Inheritance of Flower Color in Pickerelweed (Pontederia cordata L.)

LYN A. GETTYS AND DAVID S. WOFFORD

Department of Agronomy, Plant Genetics and Breeding, University of Florida Institute for Food and Agricultural Sciences, 304 Newell Hall, Box 110500, Gainesville, FL 32611-0500.

Address correspondence to L. A. Gettys at UF/CAIP, 7922 Northwest 71 Street, Gainesville, FL 32653, or e-mail: lgettys@ufl.edu.

Pickerelweed (Pontederia cordata L.) is a diploid (2n = 2x = 16), erect, emergent, herbaceous aquatic perennial. The showy inflorescences of pickerelweed make this species a prime candidate for inclusion in water gardens and aquascapes. The objective of this experiment was to determine the number of loci, number of alleles, and gene action controlling ower color (blue vs. white) in pickerelweed. Two blue-owered and one white-owered parental lines were used in this experiment to create S1 and F1 populations. F2 populations were produced through self-pollination of F1 plants. Evaluation of S1, F1, and F2 generations revealed that ower color in these populations was controlled by 2 alleles at one locus with blue ower color completely dominant to white. We propose that this locus be named white flower with alleles W and w.

Pickerelweed is classified as an obligate wetland plant (Ordnuff 1966; Barrett and Anderson 1985; Barrett and Anderson 1985; Eckert and Barrett 1994; O'Neill 1994). The different floral morphs of pickerelweed exhibit varying levels of self-incompatibility, but all morphs produce more seeds after legitimate pollination than after illegitimate pollination (Ordnuff 1966; Barrett and Anderson 1985; Barrett and Glover 1985).

The showy inflorescences of pickerelweed make this herbaceous perennial a prime candidate for inclusion in water gardens and aquascapes. The racemose inflorescence is borne at the distal end of a stem and is subtended by a single leaf-like bract. Each inflorescence measures from 5 to 20 cm in length and bears up to 250 individual flowers (although Ordnuff [1966] noted more than 450 individual flowers on a single inflorescence). Anthesis begins in the morning and flowers remain open for up to 12 h; an average of 20 individual flowers are open on any given day on a single inflorescence. The perianth is composed of 6 petaloid tepals arranged in 2 whorls of 3; tepals range in color from violet–blue to lilac to rarely white, with yellow nectar guides (eye spots) marking the median upper tepal of the floral envelope. Each flower is zygomorphic, basally connate and perfect, bearing one style and 2 sets of 3 stamens. Wild-type plants of pickerelweed produce blue or violet flowers, but plants with white flowers are sometimes seen in natural environments (Godfrey and Wooten 1979). Although uncommon in nature, white-flowered specimens of pickerelweed are much easier to locate in a retail environment; a simple search of the internet reveals that white-flowered specimens of pickerelweed are readily available from the many nurseries that sell aquatic plants.
Durbin et al. (2003) stated that variations in flower color are often transmitted in a simple Mendelian manner. Control of flower color by a single diallelic locus has been described in several species, including stokes aster (Gaus et al. 2003), morning glory (Zufall and Rausher 2003), crimson clover (Mosjidis 2000), and guayule (Estilai 1984). Genetic control of flower color is more complicated in other species; for example, Brewbaker (1962) reported that red flower color in white clover resulted from the presence of recessive alleles at 2 loci, whereas Pahlavani et al. (2004) stated that flower color in safflower was conditioned by 2 diallelic epistatic loci. Griesbach (1996) found that flower color in the common petunia was influenced by 2 loci that were responsible for the production of anthocyanins and by 2 additional loci that controlled vacuole pH.

There is no published information describing the inheritance and genetic control of flower color in pickeralweed. The objective of this experiment was to determine the type of gene action and number of loci controlling flower color in these populations of pickeralweed.

Materials and Methods

The plants used in this experiment were part of a population maintained for genetic and breeding studies at the University of Florida in Gainesville. All plants were grown in 1-l nursery containers filled with a commercially available potting mix, and nutrition was supplied by the incorporation of 10 g of controlled-release fertilizer per container. Plants were subirrigated and kept in a pollinator-free glasshouse with air temperature maintained at 27 °C (day) and 16 °C (night). During preliminary experiments, we observed that some genotypes were more floriferous when grown under long days; therefore, supplemental lighting was employed to artificially extend daylength to 16 h in this study.

One white-flowered parent (coded WM) and 2 blue-flowered parents (coded BS and BL) were utilized in this experiment. Parents were collected from natural populations throughout southern Florida; each parent was selected from a different geographically isolated location so it is unlikely they share a common ancestor. The parents WM and BL were derived from separate mixed (blue and white flowers) populations, and the parent BS was chosen from a population with only blue-flowered plants. Flower color surveys of these populations were not conducted, but we agree with the observation of Godfrey and Wooten (1979) that white-flowered plants are uncommon in nature and occur only sporadically. Each parent was self-pollinated to create the S1 families WM ⊗, BS ⊗, and BL ⊗. Cross- and reciprocal pollinations were performed between parents to create the F1 families WM × BS, WM × BL, and BS × BL. Barrett and Glover (1985) stated that emasculation was not necessary to prevent self-pollination, so anthers were removed only when their presence restricted access to the stigma (i.e., anthers borne on the long filaments of the parent WM and all anthers of the parent BS). Representative samples were selected from each F1 family and self-pollinated to generate F2 families. Cross- and reciprocal pollinations to generate F1 populations were performed between December 2001 and April 2002, whereas self-pollinations of parents and F1 plants (to create S1 and F2 populations, respectively) were conducted between January and June 2003.

Pollinations commenced with the opening of the first flowers of an inflorescence and continued until all flowers in the inflorescence had been pollinated (ca. 7–12 days). All pollinations were performed between 9 AM and 3 PM daily, and all flowers in each inflorescence were pollinated using the same method. Daily pollination data were recorded on jewelry tags placed on each inflorescence. Each completed inflorescence was enclosed in a small mesh bag and secured with a plastic-covered twist-tie until fruits were ripe (usually 23–30 days after completion of pollinations).

Fruits were collected in their mesh bag and air dried for approximately 7 days, then dehusked using a rubber-covered rubber board. Seeds were germinated under approximately 5 cm of water in glass half-pint (250 ml) bottles, with additional water added as needed to maintain a constant depth. Germination vessels were placed on a bench in the greenhouse under the temperature and light conditions described above. Germinated seeds were transferred into 612 cell packs filled with a commercially available potting mix and irrigated with an automatic mist system (irrigation events every 2 h from 6 AM until 8 PM; duration of each event 3 min) for 3–4 weeks until the seedlings were approximately 30 cm tall. Seedlings were then transplanted into 1-l nursery containers, subirrigated, and kept in a pollinator-free greenhouse under the conditions described above.

All plants were grown to reproductive maturity and evaluated for flower color. No maternal effects were noted; therefore, data for each family were pooled within each cross/reciprocal set. Data from S1 and F1 families were used to develop a working model to explain the type of gene action and number of loci controlling flower color in pickeralweed. Development of this model allowed the assignment of genotypes to parents; the model was then verified by analyses of F2 populations. All data were analyzed using goodness-of-fit (chi square or \( \chi^2 \) ) tests (Steel et al. 1997). A test for heterogeneity of the data for F2 populations from different crosses was performed to determine whether it was appropriate to pool data for all F2 progeny.

Results and Discussion

All S1 progeny in the family WM ⊗ bore only white flowers, whereas all S1 progeny from the family BS ⊗ bore only blue flowers. The family BL ⊗ segregated for flower color and was composed of 38 blue-flowered S1 progeny and 18 white-flowered S1 progeny; this segregation pattern was not statistically different from a 3 blue:1 white ratio (\( P = 0.2170 \)).

The F1 families WM × BS and BS × BL produced only blue-flowered F1 progeny (Table 1). The F1 family WM × BL segregated for flower color and was composed of 29 blue-flowered S1 progeny and 28 white-flowered S1 progeny;
Table 1. Classification of plants of pickerelweed in the F1 and F2 generations for blue or white flower color. Cross- and reciprocal pollinations are pooled within each parental set and are listed by the cross (e.g., observations attributed to WM × BS include data from WM × BS and from BS × WM)

<table>
<thead>
<tr>
<th>Parents</th>
<th>Generation</th>
<th>Genotype</th>
<th>No. of plants observed</th>
<th>Expected ratio</th>
<th>No. of plants expected</th>
<th>χ²</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>WM × BS</td>
<td>F1</td>
<td>WW × WW</td>
<td>103 0</td>
<td>— —</td>
<td>— —</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>WM × BS</td>
<td>F2</td>
<td>WW</td>
<td>855 263</td>
<td>3 1</td>
<td>838.5 279.5</td>
<td>1.299</td>
<td>0.254</td>
</tr>
<tr>
<td>WM × BL</td>
<td>F1</td>
<td>WW × WW</td>
<td>28 29</td>
<td>1 1</td>
<td>28.5 28.5</td>
<td>0.018</td>
<td>0.895</td>
</tr>
<tr>
<td>WM × BL</td>
<td>F2</td>
<td>WW</td>
<td>0 315</td>
<td>— —</td>
<td>— —</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>WM × BL</td>
<td>F2</td>
<td>WW</td>
<td>449 129</td>
<td>3 1</td>
<td>433.5 144.5</td>
<td>2.217</td>
<td>0.137</td>
</tr>
<tr>
<td>BS × BL</td>
<td>F1</td>
<td>WW × WW</td>
<td>49 0</td>
<td>— —</td>
<td>— —</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>BS × BL</td>
<td>F2</td>
<td>WW × WW</td>
<td>615 0</td>
<td>3 1</td>
<td>258.75 86.25</td>
<td>0.047</td>
<td>0.828</td>
</tr>
<tr>
<td>BS × BL</td>
<td>F2</td>
<td>WW</td>
<td>257 88</td>
<td>— —</td>
<td>— —</td>
<td>—</td>
<td>—</td>
</tr>
</tbody>
</table>

this segregation pattern was not statistically different from a 1 blue:1 white ratio (Table 1).

The simplest model that would produce the progeny types recovered in these S1 and F1 families was a model with 2 alleles at 1 locus and blue flower color completely dominant to white. Genotypes were assigned to all 3 parents using the proposed model and segregation of S1 and F1 progenies. The white-flowered parent WM was homozygous recessive (ww), the blue-flowered parent BS was homozygous dominant (WW), and the blue-flowered parent BM was heterozygous (Ww).

Fifteen F1 plants (all with blue flowers and the genotype WW) from the family WM × BS (ww × WW) were self-pollinated to produce 15 F2 families. Each F2 family produced progeny that segregated in a manner that was not statistically different from the expected 3 blue:1 white ratio (data not shown). Heterogeneity chi-square analysis revealed that all F2 families from blue-flowered F1 plants were drawn from populations with identical genotypic constitutions (data not shown); therefore, data for F2 progeny from all F2 families in the family WM × BL were pooled. These pooled progeny segregated in a manner that was not statistically different from the expected 3 blue:1 white ratio (Table 1).

Twelve F1 plants (all with blue flowers) from the family BS × BL (WW × WW) were self-pollinated to produce 12 F2 families. Eight F2 families produced only blue flowers (Table 1) and were derived from F1 plants with the genotype WW. The remaining 4 F2 families were derived from F1 plants with the genotype Ww and produced progeny that segregated in a manner that was not statistically different from the expected 3 blue:1 white ratio (data not shown). Heterogeneity chi-square analysis revealed that all segregating F2 families from blue-flowered F1 plants were drawn from populations with identical genotypic constitutions (data not shown); therefore, data for all segregating F2 progeny from F1 plants in the family BS × BL were pooled. These pooled progeny segregated in a manner that was not statistically different from the expected 3 blue:1 white ratio (Table 1).

Twelve F1 plants (all with blue flowers) from the family BS × BL (WW × WW) were self-pollinated to produce 12 F2 families. Eight F2 families produced only blue flowers (Table 1) and were derived from F1 plants with the genotype WW. The remaining 4 F2 families were derived from F1 plants with the genotype Ww and produced progeny that segregated in a manner that was not statistically different from the expected 3 blue:1 white ratio (data not shown). Heterogeneity chi-square analysis revealed that all segregating F2 families from blue-flowered F1 plants were drawn from populations with identical genotypic constitutions (data not shown); therefore, data for all segregating F2 progeny from F1 plants in the family BS × BL were pooled. These pooled progeny segregated in a manner that was not statistically different from the expected 3 blue:1 white ratio (Table 1).

Heterogeneity chi-square analysis was performed on F2 progeny from the families WM × BS, WM × BL, and BS × BL that segregated in a 3 blue:1 white ratio (Table 2). The test for heterogeneity was not significant; therefore, data for

Table 2. Test for heterogeneity of segregating F2 progeny from 3 F1 families of pickerelweed. Progeny within each F1 family segregated in a manner that was not statistically different from a 3 blue:1 white ratio

<table>
<thead>
<tr>
<th>Parents</th>
<th>Generation</th>
<th>Genotype</th>
<th>No. of plants observed</th>
<th>No. of plants expected</th>
<th>χ²</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>WM × BS</td>
<td>F2</td>
<td>WW</td>
<td>855 263</td>
<td>838.5 279.5</td>
<td>1.299</td>
<td>0.254</td>
</tr>
<tr>
<td>WM × BL</td>
<td>F2</td>
<td>WW</td>
<td>449 129</td>
<td>433.5 144.5</td>
<td>2.217</td>
<td>0.137</td>
</tr>
<tr>
<td>BS × BL</td>
<td>F2</td>
<td>WW</td>
<td>257 88</td>
<td>258.75 86.25</td>
<td>0.047</td>
<td>0.828</td>
</tr>
<tr>
<td>Sum of χ²</td>
<td>—</td>
<td>—</td>
<td>— —</td>
<td>— —</td>
<td>3.563</td>
<td>0.313</td>
</tr>
<tr>
<td>Pooled data</td>
<td>—</td>
<td>—</td>
<td>1561 480</td>
<td>1530.75 510.25</td>
<td>2.391</td>
<td>0.122</td>
</tr>
<tr>
<td>Heterogeneity χ²</td>
<td>—</td>
<td>—</td>
<td>— —</td>
<td>— —</td>
<td>1.172</td>
<td>0.557</td>
</tr>
</tbody>
</table>
all segregating F<sub>2</sub> progeny from all 3 F<sub>1</sub> families were pooled and subjected to chi-square analysis. These pooled progeny segregated in a manner that was not statistically different from the expected 3 blue:1 white ratio (Table 2).

**Conclusions**

The results of this experiment suggested that flower color in these populations of pickerelweed was controlled by 2 alleles at one locus; gene action was completely dominant, and white flower color was recessive. All progeny in this experiment segregated as expected when tested against this model. Self-pollination of white-flowered plants (genotype <em>ww</em>) produced only white-flowered offspring, whereas self-pollination of blue-flowered plants resulted in progeny with only blue flowers (parent genotype <em>WW</em>) or progeny with blue and white flowers in a 3:1 ratio (parent genotype <em>Ww</em>). We propose that this locus controlling flower color in pickerelweed be named <em>white flower</em> with alleles <em>W</em> and <em>w</em>.

Pickerelweed is used extensively as an ornamental in water gardens and aquascapes because the species is a widely adapted perennial with attractive flowers. The wild-type blue flowers of pickerelweed are always appealing to consumers, but nurseries are constantly searching for novel and exciting plants to offer their clients. White-flowered specimens of pickerelweed are readily available from many aquatic plant nurseries but propagules of pickerelweed are often derived through micropropagation (Kane and Philman 1997), which requires specialized equipment that may be unavailable to small growers. This research revealed that white flowers are the result of a recessive condition at the <em>white flower</em> locus, so white-flowered plants are true breeding for flower color. Nurseries may be able to use this information to produce white-flowered plants of pickerelweed more inexpensively by maintaining white-flowered plants for use as parents in seed production.

**Acknowledgments**

This research is presented by the senior author as partial fulfillment for the Doctor of Philosophy degree and was supported by the Florida Agricultural Experiment Station (FAES Journal Series No. R-10878). Mention of a trademark or a proprietary product does not constitute a guarantee or warranty of the product by the FAES and does not imply its approval to the trademark or a proprietary product does not constitute a guarantee or warranty of the product by the FAES and does not imply its approval to the

**References**


Darwin C. 1877. The different forms of flowers on plants of the same species. London: John Murray.


