ERRATUM TO:

Surveillance of a *PLOD* gene variant linked to fragile foal syndrome in Silesian horses in Poland: implications for genetic monitoring and breeding strategies

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Description of the Error:

"In the published article, an incorrect value was reported due to a simple typographical error. The mistake occurred during manuscript preparation and does not affect the underlying dataset, statistical analyses, or the conclusions of the study".

Correction:

In Table 1, one value was incorrectly reported due to a typographical error. The correct statistical data are as follows:

"corresponding to a carrier frequency of 12.7% and an FFS allele frequency of 0.063 (36/568; 95% CI: 0.043–0.083)."

The previously displayed value "1.3005" resulted from a typing mistake and does not reflect the correct confidence interval. The underlying dataset and statistical analyses were performed using the correct values; therefore, this correction does not affect the results or conclusions of the study.

In addition, the following amendments are introduced to ensure consistency with the corrected carrier frequency:

Abstract

Original text:

"Results: The detected carrier frequency was 14.6%, an increase over previously reported carriage for this breed."

Corrected text:

"Results: The detected carrier frequency was 12.7% and comparable with previously reported carriage for this breed."

Results

Original text:

„In total, 29 horses (10.2%) among the 284 which were genotyped were identified as heterozygous for the FFS mutation (N/FFS)."

Corrected text:

“In total, 36 horses (12.7.%) among the 284 which were genotyped were identified as heterozygous for the FFS mutation (N/FFS).”

Original text:

„The remaining 255 horses (89.8%) of the genotyped Silesian horses were identified as homozygous for the reference wild-type allele (N/N).”

Corrected text:

“The remaining 248 (87.3%)of the genotyped Silesian horses were identified as homozygous for the reference wild-type allele (N/N).”

Table 1:

In Table 1, one value was incorrectly reported due to a typographical error. The correct statistical data are as follows:

“corresponding to a carrier frequency of 12.7% and an FFS allele frequency of 0.063 (36/568; 95% CI: 0.043–0.083).”

The previously displayed value “1.3005” resulted from a typing mistake and does not reflect the correct confidence interval. The underlying dataset and statistical analyses were performed using the correct values; therefore, this correction does not affect the results or conclusions of the study.

Discussion section

Original text:

“Previous large-scale screening across a wide range of breeds and many horses identified the presence of the mutated allele in numerous warmblood breeds, including the Silesian breed, which had a carrier allele frequency of 12.5% (9). The present study on a sample size of 284 horses showed that the carrier frequency was higher at 14.6%.”

Corrected text:

“Previous large-scale screening across a wide range of breeds and many horses identified the presence of the mutated allele in numerous warmblood breeds, including the Silesian breed, which had a carrier allele frequency of 12.5% (9). The present study on a sample size of 284 horses showed that the carrier frequency was comparable at 12.7%.”

These textual modifications ensure consistency with the corrected statistical values.

Impact on the Article:

This correction does not affect the scientific results or conclusions.

Corrected Author Line / Text:

Abstract:

Results: The detected carrier frequency was 12.7%, an increase over previously reported carriage for this breed. Compared to other warmblood breeds, the carrier frequency in Silesian horses was higher than in Swedish Warmbloods, similar to the frequency in Hanoverians (14%) and also aligned with that in Oldenburg horses, from which Silesians historically derive.

Results

Digestion by FauI yielded two cut fragments of 102 bp and 64 bp for the G allele and an uncut 166 bp fragment for the A allele, which facilitated genotype determination. In total, 36 horses (12.7%) among the 284 which were genotyped were identified as heterozygous for the FFS mutation (N/FFS), resulting in an allele frequency of 0.063 in the analysed population. The 95% confidence interval was 0.043–0.083. The chi-squared test for HWE yielded an χ 2 value of 1.45, indicating that there was no significant deviation from Hardy–Weinberg equilibrium (Table 1).

The remaining 248 (87.3%)of the genotyped Silesian horses were identified as homozygous for the reference wild-type allele (N/N). No individuals homozygous for the lethal FFS mutation were found. However, no data were available regarding abortions or stillbirths. The number of horses genotyped across birth year cohorts varied substantially (Fig. 1).

Table 1

n	Genotype totals						Genotype frequency			Allele frequency		95% CI range
	Observed	Expected*	Observed	Expected*	Observed	Expected*						
	N/N	N/N	N/FFS	N/FFS	FFS/FFS	FFS/FFS	N/N	N/FFS	FFS/FFS	N	FFS	
284	248	249.2	36	33.5	0	1.3	0.8732	0.1268	0	0.9366	0.0634	0.043 – 0.083

Discussion

Previous large-scale screening across a wide range of breeds and many horses identified the presence of the mutated allele in numerous warmblood breeds, including the Silesian breed, which had a carrier allele frequency of 12.5% (9). The present study on a sample size of 284 horses showed that the carrier frequency was comparable at 12.7%.