

nomically, other than in the commercial breeding program for which I was personally responsible, little use has been made of the [doubled haploid] method in the development of homozygous diploids. Increased interest in and use of such radical techniques is likely in the future as the challenges of intensified commercial maize culture and of the highly competitive hybrid seedcorn market necessitate an increasingly high degree of responsiveness on the part of the maize breeder.”

The practicality of the method today certainly owes much to Coe’s “stock 6” and its derivatives, to improvements and techniques for genome doubling, and to the higher technical skills of maize breeders.

#### **Firsts (achieved by SSC):**

1) First haploid to doubled haploid. The first homozygous diploid derived from a haploid was out of sweet corn (Golden Cross Bantam).

2) First substantial confirmation of different rates of parthenogenesis among female parents. (Stadler obtained a frequency of about 1:100 in a diploid multiple recessive tester; most prior information suggested rates of about 1:1000.)

3) First recognition that rates of parthenogenesis were influenced by the male parent.

4) First haploids in quantity.

5) First observation of high rates of somatic chromosome complement doubling in haploids.

6) First doubled haploids in quantity.

7) First to use “embryo markers” for dry seed haploid selection (Pu, etc.).

(A major disadvantage of Pu, purple embryo marker, is — was — that it occurs widely in Corn Belt maize; Stadler told me that 15% of the then available inbreds in use had the purple plumule phenotype, hence Pu was not a “clean” marker for my purposes.)

8) First doubled haploid line(s) in successful commercial hybrid(s). (Example: DeKalb 640)

9) First “second generation” doubled haploid lines in commercial hybrid (H2386 and H2398, both ex H73xH225).

10) First cloning of haploid through reproductive process (W23 haploid).

11) First, with Sam Goodsell, to demonstrate cytoplasmic transfer through androgenesis.

12) First to demonstrate (in W22) the possibility of “fixing” high-performing substrains of long established inbreds through haploidy.

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#### **SIoux FALLS, SD**

#### **Quantitative trait loci for leaf angle, leaf width, leaf length, and plant height in IBM-94**

— Wassom, J

Modern maize varieties are more productive than varieties of a few decades ago, partly due to higher population densities and adaptations that permit vigorous growth at high densities. Plant forms that enable efficient light interception at high popula-

tion densities will increase yield production under modern field conditions. Leaf angle has been shown to affect yield especially at high densities. To determine the QTL affecting leaf traits and plant height in maize I experimented with IBM-94, a B73 x Mo17 recombinant inbred line (RIL) population developed by other researchers for genetic studies (Coe et al., *Plant Physiol* 128:9-12, 2002; Cone et al., *Plant Physiol* 130:1598-1605, 2002; Lee et al., *Plant Mol Biol* 48:453-461, 2002).

Seed for the 93 RIL constituting IBM-94 was obtained from the Maize Genetics Cooperative Stock Center (<http://maizecoop.cropsci.uiuc.edu>). In year 2006 the original seed was grown and plants were self-pollinated to produce enough RIL seed to plant replicated experimental plots at Sioux Falls, South Dakota, USA. In years 2007, 2008, and 2009 the 93 RIL were grown in randomized complete blocks with three replicates each year. Space was limited, so each plot included four plants spaced 279 mm apart in rows 76 mm apart. There were no extra spaces between plots in rows. At anthesis or soon after, the total plant height to the tassel tip and the leaf at the uppermost ear shoot were measured on the two center plants in each plot. Leaf measurements included the leaf angle from vertical, maximum leaf width, and distance from the ligule to the tip of the straightened leaf.

Statistical analysis, including analysis of variance and heritability was performed with PLABSTAT (University of Hohenheim, Germany, <https://plant-breeding.uni-hohenheim.de/-ipspwww/soft.html>). Genetic map distances of markers and molecular marker genotypes of each RIL were obtained from the Maize Genetics and Genomics Database (MaizeGDB) (<http://www.maizegdb.org>). Phenotype data for the RILs was combined with marker genotypic information and map distances from the MaizeGDB IBM2 map to analyze for QTL using PLABMQTL (University of Hohenheim, Germany, <https://plant-breeding.uni-hohenheim.de/-ipspwww/soft.html>).

There was significant variation among genotypes (Table 1; opposite page) and 1 to 3 QTL identified for each of the measured traits (Table 2). Larger plots and the larger IBM-302 population might have improved precision and enabled detection of more QTL. The total area taken up by nursery rows and experimental plots was about 50 by 75 feet, illustrating that even with limited resources the IBM-94 population and MaizeGDB data can be used for QTL mapping.

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#### **ST. PAUL, MINNESOTA**

#### **Adapted *Zea diploperennis*: *Zea diploperennis*-maize hybrid adapted to the U.S. corn belt**

— Carlson, LA; Price, SC

Experiment 1. 1979, a cross between *Zea diploperennis* No. 1190 as female parent and Minhybrid 8201 (A641 x W182B) as male was made in St. Paul (materials were furnished by John Doebley of the University of Wisconsin and Jon Geadelmann of the University of Minnesota). Approximately 6,000 F2 seeds were collected from an isolation plot of the F1 plants. In 1982