

# Inheritance of Photoperiodic Flowering Response and Stem Striping in *Salvia splendens* Sello<sup>1</sup>

C. H. Lai, Jules Janick, and T. C. Weiler<sup>2</sup>  
Purdue University, West Lafayette, Indiana

**Abstract.** The flowering response of 'St. John's Fire' salvia is day neutral and occurs between the 8-13th node under both 8 (SD) and 24 hour (LD) photoperiods. In contrast 'Bonfire' flowers between the 8-13th node under SD, and under LD flowering is delayed to the 16-19th node. Genetic experiments indicate that this difference in photoperiodic response is controlled by a single gene: *RR* flowers from node 16-20, *Rr* from node 13-17, and *rr* from node 8-13. A single dominant gene *S* conditions stem stripedness; *ss* is solid colored. *S-s* and *R-r* are independently inherited.

*Salvia splendens*, which is indigenous to Mexico,  $2n' = 32$ ,  $x = 8$  (1), is increasing in popularity as a bedding plant. Photoperiods beyond 14 hr delay flowering in some salvia cultivars, but not in others (2, 3). The maximum delay is obtained in continuous illumination (4). This study describes the inheritance of photoperiodic response and stem stripedness from crosses involving 'St. John's Fire' (SJF) which flowers at an early node in LD and SD and 'Bonfire' (BF) in which flowering is delayed in LD.

The work was conducted in late winter and spring greenhouse conditions with a 21°C minimum temp. Black cloth covered all plants from 4:30 PM to 8:30 AM. Incandescent illumination of approximately 0.0015 Langley/min was provided under the cover for plants receiving continuous lighting.

**Hybridizing salvia.** The salvia flower is hermaphroditic and naturally self-pollinating. We determined the optimum stage for crossing by emasculating flowers with a sharp forceps when the corolla tube was 1.5 cm and subsequently pollinating at various stages of maturity based on corolla length and openness of the forked stigma which ranges from 0-75°. Pollen was applied using the mature flower as a brush. A plastic bag was applied before emasculation and subsequently kept until nutlets enlarged after 2-5 days and depending on temp, darkened 3-4 weeks later.

The greatest amount of seed set was obtained with corolla length from 4.0-4.8 cm and stigma opening from 70-75° (Table 1). For hybridizing, emasculation can be performed when corolla length is  $\leq 3.0$  cm and stigma

Table 1. Determination of the optimum stage of pistil receptivity.

Time of pollination		
Corolla length (cm)	Stigma openness (degree)	Seed set (%)
1.5	0	0
1.8	10	0
2.5	20	0
3.0	35	10
3.5	45	50
4.0	70	50-80
4.5	75	50-80
4.8	75	50-80
4.8 + 1 day	75+	10
4.8 + 2 days	75+	0

opening is  $\leq 35^\circ$ ; pollinations should be made the following day.

**Flowering response to daylength.** 'BF' and 'SJF' both flowered from node 8-13 under SD but under LD flowering in 'BF' was delayed until node 16-19 (Table 2). Seedlings of reciprocal crosses between 'SJF' and 'BF' were compared under SD and LD. No difference in the flowering response occurred between reciprocal crosses in the F<sub>1</sub> so the data are combined. Of the 107 F<sub>1</sub> plants, 1 flowered at node 13, 6 flowered at node 17, and the remainder were distributed in nodes 14, 15 and 16. The F<sub>1</sub>'s, therefore, were delayed in flowering as in 'BF' under LD, but the actual number of vegetative nodes of

flowering was intermediate between 'SJF' and 'BF'

F<sub>2</sub> and backcross generations were only grown under LD and flowering ranged from node 10-20. The backcross of the F<sub>1</sub> to 'SJF' flowered from node 10-17, while the backcross of the F<sub>1</sub> to 'BF' flowered from node 14-20.

We used the ability to flower at the 13th node in LD to separate 2 classes of photoperiodic response. Plants that flowered  $\leq$  node 13 under LD were considered nonphotoperiodically responsive (NR); plants that flowered beyond the 13th node were photoperiodically responsive (PR). The 2 class segregation ratio in LD can be explained with a single gene (*R* vs. *r*) with *RR* and *Rr* genotypes being PR and *rr* genotypes being NR. Under this assumption, 'BF' is *RR* and 'SJF' is *rr*. The reciprocal F<sub>1</sub>'s are both heterozygous *Rr* and PR indicating dominance for delayed flowering in long days.

The F<sub>2</sub> ratio of 288 PR:99 NR fits the expected 3:1 ratio assuming a single gene difference (Table 3). The backcrosses segregated 1 PR:0 NR (F<sub>1</sub> × 'BF') and 1 PR:1 NR (F<sub>1</sub> × 'SJF'), as expected.

The *R* allele appeared incompletely dominant to *r* with respect to the node of flowering under LD. The *RR* genotype ('BF') flowered from node 16-19, *Rr* (F<sub>1</sub>) flowered from node 13-17, and *rr* ('SJF') flowered from node 8-11. There was some overlapping of the *RR* and *Rr* genotypes at nodes 16 and 17 but most *RR* genotypes flowered above node 17. Therefore in crosses segregating for *RR* and *Rr* (F<sub>2</sub> and F<sub>1</sub> × 'BF') all plants which flowered

Table 2. Distribution of node of first flowering in crosses involving 'SJF' and 'BF' by photoperiod.

Photoperiod	Node of 1st flower	No. of plants					
		Parents		F <sub>1</sub> (reciprocals)	F <sub>2</sub>	Backcrosses	
		SJF	BF			F <sub>1</sub> × SJF	F <sub>1</sub> × BF
SD (8 hr)	8	2	6	7	—	—	—
	9	6	1	29	—	—	—
	10	1	1	28	—	—	—
	11	1	1	16	—	—	—
	12	0	1	7	—	—	—
	13	0	0	3	—	—	—
	14-20	0	0	0	—	—	—
	Avg node no.	9.1	8.5	10.0			
LD (24 hr)	8	1	0	0	0	0	0
	9	7	0	0	0	0	0
	10	1	0	0	3	4	0
	11	1	0	0	11	16	0
	12	0	0	0	56	12	0
	13	0	0	1	29	5	0
	14	0	0	31	14	6	1
	15	0	0	42	47	12	16
	16	0	2	27	107	12	34
	17	0	6	6	72	3	27
	18	0	1	0	34	0	19
	19	0	1	0	8	0	7
	20	0	0	0	6	0	4
	Avg node no.	9.2	17.0	15.1	15.3	13.3	16.8

<sup>1</sup>Parents grown in 1972; F<sub>1</sub>, F<sub>2</sub> and backcrosses grown in 1973.

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<sup>2</sup>Graduate Research Assistant, Professor, and Assistant Professor, Department of Horticulture.

Table 3. Segregation for node of flowering under LD of crosses involving 'SJF' and 'BF'.

Cross	2 class segregation				3 class segregation				
	Node of flowering in LD		Expected ratio	P	Node of flowering in LD			Expected ratio	P
	14-20	8-13			17-20	14-16	8-13		
SJF	0	10			0	0	10		
BF	10	0			8	2	0		
F <sub>1</sub> (SJF x BF)	47	1			2	45	1		
F <sub>1</sub> (BF x SJF)	59	0			4	55	0		
F <sub>2</sub>	288	99	3:1	.50-.70	120	168	99	1:2:1	.01-.02
F <sub>1</sub> x SJF	33	37	1:1	.50-.70	3	30	37	0:1:1	.50-.70
F <sub>1</sub> x BF	108	0			57	51	0	1:1:1	.50-.70
Assumed genotype	R-	rr			RR	Rr	rr		

Table 4. Inheritance of stem striping in crosses involving 'SJF' and 'BF'.

Crosses	No. of plants		Expected ratio	P
	Striped	Non-striped		
SJF	10	0		
BF	0	10		
F <sub>1</sub> (SJF x BF)	48	0		
F <sub>1</sub> (BF x SJF)	59	0		
F <sub>2</sub>	294	93	3:1	.50-.70
F <sub>1</sub> x SJF	70	0		
F <sub>1</sub> x BF	56	52	1:1	.50-.70

from  $\geq$  node 17 were assumed to be RR while plants between 14-16 were assumed to be Rr.

The segregation for node of flowering under LD of 3 classes (8-13, 14-16, 17-20) is shown in Table 3. While the F<sub>2</sub> distribution is significantly different for the expected 1:2:1 ratio at the 5% level (P = <2%), the backcross of the F<sub>1</sub> x 'BF' fits the expected 1:1 ratio. The results support the hypothesis that while the R allele is dominant for delay of flowering, the action is incompletely dominant if the actual node of flowering is considered.

**Plant height.** Under LD 'SJF' was of short stature and 'BF' was tall. This difference in height is due to the node of flowering. In Fig. 1, the average height of parents, F<sub>1</sub>, F<sub>2</sub> and backcrosses reflects the node of flowering although heterosis of the F<sub>1</sub> was observed. Thus, plant height under LD is effectively controlled by the R-r alleles.

**Days from transplanting to visible bud.** Under LD 'SJF' flowered early and 'BF' flowered late. The difference in days to flower between these cultivars and crosses between them is also primarily due to the node of flowering (Fig. 2).

**Stem striping.** The lower stems of both cultivars are purple but 'SJF' is striped, with the purple color confined to the vascular strands, while 'BF' is solid purple. The plants are easily scored for this character at the 4th internode. The reciprocal F<sub>1</sub>'s were all striped; the F<sub>2</sub> segregated 3 striped:1 non-striped. The F<sub>1</sub> x 'SJF' were all striped, while the F<sub>1</sub> x 'BF' segregated 1 striped:1 non-striped (Table 4). We conclude that

striped vs. non-striped, (solid colored) stem is controlled by a single gene; SS and Ss are striped, ss is non-striped.

**Linkage between R and S.** The genotypes of the two cultivars with respect to photoperiodic flowering response and stem striping are:

$$\text{'BF'} = RRss$$

$$\text{'SJF'} = rrSS.$$

The 4 class F<sub>2</sub> ratio of 222 (PR, striped):66 (PR, non-striped):72 (NR, striped):27 (NR, non-striped) does not differ significantly from the expected 9:3:3:1 ratio indicating independent segregation R and S. In this type of cross, linkage cannot be determined from backcrosses. Combining the 1:2:1 ratio for node of flowering and the 3:1 ratio for stem striping ratio gives a 6 class F<sub>2</sub> ratio of 3:1:6:2:3:1. The observed segregation fits the expected (X<sup>2</sup> = 10.54, P = 5-10%) although it approaches significance. The Chi square analysis indicates that most of the deviation is due to the poor 1:2:1 fit; there is no evidence for linkage.

**Conclusion.** The discovery of a single gene that determines the node of

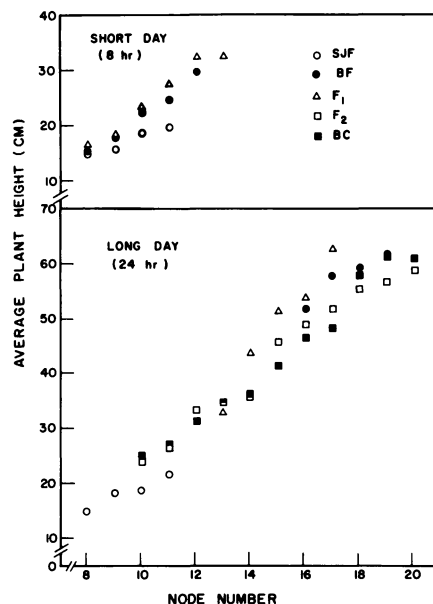


Fig. 1. Average plant height at node of first flower under long day and short day in crosses involving 'SJF' and 'BF'.

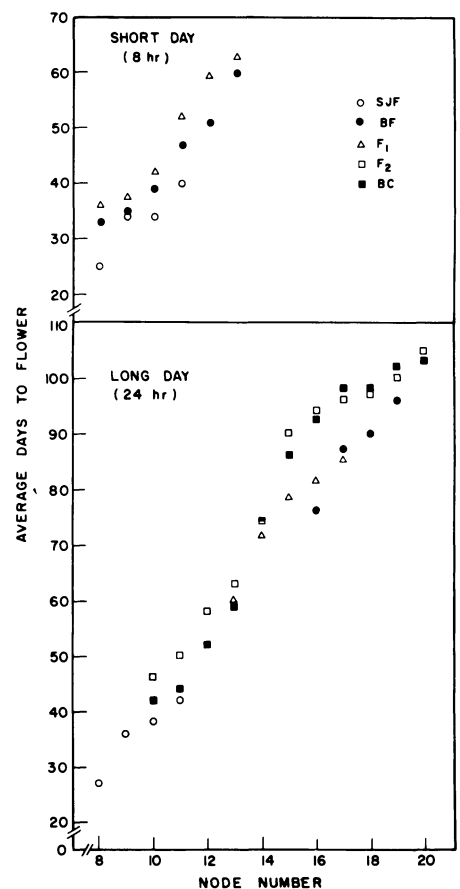


Fig. 2. Days from transplanting to visible flower bud in long day and short day in crosses involving 'SJF' and 'BF'.

flowering under LD makes it possible to clearly separate at least 2 true-breeding classes of *Salvia splendens*. One consists of plants of short stature that flower early under any daylength (rr). Further selection may result in plants of this genotype varying as to the precise node of flowering, height, and flowering date. The other class, homozygous for the R gene, is tall and late flowering under long days. Selection within these types might yield a range of genotypes with respect to plant height and days from transplanting to visible bud. Further studies should be based on F<sub>3</sub> analysis and additional crosses involving other genotypes to determine if there are other major or modifying genes.

#### Literature Cited

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