

CORRECTION

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Correction: Genome-wide identification and expression characterization of the *DoG* gene family of moso bamboo (*Phyllostachys edulis*)

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Correction: *BMC Genomics* 23, 357 (2022)
<https://doi.org/10.1186/s12864-022-08551-3>

Following publication of the original article [1], a typesetting error was identified in the **Analysis of conserved structural domains and conserved motifs of the *PeDoGs*** section.

The paragraph currently reads:

To study the structural domains of the *DoGDoGDoGDoG*

The paragraph should read:

To study the structural domains of the *DoG* family of moso bamboo, the GFF annotation file of the whole genome of moso bamboo was used to extract the

structural information of the moso bamboo *DoG* family genes. The structural domains of the moso bamboo *DoG* family were analyzed by NCBI Conserved Domain (<https://www.ncbi.nlm.nih.gov/cdd/>), and the gene structures and protein structural domains were mapped by TBtools software. The conserved motifs of the *DoG* family of Moso bamboo were predicted by using the online amino acid conserved motif analysis software MEME (<http://meme-suite.org/tools/meme>) with the following parameter settings: the motif discovery mode was classical with a predicted number of motifs of 5, and each motif occurred 0 or 1 times.

The original article [1] has been corrected.

The original article can be found online at <https://doi.org/10.1186/s12864-022-08551-3>.

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Reference

1. Zhijun Z, Peiyao Y, Bing H, et al. Genome-wide identification and expression characterization of the *DoG* gene family of moso bamboo (*Phyllostachys edulis*). *BMC Genomics*. 2022;23:357. <https://doi.org/10.1186/s12864-022-08551-3>.



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