

QTL-MAS 2010: Simulated Dataset

Maciej Szydlowski

Poznań University of Life Sciences, Poznań, Poland

QTL-MAS 2008 Uppsala

48 additive QTLs

6000 SNPs + quantitative trait

QTL-MAS 2009 Wageningen

18 additive QTLs

453 SNPs + growth trait

QTL-MAS 2010 Poznań

More complex genetic architecture

Multiple loci with small effects

Genome wide association studies

- Larger sample size
- Higher marker density
- More detected QTLs
- Average effect decreases

Epistasis

- Documented in genetic crosses with optimized power
- Effect can be as large as main QTL effect
- Can occur between loci without main effects

Imprinted genes

- Documented in mammals (>80 genes) and flowering plants
- Usually found in clusters
- Control growth and development

Pleiotropy

- Very common
- Occurs also between „unrelated” traits
- Can help predict correlated response to selection

Pedigree

- **3,226** individuals in 4 generations
- **20** founders
- **30** progeny per mating
- **900** young individuals with no progeny

Genome simulation

- 5 chromosomes × 100 Mb
- **mh** software for haplotypes
 - coalescent model
 - effective population size 5000
 - mutation rate 10^{-8} per base
 - recombination 1cM / Mb
- Gene dropping with interference

SNPs simulation

- **10'031** SNPs sampled randomly
- MAF > **0.1**
- Only unphased data available
- No errors

37 QTLs simulated

9 controlled + **28** random

30 additive QTLs (**2** major QTLs)

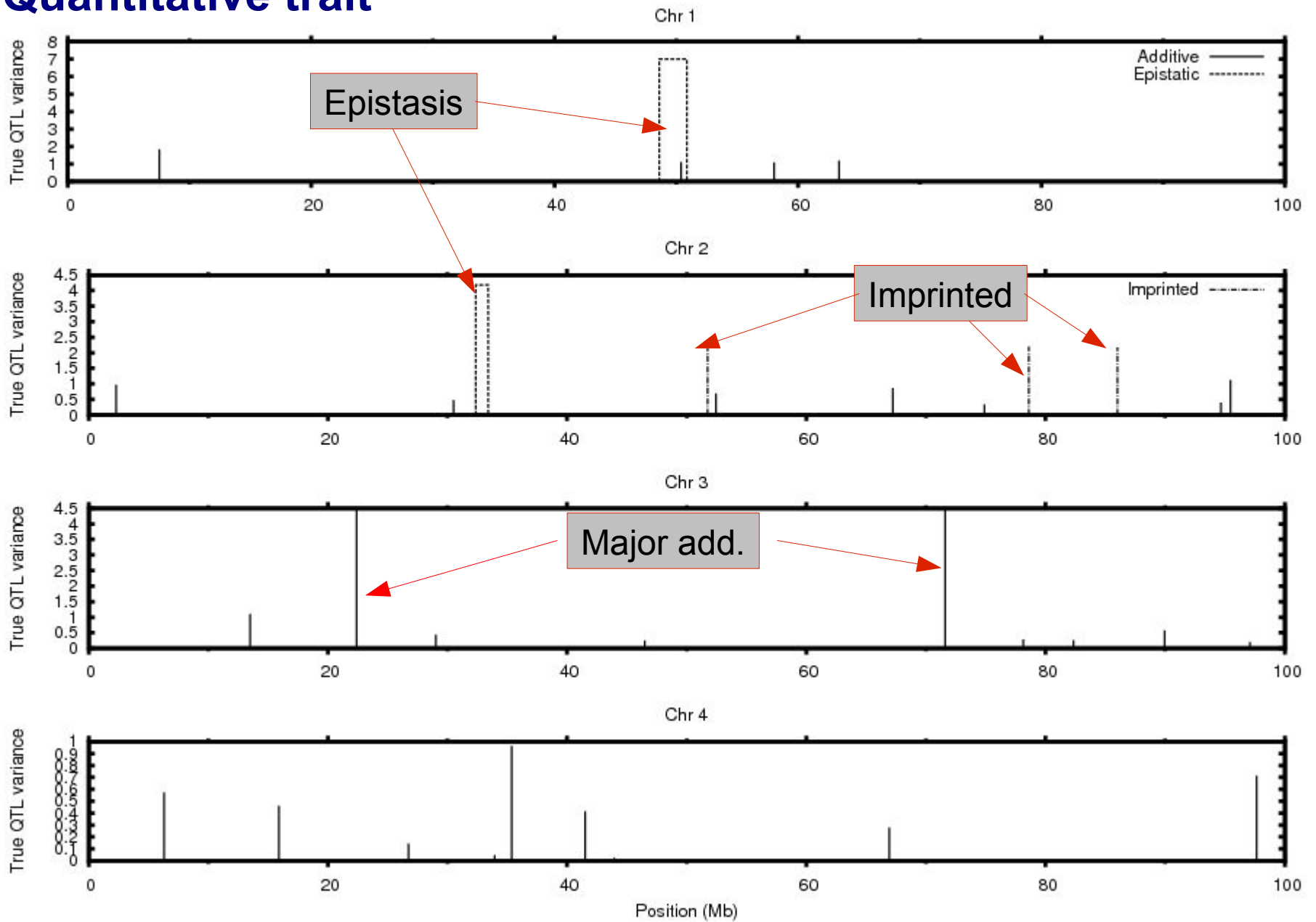
22 pleiotropic (additive)

4 epistatic QTLs (2 SNP pairs)

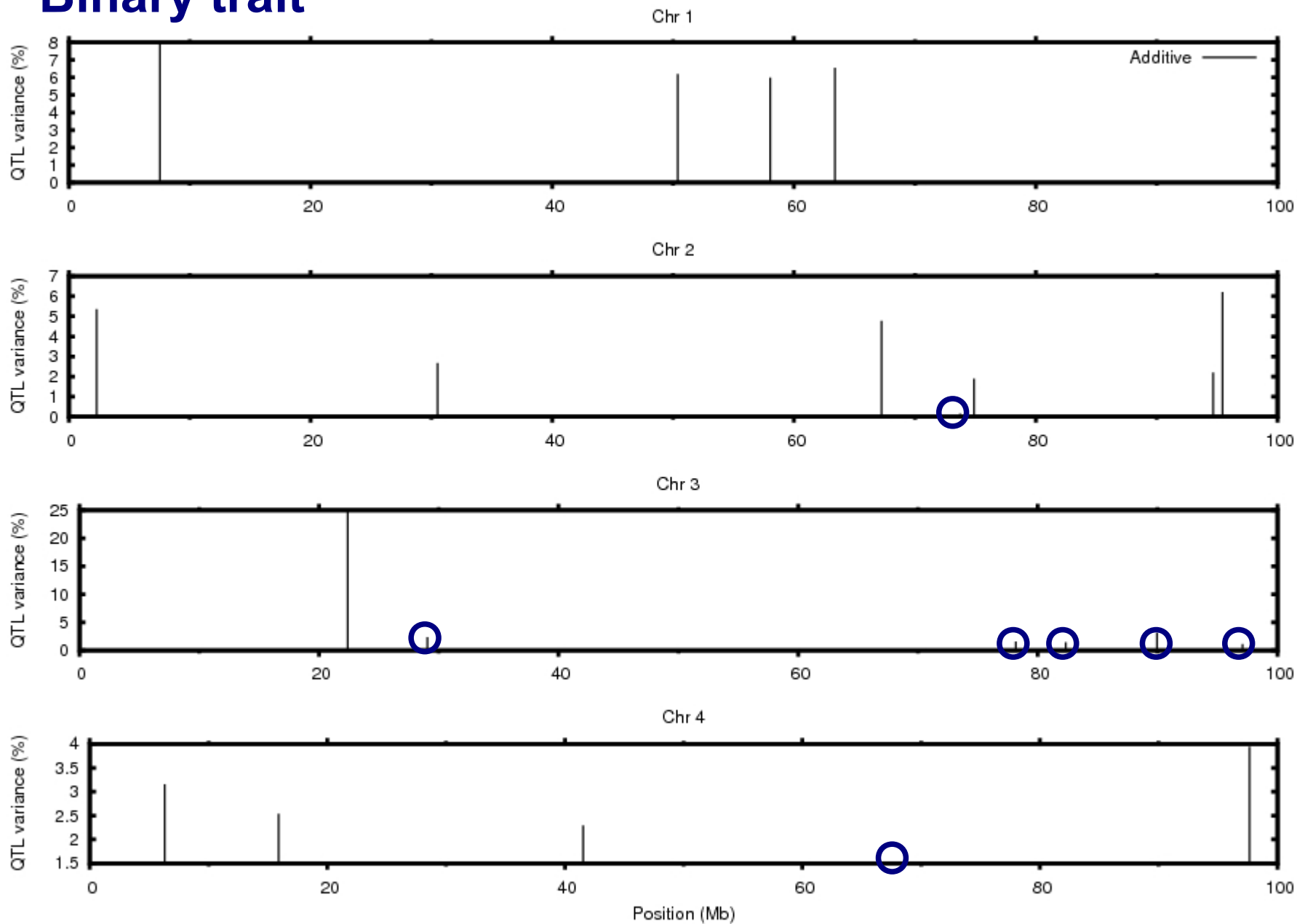
3 imprinted QTLs

8 key QTLs were genotyped

Quantitative trait



Binary trait



Breeding value definition

TBV =

+ 30 additive genes

+ 2 haplotypes (crossing-over ignored)

+ 3 imprinted genes (only for males)

Imprinted genes were excluded from breeding value of female

Heritability

Quantitative trait	0.52 males	0.39 females
Binary trait	0.48	

Genetic correlation between traits

0.59 males	0.68 females
-------------------	---------------------

Summary

- Complex genetic architecture was simulated
- Extreme effects shaped phenotypes
- Key SNPs were included in the molecular data
- Behavior of different approaches can be evaluated