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Need for sharp phenotypes in QTL detection for calving traits in dairy cattle

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Introduction

- High incidence of stillbirth and dystocia (7% and 12%, respectively, LKV 2005) is a problem due to economic and animal welfare reasons.
- QTL mapping results published in literature up to now are only partly consistent.
- EBV used for QTL detection are often estimated in a multivariate setting across parities.
- Heterogenous information for specific calving traits in multivariate models

Aim of the study

Experiment I:

- QTL mapping in German Holsteins for the calving traits stillbirth and dystocia in first and second parity, based on univariately estimated DYDs

Experiment II:

- Genome scan with deregressed proofs derived from EBV obtained from routine breeding value estimation across parities
- Similar to Kühn *et al*. (2003) using actual phenotypes

Phenotypes experiment I

Requirements for observations to be included in analysis of experiment I:

- at least five calvings per herd
- at least 30 observations (daughters) per sire

Parity specific DYDs obtained from EBV, estimated univariately and separately for first and second parity

- estimated via sire model
- without pedigree information

Model for BV estimation

$$y_{ijklmn} = H*Y_i + CM_j + CS_k + AC_l + s_m + e_{ijklmn}$$

Fixed effects:

- H*Y: herd by year
- CM: calving month
- CS: calving saison
- AC: age of calving

Random effects:

- s: effect of the sire
- e: residuals

BV estimated with an assumed heritability of 0.05 for all traits

Phenotypes experiment II

Deregressed EBV:

- Estimated simultanously via BLUP animal model in a multivariate setting
- Routine breeding value estimation in Germany
- DYDs not available
- Genetic parameters:

trait	h^2	w	gen. corr. direct/maternal
dystocia	0.05	0.15	- 0.1
stilllbirth	0.05	0.15	- 0.1

Pedigree and marker data

Pedigree:

- GDD consisting of 18 half-sib families (Thomsen *et al*. 2001)
- Second parity/all parities: 1237 progeny tested bulls
- First parity: 473 progeny tested bulls

Marker data:

- Obtained from previous analysis project (ADR I)

QTL analysis

- Univariate weighted multimarker regression (Knott *et al*. 1996)
- Permutation test with 10000 permutations
- Software: BIGMAP, ADRQLT (Reinsch 1999)
- False discovery techniques (Storey *et al*. 2002)

Results experiment I and II

QTL that show a chromosomewise error probability $p_c \leq 0.05$

	Experiment I		Experiment II
Chromosome	First parity	Second parity	All parities
4			DYS_m, STI_d
7	STI_m		
10	DYS_m	STI_m	
16		STI_d	
17	STI_m	DYS_d	DYS_m
18		DYS_d, STI_m	STI_d,STI_m
23	DYS_m		
27			DYS_d
XY	DYS_d		

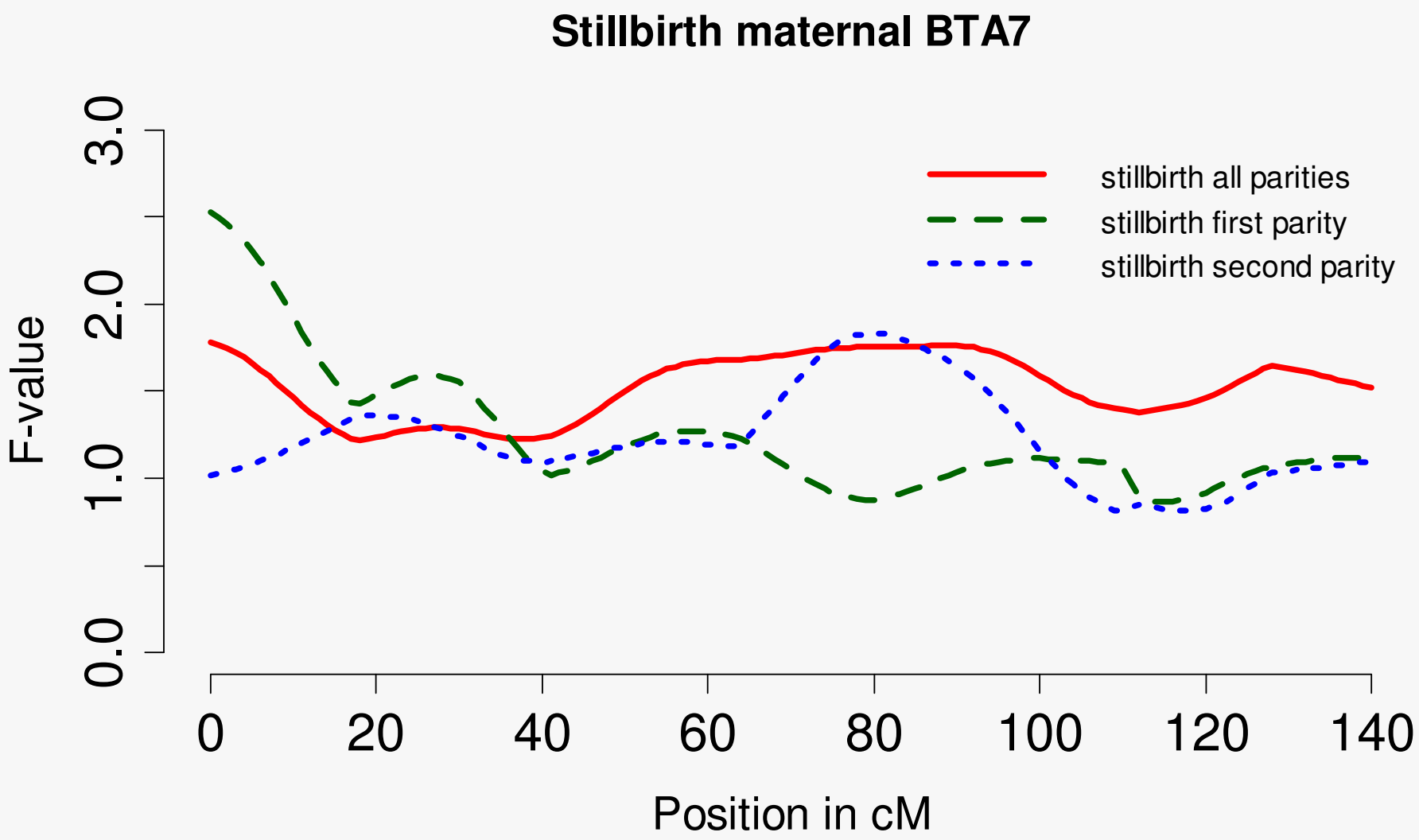
STI_m, stillbirth maternal; STI_d, stillbirth direct; DYS_m dystocia maternal; DYS_d, dystocia direct

Results

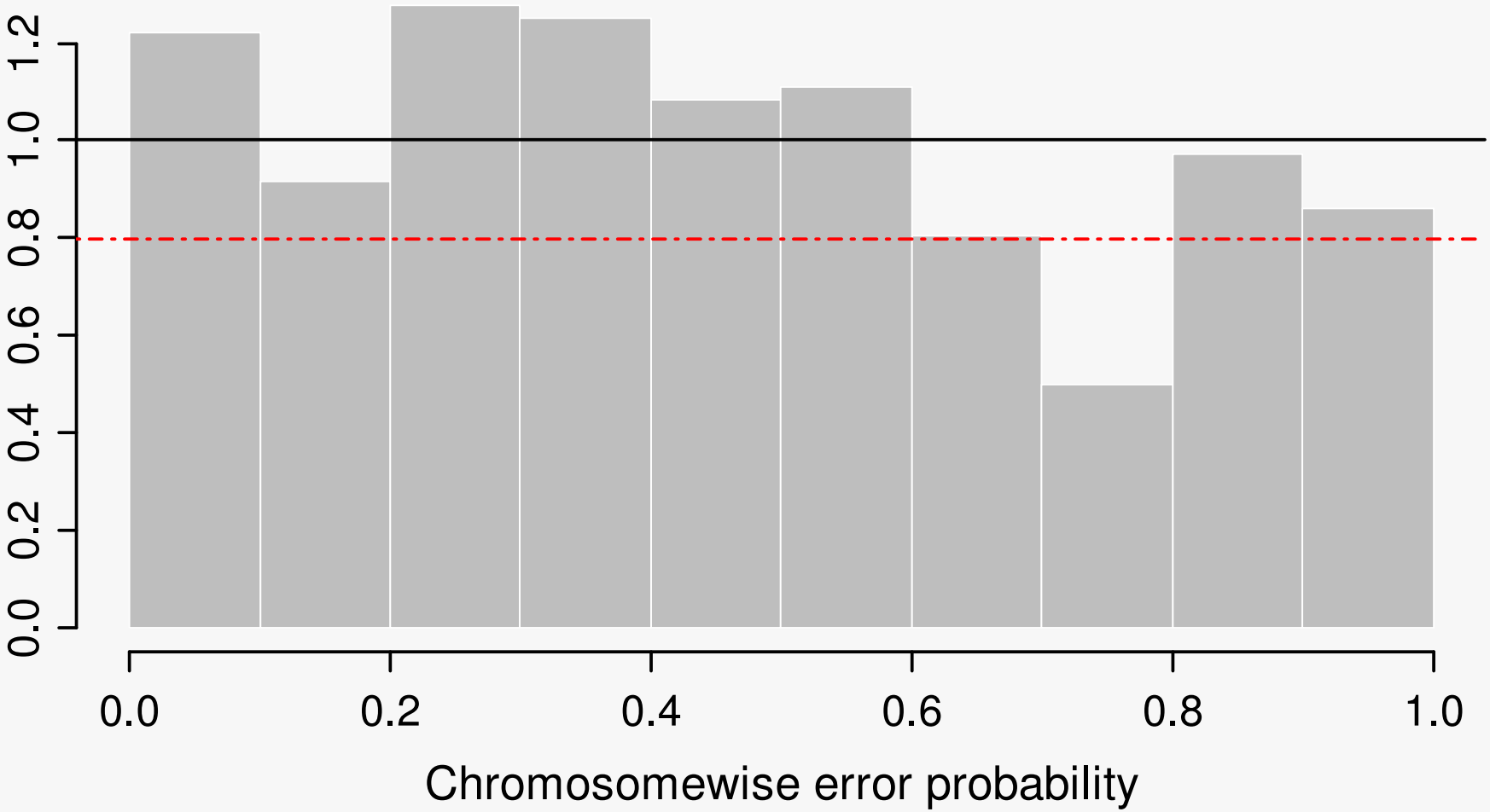
Chromosomewise error probability $p_c \leq 0.10$

- 19 significant QTL for calving traits in first parity, 13 significant QTL in second parity and 15 significant QTL for the combined phenotypes
- Some QTL mapped for first parity are not found for second parity and vice versa.
- QTL mapped with DYDs and deregressed EBV only partly consistent
- Some chromosomes showed QTL for several traits.

F-statistic BTA7 stillbirth maternal

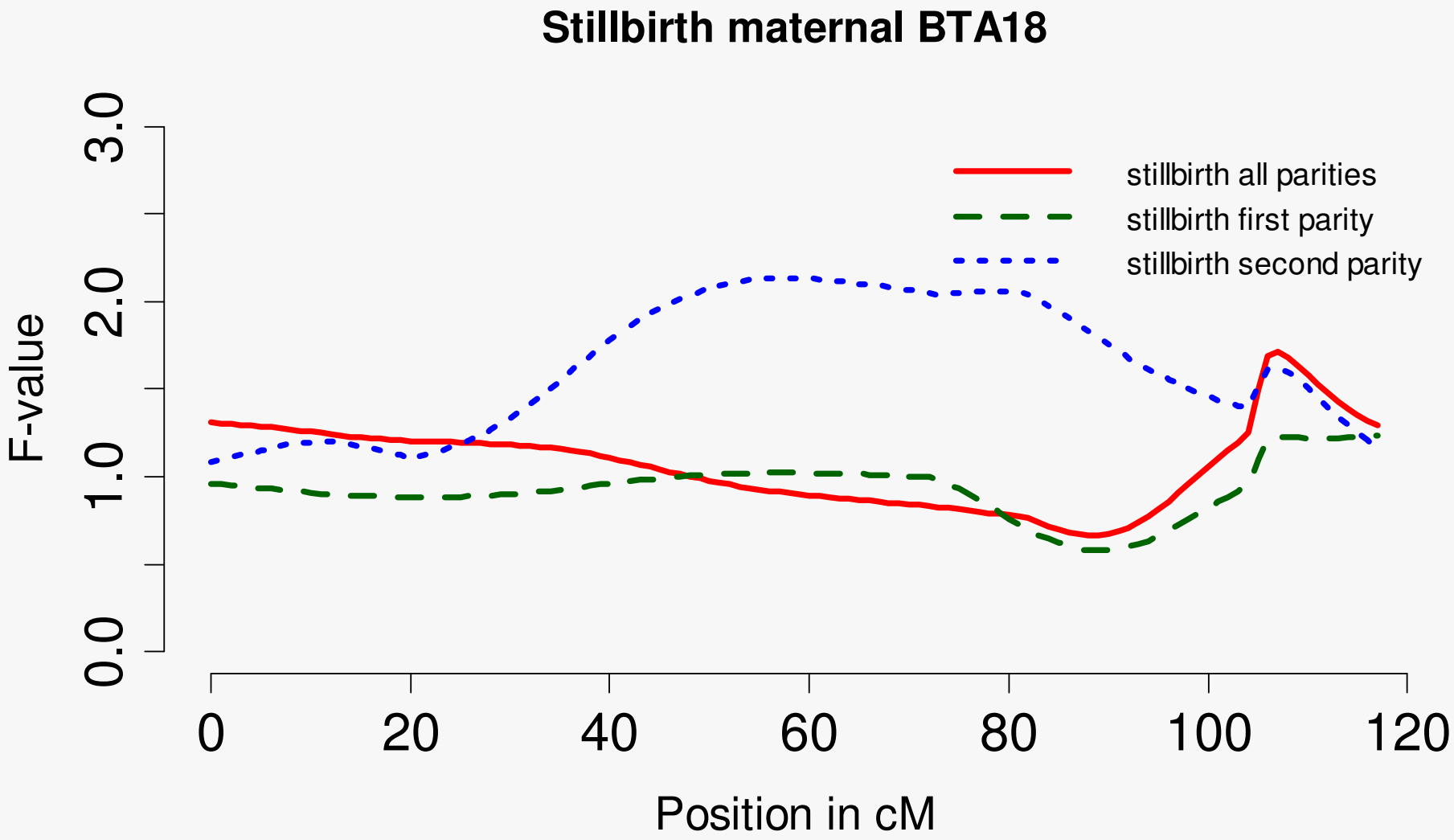


Distribution of p-values

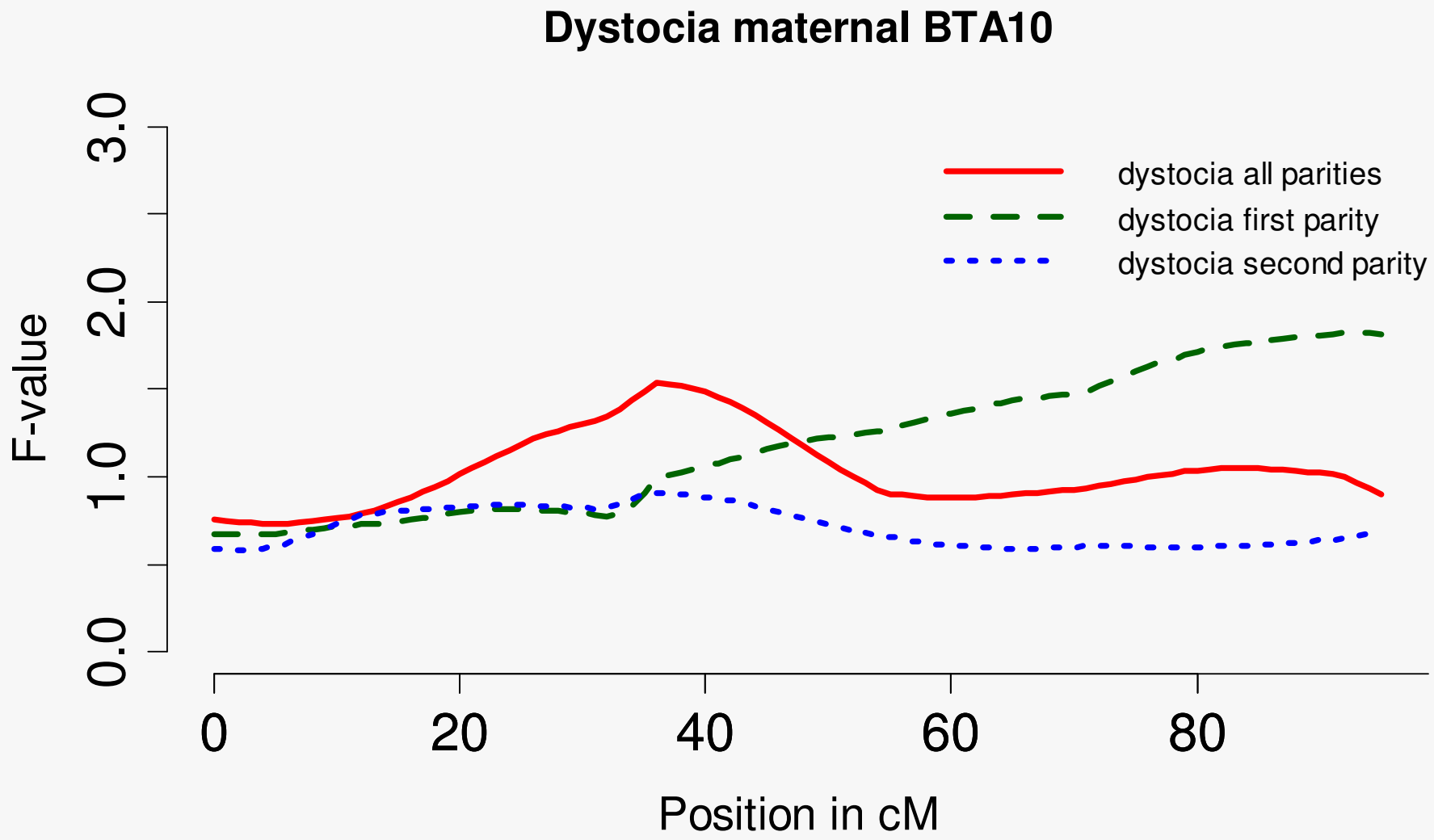


—, the expectation of the density under the assumption of all null hypotheses being true; -·- , true null hypotheses estimated with the false discovery rate

Discussion


Stillbirth maternal BTA18
stillbirth all parities
stillbirth first parity
stillbirth second parity
F-value
0.0
1.0
2.0
3.0
0
20
40
60
80
100
120
Position in cM

Discussion


Dystocia maternal BTA10
F-value
0.0
1.0
2.0
3.0
0
20
40
60
80
Position in cM
dystocia all parities
dystocia first parity
dystocia second parity

Discussion

- Calving traits in first and second parities have different genetic background
  → indicated by Philipsson (1996) and Harbers *et al*. (2000)

- Results published in literature only partly comparable, due to
  - different trait definition
  - different phenotypes
  - different populations except Kühn *et al*. (2003)

- Different data collecting systems for dystocia and stillbirth

- Different progeny testing schemes (in some countries testbulls also mated with heifers)

Discussion

- Mating of testbulls with heifers
  → more accurate phenotypes for QTL mapping
- Distinction of calving traits in parities for QTL mapping and progeny testing
- Improvements for data collecting for dystocia and stillbirth (subjective evaluation, high number of unreported cases)

Conclusions

More accurate and sharper phenotypes for breeding value estimation and QTL mapping lead to a higher power of mapping of trait specific QTL. These sharp phenotypes should be used in subsequent studies.

Thank you for your attention!

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