

**Abstract ID:-** 110

**Abstract Topic:-** Evolutionary and population genetics

**Abstract Title:-** Genetic polymorphic diversity and Ancestry among the Sindhi-Indian population based on 28 Autosomal STR's: A procurement of a forensic database

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**Aims:-**The Sindhi-Indian population lacks sufficient data for CODIS STR loci. In contrast, highly polymorphic autosomal STR loci are valuable for forensic applications and improving our understanding of population structure. This study aimed to investigate the forensic effectiveness and population genetic variation of 28 autosomal STR loci among the Sindhi population in India, as well as to explore their ancestral relationships with other populations, including Sindhi Pakistanis and other groups.

**Methods:-** The allele frequency distribution of these 28 autosomal STR loci was determined using the Microreader™ Forensic Grade kit on a sample of 350 individuals from across India. This study included 6-dye fluorescent kit amplification of 24 autosomal STR loci, 1 Y chromosome STR locus, 2 Y-indel loci, and Amelogenin. The targeted loci in this study encompassed TH01, D5S818, D21S11, D18S51, D6S1043, Y-indel, Amel, D3S1358, D13S317, D7S820, D16S539, CSF1PO, Penta D, D2S441, VWA, D8S1179, TPOX, Penta E, Y-indel, D19S433, D22S1045, D2S1338, FGA, DYS391, D1S1656, D12S391, D10S1248, and SE33.

**Results:-** These STRs exhibited high powers of discrimination (CPD), power of exclusion (CPE), and matching probability (CMP) at approximately 0.999999999999999968997, 0.99998612, and 3.1003 × 10<sup>-18</sup>, respectively. The indigenous Sindhi population demonstrated a closer genetic relationship with Indian populations, particularly Indo-European, and a more distant relationship with regional populations from Pakistan and Afghanistan

**Conclusions:-** This conclusion is based on genetic distances, a neighbor-joining (NJ) tree, a Heat map, an Multi-dimensional Scaling plot, an interactivity test, and principal component analysis (PCA) using data from the 28 autosomal STR loci. This study provides valuable forensic population genetic data for paternity testing, forensic human individual identification, and genetic research.

**Keywords:-** CODIS,Short tandem repeat(STR),Population genetics, Neighbor joining Tree