

Population Genetic Analyses of Globalfiler™ Loci for Indian Population

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GlobalFiler™ Express PCR Amplification Kit is a highly discriminative STR kit developed by Life Technologies to meet the requirements of FBI recommendations [1,2], including 21 autosomal STR loci (i.e., D3S1358, vWA, D16S539, CSF1PO, TPOX, D8S1179, D21S11, D18S51, D2S441, D19S433, TH01, FGA, D22S1045, D5S818, D13S317, D7S820, SE33, D10S1248, D1S1656, D12S391, and D2S1338), 1 Y STR locus (i.e., DYS391), 1 Y-indel locus, and Amelogenin. In this study, we did population genetic analyses with the GlobalFiler™ Express Kit for Indian population. 201 samples were collected, with consent, from unrelated individuals from different geographic regions of India. The samples were anonymized prior to analysis.

Genomic DNA was extracted from buccal swabs using Prep-n-Go™ protocol and amplified using the GlobalFiler™ Express PCR Amplification Kit (Life Technologies, WarringtonWA1 4SR, UK) in the GeneAmp 9700 PCR system (Life Technologies) according to the manufacturer's recommendations [3]. The electrophoretic separation of the amplified PCR products was performed on the ABI 3500xL Genetic Analyzer (Life Technologies). GeneScan-600 LIZ was used as the internal lane standard. The data analysis and allele identification were performed using GeneMapper1 ID-X (version 1.4) analysis software (Life Technologies).

Allele frequencies, observed heterozygosity (Ho), expected heterozygosity (He), Match Probability (MP), and Power of discrimination (PD) of each locus were calculated using a software program developed by Ge [4]. Departures from Hardy-Weinberg Equilibrium (HWE) expectations and Linkage Disequilibrium (LD) between each pair of loci were derived using Arlequin [5]. Fst values were determined using Arlequin [5].

Allele frequencies and applicable forensic statistics for all the loci are displayed in supplemental Table 1. All loci are polymorphic in all populations. Y-indel is the least informative marker as it has only two

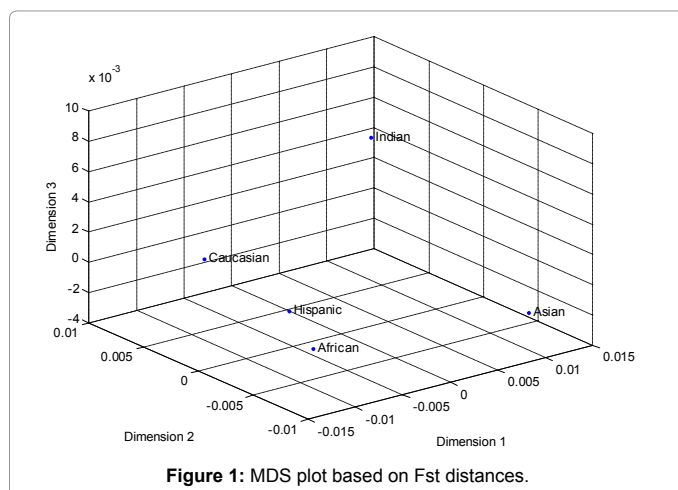
alleles. After Bonferroni correction [6] ($p\text{-value} = 0.05/21 = 0.0024$ for HWE test and $0.05/21 = 0.00024$ for LD test), no locus was departed from HWE and no pair of loci were departed from LD.

An MDS plot, based on Fst distances, of the India populations and four US major populations (i.e., Caucasian, African American, Hispanic, and Asian) [7,8] are generally consistent with geographical distances or population admixture history (Figure 1).

This study supports that the autosomal STR loci amplified with the GlobalFiler™ Express Kit have high discrimination powers in Indian population. The allele frequencies can be used in forensic and paternity testing cases.

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