

Short Term Fellowship Report

Intern's Name: Lucía Garrigós Calivares

Internship Period: September 1 to September 30, 2023

Summary:

During the internship, an extensive investigation was conducted on scientific studies providing genetic data of Argentine indigenous populations. Genetic data from eight Argentine indigenous populations were available and analyzed during the internship using the Arlequin 3.5 software. Subsequently, a bibliographic search was performed to expand the generated database, standardizing nomenclatures for mitochondrial and Y-chromosomal haplotypes.

Analysis of Previous Data:

A population genetic analysis was carried out on the previously generated data, including 12 autosomal STR markers for 502 individuals from Argentine indigenous populations belonging to the Tupí-Guaraní (Chiriguano and Guaraní), Mataco-Guaycurú (Toba, Mocoví, Wichi, and Pilagá), and Mapudungun (Tehuelche and Mapuche) linguistic groups.

Key Findings:

- Population genetic analyses of autosomal STRs revealed that, in general, there were no significant differences between the observed and expected genetic diversity under the Hardy-Weinberg Equilibrium, except for the D8S1132 marker in the Wichi population, which exhibited a high fixation index ($F=0.363$), indicative of substructure.
- All populations exhibited a significant Garza-Williamson index (greater than 0.68) for the D21S2055 marker, suggesting signals of genetic bottleneck in their history.
- Rst values grouped the populations as follows: Guaraníes-Mapuches-Tehuelches, Chiriguano-Tobas-Mocovíes-Pilagá, and Wichí, a conclusion supported by previous research (Sala et al. 2018).

Bibliographic Search and Database:

A search for open-access literature containing genetic data of Argentine indigenous populations was conducted according to the criteria of the Joanna Briggs Institute on Pubmed. Data from 20 previous studies from 1998 to the present were collected, including a wide spectrum of 17 populations and their genetic data.

Data curation was performed to create a comprehensive and standardized database, including genetic information from 1079 individuals for Y-chromosomes, 1106 individuals for mitochondrial DNA, 459 for 26 autosomal STRs, 204 for 46 InDels, and 133 for 46 SNP-AIMs.

Conclusions:

The internship has been a significant step in understanding the genetic diversity of Argentine indigenous populations. The results obtained and the expansion of the database provide a strong foundation for future research in population genetics and contribute to my doctoral thesis.

Acknowledgments:

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