

Correction

Open Access

Genetic diversity of a large set of horse breeds raised in France assessed by microsatellite polymorphism

Grégoire Leroy*^{1,2}, Lucille Callède^{1,2}, Etienne Verrier^{1,2}, Jean-Claude Mériaux³, Anne Ricard⁴, Coralie Danchin-Burge^{1,2} and Xavier Rognon^{1,2}

Address: ¹AgroParisTech, UMR1236 Génétique et Diversité Animales, 16 rue Claude Bernard, F-75321 Paris, France, ²INRA, UMR1236 Génétique et Diversité Animales, 78352 Jouy-en-Josas, France, ³LABOGENA, F-78352 Jouy-en-Josas, France and ⁴INRA, UR631 Station d'amélioration génétique des animaux, BP 52627, 31326 Castanet-Tolosan, France

Email: Grégoire Leroy* - gregoire.leroy@agroparistech.fr; Lucille Callède - lcallede@gmail.com; Etienne Verrier - etienne.verrier@agroparistech.fr; Jean-Claude Mériaux - Jean-Claude.Meriaux@jouy.inra.fr; Anne Ricard - Anne.Ricard@toulouse.inra.fr; Coralie Danchin-Burge - coralie.danchin@inst-elevage.asso.fr; Xavier Rognon - Xavier.Rognon@jouy.inra.fr

* Corresponding author

Published: 19 March 2009

Received: 12 March 2009

Genetics Selection Evolution 2009, **41**:31 doi:10.1186/1297-9686-41-31

Accepted: 19 March 2009

This article is available from: <http://www.gsejournal.org/content/41/1/31>

© 2009 Leroy et al; licensee BioMed Central Ltd.

This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/2.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Abstract

After the recent publication of our article (Leroy, *Genetics Selection Evolution* 2009 41:5), we found several errors in the published Table Three, concerning the computation of contribution to within-breed diversity (CW). We apologize to the readers for these errors, which are corrected in the present erratum.

Correction

Table Three (see Table 1 of this erratum) of our recently published paper [1] contains several errors. Here we present the corrected version of Table Three (see Table 2 of this erratum) and explain the new data. The authors regret the errors.

Results

Partition of diversity

Errors concern the computation of the CW component developed by Ollivier and Foulley [2]. In the new version, CW ranged from -1 to 0.78. As aggregate diversity D is defined as a linear combination of CW and contribution to between-breed diversity, column D had also to be corrected, and ranged from -0.30 to 1.18. Consequently, the Pearson correlation between CW and ΔGD_{WS} was found to be -1 (instead of -0.72 in the previous version), and the

Pearson correlation between D and ΔGD_T was found to be -0.59 ($P = 0.008$).

Discussion

Conservation priorities

In spite of the above modifications, the populations that contributed most to the total diversity, according to the approaches of Ollivier and Foulley [2] and Caballero and Toro [3], still remain mostly the non-endangered breeds (AR, PFS, TF) [instead of AR, PS, SF, TF in the previous version].

On the contrary, when considering the eight breeds classified as endangered or endangered/maintained by the FAO (ARD, AUX, BOUL, LAND, MER, POIT, POT, TDN) and the approach of Ollivier and Foulley [2], a change is noted for the breeds exhibiting the highest contributions to

Table 1: Original and incorrect Table Three presented in Leroy et al. (2009)

| Breed code | Nb of breeding animals in 2005 | | Pr. extinction | Agregate diversity and cryopreservation potential (Ollivier and Foulley, 2005) | | | | Loss or gain of diversity when a breed is removed and contributions to optimal diversity (Caballero and Toro, 2002) | | | |
|------------|--------------------------------|---------|----------------|--|-------|-------|------|---|------------------|---------------|-------|
| | Males | Females | | CW | CB | D | CP | ΔGD_{WS} | ΔGD_{BS} | ΔGD_T | C_i |
| AA | | | 0.11 | 0.35 | 0.85 | 0.39 | 0.10 | -0.0013 | -0.0018 | -0.0031 | 0% |
| AR | 480 | 2 130 | 0.03 | 0.29 | 10.90 | 1.25 | 0.35 | -0.0015 | -0.0010 | -0.0026 | 0% |
| ARD | 187 | 1 417 | 0.08 | -0.48 | 1.33 | -0.32 | 0.10 | 0.0031 | 0.0001 | 0.0032 | 0% |
| AUX | 24 | 248 | 0.57 | -0.19 | 3.14 | 0.11 | 1.79 | 0.0023 | -0.0005 | 0.0018 | 0% |
| BOUL | 58 | 540 | 0.24 | -0.27 | 12.35 | 0.87 | 2.95 | 0.0040 | -0.0023 | 0.0018 | 6% |
| BR | 621 | 6 380 | 0.02 | -0.38 | 5.57 | 0.16 | 0.12 | 0.0016 | 0.0009 | 0.0024 | 0% |
| CAM | 118 | 837 | 0.12 | 0.00 | 7.99 | 0.73 | 0.97 | -0.0018 | 0.0013 | -0.0006 | 0% |
| COBND | 63 | 760 | 0.21 | -0.06 | 2.42 | 0.16 | 0.52 | -0.0017 | 0.0019 | 0.0002 | 2% |
| COMT | 856 | 7 073 | 0.02 | -0.25 | 3.63 | 0.11 | 0.06 | 0.0000 | 0.0015 | 0.0015 | 0% |
| LAND | 22 | 73 | 0.74 | 0.06 | 3.99 | 0.41 | 2.95 | -0.0029 | 0.0016 | -0.0014 | 2% |
| MER | 93 | 1 012 | 0.15 | -0.04 | 10.41 | 0.91 | 1.53 | 0.0000 | 0.0001 | 0.0001 | 0% |
| PER | 183 | 2 461 | 0.07 | -0.32 | 4.60 | 0.12 | 0.34 | 0.0006 | 0.0014 | 0.0020 | 0% |
| PFS | 100 | 949 | 0.14 | 0.39 | 1.93 | 0.53 | 0.27 | -0.0055 | 0.0024 | -0.0031 | 70% |
| POIT | 39 | 199 | 0.38 | -0.43 | 12.60 | 0.75 | 4.83 | 0.0069 | -0.0030 | 0.0039 | 0% |
| POT | 94 | 910 | 0.15 | 0.19 | 1.33 | 0.29 | 0.20 | -0.0040 | 0.0024 | -0.0016 | 5% |
| PS | 369 | 8 049 | 0.04 | 0.50 | 6.17 | 1.02 | 0.22 | -0.0001 | -0.0041 | -0.0042 | 1% |
| SF | 474 | 11 700 | 0.03 | 0.45 | 1.33 | 0.53 | 0.04 | -0.0024 | -0.0013 | -0.0037 | 15% |
| TDN | 16 | 183 | 0.85 | -0.17 | 1.93 | 0.02 | 1.64 | 0.0032 | -0.0009 | 0.0022 | 0% |
| TF | 527 | 15 950 | 0.02 | 0.36 | 7.51 | 1.01 | 0.18 | -0.0002 | -0.0029 | -0.0032 | 0% |
| Sum | | | | 0 | 100 | 9.054 | | 0 | -0.043 | 0.043 | 100% |

CW = contribution to within-breed diversity; CB = contribution to between-breed diversity; D = aggregate diversity; CP = cryopreservation potential; ΔGD_{WS} = loss or gain of gene diversity within populations when breed is removed; ΔGD_{BS} = loss or gain of gene diversity between populations when breed is removed; ΔGD_T = loss or gain of total diversity when the breed is removed; C_i = contribution of the breed to optimise GD_T

Table 2: Corrected Table Three

| Breed code | Nb of breeding animals in 2005 | | Pr. Extinction | Agregate diversity and cryopreservation potential (Ollivier and Foulley, 2005) | | | | Loss or gain of diversity when a breed is removed and contributions to optimal diversity (Caballero and Toro, 2002) | | | |
|------------|--------------------------------|---------|----------------|--|-------|-------|------|---|------------------|---------------|-------|
| | Males | Females | | CW | CB | D | CP | ΔGD_{WS} | ΔGD_{BS} | ΔGD_T | C_i |
| AA | 119 | 1 443 | 0.11 | 0.18 | 0.85 | 0.24 | 0.10 | -0.0013 | -0.0018 | -0.0031 | 0% |
| AR | 480 | 2 130 | 0.03 | 0.21 | 10.90 | 1.18 | 0.35 | -0.0015 | -0.0010 | -0.0026 | 0% |
| ARD | 187 | 1 417 | 0.08 | -0.46 | 1.33 | -0.30 | 0.10 | 0.0031 | 0.0001 | 0.0032 | 0% |
| AUX | 24 | 248 | 0.57 | -0.32 | 3.14 | -0.01 | 1.79 | 0.0023 | -0.0005 | 0.0018 | 0% |
| BOUL | 58 | 540 | 0.24 | -0.60 | 12.35 | 0.57 | 2.95 | 0.0040 | -0.0023 | 0.0018 | 6% |
| BR | 621 | 6 380 | 0.02 | -0.24 | 5.57 | 0.29 | 0.12 | 0.0016 | 0.0009 | 0.0024 | 0% |
| CAM | 118 | 837 | 0.12 | 0.27 | 7.99 | 0.97 | 0.97 | -0.0018 | 0.0013 | -0.0006 | 0% |
| COBND | 63 | 760 | 0.21 | 0.24 | 2.42 | 0.44 | 0.52 | -0.0017 | 0.0019 | 0.0002 | 2% |
| COMT | 856 | 7 073 | 0.02 | -0.01 | 3.63 | 0.32 | 0.06 | 0.0000 | 0.0015 | 0.0015 | 0% |
| LAND | 22 | 73 | 0.74 | 0.48 | 3.99 | 0.79 | 2.95 | -0.0029 | 0.0016 | -0.0014 | 2% |
| MER | 93 | 1 012 | 0.15 | 0.02 | 10.41 | 0.96 | 1.53 | 0.0000 | 0.0001 | 0.0001 | 0% |
| PER | 183 | 2 461 | 0.07 | -0.10 | 4.60 | 0.33 | 0.34 | 0.0006 | 0.0014 | 0.0020 | 0% |
| PFS | 100 | 949 | 0.14 | 0.78 | 1.93 | 0.89 | 0.27 | -0.0055 | 0.0024 | -0.0031 | 70% |
| POIT | 39 | 199 | 0.38 | -1.00 | 12.60 | 0.23 | 4.83 | 0.0069 | -0.0030 | 0.0039 | 0% |
| POT | 94 | 910 | 0.15 | 0.58 | 1.33 | 0.64 | 0.20 | -0.0040 | 0.0024 | -0.0016 | 5% |
| PS | 369 | 8 049 | 0.04 | 0.01 | 6.17 | 0.57 | 0.22 | -0.0001 | -0.0041 | -0.0042 | 1% |
| SF | 474 | 11 700 | 0.03 | 0.34 | 1.33 | 0.43 | 0.04 | -0.0024 | -0.0013 | -0.0037 | 15% |
| TDN | 16 | 183 | 0.85 | -0.41 | 1.93 | -0.20 | 1.64 | 0.0032 | -0.0009 | 0.0022 | 0% |
| TF | 527 | 15 950 | 0.02 | 0.02 | 7.51 | 0.70 | 0.18 | -0.0002 | -0.0029 | -0.0032 | 0% |
| Sum | | | | 0 | 100 | 9.054 | | 0 | -0.043 | 0.043 | 100% |

CW = contribution to within-breed diversity; CB = contribution to between-breed diversity; D = aggregate diversity; CP = cryopreservation potential; ΔGD_{WS} = loss or gain of gene diversity within populations when breed is removed; ΔGD_{BS} = loss or gain of gene diversity between populations when breed is removed; ΔGD_T = loss or gain of total diversity when the breed is removed; C_i = contribution of the breed to optimise GD_T

aggregate diversity D , which are now MER, LAND and POT, instead of BOUL, MER and POIT.

Finally, since the discussion on breed conservation is based on the use of several other methods and parameters, the above new results do not change our recommendations on which breeds specifically need support.

References

1. Leroy G, Calède L, Verrier E, Mériaux JC, Ricard A, Danchin-Burge C, Rognon X: **Genetic diversity of a large set of horse breeds raised in France assessed by microsatellite polymorphism.** *Genet Sel Evol* 2009, **41**:5.
2. Ollivier L, Foulley JL: **Aggregate diversity: New approach combining within- and between-breed genetic diversity.** *Livest Prod Sci* 2005, **95**:247-254.
3. Caballero A, Toro MA: **Analysis of genetic diversity for the management of conserved subdivided populations.** *Conserv Genet* 2002, **3**:289-299.

Publish with **BioMed Central** and every scientist can read your work free of charge

"BioMed Central will be the most significant development for disseminating the results of biomedical research in our lifetime."

Sir Paul Nurse, Cancer Research UK

Your research papers will be:

- available free of charge to the entire biomedical community
- peer reviewed and published immediately upon acceptance
- cited in PubMed and archived on PubMed Central
- yours — you keep the copyright

Submit your manuscript here:
http://www.biomedcentral.com/info/publishing_adv.asp

