MITOCHONDRIAL DNA DIVERSITY IN THE MIDWEST POPULATION OF BRAZIL

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Polymorphic sites on the non-coding region of the mitochondrial DNA are useful for human population genetic studies as well as forensic investigation. Data concerning the maternal lineages from brazilian populations are scarce and most of them have been generated just for hypervariable I and II regions (HVI and HVII). In this study, we have analized the mtDNA control region of 200 unrelated individuals born in Midwest region of Brazil, which includes Mato Grosso do Sul, Mato Grosso, Goiás States and Brasilia, the Federal District. Blood samples were collected on Whatman FTA cards and processed for mtDNA sequencing by direct PCR amplification; the extension products were analyzed on a ABI 3500 Genetic Analyzer (Applied Biosystems).The haplogroups were classified using the online software HaploGrep (Phylo Tree build 17) after assembly and comparison to the revised Cambridge Reference Sequence (rCRS) using the SeqScape® Softwarev2.5. Considering historical data for each region of the country, nowadays maternal lineages in the Midwest of Brazil are expected to show significantly distinct proportions of African, European and Native-American ancestries in relation to each one in this region population as well as to those of other regions of the country, as a consequence of significative differential crosses between components of each ethnic ancestral population. The last census of the Instituto Brasileiro de Geografia e Estatística (IBGE), in 2010, showed that the Midwest region population is composed by brown (43.1 %), White (47.7 %), black (7.6 %), yellow (1.1 %) and indigenous (0,4%). Our data showed a high contribution of Native American ancestry (46.9 %), followed by African(34.4 %) and European (18.8 %) proportions. The haplogroup C was the most common. These data are in accordance with other data comparing the Brazilian geographical regions and reinforce the importance of further studies with applications in both medical and forensic genetics.

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