

Video Article

Pyrosequencing: A Simple Method for Accurate Genotyping

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Abstract

Pharmacogenetic research benefits first-hand from the abundance of information provided by the completion of the Human Genome Project. With such a tremendous amount of data available comes an explosion of genotyping methods. Pyrosequencing(R) is one of the most thorough yet simple methods to date used to analyze polymorphisms. It also has the ability to identify tri-allelic, indels, short-repeat polymorphisms, along with determining allele percentages for methylation or pooled sample assessment. In addition, there is a standardized control sequence that provides internal quality control. This method has led to rapid and efficient single-nucleotide polymorphism evaluation including many clinically relevant polymorphisms. The technique and methodology of Pyrosequencing is explained.

Protocol

The complete text protocol for this experimental approach is available in [Springer Protocols](#).

References