

## A newly identified dominant silk scar/pericarp color mutant, *Sksc1*.

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In 2014, the Maize Genetics Stock Center received a GEM (Germplasm Enhancement of Maize) stock, BGEM-0247-N, from Mike Blanco of Iowa State University that is homozygous for a mutant that confers red pericarp color to the kernel crown. The GRIN listing for this line is listed at: [PI 686017](#); and photographs of ears can be found at: [BGEM-0247-N](#). We gave this mutant the provisional designation *Sksc\*-BGEM-0247-N*. The red coloration encompasses the entire kernel crown and is reminiscent of the Navajo color pattern of *RI-nj* aleurones. However, dissection of imbibed kernels revealed that the red color is restricted to the pericarp and is not water soluble, unlike the anthocyanins in the aleurones of *RI-nj* kernels. The red coloration, lack of water solubility, and pericarp localization is similar to that of phlobaphenes of *PI* pericarp color alleles, but we have not performed a chemical analysis of the pigment.

Since the cobs of the BGEM-0247-N line are also red, we explored the possibility that *Sksc\*-BGEM-0247-N* is an allele of *p1* with a unique pericarp color pattern. We performed a series of backcrosses of *Sksc\*-BGEM-0247-N* to the inbred line 4Co63, which has white pericarp and white cobs (*p1-ww*). Progeny from the first generation outcross to 4Co63 all had red cobs and only silk scar color (rather than the strong Navajo pericarp pattern that we observed in the original BGEM-0247-N line).

Following the second backcross to 4Co63, we realized that the silk scar color trait was separable from the cob color trait. Out of 15 ears, 7 had silk scar color with white cobs, one had colorless pericarp with red cob, 4 had silk scar color with red cobs, and 3 had colorless pericarp with white cobs. This was not significantly different from a 1:1:1:1 ratio (chi-square = 5.000; df = 3; p > 0.10). The silk scar color trait also became more dilute in outcrosses, becoming a pink blush that in some cases was focused around the silk scar, or in other cases colored the entire pericarp. We conclude that the silk scar color trait is dominant or semidominant, and not linked to cob color.

Following the isolation of separate stocks that carried the silk scar color trait with white cobs (*Sksc\*-BGEM-0247-N p1-ww-4Co63*) or colorless pericarp with red cobs (*sksc\* P\*-wr-BGEM-0247-N*), we performed separate tests of linkage of the silk scar color and cob color traits with the *PI-wr* reference allele from W23. The results are summarized in Tables 1 and 2. We conclude that *Sksc\*-BGEM-0247-N* segregates independently of *p1*, and that the red cob color trait in BGEM-0247-N is a *p1* allele similar or identical to *PI-wr*. Since there are no previously characterized red pericarp color loci that segregate independently of *p1*, we have named the silk color locus *silk scar color1* (*sksc1*), and given *Sksc\*-BGEM-0247-N* the allelic designation *Sksc1-BGEM-0247-N*.

During the backcross series of *Sksc1-BGEM-0247-N* to 4Co63, we attempted to select for the more distinct strong red pericarp crown color pattern that was present in the original BGEM-0247-N line. Preliminary evidence suggests that the strongest pericarp crown color in backcrossed and selfed individuals occurs when *Sksc1-BGEM-0247-N* is homozygous with *P1-wr-BGEM-0247-N*. Whether this is due to a unique interaction between *Sksc1-BGEM-0247-N* and *P1-wr-BGEM-0247-N*, or whether it is an interaction between *Sksc1-BGEM-0247-N* and *P1-wr* alleles in general, or perhaps even other modifiers, is being explored. In order to obtain the original strong Navajo pericarp color pattern, it appears that *P1-wr* and/or other modifier(s) need to be homozygous. We hope to further characterize and map *Sksc1-BGEM-0247-N* and its modifiers in collaboration with other individuals.

Table 1. Two-point linkage data for *Sksc1-BGEM-0247-N* and *PI-wr-W23*.

Test cross: [*Sksc\*-BGEM-0247-N p1-ww-4Co63* X *sksc\*PI-wr-W23*] X *sksc\* p1-ww-4Co63*

Row No.	parentals		recombinants	
	sksc* P-wr	Sksc* p-ww	Sksc* P-wr	sksc* p-ww
2017-2491-2492	10	6	10	4
2017-2493-2494	11	3	6	9
2017-2495-2496	7	7	9	7
2017-2497-2498	9	8	5	7
2017-2499-2500	4	8	11	6
Totals	41	32	41	33
1:1:1:1 chi-square = 1.980	df = 3	NS (p>0.10)		
Reg. 0	73			
Reg. 1	74			
Total	147			
1:1 chi-square = 0.007	df = 1	NS (p>0.95)		

Conclusion: *Sksc\*-BGEM-0247-N* and *PI-wr-W23* are not linked.

Table 2. Two-point linkage data for *P\*-wr-BGEM-0247-N* and *PI-wr-W23*.Test cross: [*P\*-wr-BGEM-0247-N* X *PI-wr-W23*] X *p1-ww-4Co63*

Row No.	Parental	Recombinant
	P-wr	p-ww
2017-2467	15	0
2017-2468	14	0
2017-2469	14	0
2017-2470	15	0
2017-2471	10	0
2017-2472	15	0
2017-2477	13	0
2017-2478	14	0
2017-2483	14	0
2017-2484	14	0
2017-2485	15	0
2017-2486	12	0
Totals	165	0

% recombination between *PI-wr-BGEM* and *PI-wr-W23* < 1.2 +/- 0.9 cM