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Native American population data based on the Globalfiler® autosomal STR loci

A B S T R A C T

Native American population data are limited and thus impact computing accurate statistical parameters for forensic investigations. Thus, additional information should be generated from geographically representative tribes in North America, particularly from those that are not included in existing population databases for forensic use. The Globalfiler® PCR Amplification kit was used to produce STR genotypic data for 533 individuals who represent 31 Native American tribal populations derived from eight geographically diverse regions in North America. Population genetic estimates from 21 autosomal STRs are reported.

Dear Editor,

Present day Native American forensic STR databases do not represent the majority of tribes resident in North America. Therefore, it is necessary to generate information for a more geographically diverse representation of additional tribes to better characterize genetic variation among Native Americans [1]. For this purpose, this study analyzed samples taken from 533 unrelated and anonymous individuals with self-identified affiliation to 31 tribes. These tribes represented eight geographic regions in North America including the Arctic region, Baja California, California/Great Basin, the Southeast, Mexico, the Midwest, the Northwest, and the Southwest. Fig. S1 shows the geographical location of the sampled populations. DNA from these individuals was isolated using the QIAamp DNA Blood Mini Kit (QIAGEN, Valencia, CA). The purified DNA was quantified using the Quantifiler® Duo Quantification Kit and the 7500 Fast Real-time PCR system (Applied Biosystems, Thermo Fisher Scientific, Carlsbad, CA) and then normalized to 1.0 ng/μL. Each individual sample, along with the National Institute of Standards and Technology (NIST) Standard Reference Material (SRM) 2391c calibrant, was profiled using the Globalfiler® PCR Amplification kit (Applied Biosystems). The Globalfiler® kit interrogates 24 loci including 21 autosomal STR markers: CSF1PO, D1S1656, D2S1338, D2S441, D3S1358, D5S818, D7S820, D8S1179, D10S1248, D12S391, D13S317, D16S539, D18S51, D19S433, D21S11, D22S1045, FGA, SE33, TH01, TPOX, and VWA. Electrophoresis was conducted on the ABI 3130*xl* Genetic Analyzer (Applied Biosystems) according to the manufacturer's guidelines. Allele calls were performed with the GeneMapper1 ID-X Software v1.4 (Applied Biosystems) along with the corresponding GlobalFiler Allelic Ladder (Applied Biosystems) (Table S1).

Because forensic STR information on most of the native tribes included in this study is still lacking, frequency of alleles were computed for all tribes using the program CONVERT v1.31 [2] (Table S2), including those tribes with small sample sizes. Observed heterozygosity (H_{obs}), probability of identity (P_I), probability of paternity exclusion (PPE), and allele frequencies were estimated using the Excel-based software STR_Genotype developed at NIST (http://www.cstl.nist.gov/biotech/strbase/software.htm) which was modified to accommodate tribes with a minimum of 25 individuals. The population genetic parameters were estimated for both the pooled tribal population data and the data from nine tribes represented by 25 or more individuals, which included Apache, Cherokee, Cochimi, Cora, Eskimo, Huichol, Miwok, Seri, and Yavapai (Table S3). Shriver et al. [3] concluded that sample sizes of greater than 25 individuals did not have an appreciable effect on the genetic distance variance. The Hardy-Weinberg Exact Test was performed using Arlequin v3.5.1.2 [4] with 1,000,000 Markov chain and 100,000 dememorization steps to determine if any tribal sample showed detectable deviations from expectations of equilibrium (Table S3). Significance level was presented at $p = 0.05$, in addition to applying standard Bonferroni correction for multiple comparisons [5].

In the combined tribal dataset, there were 11 loci that exhibited statistically significant deviations from HWE based on the exact test ($p < 0.05$, Table S3), which might be expected given population substructure. After Bonferroni adjustment (21 loci: adjusted critical $p = 0.00001$), only one deviation remained statistically significant (SE33). The locus/population combination still showing significant departure from HWE following Bonferroni adjustments could reflect the observed genetic structure among Native American tribal populations [6–8]. There were fewer examples of detectable departures from HWE for individual populations ($N > 25$, Table S3). The marker SE33 exhibited the highest H_{obs} (0.85633) and PPE values (0.86330) and lowest P_I value (0.01115), making it the most variable locus when compared to the other loci in this data set. For the tribes represented by more than 25 individuals, SE33 was the most variable locus with the greatest H_{obs} and PPE values and lowest P_I values for the Apache (H_{obs}: 0.88506, PPE: 0.80612, P_I: 0.03052), Cora (H_{obs}: 0.87500, PPE:

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0.79443, P_I: 0.03271), and Yavapai tribes (H_{obs}: 0.94000, PPE: 0.81611, P_I: 0.03440).

This study used the 21 autosomal Globalfiler® loci to genotype 533 Native American tribal samples. The inclusion of additional Native American samples will yield more robust statistical estimates in casework involving these communities. For instance, an analysis based on ten North American tribes, including those that are not found in existing forensic STR databases [9] revealed an F_{ST} or θ correction factor of 0.04 which is above the conservative estimate of 0.03 recommended by the National Research Council (NRC) [6]. This is consistent with findings by Buckleton et al. [10] who concluded after extensive reviewing of articles on forensic STR profiles from approximately 500,000 individuals from 446 populations, that θ values currently used in forensic calculations are not as conservative as often considered. The greater inter-population differentiation among this study's tribal populations sheds light on the geographic isolation and genetic subdivision among these populations [9].

The study was approved by the UC Davis Internal Review Board (ID 430207-2). This correspondence follows the journal's guidelines for publication of population data [11].

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at http://dx.doi.org/10.1016/j.fsigen.2016.06.014.

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