Genomic Selection:

The Bulmer-effect,

and prospects with small reference populations

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Genomic Selection

- Large ref. pops. are required for high accuracy
- This is not always feasible
  - Traits that are difficult/expensive to record
    - Disease-resistance
    - Methane emission
    - Meat quality
    - Osteochondrosis (bone disease in horses and pigs)
  - Small breeds

Objectives

1. Quantify the Bulmer-effect for GS

2. Prospects of GS when phenotyping is limiting
    1. Optimum construction of the reference population
    2. Response to GS when ref. pops are small

1. The Bulmer-effect with GS

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Assumptions:

- Markers capture a proportion ρ^2 of the additive genetic variance
- No updating of the reference population
- Selection is based on the known genomic EBV

Variance GEBV: $\sigma^2_{EBV} = \rho^2 \sigma^2_A$

Variance GEBV in selected parents : $\sigma^2_{EBV}{}^* = (1-k)\sigma^2_{EBV}$ k = 0.7 - 0.9

Next generation: $\sigma^2_{EBV,t+1} = \frac{1}{2}(1-k)\sigma^2_{EBV,t} + \frac{1}{2}\sigma^2_{EBV,0}$

Bulmer-equilibrium variance GEBV: $\sigma^2_{EBV_{eq.}} = \frac{\sigma^2_{EBV_0}}{1+k} \approx (0.53.....0.59)\sigma^2_{EBV_0}$

1. The Bulmer-effect with GS

Response to selection: $R_{eq} = \frac{R_0}{\sqrt{1+k}} \approx (0.73....0.77)R_0$

Accuracy: $\rho_{eq.} = \rho_0 \frac{1}{\sqrt{1+k(1-\rho_0^2)}} \approx (0.83...0.86)\rho_0$ for $\rho_0 = 0.7$

Additive genetic variance: $\sigma^2_{A_{eq.}} = \sigma^2_{A_0}\left(1-\frac{k\,\rho_0^2}{1+k}\right) \approx (0.76-0.79)\sigma^2_{A_0}$ for $\rho_0 = 0.7$

- Conclusion
  - The Bulmer-effect reduces response to GS by ~25%
  - This is independent of accuracy
  - This is identical to Bulmer-effect for traditional BLUP-EBV (Dekkers, 1992)
  - This is more than with phenotypic selection

2. Prospects of GS when phenotyping is limiting

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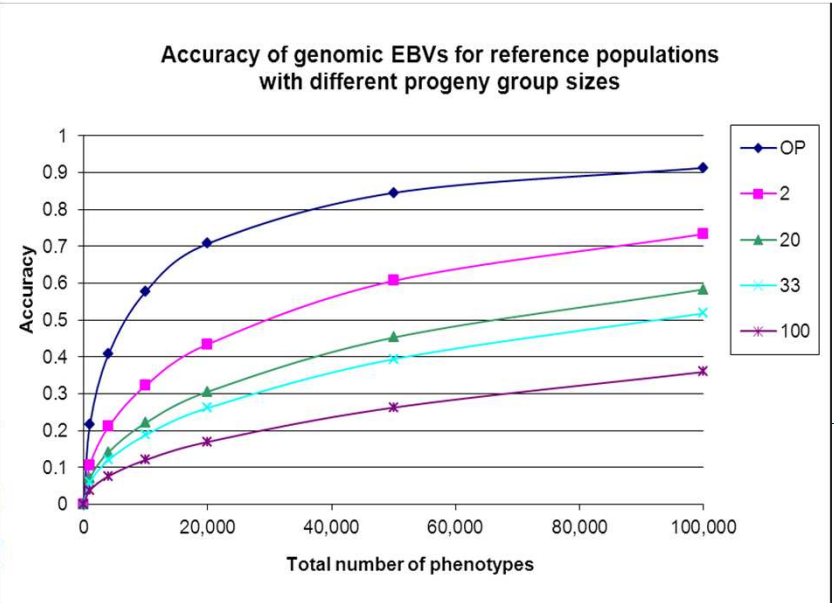
2.1 Optimal construction of the reference population with fixed # phenotypes

- Use progeny testing?
- Use own performance → phenotype and genotype same individuals?

- Accuracy GS (Daetwyler et al. 2008): $\rho = \sqrt{\frac{r^2}{r^2 + n_G / n}}$
  - r^2 = reliability of "record" in the reference population
  - n = number of individuals in the reference population
  - n_G = effective number of genetic effects to estimate

Progeny testing →
r^2 increases, but n decreases



Conclusion:
When the number of phenotypes is limiting, it is optimal to genotype and phenotype the same individuals

2. Prospects of GS when phenotyping is limiting

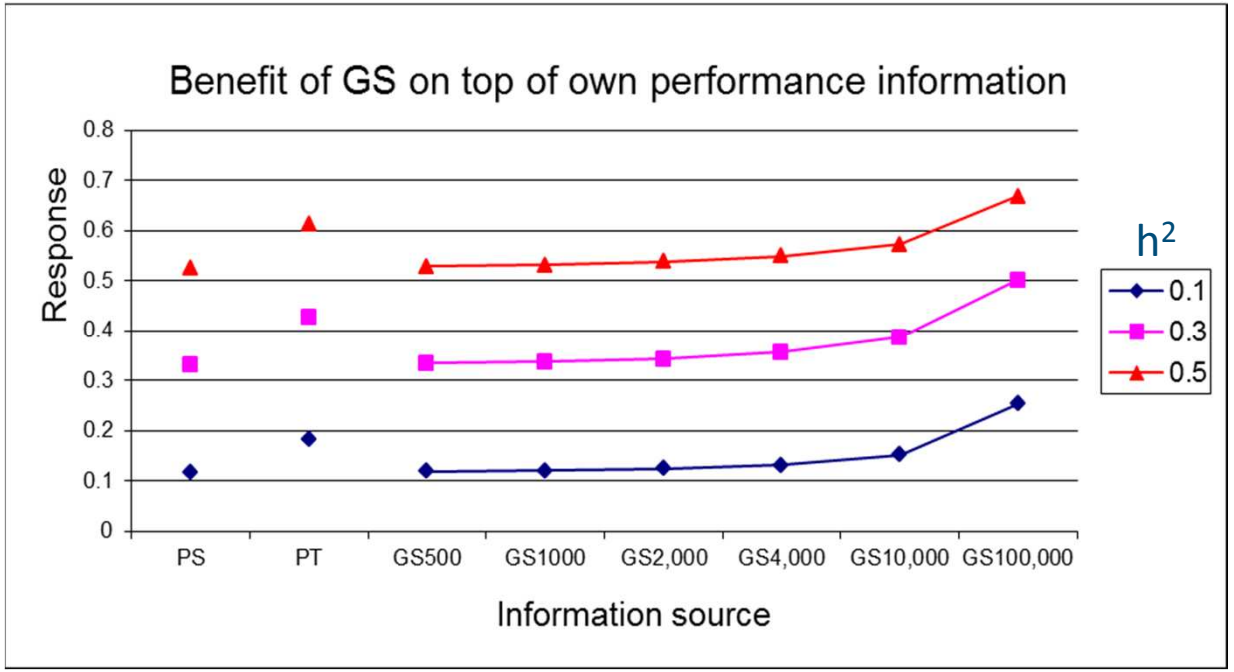
2.2 Response when reference populations are small

- Methods
  - Compare GS with traditional selection
    - Own-performance
    - Progeny testing (for traits not recordable on candidate)
  - Ref. pop. is based on own performance information
  - Deterministic simulations in SelAction
    - (Schrooten et al. 2005; Dekkers 2007)

2. Prospects of GS when phenotyping is limiting

Scenario 1: GS info available on top of own performance info

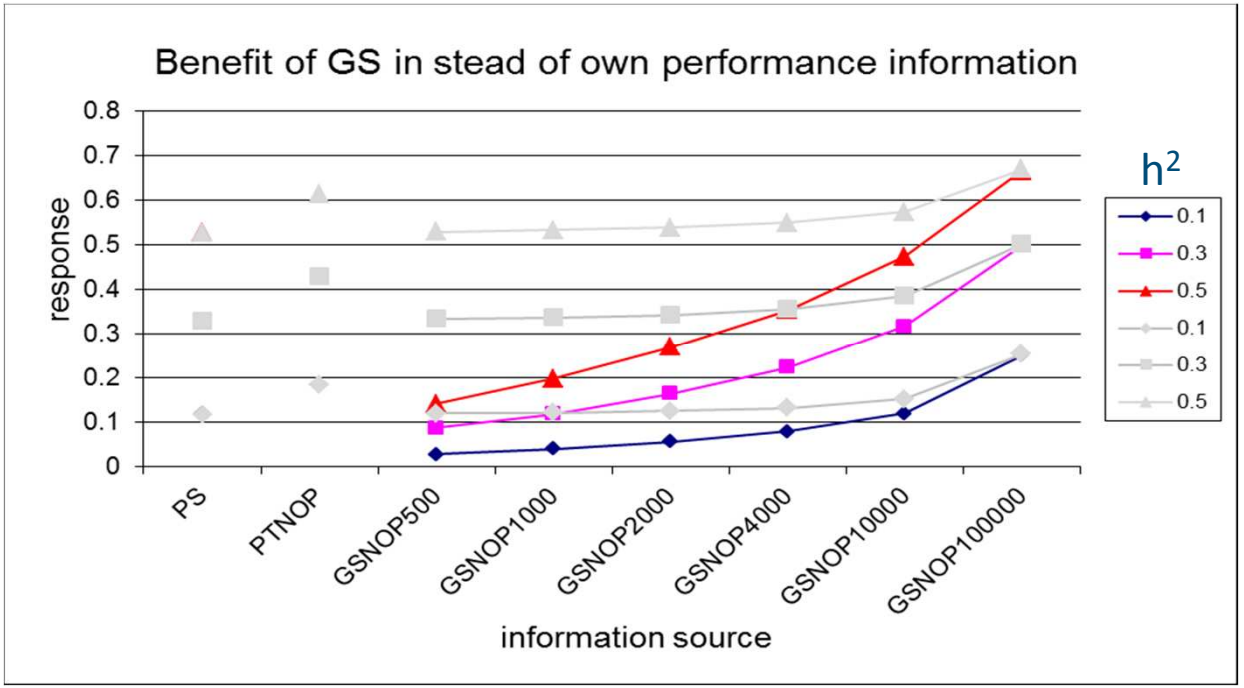
- Effect of reference population size
- No change in generation interval



Conclusion: When phenotypic info is available, GS adds little

2. Prospects of GS when phenotyping is limiting

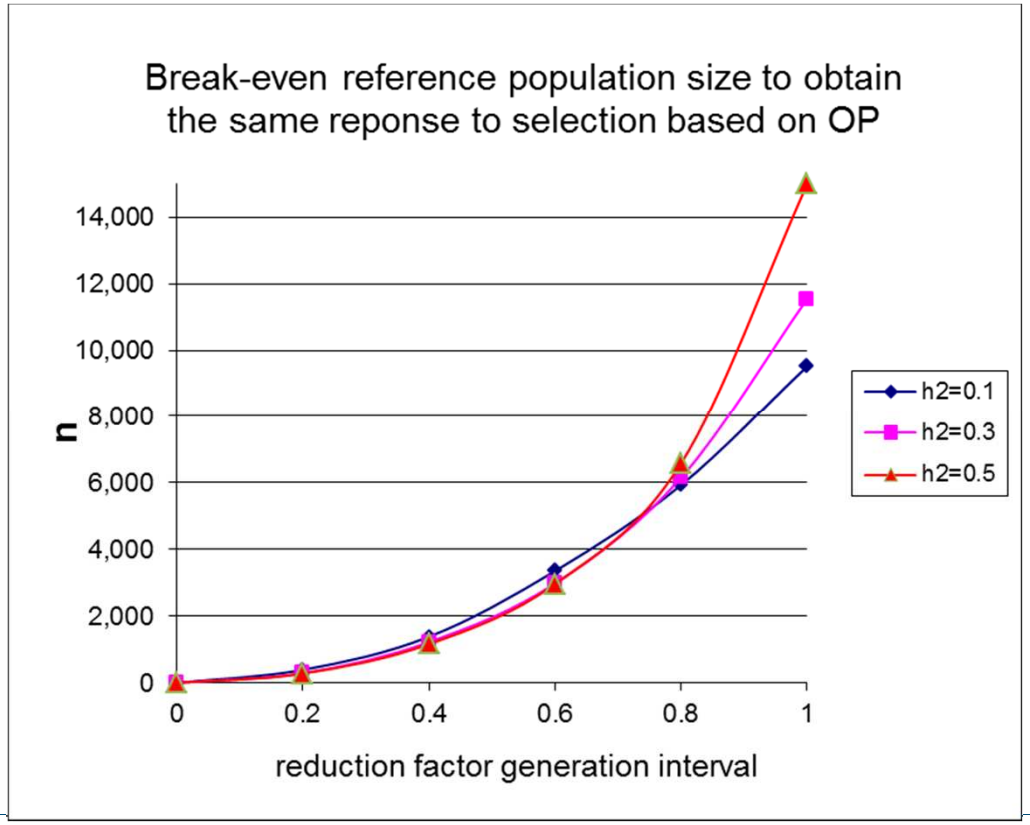
Scenario 2: GS info in stead of own performance info



2. Prospects of GS when phenotyping is limiting

Prospects when generation interval (L) can be shortened

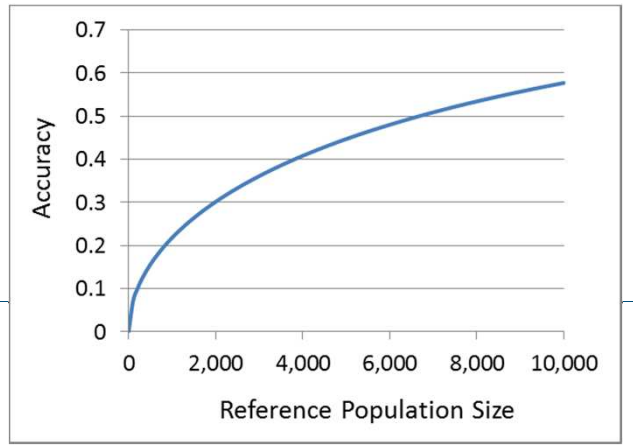
→ Break-even reference population size as function of reduction in L



- Required ref. pop. size decreases rapidly when L can be shortened.

- Same pattern with progeny testing

Originates from the non-linear relationship of ρ with n



Conclusions

- The Bulmer-effect reduces response to GS by ~25%
  - This is the same as with traditional BLUP
- When phenotyping is limiting, the same individuals should be genotyped and phenotyped in the ref. pop.
- When L cannot be reduced, large ref. pops are required to obtain same response.
- When L can be reduced, the required ref. pop. size decreases rapidly

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