

ethnic groups are officially recognized, four of which are located in French Guyana: the Aluku, the Ndjuka, the Saramaka, and the Paramaka. The aim of this study was: (1) to determine the Noir Marron settlement through genetic exchanges with other communities such as Amerindians and Europeans; (2) to retrace their origins in Africa.

Buffy-coat DNA from 142 Noir Marron, currently living in French Guyana, were analyzed using mtDNA (typing of SNP coding regions and sequencing of HVSI/II) and Y chromosomes (typing STR and SNPs) to define their genetic profile. Results were compared to an African database composed by published data, updated with genotypes of 82 Fon from Benin, and 128 Ahizi and 63 Yacouba from the Ivory-Coast obtained in this study for the same markers. Furthermore, the determination of the genomic subtype of HTLV-1 strains (env gp21 and LTR regions), which can be used as a marker of migration of infected populations, was performed for samples from 23 HTLV-1 infected Noir Marron and compared with the corresponding database. MtDNA profiles showed a high haplotype diversity, in which 99% of samples belonged to the major haplogroup L, frequent in Africa. Each haplotype was largely represented on the West African coast, but notably higher homologies were obtained with the samples present in the Gulf of Guinea. Y Chromosome analysis revealed the same pattern, i.e. a conservation of the African contribution to the Noir Marron genetic profile, with 98% of haplotypes belonging to the major haplogroup E1b1a, frequent in West Africa. The genetic diversity was higher than those observed in African populations, proving the large Noir Marron's fatherland, but a predominant identity in the Gulf of Guinea can be suggested. Concerning HTLV-1 genotyping, all the Noir Marron strains belonged to the large Cosmopolitan A subtype. However, among them 17/23 (74%) clustered with the West African clade comprising samples originating from Ivory-Coast, Ghana, Burkina-Fasso and Senegal, while 3 others clustered in the Trans-Sahelian clade and the remaining 3 were similar to strains found in individuals in South America.

Through the combined analyses of three approaches, we have provided a conclusive image of the genetic profile of the Noir Marron communities studied. The high degree of preservation of the African gene pool contradicts the expected gene flow that would correspond to the major cultural exchanges observed between Noir Marron, Europeans and Amerindians. Marital practices and historical events could explain these observations. Corresponding to historical and cultural data, the origin of the ethnic groups is widely dispatched throughout West Africa. However, all results converge to suggest an individualization from a major birthplace in the Gulf of Guinea.

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Genetic Diversity and Dynamics of the Noir Marron Settlement in French Guyana : A Study Combining Mitochondrial DNA, Y Chromosome and HTLV-1 Genotyping

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The Noir Marron are the direct descendants of thousands of African slaves deported to the Guyanas during the Atlantic Slave Trade and later escaped mainly from Dutch colonial plantations. Six