ANALYSIS OF X-STR MARKERS IN PERUVIAN POPULATIONS FROM COAST, ANDEAN AND AMAZON JUNGLE REGIONS

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Geographically, Peru is divided in three natural regions: Coast, Andes and Amazon Jungle. The Peruvian population is admixed, however; coast inhabitants are characterized to show more European ancestry, than the Andean populations which have more Quechua and Aymara ancestry. The Amazon jungle population historically is known to have the influence of multiple native populations. Nine X-chromosome STR-markers: DXS8378, DXS9902, DXS7132, DXS9898, DXS6809, DXS6789, GATA172D05, GATA31E08, and DXS7423 were analyzed in seven Peruvian populations, three Coastal: Piura, Chiclayo and Lima, three Andean: Huancayo, Puno and Cusco and one from the Amazon Jungle: Iquitos. 193 individuals between men and women were analyzed by each population. Allele frequencies and genetic distance (FST) analysis based on the number of different alleles were calculated for all population samples using ARLEQUIN software, neighbor-joining tree was built based on FSTmatrix using MEGA software. Significant differences were observed among some populations. Main differences were observed among the populations from the Coast and the Andes. A close cluster was formed by the populations from Cusco (Quechua) and Puno (Aymara). Huancayo, an Andean city, and cities from the coastal north Chiclayo and Piura were clustered together. Iquitos (Amazon Jungle) was clustered closer to coastal cities than to the Andean ones. This study contributes to show significant differences among populations with different genetic ancestry in Peru, and suggest that determining the allele frequency of genetic markers used for forensic and paternity analysis in these populations is relevant.