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Whole genome sequencing and epigenotyping for multiple generations of selection using Oxford Nanopore Technology



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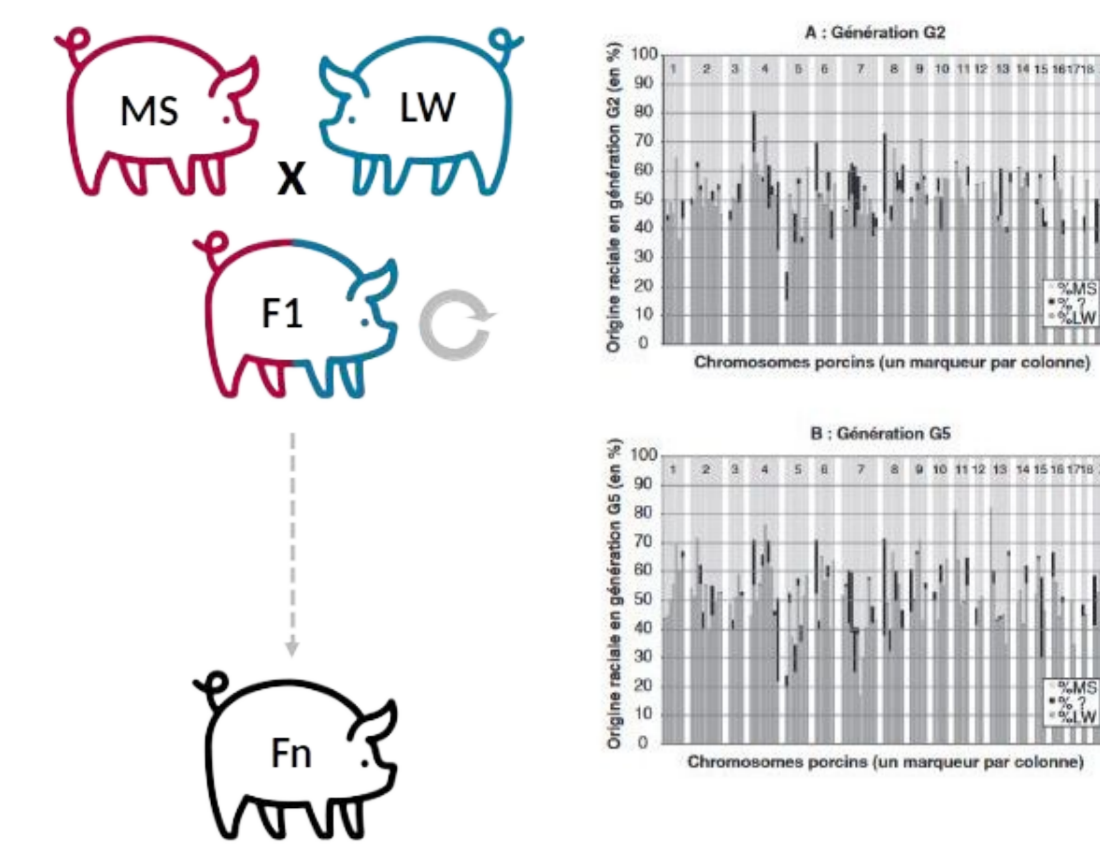
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Introduction

Context: Livestock species = controlled selection, environment and mating
Opportunity to follow the evolution of genetics and epigenetics

Question: How does genetic and epigenetic patterns evolve through time across multiple generations of selection in a commercial pig breed? Are they correlated?
Can we link these patterns to selection decisions?



Materials

Animals:

- 15 generations
- Each generation 1 pool of n = 4 to 16 boars
- Sperm

Genomics and Epigenomics:

- Oxford Nanopore Technology - PromethION Long read sequences
- + methylation
- 30M CpGs covered
- Average 30X

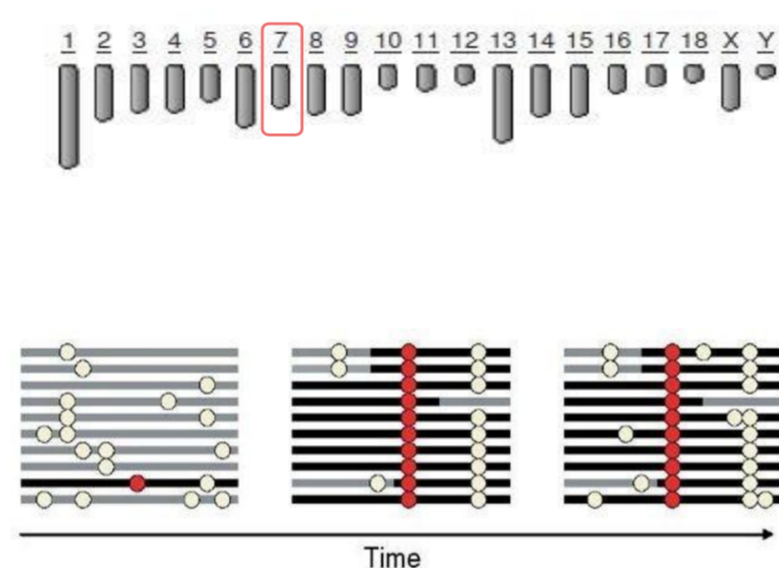
Methods

Focus on chromosome 7

(known QTLs link to selection in breed of interest)

1. Genetics:

- Evolution of allele frequencies
- Selection signature detection F_{st} (*popoolation*, Kofler et al. 2011; *pcadapt*, Luu et al. 2017, *poolfst*, Gautier et al. 2021)
- Haplotyping (*HapCUT2*, Edge et al. 2017)



2. Epigenetics:

- Differentially Methylated C (*edgeR*, Robinson et al. 2010)

3. Correlation between the two

<https://sourceforge.net/projects/popoolation2/wiki/Main/>
<https://bcm-uga.github.io/pcadapt/articles/pcadapt.html>
<https://github.com/vibansal/HapCUT2> <https://bioconductor.org/packages/release/bioc/html/edgeR.html>
<https://www.bioconductor.org/packages/release/bioc/vignettes/DSS/inst/doc/DSS.html>
<https://www.rdocumentation.org/packages/poolfst/versions/2.2.0>

Conclusions & perspectives

Conclusions:

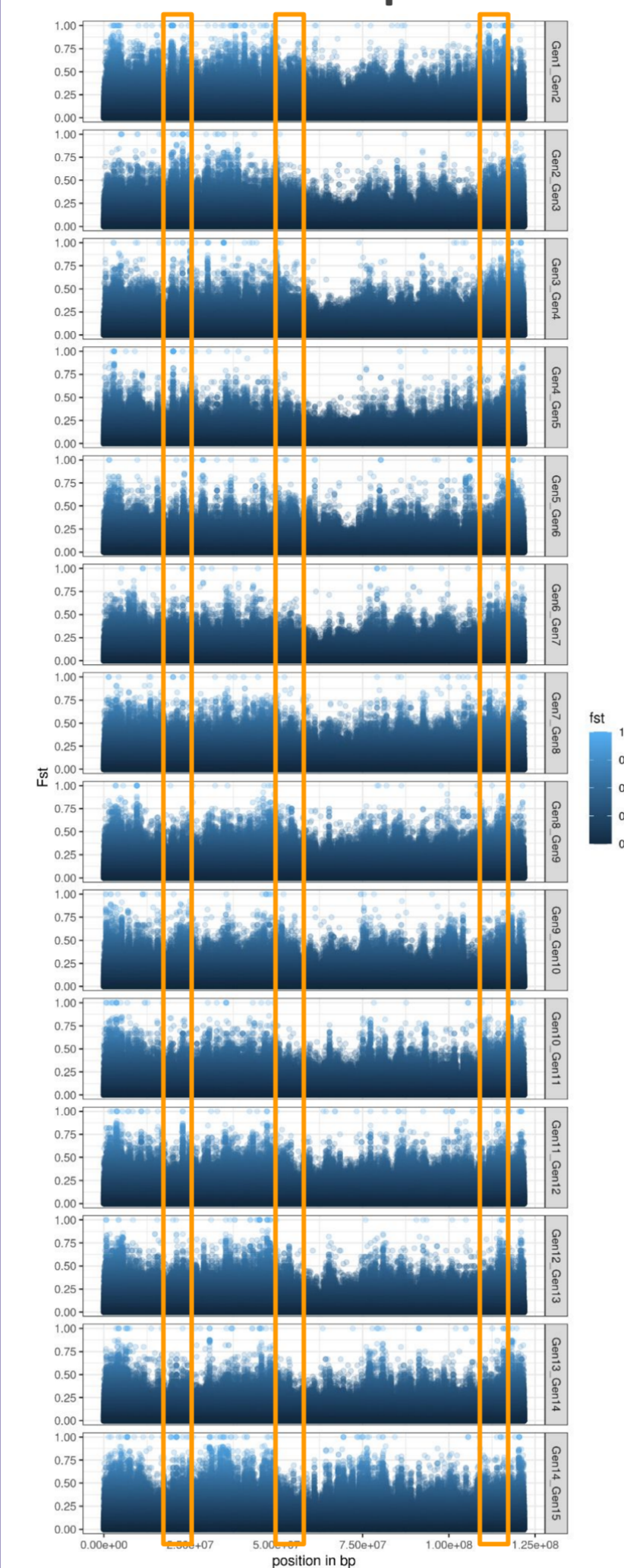
- We can identify regions showing changes in allele frequency and methylation rate through time
- Possible link with selection decision on the breed
- Evolution of methylation can be linked or not to genetics

Perspectives:

- Same analysis on the whole genome
- Link signal to genome features
- Correlated changes with breed selection decisions

Results - genetics

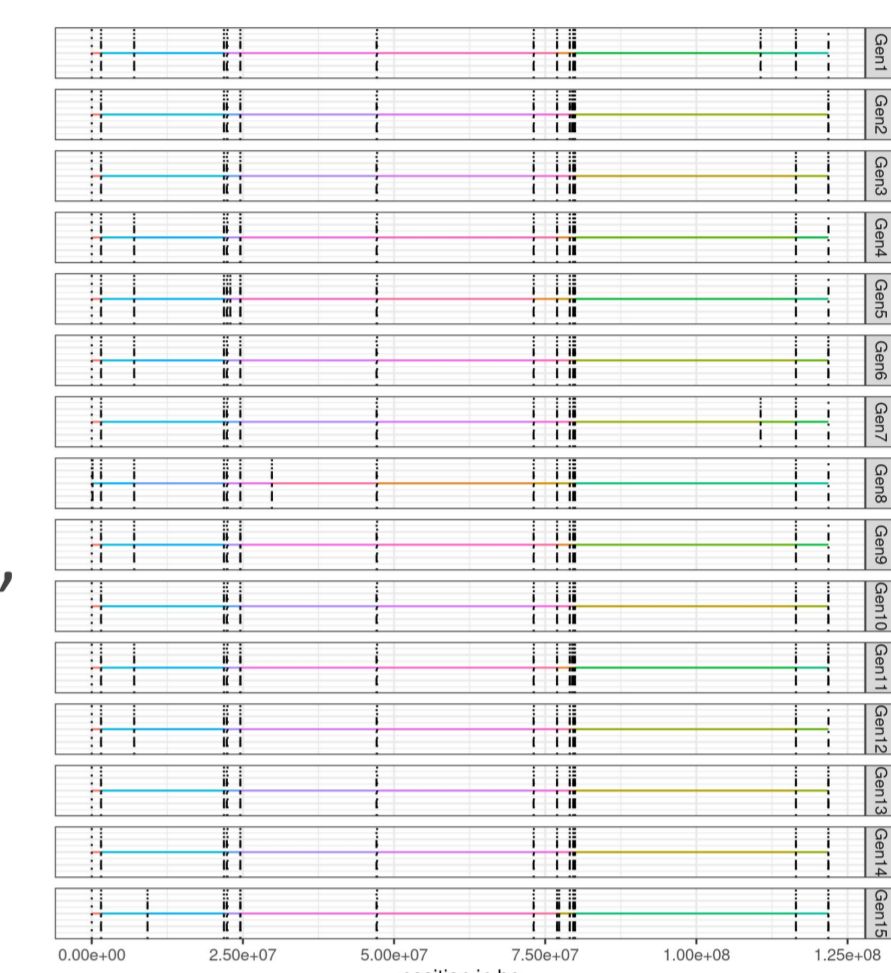
Alleles frequencies



Using F_{st} estimates we observed changes in allele frequencies in specific regions of the pig genome

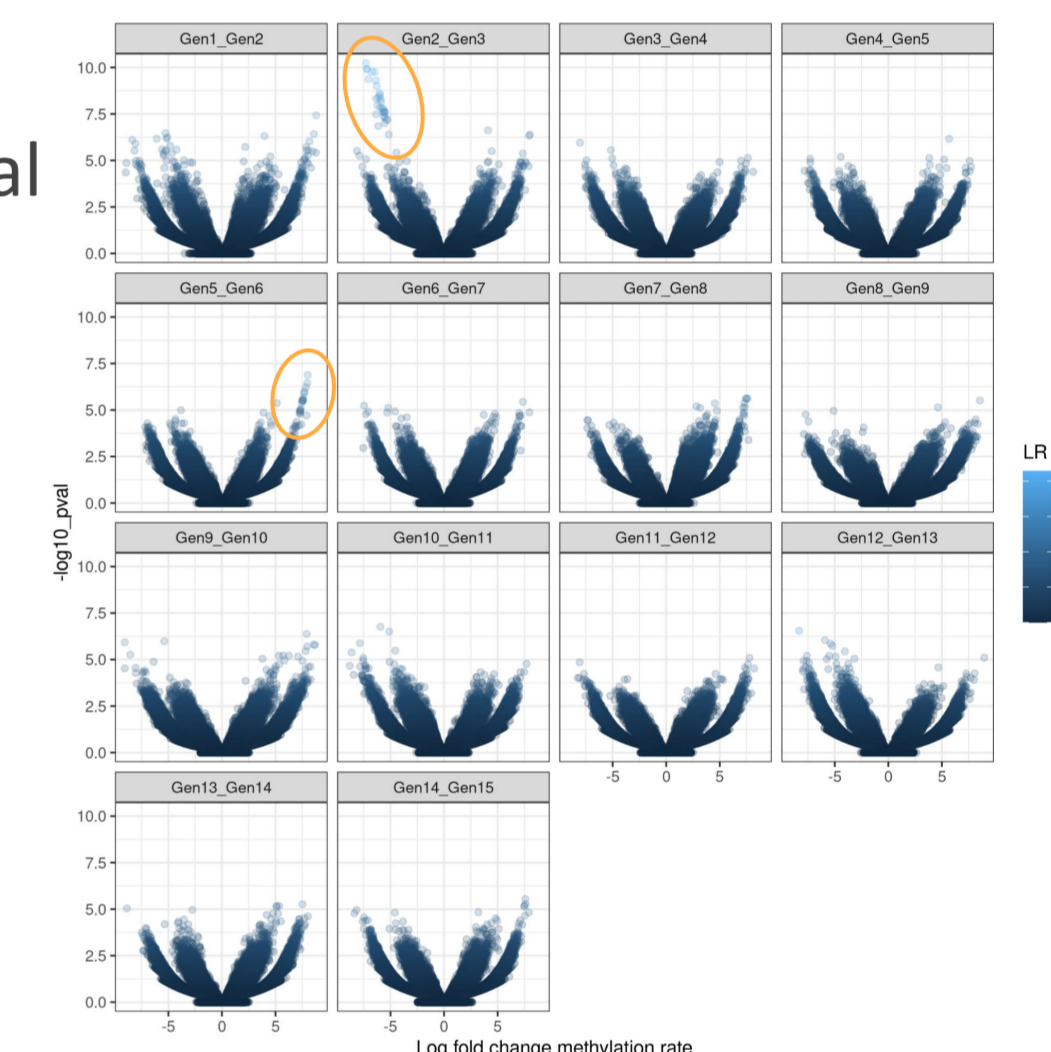
Haplotypes

Using pool-sequence data, we managed to identify between 14 and 18 haplotypes, of varying size, depending on the generation



Results - epigenetics

We saw regions harbouring differential methylation rate (epigenetic pattern) between the generations of pig selection



Results

Correlation genetics/epigenetics

The same generations contributed the most to the variation in both genetics and epigenetics patterns in our pig population

PC	Cumulative % variance	Cumulative % variance	Generation	Generation
	FREQ	METH	FREQ	METH
1	9	9	Gen8	Gen8
2	18	17	Gen1	Gen1
3	26	25	Gen15	Gen11
4	33	33	Gen10	Gen14
5	40	41	Gen4	Gen10

