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Investigating genomic adaptation to climate in local Mediterranean sheep breeds

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Introduction

- Local livestock breeds exhibit adaptive traits shaped by their long association with the local environment.
- These breeds thrive in specific climates or terrains, in contrast to more common commercial breeds.
- Genomic studies are revealing signatures of selection in these breeds, underpinning their genetic adaptation to local conditions.



Aim

The objective of this study is to investigate the interaction between the genomes of local sheep breeds and bioclimatic variables that influence their genomic structure. Furthermore, this study aims to elucidate the biological pathways and processes involved in this genomic shaping.



Materials & Methods

- 1233 individuals belonging to 59 Mediterranean sheep breeds.
- Genotypes retrieved from public datasets genotyped using the Illumina OvineSNP50 beadchip. Reference genome OARv4.0
- After quality control and filtering we obtained a final dataset of 36,809 SNPs, and 1233 individuals.
- 13 bioclimatic variables after filtering for $r^2 < 0.8$ using the *prepareENV* function of the package R.Sambada.

BIOCLIMATIC VARIABLES:

- **Temperature:**
BIO1 = Annual Mean Temperature
BIO2 = Mean Diurnal Range (Mean of monthly (max temp - min temp))
BIO3 = Isothermality (BIO2/BIO7) ($\times 100$)
BIO4 = Temperature Seasonality (standard deviation $\times 100$)
BIO5 = Max Temperature of Warmest Month
BIO8 = Mean Temperature of Wettest Quarter
BIO9 = Mean Temperature of Driest Quarter
- **Precipitation:**
BIO15 = Precipitation Seasonality (Coefficient of Variation)
BIO19 = Precipitation of Coldest Quarter
PREC6 = Precipitation in June
PREC7 = Precipitation in July
- **Position:**
Long = Longitude
Lat = Latitude

Materials & Methods

- Using a landscape genomics approach (Samβada v0.8.3), we investigated genetic signatures of environmental adaptation correcting for the ancestry fractions identified through ADMIXTURE.
- we run a null model with only the Admixture components and a full model with all the variables, then we obtained the final p-values as a chi-squared of the delta loglikelihoods of the results
- We corrected for multiple testing calculating FDR and defined the significance threshold at $FDR < 0.01$

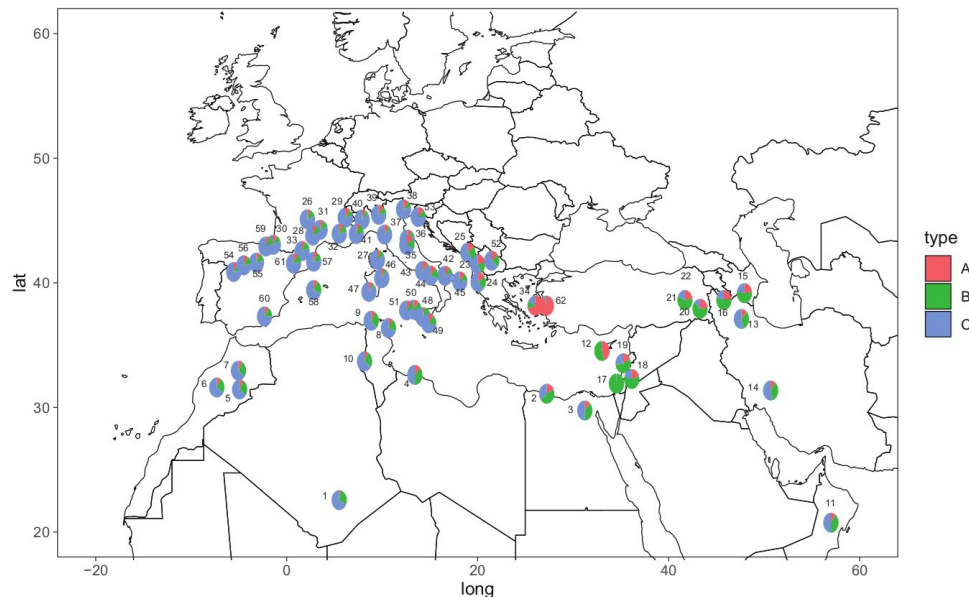


Fig. 1: Geographic distribution of the genomic components at K=3 from the ADMIXTURE analysis

Materials & Methods

- we chose the windows sizes based on LD. Merging Clusters of SNPs into a single 'window of association' when neighbouring significant SNPs had linkage disequilibrium (LD) higher than the non-syntenic background LD (nsLD) across populations and the distance between the SNPs was greater than the median distance among all the SNPs.
- Annotation of genes intercepted by neighboring regions in linkage disequilibrium with each significantly associated SNP.
- Gene prioritization / GO-terms and Pathways enrichment

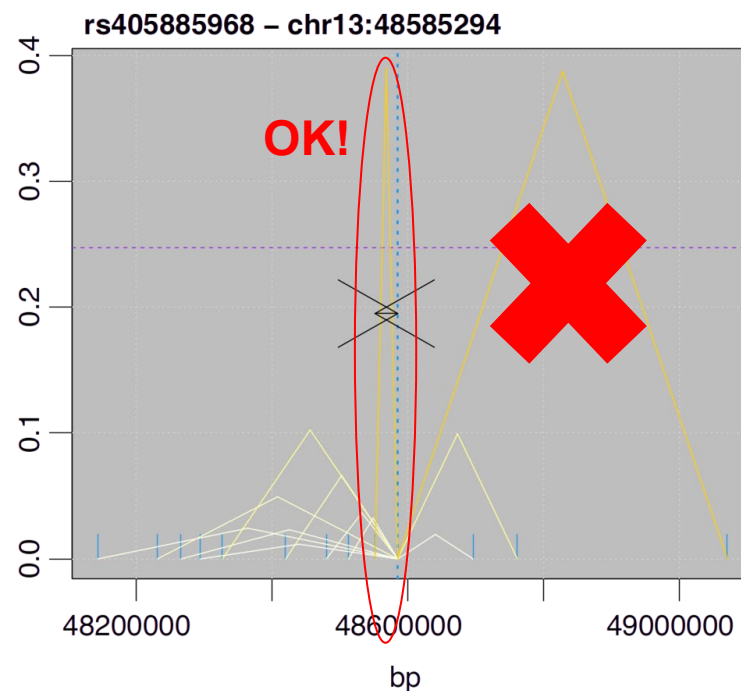


Fig. 2: *Spiderplot* representing one window obtained merging SNPs in LD. Each of the blue bars represent a SBP and each of the peaks in grades of yellow represents the LD with a neighboring SNP. In purple the threshold.

Results

- We identified several candidate genes of which many have known roles in environmental adaptation.
- By applying candidate gene prioritization, we identified genes putatively involved in metabolic pathways that are particularly relevant, as response to the ever-changing climate conditions.

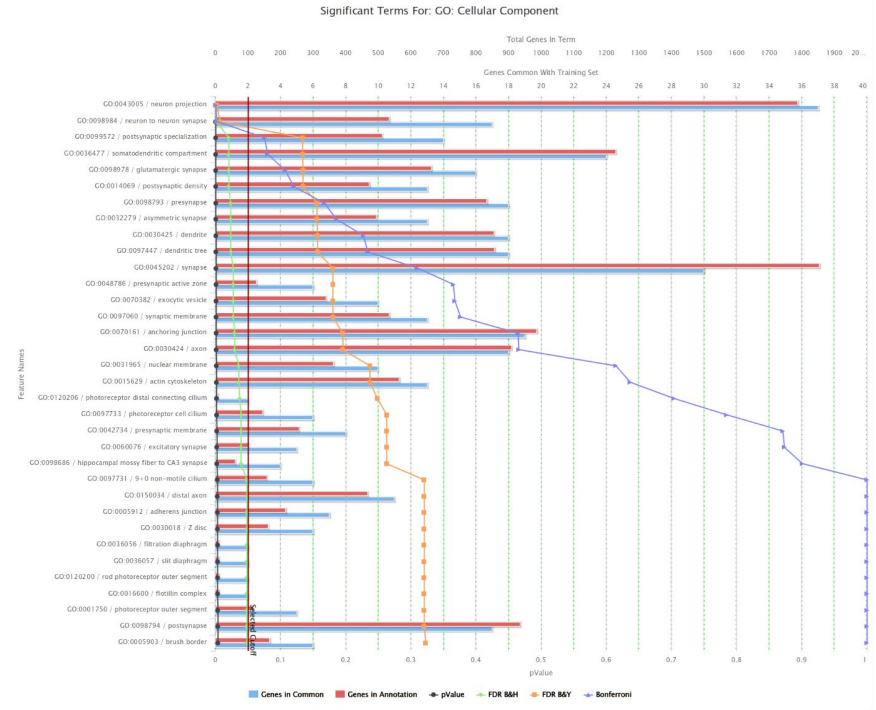


Fig. 3: GO:Cellular Components enrichment for Temperature related variables

Results: enriched GO-terms and Pathways

Category	ID	Name OXIDATIVE STRESS	FDR	Hit Count in Query List	Hit Count In Genome
GO: Molecular Function	GO:0000268	peroxisome targeting sequence binding	0.02	3	7
GO: Molecular Function	GO:0008092	cytoskeletal protein binding	0.03	24	1135
GO: Cellular Component	GO:0043005	neuron projection	2.61E-04	37	1788
GO: Cellular Component	GO:0098984	neuron to neuron synapse	1.0E-03	17	533
Pathway	M27617	REACTOME PROTEIN-PROTEIN INTERACTIONS AT SYNAPSES	0.02	7	87
Pathway	M48032	REACTOME BACTERIAL INFECTION PATHWAYS	0.03	6	71

Results

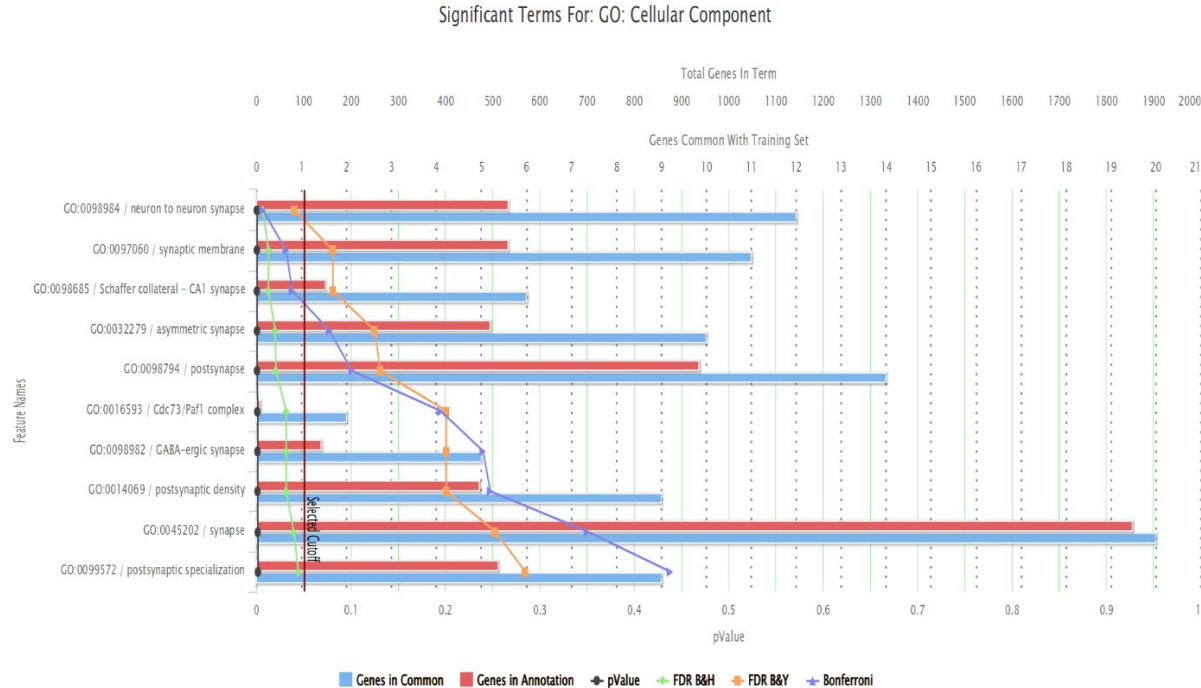


Fig. 4: GO:Cellular Components enrichment for Precipitations related variables

Results: enriched GO-terms and Pathways

Category	ID	Name	fdr	Hit Count in Query List	Hit Count in Genome
INFLUENCES METHYLATION					
GO: Molecular Function	GO:1990226	histone methyltransferase binding	0.04	3	18
GO: Cellular Component	GO:0098984	neuron to neuron synapse	0.01	12	533
GO: Cellular Component	GO:0097060	synaptic membrane	0.01	11	533
GO: Cellular Component	GO:0098685	Schaffer collateral - CA1 synapse	0.01	6	146
GO: Cellular Component	GO:0032279	asymmetric synapse	0.02	10	494
GO: Cellular Component	GO:0098794	postsynapse	0.02	14	937

Results

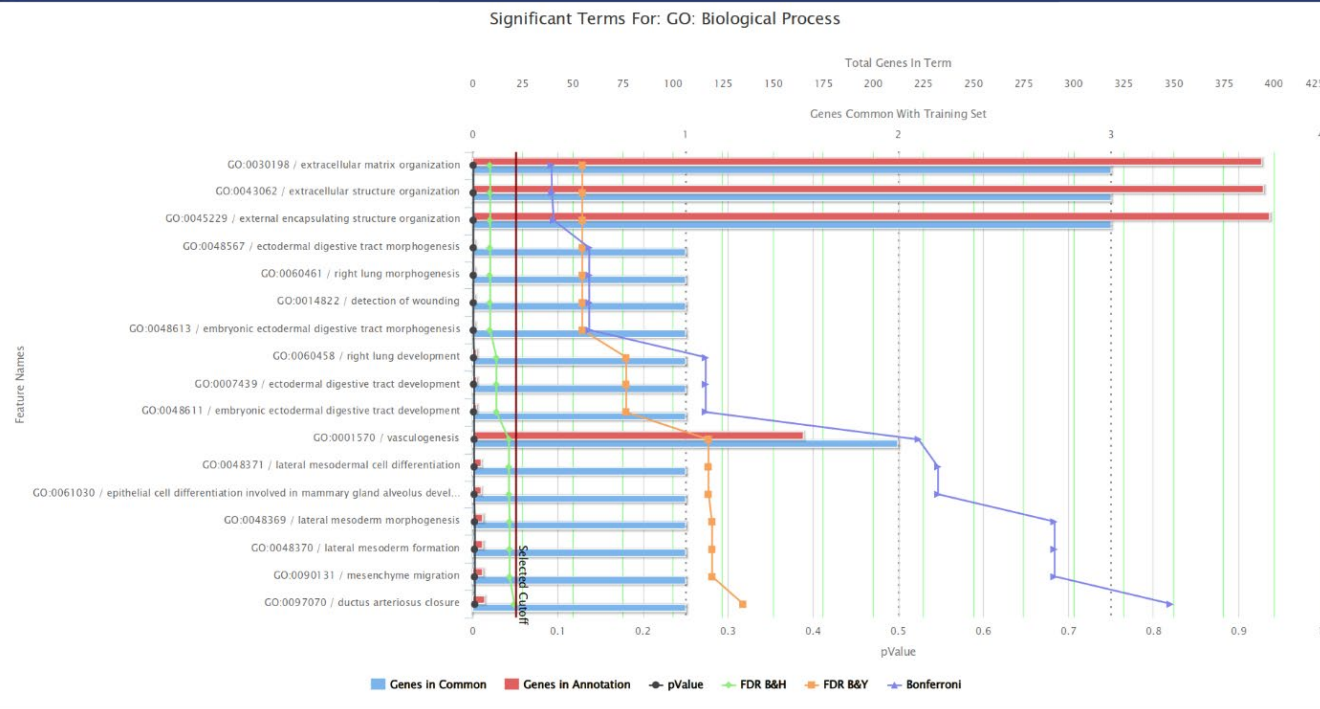


Fig. 5: GO: Cellular Components enrichment for Latitude

Results: enriched GO-terms and Pathways

Category	ID	Name	fdr	Hit Count in Query List	Hit Count in Genome
GO: Biological Process	GO:0030198	extracellular matrix organization	0.02	3	394
GO: Biological Process	GO:0043062	extracellular structure organization	0.02	3	395
GO: Biological Process	GO:0045229	external encapsulating structure organization	0.02	3	398
GO: Biological Process	GO:0048567	ectodermal digestive tract morphogenesis	0.02	1	1
GO: Biological Process	GO:0060461	right lung morphogenesis	0.02	1	1
GO: Biological Process	GO:0014822	detection of wounding	0.02	1	1

ADAPTATION TO DIVERSE DIETS

ADAPTATION TO VARYING OXIGEN LEVELS

Results

	bio1	bio2	bio3	bio4	bio5	bio8	bio9	bio15	bio19	prec6	prec7	Long	Lat
bio1	1	-0,13	-0,21	-0,08	-0,01	-0,04	-0,10	0,39	0,59	-0,10	-0,11	-0,22	-0,06
bio2	-0,13	1	0,12	-0,07	0,04	-0,04	-0,06	-0,05	-0,05	-0,15	-0,16	0,03	-0,12
bio3	-0,21	0,12	1	0,02	-0,04	-0,06	-0,07	-0,10	-0,15	-0,18	-0,18	0,12	-0,05
bio4	-0,08	-0,07	0,02	1	-0,05	-0,06	-0,01	0,05	-0,08	-0,08	-0,10	-0,03	-0,08
bio5	-0,01	0,04	-0,04	-0,05	1	0,01	-0,03	-0,05	-0,04	-0,06	-0,06	-0,05	0,02
bio8	-0,04	-0,04	-0,06	-0,06	0,01	1	-0,04	-0,06	0,02	-0,11	-0,11	-0,09	-0,04
bio9	-0,10	-0,06	-0,07	-0,01	-0,03	-0,04	1	0,00	-0,08	0,11	0,07	-0,09	-0,06
bio15	0,39	-0,05	-0,10	0,05	-0,05	-0,06	0,00	1	-0,10	0,04	-0,03	-0,11	-0,09
bio19	0,59	-0,05	-0,15	-0,08	-0,04	0,02	-0,08	-0,10	1	-0,20	-0,18	-0,14	-0,12
prec6	-0,10	-0,15	-0,18	-0,08	-0,06	-0,11	0,11	0,04	-0,20	1	0,55	-0,18	0,01
prec7	-0,11	-0,16	-0,18	-0,10	-0,06	-0,11	0,07	-0,03	-0,18	0,55	1	-0,18	-0,04
Long	-0,22	0,03	0,12	-0,03	-0,05	-0,09	-0,09	-0,11	-0,14	-0,18	-0,18	1	-0,13
Lat	-0,06	-0,12	-0,05	-0,08	0,02	-0,04	-0,06	-0,09	-0,12	0,01	-0,04	-0,13	1

Table 4: Correlation matrix displaying the relationships between the associations of single nucleotide polymorphisms (SNPs) with each bioclimatic variables.

Discussion & Conclusion

- Our analyses identified many genes Pathways and biological functions potentially involved in the adaptation to different Latitude, temperatures and precipitation levels.
- Many SNPs (and consequently genes, biological pathways and functions), are involved in the adaptation to more than one bioclimatic variable.
- Our results confirm that the adaptation process is a mixture of polygenic and pleiotropic events.





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**Thank you for your kind
attention**



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Why we did not stick on the genes

Variable	n. Chromosomes	SNPs	Genes
bio1	26	1172	486
bio2	26	365	152
bio3	26	458	191
bio4	25	236	92
bio5	23	103	42
bio8	25	185	74
bio9	26	148	59
bio15	26	246	104
bio19	26	525	244
prec6	25	645	242
prec7	26	719	276
Long	25	517	210
Lat	26	692	279