



# Correction to: Genetics and breeding for climate change in Orphan crops

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## Correction to:

**Theoretical and Applied Genetics (2021) 134:1787–1815**  
<https://doi.org/10.1007/s00122-020-03755-1>

In the original publication, several references were given incorrectly, or missing in the reference list. The correct references are listed below.

Under the sub-heading “Genome Editing”, the definition of genome editing in the first sentence is linked to the wrong reference. The correct reference should be:

Zhang H, Zhang J, Lang Z et al. (2017) Genome editing—principles and applications for functional genomics research and crop improvement. *Crit Rev Plant Sci* 36:291–309. <https://doi.org/10.1080/07352689.2017.1402989>

All other corrections refer to Table 1:

Joseph et al. (2017) should be replaced with Jarvis et al. (2017). The full reference is:

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The original article can be found online at <https://doi.org/10.1007/s00122-020-03755-1>.

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Jarvis DE, Ho YS, Lightfoot DJ, Schmöckel SM et al. (2017) The genome of *Chenopodium quinoa*. *Nature* 542:307–312. <https://doi.org/10.1038/nature213702>

Yang et al. (2014) should be cited as Yang et al. (2015) and should be referenced as:

Yang K, Tian Z, Chen C, Luo L et al. (2015) Genome sequencing of adzuki bean (*Vigna angularis*) provides insight into high starch and low fat accumulation and domestication. *Proc Natl Acad Sci U S A* 112:13213–13218. <https://doi.org/10.1073/pnas.1420949111>.

Yang et al. (2015) should be replaced with Kang et al. (2014). The full reference is:

Kang YJ, Kim SK, Kim MY, Lestari P et al. (2014) Genome sequence of mungbean and insights into evolution within *Vigna* species. *Nat Comm* 5(1):1–9.

Pati et al. (2019) should be replaced with Paritosh et al. (2019). The full reference is:

Paritosh K, Yadava SK, Singh P, Bhayana L et al. (2021) A chromosome-scale assembly of allotetraploid *Brassica juncea* (AABB) elucidates comparative architecture of the A and B genomes. *Plant Biotechnol J* 19:602–614. <https://doi.org/10.1111/pbi.13492>.

The authors wrongfully cited Mayes et al. (2020) in Table 1. This citation should be deleted.

The following references were omitted in the reference list despite appearing in Table 1:

Ha J, Shim S, Lee T, Kang YJ et al. (2019) Genome sequence of *Jatropha curcas* L., a non-edible biodiesel plant, provides

- a resource to improve seed-related traits. *Plant Biotechnol J* 17:517–530. <https://doi.org/10.1111/pbi.12995>.
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- Jiao F, Luo R, Dai X, Liu H et al. (2020) Chromosome-level reference genome and population genomic analysis provide insights into the evolution and improvement of domesticated mulberry (*Morus alba*). *Mol Plant* 13:1001–1012. <https://doi.org/10.1016/j.molp.2020.05.005>.
- Kaul T, Eswaran M, Thangaraj A, Meyyazhagan A et al. (2019) Rice Bean (*Vigna umbellata*) draft genome sequence: unravelling the late flowering and unpalatability related genomic resources for efficient domestication of this underutilized crop. *bioRxiv Prepr* 1–41. <https://doi.org/10.1101/816595>.
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- Yang J, Liu D, Wang X, Ji C et al. (2016) The genome sequence of allopolyploid Brassica juncea and analysis of differential homoeolog gene expression influencing selection. *Nat Genet* 48:1225–1232. <https://doi.org/10.1038/ng.3657>.
- Yang J, Moeinzadeh MH, Kuhl H, Helmuth J et al. (2017) Haplotype-resolved sweet potato genome traces back its hexaploidization history. *Nat Plants* 3:696–703. <https://doi.org/10.1038/s41477-017-0002-z>.
- Yasui Y, Hirakawa H, Ueno M, Matsui K et al. (2016) Assembly of the draft genome of buckwheat and its applications in identifying agronomically useful genes. *DNA Res* 23:215–224. <https://doi.org/10.1093/dnares/dsw012>.
- Zhang T, Ren X, Zhang Z, Ming Y et al. (2020) Long-read sequencing and de novo assembly of the *Luffa cylindrica* (L.) Roem. genome. *Mol Ecol Resour* 20:511–519. <https://doi.org/10.1111/1755-0998.13129>.
- Zou C, Li L, Miki D, Li D et al. (2019) The genome of broomcorn millet. *Nat Commun* 10:1–11. <https://doi.org/10.1038/s41467-019-08409-5>.

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