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Analysis of genomic variation and population structure through single-nucleotide polymorphisms of the Latvian dark-headed breed in comparison to other breeds in Latvia

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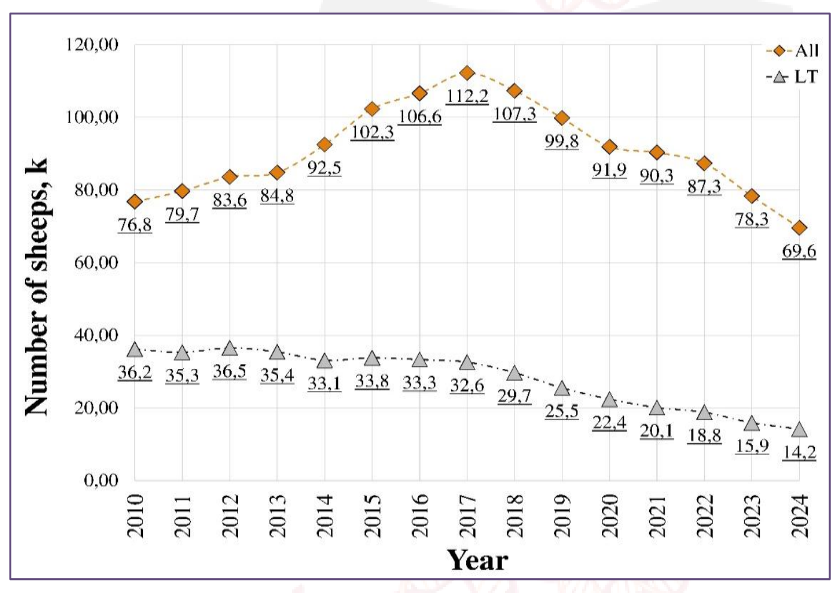
INTRODUCTION

Sheep in Latvia



In **2001**, the **Sheep Breeders Association** officially began operating in Latvia, which is authorised to carry out selection work in sheep breeding, including only breed selected in Latvia – **Latvian dark-head (*Latvijas tumšgalve*; LT).**

Latvian Dark-Head breed

Was created by crossing local Latvian sheep with Shropshire and Oxfordshire rams imported from Sweden and England. The first pedigree or breeder's book for LT rams was issued in 1939.

The **LT breed fully adapts** to local environmental conditions and holds cultural significance, contributing to traditional lifestyles, landscape preservation, and regional identity. Therefore, **genetic studies on LT** are **crucial for conserving** its diversity and **informing future breeding programs**.

AIM

This study <u>aimed</u> to evaluate the genetic diversity of the Latvian Dark-head breed and compare it with that of other dominant sheep breeds in Latvia.

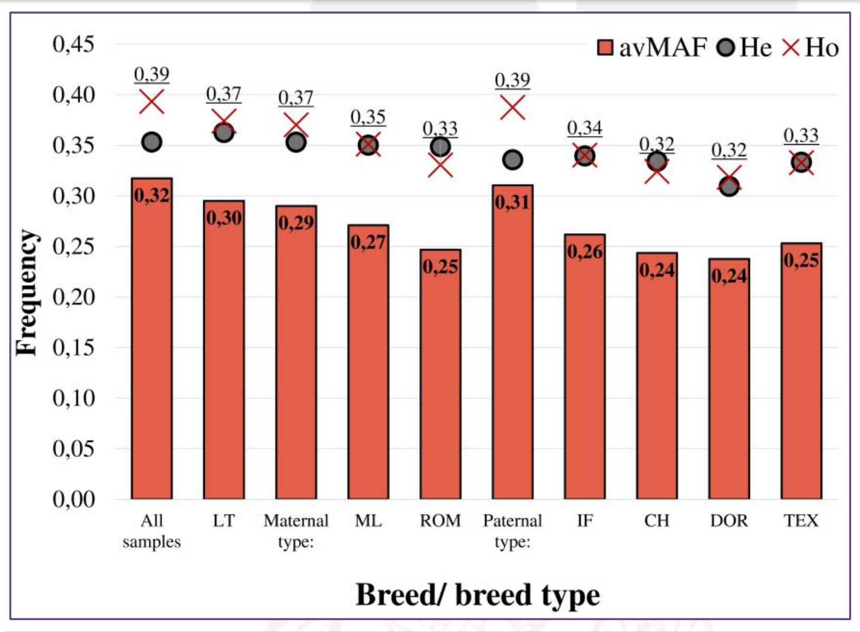
METHOD

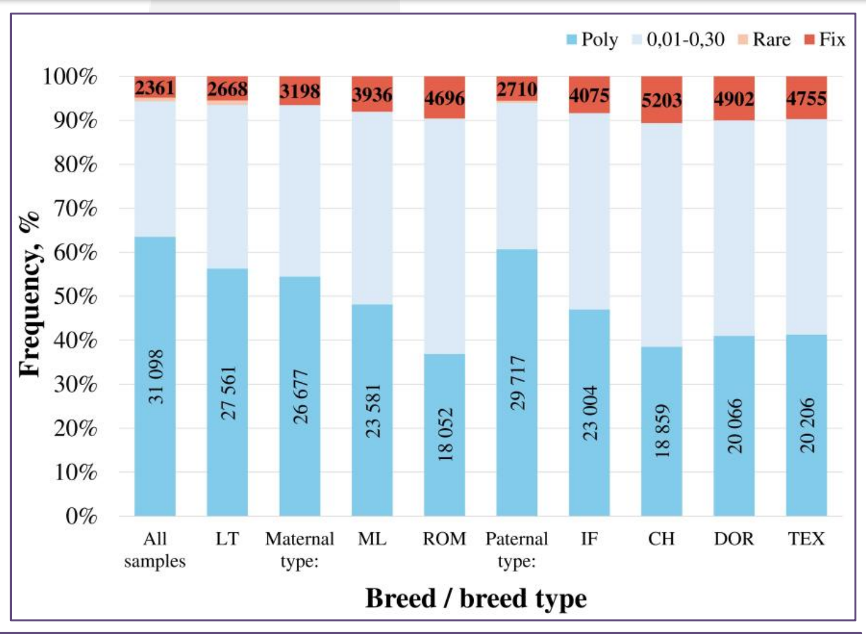
Breed	Breed type	Samples	Total by type
Latvian dark-head (LT)	Maternal	135	135
Merinolandschaf (MLS)	Maternal	26	38
Romanova (ROM)		12	
Île de France (IF)	Paternal	33	88
Charollais (CH)		14	
Dorper (DOR)		15	
Texel (TEX)		22	
Oxford Down (OX)		4	

Genotyping of SNP of the GeneSeek® Genomic Profiler™ Ovine 50K array – 48,981 SNP after quality control

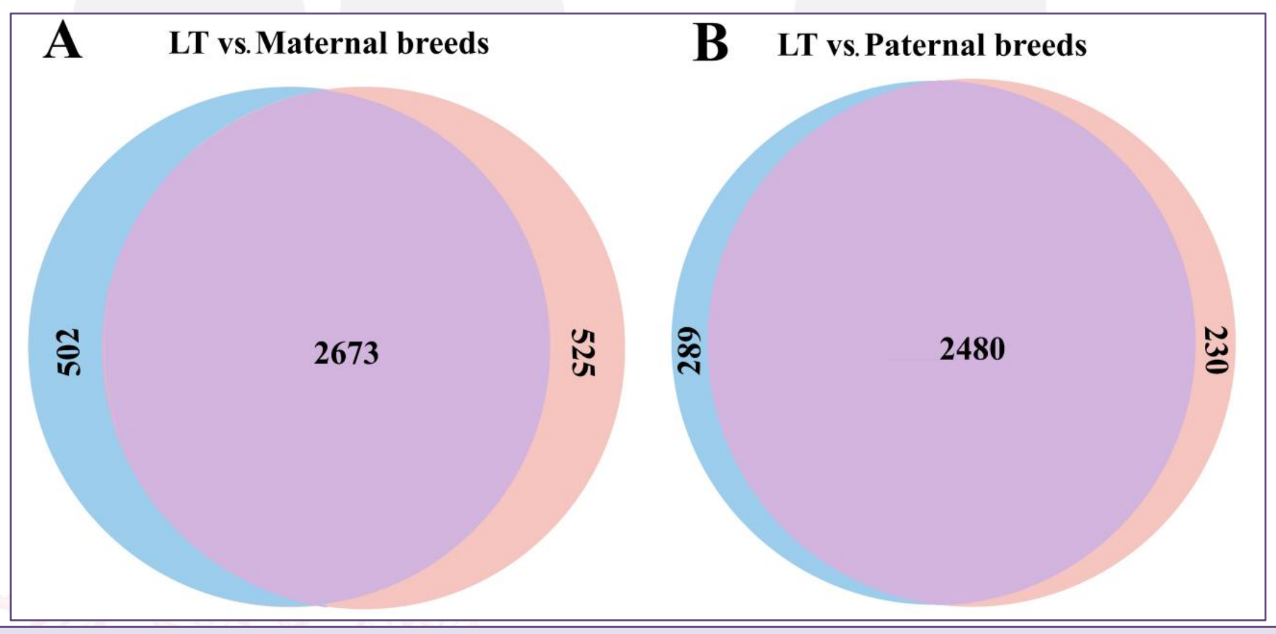
- **Basic indices of genetic diversity**: percentage of polymorphic markers, observed heterozygosity (Ho), expected heterozygosity (He), and Minor Allele Frequency (MAF)
- A **comparative analysis** to identify **fixed SNPs** (MAF=0) in the LT breed and/or its related breed types. The bootstrapping approach was used for the LT population in the comparison.
- **Principal component analysis** (PCA) and **structure analysis** (Genetic admixture) and **Genetic admixture** analysis

RESULTS & DISCUSSION

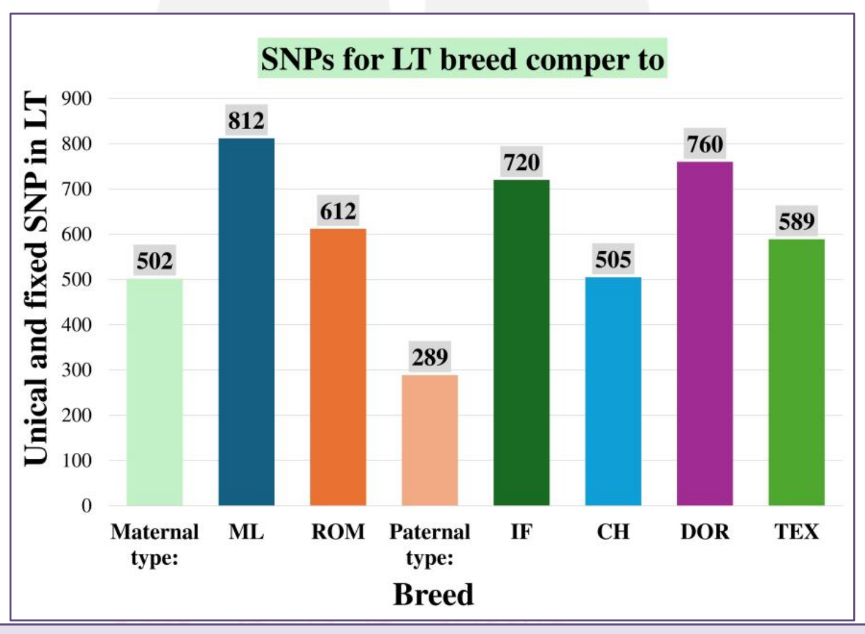




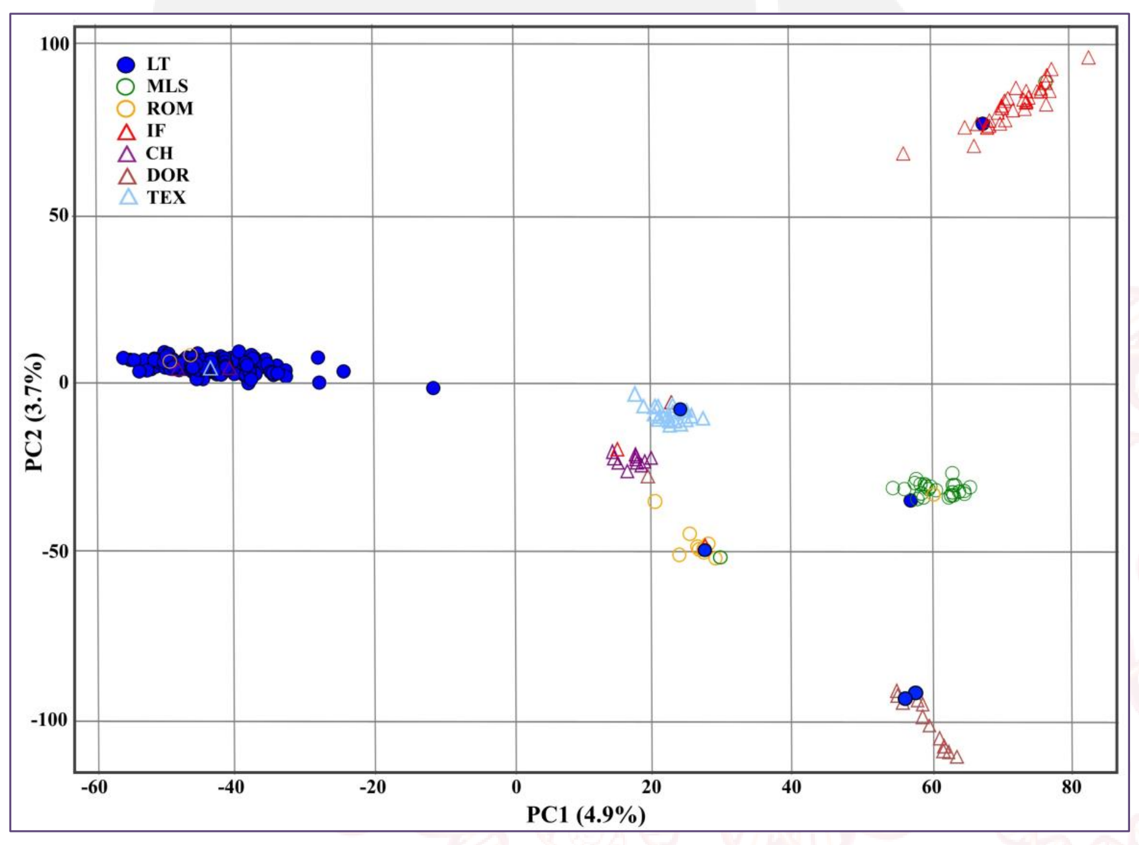
<u>In the **Latvian dark-head breed** samples:</u>
- **27’561 (56.27%) SNPs highly polymorphic** (MAF 0.3 – 0.5)
- **3’169 (5.66%) SNPs rare** (MAF <0.01)
- **2’668 (5.45%) SNPs fixed** (MAF = 0)



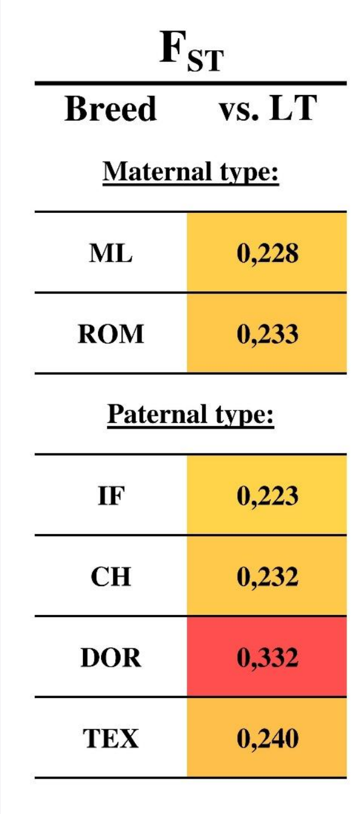
Compared to **maternal-type** or **paternal-type** breeds, **the LT breed** was differentiated by **502** (15.81% of fixed SNPs in LT) and **289** (10.44%) unique fixed SNPs.



From **all fixed SNPs**, from **289 (10.83%) to 812 (30.43%) SNPs** were **unique** to the **LT breed** compared to others.

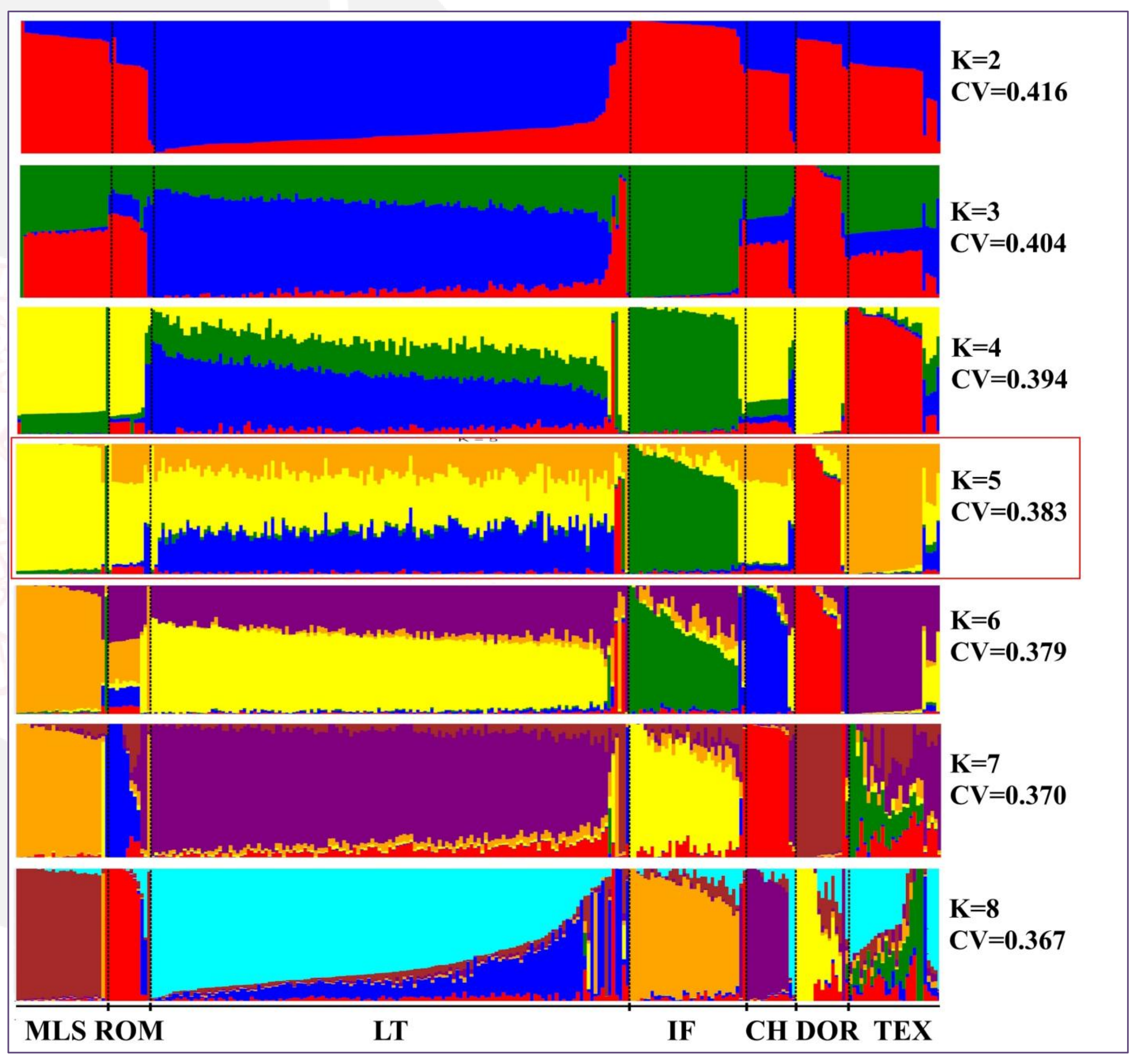


While the **LT breed**, with 99% of LT samples forming a distinct cluster, is **clearly segregated** by PC1, it is positioned **relatively close** to the TEX, CH, and ROM breeds on the PC2 axis.



F_{ST}	
Breed	**vs. LT**
<u>**Maternal type:**</u>	
ML	0,228
ROM	0,233
<u>**Paternal type:**</u>	
IF	0,223
CH	0,232
DOR	0,332
TEX	0,240

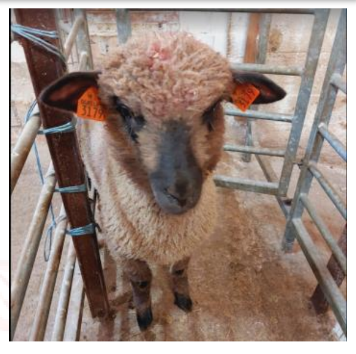
<u>**Latvian dark-head**</u> breed shows **high or very high genetic differentiation** (FST 0.22–0.33) from other breeds.



- At the initial level of analysis (**K = 2**), LT and other breeds had **different genetic component distributions**. .
- The LT breed had **three primary components** when the cluster number was increased to **K = 5**, with **one** of these components being **quite low** in other breeds.
- Cross-validation **error** improved only **little** after K = 5, where the **curve elbowed**.

CONCLUSION

The GeneSeek® Genomic Profiler™ Ovine 50K array provides a sufficiently informative of the **genetic foundation of the Latvian national sheep breed**. Facilitating novel avenues for genetic research and the advancement of genetic selection within the Latvian sheep population.



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