Host Genetic Epidemiology by Single Nucleotide Polymorphism (SNP) Analysis

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The completion of the whole human genome sequences is now a reality. Emphasis on the analysis of genetic variation on both an individual level and a population level is more important than ever. The identification and characterization of single nucleotide polymorphisms (SNP) in target genes or candidate genes plays a crucial role in identifications of disease genes and in expediting drug discovery/development. Identification of known SNPs can be easily accomplished by searching the ever-expanding public domain databases. However, discovery of new SNPs is best accomplished by sequencing a reasonable subset of the applicable population groups. Particular SNPs of interest will be the ones that effect coding changes and regulatory functions of genes. Once SNPs have been identified, the next step is to examine their frequency in disease models by accurate, cost-effective and high-throughput SNP genotyping methods. This presentation will cover the overview of principal techniques of SNP genotyping which have been developed so far. And also will be discussed the importance of well-defined disease model and error-free high-throughput SNP genotyping in candidate genes and genome-wide SNP screening in the near future.