

Localized hypermutation and associated gene losses in legume chloroplast genomes

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The structures of the two *Trifolium repens* cDNAs reported in Figure S6 of this paper are incorrect. The *T. repens* nuclear *accD*-coding region is fused to *LPD1*, not *LPD2* as reported. We incorrectly assembled full-length cDNAs from expressed sequence tags, resulting in erroneous “recombination” between *LPD1* and *LPD2* in a region of high similarity about 200 bp upstream of the *LPD1-accD* junction. Correct sequences of *LPD1-accD* and *LPD2* cDNAs from both *T. repens* and *T. pratense* have been reported by Sabir et al. (2014) and deposited in GenBank (<http://www.ncbi.nlm.nih.gov/genbank/>) with accession numbers KF781540–KF781544. We have therefore withdrawn our *T. repens* cDNA sequences from the nucleotide databases (European Nucleotide Archive accession numbers HM029367–HM029368; <http://www.ebi.ac.uk/ena/home>).

The authors apologize for any inconvenience caused by this error and thank Jin Zhang, Bob Jansen, and Tracey Ruhlman for bringing it to our attention. This correction does not affect any of the paper’s conclusions other than the name of the fusion gene.

Reference

Sabir J, Schwarz E, Ellison N, Zhang J, Baeshen NA, Mutwakil M, Jansen R, Ruhlman T. 2014. Evolutionary and biotechnology implications of plastid genome variation in the inverted repeat-lacking clade of legumes. *Plant Biotech J* doi: 10.1111/pbi.12179.