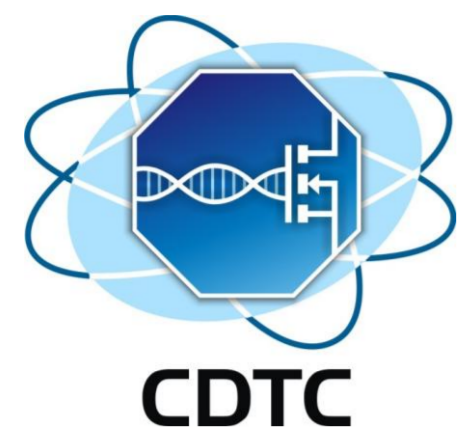# Impact of genetic markers information on breeding value accuracy and selection of replacement bulls

Rezende, F.M.[1]; Ferraz, J.B.S.[2]; Meirelles, F.V.[2]; Ibañez-Escriche, N.[3]

[1]Federal University of Uberlandia, Campus Patos de Minas, MG, Brazil, frezende@ingeb.ufu.br [2]NAP-GMABT, College of Animal Science and Food Engineering, University of Sao Paulo, Pirassununga, SP, Brazil [3]IRTA-Cataluña, Genetic and Animal Breeding, Lleida, Cataluña, Spain

Objectives

To evaluate the impact of genetic markers information on the selection of replacement bulls, comparing the reliability of breeding values estimated by classical genetic evaluation and marker assisted genetic evaluation, as well the selection conflicts when the top 10% replacement bulls were selected in each case.

Material and Methods

Data: 83,404 animals measured for post-weaning gain, scrotal circumference and muscle score, corresponding to 116,652 records on relationship matrix. A sample of 3,149 animals were genotyped for a panel, that considered, after quality control, 106 SNP markers.

Statistical analyses: Classical genetic evaluations and marker assisted genetic evaluations were performed using MTDFREML software, under animal model, as single and two-traits analyses, respectively. Markers effects were estimated by Bayesian ridge regression methodology assuming adjusted phenotypes as dependent variable and molecular breeding values (MBV) were calculated by adding the estimates for all markers.

Impact on reliability ($r_{T,I}$): The mean percentage variation between the mean accuracy of breeding values estimated by classical genetic evaluation and the mean accuracy of breeding values estimated by marker assisted genetic evaluation.

Selection conflicts: Divergences on the selection of replacement bulls based on classical and marker assisted breeding values, when the top 10% young bulls for each trait were selected.

Results

Table 1. Number of animals (N) and increments on accuracy (%) of estimates of breeding values of post-weaning gain (PWG), scrotal circumference (SC) and muscle score (MS) for genotyped and non-genotyped young bulls.

	N	PWG	SC	MS
Genotyped	1,374	6.55	1.91	9.70
Non-genotyped	2,744	0.14	0.23	0.09

Figure 2. Limiting point of top 10% and selection conflict (%).
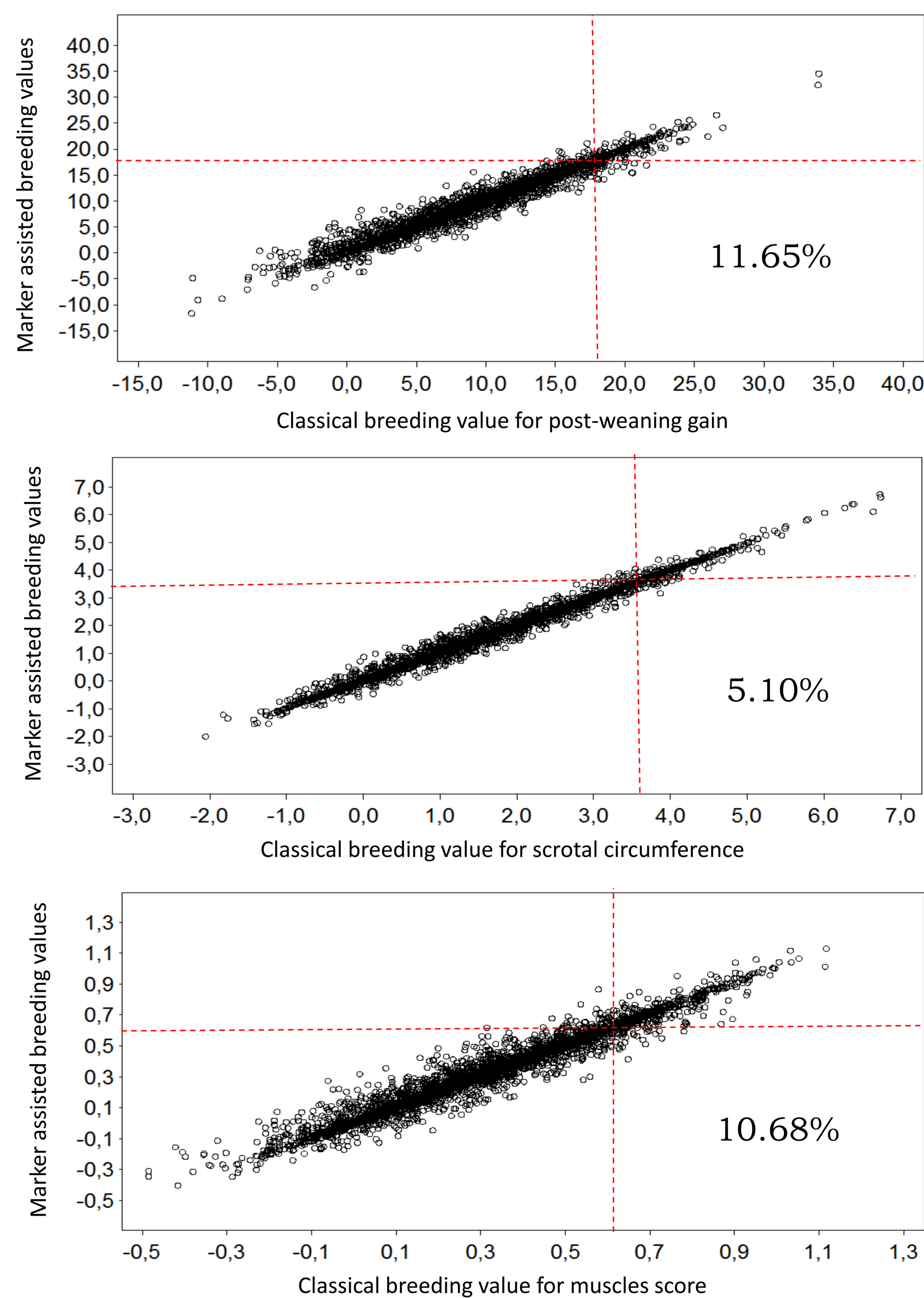
Conclusion

The use of panels of very low density markers increased the accuracy of estimates of breeding values of replacement young bulls and changed the classification of animals with breeding values close to threshold selection point.