



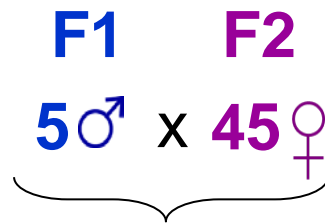
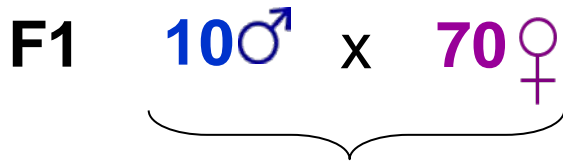
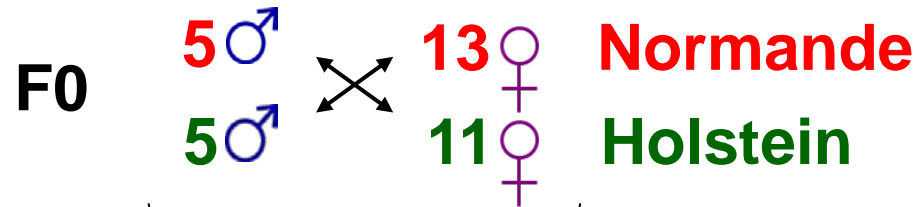
Detection of QTL controlling age at puberty and cyclicity resumption in a Holstein x Normande crossbred cattle population

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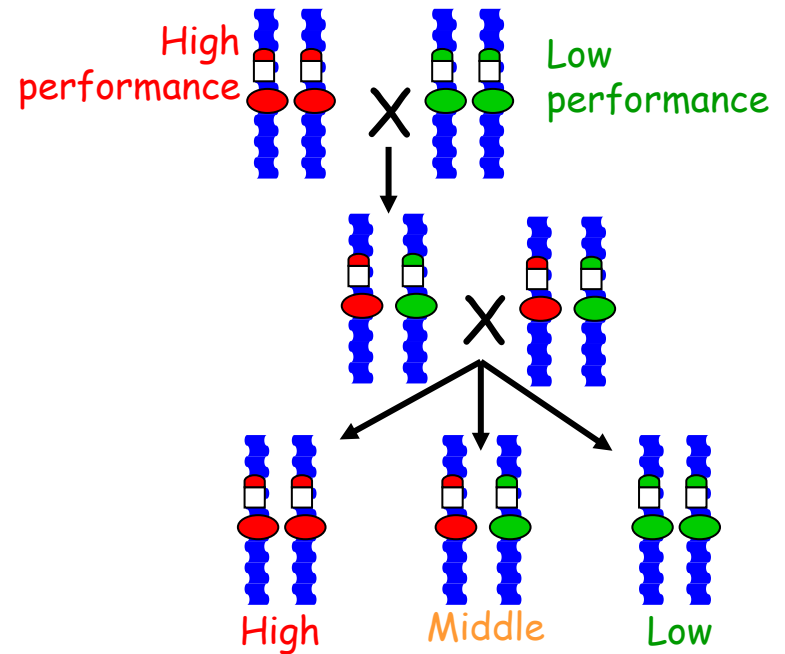
Introduction

- High interest in reproductive traits of dairy cattle
- But are usually limited to traits defined from insemination and calving dates
- Traits related to ovary activity are rarely available, because they are more difficult to record
- Goal of this study = to detect QTL responsible for ovary activity
- Crossbreeding design between Holstein and Normande breeds carried out in Le Pin INRA experimental facility

Experimental design



Why crossbreeding?



Segregation of loci fixed or at low frequency within breed

Data

- Blood progesterone (P4) assessed every 10 days until positive assay
 - ✓ from 230 days old for heifers
 - ✓ from 20 days post-partum for primiparous cows
 - ✓ from F1 to F3 generation
- Genotyping with Illumina BovineSNP50® Beadchip

⇒ 1096 heifers and 1038 cows

Traits analyzed

- Age at puberty = date of 1st ⊕ P4 assay - birth date
- Time to resumption = date of 1st ⊕ P4 assay - calving date

Trait	N	Mean (\pm SD)	h^2	r_g	r_p
Age	1096	307 d (\pm 51)	0.37	0.24	0.03
Time	1038	31.1 d (\pm 12.5)	0.17		

Models

Linkage Disequilibrium and Linkage Analysis

(Meuwissen and Goddard, 2001)

→ applied to Model 1 or Model 2

M1 : $y = \text{season} * \text{year} + \text{polygenic effect} + \text{QTL effect} + e$
(haplotypes of 6 SNP)

M2 : Age = M1 + (weaning weight / adult weight)
Time = M1 + age at calving + calving difficulty

Trait adjustments

Age at puberty	r_p
Weight ratio	-0.20

= Genetic adjustment
→ trait is different in M1 and M2

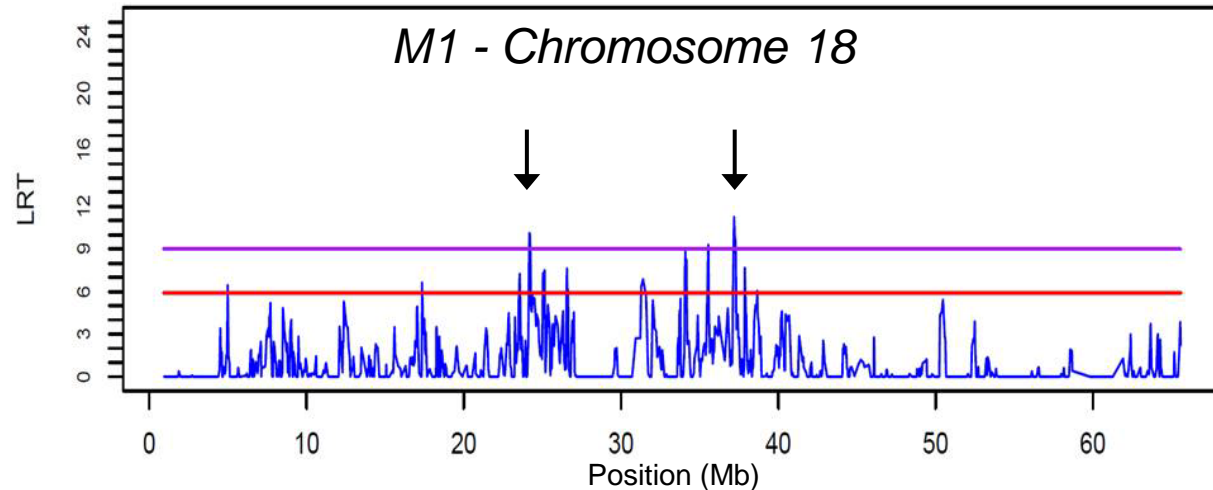
Time to resumption	r_p
Age at calving	0.13
Calving difficulty	0.09

= Environmental adjustments
→ mean can change but still
the same trait

Results: Age at puberty

Chromosome	M1
1	X
2	
3	
5	X X
8	
10	X X
11	X
12	
13	X X
14	
18	X X
21	X X X
24	X
25	
26	X
27	X
28	X
29	X X X

M1: 20 regions detected X



Results: Age at puberty

Chromosome	M1 → M2
1	X
2	
3	
5	X X
8	
10	(X X)
11	X
12	
13	X X
14	
18	(X X)
21	X X (X)
24	(X)
25	
26	(X)
27	X
28	(X)
29	X X X

M1: 20 regions detected X

M2:

✓ 8 disappeared (X)

⇒ specific to growth rather than ovarian activity ?

Results: Age at puberty

Chromosome	M1 → M2
1	X X X
2	X
3	X
5	X X
8	X X X
10	(X X)
11	X X
12	X
13	X X X
14	X
18	(X X)
21	X X (X)
24	(X)
25	X
26	(X)
27	X
28	(X)
29	X X X

M1: 20 regions detected X

M2:

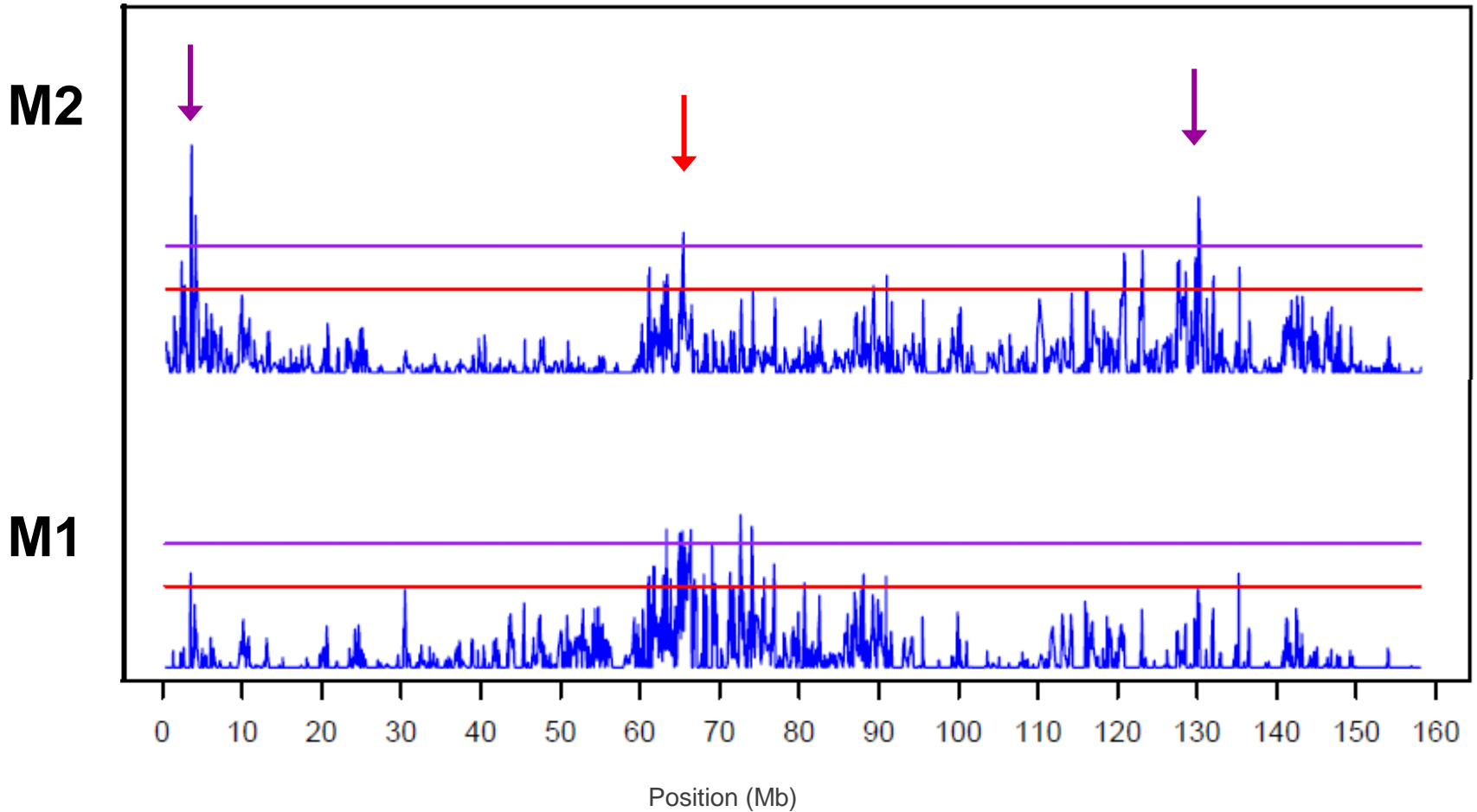
✓ 8 disappeared (X)
 ⇒ specific to growth rather than ovarian activity?

✓ 12 common regions X

✓ 12 new regions X

Results: Age at puberty

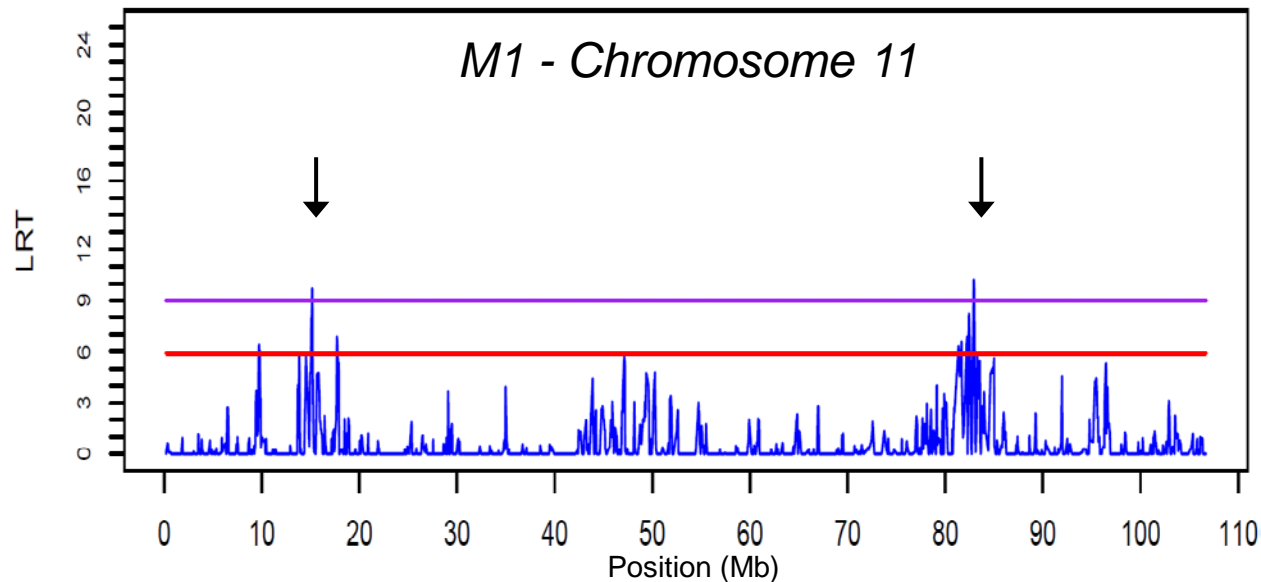
Chromosome 1



Results: Time to resumption

Chromosome	M1
1	X X
3	X X
5	
8	X
11	X X
17	X
21	X X
26	X X
27	X X

M1: 14 regions detected X



Results: Time to resumption

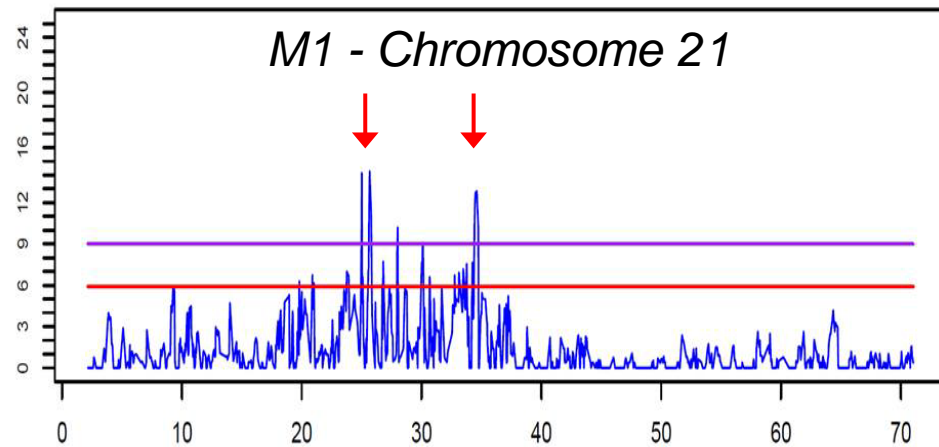
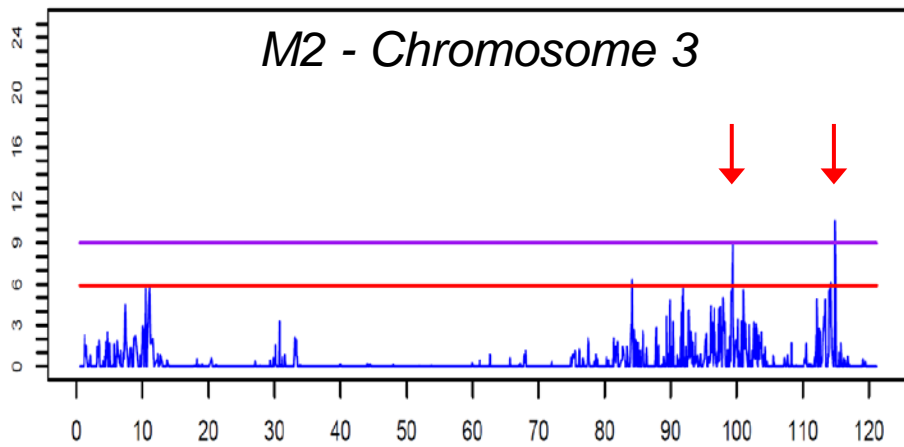
Chromosome	M1 → M2
1	X (X)
3	X X
5	
8	X
11	X X
17	X
21	X X
26	X X
27	X X

M1: 14 regions detected X

M2:

✓ 1 disappeared (X)

✓ 13 common regions X



Results: Time to resumption

Chromosome	M1 → M2
1	X (X)
3	X X
5	X
8	X
11	X X
17	X
21	X X
26	X X
27	X X

M1: 14 regions detected X

M2:

✓ 1 disappeared (X)

✓ 13 common regions X

✓ 1 new X

⇒ limited effect of calving age and calving difficulty on QTL detection

Conclusions

- Many QTL detected for both traits
- Only 2 common regions (chromosome 21) between traits
→ in agreement with their low correlation
- Age at puberty
 - ✓ More QTL probably because of a relatively higher recording accuracy and a higher heritability
 - ✓ Different trait when considering the raw measure or after adjustment for relative weight maturity
 - ✓ Strongest regions on chromosomes 13 (61Mb) and 29 (26Mb)
- Time to resumption
 - ✓ Adjustements don't affect QTL detection
 - ✓ Strongest regions on chromosomes 21 (26Mb) and 26 (33Mb)

Next...

- Genes of interest in these strongest regions ?
- Other phenotypes: analysis in process
→ colocalization of QTL?

Acknowledgements

- ✓ Le Pin experimental farm staff
- ✓ Hormonal Assay Laboratory (INRA Tours)



Thank you for your attention