Implementation of genomic selection in dairy cattle breeding schemes

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Introduction

- GEBV are available in many countries
  - GBLUP or blended GBLUP-TBLUP
  - BayesA/B/C
- Expectations high: accurate EBV of:
  - Young genotyped animals
  - Nonrecorded animals (trait nor pedigree)
    - Difficult /costly traits
  - Animals living in a different environment
  - Low heritability traits
  - More sustainable breeding scheme

AIM:

- Compare alternative designs for implementing GEBV in Norwegian Red breeding schemes

- Use stochastic simulation where accuracy of GWEBV is a result of the design
  - Deterministic: accuracy is input/ independent of design (Schaeffer et al., 2007; Kønig et al., 2009)

Methods: simulation of base population

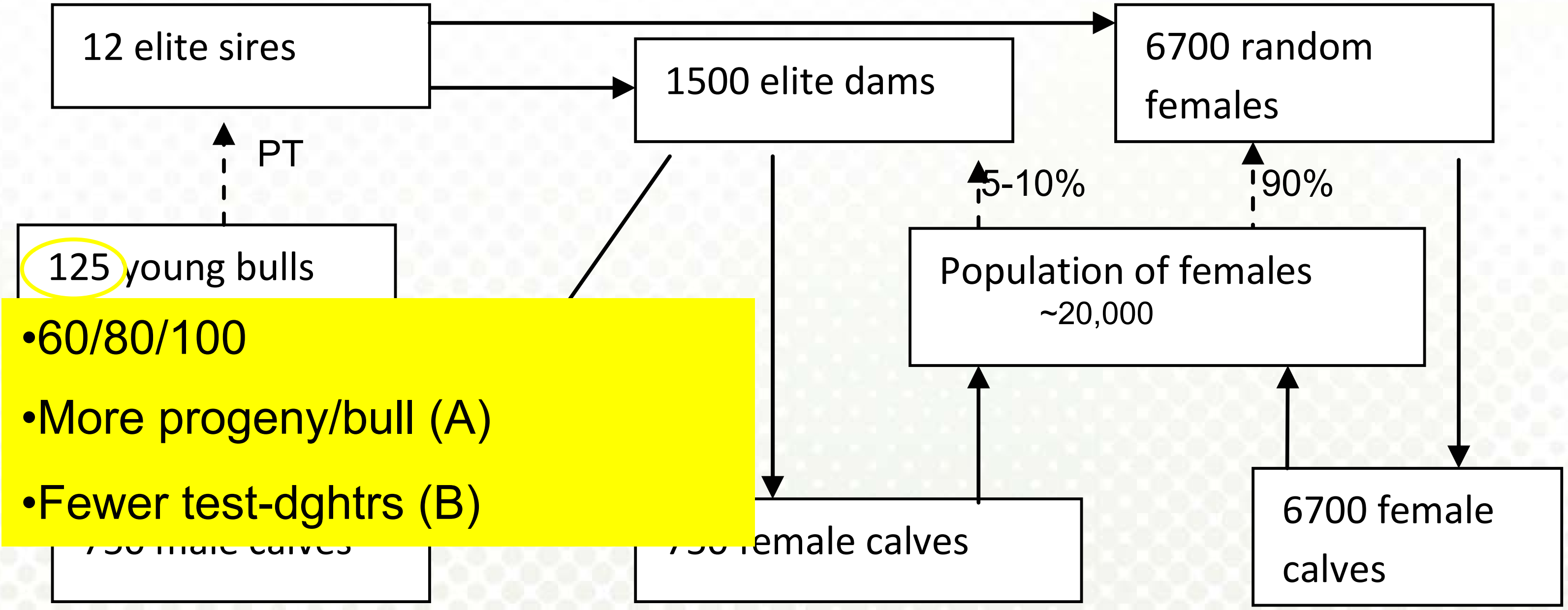
- 2,000 generations
- Ne=200 (Fisher-Wright idealised pop.)
- 30 BTAs of 1 Morgan each (10^6 bp)
- Mutation 10^{-8}/bp (infinite sites mutation mod)
- Recombination 10^{-8}/bp
- 3,000 random SNPs with MAF>.05 => QTL
  - QTL effects from reflected exponential distrib.
- 15,000 SNPs with highest MAF =>marker
  - Marker ≠ QTL

Simulation of breeding scheme

- Not possible to simulate entire Norwegian Red pop.
- Reduced size of simulated population
  - Number of selected males the same (in SD and SS)
  - Selected fractions identical (and selection intensities)
  - Selection steps for other traits: omitted
  - Non-GS larger scheme: similar G and F
- Test-daughters were not (individually) simulated
  - Reduces population size

$$DYD_i = \frac{1}{2}TBV_i + \sqrt{\frac{\frac{3}{4}V_g + V_e}{260}} * r_i$$

Preselection of young bulls (PS)

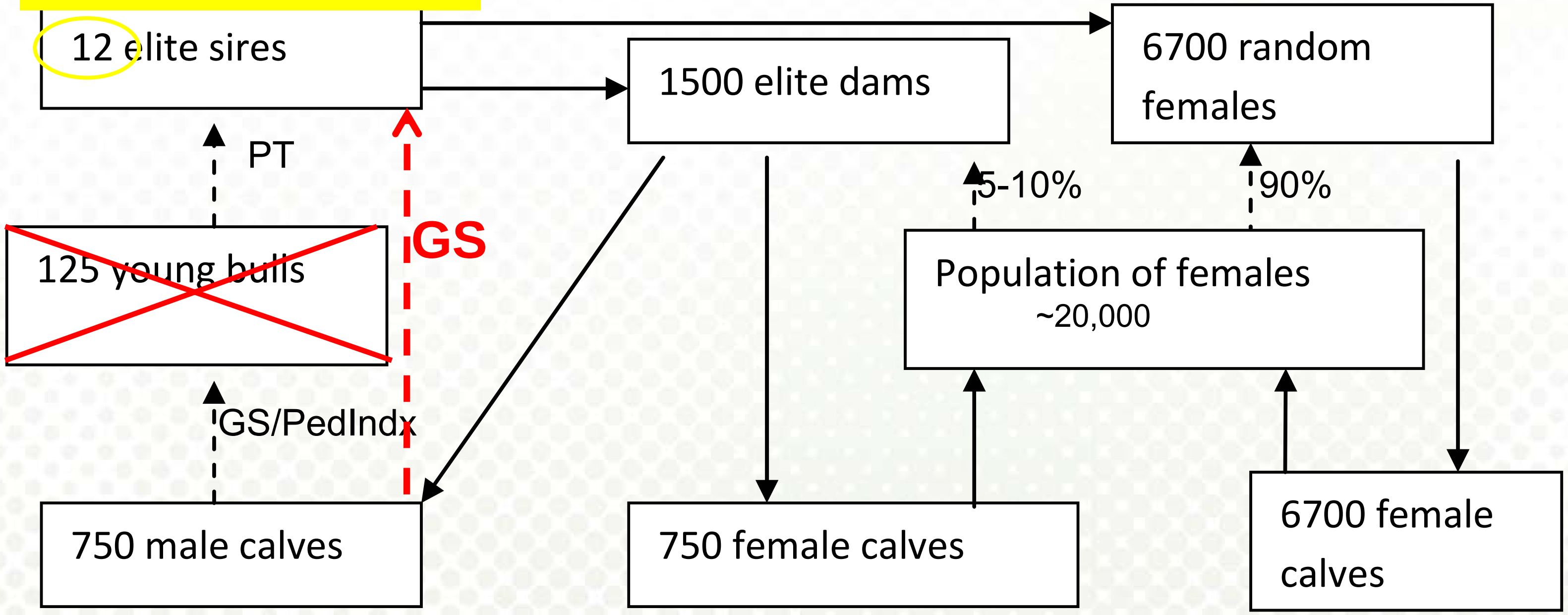


- 60/80/100
- More progeny/bull (A)
- Fewer test-dghtrs (B)

-----> Selection (TBLUP, unless stated otherwise)

Full genomic selection scheme (GS)

- 20 / 30 / 40



-----> Selection (TBLUP, unless stated otherwise)

Traits & GEBV

$$TBV_i = \sum_{j=1}^{3000} x_{ij1} g_{j1} + x_{ij2} g_{j2}$$

- $Y_i = TBV_i + e_i$
- $e_i \sim N(0, V_e)$
- V_e is adjusted so that h^2 is .01, ***.15*** or .30
- Trait recording: at 2-yr-old females (gen.interv. = 3yr)
- Progeny test: 5-yr-old sires (gen.interv. = 6yr)
- GS: only applied to young-bulls;
  - GBLUP (BLUP of marker effects; no blending):

$$y_i = \mu + \sum_{j=1}^{n} x_{ij} a_j + e_i \qquad GEBV_i = \sum_{j=1}^{n} x_{ij} a_j$$

Simulation parameters:

- 100 replicates
- Start population:
  - no genetic trend
  - Training set of 3000 progeny tested bulls
- Results for yr 13-19
  - Accuracy : yr 19

Results: preselection schemes

	ΔF	ΔG	Acc
Conv.	1	1	xx
PS_125	1.13	1.29	0.7
PS_60A	1.15	1.29	0.68
PS_60B	1.06	1.27	0.66

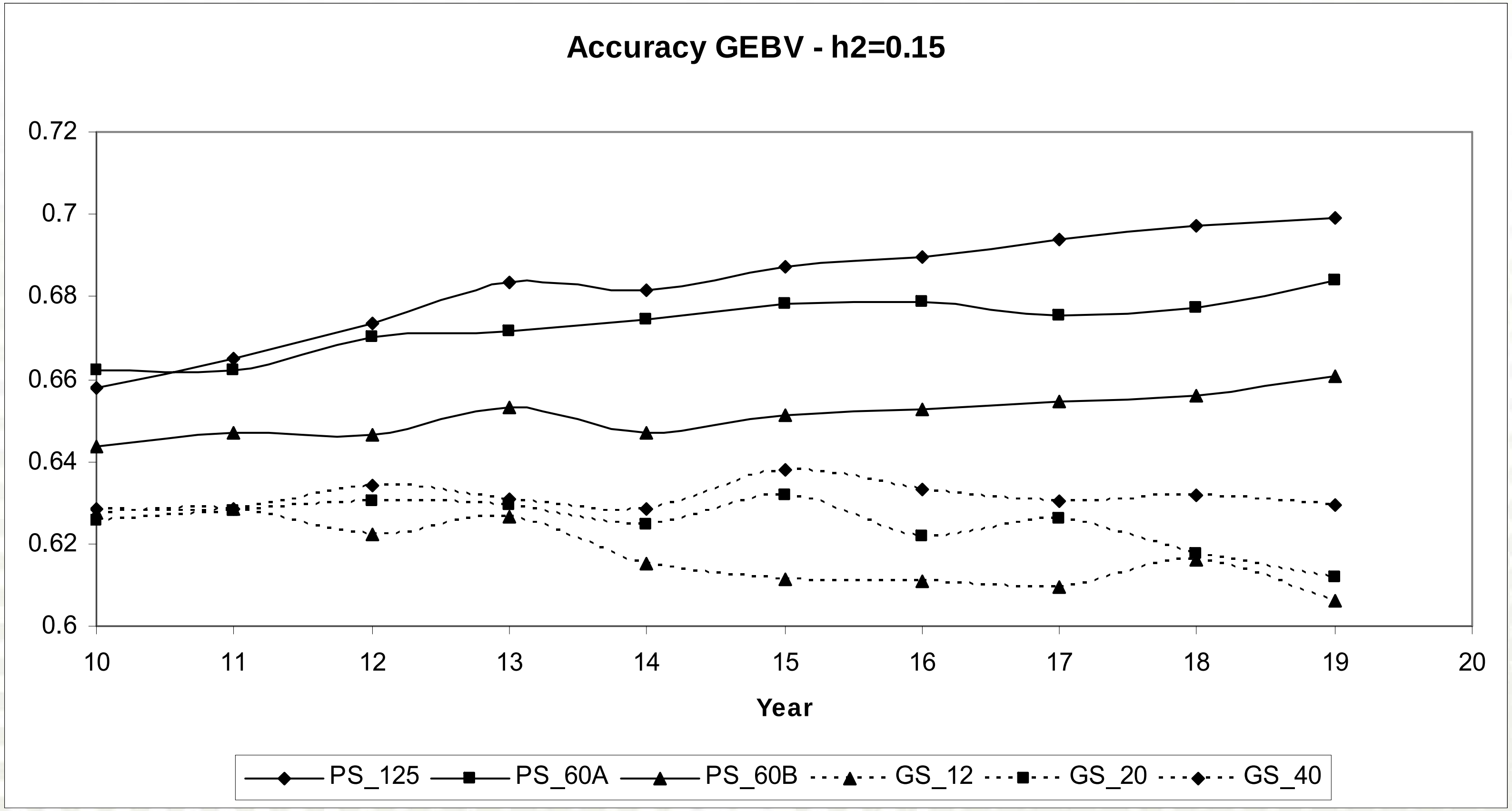
Full GS schemes

	ΔF	ΔG	Acc
Conv.	1	1	xx
GS_12	1.65	1.52	0.61
GS_30	0.8	1.42	0.63
GS_40	0.61	1.37	0.63

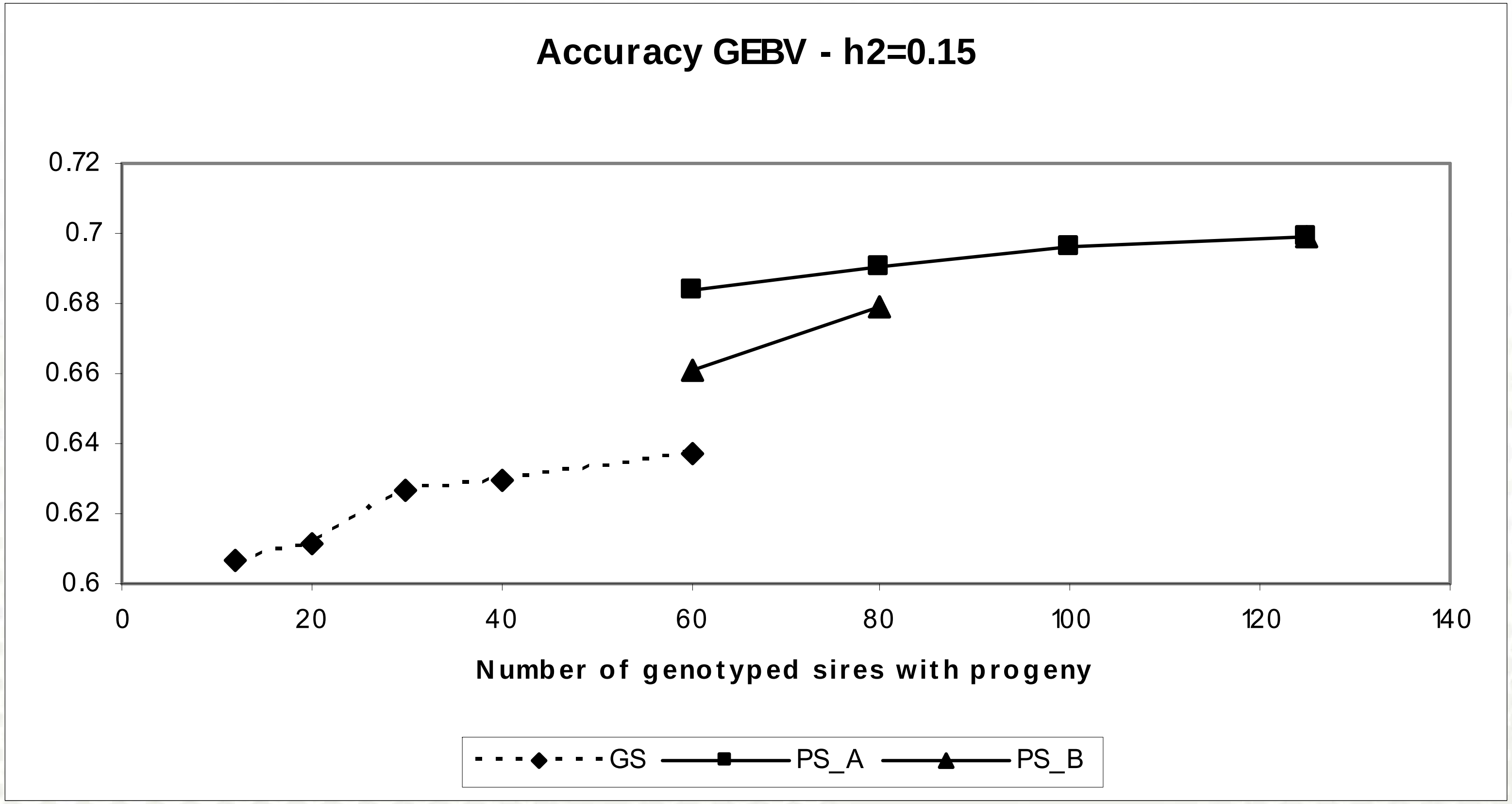
Effect of h^2 on G

h^2	0.01	0.05	0.3
Conv.	1	1	xx
PS_125	1.32	1.31	1.29
PS_60A	1.39	1.3	1.27
GS_12	1.87	1.59	1.5
GS_40	1.59	1.42	1.36

Trend in accuracy



Accuracy of GEBV



- GS less accur. at same no. of training bulls
- In GS training bulls are from generation t-2

GS versus PS

- GS highest   G (+18%)
- GS highest   F (+46%)
  - Short generation interval
  - Alleviated by selecting 30 elite sires:

    F : -20% and   G =+10%
- GS is cheapest (no progeny testing)
- BUT:
  - GS is furthest from conventional scheme (risk)
  - Has lowest accuracy (farmer acceptance)

Low heritability traits

- Schemes rank the same
- GS gives relative more extra G
- More sustainable breeding scheme
  - Functional traits more easily improved by GS
  - BUT: still need large scale recording

Including females

- For selection:
  - – Reduce generation interval in DS path
  - – Avoids preferential treatment problem
- For training:
  - – Need huge numbers
    - h^2=.15 => 6 times as many
- Work in progress (Noirin McHugh)
  - – Irish Dairy cattle

Other traits : not large scale recorded

- Idea for difficult trait:
  - – Perform experiment (~2000 records)
  - – Estimate SNP effects
  - – Select for SNP effects for ever after
  - – Accuracy reduces markedly over time
    - (Muir, 2007; Habier etal, 2007; Sonesson et al., 2009)
    - Need continuous scheme for updating SNP effects
    - Not when using genome sequence (Meuwissen&Goddard,2010)

Conclusions:

- Full GS scheme is best
  - Highest G and F
  - Can be tuned to have low F
  - Cheapest
  - BUT: most risky
- Pre-selection scheme:
  - Close to current scheme
  - Can safe some costs by reducing progeny test
    - Beneficial for farmer
  - High accuracy

Conclusions (2)

- Increased F
  - shorted generation interval in GS scheme
  - also in PS scheme
- Accuracy remained high when h^2 decreased
  - Unless h^2 became very low
  - Lower in GS than PS
    - One generation more between training and candidates
    - Kept on decreasing in scheme with few elite sires

Conclusions (3)

- More sustainable breeding schemes
  - Low h^2 traits easier to improve
  - However in practice r^2 of low h^2 trait disappointing (Luan et al., 2010)
  - Still need large scale recording
    - Re-train SNP effects