
THE RELATIVE ROLES OF MOLECULAR GENETIC AND EVOLUTIONARY FORCES IN THE UNEXPECTEDLY HIGH FREQUENCIES OF MICROVARIANT ALLELES

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It has become an increasingly common practice to use genotyping based on DNA analysis in human identification strategies. The analysis of Short Tandem Repeats (STRs) currently forms the foundation for individual identification in forensic applications. One concern that has been raised is the genetic basis for microvariant alleles and their impact on the calculation of standard forensic statistics. A population study was performed on voluntary, non felon DNA samples in Connecticut containing microvariant alleles from three different loci: humTH01, humFGA, and D21S11. Repeat region and flanking regions were sequenced both in the 5' and 3' directions. Analysis of 10 humFGA and 20 D21S11 alleles reveal that although the number of core repeat units may differ, the location of the partial repeat remains constant in each similar allele. Current thinking is that this is due to replication slippage, but results suggest that selection may play a role in this phenomenon with evolutionary or molecular stability forces perpetuating them in the population.