



Genetic variation of high-altitude Ecuadorian population using autosomal STR markers

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ABSTRACT

Fifteen autosomal STRs were analyzed in order to elucidate the differences between low and high land Ecuadorian population. Seven Ecuadorian geographic areas (Tisaleo-Mocha, Cañar, Quito, Rocafuerte, Santa Rosa, Guayaquil and Lago Agrio) from different altitudes were selected for the study. After the analysis, little genetic distances were observed between all cities, the more distant cities ($F_{ST} = 0.02354$) were Rocafuerte at an elevation of 17 m.a.s.l. and Quito at 2850 m.a.s.l. and the similar cities ($F_{ST} = 0.00033$) were Rocafuerte (17 m.a.s.l.) and Santa Rosa (10 m.a.s.l.). In conclusion, there is not a great genetic distance in the 15 STRs reported in high and low land Ecuadorian population, therefore previously reported frequencies could be used in identification and paternity cases under analysis.

1. Introduction

Ecuador, located in South America is bordered by the Pacific Ocean on the west, Colombia in the north and Peru in the east and south [1]. Ecuador is at an elevation between 4 m.a.s.l. in the coast and 3264 m.a.s.l. in the Andes region [1]. For these reasons, the aim of the present study was to compare the genetic information of 15 STRs to visualize the genetic distances between low and high land population.

2. Materials and methods

2.1. Population

The study included 328 unrelated individuals self-identified as mestizos from seven Ecuadorian provinces which are located in different high-altitudes. From the highland the selected samples were: 49 samples from Tisaleo-Mocha (~3200 m.a.s.l.) in Tungurahua province, 40 individuals from Cañar city (3125 m.a.s.l.) in Cañar province and 50 individuals from Quito (2850 m.a.s.l.) in Pichincha province. From the lowland the selected individuals were: 43 individuals from Rocafuerte (17 m.a.s.l.) in Manabí province, 47 samples from Santa Rosa (10 m.a.s.l.) in El Oro province, 50 individuals from Guayaquil (4 masl)

in Guayas province and 49 samples from Lago Agrio (418 m.a.s.l.) in Sucumbios province. The participants signed the informed consent in order to participate in the study.

2.2. DNA extraction and amplification

Blood samples on FTA card were extracted using FTA buffer (GE Healthcare), following the manufacturer's recommendation protocol [2]. The amplification was done using PowerPlex 16 system (Promega) in a single multiplex following the protocol recommended by the manufacturer [3]. Positive (2800 M) and negative control was used in the amplification process. Capillary electrophoresis was performed on the 3130 and 3500 Genetic Analyzers (Applied Biosystems). Lastly, the results were analyzed by GeneMapper v3.2 and v5 (Applied Biosystems).

2.3. Data analysis

Data were analyzed using: Arlequin v 3.5.2.2 for population genetic differences, and SPSS Statistics v24 for visual representation.

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Table 1

Genetic distances (F_{ST}) between Tisaleo-Mocha (Tungurahua), Santa Rosa (El Oro), Rocafuerte (Manabí), Lago Agrio (Sucumbios), Quito (Pichincha), Cañar (Cañar), Guayaquil (Guayas) (lower diagonal) and P-values (upper diagonal).

	Tisaleo -Mocha	Santa Rosa	Rocafuerte	Lago Agrio	Quito	Cañar	Guayaquil
Tisaleo - Mocha	–	$\leq 5e-5$	$\leq 5e-5$	$\leq 5e-5$	0.0139	0.035	0.0139
Santa Rosa	0.01806	–	0.0394	0.0121	$\leq 5e-5$	$\leq 5e-5$	$\leq 5e-5$
Rocafuerte	0.02341	0.00033	–	$\leq 5e-5$	$\leq 5e-5$	$\leq 5e-5$	$\leq 5e-5$
Lago Agrio	0.02058	0.00535	0.01380	–	$\leq 5e-5$	$\leq 5e-5$	$\leq 5e-5$
Quito	0.00607	0.02298	0.02354	0.00951	–	0.0278	0.0201
Cañar	0.00237	0.01090	0.01716	0.00973	0.00251	–	0.0433
Guayaquil	0.00561	0.01212	0.01190	0.01278	0.00492	0.00259	–

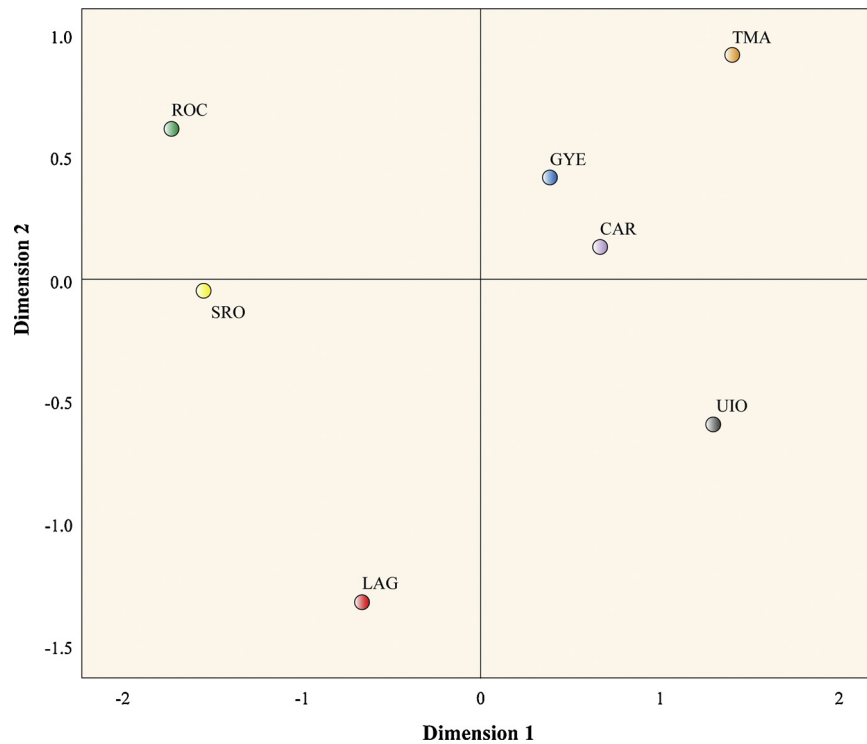


Fig. 1. Multidimensional scaling plot from the F_{ST} between the Ecuadorian cities (ROC: Rocafuerte, SRO: Santa Rosa, LAG: Lago Agrio, UIO: Quito, CAR: Cañar, GYE: Guayaquil, TMA: Tisaleo-Mocha).

3. Results

For population genetic comparison, the F_{ST} was computed between all population pairs of the seven Ecuadorian geographic provinces (Table 1).

All the p-values were statistically significant (p-value ≤ 0.05). In order to interpret the genetic distances obtained, we used the suggested values classification of Ballaux et al. [4]. Therefore, all the values were between 0–0.05 indicating little genetic distance between cities compared. The pairwise F_{ST} obtained is represented in a multidimensional scaling plot (Fig. 1) in order to visualize the similarities between the cities compared.

4. Discussion

As it was expected low distant between low and high altitude cities was found due to its same origin [5,6] and short geographic distances (the biggest distance is 796 km between Santa Rosa and Lago Agrio) that allow a constant migration inside the country [7]. Consequently, the 15 STRs could be used in the studied Ecuadorian population in forensic and kinship analysis, using the same frequencies reported [8].

5. Conclusion

In conclusion, there is not a genetic substructure evidence between low land and high land Ecuadorian population using 15 autosomal STR markers.

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None.

Declaration of Competing Interest

None.

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