

### **RIDING THE WHOLE-GENOME DATA TSUNAMI: A LANDSCAPE GENOMIC STUDY OF LOCAL ADAPTATION IN MOROCCAN SHEEP AND GOATS**

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In Morocco, like in other developing countries, small ruminants play an important role in the livelihood of a large proportion of farmers and landless shepherds. Conserving traditional breeds is essential in these countries since they are able to prosper in challenging habitats and their rich genomic resources allow them to adapt to new conditions. Therefore the key genetic features of local adaptation must be identified, notably with landscape genomic approaches, in order to support and encourage sustainable breeding of low-input livestock. To this end, the NEXTGEN project led an extended sampling campaign of local small ruminants to study local adaptation in Morocco. Over 2000 sheep and goats were sampled in small farms and flocks spread over the whole country. For each species, 164 samples were selected in order to reliably represent the environmental conditions while having an even spatial distribution. A landscape genomic approach was applied to detect selection signatures among 28 million SNPs in sheep and 19 million SNPs in goats. In summary, the habitat of each sample is characterised with environmental variables and significant genotype/environment associations point out the loci potentially under selection. Data were processed with SamBada, a specific landscape genomic software program. Preliminary results show that the method is able to process whole-genome sequence data. However the relatively low number of samples compared with the number of SNPs implies the existence of false positives among the most significant results. Measuring the spatial dependence between samples, as featured in SamBada, may facilitate their detection and interpretation. Thus combining whole-genome analysis with spatial statistics may lead to an integrated biogeoinformatic approach to study local adaptation.