MEASURING EPISTATIC INTERACTIONS BETWEEN KNOWN DNA VARIANTS FOR EYE AND HAIR COLOR TO IMPROVE STATISTICAL PREDICTION MODELS

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Forensic DNA phenotyping is an up and coming area in forensic DNA analyses that enables the physical appearance prediction of an individual from DNA left at a crime scene. At present, there has been substantial work performed in understanding what genes/markers are required to produce a reliable prediction of categorical eye and hair color from the DNA of an individual of interest. These pigmentation markers (variants from *HERC2, OCA2, TYR, SLC24A4, SLC45A2,* and *IRF4* to name a few) are at the core of several prediction systems for eye and hair color such as IrisPlex [1], HIrisPlex [2], and the Snipper 2.5 suite [3, 4]. The contribution of these markers towards prediction in most cases however, only factors in an independent effect and does not take into account potential interactions or epistasis in the production of the final phenotypic color. Epistasis is a phenomenon that occurs when a genes effect relies on the presence of 'modifier genes', and can display different effects (enhance/repress a particular color) in gene combinations rather than individually.

In an effort to detect such epistatic interactions and their influence on eye and hair color prediction models, for this current study, 874 individuals were genotyped at 61 pigmentation markers from several diverse population subsets. Each individual was phenotypically evaluated for eye and hair color by three separate independent assessments. Several analyses were performed using statistical approaches such as multi-dimensionality factor reduction (MDR) for example, in an effort to detect if there are any SNP- SNP epistatic interactions present that could potentially enhance eye and hair color prediction model performances. The ultimate goal of this study is to assess what SNP-SNP combinations amongst these known pigmentation genes should be included as an additional variable in future prediction models and how much they can potentially enhance overall pigmentation prediction model performance.

1. Walsh, S., et al., *IrisPlex: a sensitive DNA tool for accurate prediction of blue and brown eye colour in the absence of ancestry information*. Forensic Sci Int Genet, 2011. 5(3): p. 170-80.
2. Walsh, S., et al., *The HIrisPlex system for simultaneous prediction of hair and eye colour from DNA.* Forensic Sci Int Genet, 2013. 7(1): p. 98-115.
3. Ruiz, Y., et al., *Further development of forensic eye color predictive tests.* Forensic Sci Int Genet, 2013. 7(1): p. 28-40.
4. Sochtig, J., et al., *Exploration of SNP variants affecting hair colour prediction in Europeans.* Int J Legal Med, 2015. 129(5): p. 963-75.