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Correction

Brachypodium: 20 years as a grass biology model system; the way forward?

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John P. Vogel, Kai Wang, and Luis A.J. Mur*

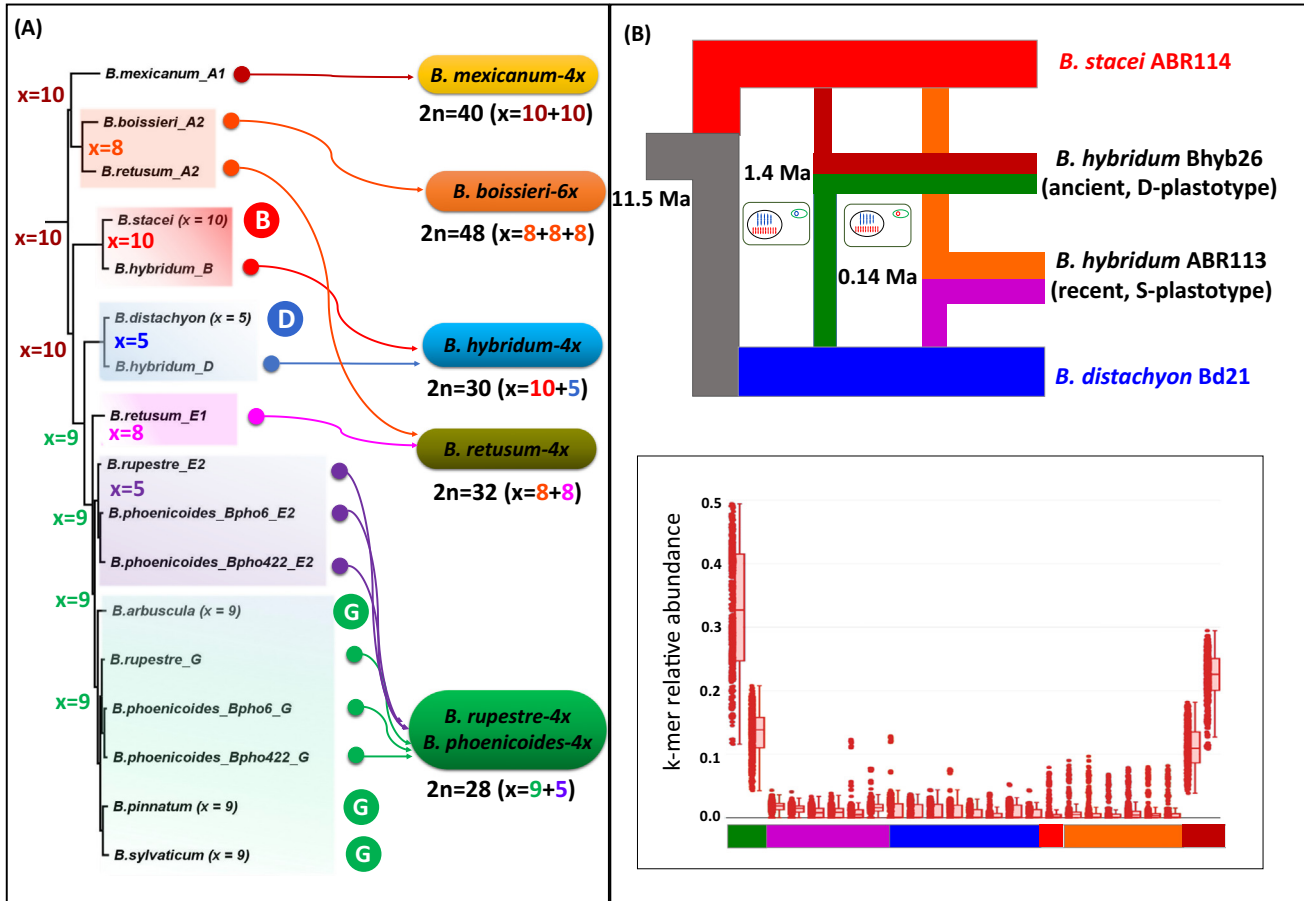
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(*Trends in Plant Science* 27, 1002–1016, 2022)

In the Feature Review article '*Brachypodium*: 20 years as a grass biology model system; the way forward?' by Robert Hasterok *et al.*, which was published in the October 2022 issue of *Trends in Plant Science*, '0.14 Ma' was incorrectly given as '0.4 Ma' in the main text on page 1004, and in [Figure 1B](#) and the affiliated figure legend on page 1005. The corrected text and Figure are below.

This change does not affect the conclusions mentioned in the paper. The authors apologize for the error.

P. 1004: "... Pangenomic and coalescence dated analyses detected multiple and bidirectional origins for the wild allotetraploid *B. hybridum*, with ancestral [*B. distachyon*-type (D) plastotypes] and recent [*B. stacei*-type (S) plastotypes] allotetraploids, originating 1.4 and 0.14 Ma, respectively ([Figure 1B](#)) [27]."





Trends in Plant Science

Figure 1. Inferred evolutionary speciation events of annual and perennial *Brachypodium* species. (A) Comprehensive evolutionary framework for the origins of *Brachypodium* diploids and polyploids based on the combined phylogenomic and comparative chromosome barcoding analyses [26]. Colours indicate the different types of (sub)genomes retrieved in the phylogenomic analysis using 322 gene-based phylogeny and subgenome detection algorithms; letters designate the karyotype profiles found in the diploids and polyploids. Allopolyploid species show different types of known (B, D, G) or orphan (A1, A2, E1, E2) diploid progenitor subgenomes [*Brachypodium hybridum*-4x (B, D), *Brachypodium retusum*-4x (A2, E1), *Brachypodium phoenicoides*-4x (E2, G), *Brachypodium rupestre*-4x (E2, G)], whereas putative autoploid (or segmental allopolyploid) species show the same type of orphan progenitor subgenome [*Brachypodium mexicanum*-4x (A1A1), *Brachypodium boissieri*-6x (A2A2A2)] (modified from [26]). (B) Evolutionary allopolyploidisation scenarios for the origins of the two types of *B. hybridum* lines; ancient *B. hybridum* (reference genome Bhyb26, showing maternal plastome D inherited from *B. distachyon*) and recent *B. hybridum* (reference genome ABR113 showing maternal plastome S inherited from *B. stacei*) were formed from distinct hybridisation and genome doubling events 1.4 and 0.14 Ma, respectively. Stylised plant cell diagrams with colour coding indicating the origins of the plastomes (circles) and nuclear genomes (haploid chromosome numbers) of ancient and recent *B. hybridum* lines (*B. distachyon*-type D genomes, blue; *B. stacei*-type S genomes, red). The datings were inferred from the coalescence-based and cross-bracing analyses of Gordon *et al.* 2020 (modified from [27]). Abundance of a repeat k-mer class that expanded in the D and S subgenomes of the ancient but not the recent hybrids, nor in the progenitor genomes, indicates a postpolyploidisation evolutionary novelty. Genomes and subgenomes are indicated by their respective colour codes in the bar below the x axis and correspond to those indicated in the above cladogram: from left to right, ancient *B. hybridum* D subgenome (green), recent *B. hybridum* D subgenome (purple), *B. distachyon* D genome (blue); *B. stacei* S genome (red); recent *B. hybridum* S subgenome (orange); ancient *B. hybridum* S subgenome (brown) (modified from [27]).