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QTL mapping of suppressor of plant blotching1, modifiers of an epiallele

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P11-Blotched is an epigenetically regulated allele (an epiallele) of the purple plant1 gene, which activates synthesis of purple anthocyanin pigments. We identified a modifier called Suppressor of plant blotching 1 (Spb1), which leads to increased pigmentation in P11-Blotched plants. This phenotype is correlated with higher levels of P11-Blotched mRNA and an altered pattern of DNA methylation on the P11-Blotched gene. These features suggest that the effect of Spb1 may be to epigenetically alter the organization of P11-Blotched chromatin. An F2 population generated from a cross between two P1-Blotched plants (P1-Blotched; Spb X P1-Blotched, no Spb) showed a continuous distribution and transgressive segregation suggesting a polygenic trait. Individuals were genotyped at 104 SSR loci and anthocyanin content was quantified. Mapmaker and QTL cartographer software analysis of 211-individual and 279-individual F2 populations both identified QTL on chromosomes 5, 6, 7 contributed by Spb and non-Spb parents. Epistacy and ANOVA analysis of a ~1400 F2 population indicates that epistatic interactions are extremely important for high anthocyanin levels. The QTL intervals identified in both studies contain a number of candidate genes that might influence pigmentation of P11-Blotched. One of these genes—intensifier 1--was previously shown to be capable of increasing anthocyanin accumulation, although the mechanism of action is uncertain. Other candidates in the QTL intervals are several chromatin genes with likely, but as yet uncharacterized, roles in epigenetic regulation. The Chromosome 6 QTL spans a region that contains the p11 locus, however, no sequence polymorphism between the two parental P1-Blotched alleles has yet been identified. This might suggest that the chromosome 6 QTL is due to chromatin inherited from Spb, rather than DNA polymorphism at p11.