

CORRECTION

Open Access



Correction: A genome-wide scan to identify signatures of selection in two Iranian indigenous chicken ecotypes

Elaheh Rostamzadeh Mahdabi, Ali Esmailzadeh, Ahmad Ayatollahi Mehrgardi and Masood Asadi Fozi*

Correction to: *Genet Sel Evol* (2021) 53:72

<https://doi.org/10.1186/s12711-021-00664-9>

After publication of this work [1], we noticed that (1) we had not clearly stated that the data are publicly available and (2) we had not cited the original paper [2]. Therefore, the following sections “Background”, “Methods”, “Availability of data and materials” and “References” are incomplete and should be amended as follows.

Background

Page 1, first paragraph of the “Background” section where we stated “that domestic chicken originated from the Red Jungle fowl (*Gallus gallus*) in the south and Southeast Asia”, the following sentence is missing:

“Recently, a comprehensive study, which analyzed 863 whole-genome sequences from a worldwide sampling of chickens and representatives of all four species of wild jungle fowl and each of the five subspecies of red jungle fowl (RJF), concluded that domestic chickens were initially derived from the RJF subspecies *Gallus gallus spadiceus* whose present-day distribution is predominantly in southwestern China, northern Thailand and Myanmar [2]”.

Methods

Sampling and genome sequencing

Page ‘3’, first paragraph, line ‘10’ where we described the preparation of DNA samples, the following sentence is missing:

“Whole-genome sequencing of the samples using the next-generation sequencing technique was conducted within the framework of the Global Chicken Genome Project (<http://chicken.yнау.edu.cn/index/about/index.html>) led by the Kunming Institute of Zoology, Chinese Academy of Sciences (KIZ-CAS) and described by Wang *et al.* [2–5]”.

Availability of data and materials

The following sentence “The datasets used for the current study are available from the corresponding author upon reasonable request” should read:

“The datasets used for the current study were from Wang *et al.* [2]. The raw sequencing data, alignment of BAM files, and genotypes (VCF) are available in the ChickenSD database (<http://bigd.big.ac.cn/chickensd/>)”.

Published online: 19 April 2022

References

1. RostamzadehMahdabi E, Esmailzadeh A, AyatollahiMehrgardi A, Asadi FM. A genome-wide scan to identify signatures of selection in two Iranian indigenous chicken ecotypes. *Genet Sel Evol.* 2021;53:72. <https://doi.org/10.1186/s12711-021-00664-9>.

The original article can be found online at <https://doi.org/10.1186/s12711-021-00664-9>.

*Correspondence: masadi@uk.ac.ir
Department of Animal Science, Faculty of Agriculture, Shahid Bahonar University of Kerman, 22 Bahman Blvd, Kerman, Iran



© The Author(s) 2022. **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>. The Creative Commons Public Domain Dedication waiver (<http://creativecommons.org/publicdomain/zero/1.0/>) applies to the data made available in this article, unless otherwise stated in a credit line to the data.

2. Wang MS, Thakur M, Peng MS, Jiang Y, Frantz LAF, Li M, et al. 863 genomes reveal the origin and domestication of chicken. *Cell Res.* 2020;30:693–701.
3. Wang MS, Zhang JJ, Guo X, Li M, Meyer R, Ashari H, et al. Large-scale genomic analysis reveals the genetic cost of chicken domestication. *BMC Biol.* 2021;19:118.
4. Wang MS, Li Y, Peng MS, Zhong L, Wang ZJ, Li QY, et al. Genomic analyses reveal potential independent adaptation to high altitude in Tibetan chickens. *Mol Biol Evol.* 2015;32:1880–9.
5. Wang MS, Otecko NO, Wang S, Wu DD, Yang MM, Xu YL, et al. An evolutionary genomic perspective on the breeding of dwarf chickens. *Mol Biol Evol.* 2017;34:3081–8.

Publisher's Note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Ready to submit your research? Choose BMC and benefit from:

- fast, convenient online submission
- thorough peer review by experienced researchers in your field
- rapid publication on acceptance
- support for research data, including large and complex data types
- gold Open Access which fosters wider collaboration and increased citations
- maximum visibility for your research: over 100M website views per year

At BMC, research is always in progress.

Learn more biomedcentral.com/submissions

