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Genomic predictive ability for growth, carcass and temperament traits in Nelore cattle

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The Team

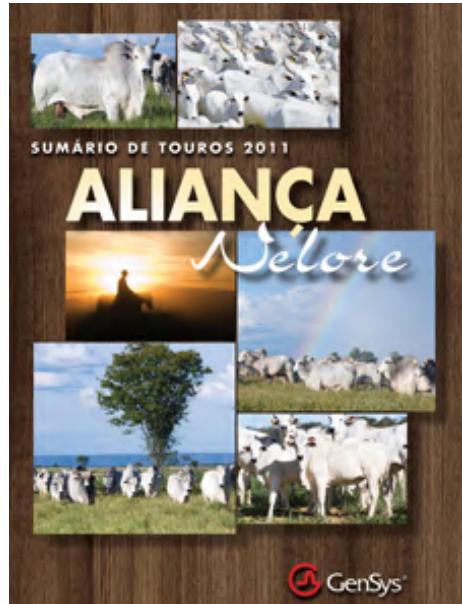


Zebu Genomic Consortium

The Breed



The Samples

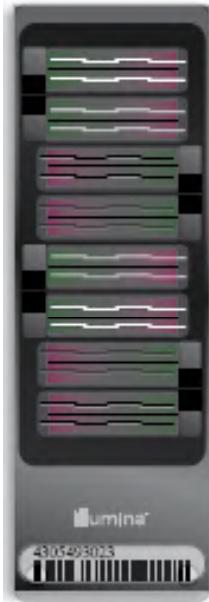


685 Nelore bulls (after QC)

Average accuracy: **0.81** to **0.88**

The SNPs

777,962 total SNPs

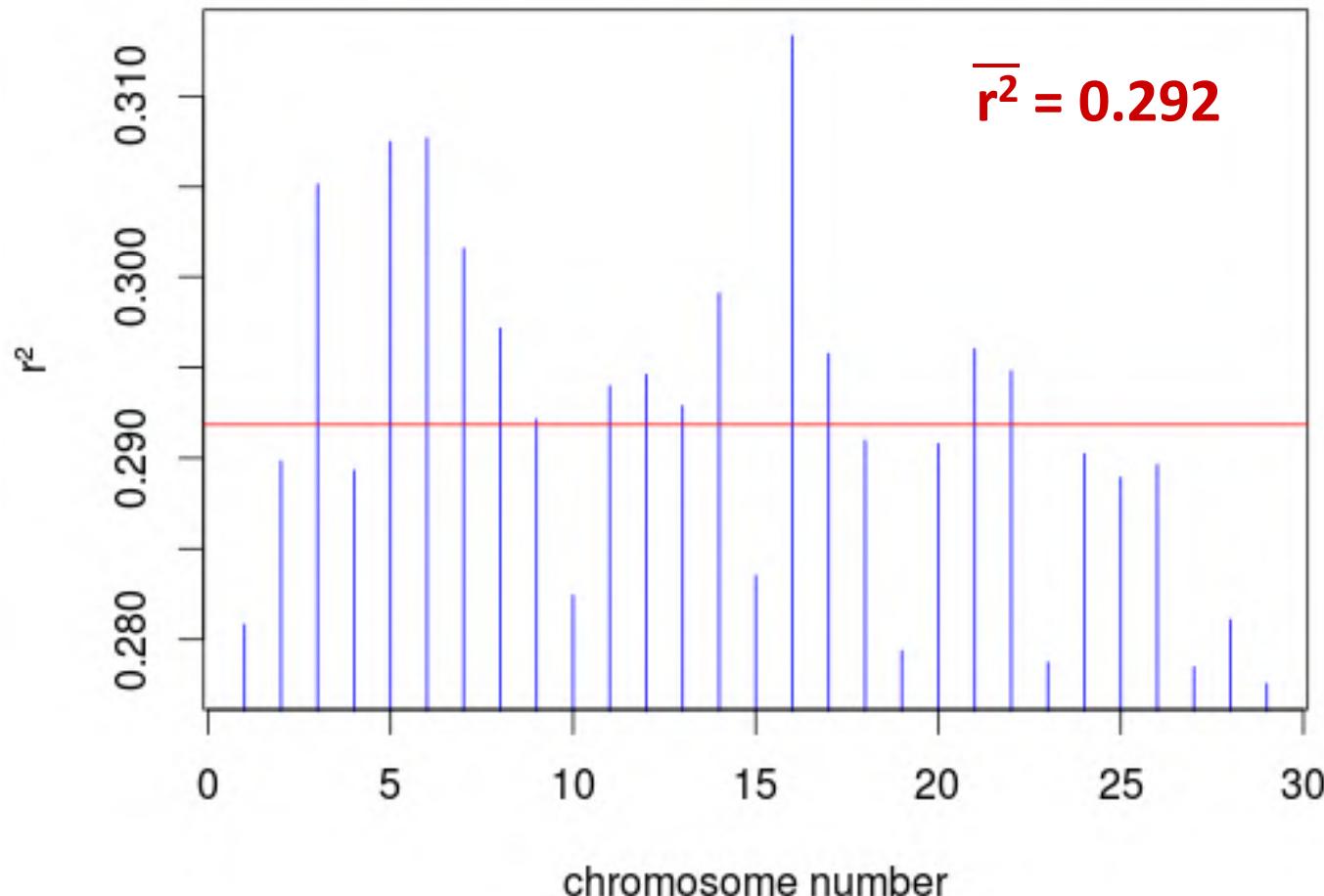


- 42,669 non-autosomal
- 54 same position
- 174,532 MAF only
- 1,539 HWE only
- 98,472 SNP call rate only
- 1,577 both MAF and HWE
- 15,058 both MAF and call rate
- 12,810 both call rate and HWE
- 1,561 MAF, call rate and HWE
- 109,452 $r^2 > 0.995$

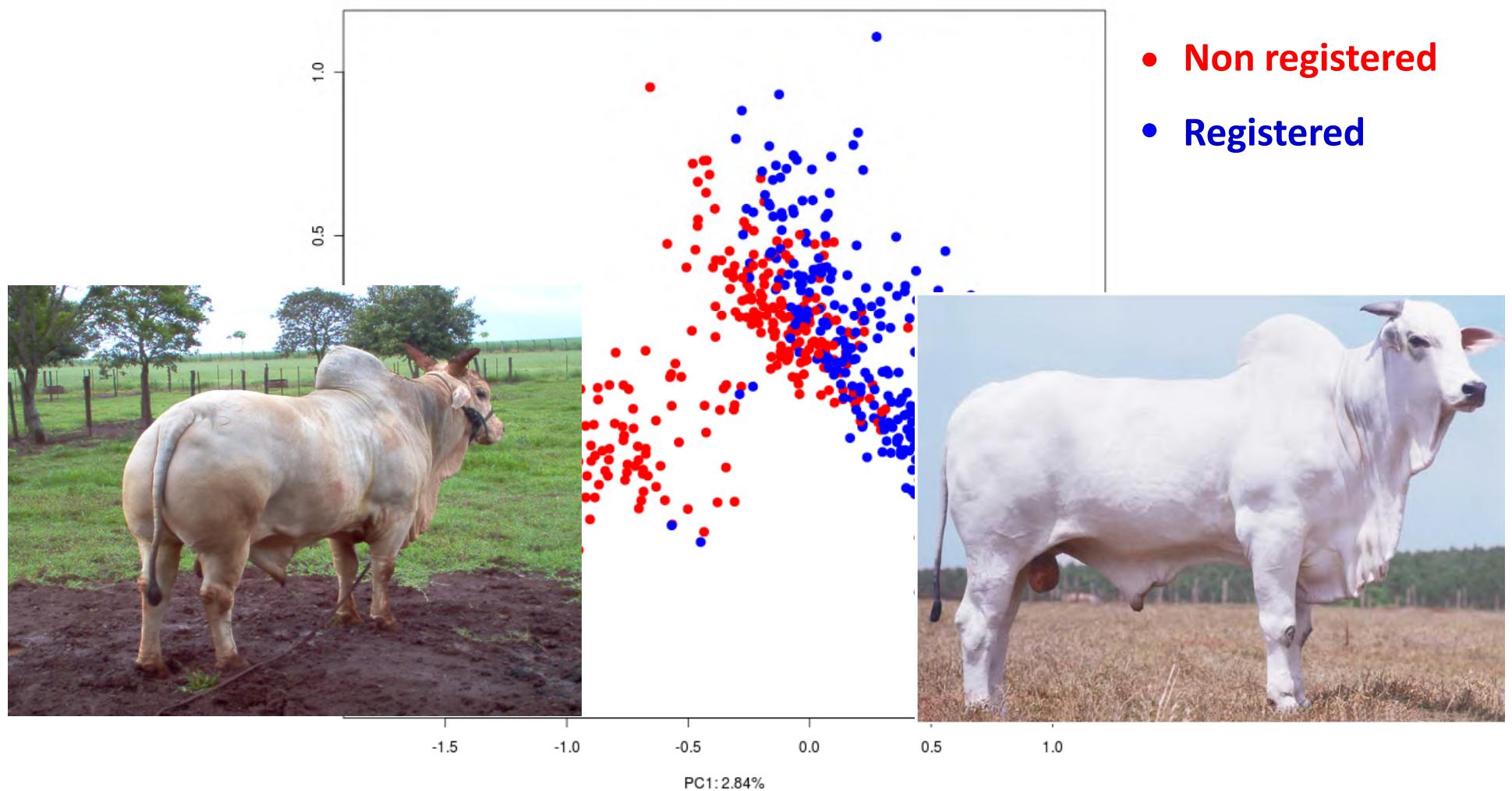
320,238 SNPs after QC

Linkage Disequilibrium

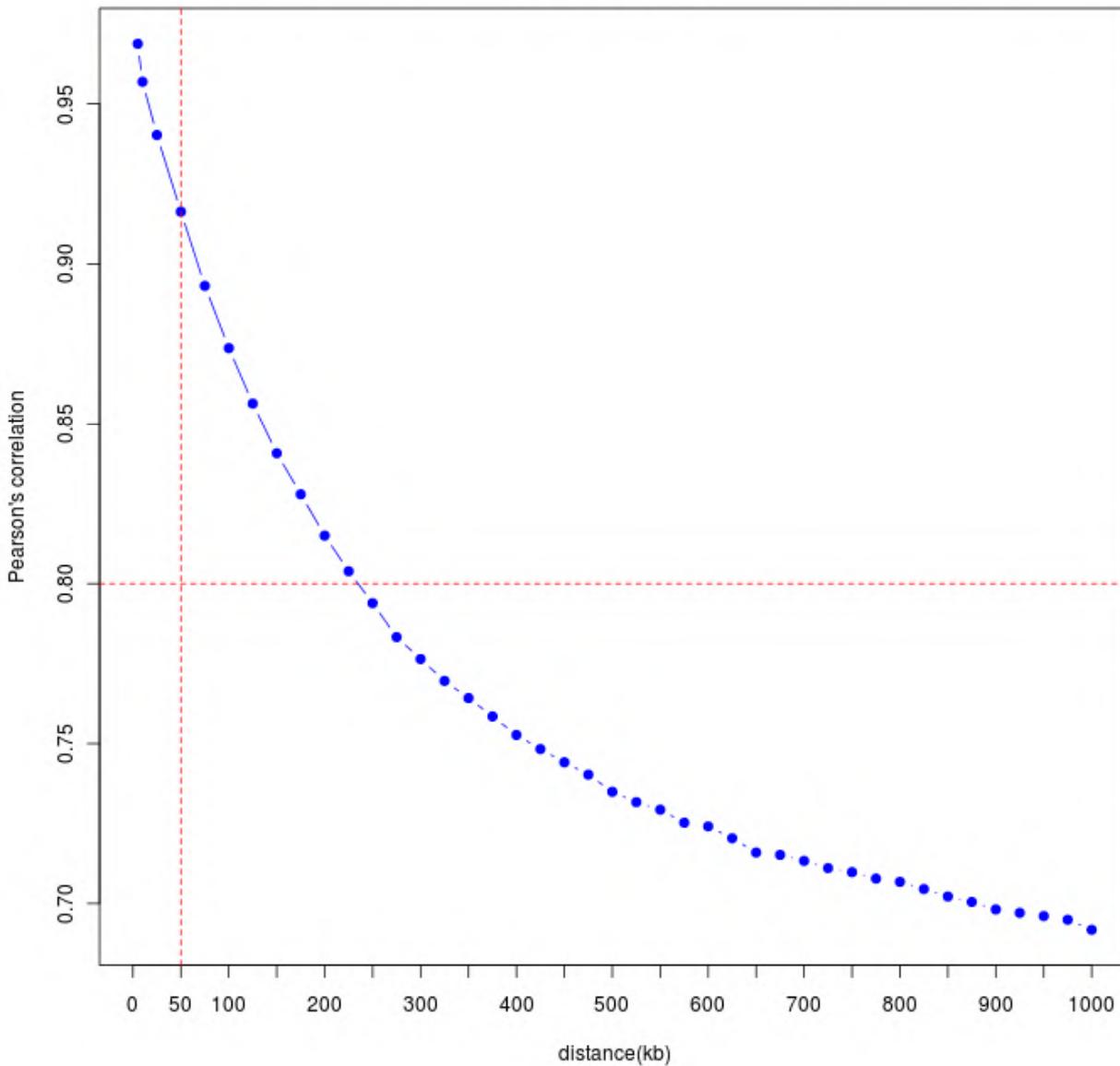
(adjacent markers)



PCA Genomic Kinship



Phase Persistency Nelore “subgroups”



The Traits

Birth weight (BW)

Weaning weight (WG)

Carcass conformation (Cw)

Finishing precocity (Pw)

Muscling (Mw)

Navel (Nw)

birth

weaning (~7m)

“yearling” (~18m)

cow

Yearling weight (PWG)

Carcass conformation (Cy)

Finishing precocity (Py)

Muscling (My)

Navel (Ny)

Temperament (Ty)

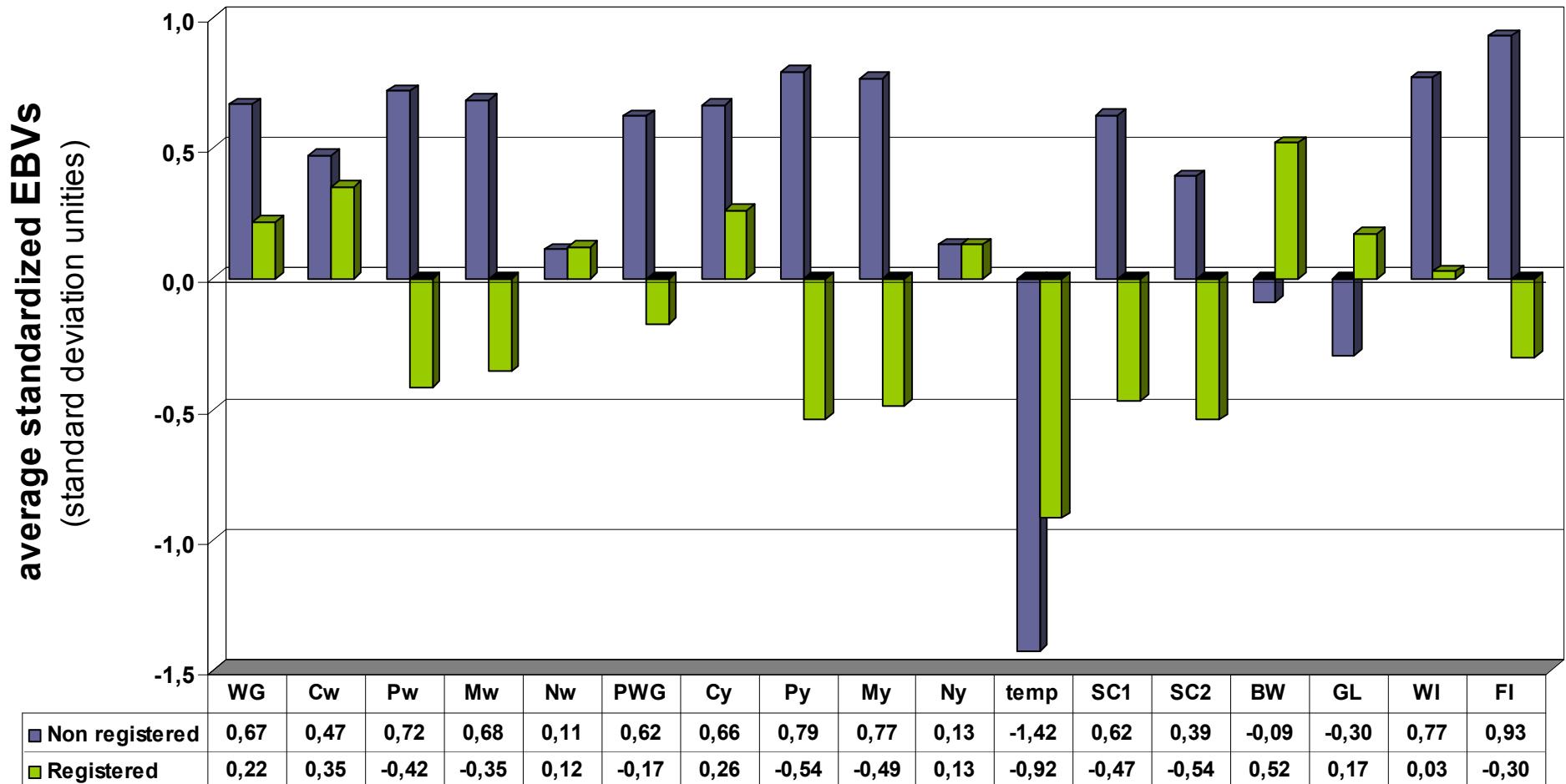
Scrotal circumference (SC)

Age at first calving (*phase 2*)

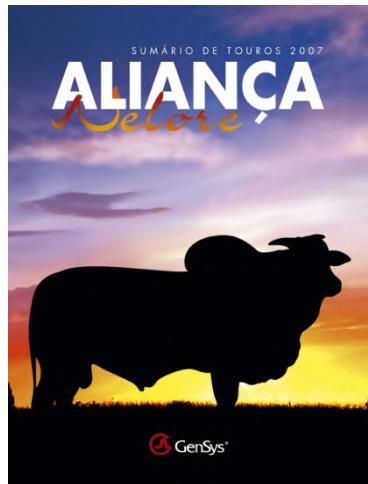
Gestation Length (GL)

Mature weight (*phase 2*)

Average standardized EBVs - Nelore “subgroups”

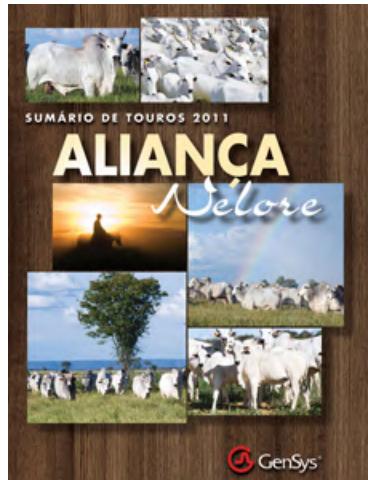


Training and Testing Groups



Training

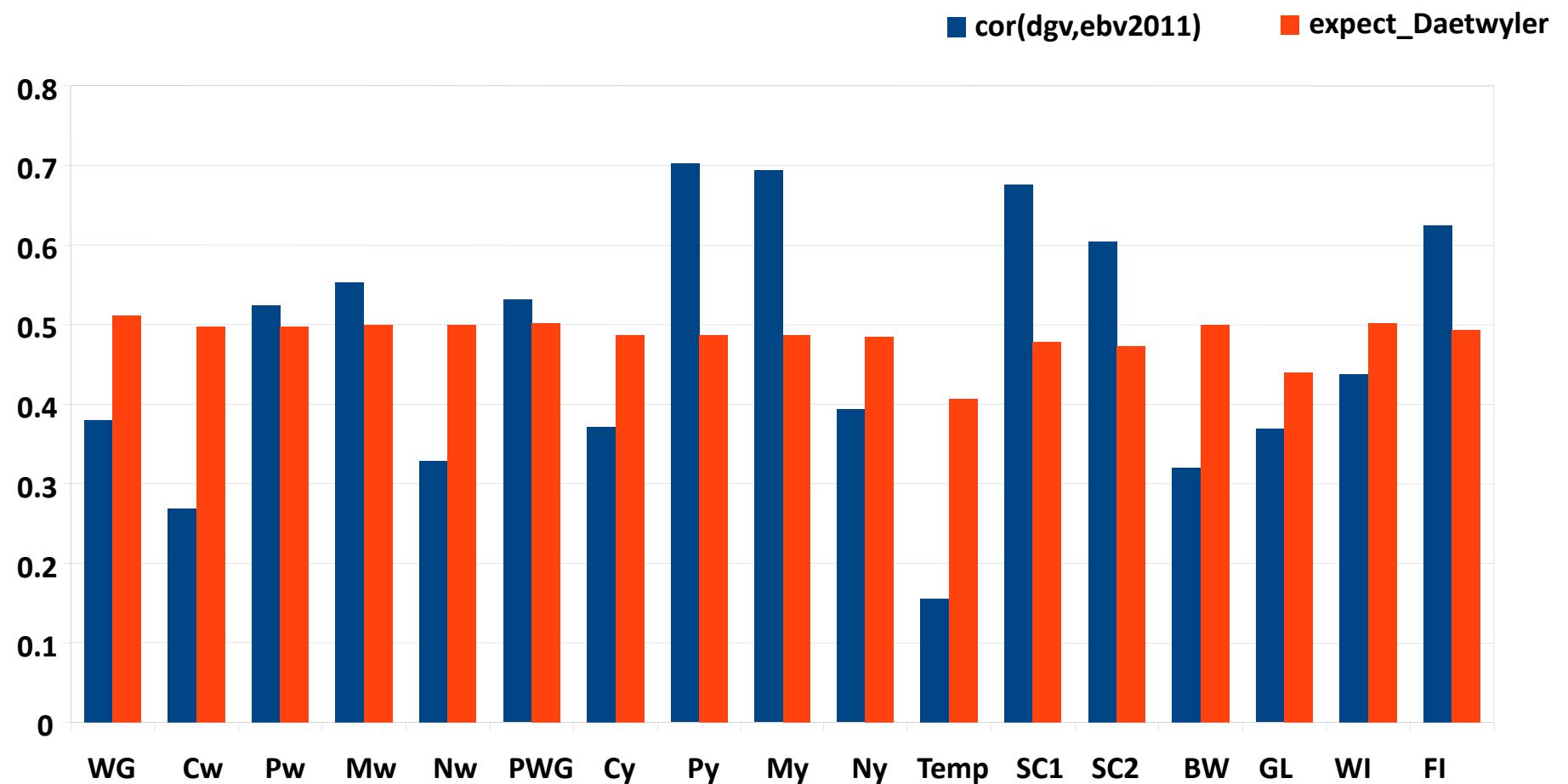
Sires with proofs in Nelore Aliance 2007
~ 470 sires (70%)



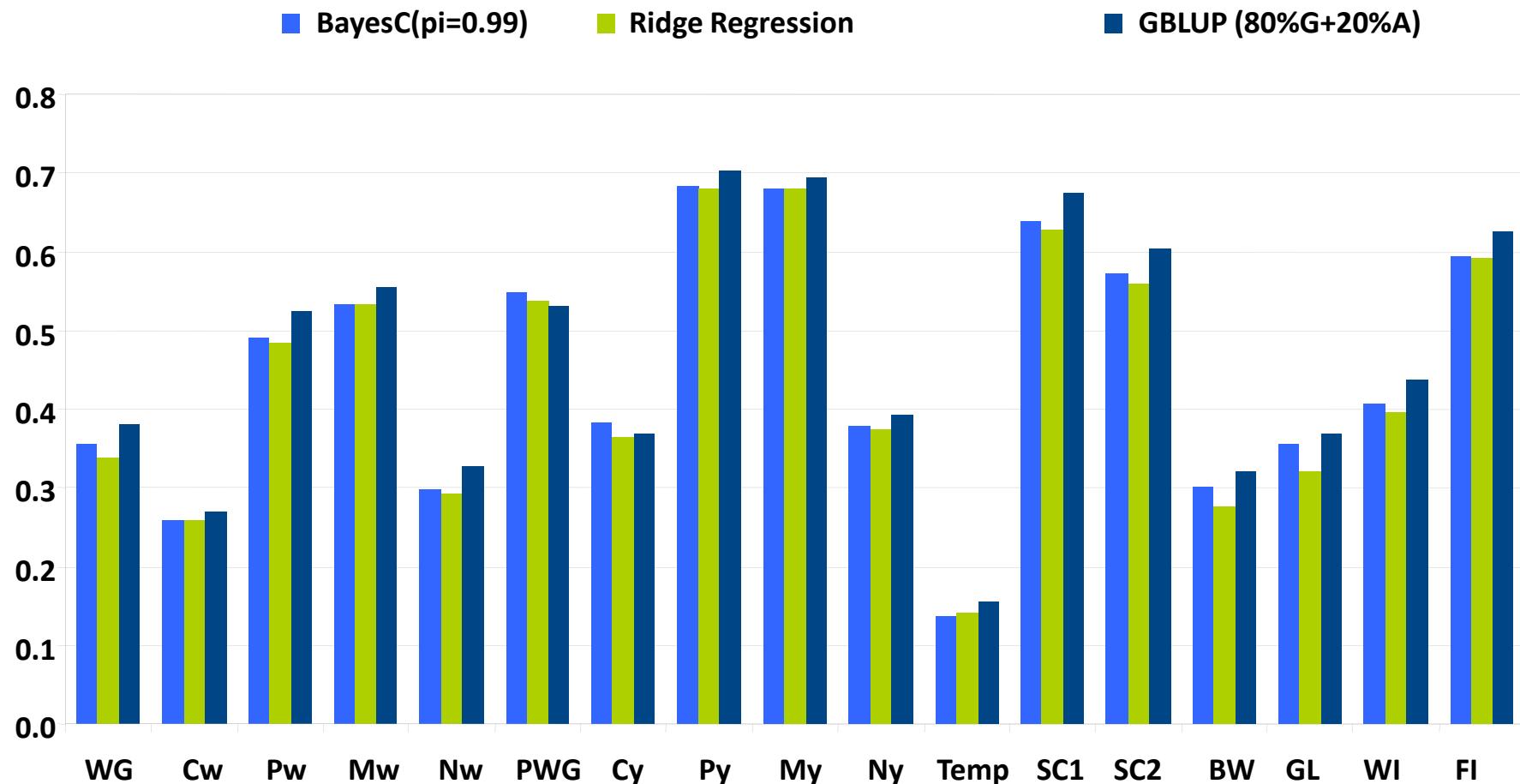
Testing

Sires without proofs in 2007 but with
proofs in Nelore Aliance 2011
~ 190 sires (30%)

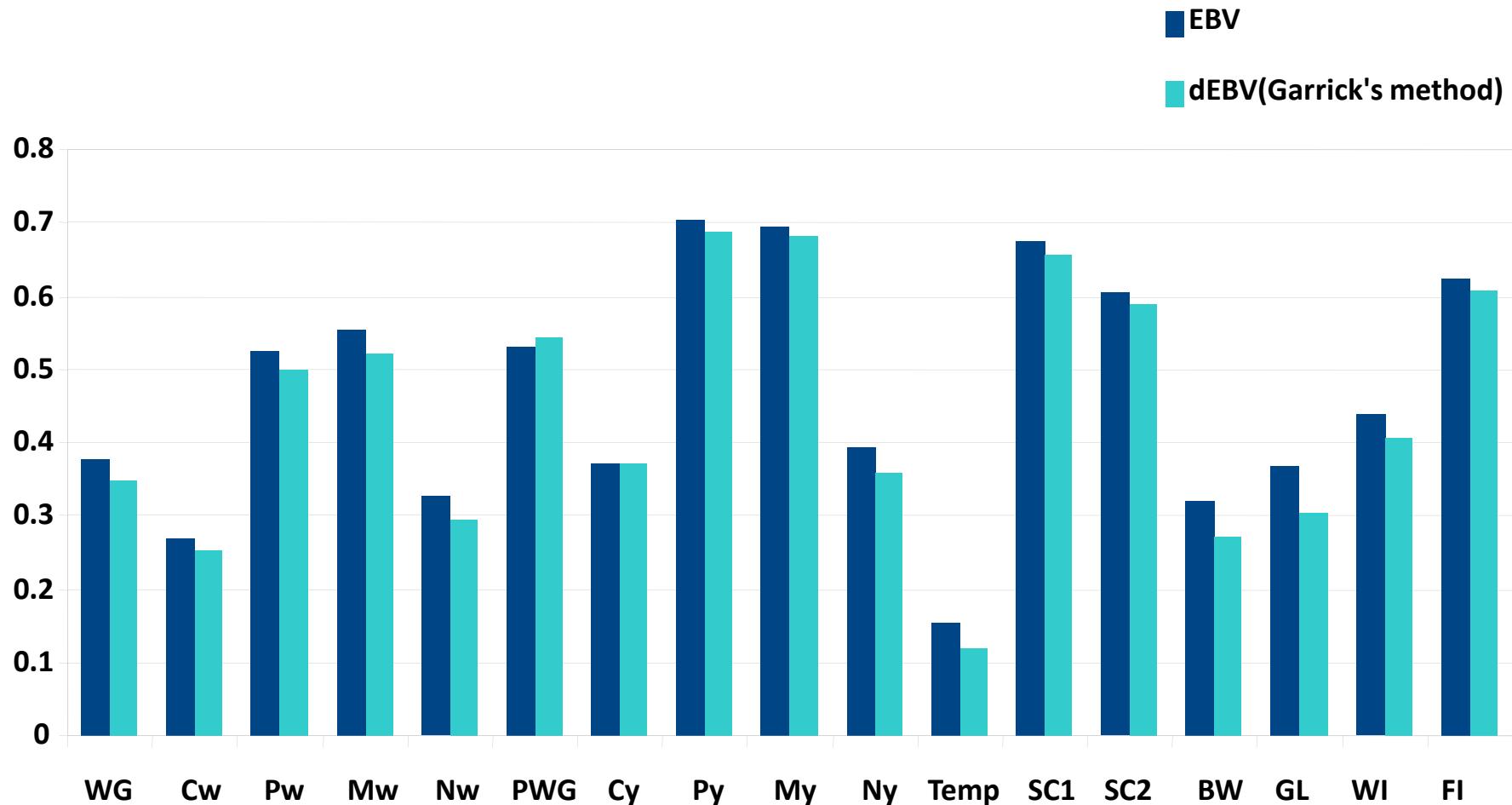
Predictive ability GBLUP



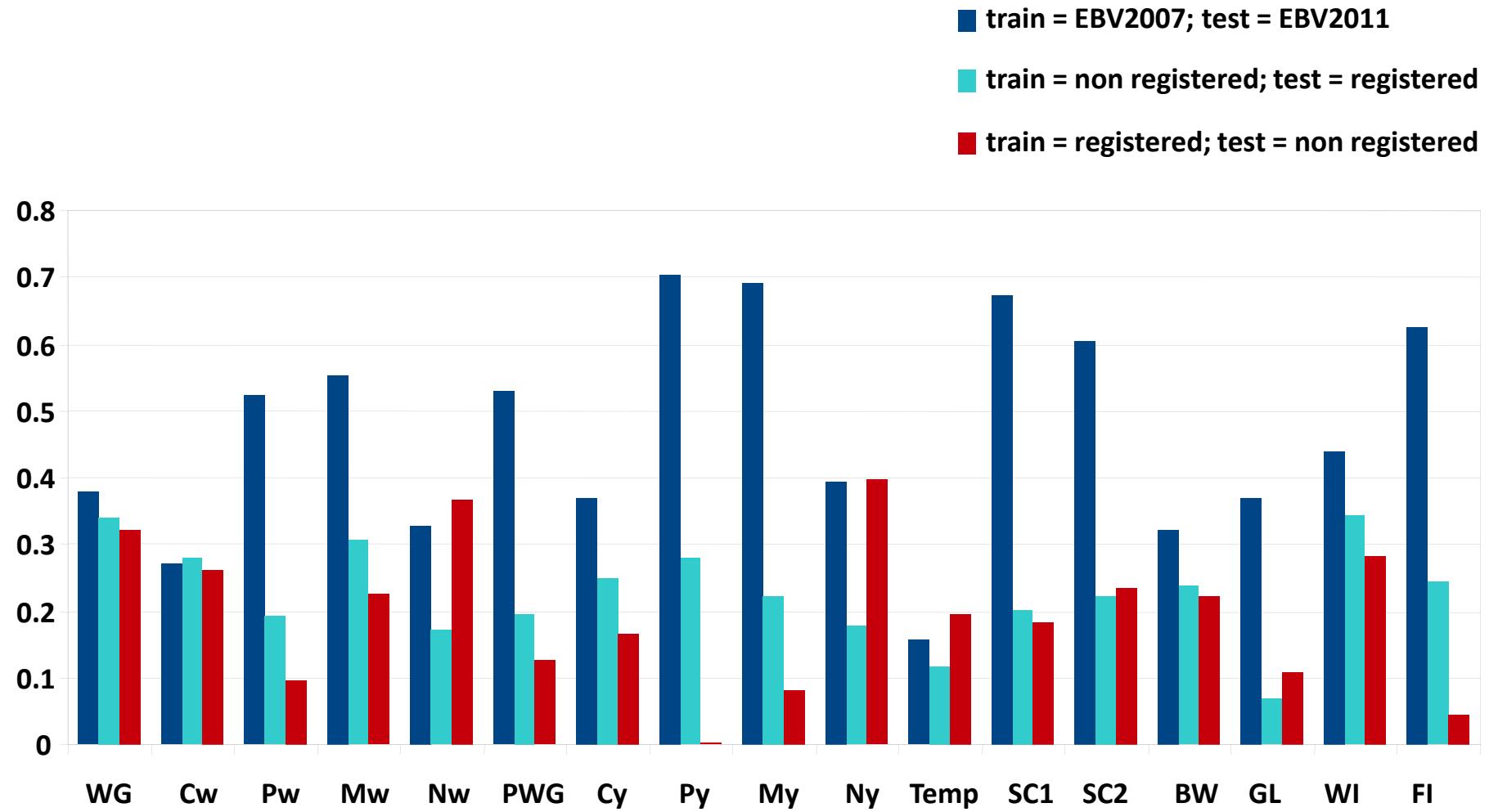
Predictive ability different methods



Predictive ability different pseudo-phenotypes (GBLUP)



Predictive ability Nelore “subgroups” (GBLUP)



Summary

- ✓ Reasonable predictive ability (encouraging further studies)
- ✓ Almost no difference between GS methods
- ✓ Similar predictive ability with different pseudo-phenotypes
- ✓ Good prediction equation for the Nelore breed need to consider animals from different “subgroups”

Acknowledgements

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Embrapa

GenSys