

## Incongruence and the Phylogeny of the *Triticeae* (Poaceae)

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**Abstract:** Despite its economic importance the phylogeny of the tribe remains largely unsettled. The vast majority of the species are allopolyploids, with an apparently known history, but the relationships of their diploids progenitors are obscure. Nearly all phylogenies of the *Triticeae* (Poaceae), which have been based on more than a single data set, show a high level of incongruence between different data partitions. The contribution of individual data sets from different genome compartments are explored in this analysis based on eight data sets, viz. nucleotide sequences from three plastid genes (*rbcL*, *ndhF*, and *rpoA*), one mitochondrial gene (*coxII*), two single-copy nuclear genes (*DMC1* and *EF-G*), one multi-copy nuclear region (ITS), and morphology.