

Corrections

EVOLUTION

Correction for “Origin, inheritance, and gene regulatory consequences of genome dominance in polyploids,” by Margaret R. Woodhouse, Feng Cheng, J. Chris Pires, Damon Lisch, Michael Freeling, and Xiaowu Wang, which appeared in issue 14, April 8, 2014, of *Proc Natl Acad Sci USA* (111:5283–5288; first published March 24, 2014; 10.1073/pnas.1402475111).

The authors note that Fig. 2 and its corresponding legend appeared incorrectly. The corrected figure and its corrected legend appear below.

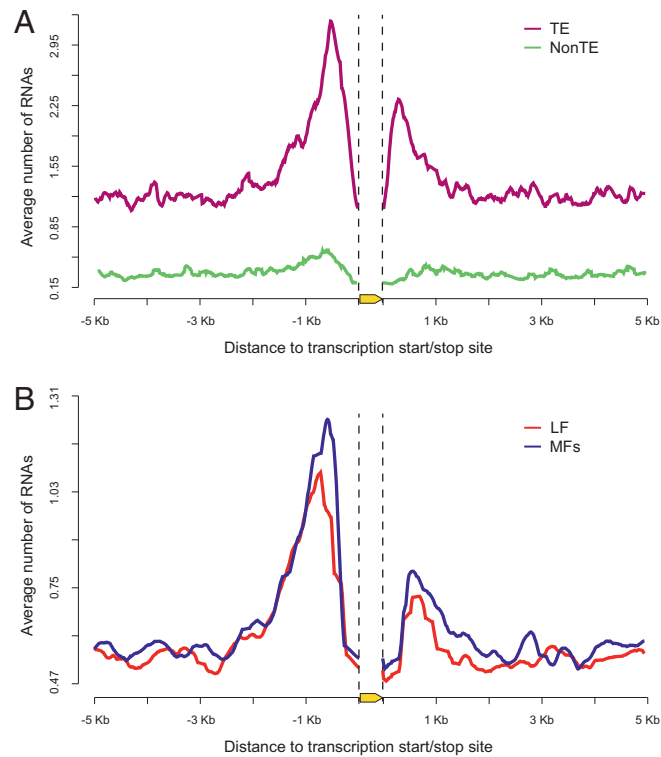


Fig. 2. Twenty-four-nucleotide smRNAs were enriched in TEs flanking LF *B. rapa* genes (gene space is represented by yellow arrow). In the y axis, the number of unique, perfectly mapped 24-nt RNAs was averaged in a 100-bp sliding window moving in 10-bp increments through each flanking region of *B. rapa* genes. All genes have an Arabidopsis ortholog. In the x axis, kilobytes from the start and end of transcription are shown. (A) Overall targeting level distribution of 24-nt RNA molecules to flanking sequences of the average *B. rapa* gene, with (green) and without (red) known transposons being hard-masked. (B) Overall targeting level distribution of 24-nt RNA molecules to flanking TE sequences outside of the gene (everything but TEs masked) of *B. rapa* genes, with subgenome location of these genes differentiated by LF (red) or MFs (blue, MF1 and MF2). Genes from subgenome LF and MFs were calculated separately.

www.pnas.org/cgi/doi/10.1073/pnas.1405833111

PLANT BIOLOGY

Correction for “Natural variation of rice strigolactone biosynthesis is associated with the deletion of two *MAX1* orthologs,” by Catarina Cardoso, Yanxia Zhang, Muhammad Jamil, Jo Hepworth, Tatsiana Charnikhova, Stanley O. N. Dimkpa, Caroline Meharg, Mark H. Wright, Junwei Liu, Xiangbing Meng, Yonghong Wang, Jiayang Li, Susan R. McCouch, Ottoline Leyser, Adam H. Price, Harro J. Bouwmeester, and Carolien Ruyter-Spira, which appeared in issue 6, February 11, 2014, of *Proc Natl Acad Sci USA* (111:2379–2384; first published January 24, 2014; 10.1073/pnas.1317360111).

The authors note that, in the Acknowledgments, the statement “Bala sequencing was supported by European Union FP6 Project 015468 (“CEDROME”) and a Monitoring Agricultural Resources grant” should instead appear as “Bala sequencing was supported by European Union FP6 Project 015468 (“CEDROME”) and a Mars grant.”

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PHYSIOLOGY

Correction for “Ion channel-kinase TRPM7 is required for maintaining cardiac automaticity,” by Rajan Sah, Pietro Mesirca, Marjolein Van den Boogert, Jonathan Rosen, John Mably, Matteo E. Mangoni, and David E. Clapham, which appeared in issue 32, August 6, 2013, of *Proc Natl Acad Sci USA* (110:E3037–E3046; first published July 22, 2013; 10.1073/pnas.1311865110).

The authors note that they “inadvertently omitted crediting Dr. Andreas Ludwig (Friedrich-Alexander-Universität Erlangen-Nürnberg) for providing the HCN4-CreERT2 line for sinoatrial deletion of TRPM7. We apologize for this oversight.” The above credit statement should be added to the Acknowledgments.

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