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## INFERRING PATERNAL HISTORY OF RURAL AFRICAN-DERIVED BRAZILIAN POPULATIONS FROM Y CHROMOSOMES

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About four million Africans were brought to Brazil as slaves during four centuries. Many communities, named quilombos, were founded by runaway or abandoned African slaves. - ere are many quilombo remnants in the 'Vale do Ribeira' region in the southern part of São Paulo State, Brazil. In order to shed light on their origins, patterns of genetic diversity and to estimate genetic admixture, we used 19 biallelic Y chromosome markers (YAP, M3, M242, M168 and M2) and a set of 17 microsatellites (AmpFISTR Yfiler, Applied Biosystems) to determine haplotypes and haplogroups. - e aim of the study was to investigate how Amerindians, Europeans and Africans contributed to the Y chromosome pool in ten African-derived populations (about 300 individuals) from 'Vale do Ribeira' region. Allelic and haplotype frequencies were estimated by direct counting using the Arlequin ver 3.5 software (Excoffier and Lischer, 2010; Mol Ecol Resour. May; 10(3): 564-7). Haplotype diversity and degrees of interpopulational genetic variation ( $F_{ST}$ ) were inferred using the same software. Y-chromosomal haplogroups predictions based on the set of microsatellites were generated using Haplogroup Predictor (<http://www.hprg.com/hapest5/>). Admixture analysis based on the biallelic markers indicated that 32.2% of Y chromosome lineages were African, 60.9% are European and a small proportion, Amerindian (7.0%). Further analysis based on microsatellites allowed identification of 99 different haplotypes, classified into 12 distinct haplogroups. - e most frequent were haplogroups R1b (39.5%, European), E1b1a (33.0%, African) and Q (7.8% Amerindian). - e remaining haplotypes (19.8%) were classified into several different European haplogroups. - e presence of predominant haplotypes and genealogical data indicate a pattern of origin of quilombos from a limited number of male individuals, some of them having a key role in the foundation of these populations. - e genetic distances ( $F_{ST}$ ) analysis indicated that the ten populations studied, geographically close, have a low degree of genetic differentiation (mean  $F_{ST} = 0.089$ ,  $p < 0.001$ ), indicating that they are genetically very similar, a phenomenon that may be explained by high degree of gene flow between them. - is study helped to highlight the history of social interactions during the setting and establishing of the 'Vale do Ribeira' populations.

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