B154 Autosomal STRs Data on Two Aboriginal Populations of Guatemala

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After attending this presentation, attendees will learn data and parameters of forensic interest (HWE, PD, PE) of the Kiche and Qeqchi aboriginal Guatemala population for the 15 STR loci included in the Identifiler kit (Applied Biosystems - ABI). These data are of great interest for the forensic community, since they are necessary to perform statistical calculations, both in the paternity and forensics fields, after DNA identification analysis.

This presentation will impact the forensic community and/or humanity by providing exact and reliable data to perform appropriate statistical calculations in forensic and paternity cases, and also for anthropological studies.

Short tandem repeat (STR) loci are the most informative PCR- based genetic markers available to date for attempting to individualize biological material. The CODIS system includes 13 of the most informative STR loci available that can be amplified simultaneously using different available commercial kits.

In order to establish the appropriate statistical calculations for paternity and forensic cases, it is necessary to generate independent databases for all different populations, including the aboriginal populations, since some allele frequencies are statistically different from the mestizo general populations of the geographical areas where they are set.

Guatemala is the largest country in Central America, and its total population approximately twelve million (12,000,000) people, most of them mestizo population. There are several aboriginal populations, and the Kiche and Qeqchi groups are the largest ones, and represent approximately 750,000 and 475,000 individuals respectively.

This paper presents allele distribution data in the two main aboriginal populations from Guatemala. The data demonstrate that these loci can be useful for providing estimates of the frequency of a DNA profile in forensic identity testing and that a multiple locus profile is extremely rare in all the population.

Blood samples were obtained from 50 Kiche and 50 Qeqchi unrelated individuals (N=50) residing in Guatemala, and spotted on FTA® paper (Whatman, Florham Park, NJ). DNA samples were purified and amplified for the 15 loci included in the AmpF/p Identifiler® kit (Applied Biosystems, Foster City, CA). Samples were analyzed using the ABI PrismTM 310 Genetic Analyzer (PE Biosystems, Foster City, CA) according to the manufacturers' recommended protocols.

All 15 loci are highly polymorphic in both aboriginal populations.

For the Kiche group, the highest heterozygosis is shown by the D21S11 and D2A1338 loci, with a value of 0.880 in both. The most discriminating loci are D18S51 (PD 0.988) and FGA (0.948). The combined probability of exclusion for the 15 STR loci is 0.9999905.

For the Qeqchi group, the highest heterozygosity is shown by the FGA locus (0.88) and by the D21S11 locus (0.86). The most discriminating loci in this population are D18S51 (PD 0.951) and FGA (0.948). The combined probability of exclusion for the 15 STR loci is 0.9999943.

A resume of the PD and PE are shown in these tables:

KICHE POPULATION RESULTS

Locus	PD (Obs)	PD (Exp)	PE
1 D8S1179	0.90720000	0.90999226	0.55322870
2 D21S11	0.92160000	0.93949044	0.63145665
3 D7S820	0.86080000	0.86225572	0.45552161
4 CSF1PO	0.85040000	0.86339508	0.45965489
5 D3S1358	0.70320000	0.74253556	0.30551385
6 THO1	0.78000000	0.77330634	0.33111315
7 D13S317	0.92880000	0.93952164	0.63121708
8 D16S539	0.90000000	0.89997556	0.52859863
9 D2S1338	0.91840000	0.93838408	0.62846046
10 D19S433	0.93440000	0.94435326	0.64706071
11 vWA	0.83120000	0.84778954	0.43906759
12 TPOX	0.81120000	0.82236666	0.39062732
13 D18S51	0.94880000	0.95797906	0.69273671
14 D5S818	0.83360000	0.83061556	0.41482609
15 FGA	0.94800000	0.95998312	0.70014183
Total	>0.99999999	>0.99999999	0.99999055

QEQCHI POPULATION RESULTS

Locus	PD (Obs)	PD (Exp)	PE
1 D8S1179	0.91760000	0.93016618	0.60471043
2 D21S11	0.90400000	0.92812984	0.60027251
3 D7S820	0.87040000	0.89459556	0.52115496
4 CSF1PO	0.82080000	0.84799684	0.43574904
5 D3S1358	0.72640000	0.74592276	0.31294708
6 THO1	0.72160000	0.77057716	0.32637633
7 D13S317	0.93040000	0.93643780	0.62195132
8 D16S539	0.90480000	0.89938336	0.52605302
9 D2S1338	0.90960000	0.92523294	0.59183097
10 D19S433	0.93360000	0.94746280	0.65566656
11 vWA	0.88320000	0.90991524	0.55630269
12 TPOX	0.82160000	0.81669844	0.38157896
13 D18S51	0.95120000	0.96693342	0.72771031
14 D5S818	0.86640000	0.86787364	0.47172256
15 FGA	0.94800000	0.96278862	0.71103911
Total	>0.99999999	>0.99999999	0.99999433

In conclusion, two independent databases have been established for 15 STRs loci (including the 13 CODIS core loci) for the aboriginal Kiche and Qeqchi populations of Guatemala. All loci are highly polymorphic and can be used for human identification investigations.

Forensic Science, STRs, Guatemala