Traceability of the PGI product "Vitellone Bianco dell'Appennino Centrale" by SNP markers

R. Negrini, E. Milanesi, F. Filippini, S. Dunner, H. Leveziel, J. Williams, A. Valentini & P. Ajmone Marsan

Published online: 15 Mar 2016.

Submit your article to this journal ⬈

Article views: 29

Traceability of the PGI product "Vitellone Bianco dell'Appennino Centrale" by SNP markers

R. Negrini[1], E. Milanesi[2], F. Filippini[3], S. Dunner[4], H. Leveziel[5], J. Williams[6] , A. Valentini[7], P. Ajmone Marsan[1]

[1] Istituto di Zootecnica. Università Cattolica del S. Cuore, Piacenza, Italy
[2] Istituto di Zootecnia Generale. Università di Milano, Italy
[3] ANABIC, Perugia, Italy
[4] Depatimento de Producción Animal. Universidad Complutense, Madrid, Spain
[5] Faculté des Sciences et Techniques. UGEMA Limoges, France
[6] Parco Tecnologico Padano. Lodi, Italy
[7] Dipartimento di Produzioni Animali. Università della Tuscia, Viterbo, Italy

Corresponding author: Riccardo Negrini, Istituto di Zootecnica, Facoltà di Agraria, Università Cattolica del Sacro Cuore, Via Emilia Parmense 84, 29100 Piacenza, Italy - Tel. +39 0523 599205 - Fax: +39 0523 599276 - E-mail: riccardo.negrini@unicatt.it

ABSTRACT

Traceability of meat has become a key aspect of food-quality assurance and a priority for EU countries, to meet consumer demand for comprehensive and integrated food safety policies. In this context, the traceability of animals and animal products at the breed level might play a key role as it would enable the certification of regional products linked to particular breeds. Technologies based on DNA analysis have the potential to achieve this goal by-passing the large scale and systematic biological sampling necessary for individual fingerprinting.

The objective of this work was to test the power of a SNP panel to trace PGI "Vitellone Bianco dell'Appennino Centrale", a product linked to three breeds: Chianina, Marchigiana and Romagnola.

A total of 180 unrelated animals belonging to PGI-allowed breeds (Chianina n=22; Romagnola n=22; and Marchigiana n=22) and PGI-not allowed breeds (Piemontese n=22, Maremmana n=24, Italian Red Pied n=24, Italian Brown n=22, Italian Friesian n=22) were sampled and genotyped with a panel of 130 SNP in 90 independent genes.

Individual genotypes were assigned to breed by Bayesian based clustering approach. In particular the SNP data were analysed by the Rannala and Mountain approach implemented in the software Geneclass 2 (file:///C:/Software/GeneClass2/Help/index.htm).

The SNP-based molecular approach in combination with Bayesian assignment algorithms allowed an overall correct assignment of more than 95% of individuals to their breeds of origins. This percentage increase to 96% grouping the breeds allowed in a unique cluster.

Sorting the SNPs by their Gst values and using the 90 showing a value higher than 0.01, we maintain the same rate of allocation success indicating that selecting SNPs for their informative content will reduce the number of markers required for a reliable traceability at breed level, reducing the laboratory effort and consequently the cost for the large scale application of the method

Our results suggest that SNP markers in combination with Bayesian algorithm can be exploited in allocation studies and are able to trace "Vitellone Bianco dell'Appennino Centrale". The main advantages of SNP are their abundance and the potential of full automation.