Selection trace from runs of homozygosity in French dairy sheep

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Introduction

Runs of homozygosity (ROH) are contiguous homozygous segments of the genome where the haplotypes inherited from each parent are identical

ROH-based inbreeding:

(1) Distinguish recent from ancient inbreeding

(2) Improve the understanding of inbreeding depression

Introduction

The occurrence of ROH is not randomly distributed across the genome, and islands of ROH may be the result of selective pressure

Objective:

To use F_{ST} and ROH to explore selective pressure in French dairy sheep breeds and subpopulations

Material

Manech Tête Rousse (MTR)

Manech Tête Noire (MTN)

Basco-Béarnaise (BB)

Lacaune (LAC)

Lacaune (LAC) has since 1976 two subpopulations (separated breeding schemes):
- LACCon: Lacaune Confederation
- LACOvi: Lacaune Ovitest

Material

Breed / Subpopulation	Genotyped individuals
BB	321
MTN	329
MTR	1,906
LACCon	3,030
LACOvi	3,114

50K chip: 38,287 autosomal SNP distributed in 26 autosomes

and 8,700 genotyped rams
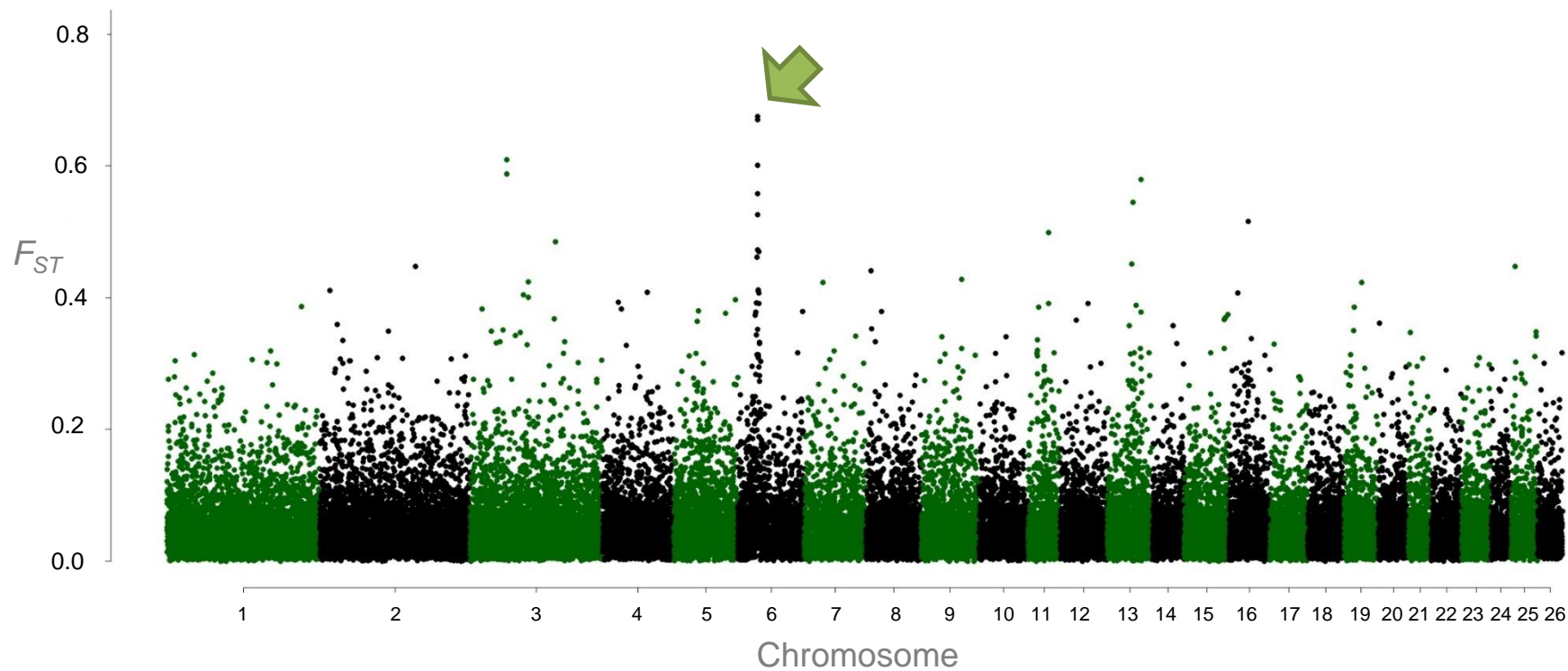
Methods

Genetic differentiation coefficient

Plink software (Purcell et al. 2007) to calculate F_{ST} (Weir &

Cockerham 1984)

Runs of homozygosity

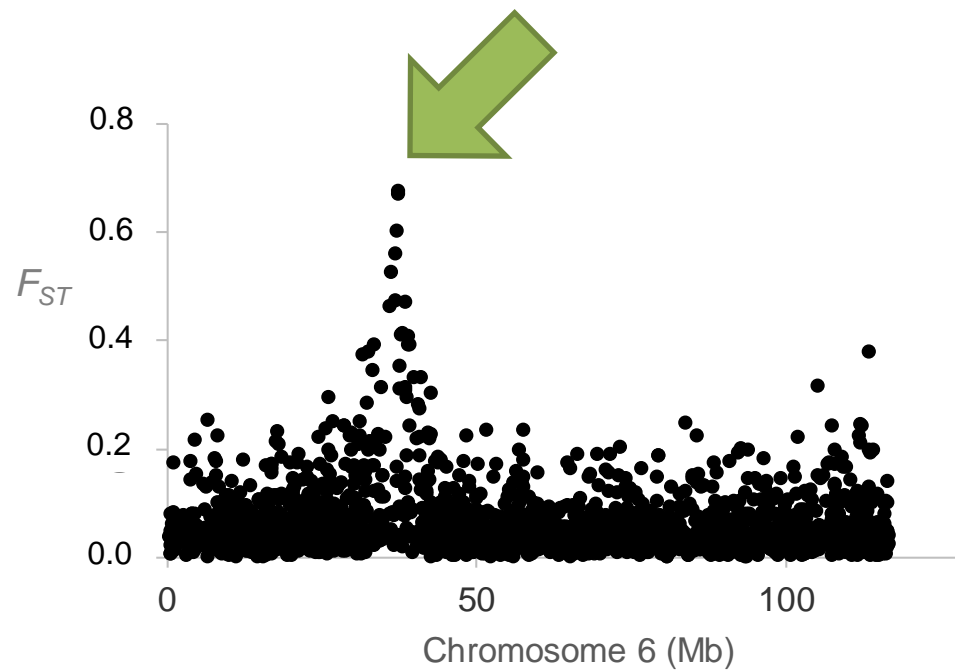Software detectRUNS (Biscarini et al. 2018)

Results

Results

SNP name	F_{ST}	P-value	POSITION (Mb)
OAR6_41583796.1	0.68	4.03×10^{-9}	**37.42**
OAR6_41709987.1	0.67	4.01×10^{-9}	**37.54**

Results

F_{ST} for SNP OAR6_41583796.1

	BB	MTN	MTR	LACCon	LACovi
BB		0.08	0.13	0.65	0.78
MTN			0.40	0.48	0.64
MTR				0.78	0.86
LACCon					0.02
LACOvi					

Similar results were observed for SNP OAR6_41709987.1

Results

Allele frequency

	OAR6_41583796.1	OAR6_41709987.1
BB	0.80	0.80
MTN	0.62	0.62
MTR	0.95	0.94
LACCon	0.13	0.13
LACOvi	0.07	0.07

Both SNPs were in nearly complete linkage disequilibrium ($r^2 = 0.98$)

Results

ROH

Chromosome 6

LACOvi

LACCon

MTR

MTN

BB

35 – 40 Mb

Mbps
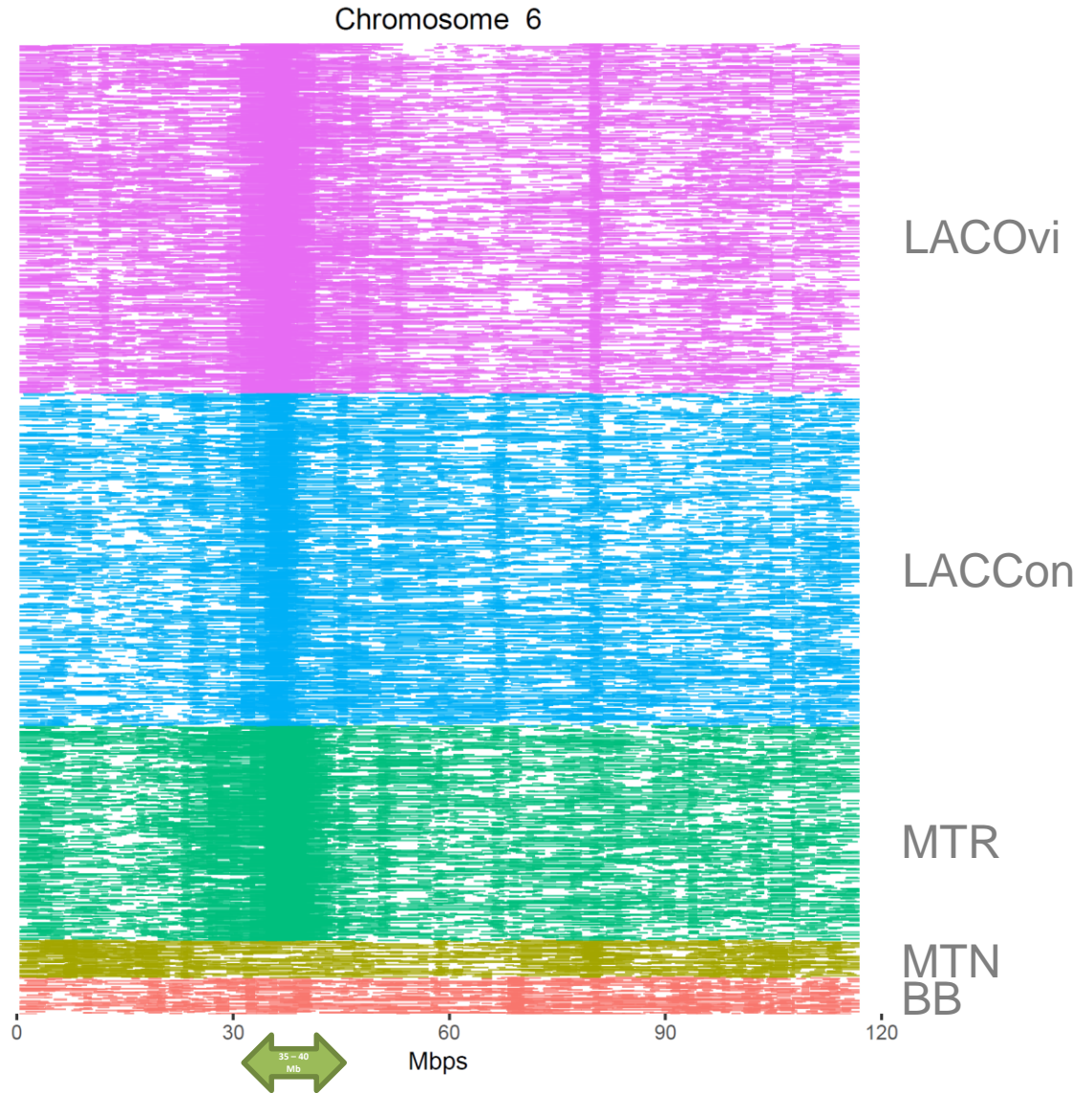
Results

- Signal confirmed in the literature (e. g. Naval-Sánchez et al. 2018; Rochus et al. 2018)

- Associated genes to this position: **NCAPG** and **LCORL**, implicated in controlling weight and stature

- Probably, Lacaune has been selected for bigger animals and MTR for smaller ones

Summarising…

Single marker F_{ST} and ROH analyses **agree that**

selection signatures exists around markers

OAR6_41583796.1 and OAR6_41709987.1, and the

associated genes to this position are *NCAPG* and *LCORL*

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ardi
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Thanks for your attention!

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