



Correction

Correction: Weighted Genomic Best Linear Unbiased Prediction for Carcass Traits in Hanwoo Cattle. *Genes* 2019, 10, 1019

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The authors wish to make the following corrections to this paper [1]:

In Equations (2) and (3), variable M is used for a matrix of centered genotypes but different variables (Z) are used in equation 4 and in some equations (points 1, 3 and 6) of the iterative steps in the algorithm of the WGBLUP approach for the same matrix. Thus, the authors would like to change the variable Z to M in Equation (4) as well as on the iterative steps in the algorithm of the WGBLUP approach. The correct expression for Equation (4) is given as

$$\hat{\mathbf{u}} = \mathbf{D}\mathbf{M}\mathbf{1} \mathbf{G}^{-1}\hat{\mathbf{g}}$$

For the iterative steps in the algorithm of the WGBLUP approach, the correct expressions are given as

- 1. Set parameters to t = 1, $D_{(t)} = I$, $G_{(t)} = MD_{(t)}M\prime\lambda$, where $\lambda = \frac{1}{\sum_{i=1}^{m}2p_{i}(1-p_{i})}$;
- 3. Compute SNP effects as $\hat{\mathbf{u}}_{(t)} = \lambda D_{(t)} \mathbf{M} / \mathbf{G}_{(t)}^{-1} \hat{\mathbf{g}};$
- 6. $G_{(t+1)} = MD_{(t+1)}M\lambda$ was calculated;

Note that on the above steps, a Z (now M) variable for point 1 and a prime on the Z (now M) for points 3 and 6 were also missing on the original version. Likewise, \hat{a}_g was changed to \hat{g} in point 3.

The authors would like to apologize for any inconvenience caused. The changes do not affect the scientific results. The manuscript will be updated, and the original will remain online on the article webpage, with a reference to this correction.

Genes **2020**, 11, 1013

Conflicts of Interest: The authors declare no conflict of interest.

References

1. Lopez, B.I.; Lee, S.-H.; Park, J.-E.; Shin, D.-H.; Oh, J.-D.; de las Heras-Saldana, S.; van der Werf, J.; Chai, H.-H.; Park, W.; Lim, D. Weighted genomic best linear unbiased prediction for carcass traits in Hanwoo cattle. *Genes* **2019**, *10*, 1019. [CrossRef] [PubMed]



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