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The effect of inbreeding on the prediction of genomic values

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ABSTRACT: The objective of this work was to evaluate the accuracy of genomic breeding values for simulated traits of different heritabilities in populations with different levels of inbreeding. The genotypes and phenotypes were simulated based on the structure of an experimental population of White Leghorn hens. The phenotypes for percentage of total egg production (TEP) and egg weight at 32 weeks (EW) were simulated with heritabilities of 0.15 and 0.37, respectively, and varying the matting type (more related, less related and random mating individuals, called REC1, REC2, and REC3, respectively) along 10 generations. The last four generations were genotyped. A GBLUP model was used to predict the genomic values using the information of markers. The accuracies of the predicted genomic values using the GBLUP model was not influenced by the level of inbreeding and the heritability of the trait.
Keywords: Genomic selection; Inbreeding; Simulation

Introduction

The genomic selection was first proposed by Meuwissen et al. (2001) and it has been used to improve the accuracy of the predicted breeding values with the help of molecular markers that cover an extensive proportion of the genome. Despite of all the improvements in predicting the breeding values using marker information, the inbreeding must be avoid with genomic control (Sonesson et al., (2012)).

The inbreeding causes loss of genetic variability of productive and reproductive traits, and economic losses, consequently. Muir (2000) reported that the first consequence of the inbreeding is the loss of some alleles in the population due to the genetic drift. Thus, the aim of this work was to evaluate the accuracy of genomic breeding values for traits of different heritabilities on populations with different inbreeding levels, and to evaluate the genetic trends of them in each scenario.

Materials and Methods

Historical population. The data set was simulated based on the genome of White Leghorn hens. All simulations were done using the QMSim program (Sargolzaei and Schenkel, (2009)). The historical populations were simulated with an effective population size (Ne) of 1100 breeding animals with random mating with 50% of males and 50% of females along 1000 generations of constant size. After 1000 generations, it was simulated a bottleneck along 20 generations (generation 1001 to 1020) decreasing the Ne gradually from 1000 to 640 breeding animals. The bottleneck was important to generate the linkage disequilibrium and random drift, and it mimics the process of domestication, in which decreased the Ne (Henson, (1992)). After that, the historical populations were expanded for three generations (1021 to 1023) under random mating of 80 males with 560 females from generation 1020 to 2013. The proportions of males to females were 1:7 with four progenies for each female, totaling 2240 animals at generation 1023. The genetic drift and recurrent mutation occurred until generation 1020, and the mutation rate was $2{,}5x10^{-5}$ for SNP markers and QTL.

Recent population. After the historical populations, three different scenarios with different mating systems were simulated in each recent population. The recent populations REC1, REC2, and REC3 were simulated maximizing the inbreeding, minimizing the inbreeding and random mating individuals, respectively. Two traits were simulated, one with heritability of 0.15 and other of 0.37. Those ones were simulated based on the heritabilities and phenotypic variances for percentage of total egg production and egg weight, reported by Savegnago et al. (2011). The phenotypic variances for these traits were 130.32 and 16.11kg², respectively.

Genome. The genome was simulated for REC1, REC2, and REC3 based on the genome of the *Gallus gallus* 4.0 (NCBI, (2013)), with eight macrochromosomes and 19 microchromosomes totaling 958Mb (10^6 base pairs). Only the autosomes were simulated and the microchromosomes 16 and 32 were omitted because QMSim cannot simulate chromosomes with less than 1Mb. The number of simulated QTL was 3747, which were all QTL reported for *Gallus gallus* (Hu et al., (2013)), and 49978 SNPs equally spaced along the genome with 52.17Mb between adjacent SNPs.

Training and validation sets. The data set of each scenario (REC1, REC2, and REC3) was splited in training and validation data sets. In the first one, the phenotypes and genotypes were used to estimate the marker effects. The validation sets were used to predict the genomic breeding values. The divisions of the data sets were made using 960 animals of the generations seven, eight and nine (individuals with the highest accuracies), and 1120 animals from the 10th generation to validate the models.

Genomic BLUP. The GBLUP as implemented in the GS3 software (Legarra et al., (2013)) was used to estimate the SNP effects. This model assumes equal effect for all SNPs. The de-regressed EBVs (Garrick et al., (2009)) of the traits were used as response variables of the model because they were simulated as sex-dependent

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Table 1. Correlation and standard errors (into parentheses) between the simulated and predicted genomic values and the predicted genomic values.

Trait[1]	Inbreed Level[2]	Training Sets		Validation Sets	
		N	Train Accuracy[3]	N	Validation Accuracy[4]
TEP	REC1	960	$0.61(0.11)^{AB}$	1120	$0.37(0.07)^{A}$
	REC2		$0.51(0.04)^{B}$		$0.36(0.04)^{A}$
	REC3		$0.54(0.05)^{B}$		$0.39(0.07)^{A}$
EW	REC1	960	$0.73(0.02)^{A}$	1120	$0.45(0.06)^{A}$
	REC2		$0.62(0.05)^{AB}$		$0.42(0.03)^{A}$
	REC3		$0.61(0.05)^{B}$		$0.45(0.04)^{A}$

[1] TEP = Percentage of total egg production; EW = Egg weight at 32 weeks of age;
[2] REC1, REC2, REC3 = recent populations with more related, less related and random mating individuals, respectively.
[3] Different letters indicated significant differences according to the Tukey test ($p<0.05$).
[4] No significant differences according to the Tukey test ($p>0.05$).

traits. The predicted breeding values using the genomic information in the test population were calculated by summation of each SNP effect multiplied by the respective number of allele copies. The accuracy of the predictions was calculated by the correlation between the simulated and the predicted genomic values. Five repetitions were done on each scenario. The Tukey test was used to test if there were significant differences ($p<0.05$) between the average of the accuracies among the scenarios.

Genetic trends. The genetic trends were calculated for each trait as the regression of the breeding values in each generation of the recent population. Each regression coefficient (b) was divided by the respective phenotypic mean of the trait only for comparison purposes of the genetic gains per generation, once the units of each trait were different (percentage for egg production and grams for egg weights).

Results and Discussion

The higher values of accuracies were 0.61 ± 0.11 for TEP, and 0.73 ± 0.02 for EW in REC1. The accuracies of the genomic breeding values for the TEP and EW had significant differences ($p < 0.05$) between the training populations REC1, REC2, and REC3. There were no significant differences ($p > 0.05$) of the accuracies between the testing populations (Table 1).

The REC1 scenarios had higher linkage disequilibrium compared to the other scenarios and it can be a factor that affects the accuracies of the genomic breeding values, once its prediction had higher accuracies compared to the other scenarios in its training sets. The differences on the heritabilities and the inbreeding levels did not affect the accuracy of the genomic breeding values in the validation sets.

The slope of the genetic trends for TEP and EW in REC1, REC2, and REC3 (Figure 1) were statistically different from zero according to the t-test ($p < 0.05$). The genetic trends indicated that the genetic gain per year were higher for TEP, especially at the scenario REC1 (high inbreed level). But for EW, the scenario REC1 presented the lowest genetic gain compared to REC2 and REC3 for this trait. The higher genetic gains for TEP was due because it was simulated with much higher genetic variance than EW notwithstanding TEP had lower heritability than EW.

Conclusion

The five replicates did not provide sufficient support to reject hypothesis of equality of the accuracy between the simulated traits and scenarios.

Literature Cited

Garrick, D.J., Taylor, J.F., and Fernando, R.L. (2009). Genet. Sel. Evol., 41:55.

Henson, E.L. (1992). FAO Anim. Prod. Health.

Hu, Z.L., Park, C.A., Wu, X.L. et al. (2013). Nucleic Acids Res. 41:D871-D879.

Legarra, A., Ricardi, A., and Filangi, O. (2013). Available in < http://genoweb.toulouse.inra.fr/~alegarra/ >.

Meuwissen, T.H.E., Goddard, M.E., and Hayes, B.J. (2001). Genetics, 157: 1819-1829.

Muir, W.M. (2000). J. Anim. Sci., 79:1-11.

NCBI, National Center for Biotechnology Information. EUA. (2013). Available in <http://www.ncbi.nlm.nih.gov/genome/111?project_id=10808>.

Sargolzaei, M., and Schenkel, F.S. (2009). Bioinformatics, 25:680–681.

Savegnago, R.P., Caetano, S.L., Ramos, S.B. et al. (2011). Poult Sci., 90:2174–2188.

Sonesson, A.K., and Meuwissen, T.H.E. (2000). Genet. Sel. Evol., 32:231-248.

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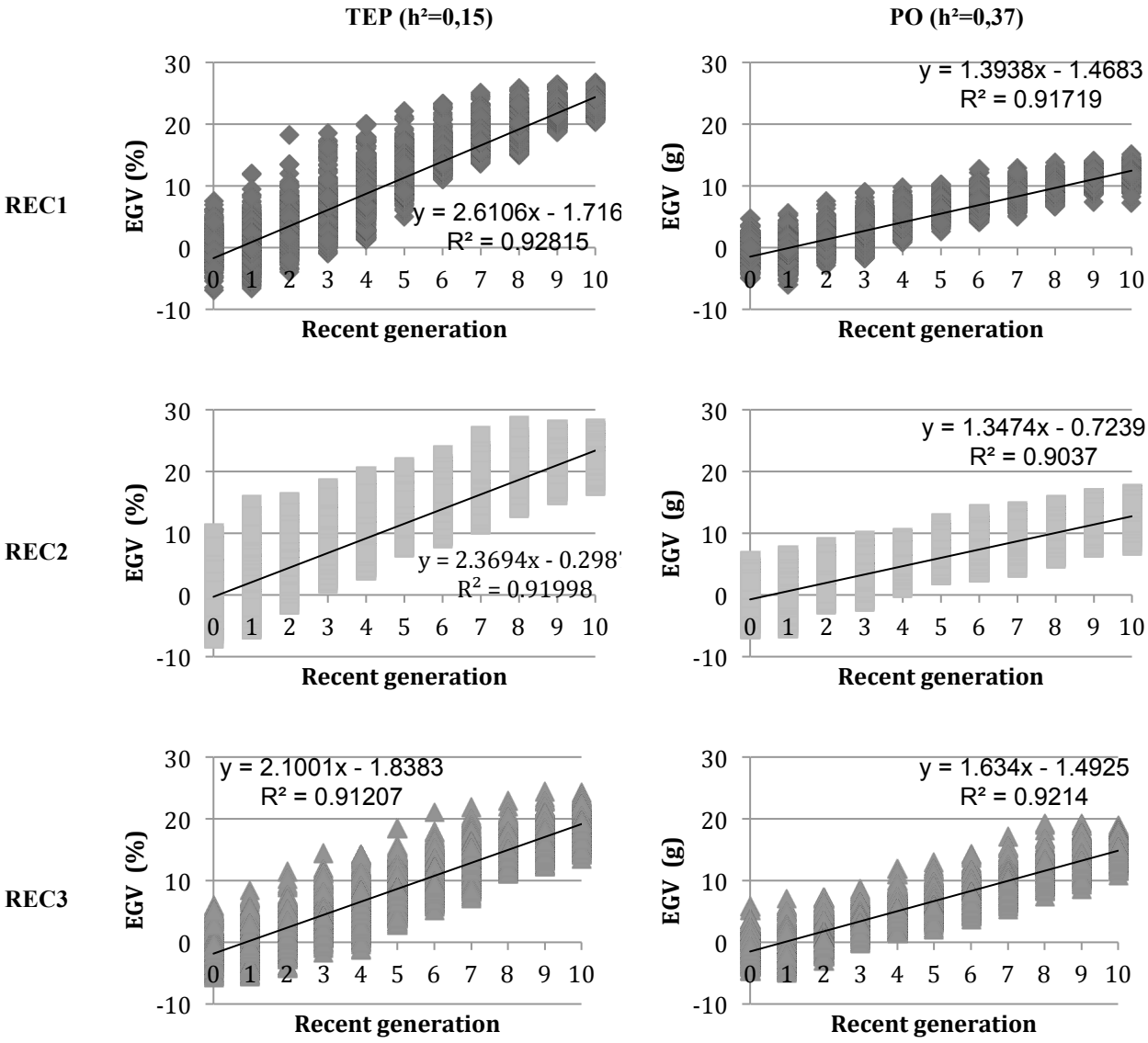

Figure 1. Genetic trends for the percentage of total egg production (TEP), egg weight at 32 weeks of age (EW) in scenarios REC1, REC2, and REC3 (recent populations with more related, less related and random mating individuals, respectively). EGV = Predicted genomic value; R^2 = coefficient of determination.

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