EVALUATION OF LINKAGE DISEQUILIBRIUM OF MARKER SETS D7S820-rs2307978 AND D12S391-rs1610919 IN BRAZILIAN SAMPLES OF SÄO PAULO STATE

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One of the most promising developments in the analysis of degraded and/or low copy number DNA is to use insertion-deletion polymorphisms (InDels) because they are biallelic polymorphisms with short amplicons and can be analyzed in multiplexed reactions, and exhibit low mutation rate. In addition, as length-based polymorphisms, InDels can be analyzed with the same simple dye-labelled PCR primer methods as standard forensic STRs. Separation and detection of fluorescent dye-labelled PCR products by capillary electrophoresis eliminate the multiple step protocols required by SNP typing. An example is the 38plex-HID reaction standardized by Pereira et al. (2009) for analysis of 38 autosomal InDels for human identification. The combination of InDels and STRs is interesting, but it is important to know the independence of the markers used to achieve a good discrimination power. In this context, Fondevila et al. (2012) have cited two pairs of markers STR-InDel very close in the genome to be considered independent: D7S820-rs2307978 and D12S391-rs1610919, these two INDELs are analyzed in the 38plex-HID described by Pereira et al. (2009). To assess the linkage disequilibrium (LD) of these two sets of markers, we analyzed 100 individuals from state of São Paulo, Brazil, using PowePlex 21 System (Promega) and 38plex-HID. LD analysis was performed in Arlequin v. 3.1 software and it did not confirm associations between any of the marker pair investigated with p = 0.43988 (+- 0.00410) for the pair D7S820-rs2307978 and p = 0.99606 (+- 0.00050) for the pair D12S391-rs1610919. These results suggest that there is independence between these markers in the population sampled of the state of São Paulo, Brazil.

References

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