FORENSIC EFFICIENCY OF THE KIT INVESTIGATOR ARGUS X-12 IN TWO MESTIZO AND SEVEN AMERINDIAN POPULATIONS FROM MEXICO

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The current Mexican population is mostly constituted by Mestizos (~90%), who speak Spanish and live in both urban and rural regions all through the country [1]. However, most of the human genetic diversity from Mexico is contained in their Native American groups, which constitute ~10% of the total population. They represent > 68 Amerindian groups living in 156,557 indigenous settlements from 803 localities concentrated in the Southeast region of the country where > 85 languages and/or linguistic variants are spoken [2]. Although Mexican populations have been largely studied to validate the application of autosomal STRs [1], none Mexican population has been analyzed with the Investigator Argus X-12 kit (Qiagen), which allow solving complex relationship cases due to its X-linked inheritance pattern. Therefore, we determined the allele frequency distribution and statistical parameters of forensic efficiency concerning the kit Investigator Argus X-12 (Qiagen) in a total sample of 482 unrelated Mexican females, including three Mestizo –admixed– populations (*n*= 144) and seven Amerindian groups (*n*= 338) from the main regions of the country. The following forensic efficiency parameters were estimated on-line (http://www.chrx-str.org/): Het: heterozygosity observed; PIC: Polymorphism information content; power of discrimination in females (PD_f) and males (PD_m), and the Median exclusion chance for trios (MEC_T) and duos (MEC_D) according to Desmarais et al. [3]. Most of the 12 X-STRs were in agreement with Hardy-Weinberg expectations in all 10 Mexican populations. The combined Power of discrimination (PD) and Median exclusion chance (MEC) of this genetic system were > 99.99%. Although most of the Mexican populations showed significant pairwise differentiation, a close relationship was evident between Amerindian groups and nearby Mestizos from the West and Southeast regions, in agreement with historical records, previous genetic studies, and X-linked inheritance pattern expectations. We thank the financial support from Qiagen and CONACYT (grant N° 129693 to H-RV and the scholarship to I-CT).

References

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