A54   A SNP Based Assay to Predict Hair Pigmentation

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After attending this presentation, attendees will learn how human hair pigmentation can be predicted based on single nucleotide polymorphisms (SNPs).

This presentation will impact the forensic science community in the identification of victims, suspects, and unidentified remains when reference samples are not available for traditional forensic DNA comparison. The ability to predict hair pigmentation will permit a more accurate description of an individual's physical appearance, thereby increasing the ability of family, friends, detectives, and the like, to make an identification, which is critical in many investigations.

Hair pigmentation is determined by the interaction of many genes and their corresponding protein products during melanogenesis. Two pathways exist for this, one that leads to eumelanin, a black/brown pigment, while the other leads to pheomelanin, a red/yellow pigment. It is the relative abundance of these two products that determines hair color.

Previous research has lead to a SNP assay that correlates with red hair pigmentation. However, due to the more complicated nature of the eumalanin pathway, a similar assay for blonde/brown hair pigmentation has not yet been developed. In an effort to begin understanding the factors that contribute to blond/brown hair color, researchers have investigated SNPs within genes in the eumalanin pathway. Examples include tyrosinase; tyrosine related protein 1; solute carrier families 24 member 5, 45 member 2, and 24 member 4; oculocutaneous albinism type II; KIT ligand gene; immune regulatory factor 4; and HEct domain RCc1 domain protein 2. However, an individual's population ancestry also influences hair pigmentation, so it needs to be accounted for.

In order to develop a SNP-based assay for hair pigmentation that considers ancestry, 18 SNPs within the aforementioned genes were amplified and genotyped from African-Americans with at least 25% West African ancestry; Europeans with at least 90% European ancestry; and Brazilians with at least 25% West African ancestry. The genotypic data along with the melanin index, a numerical measurement of melanin content, were combined and used to create a predictive model for hair pigmentation. Significant SNPs in the prediction of hair pigmentation and a preliminary model based upon these SNPs will be presented.

Hair Pigmentation, Single Nucleotide Polymorphism, DNA