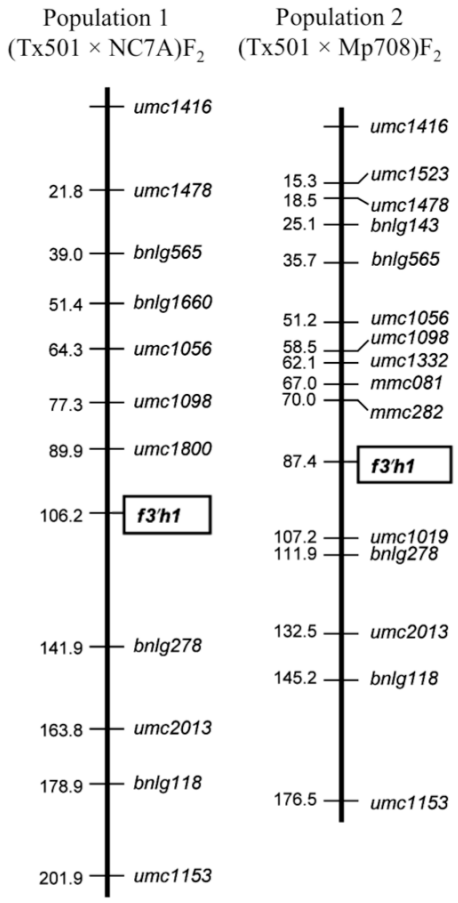

FIGURE S1.—*Zmf3′h1* maps to the *pr1* locus on chromosome 5L. Genetic linkage mapping of *Zmf3′h1* SNP marker on chromosome 5 for (Tx501 x NC7A) and (Tx501 x MP708) F_2 populations. The position of *Zmf3′h1* is indicated on both maps and corresponds to the *pr1* locus. Cumulative distances given in centimorgans are indicated to the left of the chromosome and marker loci are indicated to the right.

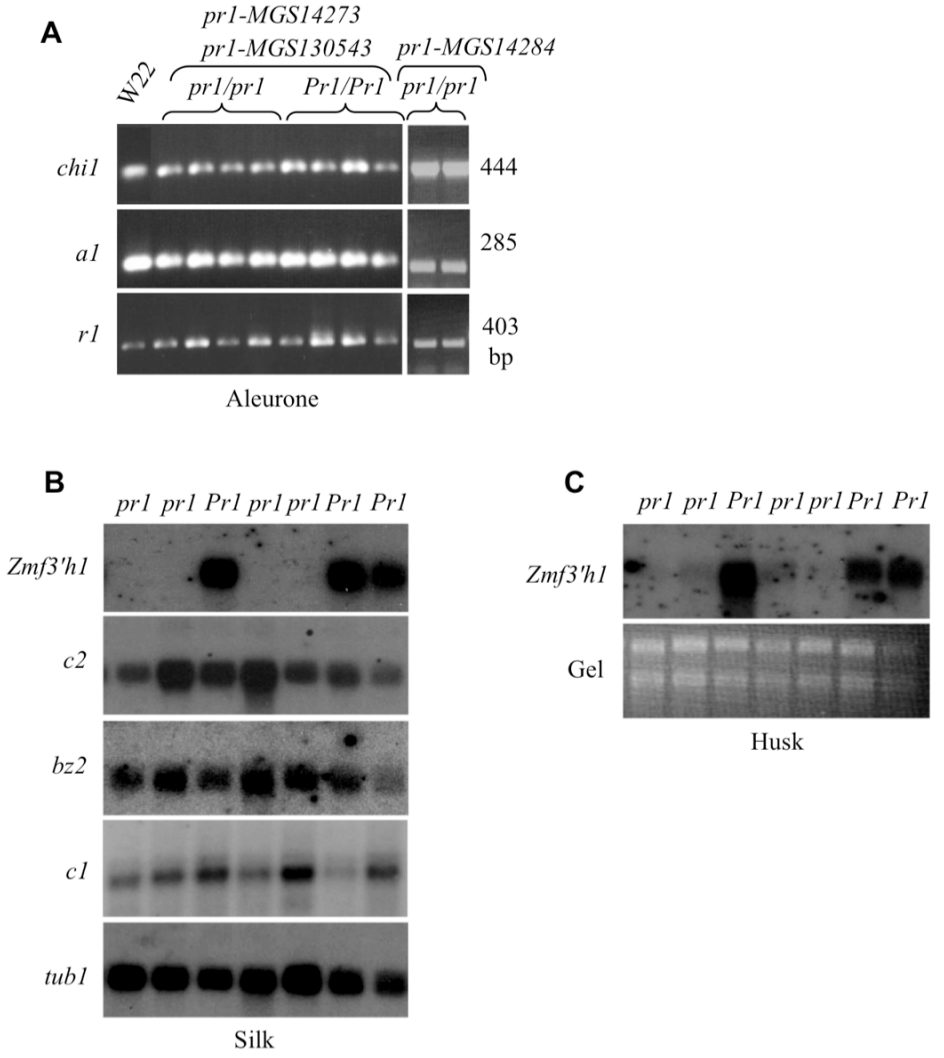

FIGURE S2.—RT-PCR and RNA hybridization analyses were performed on total RNA extracted from developing aleurones, young silks and young husk collected from plants segregating for *Pr1* and *pr1*. (A) RT-PCR for expression of anthocyanin genes *chi1*, *a1*, and transcription factor, *r1* in aleurone tissues of *pr1/pr1* and *Pr1/Pr1* plants. (B) Gel blot of RNA isolated from silk tissues was hybridized to *Zmf3'h1*, *c2*, *bz2*, *c1*, and *α-tubulin1* specific probes. (C) Husk RNA gel blot hybridized with *Zmf3'h1* probe. Ethidium bromide stained gel picture shows loading control for RNA in each lane.

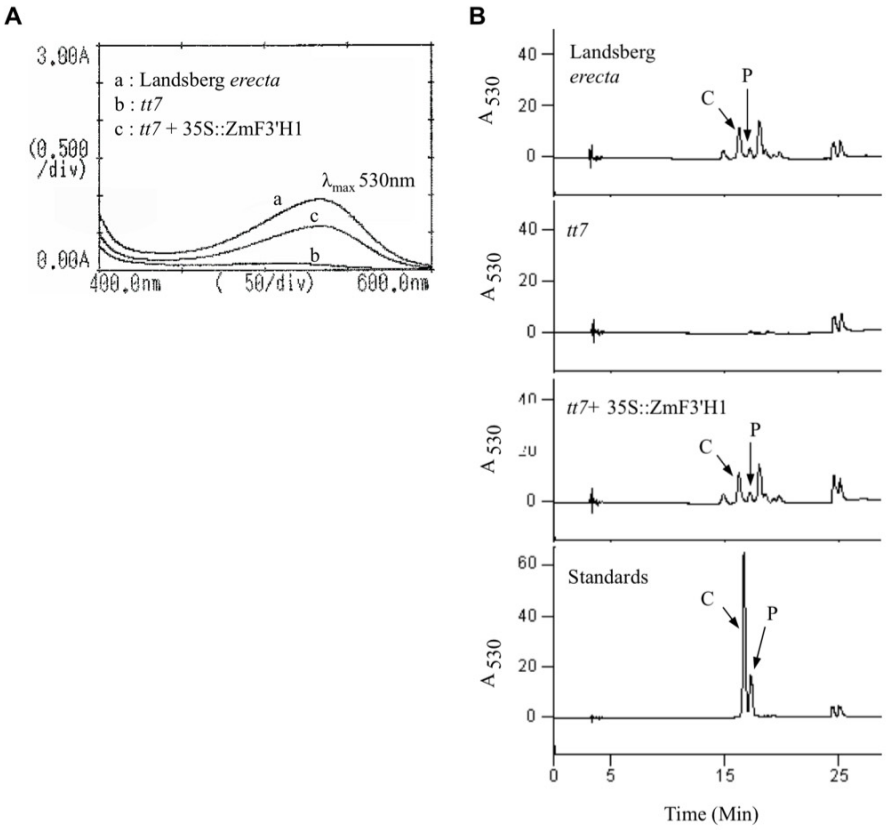

FIGURE S3.—Biochemical analysis of *Zmf3'h1* complemented Arabidopsis *tt7* mutant. (A) Spectrophotometric analysis of methanolic extracts from 10 day old seedlings grown on a minimal medium (a) Landsberg *erecta*, (b) 35S::ZmF3'H1 complemented *tt7*, (c) *tt7*. (B) HPLC analysis of anthocyanins present in hydrolyzed methanolic extracts of 10 day old seedlings from Landsberg *erecta*, *tt7*, and *Zmf3'h1* complemented *tt7* mutant. The standards for cyanidin and pelargonidin are also shown. C, cyanidin; P, pelargonidin; and CG, cyanidin glycosides.

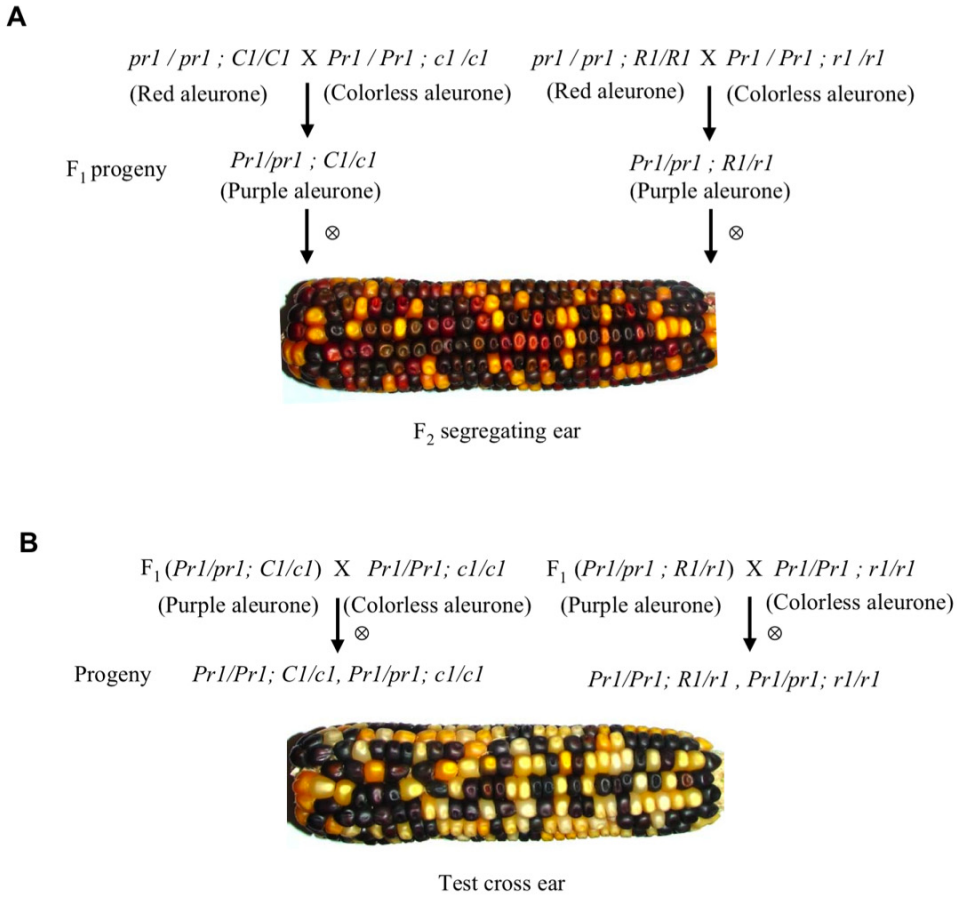

FIGURE S4.—Genetic assays to study regulation of *pr1* by the anthocyanin regulatory genes *c1* and *r1*. (A) Crossing scheme used to develop F_1 and F_2 progenies. Purple, red, and colorless kernel aleurone phenotypes were observed in F_2 segregating ears. (B) Crossing scheme used to develop the F_1 and test cross progenies. Purple and colorless kernel aleruone phenotypes were seen in representative test cross ears.

TABLE S1

PCR primers used in RT-PCR analysis

Gene	Primer combination		Product (bp)	Reference
pr1	5F3H-F2	5′-GAGCACGTGGCGTACAACTA-3′	771	This Study
	ZMR4	5′-AAACGTCTCCTTGATCACCGC-3′		
c2	CHSF	5′-TCGATCGGTCTCTCTGGTACAACGTA-3′	549	This Study
	CHSR	5′-TACATCATGAGGCGGTTCACGGA-3′		
chi1	CHIF	5′-GTGCGGAATTTAACATGGCGTGC-3′	444	This Study
	CHIR	5′-CGGCGCGAAAGTCTCTGGCTT-3′		
a1	A1	5′-CAATTCGTTGAACATGGAAGTAAG-3′	285	Piazza *et al.*, 2002
	A2	5′-CAATTCGTTGAACATGGAAGTAAG-3′		
bz2	BZ2F	5′-ATATGCGAGTCCGCAGTCATCGT-3′	379	This Study
	BZ2R	5′-TCGATGAGTGAGAGGCCGTGAA-3′		
c1	PL6	5′-TCGGACGACTGCAGCTCGGC-3′	313	Piazza *et al.*, 2002
	AC1	5′-CACCGTGCCTAATTTCCTGTCCGA-3′		
r1	OR31	5′-ATGGCTTCATGGGGCTTAGATAC-3′	403	Piazza *et al.*, 2002
	OR32	5′-GAATGCAACCAAACACCTTATGCC-3′		
actin	ActinF	5′-CCTTCGAATGCCCAGCAATG-3′	202	This Study
	ActinR	5′-GAGGATCTTCATTAGGTGGT-3′		
gapdh	GAP1	5′-AGGGTGGTGCCAAGAAGGTTG-3′	621	This Study
	GAP2	5′-GTAGCCCCACTCGTTGTCGTA-3′		
tubulin	Tub1	5′-AGGATCCACTTCATGCTTTCCTCC-3′	546	This Study
	Tub2	5′-CACCTTCCTCACCCTCATCAAACT-3′		

TABLE S2

Primers for PCR amplification

Primer combination	Primer sequences	Product (bp)
ZF3F2 ZF3R2	5′-AGTGCGAGGTGGACGGGTTC-3′ 5′-GCAGACGGCAGCAGTCTCCCCT-3′	387
OSF1 ZMR4	5′-CATACGGCCATGGACGTTGTGCCT-3′ 5′-AAACGTCTCCTTGATCACCGC-3′	1276
SBF12 SBR22	5′-CTTCTAGAACCGAG-3′ 5′-TTGGAT CCCCTACTCCGCTGCGTAT-3′	1788
P-1 P-2	5′-TGACTTGCACCTCCTTGTTCTGTC-3′ 5′-TTTAGTGCACAACCTTTAGGG-3′	441
P-3 P-4	5′-GTACGAAATTCCAGATCGCGGGTA-3′ 5′-ATAGCCACATGGTGTGGTGCGG-3′	349
MGR1 JSR01	5′-CACTGATACCCACGTACAACGCTT-3′ 5′-GTTCGAAATCGATCGGGATA-3′	1547
MGR2 JSR01	5′-TTGCGCTCGTACGGGAAAGGTA-3′ 5′-GTTCGAAATCGATCGGGATA-3′	670
MGF1 JSR05	5′-GTACGAAATTCCAGATCGCGGGTA-3′ 5′-CGTCCCGCAAGTTAAATATGA-3′	588