2014-05-09 nytt kravsett

WE CLAIM:

1. A method of asymmetric PCR comprising:
- providing a nucleic acid sample to be used as a target template
- identifying target template(s)
- performing a polymerase chain reaction, utilizing highly complementary primers wherein either the forward or the reverse primer concentration is decreased to unblock the PCR reaction by initially promoting linear amplification which will progressively shift towards exponential amplification by the COMplementary-Primer-ASymmetric (COMPAS)-PCR;
- identifying the amplified nucleotide target sequence(s);

2. The method of claim 1 wherein the highly complementary primers have a common overlapping DNA target sequence.

3. The method of claim 2 wherein the overlapping DNA target sequence is direct tandem repeats.

4. The method of any one of claims 3 wherein the direct tandem repeat target is in the 5S-rDNA region.

5. A method for detecting, identification or monitoring salmonid species comprising: - providing a nucleic acid sample from salmonid to be used as (a) target template(s); - performing a polymerase chain reaction (PCR) applying COMplementary-Primer-ASymmetric (COMPAS)-PCR according to any one of claims 1-4, to amplify a nucleic acid target sequence of the template (s), utilizing a set or several sets of highly complementary primer pair(s) capable of priming said target(s);
- identifying the amplified nucleotide target sequence(s);
- determining the species.

6. The method of any one of claims 1-5 wherein the determination of the species is performed by a melting curve analysis of the PCR product or by electrophoresis analysis.

7. The method of any one of claims 1-5 wherein the forward primer is extended in the 3´ end to favor priming to the target and not to the reverse primer.

8. The method of any one of claims 1-7 wherein the reverse primer is extended in the 3´ end to favor priming to the target and not to the forward primer.

9. The method of any one of claims 1-8 wherein either the reverse or the forward primer has a SNP at its 3' end.

10. The method of any one of claims 1-9 wherein the primers in the primer pair are oligonucleotides each having a length of about 12 to about 30, preferably about 20 bp.

11. The method of any one of any one of claims 1-10, wherein the complementary set of primers is selected from a set of primer pair (s) wherein the forward primer is selected from Table 1 or a complementary sequence thereof and the reverse primer is selected from Table 2 or a complementary sequence thereof.

12. The method of claims 5-11, wherein said salmonid comprises *Salmo trutta, Salmo salar* and hybrids thereof.

13. Oligonucleotide primer pairs, selected from the oligonucleotides of Tables 1 and 2 or oligonucleotides with complementary sequences or their functional equivalent sequences.

14. Kit for detecting and identification of salmonid species, comprising a collection of oligonucleotide primer pairs selected from Tables 1 and 2 or complementary sequences thereof, in any combinations, capable of detecting salmonid species by the method of any one of claims 1-12.

15. Use of a method of any one of claims 1-12.

16. Use of the oligonucleotide primer pairs of claim 13.

17. Use of the kit of claim 14.