435. Optimizing sampling strategies for sib test schemes in a broiler breeder program

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Abstract

In broiler breeding there is a known genotype by environment interaction for bodyweight measured in a bio-secure (BW_B) or in a commercial environment (BW_C), thus a sib test scheme to record and use BW_C records is beneficial. This study estimated a genetic correlation of 0.59 between BW_B and BW_C. To optimize the sib scheme, different genotype proportions (25, 50, 75%) and sampling strategies were studied. No pedigree information was available for birds in the commercial environment unless they were genotyped. Genotyping based on phenotypes, heaviest and lightest, resulted in the highest accuracy compared to random genotyping 0.88 vs 0.80 at 25%, 0.94 vs 0.89 for 50 and 0.97 vs 0.95 at 75% genotyped. No bias was observed with random sampling, however bias was detected with sampling based on phenotypes (0.58 at 25%, 0.76 at 50 and 0.91 at 75%).

Introduction

Broiler poultry breeding companies keep and select their genetic pure lines in a bio-secure environment to reduce the risk of any diseases. However, this environment differs from the environment in which commercial broilers are usually reared. Because the selection environment does not completely reflect the commercial environment, a genotype by environment interaction (G×E) is likely present. The G×E causes the expressions of different phenotypes to be affected (Kolmodin and Bijma 2004) and thereby lead to reranking of families in different environments. A genetic correlation between body weight of the same purebred broiler line in a bio-secure and in a commercial environment was reported between 0.46-0.69 (Chu *et al.* 2019; Kapell *et al.* 2012). Therefore, it would be valuable for broiler breeder companies to set up a sib scheme test design to increase the genetic gain in body weight in a commercial environment. This study explored different genotyping strategies and proportions of birds to be genotyped to optimize a broiler breeding sib scheme set up. The two following strategies were chosen: the first is Random sampling (RND), this strategy is known to result in higher accuracies and lower bias compared to genotyping strategies based on mean phenotypes or best phenotypes (Howard *et al.* 2018; Jiménez-Montero *et al.* 2012). The second strategy is sampling based on Extreme phenotypes (EXT), the heaviest and lightest birds are chosen to be genotyped. This strategy has been found to result in the highest accuracies of breeding values compared to random sampling (Boligon *et al.* 2012; Howard *et al.* 2018; Jiménez-Montero *et al.* 2012). Additionally, three different proportions of genotyped birds were studied: 25, 50 and 75% of the available birds in the commercial environment.

Materials & methods

Phenotypes and genotypes. Data was provided by the poultry breeding company Cobb-Vantress, Inc. (Siloam Springs, Arkansas, USA). The data included performance information collected on pure-line broiler chickens that were either raised in a pedigree bio secure environment (Env B) or in a commercial environment (Env C). Once a bird is placed in Env C, they cannot return to Env B and will therefore be excluded from the breeding program. Of all birds hatched in one selection round, about 30% were placed in Env C, this was found to be sufficient by Chu *et al.* 2018 considering selection intensity, inbreeding and accuracy. These birds were all either full or half sibs of the other 70% birds that were placed in Env B. Data was collected over approximately 3.5 generations. The number of body weight phenotypes and the number

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of genotypes are represented in Table 1. Body weight was recorded in both environments at the same age. Birds included in this study were offspring from 519 Sires and 2,368 Dams. Genotypes were collected on all birds in Env C but only on a selected amount of birds in Env B (Table 1). All chicks placed in Env B have a known pedigree and the selection candidates are genotyped.

Sampling strategies for Env C. Having all chicks in Env C genotyped, allowed to retrospectively evaluate different sampling strategies. For each strategy, to reflect a scenario in which chicks placed in Env C are hatched in a commercial hatchery, animals that were not sampled in Env C were assumed to have no pedigree, and were therefore not included in the ssGBLUP analysis. The following sampling strategies are studied: Random sampling (RND): based on the proportion, X chicks were randomly sampled. Extreme phenotypes sampling (EXT), based on the proportion, 0.5X birds were sampled based on the highest body weight and 0.5X birds were sampled based on the lowest body weight.

Statistical analysis. A multivariate pedigree based model was used to estimate variance and covariance components. The multivariate model included six traits; BW_B, BW_C, White Meat Percentage (WMPct), Leg Quarter Percentage (LegQPct), Gain and Feed Efficiency (FE). BW_B, WMPct, LegQPct and FE and Gain were only recorded in Env B. BW_C was only recorded in Env C. All traits were corrected for gender and contemporary group. Additionally, for both BW_B and BW_C a random permanent maternal environmental effect was added to the model.

$$y_{BwB + BwC} = Xb + Za + Wc + e \qquad (1)$$

$$y_{Gain + RFI + BRM\% + LegQ\%} = Xb + Za + e \qquad (2)$$

X, Z and W are incidence matrices; where a, c and e are vectors for direct additive genetic, environmental maternal and residual effects, respectively. These random effects were assumed to be normally distributed $a \sim N(0,A\sigma_a^2)$, $c \sim N(0,I_d\sigma_c^2)$ and $e \sim N(0,I\sigma_e^2)$, where A is the pedigree relationship matrix and I_d the dam's identity matrix and I the identity matrix for all individual birds.

The variance components were estimated with the use of AIREML procedure in the DMUAI program from DMU (Madsen and Jensen 2013). Estimated variance components were used in single-step genomic BLUP (ssGBLUP) to estimate breeding values with the use of BGF90 (Misztal *et al.* 2002). The ssGBLUP models were identical to models described above (Misztal, *et al.* 2009). For computational reasons APY method (Misztal *et al.* 2014) was used to compute the inverse of the G matrix used in ssGBLUP. Core animals included parents and all selection candidates.

Validation. Validation was done using LR method (Legarra and Reverter 2018) to evaluate the differences in GEBV accuracies and bias. Full data contained all genotypes on all birds raised in Env C, the reduced data only contained a proportion of the genotyped birds in Env C based on each strategy. The number of genotypes in Env B remained the same across all strategies. Accuracies of different scenarios were measured by the correlation of GEBVs between the full data and reduced data. Dispersion bias was evaluated by the

Table 1. The number of phenotypes and genotypes used in this study.

	Phenotypes	Genotypes
BW_B	87,381	26,867
BW_C	34,863	34,816

slope of the regression of GEBVs from the full data on the GEBVs of the reduced data for the different strategies.

Results & discussion

Accuracy. Table 2 shows the accuracy of different ratios and different strategies of genotype sampling. The EXT clearly shows an advantage over RND sampling in terms of accuracy, especially at lower sampling rates (0.88 vs 0.80 at 25%, resp.). The magnitude of the advantage disappears as sampling proportion increases (0.94 vs 0.89 at 50% and 0.97 vs 0.95 at 75% of birds genotyped resp.). This increased accuracy of EXT over RND is in accordance with multiple other studies (Boligon *et al.* 2012; Howard *et al.* 2018; Jiménez-Montero *et al.* 2012).

Bias. Table 2 shows that bias is virtually absent for RND, while considerable for EXT, especially at a lower proportion (0.58 at 25% genotyped). When the sampling proportion increases the bias decreases for EXT but is still present even at 75% (0.76 at 50% and 0.91 at 75% genotyped). It is known that with an increase in the number of genotypes there is a decrease in bias (Daetwyler *et al.* 2012) and that genotyping randomly reduces bias compared to sampling based on phenotypes or family index (Boligon *et al.* 2012; Howard *et al.* 2018; Jiménez-Montero *et al.* 2012).

Table 2. Accuracies (r) and regression slopes (β) across strategies and proportions.

Strategy	Ratio	$r_{f\text{-}r}$	SE	$\beta_{f\text{-}r}$	SE
Random	25%	0.80	0.007	0.98	0.008
Extreme phenotypes	25%	0.88	0.005	0.58	0.003
Random	50%	0.89	0.005	0.98	0.005
Extreme phenotypes	50%	0.94	0.002	0.76	0.003
Random	75%	0.95	0.002	1.01	0.004
Extreme phenotypes	75%	0.97	0.001	0.91	0.002

Conclusions

In a sib test scheme where siblings tested in a commercial environment are removed from the breeding program and the correlation between body-weight measured in two different environments is 0.59, the following genotype strategies are advised for different proportions. When the genotyping is limited to less than 75% of all animals, it is advisable to sample animals based on extreme phenotypes as this strategy results in the highest accuracy. However, caution should be taken with interpreting the breeding values as this strategy shows higher levels of bias. When the sampling ratio is 75% or higher, random sampling of animals is recommended as this reduces the bias and shows similar accuracy compared to extreme phenotyping strategy.

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