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S2-O3 Harnessing landscape genomics to unravel adaptation to water stress in sheep from south-west Europe

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Extensive sheep production systems in semi-arid regions are highly dependent on rainfall patterns and are therefore increasingly vulnerable to climate change-induced water stress. Here, we aimed to identify genes and biological processes putatively involved in adaptation to water stress in 22 autochthonous sheep breeds from Spain, one of the European hotspots for drought severity. To this end, we genotyped around 54,000 single nucleotide polymorphisms (SNPs) in >1000 animals using the Illumina Ovine SNP50 BeadChip and characterised water availability at the sampling sites. Latent factor mixed models (LFMMs) were used to identify gene-environment associations (GEAs) and the Ensembl database was used to annotate the significant associations found. To correct GEAs for population stratification, we quantified genetic structure and the number of ancestral populations using a sparse non-negative matrix factorisation (sNMF) algorithm. We found moderate levels of structuring with pairwise *F*STs ranging from 0.03 to 0.14 and evidence for 16 ancestral populations, suggesting a complex demography with high levels of admixture. We found 13 significant SNPs with an expected false discovery rate of 5%, with most associations highlighting the covariance between temperature and precipitation as a major selective driver. Candidate genes in linkage disequilibrium with significant SNPs were involved in processes ranging from the molecular level (e.g. chromatin organisation) to the cellular and organismal level (e.g. cytoskeletal organisation and anatomical structure development). Our findings provide new insights into the genetic basis of adaptation to water stress, and highlight the need for genome-informed strategies to enhance sheep resilience in semi-arid regions.