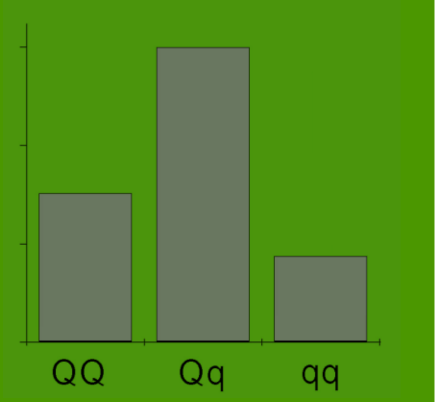
EAAP Annual Meeting 2012
Bratislava, Slovakia

Christian-Albrechts-Universität zu Kiel
Institut für Tierzucht und Tierhaltung

Estimation of dominance effects in paternally genotyped populations



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Introduction

Dominance effects are expected to be important in functional traits.

To estimate dominance effects it is essential to know both phenotype and genotype in the *same* individual.

In diary cattle breeding value estimation are based on genotypes of the sires and daughter phenotypes.

Problem:

How to make dominance obtainable in this scenario?

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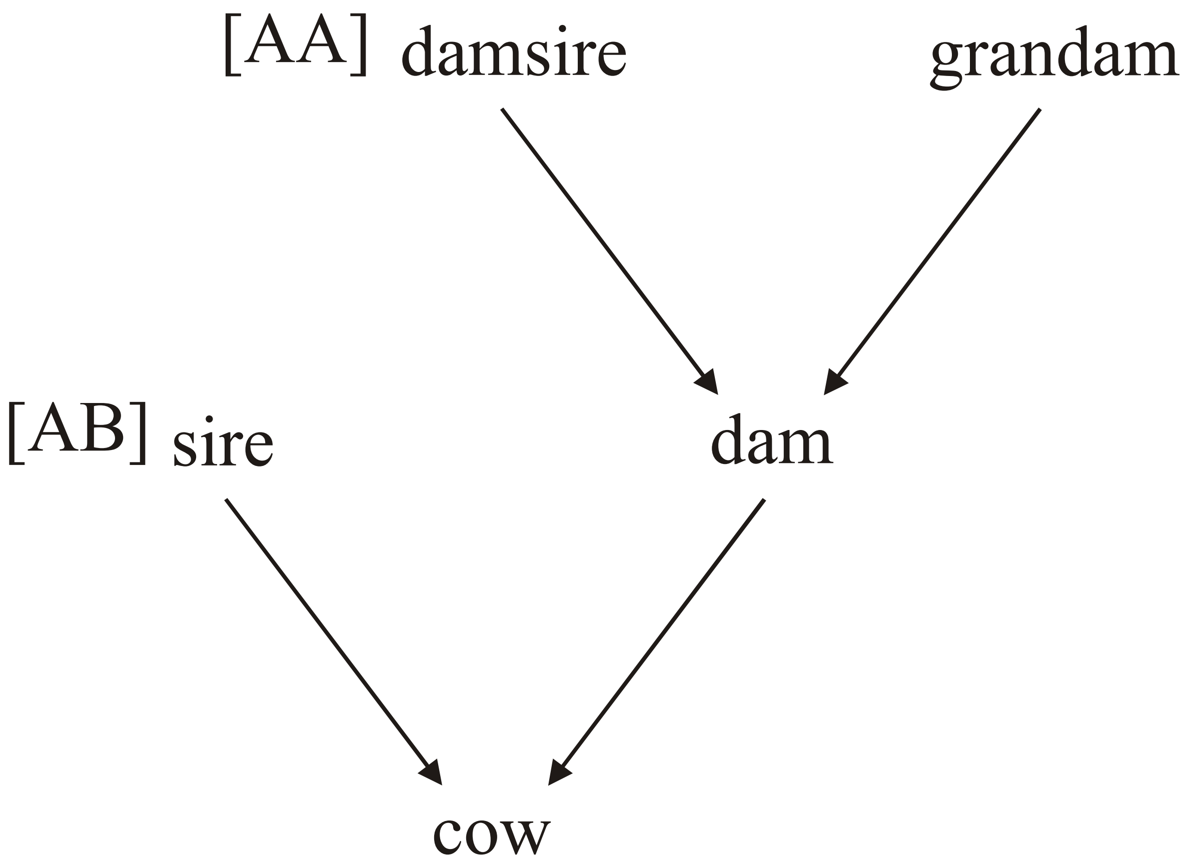
How to make dominance obtainable in this scenario?

Approach:

Deriving genotype probabilities in cows,
application of these data in QTL analysis.

Genotype probability derivation



[AA] damsire

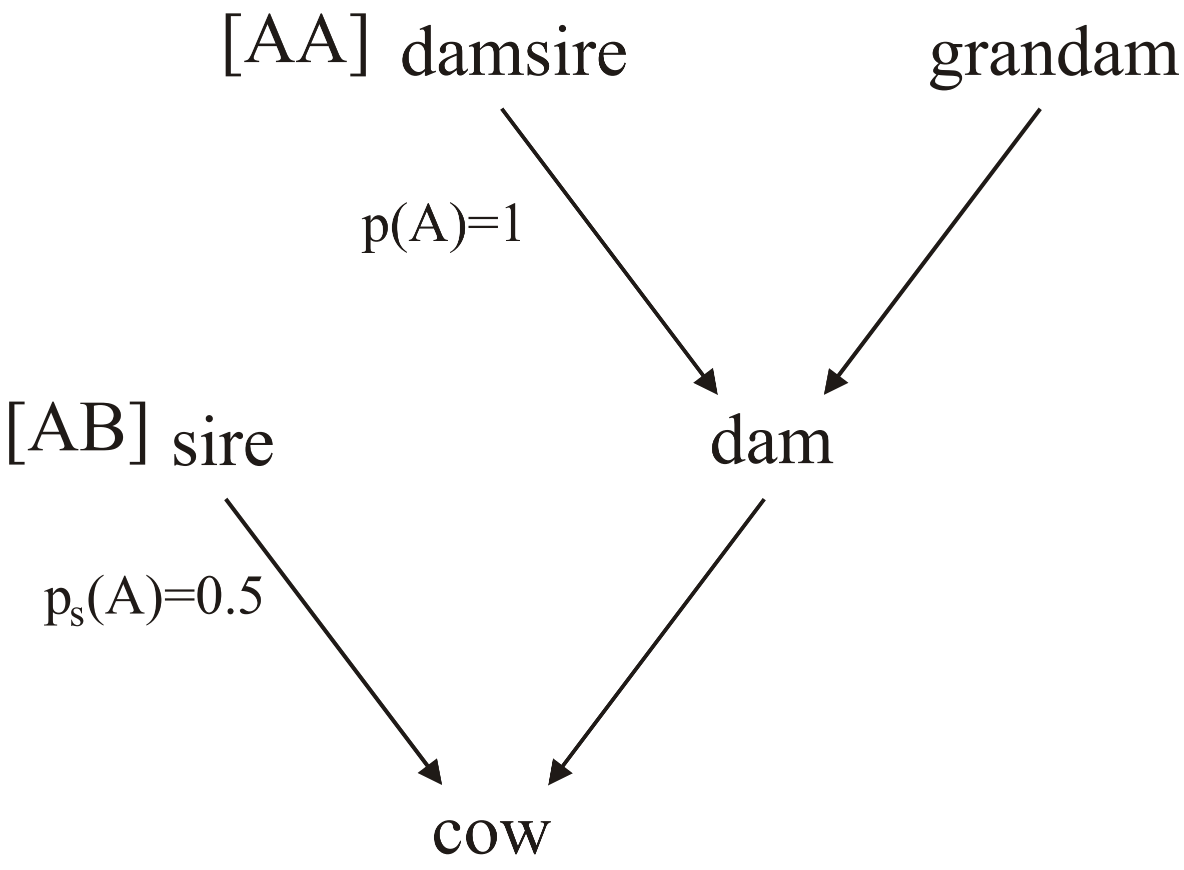
grandam

[AB] sire

dam

cow

Genotype probability derivation



[AA] damsire

grandam

$p(A)=1$

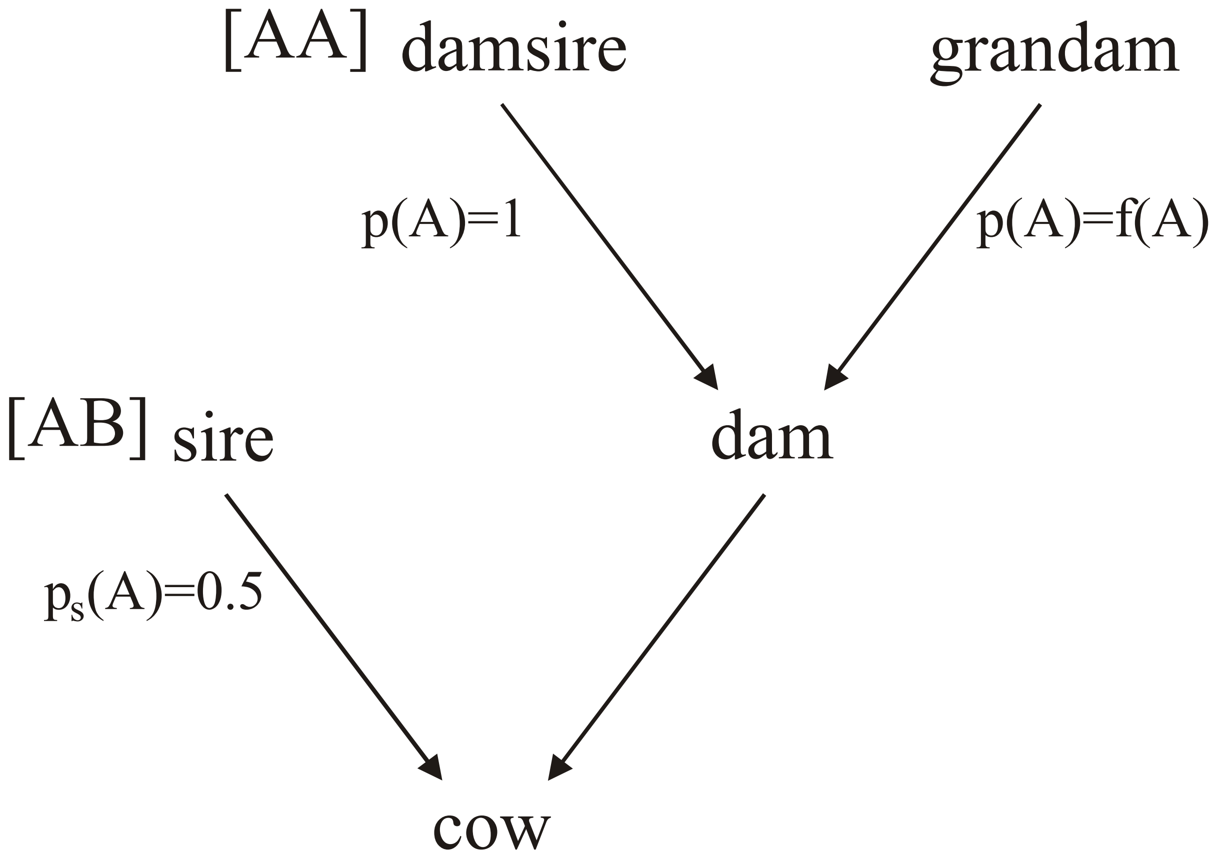
[AB] sire

dam

$p_s(A)=0.5$

cow

Genotype probability derivation



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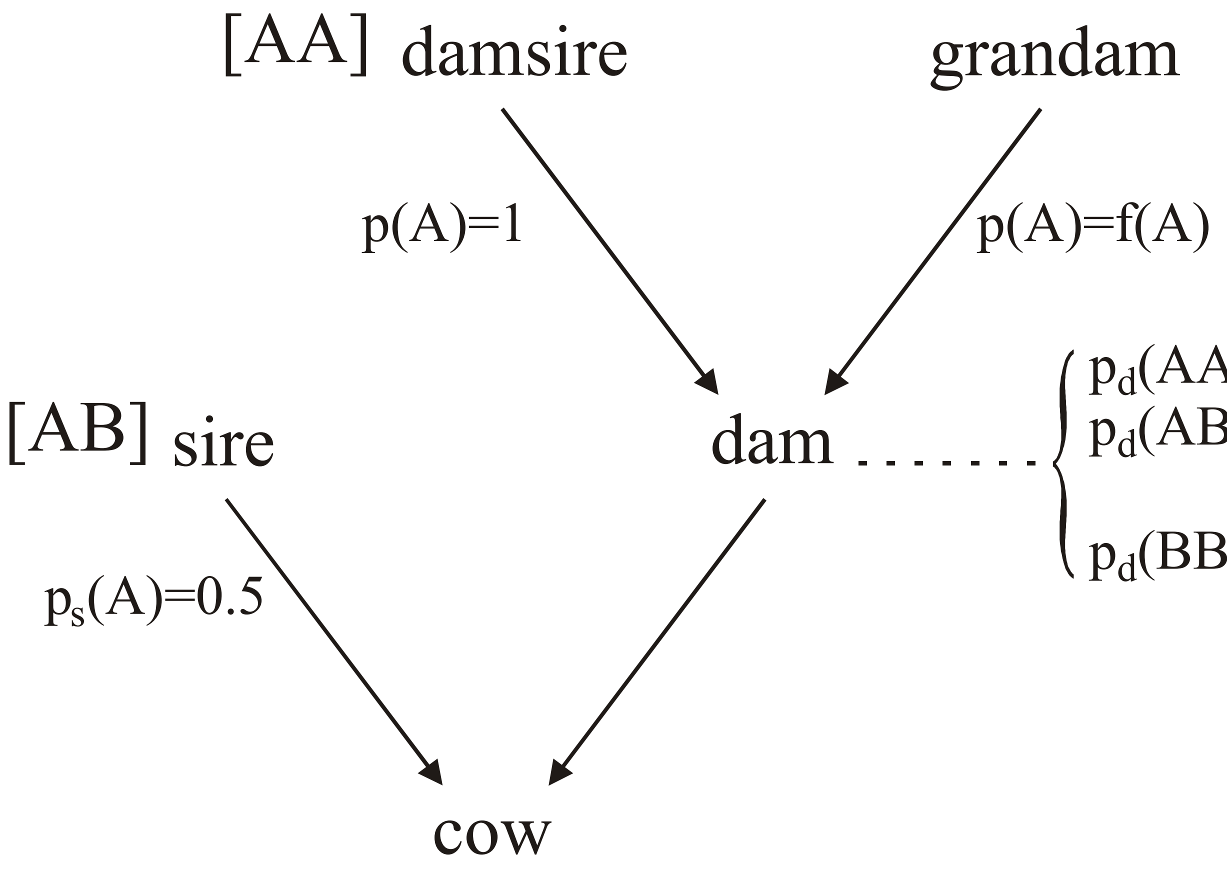

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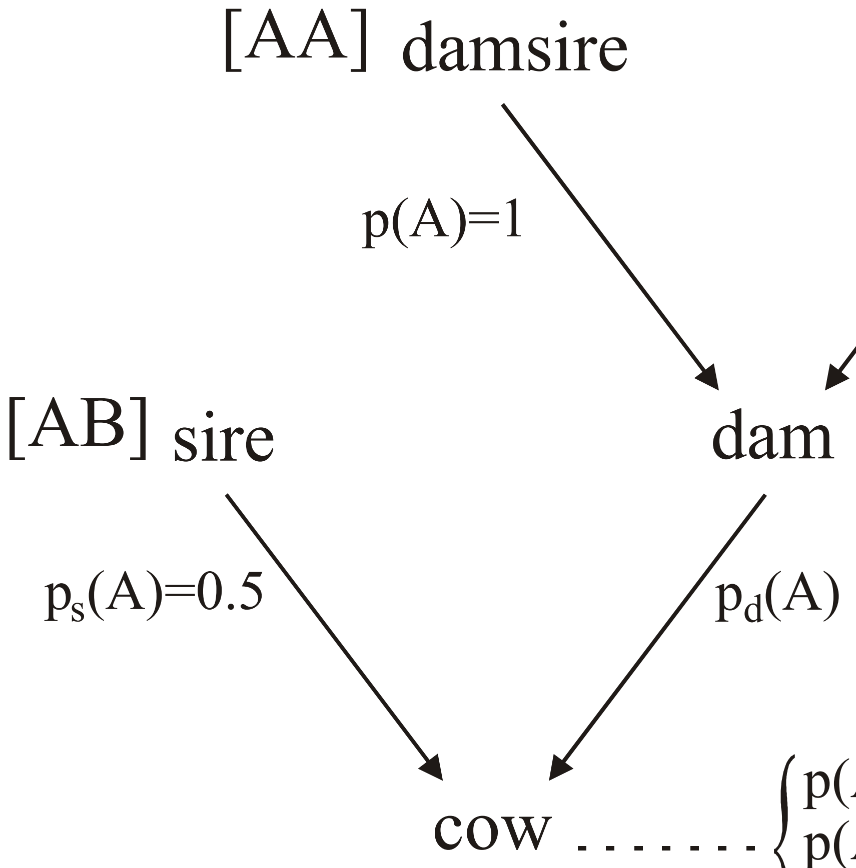
$$\begin{cases} p_d(AA) = p(A)\,f(A) \\ p_d(AB) = p(A)\,(1-f(A)) \\ \qquad\qquad + (1-p(A))\,f(A) \\ p_d(BB) = (1-p(A))\,(1-f(A)) \end{cases}$$

Genotype probability derivation



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$p_d(A)$

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\begin{cases}
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\end{cases}
$$

$$
\begin{cases}
p(AA) = p_s(A)\,(p_d(AA)+0.5p_d(AB)) \\
p(AB) = p_s(A)\,(0.5p_d(AB)+p_d(BB)) \\
p(BB) = (1-p_s(A))(0.5p_d(AB)+p_d(BB))
\end{cases}
$$

Simulation studies

- Simulated populations were build, different population sizes and structures.

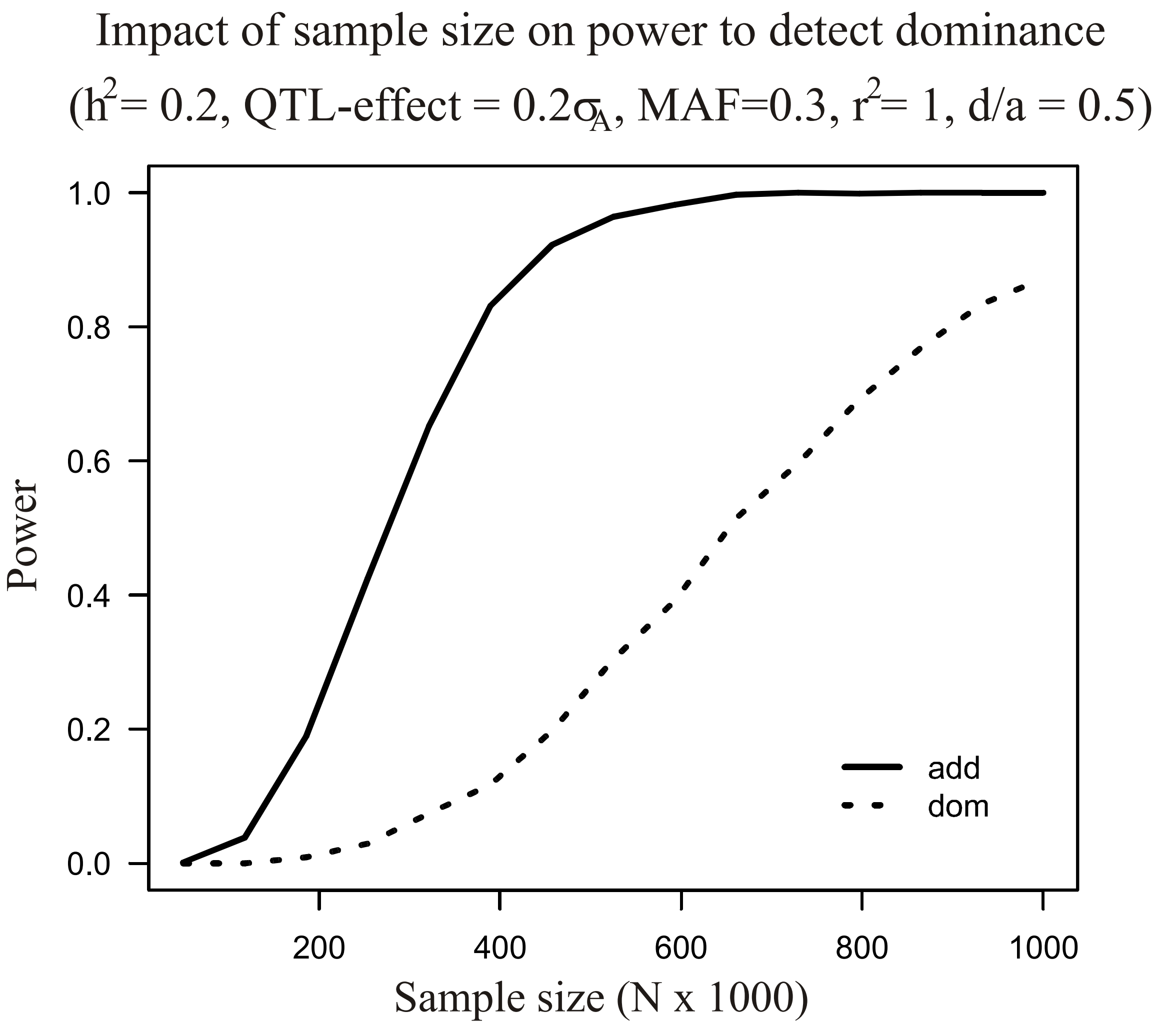
- Genotyp probabilities were calculated for the cows, their “real” genotype were sampled based on these probabilities.

- A normally distributed phenotype was assigned to the cows based on their genotype.

-Various scenarios were calculated testing sample size, family structure, MAF, heritability, linkage disequilibrium, variance explained by the QTL.

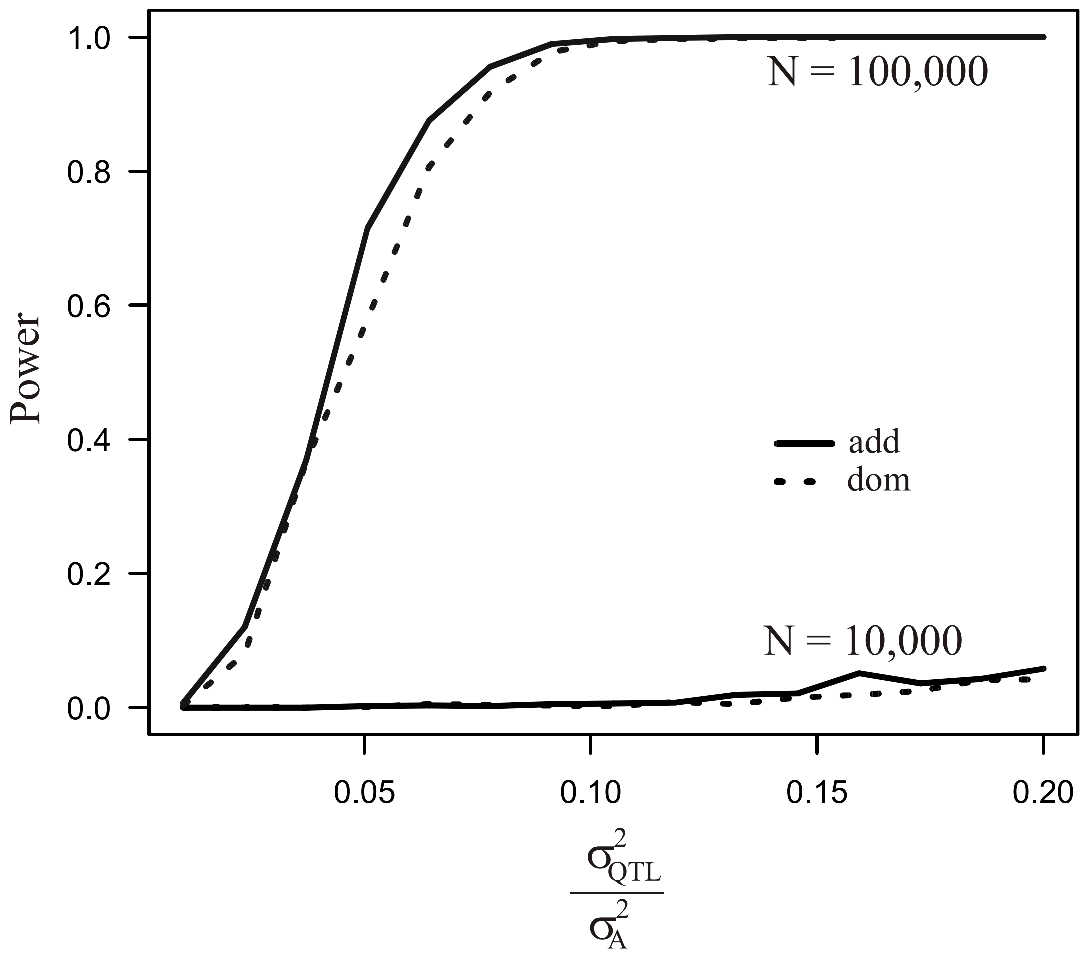
- Stratification adjustment was tested.

Simulation studies – sample size



Simulation studies – variance component

Impact of variance explained by the QTL
($h^2 = 0.25$, MAF = 0.3, $r^2 = 1$)



Pratical application - avaliable data

Application to a real data set:

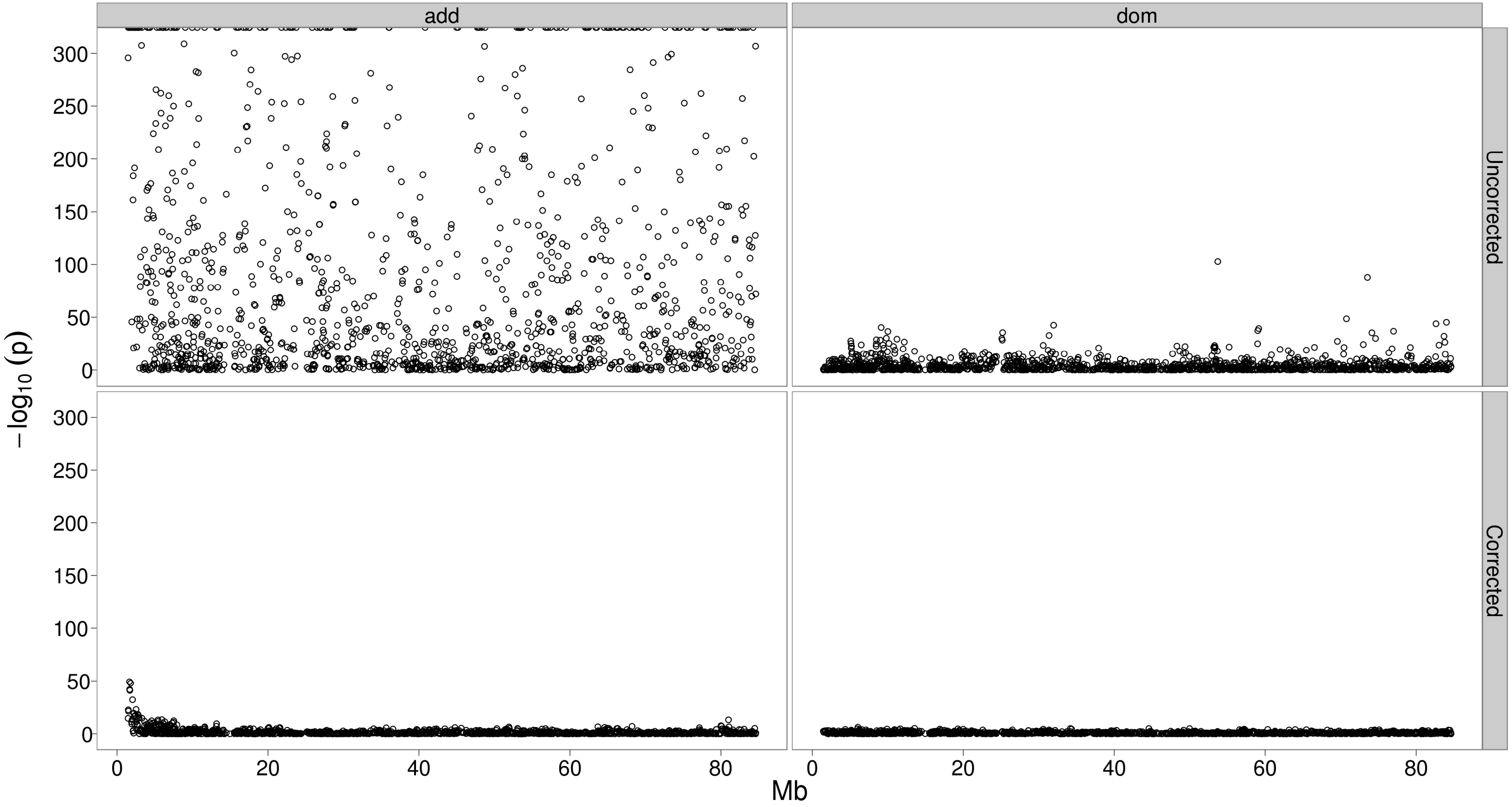
- Phenotypic and pedigree information of 847,000 german holstein cows.
- Yield deviations for the traits milk, proteine and fat yield and somatic cell count
- Genotype information for 3200 Holstein bulls, genotyped with Illumina BovineSNP50 BeadChip

- Data set was build comprising 470,000 cows and 2,081 bulls with 86,254 different sire-damsire combinations.

- Implementation using shell script and R, utilization of REML (ASReml) for linear mixed models.

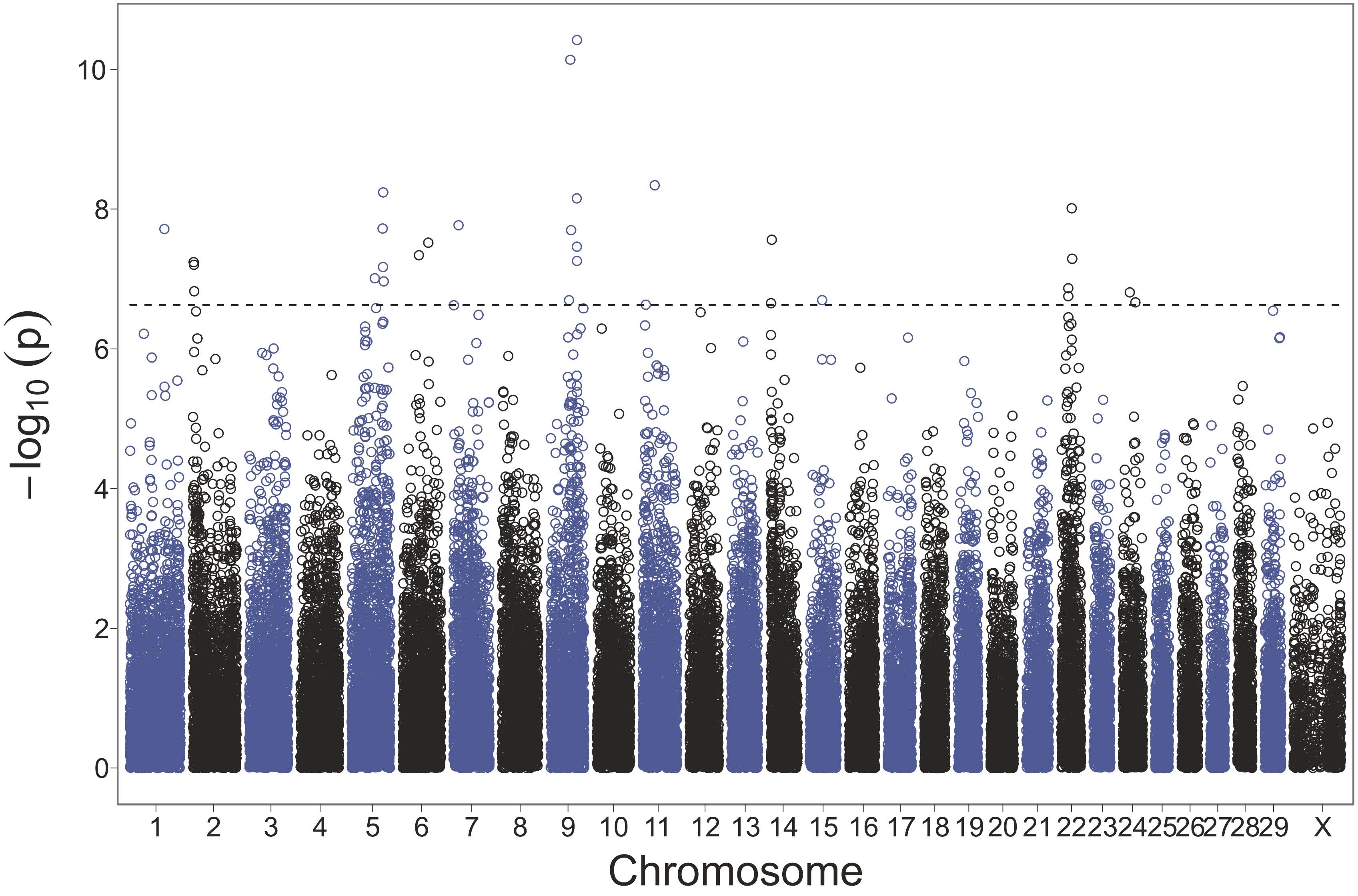
Real data - stratification correction

A mixed model including pedigree-based relationship matrix corrects stratification effectively.



Real data – genome scan

First genome scan for dominance and fat yield



Real data – results

Results from first analyses,
with $p<0.01$ after bonferroni correction:

milk yield	29 SNP on 15 Chromosomes
fat yield	30 SNP on 11 Chromosomes
protein yield	59 SNP on 17 Chromosomes

Most prominent dominance found on

BTA09	47-100MB	milk & protein yield, fat yield & content
BTA14	0-4MB	fat yield
BTA22	21-39MB	milk yield, fat yield & content

- QTL already described for yield traits there, but without dominance.
- Dominance found in *DGAT1* region is in accordance to the results from Kühn *et al.* (2006).
- On BTA09 62MB strong dominance for milk yield without additive effect was found.

Conclusion

The results of the first application demonstrates the posibility to detect dominance effects relying on large samples of phenotyped cows and deduced genotype probabilities.

It is a promising way to make use of the existing comprehensive data in cattle to detect dominance effects without additional cost.

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Thank you for your attention.

Acknoledgements

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