

POPULATION GENETICS: MATHEMATICAL PROBLEMS

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The use of polymorphic marker systems in paternity testing and the quantification of the contained information by way of a posterior probability or likelihood ratio is based on the knowledge of the formal genetic model for the given polymorphism, i.e. the genotype(s)-phenotyp relationship, and the population genetic parameters contained in the gametic as well as genotypic frequencies. The likelihood calculation, which generally uses simplifying assumptions regarding such evolutionary forces as selection, migration and deviation from Hardy-Weinberg equilibrium, depends on the availability of gametic frequencies from population studies. Gene frequencies from single locus marker systems with known mode of inheritance are straight forward to estimate by way of gene counting or maximum-likelihood estimation. The introduction of closely linked loci into paternity testing creates numerous problems by way of additional parameters such as linkage disequilibria and recombination fractions. Whereas the power of such highly polymorphic systems is desirable, its quantification can only be achieved by way of large samples of unrelated individuals and in complicated situations only by way of population studies on the level genotyped parents from random families.