Factors affecting accuracy of estimated effective number of chromosome segments for small breeds

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WAGENINGEN
UNIVERSITY & RESEARCH

100years
1918 — 2018

Acknowledgement

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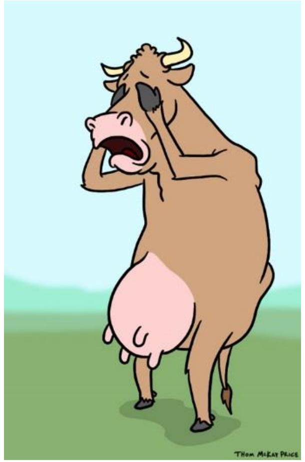
EUROPEAN RESEARCH AREA ON SUSTAINABLE ANIMAL PRODUCTION

Project **ReDiverse**

ReDiverse

- Biodiversity within and between European Red dairy breeds
- Red dairy breeds often produce less > increasingly replaced on the farm
- Make small breeds more lucrative for farmers
- Genomic selection
- Increase genetic improvement



http://www.thommckayprice.com/2016/04/sad-cow.html

Genomic selection

- Red dairy breeds are often numerically small
- Breed-specific RP is challenging

- Alternative - multi-breed RP

- Choose breeds that are relevant
- **Effective number of chromosome segments (M_e)**

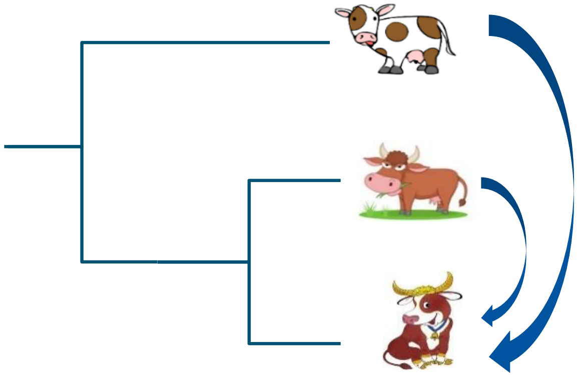
M_e

- Indicator of relatedness & expected accuracy
- M_e - within the population and across two populations
- Within M_e - Chrom segments that are segregating independently

$$M_{e,w} = \frac{1}{Var(G_{ij} - A_{ij})}$$

- Across or between M_e - consistency of LD between populations

$$M_{e,a} = \frac{1}{Var(G_{pop1_i pop2_j} - A_{pop1_i pop2_j})}$$



Numerically small breeds

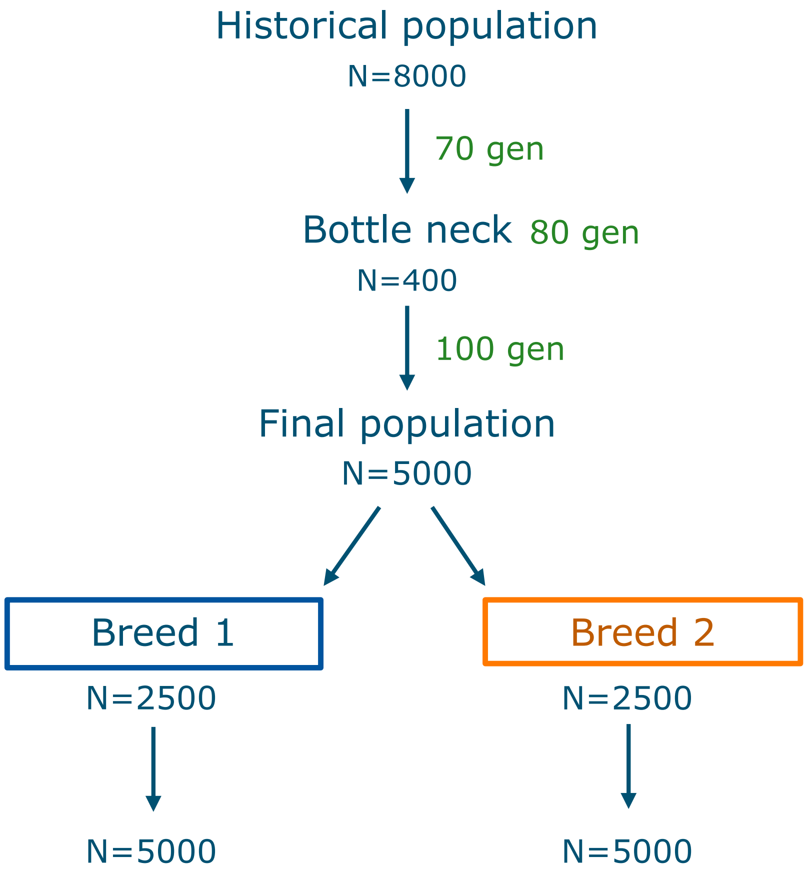
- Previous studies estimating $\mathrm{M_e}$ used large number of individuals
- May not be feasible for many ERDB
- Numbers of genotyped animals differ between breeds
- Impact on $\mathrm{M_e}$?

Objective

Effect on estimated $\mathbf{M_e}$

- Number of genotyped individuals
- Discrepancy in number of genotyped individuals in two breeds
- Marker density

Simulation study



Historical population

N=8000

70 gen

Bottle neck 80 gen

N=400

100 gen

Final population

N=5000

Breed 1

N=2500

N=5000

Breed 2

N=2500

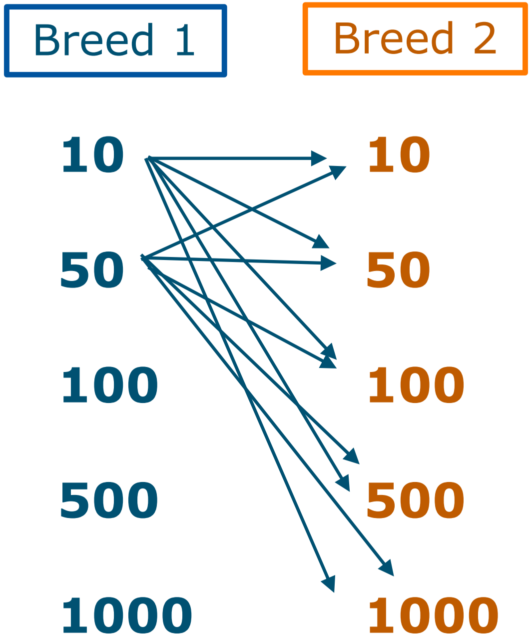
N=5000

- Mating males 50
- Mating females 2500
- Selection based on EBVs
- 100 generations

- Genome 30 Chr
- 720k SNPs
- ~9000 QTLs

- QMSim

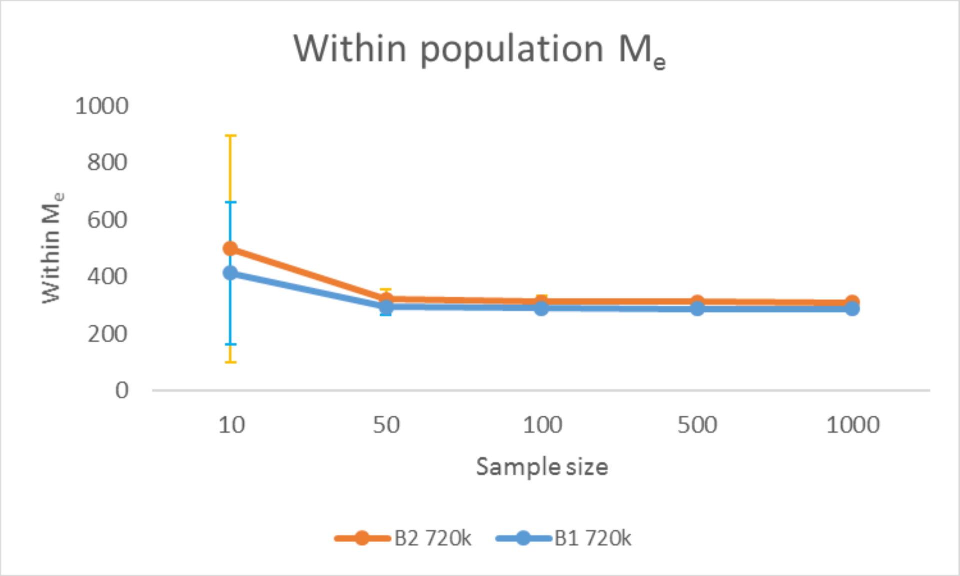
Scenarios



- Generation 10
- Sampling 50x
- Estimate M_e with calc_grm

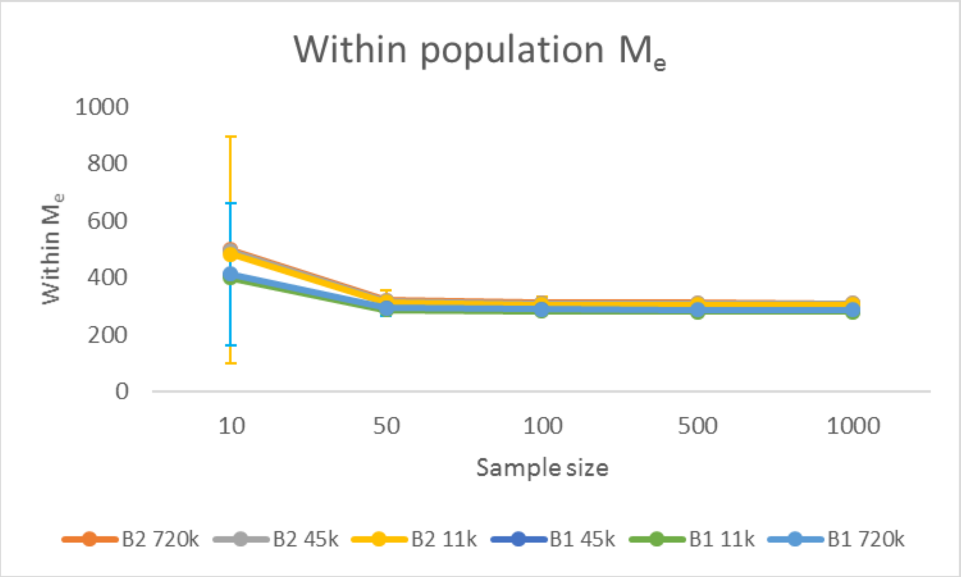
- SNP density 720k
- Selecting every 16th > 45k
- Selecting every 64th > 11k

Results – Within M_e



720k

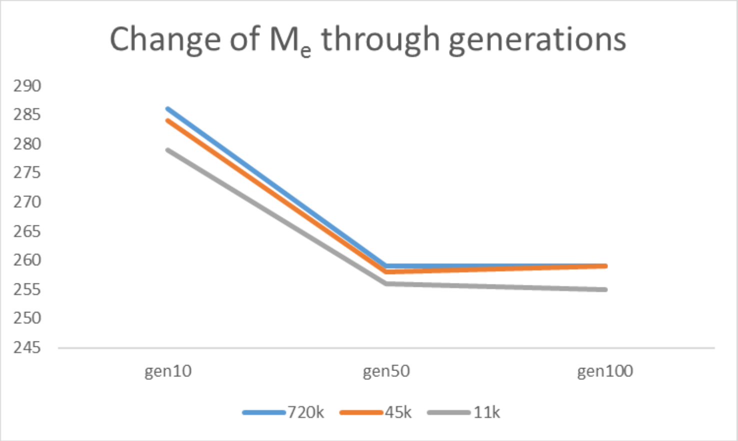
Results – Within M_e



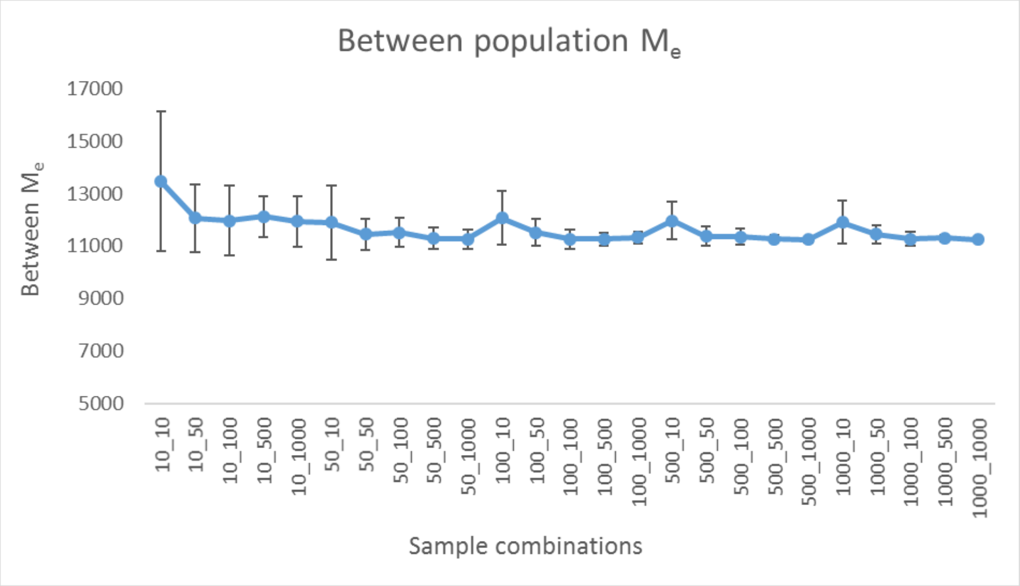
720k

45k

11k

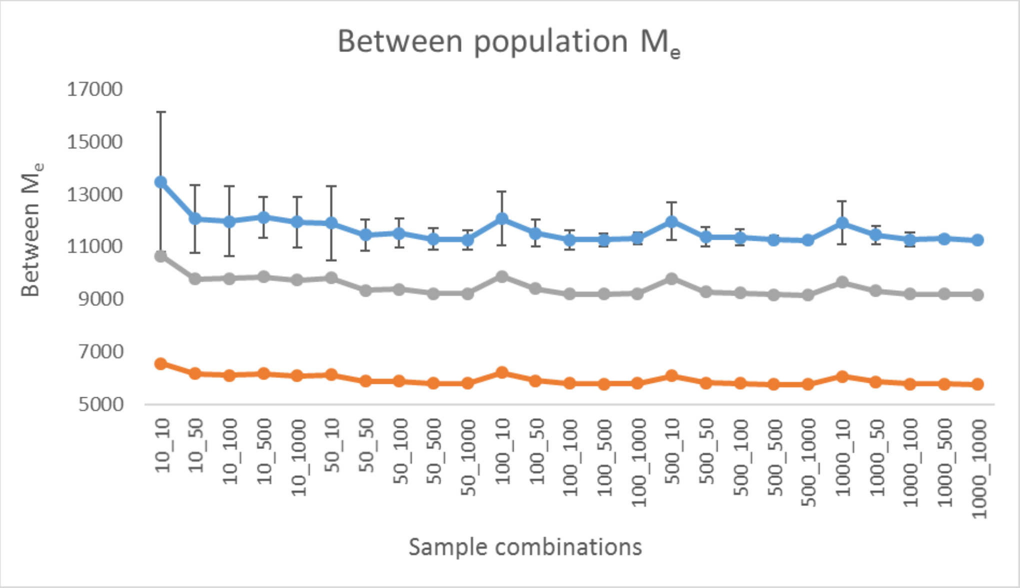


Results – Between M_e



720k

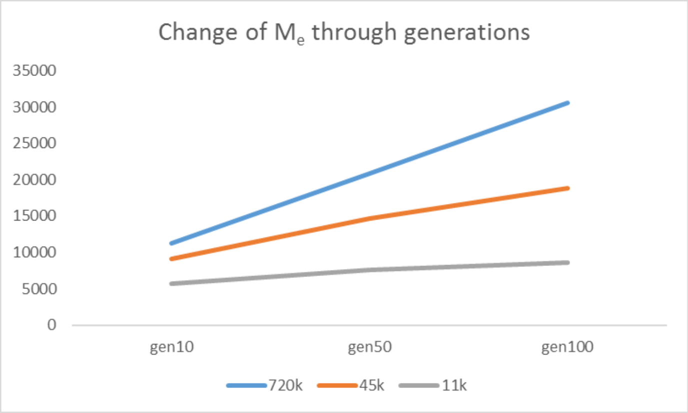
Results – Between M_e



720k

45k

11k



Conclusion

- Using less than 50 individuals may affect accuracy of within and between $\mathrm{M_e}$
- High density SNPchip > higher value of between $\mathrm{M_e}$
- SNPchip density important to accurately estimate between $\mathrm{M_e}$
- Results can serve as guidelines for
  - GP in numerically small breeds
  - When testing if implementation of GS is expected to be beneficial (by keeping initial costs minimal)