A BC$_2$S$_3$ Maize-Teosinte RIL Population for QTL Mapping

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The Doebley laboratory developed a set of 866 maize-teosinte BC$_2$S$_3$ recombinant inbred lines (RILs). The maize parent of these lines was an U.S. maize inbred line, W22, and the teosinte parent was *Zea mays* ssp. *parviglumis* (CIMMYT accession 8759) from the Balsas region of southwestern Mexico. W22 was used as the ear parent for the F1 and the recurrent parent for the two generations of backcrossing. The lines were scored for over 50,000 marker loci using genotyping-by-sequencing (GBS) technology and phenotyped for 16 traits during three field seasons. QTL analysis is summarized in the PhD dissertation of Shannon (2012), which is available at Doebley lab website (http://teosinte.wisc.edu/). This set of lines have been extensively used to map QTLs for many traits, including seed shattering (Lin et al. 2012), leaf number (Li et al. 2016), kernel row number (Calderón et al. 2016), shoot apical meristem morphology (Leiboff et al. 2016), vascular bundle number (Huang et al. 2016), tassel related traits (Xu et al. 2017b), nodal root number (Zhang et al. 2018), and leaf morphological traits (Fu et al. 2019). Also, several QTLs have been fine-mapped to single gene including *grassy tillers1* (*gt1*) for prolificacy (Wills et al. 2013), *prolamin-box binding factor1* (*pbf1*) for kernel weight (Lang et al. 2014), *glossy15* (*gl15*) for vegetative phase changes (Xu et al. 2017a), as well as several genes for flowering time: *ZmCCT10* (Hung et al. 2012), *Zea Agamous-like1* (*zagl1*) (Wills et al. 2017), *ZmCCT9* (Huang et al. 2018), *ZCN8* (Guo et al. 2018), and *ZmMADS69* (Liang et al. 2018). In addition to phenotypic traits, it has also been used for a comprehensive genome-wide eQTL analysis to study the changes in gene expression during maize domestication (Wang et al. 2018).

We report here that seeds of this RIL set are available at Maize Genetics Stock Center, GBS marker data available at the Cyverse Discovery Environment: http://datacommons.cyverse.org/browse/iplant/home/shared/panzea/genotypes/GBS/v23/teoW22_BC2S3_GBS_phased_genos_imputed_20110423.zip and phenotype data available at figshare database (https://figshare.com/s/0d3aa121f8393c9b4720). We hope this valuable resource will be useful for the maize community on QTL mapping and gene cloning of domestication traits or any further studies.

Keywords: maize, teosinte, RIL, domestication

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