Forensic Science International

Volume 164, Issue 1, 1 December 2006, Pages 20-32

Developing a SNP panel for forensic identification of individuals

Kenneth K.Kidd[a], Andrew J.Pakstis[a], William C.Speed[a], Elena L.Grigorenko[b], Sylvester L.B.Kajuna[c], Nganyirwa J.Karoma[c], Selemani Kungulilo[d], Jong-JinKim[e]Ru-BandLu[f], AdekunleOdunsi[g], FridayOkonofua[h], Josef Parnas[i], Leslie O.Schulz[j], Olga V.Zhukova[k], Judith R.Kidd[a]

https://doi.org/10.1016/j.forsciint.2005.11.017

Abstract

Single nucleotide polymorphisms (SNPs) are likely in the near future to have a fundamental role in forensics in both human identification and description. However, considerable research is necessary to establish adequate scientific foundations for these applications. In the case of identification, because allele frequencies can vary greatly among populations, the population genetics of match probabilities is a critical issue. Some SNPs, however, show little allele frequency variation among populations while remaining highly informative. We describe here both an efficient strategy for identifying and characterizing such SNPs, and test that strategy on a broad representation of world populations. Markers with high heterozygosity and little frequency variation among African American, European American, and East Asian populations are selected for additional screening on seven populations that provide a sampling of genetic variation from the world's major geographical regions. Those with little allele frequency variation on the seven populations are then screened on a total of 40 populations (∼2100 individuals) and the most promising retained. The preliminary panel of 19 SNPs, from an initial selection of 195 SNPs, gives an average match probability of $<10^{-7}$ in most of 40 populations studied and no greater than 10^{-6} in the most isolated, inbred populations. Expansion of this panel to ∼50 comparable SNPs should give match probabilities of about 10^{-15} with a small global range.