The Effect of Locus Selection on Sibship Calculations

Francis A. Chiafari, and Robert E. Wenk
Baltimore Rh Typing Laboratory

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Many different systems are available for the determination of extended family blood relationships. We demonstrate, by example and by calculation, that sibship (SI) and half sibship (HSI) indices are maximized by the high locus information content currently generated only at VNTR loci.

The SI and HSI ratios are useful in determining a hypothesized relationship between two persons whose parents are not typed. Allele sharing at a locus favors relationship of the pair with a likelihood magnitude that is inversely related to the shared allele(s) population frequencies. The magnitude of finding two shared allele(s) at a locus is determined less by the population frequency of alleles than by the ability of hypothetical parents to donate a particular set of gametes. High information content loci, therefore, perform best for sibship analyses because they maximize the relative probabilities of allele sharing by decent verse allele sharing by chance. Practical experience and sample calculation both indicate the greater value of loci with high information content.

VNTRs, of the loci commonly in use, consistently fulfill the information content requirements of extended family blood relationship likelihood ratios. Testing a greater number of relatively low information content loci will not work as an alternative strategy.