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BIOMARK programme

Effects of six QTL on growth, carcass composition and meat quality traits in French commercial pig populations

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In **pigs**, many **QTL** have been detected in crosses between divergent breeds; results are not directly transposable in **commercial populations**

Objectives of the BIOMARK programme

Production of sire families to estimate the effects of **6 QTL** on a **large number of traits**

Investigate the **genetic variability** of these QTL in **French commercial populations**

Fine mapping of these QTL
➔Causal polymorphisms

Sire families

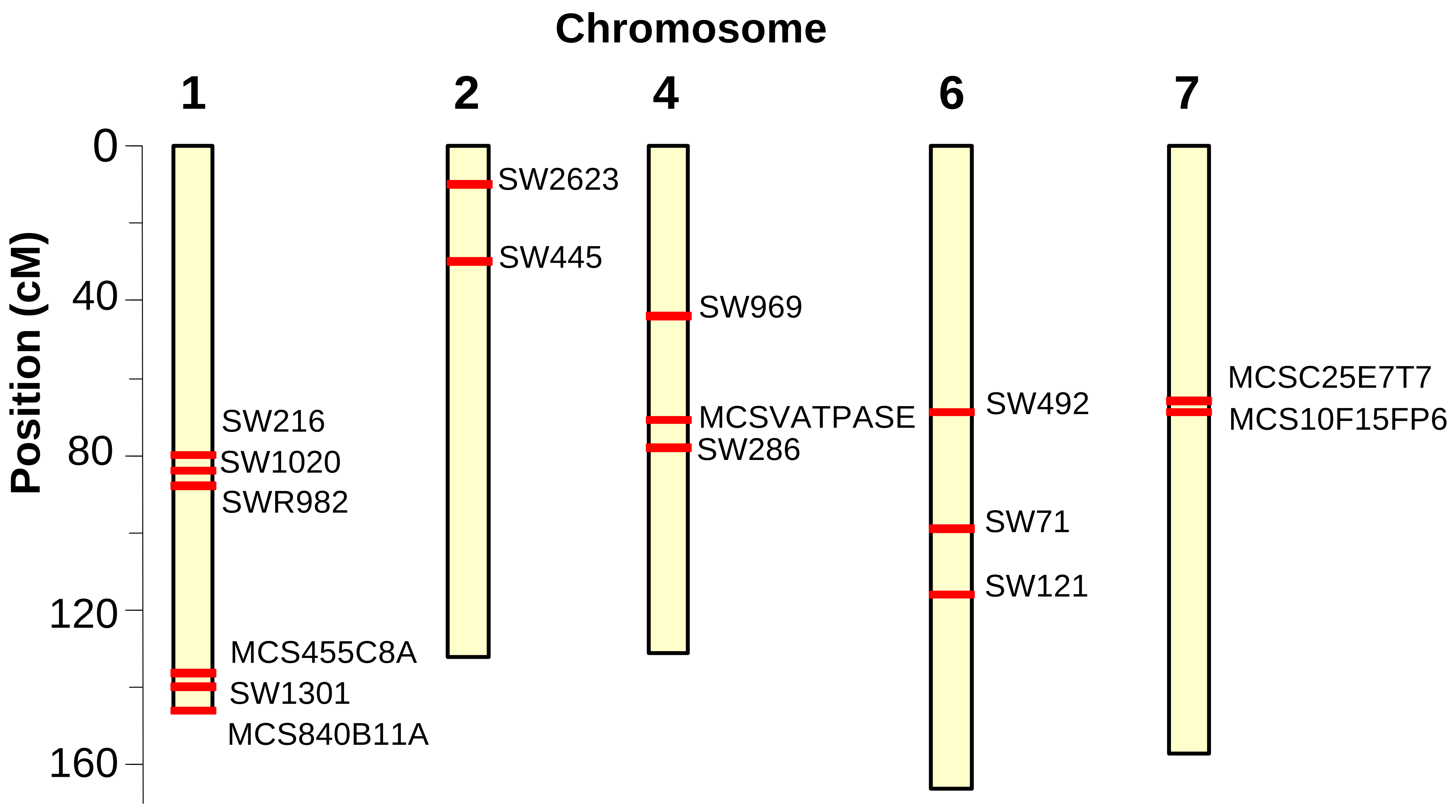
45 families from experimental populations

20 families from commercial populations
- **16 produced in INRA experimental units**
- 4 produced in selection herds

Genetic Type (GT) of sire	Number of sires	Number of progeny
Large White (LW)	6	65 to 107
Piétrain (PI)	3	34 to 92
Duroc (DU)	2	72 and 110
French Landrace	4	85 and 120
Other GT §	5	56 to 129
Laconie	10	23 to 97
PI x LW	3	57 to 79
DU x LW	4	86 to 114
(LW x PI) x LW	16	30 to 191
(LW x Meishan) x LW	12	121 to 282

§ P76, Redone, Taïzumu and DRB

6 regions / 16 markers



67 traits

Production: growth, body composition

Meat quality: pH, colour…

Other traits: leg score, number of teats

Results

(16 commercial families)

891 significant results at a 5% nominal level ~ 144 expected false positives

Significant effects of the 6 regions investigated are found in at least 2 families

Effects vary from **0,1 to 1,4 phenotypic standard deviation**

Conclusion

QTL explaining differences between divergent breeds also affect the **genetic variability within French commercial populations**

➔ The results open possibilities for **marker assisted selection** in French commercial populations, but **fine mapping** of these regions (with SNP) is previously required

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