

AUTHOR CORRECTION

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Author Correction: DNA methylation remodeling and the functional implication during male gametogenesis in rice

Xue Li^{1†}, Bo Zhu^{1†}, Yue Lu², Feng Zhao¹, Qian Liu¹, Jiahao Wang¹, Miaomiao Ye¹, Siyuan Chen¹, Junwei Nie³, Lizhong Xiong¹, Yu Zhao¹, Changyin Wu¹ and Dao-Xiu Zhou^{1,4*}

[†]Xue Li and Bo Zhu contributed equally to this work.

The original article can be found online at <https://doi.org/10.1186/s13059-024-03222-w>.

*Correspondence: dao-xiu.zhou@universite-parisaclay.fr

¹ National Key Laboratory of Crop Genetic Improvement, Hubei Hongshan Laboratory, Huazhong Agricultural University, Wuhan 430070, China

² Key Laboratory of Plant Functional Genomics of the Ministry of Education/ Jiangsu Key Laboratory of Crop Genomics and Molecular Breeding, College of Agriculture, Yangzhou University, Yangzhou 225009, China

³ Vazyme Biotech Co., Ltd, Nanjing 210000, China

⁴ Institute of Plant Science Paris-Saclay (IPS2), CNRS, INRAE, Université Paris-Saclay, 91405 Orsay, France

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Following publication of the original article [1], the authors identified an error in Fig. 2. In Fig. 2B, a wild type pollen picture was wrongly used to represent *cmt3b* pollens that in fact are of wild type phenotype.

The incorrect and correct Fig. 2 is published in this correction article and the original article [1] has been updated.



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Incorrect figure:

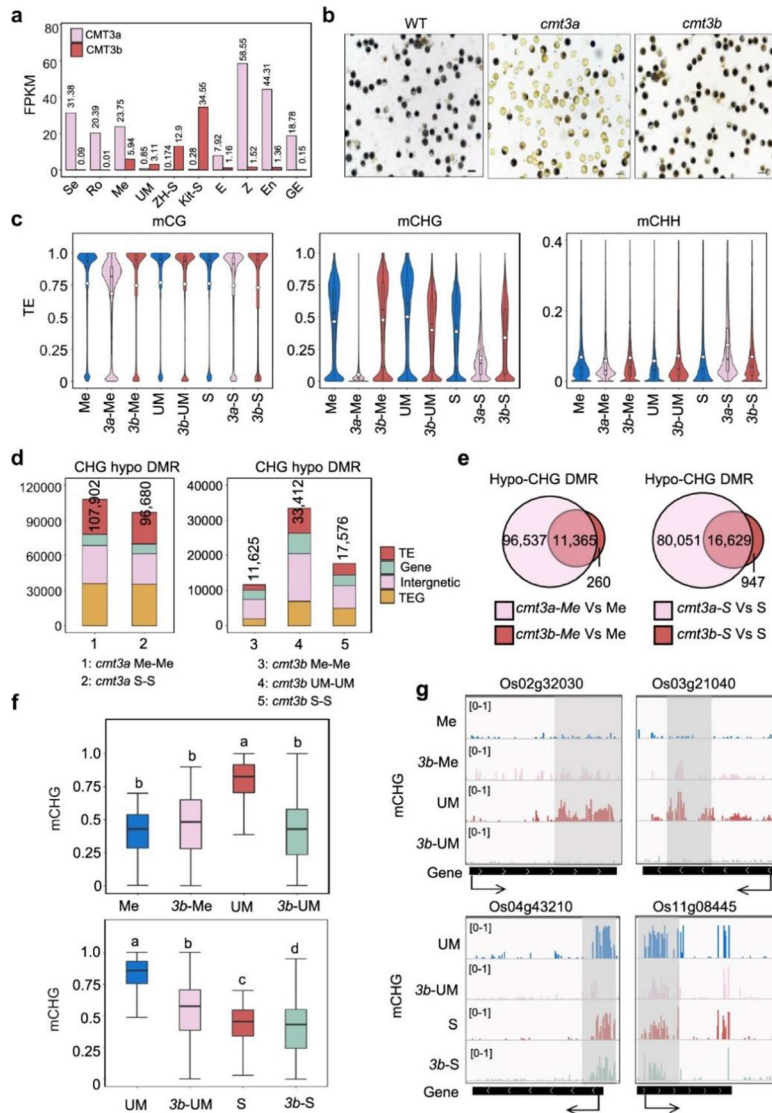


Fig. 2 Effects of *cmt3a* and *cmt3b* mutations on DNA methylation in meicyte, microspore and sperm. **a** Transcript levels in FPKM of rice CMT3a and CMT3b in seedling (Se), roots (Ro), meicyte (Me), unicellular microspore (UM), sperm (S), egg (E), zygote (Z), endosperm nuclei (En, 1.5 days after fertilization) and globular embryo (GE, 3 days after fertilization) from RNA-seq data. The sperm (Kit-S) in Kitaake background was reported by Anderson et al., (2013). **b** The pollen grains of wild type and *cmt3a* and *cmt3b* mutants were I2-KI stained. Bars = 50 μ m. **c** Violin plots comparing overall cytosine methylation levels of wild type and *cmt3a* and *cmt3b* mutant meicyte (Me), unicellular microspore (UM) and sperm (S). The average methylation levels (white dots) and median values (black bars) in transposable elements (TE) are shown. Values of the methylomes are averages from the two replicates. **d** Number of differential methylated regions (DMR) in *cmt3a* and *cmt3b* relative to wild type. Relative portions in TE (> 500 bp), TEG, gene, and Intergenic regions are indicated by different colors. **e** Venn diagrams showing overlapping of hypo-CHG DMRs in *cmt3a* and *cmt3b* meicyte (left) and sperm (right) relative to wild type cells. **f** Box plots of DNA methylation levels of hypo-CHG DMRs in meicyte (Me) versus microspore (UM) (upper) and sperm (S) relative to microspore (UM) (lower) in wild type, *cmt3a* (3a) and *cmt3b* (3b) cells. The significance was calculated with multiple comparison tests. Different letters on top of the bars indicate a significant difference ($p < 0.05$). **g** Genome Browser screen captures showing high CHG methylation sites in microspore relative to meicyte and sperm decreased in *cmt3b* mutants (highlighted by grey)

Correct figure:

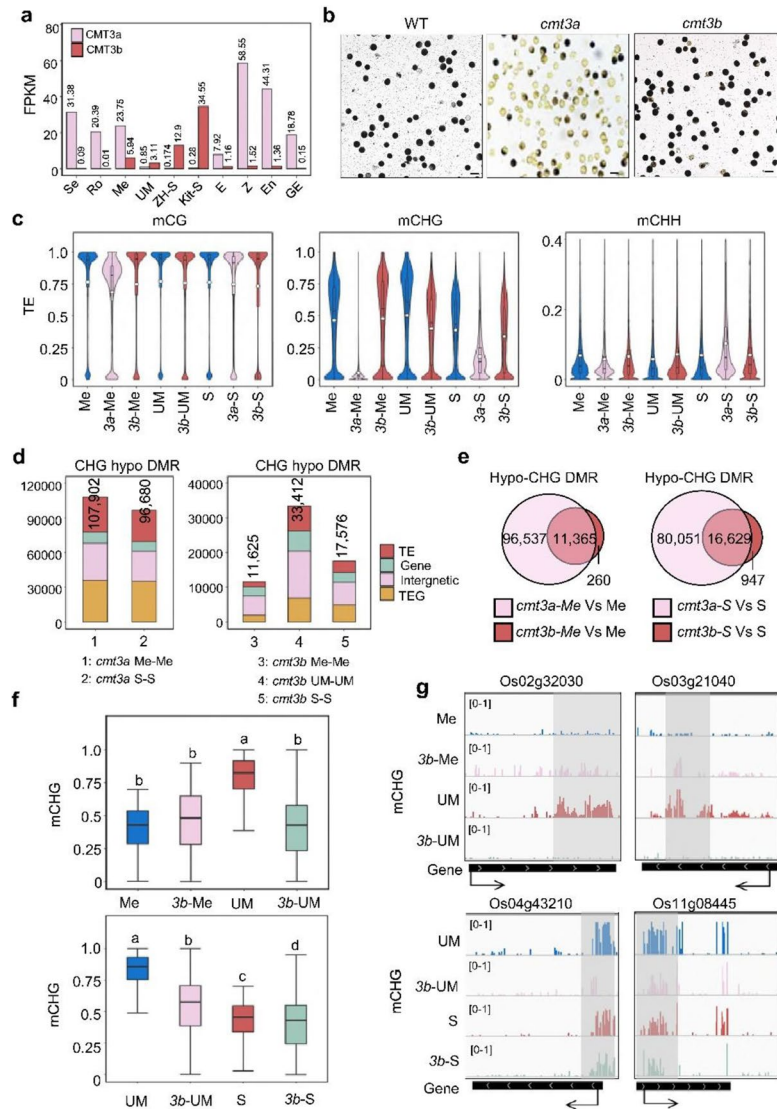


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Reference

1. Li X, Zhu B, Lu Y, et al. DNA methylation remodeling and the functional implication during male gametogenesis in rice. *Genome Biol.* 2024;25:84. <https://doi.org/10.1186/s13059-024-03222-w>.