Unravelling local adaptation in the genome of British sheep

Supervisory team:
Main supervisor: Dr Pablo Orozco-terWengel (Cardiff University)
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Host institution: Cardiff University
Project description:

Understanding how species adapt to the environment they live in is a major goal in evolutionary biology. This is of particular value in light of climate change, where extant species will have to adapt to warmer and potentially harsher conditions relatively fast. However, identifying the genomic regions involved in local adaptation has been a challenging problem because the tools to survey species' genomes have only become available in the last two decades, e.g. SNP arrays and whole genome sequencing. The aim of this project is to analyse British sheep occurring in contrasting environments (mountain vs. lowland) using the OvineSNP50 arrays (~51,000 SNPs) to identify genetic variation linked to local adaptation in the UK's heterogeneous agricultural landscape. Additionally, the SNP arrays data will be analysed in combination with whole genome data for a population of Iranian wild mouflon (the sheep's ancestor) and other sheep breeds in order to identify genomic signatures of selection specific to the domestication event.

The PhD student will be based 80% at Cardiff University, where the research group specialises in identifying signatures of selection using next generation sequencing in livestock and wildlife, and 20% at Bristol University, a world leader in the development of statistical approaches to study demographic history using genetic data. For this project the PhD student will be trained in sample preparation for SNP chip analysis and bioinformatics analyses (e.g. data quality filtering, demographic analyses, and identifying signatures of selection). This experimental design will allow the PhD student to compare populations of British mountain vs. lowland sheep, in the equivalent of a replicated experiment, to identify specific signatures of local adaptation to the environment where these populations live in, while controlling for confounding factors such as the demographic history (to be simulated with approximate Bayesian computation) and the selection signature left by the domestication process (to be accounted for by comparing domestic sheep against Iranian wild mouflon).

Informal enquiries are also encouraged. Please contact Dr. Pablo Orozco-terWengel at 'Orozco-terWengelPA@cardiff.ac.uk'.

Further information can be found at:
http://www.cardiff.ac.uk/biosciences/research/divisions/organisms-and-environment