

Proceeding Paper

Comparative Study of the Phenotypic and Molecular Genetic Diversity of “Tergui” Camel Population in the Hoggar Region (South Algeria) [†]

Derradji Harek ^{1,2,*} , Hacene Ikhlef ², Youcef Amine Cherifi ³, Rachid Bouhadad ⁴ and Fodil Arbouche ⁵ 

¹ Higher National Agronomic School-ENSA (ex. INA), Algiers 16000, Algeria

² National Institute of Agronomic Research of Algeria (INRAA), Algiers 16010, Algeria; h.yakhlef@ensa.dz

³ Molecular and Cellular Genetics Laboratory, University of Science and Technology of Oran Mohamed-Boudiaf USTOMB, Oran 31000, Algeria; cherifi.youcef@gmail.com

⁴ Laboratoire Ecologie Animale, Université des Sciences et de la Technologie Houari Boumediene USTHB, Bab Ezzaouar, Algiers 16111, Algeria; rbouhadad@yahoo.fr

⁵ Department of Agronomy, University of Ghardaia, Ghardaia 47000, Algeria; arbouchefodil@yahoo.fr

* Correspondence: derradji11@gmail.com

[†] Presented at the 10th International Seminar of Veterinary Medicine: Camelids in Algeria & Maghreb, Constantine, Algeria, 20–21 December 2022.

Abstract: In the framework of the sustainable management of the genetic diversity (morphometric and molecular) of the “Tergui” camel population represented by the phenotypes (Abahou, Amelal, Alemlagh, Atelagh, and Azerghaf), surveys in the Hoggar area of 87 individuals from 11 localities were conducted in order to estimate the variability of the inter-intra-population. The morphological results provide full information about the structure of this population and demonstrate an important polymorphism. The results of the genotyping of the DNA with 20 microsatellite markers made it possible to demonstrate inter- and intra-population genetic variability characterized by a high rate of heterozygosity (Hnb) and effective alleles. The rate of heterozygosity in our phenotypes varied from 0.56 to 0.63, which is higher than that observed in foreign populations ranging from 0.537 to 0.629. A total of 169 alleles of 20 microsatellite loci were detected. The mean number of alleles per locus was 7.15, 6.15, 3.10, 4.45, and 3.25 for Abahou, Amelal, Alemlagh, Atelagh, and Azerghaf, respectively. The loci evaluation showed higher PIC values greater than 0.5, which are considered very instructive. The heterozygous values observed for all the loci analyzed were lower than expected, which could be attributed to inbreeding in the population or subdivision of the studied population into distinct breeds and phenotypes. On the other hand, the number of observed alleles is higher and has shown a frequency that exceeds 7.3%. The genetic differentiation values between the phenotypes analyzed were much lower and the level of differences accounted for 1.1% of the total genetic variation. All loci contributed to this differentiation with FST values being moderately low and similar but very significant ($p < 0.001$). The overall FST value was similar but slightly higher than that of 0.9%. The genetic similarity between the phenotypes and the classification methods (AFC and DACP) gave results similar to the phenotypic characteristics, and showed that they appear to be genetically very similar, thereby supporting the decision to consider them only mildly differentiated.

Keywords: dromedary; genetic characterization; genetic variability; microsatellite; *Camelus dromedarius*; Tamanrasset



Citation: Harek, D.; Ikhlef, H.; Cherifi, Y.A.; Bouhadad, R.; Arbouche, F. Comparative Study of the Phenotypic and Molecular Genetic Diversity of “Tergui” Camel Population in the Hoggar Region (South Algeria). *Biol. Life Sci. Forum* **2023**, *22*, 6. <https://doi.org/10.3390/blsf2023022006>

Academic Editors: Amira Leila Dib, Said Boukhechem, Hithem Bougherara and El-Hacene Bererhi

Published: 30 March 2023



Copyright: © 2023 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

1. Introduction

Genetic resources are the most valuable and strategically important commodity because many indigenous populations, races, and ecotypes contribute to human needs and could generate much more than they currently do. In order to ensure the sustainability of species and avoid their extinction, the study and management of biodiversity allows us to

accumulate knowledge and orient towards their economic value on the genetic level and to qualify biodiversity as a potential source of permanent income on a global scale [1].

An effort has been made to determine, through the analysis of genetic diversity, the different phenotypes (ecotypes) of the “Tergui” population that have until now only been differentiated based on phenotypic appearance, geographical location, or tribal property. It was agreed that variations in the main morphological criteria, genotype, and performance that make up populations were not sufficient to describe them as “races”. This study deals with the camel’s genetic variability; its main objective is to characterize the genetic diversity of the “Tergui” camel population in the Hoggar region based on the phenotypic and molecular criteria, to analyze it within and between ecotypes, and to highlight the prospects of its exploitation in systems of sustainable livestock.

2. Material and Methods

The study was carried out throughout the Hoggar region. Initially, a pre-survey in order to select the localities, range, and degree of diversity of the phenotypes encountered with maximum representativeness was conducted [2], covering 11 localities and a part of Tamanrasset: Tamanrasset, Izernene, Asskrem, Tin-Amzi, Tarahnent, Izerzi, In-Amguel, Hirafok, Silet, and Abalessa. The morphologic methodology was based on dimensionless dimensional space, and then sampling the DNA extraction of the blood samples of 87 animals.

3. Results and Discussion

The usefulness of microsatellite and phenotypic observed in all the ecotypes (Abahou, Amellal, Alemlagh, Atelagh, and Azzerghaf) had high heterozygosity values (0.62, 0.63, 0.62, 0.59, and 0.62, respectively). The number of alleles observed is higher, and most of private alleles (55) were at very low frequencies (below 3%), although two alleles unique to Abahou population CVRL7 (292) and CMS9 (237) showed a frequency that exceeded 7.3%. Genetic differentiation values among the five analyzed camel populations are much lower, and the level of differences explained 1.1% of the total genetic variation. All loci contribute to this differentiation, with F_{ST} values being moderately low and similar for all of the studied systems, and yet still very significant ($p < 0.001$). Our overall F_{ST} value was similar to but slightly higher than the 0.9%. However, it was smaller than those previously found between Indian camel breeds ($F_{ST} = 8.2\%$, [3] and Tunisian camel populations ($F_{ST} = 9\%$), [4]. The genetic similarity between the Algerian Tergui populations was further illustrated using genetic distances, correspondence analysis, and clustering methods (DAPC). These three classical estimates are based on genetic relationships, and gave similar results. The neighbor-joining tree (DR) showed a clear subdivision of the breeds into tree main groups, each divided into subgroups, and the Azerghaf population was more closely related to Abahou–Amelal group than the Alemlagh–Atelagh group. Our estimates for the relationship of the indigenous population is similar to the one reported by the phenotypic, where it has been pointed out using characteristics (color). Furthermore, the genetic similarity of the Tergui populations was also demonstrated using the FCA and the DAPC clustering approaches. These results could be explained by the two populations being common ancestors, with an extensive gene flow between the five Tergui populations.

4. Conclusions

This study on the genetic diversity of the camel’s “Tergui” through the five phenotypes revealed great phenotypic diversity, which is due to the presence of a number of mutations with a visible effect. The genetic polymorphism was studied morphologically and molecularly. It appears the population that is geographically neighboring is genetically close, and there seems to be a significant divergence between geographically distant populations (cases of the Abahou and Azerghaf phenotypes). Moreover, the analysis as well as the genetic distances show that they appear to have a genetic kinship. The use of microsatellite markers made it possible to confirm the genetic diversity observed at

the morphological level. The genotyping results presented, even though the number of loci studied is quite large, and provided an initial estimate of camel gene diversity. In addition, it shares a large genetic base, despite the appearance of regional differences with a fairly high inbreeding rate of 15%. Indeed, the population seems threatened by the lack of management of genealogies in the herds and by crossbreeding, which could lead to a change in its genetic structure towards homozygosity. It appears, then, that the lack of a livestock management program for a given type of production and the importance of the uncontrolled migration of individuals among the herds both cause a continuous flow of genes between the phenotypes.

Author Contributions: Conceptualization, D.H. and F.A.; methodology, D.H.; Y.A.C. and F.A. software, D.H.; validation, H.I.; F.A.; R.B. and D.H.; formal analysis, D.H.; investigation, D.H., F.A.; resources, D.H.; data curation, D.H.; writing—original draft preparation, D.H.; writing—review and editing, D.H.; visualization, D.H.; supervision, D.H.; project administration, D.H.; funding acquisition, D.H. All authors have read and agreed to the published version of the manuscript.

Funding: This research received no external funding.

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: The data presented in this study are available upon request from the corresponding author.

Acknowledgments: This work was carried out within the framework of the surveys conducted in Algeria for the development of camel breeding, which was supported by the National Institute of Agronomic Research of Algeria (INRAA). We acknowledge the help of many colleagues from other institutions and universities. The authors are also grateful to the Direction des Services Agricole and the Chamber of Agriculture of the Tamanrasset Wilayate, which facilitated the logistics for the realization of the surveys, as well as to the camel breeders of the region who gave their time for the collection of data.

Conflicts of Interest: The authors declare no conflict of interest.

References

1. Food and Agriculture Organization of the United Nations. *Developing the Institutional Framework for the Management of Animal Genetic Resources*; FAO Animal Production and Health Guidelines, No.6; FAO: Rome, Italy, 2011.
2. Woolliams, G.A.; Pilling, D.; Scherf, B. Surveying animal genetic resources to manage biodiversity. *Anim. Genet. Resour.* **2010**, *47*, 23–30. [[CrossRef](#)]
3. Vijn, R.K.; Tania, M.S.; Mishra, B.; Kumar, S.T.B. Genetic Diversity and Differentiation of Dromedarian Camel of India. *Anim. Biotechnol.* **2007**, *18*, 81–90. [[CrossRef](#)] [[PubMed](#)]
4. Ahmed, M.O.; Salem, F.B.; Bedhiab, S.; M'Naouer, D. Analyse moléculaire de la diversité génétique des dromadaires (*Camelus dromedarius*) en Tunisie. *Biotechnol. Agron. Soc. Environ.* **2010**, *14*, 399–408.

Disclaimer/Publisher's Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.