



THE UNIVERSITY OF GEORGIA

COLLEGE OF AGRICULTURAL & ENVIRONMENTAL SCIENCES



Choices in genomic evaluation for small populations

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Background

- Small Holstein populations
 - Croatia 40k
 - Macedonia 35K
 - Slovenia 35K
- International trade of genetic material
 - Semen & embryos
 - Pregnant heifers
- Incomplete relationship (lack of deep pedigree)
- National genomic breeding programs - small reference population
- Selection of young animals?
- Progeny testing?

Background

- Choices for small populations are:
 - If data is available include proven bulls/dam into evaluation
 - Pedigree;
 - Phenotypes;
 - Genomic.
 - Become part of other breeding program
 - Participate into consortia.

Background

- Simulation study
- Test different sources of information from connected small (P_S) and large population (P_L)
- 4 cases

Material

- Large population

- 2K ♂ and 20K ♀ 20 generations
- $h^2 = 0.3$
- Replacement sire=0.9; dam=0.3
- Selection criterion - high EBV,
- Genotypes for generations 14-20th

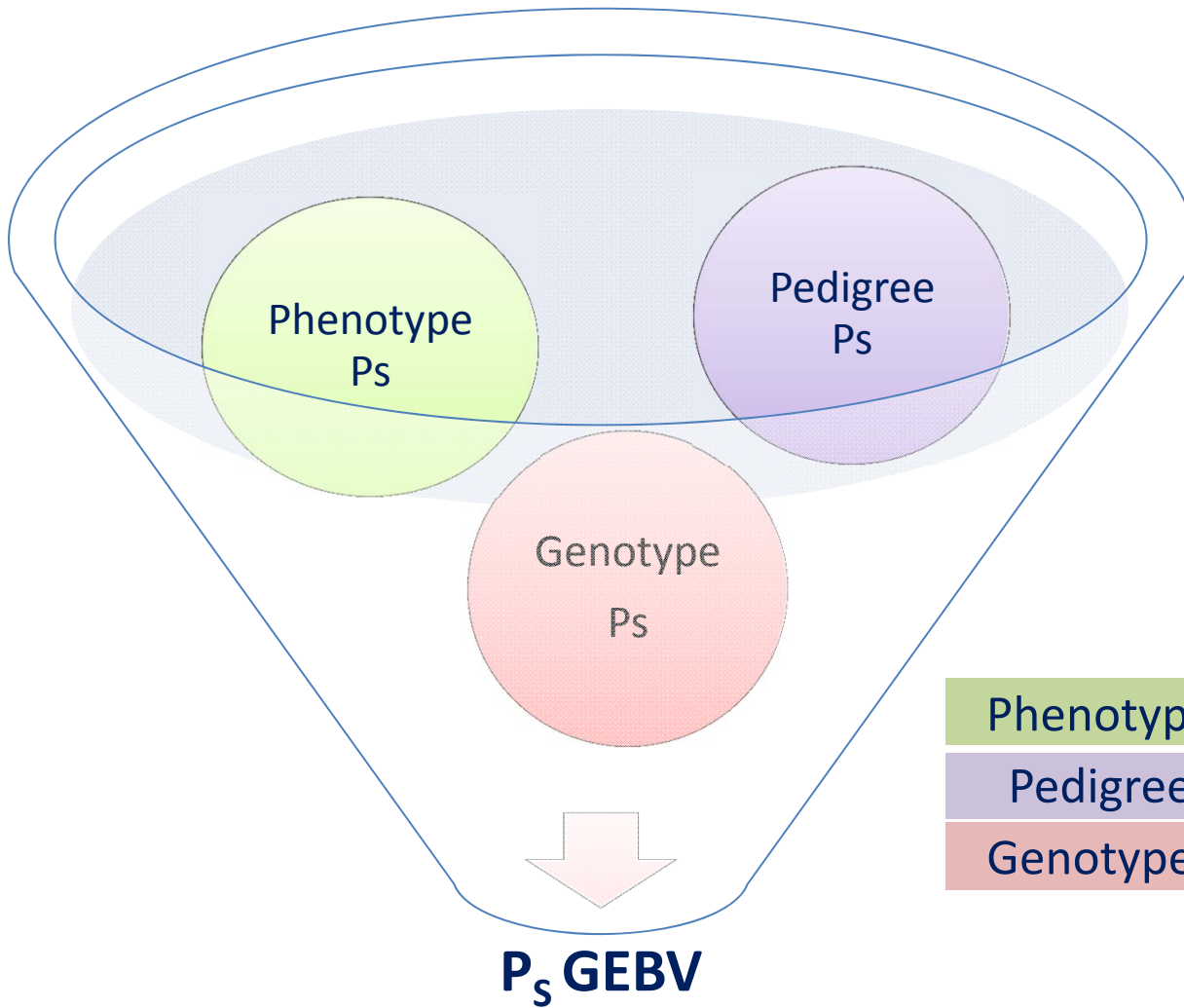
- Small population

- 150 ♂ x 2000 ♀ (P_L 18 g)
- 2nd gen + 100 ♂ (P_L 19 g)
- $h^2 = 0.3$
- Replacement sire=0.5; dam=0.3
- Selection criterion - phenotype,
- Genotypes for 1-3 generations (6000 animals total)

Material

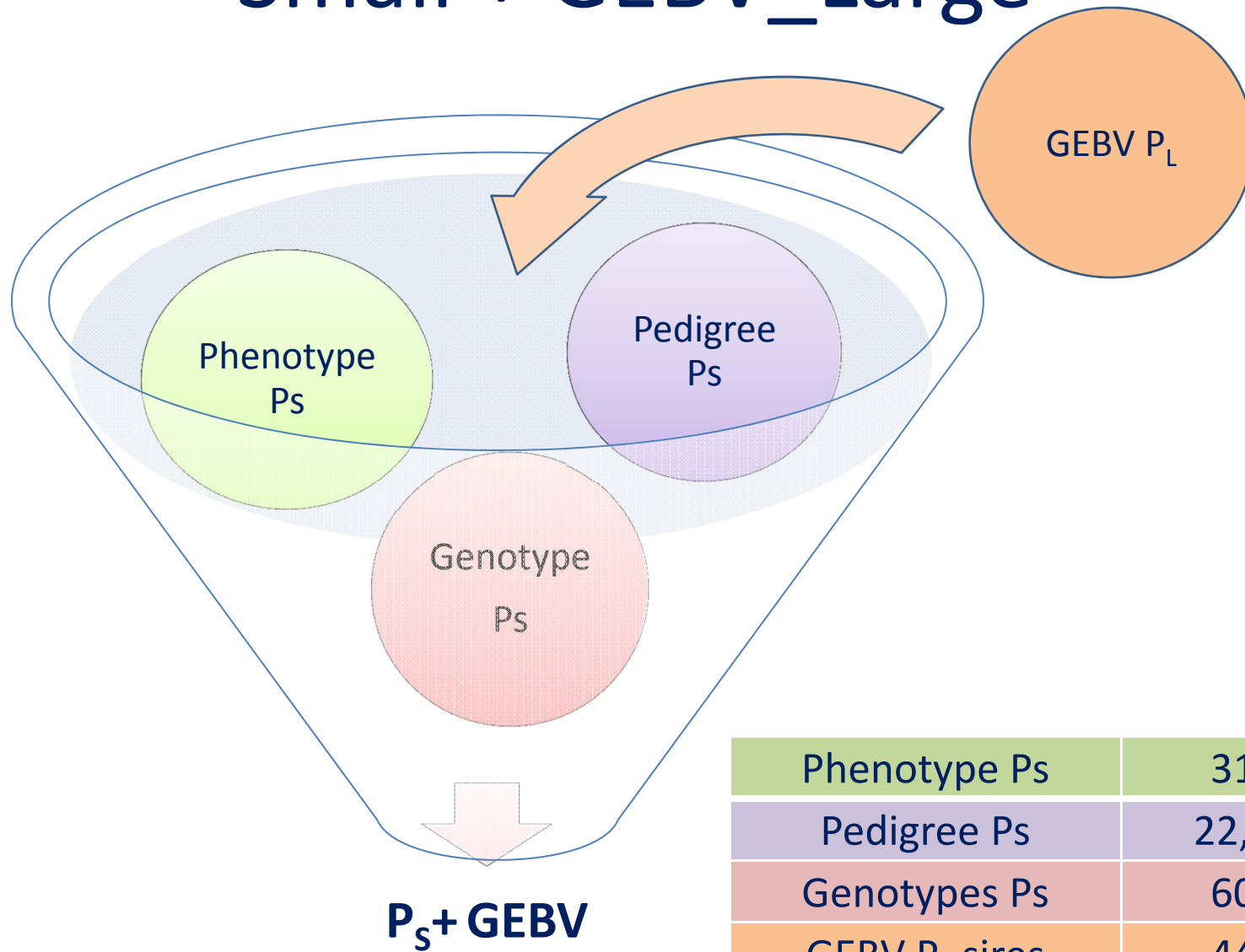
- Genomic
 - 45000 biallelic SNP
 - 29 chromosomes
 - 450 QTLs
- Average of 5 replicates

Small



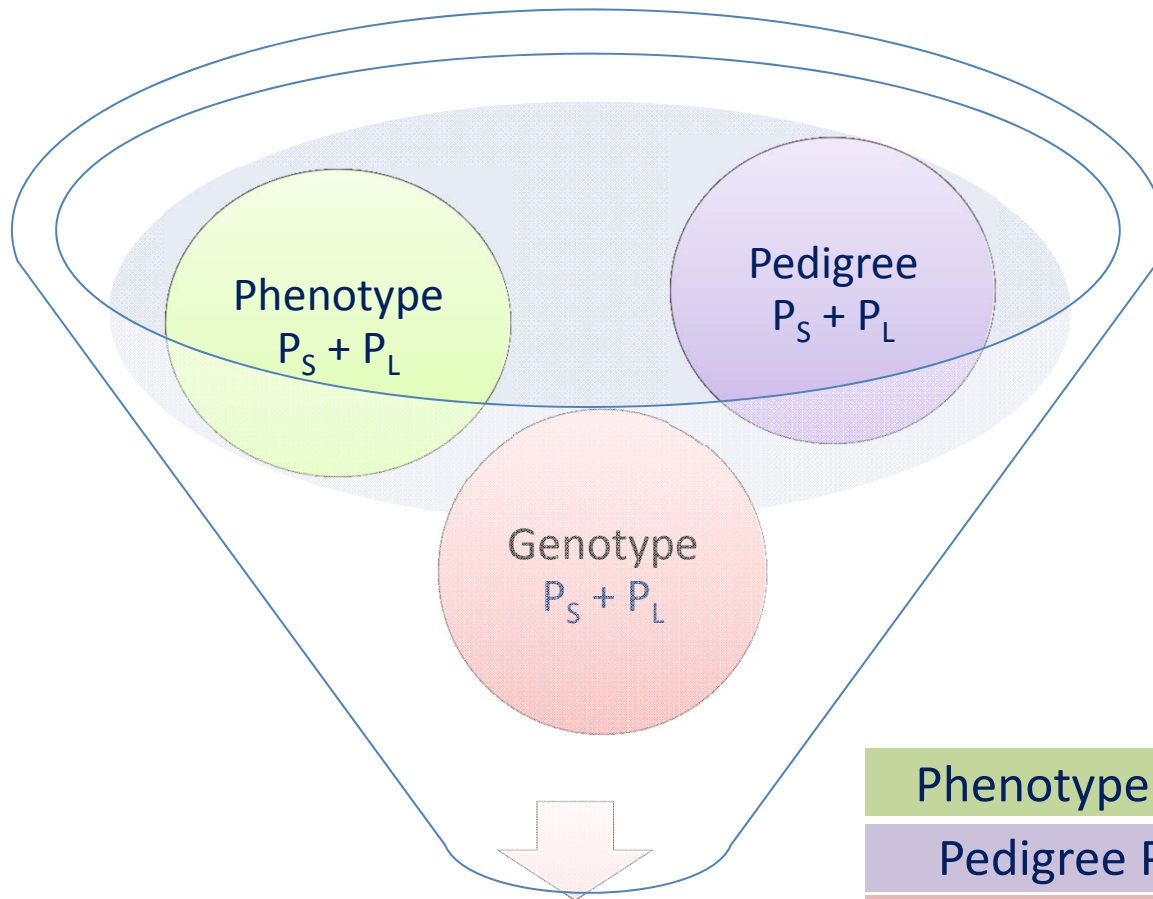
Phenotype Ps	3166
Pedigree Ps	22,885
Genotypes Ps	6000

Small + GEBV_Large



Phenotype P _s	3166
Pedigree P _s	22,885
Genotypes P _s	6000
GEBV P _L sires	4475

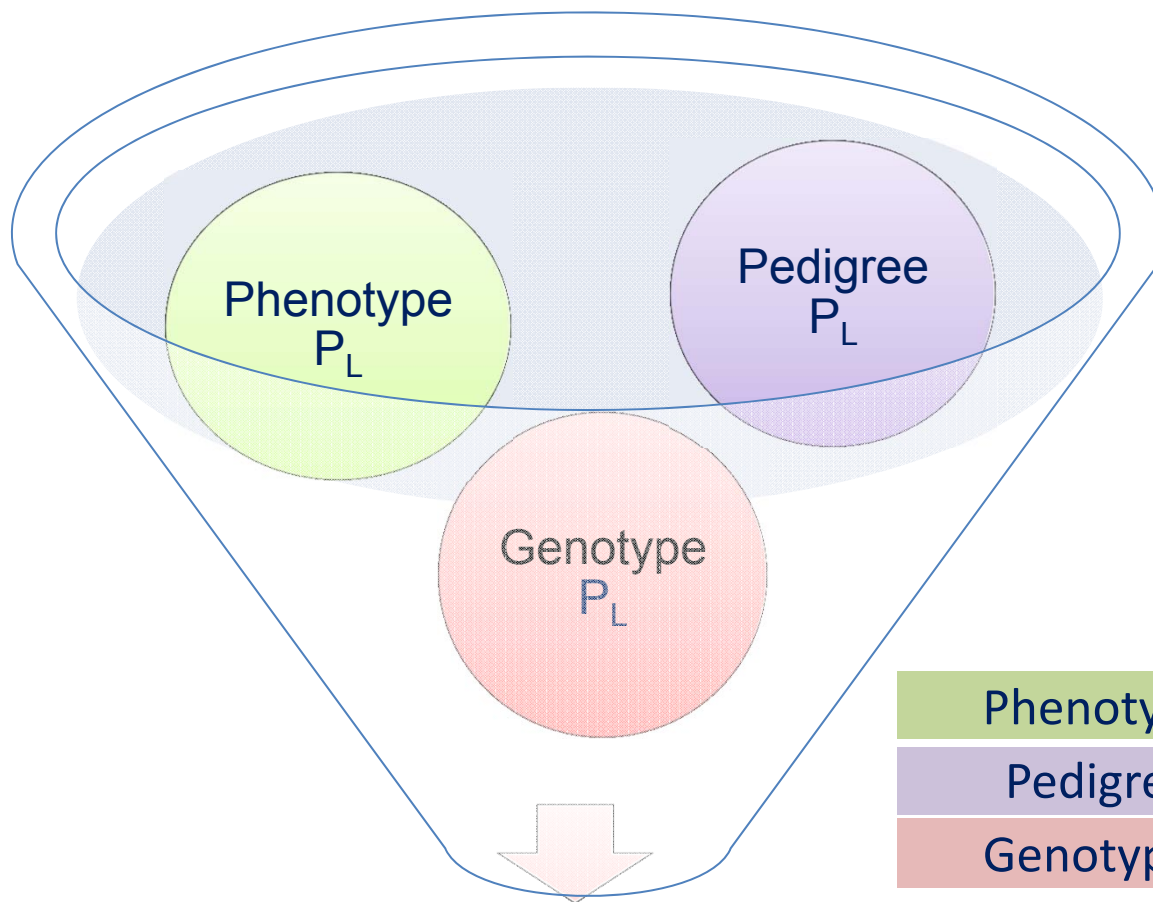
Small + Large



$P_S P_L$ GEBV

Phenotype $P_S + P_L$	224746
Pedigree $P_S + P_L$	425684
Genotypes $P_S + P_L$	59558

SNP_Large



Phenotype P_L	221,580
Pedigree P_L	402,829
Genotypes P_L	53,558

$$\text{SNP effect} * \text{SNP}(P_S) = P_{L\text{-SNP}} \text{ GEBV}$$

Methods

- BLUPF90 family (Miształ et al., 2015)
- Genetic connection between PL and PS (r_g) – REML
- Small and Small+Large, Genomic EBV - ssGBLUP
- Small+GEBV_Large - ssGBLUP with external information
- SNP_Large - ssGBLUP extended to calculate SNP effects
- Model:

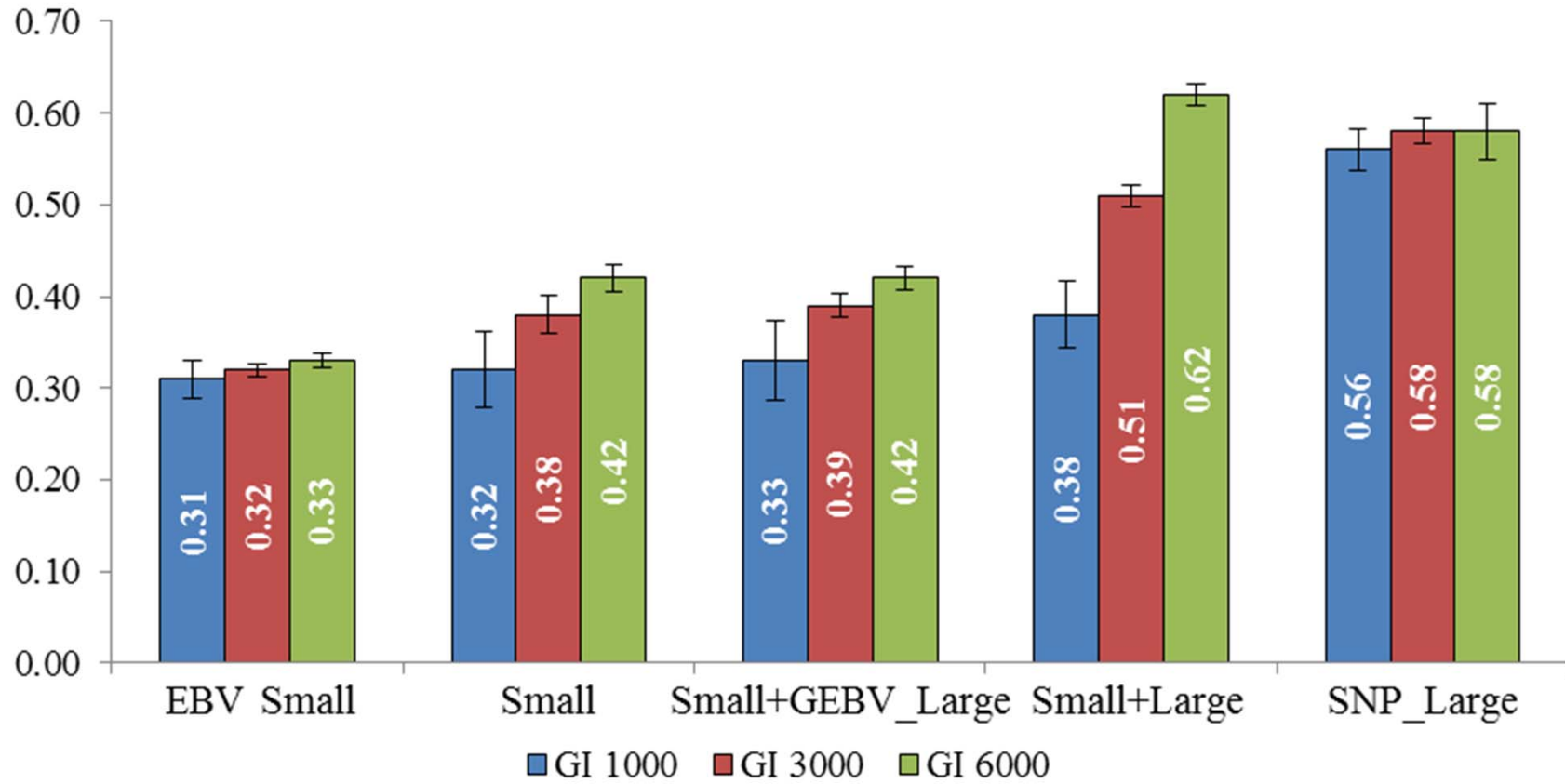
$$\mathbf{y} = \mathbf{1}\mu + \mathbf{Z}\mathbf{a} + \mathbf{e}$$

- \mathbf{Z} incidence matrix for the random effect in \mathbf{a} .
- $\mathbf{a} \sim N(0, \mathbf{H}\sigma_a^2)$; σ_a^2 \mathbf{H} matrix that combines pedigree and genomic relationships

Validation

- Correlation GEBV-TGEBV
- Validate
 - 1000 genotypes of P_S (334 in 3rd generation)
 - 3000 genotypes of P_S (1000 in 3rd generation)
 - 6000 genotypes of P_S (2000 in 3rd generation)
- $r_g = 0.84 \pm 0.019 (P_L - P_S)$

Results



Achievements

- Small population stand alone
 - Moderate accuracies
 - Need to increase daughter groups per sire in P_s
- Small population + external GEBV of sires
 - slightly improve the accuracy
 - add complexity to the evaluation

Achievements

- Join evaluation of P_S and P_L
The highest accuracies
- SNP effects for P_L to assess GEBV
Considerably high accuracies
Constant over replicates
No need pedigree and performance of P_S
Constrain - prediction of GEBV for animals with SNPs
all candidates need to be genotyped

Practical implementation

- Small population
 - share genomic in consortia
 - young animals - DGV
 - continue breeding program with GI (verify realization of GEBV)
 - Check genetic gain
- Large population
 - identifying animals with high GEBV and low inbreeding

Thank you!