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ERRATUM

Polyphenol oxidase (PPO) in wheat and wild relatives: molecular evidence for a multigene family

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Towards the right-hand side of Fig. 3, between the dashed and continuous brackets, Greek letters were used to indicate some groupings. However, these were incorrectly rendered as question marks. The correct figure is given here.

The online version of the original article can be found at http://dx.doi.org/10.1007/s00122-007-0514-4.

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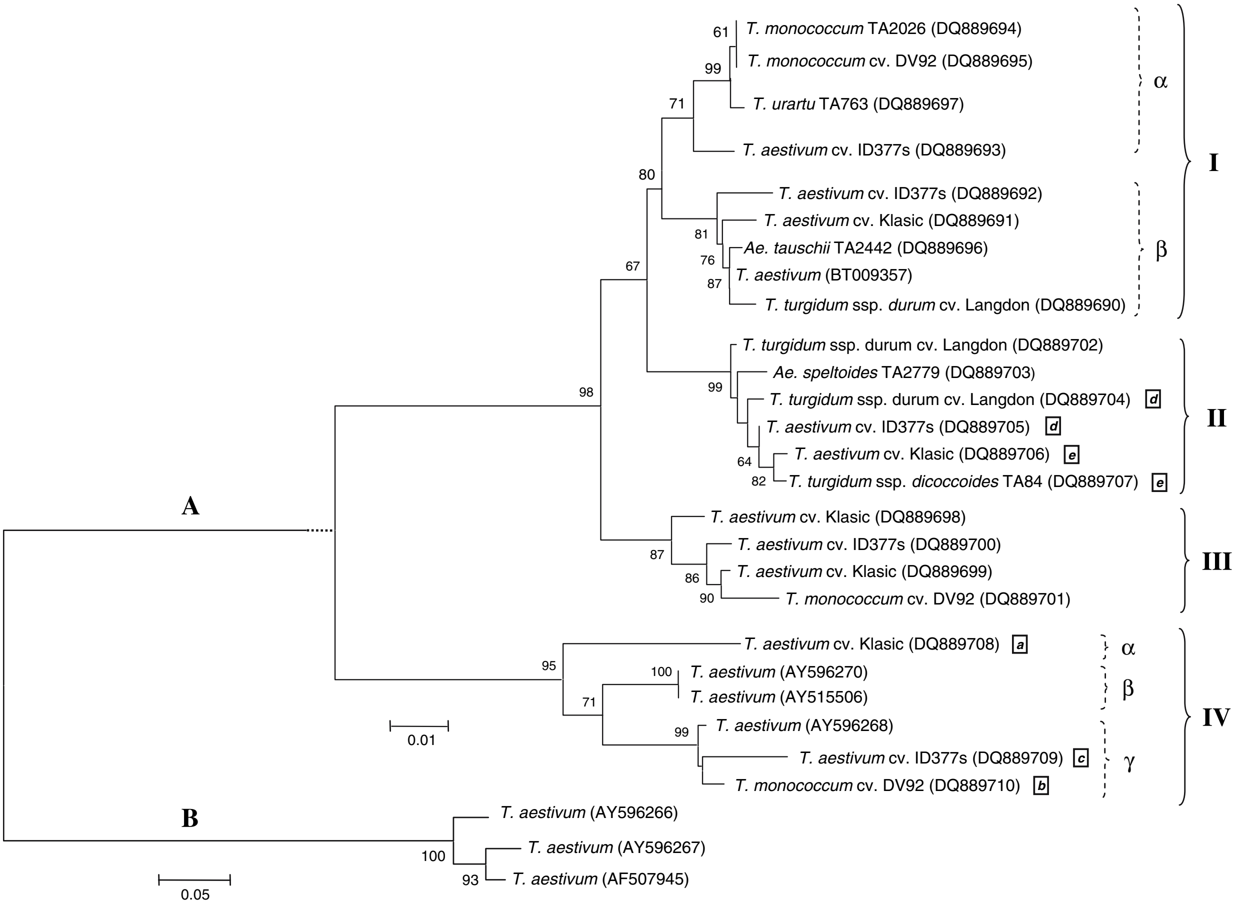

Fig. 3 Phylogenetic analysis of the PPO gene family. The tree was derived by neighbor-joining distance analysis using 28 sequences of about 440 nucleotides (excluding gaps and introns). Bootstrap values over 60% are indicated. The seed specific PPO subtree (**a**) was re-grafted to a different scale and appended to the main backbone tree as indicated by a broken horizontal line. **b** Shows the branch of non-seed PPO sequences. Genes are labeled by species name, accession identifier, and GenBank accession number (in *parentheses*). Intron presence is indicated by the corresponding number in a square box. *Scale bar* indicates the number of nucleotide substitutions per site