

Results from the Sustainable Solutions for Small Ruminants (3SR) Project

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Background

To remain sustainable, sheep and goat producers will need to continue to address the challenges of disease and improved efficiency. Genomic tools and technologies are likely to play a crucial role in helping to address these challenges. In 2009 there was still a need to improve the underpinning genomic tools such as a well annotated and complete reference sequence and effective, affordable selectable genetic markers. The 3SR project was therefore funded to help address this and to develop relevant resources.

Activity highlights

Sequencing of over 50 animals has been carried out to help improve the quality of the reference sheep genome (coordinated by the International Sheep Genomics Consortium – ISGC), while large scale RNA sequencing has been performed to help with the sheep genome annotation.

Helped the International Goat Genome Consortium (IGGC) to develop a high density (50K) SNP chip for goats.

Genotyped over 4000 sheep and 2000 goats using the respective 50K SNP chips.

Over 7000 50K genotypes analysed from 11 sheep populations and over 2000 50K genotypes analysed for goats.

Controlled challenge studies were carried out for mastitis (in sheep and goats) and nematodes (sheep) to explore the mechanisms of resistance.

Functional studies of genes involved in ovulation rate in several sheep breeds were carried out to support the biological understanding of the mutations discovered.

Project at a glance

- Total value: >€5m (of which €2.99m EC FP7 grant)
- Consortium: 14 partners in 11 countries
- Duration: 3.5 years from May 2010
- Traits of interest: mastitis, nematode resistance, ovulation rate, paratuberculosis

A global consortium



Key results

Identified causative mutations affecting ovulation rate in Grivette (French) and Olkuszka (Polish) sheep, and 2 candidate genes for sterility were identified in Cambridge sheep and continue to be investigated.

Small regions of the genome were identified that have a significant effect on mastitis susceptibility and nematode resistance. Genetic markers for these regions are being validated in commercial populations.

Helped the ISGC deliver sheep reference genome v3.1.

Produced over a terabyte of RNA-seq data that is being used to annotate the sheep genome.

Confirmed genetic variation to paratuberculosis in sheep (heritability 0.28 ± 0.10)

Open access Genome Browser developed <http://genome.itb.cnr.it/gb2/gbrowse/oarv3.1/>

A whole-genome radiation hybrid (RH) map was produced for goats, containing more than 30,000 markers ordered across the chromosomes.

Led the establishment of the goat AdaptMap project which aims to coordinate and collate the research data across a number of projects (including 3SR)



Visit www.3srbreeding.eu for further information



3SR: Sustainable Solutions for Small Ruminants is a Collaborative Project supported by funding from the 7th Framework Programme of the European Union. This publication represents the views of the Authors, not the European Commission. The Commission is not liable for any use that may be made of the information.