Abstract 24

RECENT HUMAN PHYLOGENIES ON SOUTHEAST OF BRAZIL USING AUTOSOMIC STR LOCI

Rodrigo S. Moura-Neto[1,2], Glaucia G. M. Silva[2], Rosane Silva[3], Adriana A. Debes-Bravo[4], Luciana F. Morganti[4] and Sergio P. Bydlowski[4,5]

[1] Instituto de Biologia, Universidade Federal do Rio de Janeiro, Rio de Janeiro, RJ, Brazil
[2] Instituto de Pesquisas e Perícias em Genética Forense, Polícia Civil do Estado do Rio de Janeiro, RJ, Brazil
[3] Instituto de Biofísica Carlos Chagas Filho, Universidade Federal do Rio de Janeiro, Rio de Janeiro, RJ, Brazil
[4] Divisão de Pesquisa e Biologia Molecular, Fundação Pró-Sangue Hemocentro de São Paulo, São Paulo, SP, Brazil
[5] Departamento de Hematologia, LIM-31, Faculdade de Medicina da Universidade de São Paulo, São Paulo, SP, Brazil

---

We have investigated the use of nine STR loci (CSF1PO, TPOX, TH01, vWA, F13A01, FESFPS, F13B, D16S539, D7S820, and D13S317), routinely applied in forensic analysis, for delineating phylogenetic relationships among 5 different geographic groups in Southeast of Brazil, comprising the three major ethnic groups (European- ,African- ,and Asian-descents). The resulting tree topology was consistent with the ethno-history and , corroborating that obtained using classical genetic polymorphisms. The results showed a low coancestry coefficient value across our population. The highest value obtained was 0.0159, taking the São Paulo Asian-descendants and Rio de Janeiro European-descendants. The data corroborate the notion of human phylogenies well defined clusters of ethnogeographic origins: African, Caucasian, Greater Asians and Amerindians. It it seems reasonable to assume the absence of any population substructure in the São Paulo and Rio de Janeiro databases. Our data on coancestry coefficient ($\theta = 0.0045$) do not support any calculations that may infer ethnic background and the UPGMA tree analysis has shown no significant genetic distance among the studied groups. Therefore, the profiles of nine STRs on both analyses, PCA and Genetic Distance Analysis, were essentially similar, and agreed to those data described for other genetic systems already described. Supported by: CNPq, FAPERJ,