

ERRATUM

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Erratum to: SNP-based analysis of genetic diversity reveals important alleles associated with seed size in rice

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Erratum

Unfortunately, the original version of this article [1] contained two errors within the text. On page 2 within the Background section the sentence: “Sasanishiki is a high-yielding indica cultivar” should have read: “Sasanishiki is an average-yielding japonica cultivar”.

Also at the end of page 2 in the Results section the sentence: “Consistent with the phenotypical classification, the varieties from China, Guichao2, Nanjing11 and Nanjing35 were grouped into the *indica* type, together with IR36 and IR24 from IRRI; the varieties from Japan, Sasanishiki, Koshihikari, Habataki, and Asominori were grouped into *japonica*, together with USSR5 from Russia; the varieties N22 and Kasalath from India were grouped into *aus*.” should have read: “Consistent with the phenotype classification, the varieties from China, Guichao2 and Nanjing11 were grouped into the *indica* type, together with IR36 and IR24 from IRRI; the varieties from Japan, Sasanishiki, Koshihikari, and Asominori were grouped into *japonica*, together with USSR5 from Russia; the varieties N22 and Kasalath from India were grouped into *aus*.”

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References

1. Weijie T, Tingting W, Jian Y, Juan S, Yue J, Jun Y, et al. SNP-based analysis of genetic diversity reveals important alleles associated with seed size in rice. *BMC Plant Biol.* 2016;16:93.

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