ALLELIC FREQUENCY OF 17 STR LOCI FROM PANAMANIAN GENERAL POPLULATION

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We studied the allelic frequencies of 17 STR loci (D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, TPOX, D18S51, D5S818, FGA, Penta E and Penta D) for a sample of 528 unrelated individuals from the general population of Panama. The samples were collected upon acceptance of each individual who signed an informed consent, finger stick was completed and sample placed on FTA cards (www.whatman.com).

Panama's geographical position facilitates the transit between the Americas, for centuries individuals with different ethnic backgrounds and from a variety of countries have passed thru the isthmus or have established themselves in the country.
Currently in Panama the only published allelic frequencies data are from the 9 STR markers from the Multiplex Systems GenePrint kit (Silver Stain Detection) in 102 individuals [1].

With the use of the new STR markers for forensic and human identification purposes, we have identified a lack of information about the allele frequencies from these new autosomal markers in the Panamanian population. This work aims to fill the lack of information for forensic purposes and the determination of paternity or consanguinity.
The Panamanian population is 3.4 million people according to the last national census [2] and is composed primarily of mestizos, which are a mixture of native Indians from the pre-Hispanic era, the European colonizers, Africans in the era of colonization and finally a wave of people from Caribbean descent of African slaves as well as Asians and Europeans who arrived in Panama for the construction of the canal. In the last century, Panama has received a large number of immigrants from around the world, including Central and South America [3] [4].

Genomic DNA was obtained from dried blood placed on Whatman FTA cards, and the purification was done according to manufacturer's protocol (www.whatman.com). The PCR was performed by protocol suggested by the manufacturers of PowerPlex 16 HS (www.promega.com) and AmpFlSTR Identifiler (http://www.invitrogen.com).
Typing was done on an ABI Prism 310 (http://www.invitrogen.com) and the assignments of alleles were completed using reference internal sizes standards according to manufacturer's instructions of the kits and the GeneMapper V 3.2 software (http:// www.invitrogen.com).

The determination of the data was done according to the guidelines of the Paternity Testing Commission of the International Society for Forensic Genetics (www.ISFG.org) [5]. The proficiency tests are performed with Spanish and Portuguese speaking groups along with (www.gep-isfg.org) and Laboratorio Clinico Genetix, is acreditated with DGNTI-COPANIT-ISO/IEC 17025-2006.

Allele frequencies, matching probability, power of discrimination and probability of exclusion were calculated using Powerstats version 1.2 [6]. Hardy–Weinberg equilibrium, expected heterozygozity, observed heterozygozity and population differentiation tests were carried out with the Arlequin software version 3.5 [7].

The forensic information and the frequency data base are provided in the supplemental material with the forensic data found. The power of matching for the 17 loci is 1 x 4.67691 $^{-19}$, the power of discrimination is .99999999999999999532309 and power of exclusion is 0.9999997342.

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