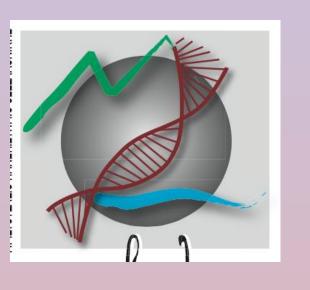


Genome-wide SNP profiling of Greek sheep with worldwide domestic breeds revealing population and admixture patterns



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Introduction

Greece hosts one of the largest and highly diverse pools of animal genetic resources in the Mediterranean region, where numerous sheep breeds have been regionally selected for centuries. Several factors have been involved in breed formation processes of Greek sheep such as the geographic isolation (e.g., island and mainland Greece), genetic drift, human-mediated selection, crossbreeding and transhumance. Greek sheep have been poorly studied in global scale genetic analysis. The present study focuses on the genome-wide characterization of population structure, diversity, and admixture patterns of local Greek domestic sheep collectively analyzed with 38 global breeds from the Sheep HapMap project.

Materials and Methods

- ♦ **Blood sampling:** 1,008 Greek domestic sheep from 5 different breeds/23 locations (Figure 1)
- ♦ **DNA extraction and genome-wide genotyping** using the OvineSNP50 Genotyping BeadChip v2 **52,152 SNPs**
- ♦ Joint analysis with ~2,000 published 50K sheep genotypes of 38 breeds Sheep HapMap and iSAGE projects
- **♦ Genotype quality control & selection of representative genotypes**
- ♦ **Population structure:** principal component analysis (**PCA**) and model-based clustering (**Admixture**)
- \diamond Genetic differentiation & diversity: pairwise F_{ST} & heterozygosity/inbreeding levels (\mathbf{H}_0 , \mathbf{H}_e , F_{IS}) using PLINK v1.9



Results & Discussion

Global PCA

The global clustering is attributed to the geographic origin of breed formation

Greek sheep represent an intermediate genetic link between Asia and Europe, indicating crosscontinent and within Europe genetic clines (Figure 2)

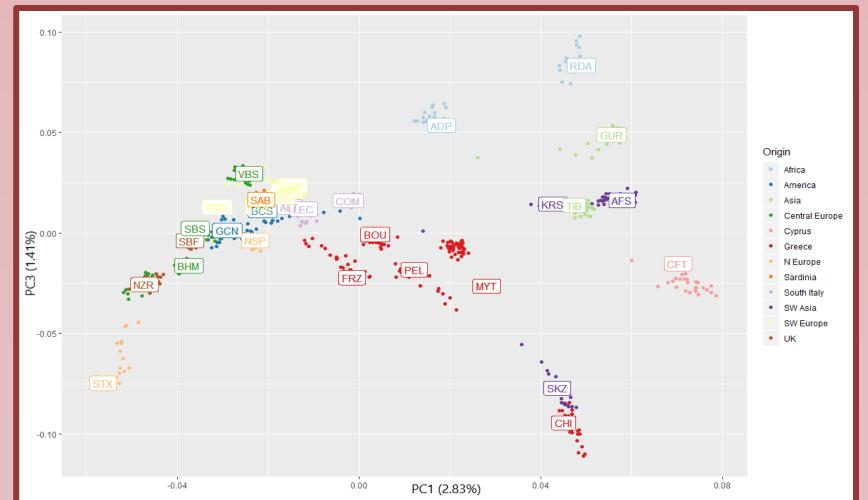


Figure 2: PCA analysis of global sheep level colored by geographic origin. First and third principal components depicted a central position of four Greek sheep breeds between Asian, African, and European sheep

Local PCA

Fat-tailed Asian origin of CHI and thin-tailed Zackel origin of BOU, PEL, MYT and FRZ may be related to the genetic differentiation between these clusters

MYT and PEL were not adequately differentiated due to high genetic relatedness (Figure 3)

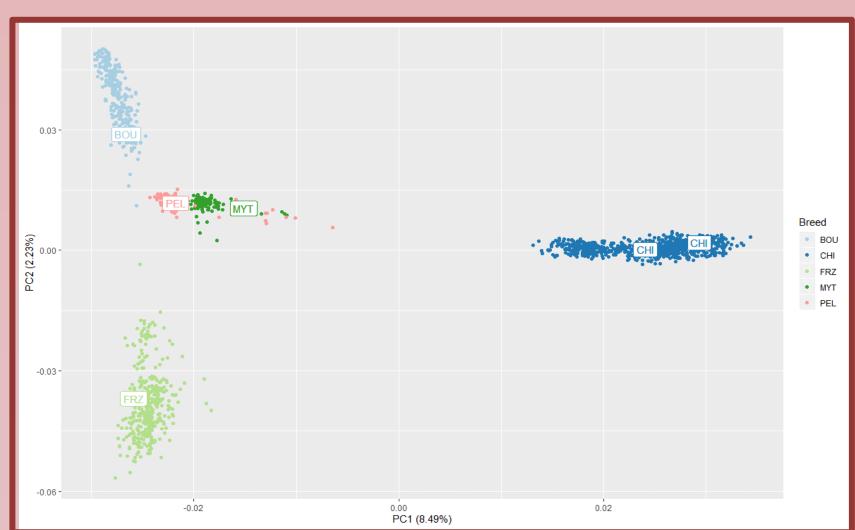


Figure 3: PCA analysis of Greek sheep colored by breed. First and second principal components revealed the relatedness among the five Greek developed breeds.

Global Admixture

Asian and European genetic components were clearly observed (K=2) while the optimal K=35 differentiated the majority of global breeds Mediterranean sheep were represented by a distinctive genetic cluster (K=8-14) (Figure 4)

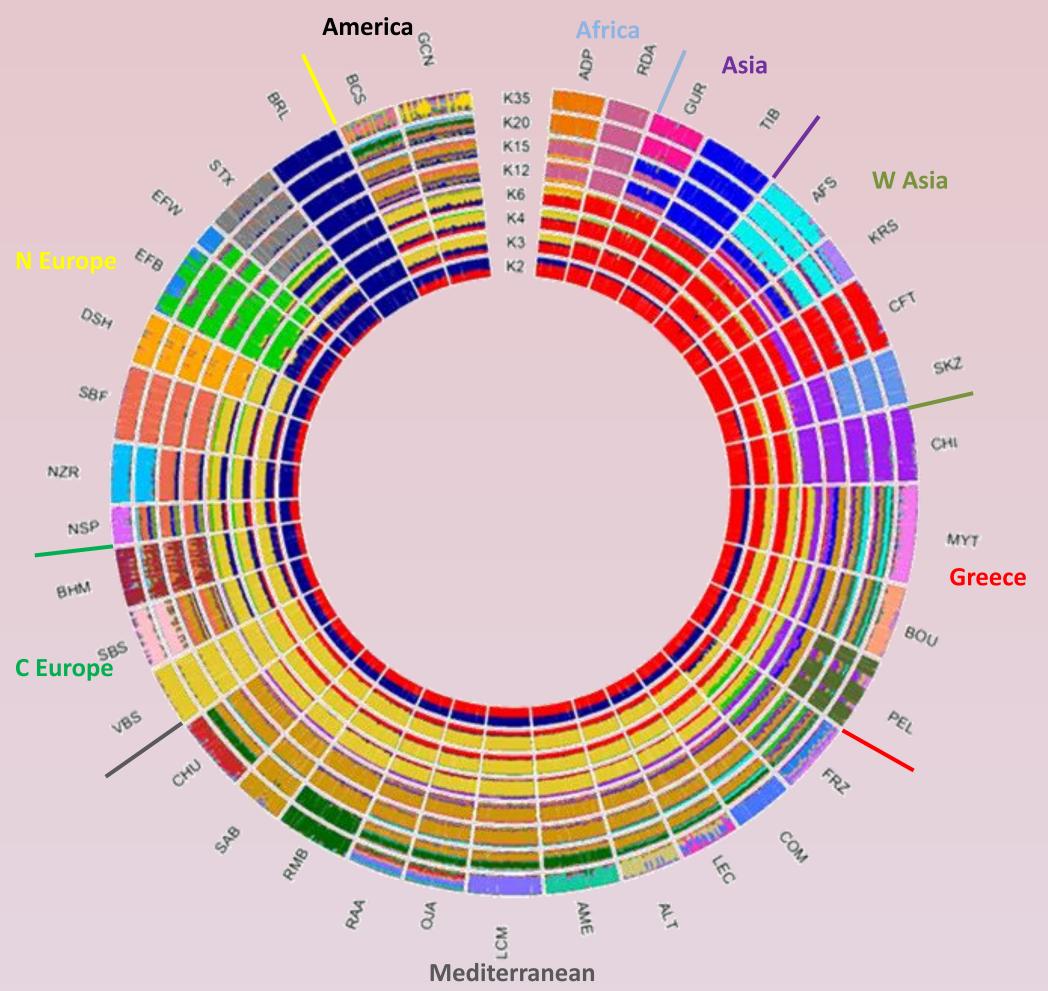


Figure 4: Circular representation of global sheep population structure results obtained with Admixture software for K = 2, 3, 4, 6, 12, 15, 20 and 35.

Local Admixture

The optimal K-value (K=5) clearly differentiated the respective five Greek breeds

Recent admixture events (K=8-13) were attributed crossbreeding for genetic improvement purposes (Figure 5)

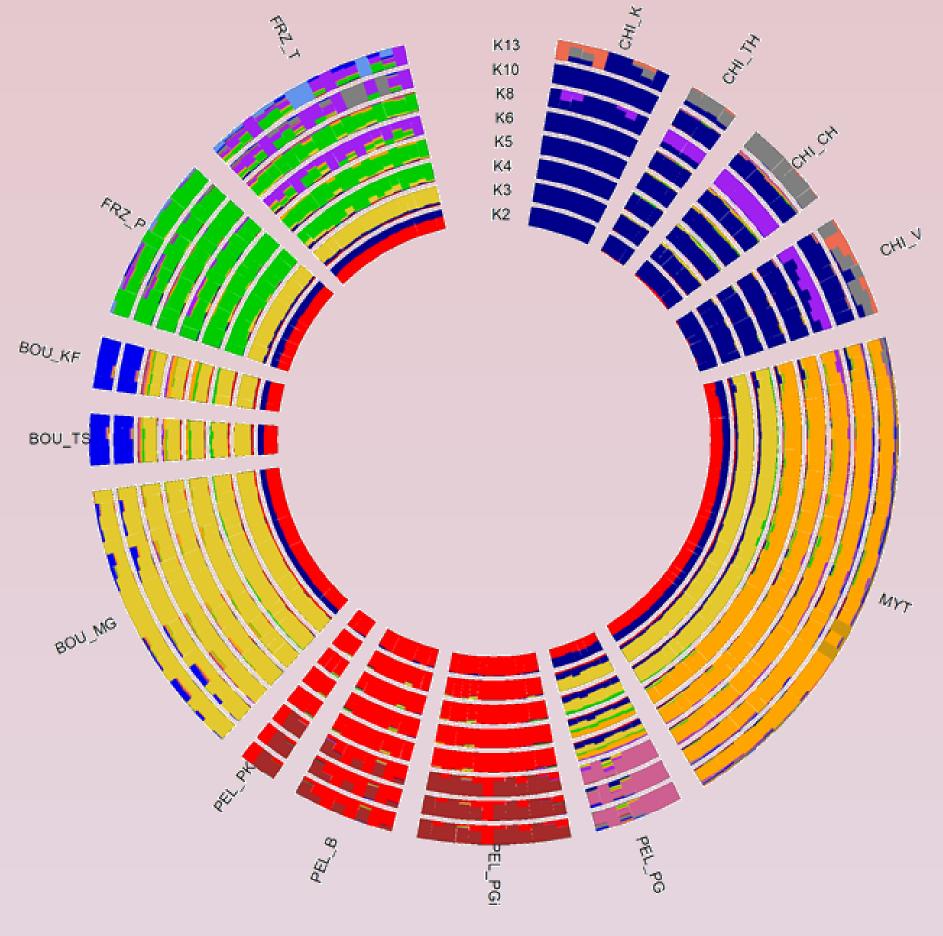


Figure 5: Circular representation of population structure results for representative local sheep obtained with Admixture software for K = 2-5, 6, 8, 10 and 13. The respective sampling sites are also depicted excluding Mytilini sheep due to highly-frequent animal exchange between farms

References

Kijas JW, Lenstra JA, Hayes B et al. (2012) Genome-wide analysis of the world's sheep breeds reveals high levels of historic mixture and strong recent selection. PLoS Biology 10, 2 Chang CC, Chow CC, Tellier LCAM et al. (2015). Second-generation PLINK: rising to the challenge of larger and richer datasets. GigaScience, 4.

Zhou X, Stephens M. Genome-wide efficient mixed-model analysis for association studies (2012). Nature Genetics 44:821–4.

Alexander DH, Novembre J, Lange K (2009). Fast model-based estimation of ancestry in unrelated individuals. Genome Research, 19:1655–1664

Naval-Sanchez M, Nguyen Q, McWilliam S et al. (2018). Sheep genome functional annotation reveals proximal regulatory elements contributed to the evolution of modern breeds. Nature Communications, 9:859

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Global genome-wide diversity metrics

Genome-wide average diversity of Greek sheep estimated similar to previously studied Mediterranean and Asian sheep while higher from Central and North European sheep

Negative average inbreeding observed for several breeds, indicating that heterozygosity levels estimated higher than expected (Table 1)

Average observed (He) and expected (He) beteregygosity and

Origin	Breed	No.	H _o	H _e	F _{IS}
Greece	Chios	802	0.326	0.328	0.007
	Mytilene	105	0.370	0.380	0.027
	Boutsko	291	0.366	0.374	0.021
	Pelagonia	59	0.351	0.356	0.015
	Frizarta	352	0.376	0.378	0.004
Italy	Comisana	24	0.375	0.364	-0.03
	Leccese	24	0.350	0.367	0.049
	Altamurana	24	0.363	0.365	0.006
Central Europe	Valais Blacknose Sheep	24	0.304	0.315	0.030
	Black-Headed Mutton	24	0.333	0.336	0.007
North Europe	Dorset Horn	21	0.319	0.292	-0.09
	Border Leicester	48	0.291	0.712	-0.00
	East-Friesian White	9	0.319	0.297	-0.07
	Old Norwegian Spaelsau	15	0.342	0.348	0.020
Asia, SW Asia	Tibetan	37	0.326	0.339	0.040
	Afshari	37	0.358	0.347	-0.03
	Karakas	18	0.357	0.341	-0.04
	Cyprus Fat Tail	30	0.329	0.313	-0 05