

Selection trace from runs of homozygosity in French dairy sheep



S. T. Rodríguez-Ramilo, A. Reverter, A. Legarra



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

Selection trace from runs of homozygosity in French dairy sheep



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

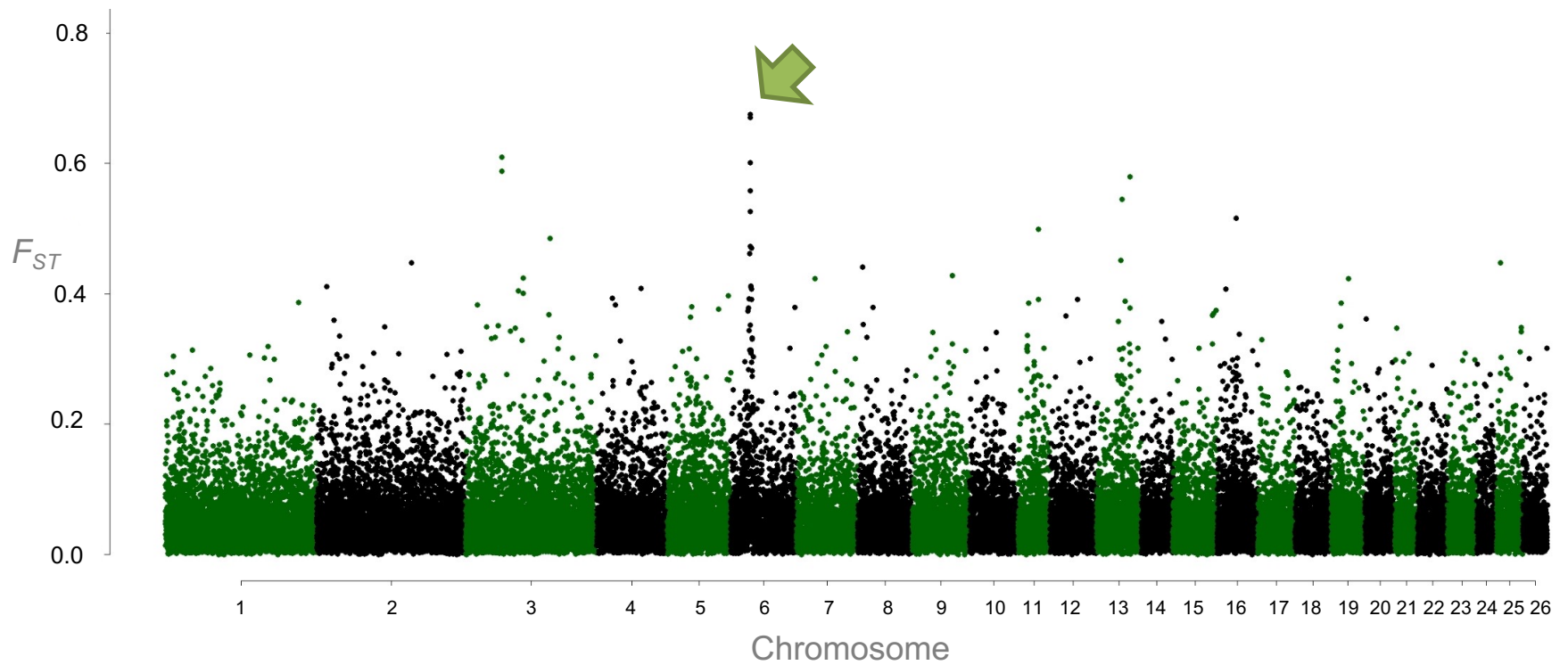
Plink software (Purcell et al. 2007) to calculate F_{ST} (Weir & Cockerham 1984)

Runs of homozygosity

Software detectRUNS (Biscarini et al. 2018)



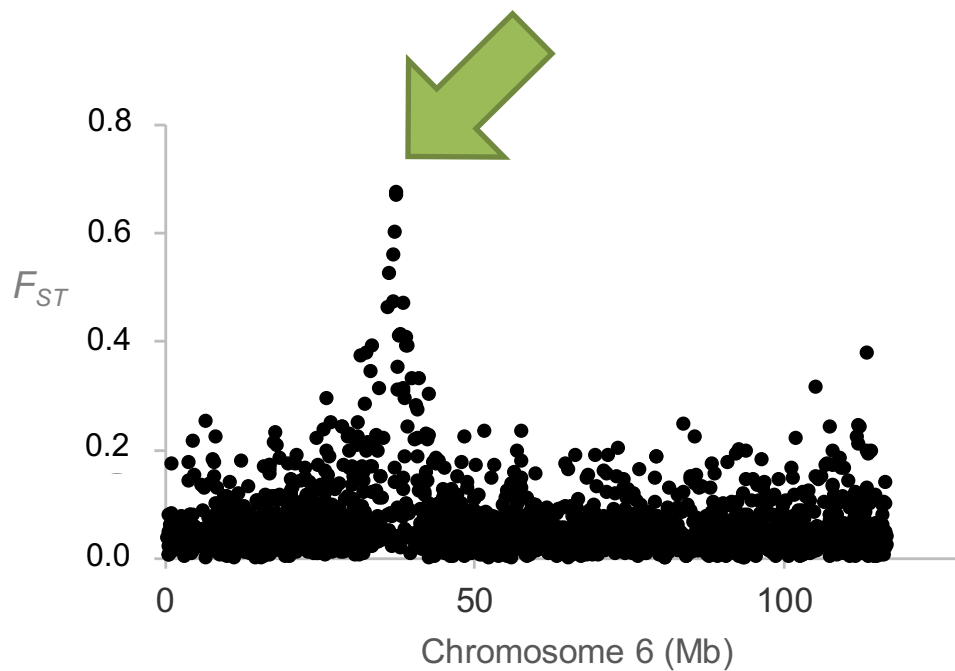
Results





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

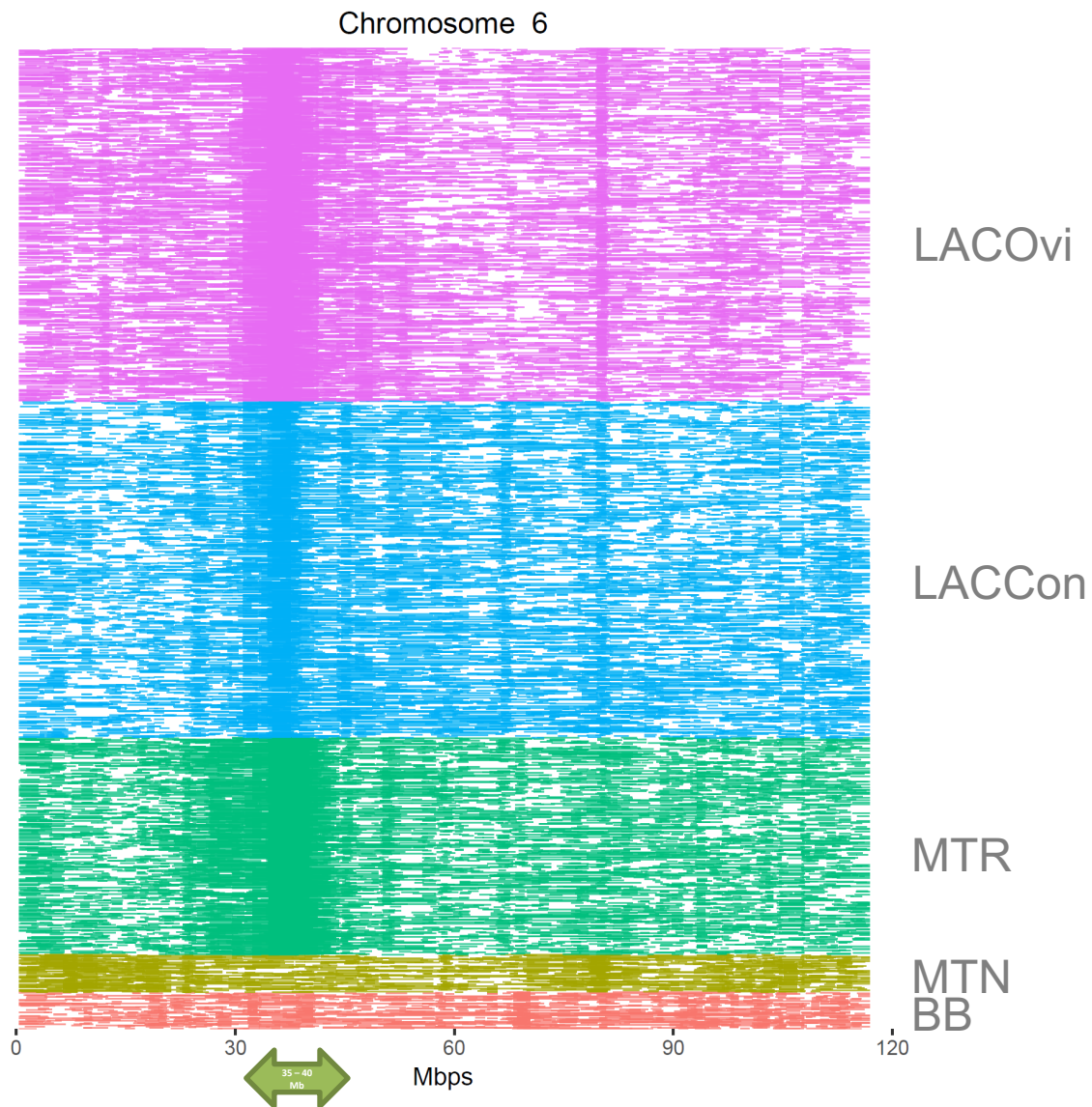
	OAR6_41583796.1	OAR6_41709987.1
BB	0.80	0.80
MTN	0.62	0.62
MTR	0.95	0.94
LACCon	0.13	0.13
LACovi	0.07	0.07

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



Results

ROH





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***



Acknowledgements



INRA project: GDivSelGen

Thanks for your attention!

E-mail: silvia.rodriguez-ramilo@inra.fr