

DNA-based selection calls for new measures of inbreeding

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Collaboration:

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The motive

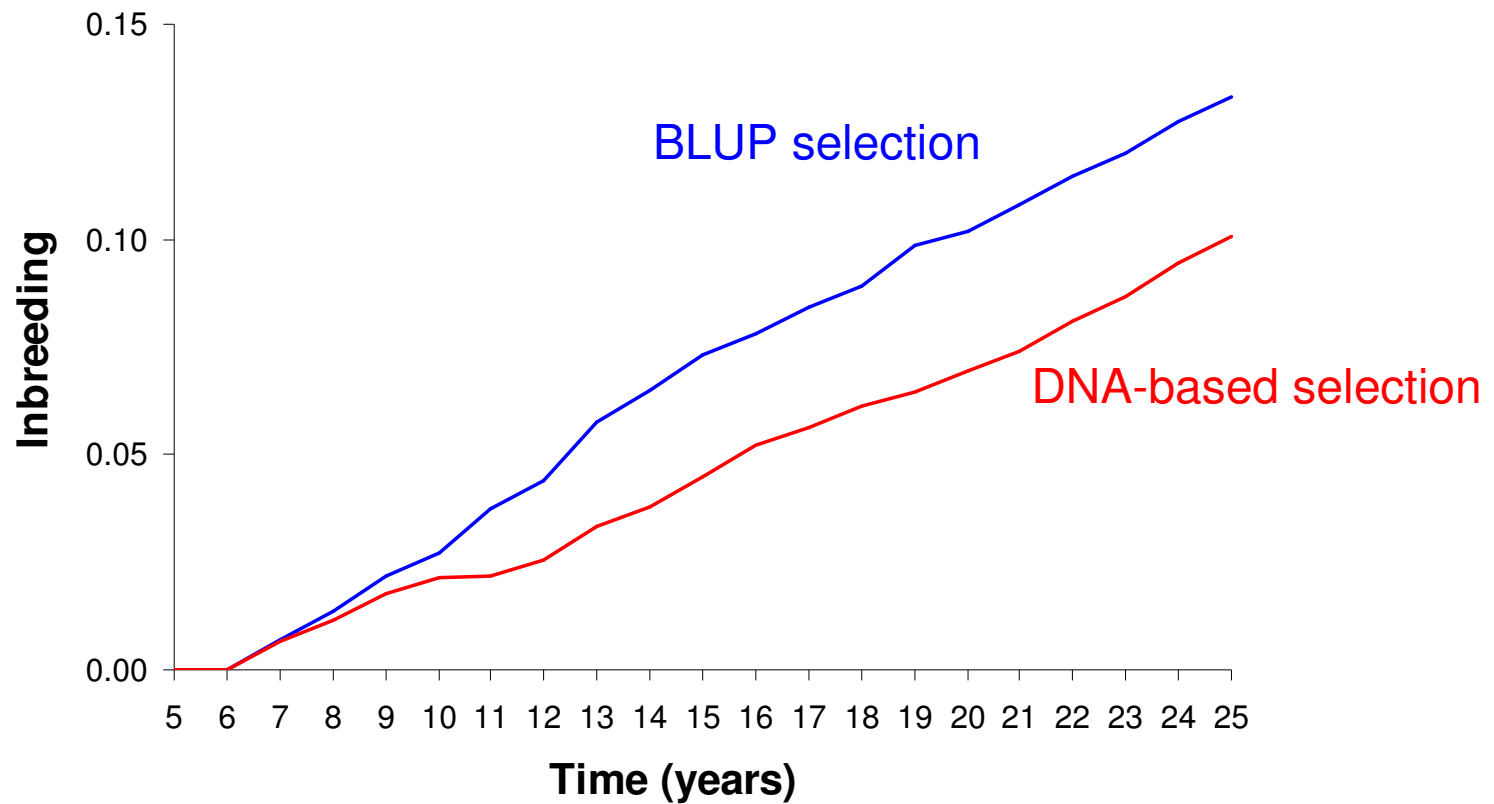
Modern dairy cattle breeding:

- Use of DNA information is inevitable
- Inbreeding is an actual problem
- Relevant to ask the question:

***What happens with
inbreeding when DNA
information is used?***

The motive

Use of DNA information reduces inbreeding



However...

Traditional inbreeding measures:

- Based on pedigree
- Assumes neutrality

If locus is under selection:

true inbreeding > pedigree estimated

- DNA information → selection pressure on QTL ↑

So...

*What happens with true inbreeding
when DNA information is used?*

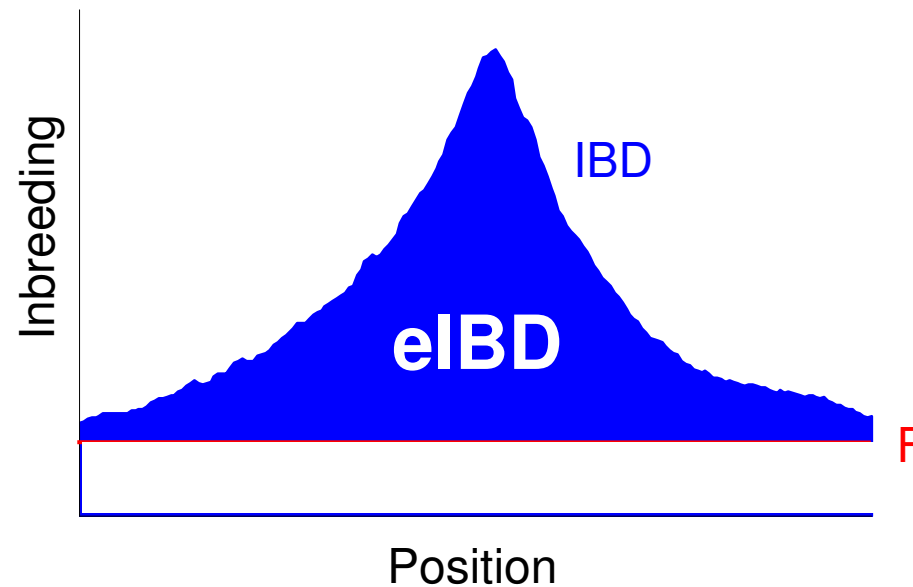
Stochastic simulation

- Dairy cattle population
- Single trait, $h^2=0.04$
- Finite-locus model
- Number of QTL: 30, 100, 300
- Selection criteria:
 - BLUP
 - True breeding values



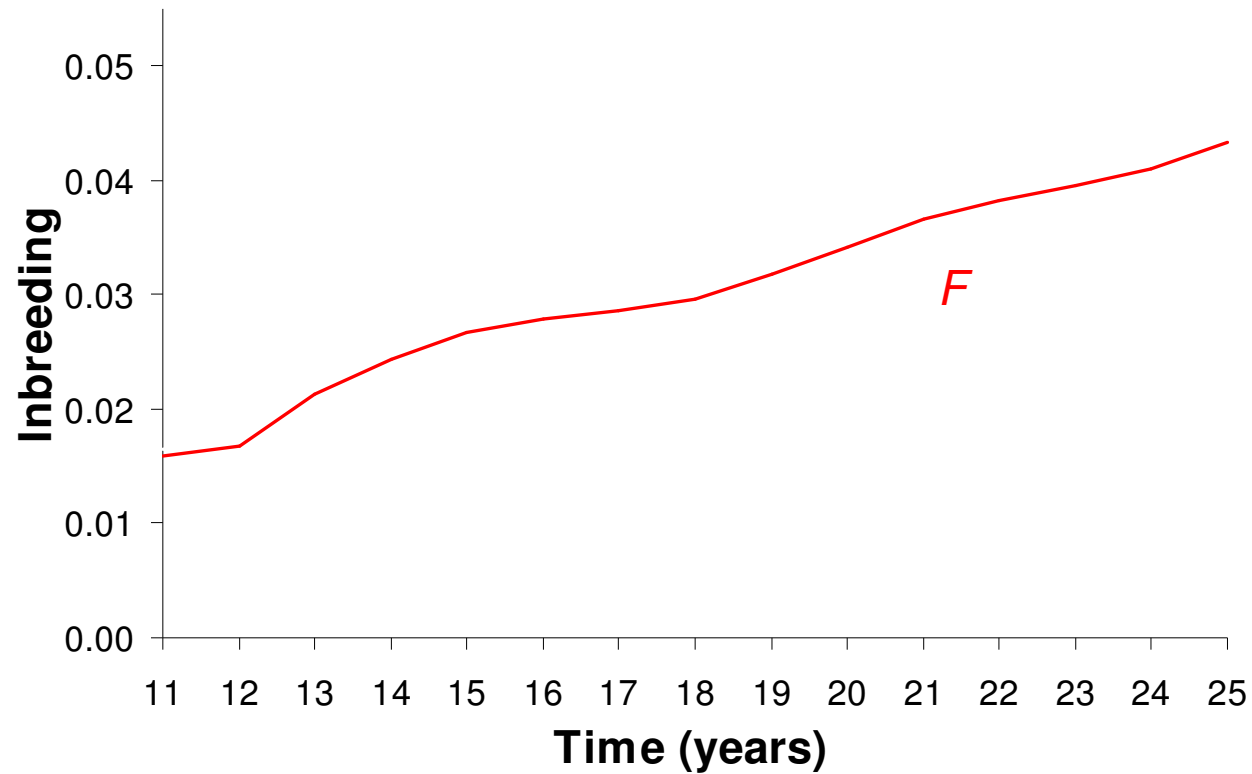
Measures of inbreeding

- F : Estimated from pedigree
- IBD : True inbreeding in QTL
- eIBD: Hitchhiking



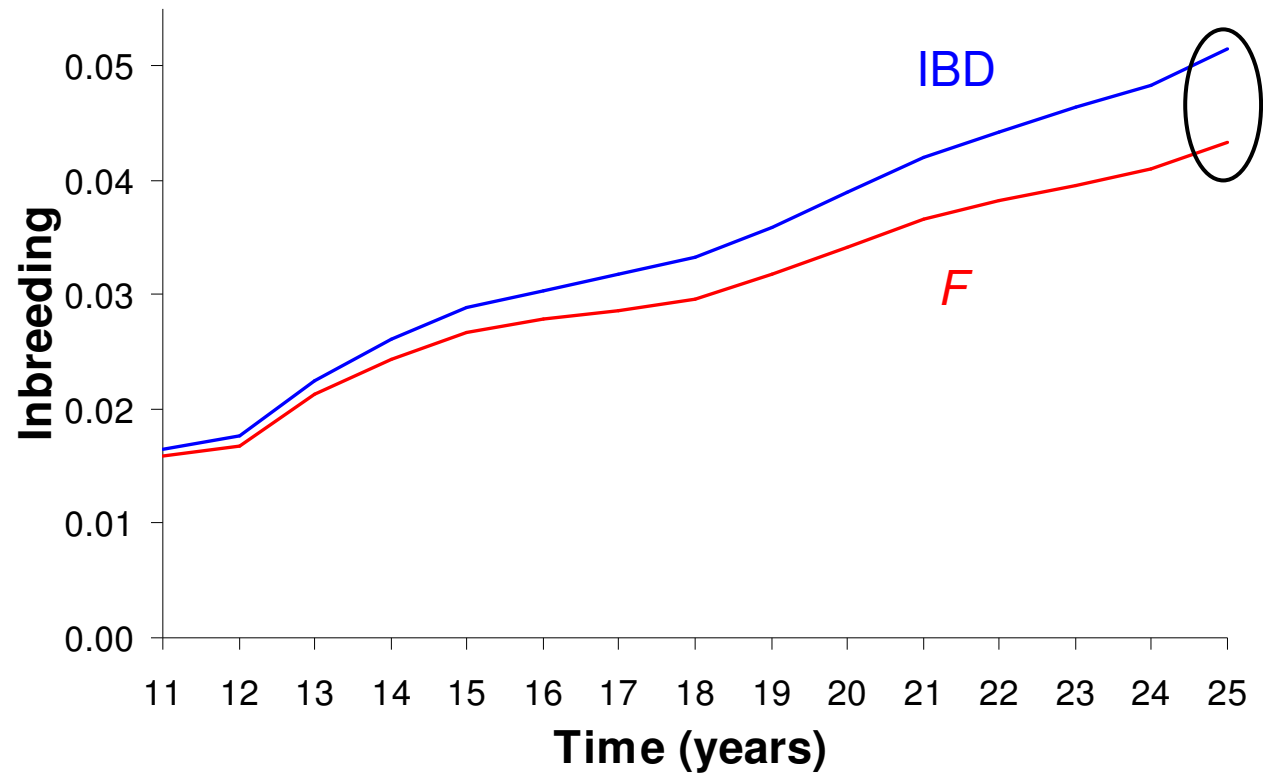
Results

True vs. pedigree estimated inbreeding:



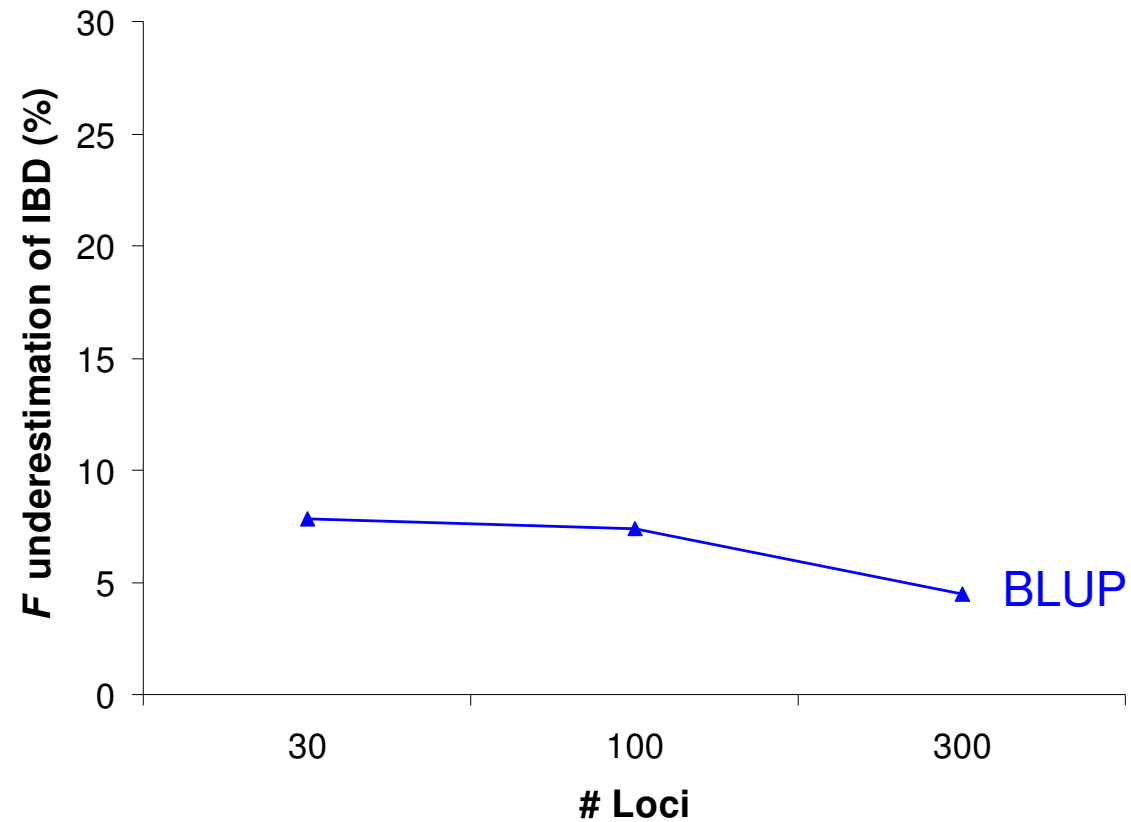
Results

True vs. pedigree estimated inbreeding:



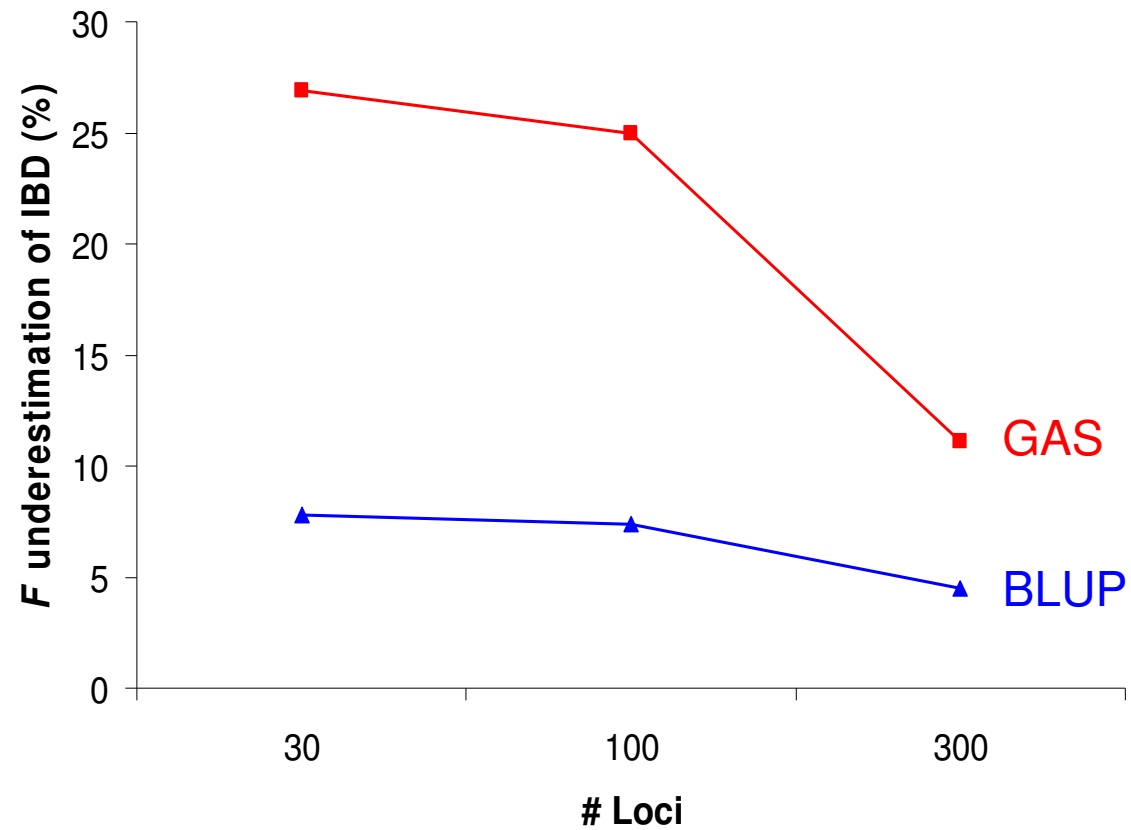
Results

True vs. pedigree estimated inbreeding:



Results

True vs. pedigree estimated inbreeding:



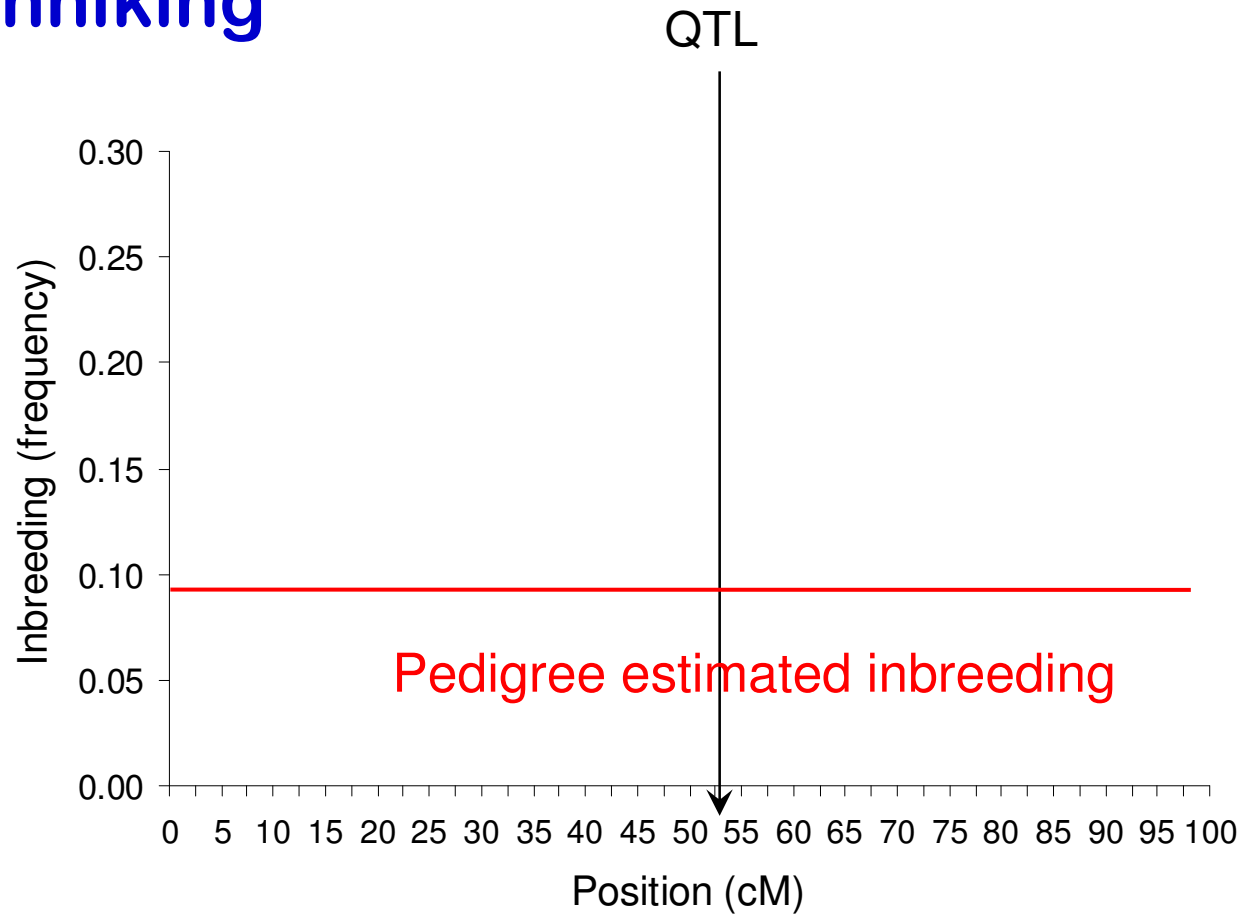
Results

Funderestimates IBD in QTL

- $GAS > BLUP$
- Few loci $>$ many loci

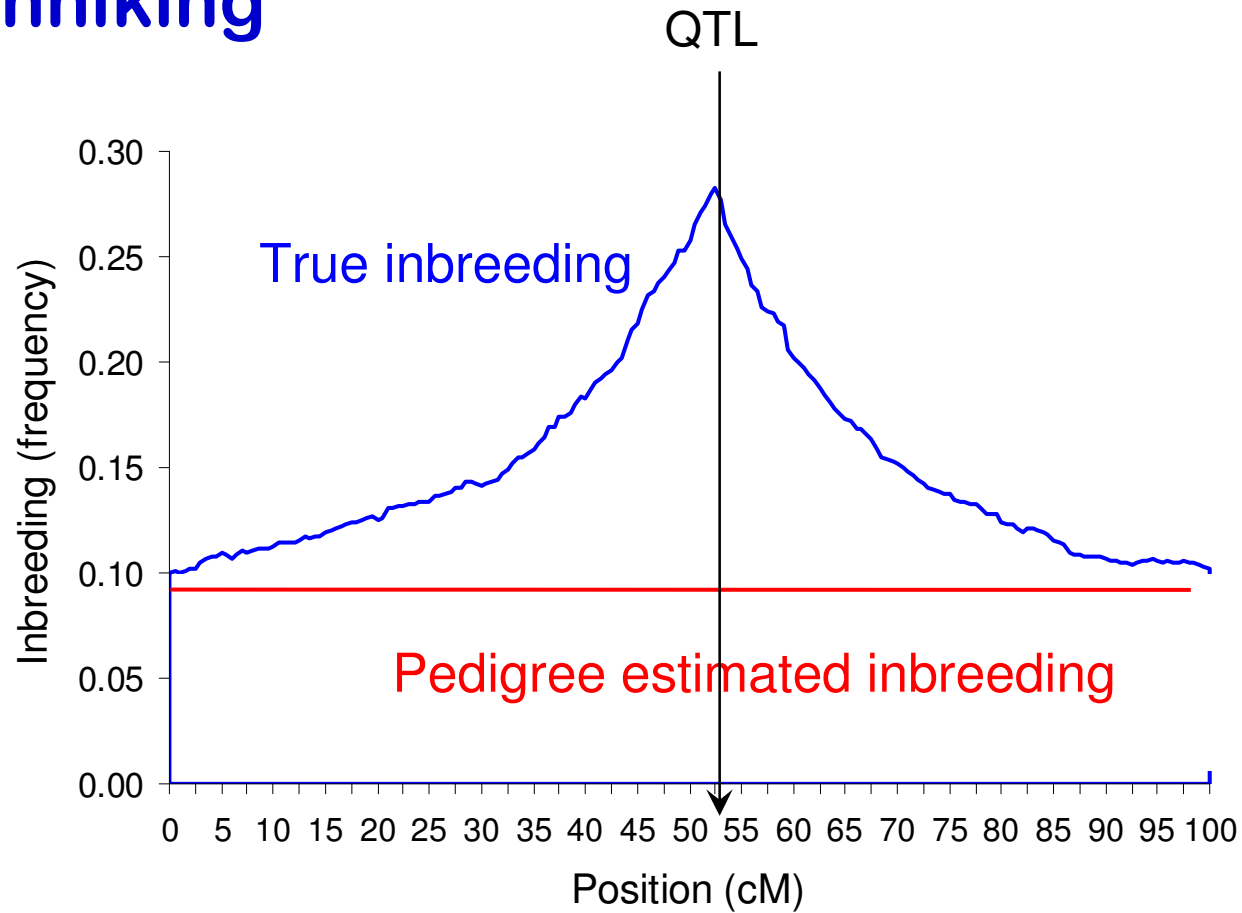
Results

Hitchhiking



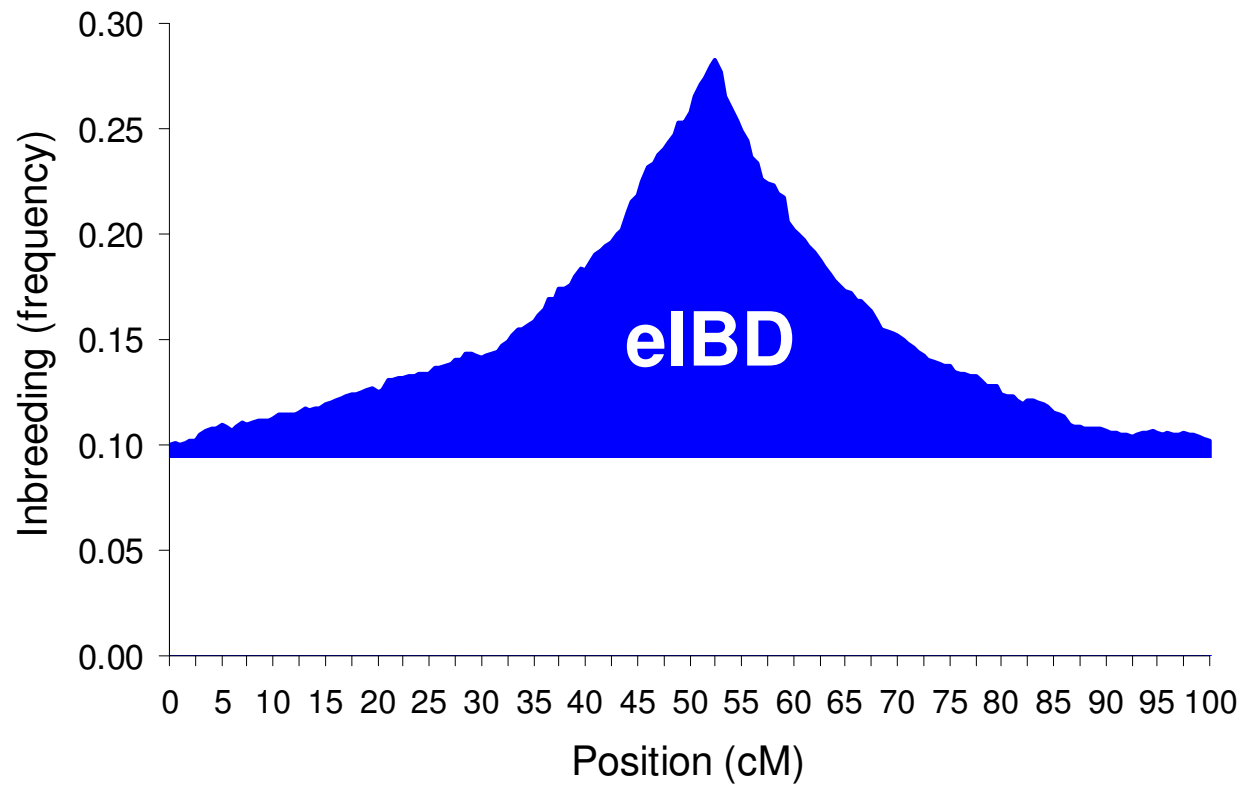
Results

Hitchhiking



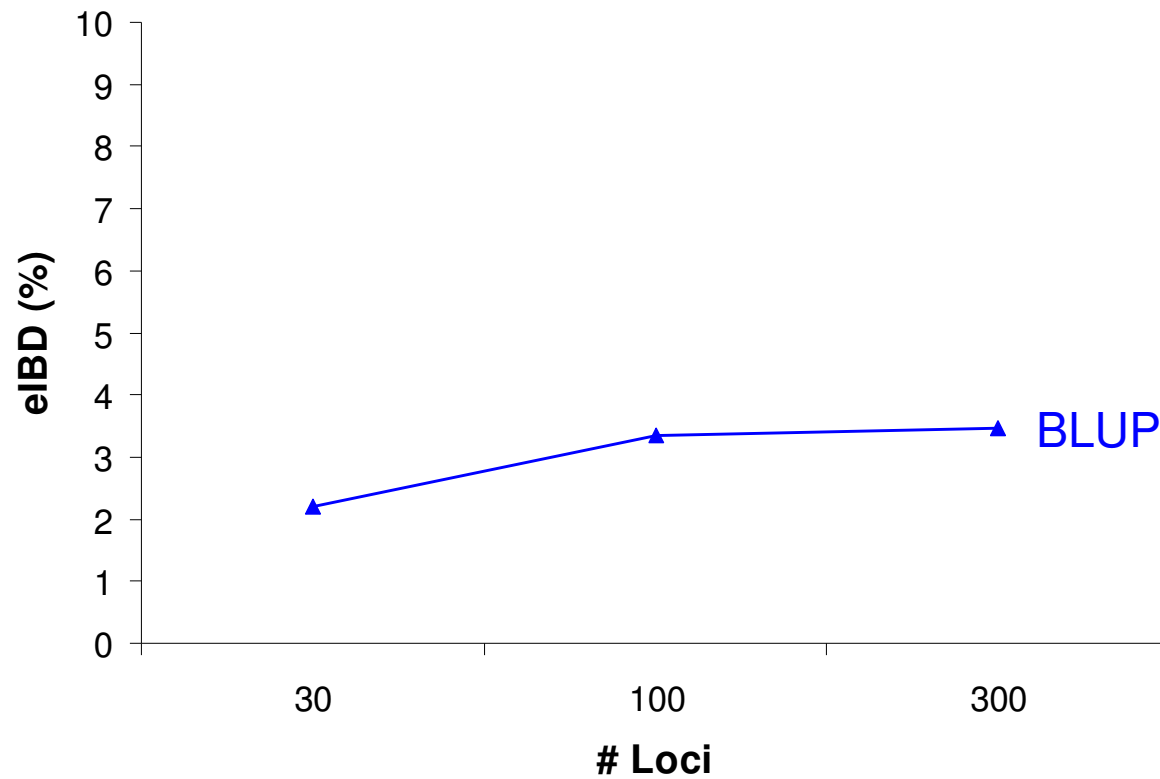
Results

Hitchhiking



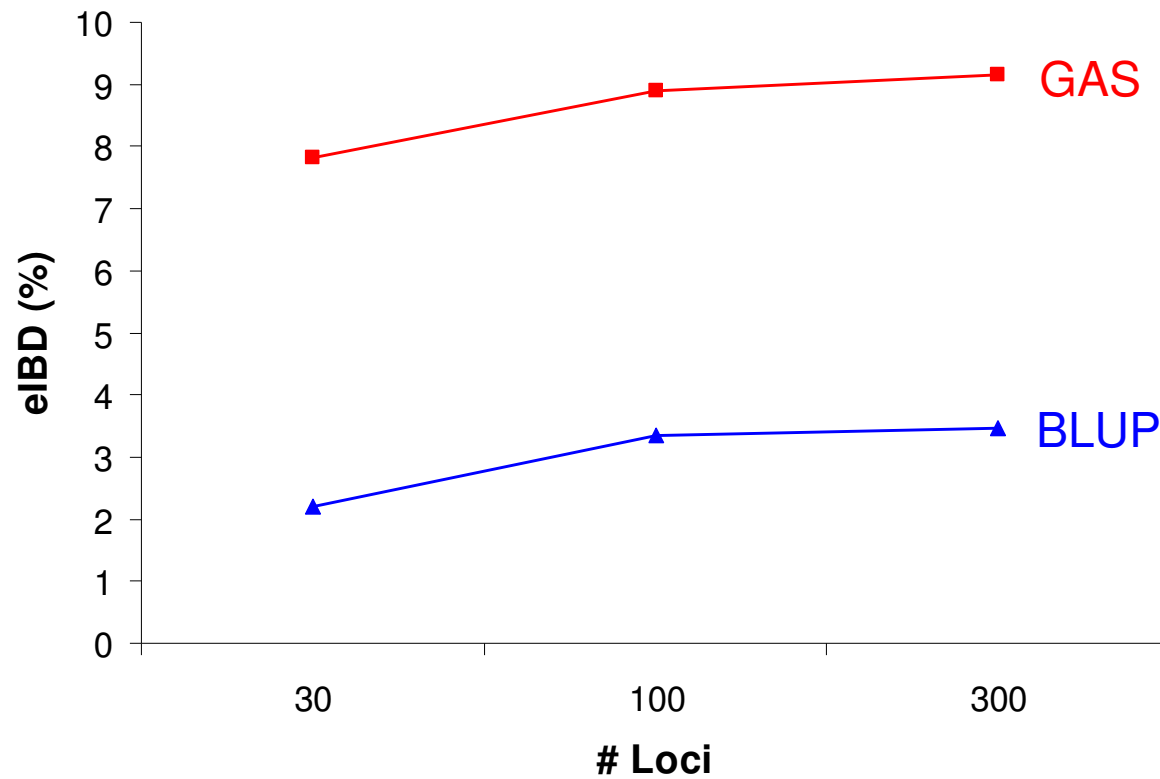
Results

Hitchhiking - global effect



Results

Hitchhiking - global effect



Results

Funderestimates total IBD in the genome

- $GAS > BLUP$
- Few loci $<$ many loci

Use of DNA information...

Decreases inbreeding in the population

BUT...

Increases selection intensity in selected loci

→ Large amount of hitchhiking

→ F underestimates IBD

→ **Deteriorates traditional measure of inbreeding**

Conclusion

**DNA-based selection calls for
new measures of inbreeding**