

Changes in allele frequency

with genomic, BLUP and phenotypic selection
at varying number of QTL and heritability

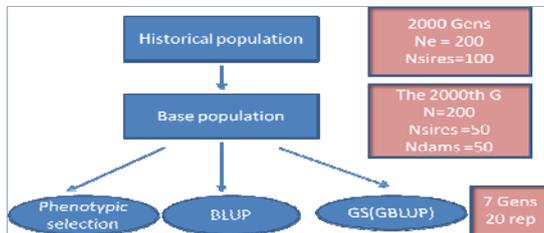
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Background and aim

- Increases in the allele frequency of favourable alleles in populations drive the genetic improvement
- Use of SNP chips and genomic selection may optimize long-term genetic response
- We compare the effect of genomic selection (GBLUP) with phenotypic selection and BLUP in terms of allele frequency changes by stochastic simulation

Simulation study

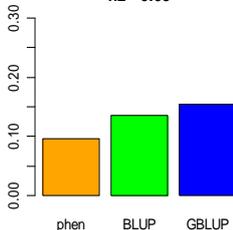


- The simulated genomes consisted of 4 chromosomes each with a size of 1M
- The number of loci is 10,000 for each chromosome - after reaching the mutation-drift equilibrium 2237 of them were chosen as markers
- We compared the realized allele frequency changes under different heritabilities (0.05-0.5) and different number of QTL (10-500)

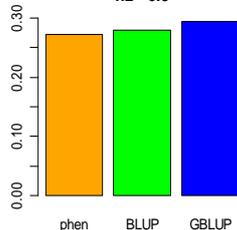
Main findings

- Irrespective of the number of QTL, GBLUP changes allele frequencies of QTL faster
- The relative effect of GBLUP on allele frequencies was larger at lower heritabilities and fewer QTL
- GBLUP results in faster changes in allele frequencies at linked markers.
- GBLUP leads to larger inbreeding at linked loci
- GBLUP results in a signature of selection with faster changes in allele frequencies both at QTL and linked markers → higher response to selection.

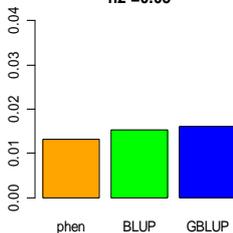
change in frequency of 10 QTL
 $h^2 = 0.05$



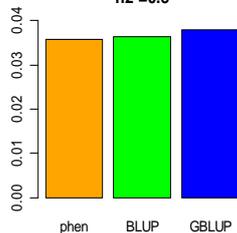
change in frequency of 10 QTL
 $h^2 = 0.5$



change in frequency of 500 QTL
 $h^2 = 0.05$



change in frequency of 500 QTL
 $h^2 = 0.5$



The average of marker allele frequency changes
under intermediate heritability

