

Microsatellite mapping of QTL for meat quality and production traits in Duroc x Large White pigs

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15 MEAT QUALITY TRAITS

13 GROWTH & CARCASS TRAITS

Interval mapping analyses with the QTLMAP software

* 5% genome-wide = significant QTL / 5% chromosome-wide = suggestive QTL

2 significant QTL + 29 suggestive QTL

Fatty acid composition **FAC**

* 2 significant QTL on SSC 10 and 14
7 suggestive QTL on SSC 1, 5, 10, 11, 13, 14

Intramuscular fat content **IMF**

3 suggestive QTL on SSC 1, 13 and 15

Ultimate pH, meat colour criteria & water holding capacity

20 suggestive QTL on SSC 4, 5, 6, 7, 8, 9, 11, 13, 14, 15 and 17

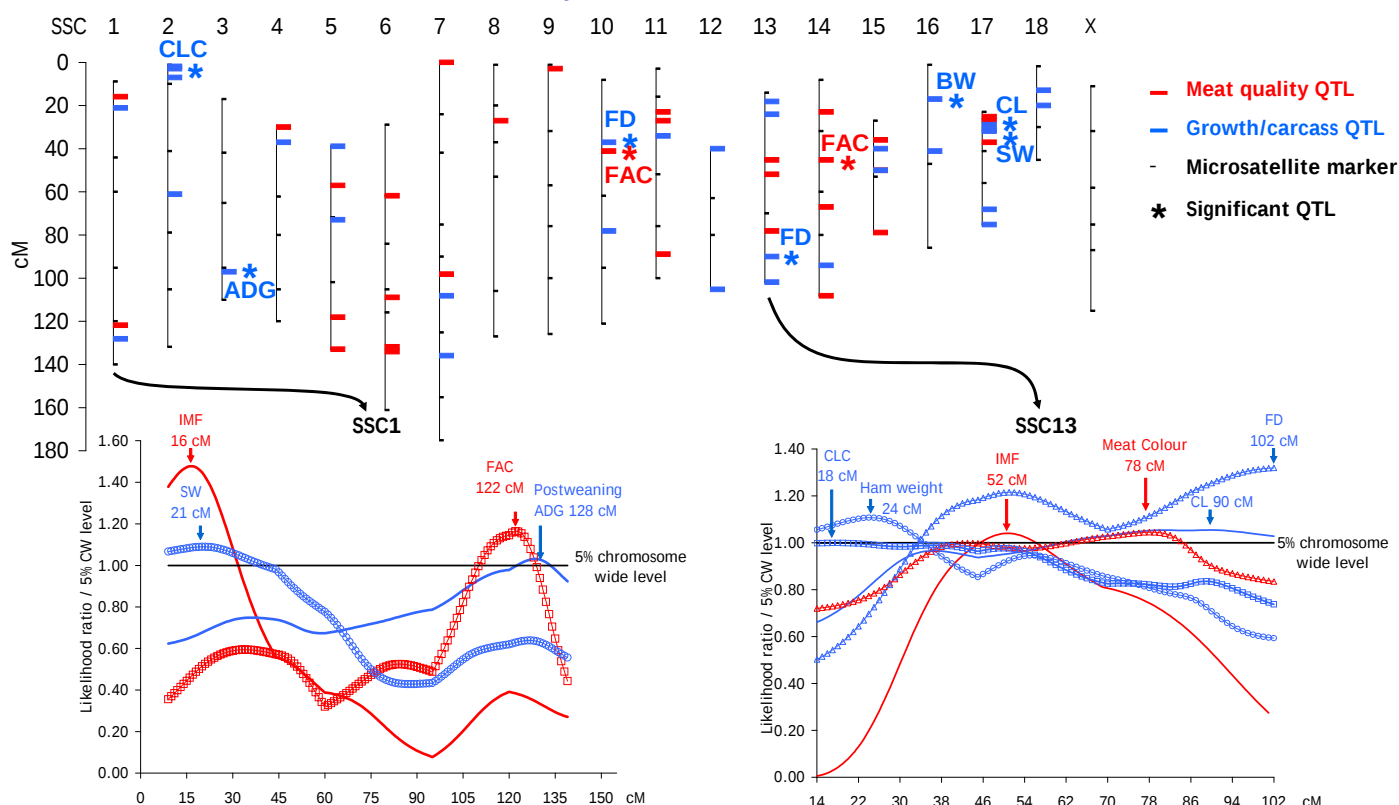
7 significant QTL + 26 suggestive QTL

Growth traits

* 2 significant QTL on SSC 3 (postweaning **ADG**) and 16 (birth weight **BW**)
7 suggestive QTL on SSC 1, 2, 10, 12, 15 and 17

Carcass traits

* 5 significant QTL on SSC 2 (lean content **CLC**), 10 and 13 (fat depth **FD**),
17 (carcass length **CL**, shoulder weight **SW**)
19 suggestive QTL on SSC 1, 2, 4, 5, 7, 11, 12, 13, 14, 15, 16, 17 and 18



CONCLUSION

- ✓ Several significant and numerous suggestive QTL detected in the F2 Duroc x Large White population
- ✓ Only some sires are heterozygous for each identified QTL
 - All QTL are segregating in at least one of the purebred founder population
 - Meat quality and production traits may be improved in purebred populations through marker-assisted or genomic selection programmes