Strain Specific Detection Made Easy By Genome Sequencing

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Abstract:

The recent developments of low cost genome sequencing technologies have enabled sequencing of bacterial strains on a routine basis. The challenge of today is to digest the amounts of data. One possible application amongst many is the identification of strain specific sequences. Strain identification is a valuable tool in many aspects of microbiological work. It is employed by culture collections to prove authenticity of their deposits. In ecological studies and biotechnological systems it can be used for the tracking of specific strains. Only very few strains can be identified and enumerated based on unique phenotypic characteristics which allow for their positive selection. Generally strain identification is therefore often performed by so called fingerprinting methods which can be based on chromosomal DNA restriction fragments (PFGE) or PCR-fragments (REP-PCR, RAPD). Although PCR-based methods are faster than PFGE, they both have a small dynamic range and are far too laborious for detecting and quantifying specific strains in investigations with increased sample number. Quantitative PCR targeted to strain specific sequences allows rapid detection and quantification of specific strains in a high number of complex samples. Up to now the challenge has been to identify possible target sequences. Sequencing of unique RAPD- or AFLP-fragments and subtractive hybridization are some of the techniques, which have been utilized for this purpose. With the "Genomics Workbench" software from CLC-bio (Aarhus, Denmark) and the output of Illumina/Solexa Next Generation Sequencing of a set of 35 relevant strains the identification of sequences specific for one of the strains is a matter of hours. This approach will be presented for strain specific detection in the species *Lactococcus lactis*.

Key words: Next Generation Sequencing, Quantitative PCR, Strain Specific Detection, Lactococcus