

## ORANGE COTYLEDONS: A NEW GENE FOR COTYLEDON COLOR

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In a previous paper (1) we described a new color of pea cotyledons, viz. orange. The F1 seeds of the cross Wt 11145 x Wt 3527 were dark yellow and the F2 segregated 3:1 for orange vs yellow. It was not possible to determine if the character orange cotyledons was controlled by an allele of gene I or was an effect of a separate locus.

A survey of accessions in the Wiatrowo collection revealed extensive variation for cotyledon color. The 1619 accessions observed could be divided into five color groups: green (327 accessions); whitish or bleached green (26); light yellow (204); yellow (732); dark yellow (315); and light orange (15 accessions). However, the collection contained no line with orange or brick cotyledons. Thus, the accession Wt 11145, originating from China, was the only pea with the character orange cotyledons.

To elucidate the genetics of orange cotyledons, we analyzed the cross of Wt 11145 (orange cotyledons) x WL 145, the type line for recessive *i* (green cotyledons). The expression of cotyledon color in the parental lines was observed as a frame of reference. Among 316 seeds from five selfed plants of the type line for *i* (green cotyledons), seven seeds were actually yellow without any trace of green, 20 were yellow with traces of green, 33 were bleached green, 155 were celadon green, and 101 were dark green. This gives a picture of the range of expression of the allele *i* in this particular line. This problem, sometimes referred to as bleaching, is well-known to breeders. A similar range of variation was observed in seeds of line of the second parent, Wt 11145. Among 320 seeds from five plants, 5 were dark yellow, 51 light orange, 214 orange and 50 brick red.

The F1 seeds of cross Wt 11145 x WL 145 (and reciprocal) were light orange. The colors of the F2 seeds are shown in Table 1, where it appears that the colors of the parental lines were all represented. Line Wt 11145 manifested the colors of column 14, 15, 16, and line WL 145 included the colors of the column 1, 4, 6, and 7. Classes found in the F2 seeds included yellow (col. 13), green (col. 5), and green on dark yellow, light orange, or brick background (col. 2, 3, 8, 9, 10, 11, and 12).

The appearance of green and yellow clearly indicates that orange is inherited independently of yellow: celadon green, i.e., the gene *I*.

Adding the data in the columns of Table 1, as grouped above, into four classes corresponding to a two-gene segregation produces the result given in Table 2. Chi-square for heterogeneity between the reciprocal crosses was 67.7 and highly significant. This might be due either to difficulties in classifying the green fraction and/or to a maternal influence on color.

The segregation in yellow:green with WT 11145 as female was 238:63, ( $X^2_{3:1} = 2.56$ ); the segregation orange:non-orange was 229:72 ( $X^2_{3:1} = 0.16$ ). In the reciprocal cross, the segregation in *I* of 344:97 ( $X^2_{3:1} = 2.05$ ) is quite acceptable. In the case of orange:nonorange the segregation 290:151 ( $X^2_{3:1} = 20.4$ ) is taken to indicate that the separation orange:non-

orange was not successful among the *i* seeds. Inasmuch as the classification of the green class is uncertain and will need confirmation in the fit to a 9:4:3 segregation was calculated (Table 3). As the  $\chi^2$  for 9:4:3 is not significant, the two-gene hypothesis is accepted.

Though the F3 results are not yet available, we feel these data are sufficient to propose a new gene, as yet provisional, the dominant allele of which determines orange cotyledons. This gene is most probably inherited independently of *I*. We propose the symbol of *Ore*.

1. Blixt, S. and W. K. Swiecicki. 1983. PNL 15:9-10.

Table 1. Distribution of cotyledon colors in an F<sub>2</sub> population from the reciprocal crosses between a line with orange cotyledons, Wt 11145, and the type line for *I*, green cotyledons, WL 145.

Cross	Phenotype (see footnotes)																		
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17		
Wt 11145 x WL 145	2	2		3			13	27		16			54	117	24	34	9		
WL 145 x Wt 11145	6		1	40	1	1	11	8	1	4	1	23	93	129	41	52	29		
1. Yellow with traces of green							7. Bleaching green on yellow							13. Yellow					
2. Dark-yellow with traces of green							8. Bleaching green on dark-yellow							14. Dark-yellow					
3. Light-orange with traces of green							9. Bleaching green on light-orange							15. Light-orange					
4. Celadon green							10. Bleaching green on orange							16. Orange					
5. Green							11. Bleaching dark-green on light-orange							17. Brick					
6. Dark-green							12. Bleaching dark-green on orange												

Table 2. Distribution for cotyledon color in F<sub>2</sub> of cross Wt 11145 x WL 145 and reciprocal. Same data as in Table 1, but grouped into four classes (see text).

Cross		Cotyledon color				Total
		Orange	Green on orange	Yellow	Green	
Wt 11145	Observed	184	45	54	18	301
	Expected	170	56	56	19	301
x	9:3:3:1					
WL 145	X <sup>2</sup>	1.15	2.16	0.07	0.05	3.44 NS
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WL 145	Observed	251	39	93	58	441
	Expected	248	83	83	27	441
x	9:3:3:1					
	X <sup>2</sup>	0.04	23.32	1.20	35.59	60.16***
Wt 11145	Corr.	226	64	118	33	441
	Expected					
	X <sup>2</sup>	2.76	9.77	5.30	18.94	36.77***

Table 3. F<sub>2</sub> distribution for cotyledon color in combined populations from cross Wt 11145 x WL 145 and reciprocal group into three classes.

	Cotyledon color			
	Orange	Green	Yellow	Total
Observed	435	160	147	742
Expected	417	186	139	742
X <sup>2</sup> for 9:4:3	0.78	3.63	0.46	4.87