

PRODUCTION OF A MULTIPARENTAL RIL POPULATION FOR HIGH-RESOLUTION MAPPING IN MAIZE

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The development of advanced cross designs that might boost the power of detection of the genetic bases of complex traits remain a crucial goal of modern plant genetics. Here we describe the program currently ongoing for the development of an innovative advanced Recombinant Inbred Lines population, aimed at the genetic and molecular dissection of complex traits in maize. Eight maize inbred lines were selected to include a wide genetic variability for the expression of complex phenotypes and crossed according to a half-diallel design. This genetic material was used as the starting point for producing an extended (>2000) maize 8-ways RIL (8W-RIL) to be used for high-resolution QTL mapping. According to what estimated by The Complex Trait Consortium, which first proposed this model for mouse, such a material should allow mapping QTL with effect size >5% of the total variance to an interval of 0.5 cM using fewer than 1000 lines.

Twenty-eight F₁ hybrids from the 8x8 half-diallel were crossed so that only crosses between entries with no parents in common (e.g. cross AB x CD) were allowed (but not AB x AD or AB x BF, etc.). Such obtained 4-ways hybrids (210) were bulked in 70 pools, each composed by all the three 4-ways hybrids bearing the same alleles in all possible parent-of-origin *cis* combinations (e.g. "ABCD" pool included ABxCD, ACxBD and ADxBC 4-ways hybrids). 8-ways hybrids were then produced by crossing complementary 4-ways hybrids pools (e.g. ABCD x EFGH, CDFG x ABEH, etc.).

The production of 8W-RIL by single-seed descent is currently at the third selfing generation (8W-RIL F₃). Performing two generations of selfing per year, we expect to obtain a 8W-RIL F₆ mapping population by the end of 2010, whereas the molecular characterization of parental lines is scheduled to start in the fall of 2009. All 2-ways hybrids, 4-ways hybrids and 8-ways highly-recombinant hybrids plus the parental inbreds will also be available for phenotypic evaluation of complex traits, including heterotic traits.