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Characterization of a recombinant inbred line population for quantitative trait locus mapping

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Eukaryotes can regulate gene expression by epigenetic mechanisms at the chromatin level. One epigenetically regulated gene in maize is P11-Blotched, an allele of purple plant1, which activates anthocyanin pigment production. Normally, P11-Blotched leads to a variegated pattern of pigmentation, but its pigment level can be increased by a modifier called Suppressor of plant blotching (Spb). At the molecular level, Spb alters the chromatin packing of P11-Blotched, leading to less tightly packed chromatin and higher gene expression. The genetic identity of Spb is not yet known, although preliminary results indicate the Spb-enhanced pigment phenotype is a quantitative trait. As a step toward isolating the genes for Spb, a mapping population of Recombinant Inbred Lines (RILs) was generated by inbreeding the progeny of an F2 derived from a cross of P11-Blotched with Spb to a less pigmented P11-Blotched stock. Genotypes were determined for 188 RILs using microsatellite or simple sequence repeat (SSR) markers. RILs were evaluated for residual heterozygosity, breakpoint locations, and heterozygous chromosomal positions. A map was created and will be used as the foundation for mapping Spb and for estimating the heritability of the Spb phenotype.