Registration of IBM2 SYN10 Doubled Haploid Mapping Population of Maize

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The IBM2 SYN10 Doubled Haploid (DH) mapping population of Maize (Zea mays L.) is a set of 360 doubled haploid lines (Reg. No. MP-1, NSL 445573 MAP) produced from a randomly mated population derived from [B73 (PI 550473) × Mo17 (PI 558532)] SYN10 population (Lamkey, 1992; Russell, 1972).

(B73 × Mo17) SYN10, obtained from A.R. Hallauer at the Department of Agronomy, Iowa State University, Ames, was crossed to an inducer line to generate haploid kernels in 2002, followed by a chromosome doubling step and line increase in 2003. Four hundred and fifty plants were used to make crosses in the induction nursery. These DH lines are yellow-seeded maize with dent endosperm.

Having undergone 10 generations of recombination, followed by the double haploid process, this population offers a genetic tool to the maize community. These germplasm lines combine agronomic performance with exceptional genotypic properties that should be of value to breeders developing high-value maize germplasm.

Based on observational plots in a single replication at one location, average across plot population, plant height ranged from 47 to 109 cm, and average ear height ranged from 14 to 94 cm. Time to reach 50% male flowering ranged from 1269 heat units (HU; 63 d) to 1741 HU (87 d). Plant height, ear height, and flowering time data were used for evaluation. By comparison, the parental lines provided an average plant height, ear height, and male flowering of 216 cm, 87 cm, and 1478 HU for B73, and 229 cm, 90 cm, and 1481 HU for MO17, respectively. These IBM2 Syn10 DH lines exhibited a high degree of phenotypic variability between lines within the population structure compared to conventionally derived lines, allowing the identification of economically important genes. They can also be useful for other genetic recombinant studies.

The IBM2 Syn10 DH lines will facilitate development of high-density genetic maps of maize, which will be useful in development of a physical map and genetic fine mapping. An accurate physical map facilitates the sequencing of the maize genome, whereas fine mapping of genes will lead to cloning and studying gene function.

This is the second significant donation of maize materials Pioneer made in 2004. In March 2004, the National Corn Growers Association announced Pioneer, Monsanto, and Ceres, Inc., corn genome sequence data to significantly accelerate the identification of genes within the entire corn genome (Anonymous, 2004). A complete gene sequence would significantly speed the rate of discovery and crop improvement. In late 2004, Pioneer released seed of this population and SSR marker genotypes of all the lines from 20 public SSR markers to the Maize Genetics Stock Center, University of Illinois, Champaign, IL, 61801.

Small quantities of seed may be obtained from the Maize Genetics Stock Center. We ask that appropriate recognition be given when this germplasm contributes to future research.

References