

SCIENTIFIC REPORT: EXCHANGE GRANT

Ref Number 3723.

Document describing the following information:

- Purpose of the visit
- Description of the work carried out during the visit
- Description of the main results obtained
- Future collaboration with host institution (if applicable)
- Projected publications/articles resulting or to result from your grant
- Other comments (if any)

ESF activity: LESC; Advances in Farm Animal Genomic Resources; Genomic-Resources

Project title: Identification of signals of selection in the genomes of Spanish dairy sheep breeds.

Candidate researcher: Dr. Beatriz Gutierrez Gil. Postdoctoral researcher at the University of León, León (Spain).

Host researcher: Dr. Pamela Wiener. Career Track fellow at The Roslin Institute, The University of Edinburgh (United Kingdom).

A) Purpose of the visit: The main objective of the visit was to perform different analyses to identify selection sweeps in dairy sheep. The Spanish group of the candidate researcher, Dr Beatriz Gutiérrez-Gil, established at the University of León (Spain), has a long tradition in the field of dairy sheep genetics and has performed several studies to gain knowledge on the quantitative and molecular genetics aspects that control the architecture of traits of interest in dairy sheep. At the molecular level, this group has performed genome scans for detection of QTL influencing milk production traits, morphological traits and disease resistance in Churra sheep, a highly specialized autochthonous breed of the region of Castilla y León. These genome scans were initially based on microsatellite genotyping (181 markers analysed; Gutiérrez-Gil et al., 2008, 2009a) and have been recently been performed using the OvineSNP50BeadChip (with about 45000 markers analysed after quality control). This medium-density high throughput SNP genotyping platform also offers the opportunity to perform selection sweeps, a complementary methodology to identify regions of the genome that have undergone selection pressure and that has not previously been implemented by the group of the University of León.

Based on previous collaborations between Dr Beatriz Gutiérrez-Gil and Dr Pam Wiener during Beatriz' postdoctoral fellowship at the Roslin Institute, Edinburgh (UK), this visit was planned as an opportunity to apply a method of selection sweep mapping that Pam Wiener has recently developed to identify selection sweeps in dairy sheep. This method is based on a regression approach for detection of regions with decreased heterozygosity (Wiener & Pong-Wong, 2011). Additionally analyses based on basic F_{st} and heterozygosity calculations across the genome would be performed, which would give us also the good opportunity to compare the results between methodologies and to implement the method described by Wiener and Pong-Wong (2011) on a whole-genome dataset.

B) Description of the work carried out during the visit: With the purpose described above we have analyzed a number of samples from four Spanish sheep breeds analyzed with the *Illumina OvineSNP50BeadChip*. Three of the breeds studied are autochthonous sheep breeds from the region of Castilla y León, where the University of León is located: Churra (dairy aptitude breed and also exploited for lamb production), Castellana and Ojalada (these two breeds are used mainly for lamb production, although the Castellana breed is also milked). Another Spanish breed included in our analyses was Rasa Aragonesa, specialized in meat production. The number of samples analysed were 96 for Churra and 24 for each of the other three breeds. After an initial quality control, we analyzed a total of 44546 SNPs distributed across the 26 autosomic ovine chromosomes

We performed three different analyses:

- 1) **Calculations of pairwise Fsts:** We estimated averaged pair-wise Fst values between Churra and each of the other three non-dairy breeds, using sliding windows of 9, 13 and 17 SNPs. Two different thresholds (quantiles of 0.005 and 0.0005) were considered for the identification of the top regions derived from this analysis.
- 2) **Calculations of Normalized Heterozygosity:** For each breed, we calculated normalized heterozygosity values averaged in sliding windows of 9, 13 and 19 SNPs individually for all the breeds included in the Fst calculations. Based on the normalized values and following Rubin et al. (2010), the estimates showing values lower than -6 were considered as significant.
- 3) **Regression-based analysis for detection of regions of decreased heterozygosity:** This method assumes that heterozygosity was at similar levels across the genome prior to the selective sweep and that an asymptotic increase in marker variation (heterozygosity) with increasing distance from a locus under directional selection will be observed. For each breed under study three different bracket sizes from the test positions (5, 10 and 20 Mbp on either side of the test positions) and three different thresholds (quantiles of 0.01, 0.005 and 0.0005) were considered for the selection of the most interesting regions revealed by this analysis.

C) Description of the main results obtained: The three different analyses applied have yielded a large number of regions to consider depending of the breed or pair of breeds analyzed, and also depending on the different parameters considered (top levels and bracket or window size). As we had previously foreseen in our project proposal, and based on the short length of the ESF funded stay (2 weeks), we did not have time during the visit to study and compare in detail the regions identified by the different analyses. This will be done by Beatriz Gutierrez from her home place of work in León (Spain) who will keep in touch with Dr Wiener through email and videoconferences to discuss the results.

D) Future collaboration with host institution: Since her postdoctoral stay at Roslin between 2004 and 2007, Beatriz Gutiérrez has been in contact with Dr. Pam Wiener who supervised her work during that period, mainly related to the preparation of manuscripts and meeting abstracts describing results that were generated at the end of

Beatriz's stay (Gutiérrez-Gil et al., 2009b; 2010; Wiener & Gutiérrez-Gil, 2009, Wiener et al., 2011; Gutiérrez-Gil et al., 2012). In the short term, the two researchers will continue the collaboration initiated through this short visit with the aim of discussing and interpreting the results and writing a manuscript for their publication. The analyses performed in this visit are of interest to both researchers and their corresponding research groups and they hope to extend these analyses in a future collaborative project, possibly focused on a multi-species (sheep, cattle, goats) genetic analysis of dairy traits.

E) Projected publications/articles resulting or to result from the grant: We expect to publish the results of these analyses regarding selection sweep mapping in dairy sheep in a full research article in an SCI journal. We have not determined the target journal at this point.

F) Other comments: The two researchers involved in the work performed during this stay acknowledge the European Science Foundation for the program "Exchange Grants" which has provided them the opportunity to initiate the collaborative work here described. Any publications on this work will acknowledge the support of the European Science Foundation.

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