B27 The Forensic Uses of SNP Profiles

Bruce S. Weir, PhD, Amanda B. Hepler, PhD, and Amy D. Anderson, PhD, North Carolina State University, Bioinformatics Research Center, Campus Box 7566, Raleigh, NC 27695-7566*

After attending this presentation, attendees will know of the recent availability of massive SNP datasets that can help forensic scientists under- stand population structure and estimate relatedness between the donors of two or more DNA profiles.

This presentation will impact the forensic community and/or humanity by demonstrating how although the forensic community has a large investment in STR genetic markers, current work in human genetics has shown that SNPs are the markers of choice. These markers have much to offer forensic science.

Current efforts in human genetics, such as the International HapMap project, have made available population data on over one million single nucleotide polymorphisms (SNPs). Data are publicly available for various African, African-American, Asian and Caucasian populations. These very large datasets have made it possible to provide new information relevant to the forensic uses of DNA.

The ability to average over many SNPs in the same region of the genome has led to much more reliable estimates of the population-structure parameter theta that is central to the calculation of match probabilities for both single-contributor and multiple-contributor stains. When this esti- mation is done it becomes clear that different values should be used for the CODIS STR markers. Recent publications in population genetics have sug- gested that the usual population-average values of theta be replaced by pop- ulation-specific values, and when this is done for regions around the CODIS markers it appears that some of these regions may have been affected by natural selection. This, in turn, may require larger values of theta than would otherwise have been used. Numerical values will be shown.

The large number of SNP markers that can now be typed simply and cheaply means that it is possible to provide direct estimates of the degree of relatedness between a set of remains and a living person, or between two sets of remains. This would be an attractive alternative to using likelihood ratios of the probabilities of two profiles under alternative hypothesized relationships and prior probabilities of those relationships. The numbers of SNPs needed to distinguish among classes of relatives is very large, but large numbers are now available. Numerical results will be shown.

It can be expected that very dense SNP datasets will hasten the day when phenotypic attributes can be predicted from DNA profiles.

DNA SNP Profile, Population Structure, Relatedness

 ** Presenting Author*