

CORRECTION

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# Correction to: Development of a genetic evaluation for hair shedding in American Angus cattle to improve thermotolerance

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**Correction:** *Genet Sel Evol* (2020) 52: 63

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In Durbin et al. [1], the correlation between partial and full breeding values,  $\rho_{p,w}^v$ , was reported as a measure of prediction accuracy, which is not correct; the metric  $\rho_{p,w}^v$  is the ratio between prediction accuracy in the partial dataset and prediction accuracy in the whole dataset. We have now calculated accuracy as follows:

$$\widehat{acc}_{LR} = \sqrt{\frac{cov(\hat{u}_w, \hat{u}_p)}{(1 - \bar{F})\hat{\sigma}_u^2}},$$

where *cov* is the covariance and  $\bar{F}$  is the average inbreeding coefficient of the animals in the partial dataset. The equation for  $\widehat{acc}_{LR}$  is adapted from [2].

Across the 10 cross-validation iterations, the average accuracy was  $\widehat{acc}_{LR} = 0.547$  (minimum = 0.539, maximum = 0.554).

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#### References

1. Durbin HJ, Lu D, Yampara-Iquise H, Miller SP, Decker JE. Development of a genetic evaluation for hair shedding in American Angus cattle to improve thermotolerance. *Genet Sel Evol.* 2020;52:63. <https://doi.org/10.1186/s12711-020-00584-0>.
2. Macedo FL, Reverter A, Legarra A. Behavior of the linear regression method to estimate bias and accuracies with correct and incorrect genetic evaluation models. *J Dairy Sci.* 2020;103:529–44.

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