Genetic distances among Burlina, Holstein Friesian and Brown Swiss cattle breeds



C. Targhetta*, M. De Marchi, C. Dalvit, P. Carnier, F. Gottardo, I. Andrighetto and M. Cassandro

Department of Animal Science, University of Padova, Agripolis, 35020, Legnaro, Padova, Italy

*corresponding author: chiara.targhetta@unipd.it

AIM

Aim of this study was to asses genetic distances among the rare Burlina breed and two world-wide breeds, the Holstein Friesian and the Brown Swiss, using AFLP molecular markers.

INTRODUCTION

Burlina is a small size cattle breed (height: 125 cm; body weight: 400 kg) with a black and white coat, reared only in the mountain area of the Veneto region in the North of Italy. There are about 400 animals; 273 dairy cows are included in the national milk recording system and their milk is used to produce local cheeses (e.g. Morlacco cheese).

According to the AIA (2001), phenotypic performances of Burlina dairy cows are: 4,083 kg of 305-lactation milk yield, 3,56% of fat, 3,21% of protein, 62 months of age at calving, 1.5 insemination for calving and 389 days of calving interval.

The lack of knowledge of genetic characteristics of Burlina cattle breed suggests more investigation in order to help protecting it and identifying its products, and also to assess genetic relations with other diffuse cattle breeds.

In this work we used AFLP to obtain genetic information on Burlina breed. Together with microsatellites, AFLP are the most widely adopted molecular markers. Even if microsatellites are more informative than AFLP, the latter are much simpler to be developed, because they don't need a preliminary identification of DNA sequences. Thus, they prove to be very useful for direct and time saving genetic analysis.



MATERIAL AND METHODS

Genomic DNA was extracted from whole blood obtained from 39 Burlina cows, 43 Brown Swiss cows and 44 Holstein Friesian animals.

White blood cells were lysed with a SDS buffer and the nucleic acid was then isolated with ammonium acetate and purified with isopropilic alcohol and ethanol 70%.

AFLP genotyping was carried out using the restriction endonucleases *EcoR*I and *TaqI* and three primer combinations in the second amplification step, following the protocol described by Barcaccia *et al.* 1999.

Data obtained by dominant scoring of 36 AFLP markers were used to calculate heterozigosity (H) and Polymorphism Information Content (PIC), supposing population to be at Hardy Weinberg equilibrium (Nei, 1987).

Genetic similarities of all possible pairs of genotypes were estimated using a Jaccard index (Ajmone-Marsan, 1997).

A factorial analysis was carried out using the software Genetix (4.01 version, Belkhir, 1998), in order to define latent variables which explain the whole genetic similarity relation system existing among individuals.

Breed	Animals N.	Н	PIC
All	126	0.373	0.295
Holstein Friesian	44	0.359	0.284
Brown Swiss	43	0.311	0.254
Burlina	39	0.308	0.246

Table 1. Values of H (Heterozigosity) and PIC(Polimorphism Information Content) for thethree breeds examined.



	Brown Swiss	Burlina	Holstein Friesian
Brown Swiss	0.610		
Burlina	0.493	0.560	
Holstein Friesian	0.556	0.484	0.549

Table 2.Jaccard similarities between and withinbreeds.

RESULTS AND DISCUSSION

As reported in Table 1, H values for the three breeds considered in the study range from 0.308 (Burlina) and 0.359 (Holstein Friesian), and PIC values are between 0.246 and 0.284. Burlina seems to have smaller genetic variability than the other two breeds; this result is consistent with the limited population size (about 400 animals) and distribution of this breed.

Genetic similarities calculated between Burlina and Brown Swiss (0,493) and between Burlina and Holstein Friesian (0,484) are similar, and smaller than the one obtained comparing the two world-wide breeds (0,556). This result points out that Burlina tends to differ of the same extent from both Brown Swiss and Holstein Friesian (Table 2).

Applying the factorial analysis, it is possible to define three main factors expressing together about 23% of the total variability. In particular, factor 1 allows separating clearly Burlina from the other two breeds, confirming the evidence found with genetic similarities. Moreover, factor 3 permits to distinguish between Brown Swiss and Holstein Friesian for a substantial part of individuals (Figure. 1).

CONCLUSION

Genetic characterization of Burlina breed with the use of AFLP molecular markers points out that there is a genetic difference between Burlina and the other two world-wide breeds examined. This evidence is confirmed by both genetic similarities data and factorial analysis.

Results obtained in this study suggest that AFLP fingerprinting technique can be suitable for the characterization of local cattle populations, even if the small values calculated for PIC, also due to the biallelic nature of these markers, advise increasing the number of molecular markers in the analysis.

Moreover, the application of this methodology could be very interesting to define a genetic traceability system for cattle breeds and products, which would be a very important step for the conservation of rare breeds and for the valorization of their products.

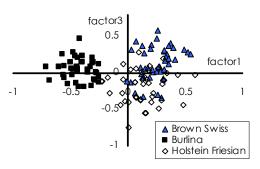


Figure 1. Distribution of individuals according to factorial analysis (factor1 and factor3)

REFERENCES

Ajmone-Marsan P., Valentini A., Cassandro M., Vecchiotti-Antaldi G., Berthi G., Kuiper M. 1997 AFLP markers for DNA fingerprinting in cattle, Animal genetics 28, 418-426

Barcaccia G., Mazzuccato A., Albertini E., Zethof J., Gerats A., Pezzotti M., Falcinelli M., 1978 Inheritance of pathogenesis in *Poa pratensis* L.: auxin test and AFLP linkage analysis support monogenic control, Theoretical and Applied Genetics, 97, 74-82

Nei M., 1987 Molecular Evolutionary Genetics, Columbia Univ. Press, New York

Belkhir K., Borsa P., Goudet J., Chikri L., L. & Bohnomme F. 1998 GENETIX, logiciel sous Windows TM pour la génétique des populations. Laboratoire Génome et Populations, CNRS UPR 9060, Université de Montpellier II, Montpellier, France

ACKNOWLEDGMENTS

Research financed by a grant of the Veneto Region. The authors wish to thank the laboratory of the Department of Agronomy, Environment and Crop Production, University of Padova, for the technical support to the study.

55th Annual Meeting of the European Association for Animal Production Bled, Slovenia – September 5th – 9th, 2004