Use of Single Nucleotide Polymorphism (SNP) in Toxicogenomic Research

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There are many different types of variation in human genome. Single nucleotide polymorphism (SNP) is the most abundant among them. There are estimated to be as much as 10 million SNPs in human genome. These differences are believed to be the major determinants of individual differences against disease susceptibility and different reactions to drugs. Since genetic variation plays an important role in many diseases, a major focus of the human genome project has been to identify a large number of uniquely mapped single nucleotide polymorphisms (SNPs) to serve as tools in genetic studies of complex traits. Many international efforts like The SNP Consortium (TSC) and International HapMap Project has done a great job of mapping variations and their relationships as a haplotype on human genome.

As individual's response to a drug varies according to the genetic make up of the individual, a person's responses against toxic substances should in part be directed by the genetic polymorphisms. Up to now, toxicogenomic researches are focused on expression pattern changes against substances. By evaluating a toxic effects of compounds show account for the genetic bases also. Investigating genetic determinants for susceptibility against harmful chemicals should shed new lights on evaluating toxicity of a compound.