

CORRECTION

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Correction to: Genomic evaluation for a three-way crossbreeding system considering breed-of-origin of alleles

Claudia A. Sevillano^{1,2*}, Jeremie Vandenplas¹, John W. M. Bastiaansen¹, Rob Bergsma² and Mario P. L. Calus¹

Correction to: *Genet Sel Evol* (2017) 49:75

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After publication of our article [1], we found a typo in the formula to build the genomic relationship matrix using allele frequencies across all genotyped pigs (matrix) and the genomic relationship matrix using breed-specific allele frequencies (matrix), and we noted that the description to this formula is not very clear. In this paper, we describe the corrected formula and provide a clarification.

In the paragraph *Genomic relationship matrix using allele frequencies across all genotyped pigs (G_A matrix)*, page 4, second column, line 21, a “2” is missing in the formula, i.e., it incorrectly says that \mathbf{D} is diagonal with $D_{jj} = \frac{1}{p_j(1-p_j)}$.

Instead, \mathbf{D} is diagonal with $D_{jj} = \frac{1}{2p_j(1-p_j)}$.

Similarly, in the paragraph *Genomic relationship matrix using breed-specific allele frequencies (G_B matrix)*, page 4, second column, line 33, a “2” is missing in the formula, i.e., it incorrectly says that \mathbf{D}^B is diagonal with $D_{jj}^B = \frac{1}{p(1-p_{Bj})}$.

Instead, \mathbf{D}^B is diagonal with $D_{jj}^B = \frac{1}{2p_{Bj}(1-p_{Bj})}$.

In the same paragraph, page 4, second column, line 29, \mathbf{p}_B is confusingly defined as: “The vector of the frequencies of the counted allele (p_{Bj}). p_{Bj} was obtained by summing the contribution of each pure breed j and the weighted contribution of the CB. The weight was 0.5 for S, and 0.25 for LR and LW.”

For clarification, \mathbf{p}_B is the vector of the frequencies of the counted allele at locus j (p_{Bj}). For PB, p_{Bj} was specific for each breed B (i.e., S, LR, and LW). For CB, p_{Bj} was the weighted contribution of each breed. The weights considered for the CB were 0.5 for S, 0.25 for LR and 0.25 for LW.

The original article was corrected.

Author details

¹ Wageningen University & Research Animal Breeding and Genomics, 6700 AH Wageningen, The Netherlands. ² Topigs Norsvin Research Center, 6640 AA Beuningen, The Netherlands.

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Reference

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*Correspondence: claudia.sevillanodelaguila@wur.nl

¹ Wageningen University & Research Animal Breeding and Genomics, 6700 AH Wageningen, The Netherlands

Full list of author information is available at the end of the article