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Master Thesis Defense

Entitled

*SHORT TANDEM REPEAT DIVERSITY IN PAKISTANI AND INDIAN POPULATION LIVING IN
UNITED ARAB EMIRATES*

By

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Abstract

Short Tandem Repeats (STRs), have become increasingly popular markers of choice due to its wide array of advantages in the sector of forensic investigation. It is most commonly associated with paternity testing, individual identification and population diversity studies. Genetic research being vital in these associations, it is necessary to expand genetic research into specific populations, even those residing in the same geographic region such as Pakistani and Indian in United Arab Emirates (UAE). This study focuses on 23 autosomal STR loci, namely D3S1358, vWA, D16S539, CSF1PO, TPOX, D8S1179, D21S11, D18S51, D2S441, D19S433, TH01, FGA, D22S1045, D5S818, D13S317, 7S820, D10S1248, D1S1656, D12S391, D2S1338, D6S1043, Penta D and Penta E which were evaluated in a total of 701 Pakistani and Indian populations, living in UAE. Blood samples was collected using FTA cards. The studied loci were amplified using VeriFiler™ Express PCR Amplification Kit. The amplified PCR products was electrophoresed on ABI 3500 Genetic Analyzer. Arlequin and Powerstats software was utilized to analyze the forensic parameters and population structure analysis. A total of 248 alleles and 298 alleles was observed in the Indian and Pakistani population, respectively. In the entirety of the studied loci, prominent result was attained for Penta_E, as it revealed the most favorable statistics. The genetic diversity among both the populations, ranged from 70%(TPOX)-92%(Penta_E). The combined probability of power of exclusion, power of discrimination and match probability in the Indian population was 5.20801E-06, 0.186910122 and 5.39427E-29, accordingly. Whereas, in the Pakistani population, the combined probability was 4.78349E-06, 0.205495754 and 2.90381E-29. The results obtained confirmed that these 23 loci are suitable to be used for individual identification and population diversity studies in forensic practice. The achieved data can aid in developing and enhancing databases to improve knowledge of the patterns of genetic diversity globally as well as to have further understanding about population genetic structure.

Keywords: Short tandem repeats, individual identification, population diversity, power of discrimination.