polynucleotides having a lower homology are not hybridized.

[0018] Specific stringent conditions are conditions including incubating a specimen having a base sequence complementary to a desired base sequence and suspected of having *Staphylococcus argenteus* in a hybridization solution (50% formamide, 10×SSC (0.15 M NaCl, 15 mM sodium citrate, pH 7.0), a 5× Denhardt's solution, 1% SDS, 10% dextran sulfate, 10 μg/ml of denatured Salmon Sperm DNA, and a 50 mM phosphate buffer (pH 7.5)) at about 42°C to about 50°C, and then washing using 0.1×SSC, 0.1% SDS at about 65°C to about 70°C.

[0019] Primers and probes are designed so that they do not cause a cross reaction with sequences of other related species, but can be appropriately changed according to the system used for detecting an amplification product and the like, and other conditions. When an amplification product having a length of 100 to 200 bases is generated, for example, it is preferable to target a base sequence from position 217 to position 331 of the base sequence shown in SEQ ID NO: 3 or 4. Primers and probes are designed to have a base sequence comprising at least 10 consecutive bases in the base sequence constituting such a target. It is preferable to design primers so that there is a mismatch with a *Staphylococcus* bacterium other than *Staphylococcus argenteus* at the end of the primer, particularly at the 3' end.

[0020] Examples of first primers targeting a nuc gene of *Staphylococcus argenteus* include one which has a base sequence shown in SEQ ID NO: 9 or a base sequence comprising at least 10 consecutive bases in a base sequence in which one or several bases are deleted, substituted, inserted, or added in the base sequence shown in SEQ ID NO: 9, and has the same function as that of the base sequence shown in SEQ ID NO: 9.

5'- TTCCACTTCTATTTTCTTAGCATTC-3' (SEQ ID NO: 9)

[0021] Examples of second primers targeting a nuc gene of *Staphylococcus argenteus* include one which has a base sequence shown in SEQ ID NO: 10 or a base sequence comprising at least 10 consecutive bases in a base sequence in which one or several bases are deleted, substituted, inserted, or added in the base sequence shown in SEQ ID NO: 10, and has the same function as that of the base sequence shown in SEQ ID NO: 10.

5'- ATTAATTGATACGCCYGAAACG-3' (SEQ ID NO: 10)

[0022] The length of the first and second primers is arbitrary, and can be, for example, appropriately set to be within a range of about 10 bases to about 35 bases, and is preferably at least 10 bases or more.

[0023] The ratio of the first primer and the second primer is not particularly limited, and may be the same as or different from each other. When the primer set is used in an asymmetric PCR method, the concentration of one primer can be adjusted to be higher than the concentration of the other primer.

[0024] *Staphylococcus* bacteria are classified into coagulase-positive ones and coagulase-negative ones. For example, *Staphylococcus argenteus* is coagulase positive. Coagulase-negative *Staphylococcus* bacteria (CNS) include a *Staphylococcus* bacterium called *Staphylococcus epidermidis* frequently found in clinical materials, and it is necessary for *Staphylococcus argenteus* to be differentiated from such coagulase-negative *Staphylococcus* bacteria as well. Since coagulase-negative *Staphylococcus* bacteria do not have a nuc gene fragment, these are suitable to be differentiated.

[0025] Primers based on a base sequence of SEQ ID NO: 10 can also be used as forward primers for detecting the presence of *Staphylococcus schweitzeri*.

[Table 1]

SEQ ID NO: 6: *S. aureus* primer	GTAGCGAAAWAGAAAAACCTC
SEQ ID NO: 7: *S. aureus* primer	ATACTTATTAAGTGCTGGCATATG
SEQ ID NO: 8: *S. aureus* probe	CCCTATAAGTAATATTGAAAC
SEQ ID NO: 9: *S. argenteus* primer	TTCCACTTCTATTTTCTTAGCATTC
SEQ ID NO: 10: *S. argenteus*/*schweitzeri* primer	ATTAATTGATACGCCYGAAACG
SEQ ID NO: 11: *S. schweitzeri* primer	TTCAACTTCAATTTTYTTAGCATTC
SEQ ID NO: 12: *S. argenteus*/*schweitzeri* probe	CATATTTTTCAACGCCT

[0052] Confirmation of Nucleic Acid Amplification

Genomic DNAs extracted from an *S. aureus* JCM5676 strain and an *S. argenteus* JCM31982 strain were used as templates, and amplification by real-time PCR was performed using primers of SEQ ID NOs: 6 and 7 or primers of 9 to 11. A TaKaRa Multiplex Assay Kit Ver. 2 (Takara Bio Inc.) was used as a reagent for amplification, and EvaGreen (Biotium) was used as an intercalator dye. The primers and the genomic DNAs were added so that each primer has a final concentration of 0.2 μM and the genomic DNAs as templates have a concentration