In silico pathogenesis

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In the June 8 Science, Grupe *et al.* describe the creation of a murine single nucleotide polymorphism (SNP) database and a linkage prediction program to map disease-related loci in mice (*Science* 2001, **292**:1915-1918). The database contains data on hundreds of SNP alleles across 15 inbred mouse strains. The computational methods scan the database to perform *in silico* prediction of chromosomal regions related to phenotypic and pathophysiological traits. Grupe *et al.* demonstrate that SNP-based genotyping of pooled DNA samples required about 20 times fewer PCR reactions than conventional microsatellite genotyping. They tested whether the SNP database and computer algorithms could predict regions of interest (quantitative trait loci, QTL). The approach was able to localize known regions, such as the major histocompatibility complex locus on chromosome 17, and to predict regions involved in disease-related traits such as allergic asthma and alcohol dependency. The average size of a predicted region was 38 cM. The authors claim that QTL analysis can be reduced from months of breeding experiments to milliseconds of computer time, facilitating attempts to identify QTL in complex disease models.

References

1. *Science* , [http://www.sciencemag.org]

2. Murine single nucleotide polymorphism database , [http://mouseSNP.roche.com]