



D9 SNP Based Ancestry Informative Markers for the Inference of Biogeographical Ancestry (i.e., “Race”) and the Estimation of Admixture: Application for the Louisiana Serial Killer Case

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After attending this presentation, attendees should retain that SNP based DNA tests for forensics exist and have been used in a high profile case.

The impact of this work became evident in the recent Louisiana Serial Killer case where we determined by a SNP based DNA test that the suspect was 85% Sub-Saharan African & 15% Native American. The Louisiana task force, following eyewitness accounts and an FBI profile that the suspect was a caucasian, had run out of leads. We performed our DNA Witness 2.0 test and two months later the task force had the man linked to 6 homicides through STR typing in custody. The alleged murderer was, in fact, African American. This test could aid in any case where there is a biological sample left at the crime scene and you have no suspect or conflicting eye witness accounts of what ancestry your suspect is. The true impact to society comes when this investigative tool is utilized to expedite the investigation thus getting criminals off the streets before they have time to strike again.

Biogeographical Ancestry is the heritable component of “race,” but to date, no method has been described to accurately measure genetic structure within individuals. Socio-cultural and geo-political metrics for measuring human “race” are human and not natural constructs, therefore eye-witness accounts and the investigative interpretation of these accounts are notoriously unreliable. In this presentation, we present novel markers and methods by which to do this. We mined the human genome sequence for candidate Ancestry Informative Markers, validated them on an ultra-high throughput genotyping platform and established parental population allele frequencies. Using 71 of the most informative AIMs, covering most of the chromosomes, and coalescing the human population to four main continental population groups (sub-Saharan African, East Asian, Indo-European and Native American), we use a maximum likelihood method to determine individual BGA admixture proportions and their associated confidence intervals. We observed that self-reported population affiliations correlated almost perfectly with the majority BGA population affiliation determined for a sample of 3,300 international samples. BGA admixture results were surprisingly frequent, and when observed, were generally not inconsistent with anthropological and geopolitical history. The admixture proportions produced tracked in family pedigrees in a manner consistent with the law of independent assortment, and simulation revealed that the markers relevant for resolving the group affiliations functioned independently within the confines of our algorithm. Because a large number of high D value markers were used, the test was surprisingly robust; reasonable levels of simulated allele frequency errors that could be caused by biased parental sampling had no significant impact on the BGA proportions determined. Combined, these results show that BGA admixture can be reliably read from the DNA. In March of 2003, we applied this technology to assist with the Louisiana Multi-Agency Homicide Task Force Serial Killer Case, which had been bogged for the prior year. Prior to testing, and based on two separate eye-witness accounts, the killer was believed to be a Caucasian, or European American individual. The results of the test suggested that this profile was not accurate and that the killer was of 85% sub-Saharan and 15% Native American BGA. Based on these results, DNAPrint advised the Louisiana Serial Killer Task Force to abandon dragnets of Caucasians and focus exclusively on African Americans of average African American skin tone. The Task Force embraced this result, and within two months, their shift in focus towards leads consistent with the BGA profile resulted in the swabbing of an African-American individual that was eventually matched with the crime scenes through STR profiling. The case represents the first successful application of a multi-factorial post-human genome test for forensic sciences that the Company is aware of. We will also present progress made for other genome-based methods of physical profiling, such as the inference of human iris and hair color within individuals of mainly Indo-European descent.

Biogeographical Ancestry (BGA), Ancestry Informative Markers (AIM), Louisiana Serial Killer