

oligonucleotide) method, a PCR-SSP (sequence specific primer) method, or a modified method thereof may be used. The PCR-SSO method is a typing method according to the presence or absence for formation of an aggregate with the probe, using a probe that hybridizes specifically with a specific allele (allele-specific probe). The PCR-SSP method is a method for typing according to the presence or absence for a PCR product when carrying out PCR using a primer that hybridizes specifically with a specific allele (allele-specific probe). Examples of the modified method thereof include an Invader method, a TaqMan probe method, a QProbe method, and a Scorpion-ARMS method. A detection method using fluorescence is preferred due to its superior detection sensitivity, and a method using a probe or primer that recognizes a specific allele, an Invader (registered mark) method, a TaqMan probe method, a QProbe method, and a Scorpion-ARMS method is preferred due to its superior detection sensitivity and accuracy. For example, the probe or primer used for the typing of the bases of (a) to (c) can be synthesized by designing by an ordinary method, for example, based on the base sequence 1 or 2.

[0039]

In the case of the typing by a sequence analysis method, the bases of (a) can be typed by carrying out PCR with a PCR primer (a primer-1 and a primer-2 in FIG. 3) for the amplification of a region having the bases of (a) interposed therein and analyzing the base sequence of the obtained amplification product, using a genomic DNA or mRNA derived from a test subject (hereinafter sometimes simply referred to as a “genomic DNA”) as a template, for example, as shown in Figure 3. Similarly, the bases of (b) and (c) can be typed by carrying out PCR with a PCR primer (a primer-3 and a primer-4 in FIG. 3) for the amplification of a region having the bases of (b) and (c) interposed therein and analyzing the base sequence of the obtained amplification product. The six bases of (c) in FIG. 3 represent the 437th base, the 441st base, the 443rd base, the 444th base, the

A*24:02/A*24:02	C	G	C	+	+	○
A*24:02/A*24:08	A/C	C/G	C	+	+	○
A*24:20/A*32:01	A/C	C/G	C	-	+	×
A*32:01/A*24:04	C	C/G	C/G	-	-	○

[0055]

[Example 2]

In the same manner as in Example 1 except that the primer-5 shown in Table 9 was used instead of the primer-4, PCR was carried out, using a genomic DNA extracted from a biological sample collected from a test subject, in which the HLA-A type is a [A*24:02/A*24:02] homotype, a heterotype of [A*24:02/A*24:08], a heterotype of [A*24:20/A*32:01], and a heterotype of [A*32:01/A*24:04], as a template. As a result, in all the cases where any genomic DNA was used as a template, PCR products were obtained by PCR, using the primers-3 and -5. Therefore, the genomic DNA of all the test subjects was typed such that the 437th base was C, the 441st base was T, the 443rd base was G, the 444th base was C, the 447th base was T, and the 449th base was C. As a result of the sequence analysis of each PCR product, the same determination results as those of Example 18, as seen from Table 12, were obtained. However, when using a genomic DNA derived from the heterotype of [A*32:01/A*24:04], only two types, C and G, of the bases of (b) were typed in Example 1, but in this Example, only one type, C, of the bases of (b) was typed.

[0056]

[Table 12]

	(a)	(b)	Type	Determination	Errata
A*24:02/A*24:02	C	G	+	+	○
A*24:02/A*24:08	A/C	C/G	+	+	○
A*24:20/A*32:01	A/C	C/G	-	+	×
A*32:01/A*24:04	C	C	-	-	○