extracting unit, and suitable for subjecting the nucleic acid sample of the fetuses to amplifying, to obtain an amplification product containing the polymorphic site, wherein

for vWA, oligonucleotides shown as SEQ ID NO: 1 and SEQ ID NO: 2 are used as PCR primers;

for TPOX, oligonucleotides shown as SEQ ID NO: 3 and SEQ ID NO: 4 are used as PCR primers;

for D3S1358, oligonucleotides shown as SEQ ID NO: 5 and SEQ ID NO: 6 are used as PCR primers;

for D16S539, oligonucleotides shown as SEQ ID NO: 7 and SEQ ID NO: 8 are used as PCR primers;

for D5S818, oligonucleotides shown as SEQ ID NO: 9 and SEQ ID NO: 10 are used as PCR primers;

for CSF1PO, oligonucleotides shown as SEQ ID NO: 11 and SEQ ID NO: 12 are used as PCR primers;

for D11S2368, oligonucleotides shown as SEQ ID NO: 13 and SEQ ID NO: 14 are used as PCR primers;

for D2S1338, oligonucleotides shown as SEQ ID NO: 15 and SEQ ID NO: 16 are used as PCR primers;

for D8S1179, oligonucleotides shown as SEQ ID NO: 17 and SEQ ID NO: 18 are used as PCR primers;

for D13S317, oligonucleotides shown as SEQ ID NO: 19 and SEQ ID NO: 20 are used as PCR primers;

for D21S1437, oligonucleotides shown as SEQ ID NO: 21 and SEQ ID NO: 22 are used

as PCR primers;

for D16S3391, oligonucleotides shown as SEQ ID NO: 23 and SEQ ID NO: 24 are used

as PCR primers;

for Penta E, oligonucleotides shown as SEQ ID NO: 25 and SEQ ID NO: 26 are used as

PCR primers;

for D12S1064, oligonucleotides shown as SEQ ID NO: 27 and SEQ ID NO: 28 are used

as PCR primers;

for D12S391, oligonucleotides shown as SEQ ID NO: 29 and SEQ ID NO: 30 are used

as PCR primers;

for D6S1043, oligonucleotides shown as SEQ ID NO: 31 and SEQ ID NO: 32 are used

as PCR primers;

for D19S433, oligonucleotides shown as SEQ ID NO: 33 and SEQ ID NO: 34 are used

as PCR primers,

a library constructing unit, connected to the amplifying unit, and suitable for constructing a sequencing library for the nucleic acid sample of the fetuses;

a sequencing unit, connected to the library constructing unit, and suitable for subjecting the sequencing library sequencing, to obtain a sequencing result; and

a genotype determining unit, connected to the sequencing unit, and suitable for determining a polymorphism type based on the sequencing result for the STR polymorphic site consisting of vWA, TPOX, D3S1358, D16S539, D5S818, CSF1PO, D11S2368, D2S1338, D8S1179, D13S317, D21S1437, D16S3391, Penta E, D12S1064, D12S391, D6S1043 and D19S433,

and

an analyzing apparatus, connected with the genotyping apparatus, and suitable for comparing the polymorphism type of the fetuses with corresponding polymorphic site of parents thereof; and determining whether the twins are the fraternal twins based on a comparing result,

wherein it is determined that the twins are the fraternal twins in the case that for at least one of STR polymorphic sites, it is heterozygous in paternal genome and its allele have two copy numbers both different from that in pregnant genome which is detectable in the nucleic acids sample.