A63 A Study of Recombination Between 15 X-Chromosomal Short-Tandem Repeat Markers in Multigenerational Family Pedigrees

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After attending this presentation, attendees will have a better understanding of the considerations involved in utilizing multiple Short Tandem Repeat (STR) markers located on the X chromosome after viewing the results of an NIJ-funded study into the recombination rate of 15 X chromosomal STR (X STR) markers that have previously been shown to be highly polymorphic in United States populations.

This presentation will impact the forensic science community by providing an understanding of how the organization of 15 X STRs across the chromosome affects their practical application in the forensic laboratory while increasing awareness of their potential utility. In addition, this presentation will describe one of the hurdles that must still be addressed for this marker system prior to routine use, prompting other scientists and laboratories to contribute to the accumulation of this important foundational data.

X-chromosomal STR (X STR) markers have recently been recognized as useful tools to supplement traditional kinship testing in the forensic setting. Development of assays allowing the multiplex detection and analysis of various combinations of X STRs has spawned numerous publications reporting the standardization of repeat structure and distribution of allele frequencies in a number of populations across the globe. However, far fewer studies have been published exploring the practical implications of utilizing markers located on a single chromosome.

According to the 1991 report of the International Society for Forensic Genetics (ISFG; formerly ISFH (Hameogenetics)) relating to the use of DNA polymorphisms in paternity testing, questions of independent assortment must be addressed for any forensic marker system. For autosomal STRs, this ensures that the product rule can be used to multiply individual marker frequencies together to determine the overall rarity of a profile. It does not preclude the use of linked markers, however, Y chromosomal STRs, for example, are linked to one another and are considered together as a group called a haplotype. Haplotype frequencies are measured directly from population data, and the counting method is used to determine the rarity of the profile. It follows that X chromosomal STRs may require a combination of the two techniques: the organization of several physically close markers into linkage groups, forming haplotypes, whose frequencies could then be multiplied together once independent assortment of the groups or "blocks" was established. Early linkage studies produced a map of the X chromosome that divided 16 X chromosomal STRs into four linkage groups and most subsequent studies have employed this model when considering markers to include in novel multiplexes as well as a currently available commercial X STR kit.

At the Armed Forces DNA Identification Laboratory, two multiplexes consisting of a total of 15 X STR markers (DXS 89, DXS9902, DXS7132, DXS7130, DXS6795, DXS10147, DXS8378, DXS7423, HPRTB, DXS101, DXS7424, GATA31E08, GATA172D05, GATA165B12, and DXS6803) have been characterized and allele frequencies determined for several different populations. In order to evaluate the organization of these markers into the four proposed linkage groups, 58 families (832 individuals) satisfying the requirements of linkage study (multiple generations and offspring) have been acquired and investigated. In this presentation, the results of this NIJ-funded study, demonstrating recombination between markers within the same proposed linkage group as well as confirming a mutation rate for X STRs on the order of 10^{-4} will be presented. These results confirm the hypothesis that for these 15 markers, recombination is not a negligible factor in the statistical interpretation of an association between individual and/or family profiles.

The opinions and assertions contained herein are solely those of the authors and are not to be construed as official or as views of the United States Department of Defense, the United States Department of the Army, or the National Institute of Justice.

Recombination, Linkage, X STRs

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