Docket #: S06-022

Multiplex DNA Amplification

Precise amplification of selected portions of genomic DNA is highly desirable for many DNA analysis purposes, for example the sequencing of multiple genes involved in a certain disease. The standard approach is currently using single polymerase chain reactions (PCR) one for each amplicon with a single specific primer pair. Several attempts have been made to perform a multiplex PCR where many primer pairs are used simultaneously in one reaction in order to reduce reagent and sample consumption, and thus cost. These attempts have been rather unsuccessful since using many PCR primers in one reaction gives rise to many false amplicons, as well as the desired amplicons. The risk of generating false amplicons increases dramatically upon increasing the number of primer pairs. These false amplicons then limit the utility of the amplification product for purposes such as SNP-detection, gene copy number analyses and sequencing.

Researchers at Stanford have developed a patented strategy for efficiently removing the false amplicons from the amplification pool while leaving only the correct ones for further amplification or for their direct analysis.

Applications

- Sequencing of multiple genes
- SNP detection
- Gene copy number analyses

Advantages

- Multiplex PCR currently requires extensive optimization and is rarely performed for more than 10 amplicons at a time. However, one could potentially perform hundreds of reactions at the same time using this very cost- and time-efficient method without incurring contamination by artefacts.

Publications

- Simon Fredriksson, Johan Banér, Fredrik Dahl, Angela Chu, Hanlee Ji, Katrina Welch, and Ronald W. Davis: "Multiplex amplification of all coding sequences within 10 cancer genes by Gene-Collector" *Nucleic Acids Res. 2007 April; 35(7): e47*

Patents

- Published Application: WO2008033442
- Published Application: 20110212490
- Issued: 8,293,501 (USA)

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