

Decay of accuracy of genomic predictions over time in broilers

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Introduction

- Accuracy of predictions is an important component of the selection response
- Accuracy is a function of the genetic variance captured by markers, accuracy of estimation of marker effects, amount and distribution of data available, heritability, and statistical method used

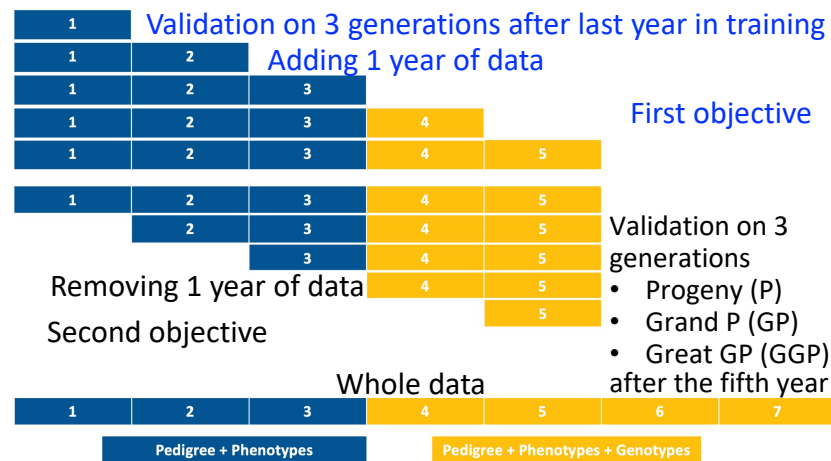
Objectives

- To investigate trends for prediction accuracies over time in a population of accumulated data
- To test if data from distant generations are useful to maintain prediction accuracies in selection candidates

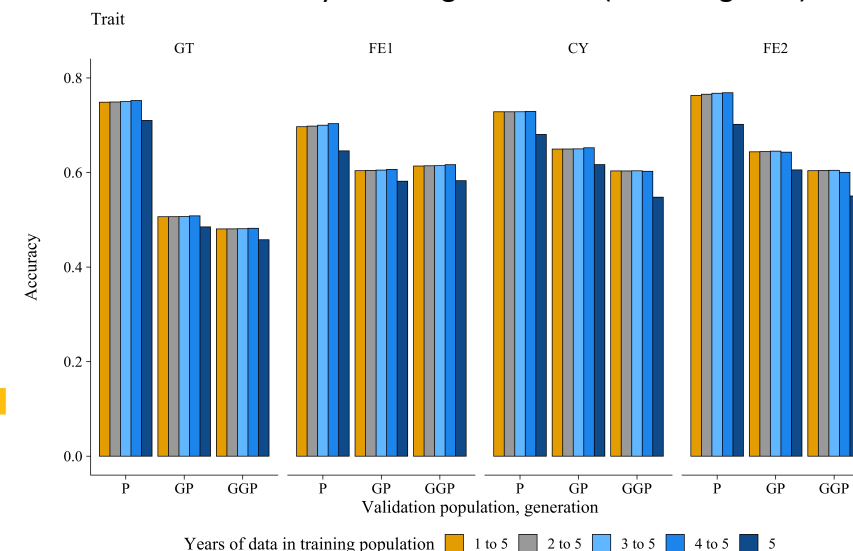
Materials and methods

- Phenotypes
 - 820K for a growth trait (GT)
 - 200K for 2 feed efficiency traits (FE1 and FE2)
 - 42K for a carcass yield trait (CY)
 - Pedigree
 - 1.2M animals (7 years)
 - Genotypes
 - 150K animals (last 4 years of data)
- 4-trait animal model using APY with 5,173 core animals
Linear Regression method for validation

$$Accuracy = \frac{cov(\hat{u}_w, \hat{u}_p)}{(1 - \bar{F})\sigma_a^2}$$

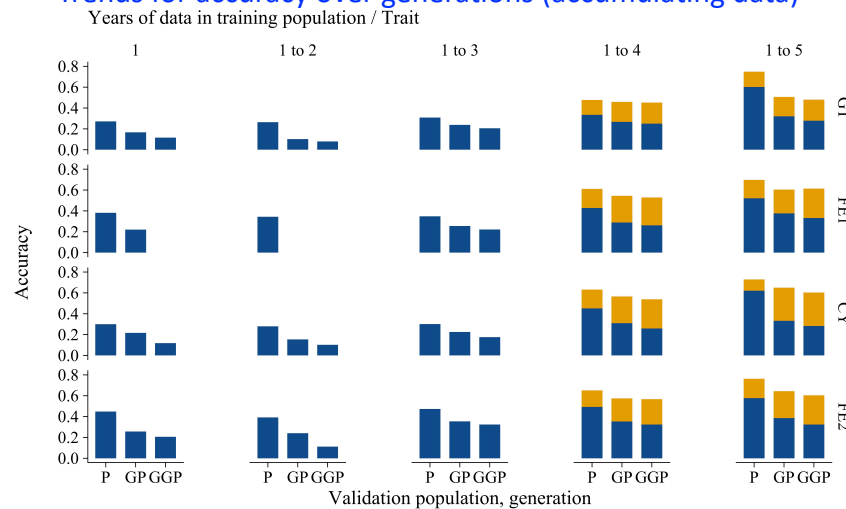


Trends for accuracy – last 3 generations (removing data)



Results

Trends for accuracy over generations (accumulating data)



Source of information additional to pedigree: Genotypes (yellow), Phenotypes (blue)

Conclusions

- Accuracy was nearly stable adding up to 3 years of data (no genotypes)
- Inclusion of genotypes in addition to pedigree and phenotypes increased accuracy 54% for GT, 76% for FE1, 110% for CY, and 38% for FE2
- On average, 74% of the increase was due to genomics
- Persistence of predictions was poor under BLUP, much better with ssGBLUP
- Two most recent years of data produced persistent accuracies of GEBV for selection candidates

