Table 1. Inheritance of bitterness in the fruit of the cross of ‘Green Striped Cushaw’ (‘G S Cushaw’) pumpkin with ‘Goldbar’ squash.

<table>
<thead>
<tr>
<th>Pedigree</th>
<th>Expected ratio</th>
<th>Classification</th>
<th>Chi square</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Bitter</td>
<td>Nonbitter</td>
</tr>
<tr>
<td>G S Cushaw</td>
<td>---</td>
<td>0</td>
<td>10</td>
</tr>
<tr>
<td>Goldbar</td>
<td>---</td>
<td>0</td>
<td>10</td>
</tr>
<tr>
<td>(G S Cushaw x Goldbar F₁)</td>
<td>1:1</td>
<td>109</td>
<td>103</td>
</tr>
<tr>
<td>G S Cushaw x Goldbar</td>
<td>1:3</td>
<td>81</td>
<td>33</td>
</tr>
<tr>
<td>(G S Cushaw x Goldbar F₁)</td>
<td>1:1</td>
<td>109</td>
<td>103</td>
</tr>
<tr>
<td>G S Cushaw x Goldbar #3</td>
<td>1:3</td>
<td>6</td>
<td>29</td>
</tr>
<tr>
<td>G S Cushaw x Goldbar #6</td>
<td>1:3</td>
<td>47</td>
<td>155</td>
</tr>
<tr>
<td>Pooled Cushaw backcrosses</td>
<td>---</td>
<td>86</td>
<td>265</td>
</tr>
<tr>
<td>Homogeneity</td>
<td>---</td>
<td>27:37</td>
<td>3:12</td>
</tr>
<tr>
<td>G S Cushaw x Goldbar #2 F₂</td>
<td>27:37</td>
<td>14</td>
<td>34</td>
</tr>
<tr>
<td>C S Cushaw x Goldbar #3 F₂</td>
<td>27:37</td>
<td>16</td>
<td>34</td>
</tr>
<tr>
<td>G S Cushaw x Goldbar #6 F₂</td>
<td>27:37</td>
<td>16</td>
<td>34</td>
</tr>
<tr>
<td>G S Cushaw x Goldbar #7 F₂</td>
<td>27:37</td>
<td>13</td>
<td>34</td>
</tr>
<tr>
<td>Pooled F₂ populations</td>
<td>27:37</td>
<td>114</td>
<td>65</td>
</tr>
<tr>
<td>Homogeneity</td>
<td>---</td>
<td>---</td>
<td>5.203</td>
</tr>
</tbody>
</table>

Numbers following crosses identify individual F₂ plants.

Bitterness in cucurbit fruit has been shown in several studies to be dominant to nonbitterness. Possibly, the edible, cultivated cucurbit cultivars originated from wild bitter species following recessive mutation (4). If a sequential series of biochemical reactions, each under gene control, is necessary for the production of cucurbitacins in cucurbit fruit, mutation of any one of these genes could interfere with cucurbitacin development and result in the production of nonbitter fruit. Although several genes affecting bitterness and the suppression of bitterness in fruit have been identified in this and other studies, it is possible, and even likely, that cucurbit species and cultivars exist that are nonbitter because of other, as yet unidentified, recessive mutations.

Literature Cited


Two Genes that Induce Brachytic Dwarfism in Peach

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Additional index words. Prunus persica, dwarfing genes

Abstract. crosses between brachytic dwarf (dwf) and standard (tall) trees in the peach breeding stock of the Univ. of California at Davis revealed two recessive genes with distinguishable effects on stature. It was concluded that one of these is the Dw/dw gene postulated by Lammerts. This gene was introduced to the United States through PI 41395, ‘Swatow’, in 1915. In homoyzogotes it affects a reduction in the internode length over that of standard trees from 18 ± 3.1 mm to 7.7 ± 2 mm, which results in 6-year-old trees averaging 1.37 ± 0.25 m in stature at Davis, Calif. The recessive allele, dwf₁, of the other gene, Dw/dwf₂, is hypostastic to the Dw allele of the Dw/dw gene. It was found to be present, but not expressed, in the standard (tall cultivars Kearney, Red Cal, and Fire Red). Doubly recessive homozygotes (of genotype dwf₁dwf₁, dwf₂dwf₂) have an internode distance of 4.4 ± 0.8 mm and a stature, at 6 years, of 0.92 ± 0.18 m.

True breeding cultivars of dwarf peach have been reported to differ widely in stature at maturity. For example, some dwarf (dwf) cultivars are reported to have mean statures of about 0.61 m. Others have mean statures of about 2.44 m (7). This difference implies that two or more genes have significant effects on stature in this species. However, the language describing these Dwf peach cultivars is insufficiently precise to determine, with any certainty, whether a few or many genes are involved.

Data concerning the inheritance of these dwarf forms are meager. Lammerts (6) studied a dwarf phenotype, ‘Bushy’, which he described as “somewhat brachytic, bushy, with shorter internodes, that reaches a stature of 0.46 to 0.91 m by the end of the second year”. He postulated this phenotype to be under the control of two recessive genes, symbolized bu₁ and bu₂. However, Lammerts based this postulate on the segregation of ‘Swatow’ (1). Tukey reported that the stature of ‘Swatow’ reaches only 0.92 m in 4 years, due to a reduced internode distance of about 6 mm (7). Lammerts postulated this dwf phenotype to be under the control of a single recessive gene, dwf.

However, he drew this conclusion from the segregation (56 tall : 16 dwarf) of only one F₁ family derived from ‘close’ [sic] pollination within the standard cultivar Babcock. No test of this postulate has been reported.

Lammerts also studied the cultivar Chinese Dwarf Mandarin. This cultivar was obtained from one of the seeds in the 1915 USDA acquisition, PI 41395, given the name, ‘Swatow’ (1). Tukey reported that the stature of ‘Swatow’ reaches only 0.92 m in 4 years, due to a reduced internode distance of about 6 mm (7). Lammerts postulated this dwf phenotype to be under the control of a single recessive gene, dwf.
been introduced to the United States from China in 1915 (1). The origin of the four dwf genotypes acquired by the Plant Introduction Agency. Tukey reports it to be a derivative of the 1915 ‘Swatow’ in­
troduction (7). R.L. Ludekens, (L.E. Cooke Co., Visalia, Calif. personal communication) attests to the correctness of Brooks and Olmo’s report (7). The mean and sd of internode lengths reported here was calculated from the measured distance between ten consecutive nodes, taken from the center of shoots, on about 2000 dwf and 500 dbl dwf seedlings in the Univ. of California, Davis breeding stock. The range of plant statures was taken from the same breeding stock. 

Test crosses
Tall x dwf
519,99-107 x 2,40-148 Dw/dw x dw/dw 68:56 62:62
524,103-5 x 2,40-148 Dw/dw x dw/dw 19:23 21:21
522,105-39 x 4,40-33 Dw/dw x dw/dw 31:37 34:34
504,26-1 x 4,4-38 Dw/dw x dw/dw 73:65 66:66

*Dw/dw, Dw2/Dw2
*Dw/Dw, Dw2/Dw2
*Dw/Dw, Dw2/Dw2
*Dw/Dw, Dw2/Dw2

Tall F1 (selfs)†
519,99-5 (x) Dw/dw (x) 44:10 40:13
518,87-18 (x) Dw/dw (x) 92:23 86:29
96,2-11 (x) Dw/dw (x) 111:42 115:38
99,2-13 (x) Dw/dw (x) 52:22 45:19
504,23-4 (x) Dw/dw (x) 225:81 229:76

†These parents were isolated from other genotypes. Thus 20% outcrossing was not expected to affect segregation ratios.

<table>
<thead>
<tr>
<th>Parents</th>
<th>Postulated genotype</th>
<th>Obs segregation tall:dwf:dbl dwf</th>
<th>Expected segregation tall:dwf:dbl dwf</th>
</tr>
</thead>
<tbody>
<tr>
<td>tall (x)</td>
<td>Dw/Dw, Dw2/Dw2</td>
<td>214:0:0</td>
<td>214:0:0</td>
</tr>
<tr>
<td>Kearney (x)</td>
<td>Dw/Dw, Dw2/Dw2</td>
<td>132:0:0</td>
<td>132:0:0</td>
</tr>
<tr>
<td>Red Cal (x)</td>
<td>Dw/Dw, Dw2/Dw2</td>
<td>92:0:0</td>
<td>92:0:0</td>
</tr>
<tr>
<td>dwf (x)†</td>
<td>dw/dw, Dw/Dw2</td>
<td>0:41:0</td>
<td>0:41:0</td>
</tr>
<tr>
<td>7 (x)</td>
<td>dw/dw, Dw/Dw2</td>
<td>0:24:0</td>
<td>0:24:0</td>
</tr>
<tr>
<td>8 (x)</td>
<td>dw/dw, Dw/Dw2</td>
<td>0:236:0</td>
<td>0:236:0</td>
</tr>
<tr>
<td>16 (x)</td>
<td>dw/dw, Dw/Dw2</td>
<td>0:1:2</td>
<td>0:0:3</td>
</tr>
<tr>
<td>dbi dwf (x)†</td>
<td>dw/dw, dw2/Dw2</td>
<td>0:5:29</td>
<td>0:7:28</td>
</tr>
<tr>
<td>5,18-21 (x)</td>
<td>dw/dw, dw2/Dw2</td>
<td>0:3:16</td>
<td>0:4:15</td>
</tr>
<tr>
<td>6,18-181 (x)</td>
<td>dw/dw, dw2/Dw2</td>
<td>0:1:9</td>
<td>0:2:8</td>
</tr>
</tbody>
</table>

*These parents were surrounded by dw/dw, Dw/Dw2 genotypes. Consequently outcrosses were expected to generate some dwf offspring of genotype Dw/dw Dw2/Dw2 (see Materials and Methods).

Table 2. Observed and expected segregation for three plant forms, standard (tall), dwarf (dwf), and double dwarf (dbl dwf) among the progeny of self-pollinated standard, dwarf, and double dwarf peach trees.

<p>| Table 1. Segregation of the postulated recessive gene dw in peach trees. |</p>
<table>
<thead>
<tr>
<th>Matings</th>
<th>Postulated genotypes</th>
<th>Observed segregation tall:dwf:dbl dwf</th>
<th>Expected segregation tall:dwf:dbl dwf</th>
</tr>
</thead>
<tbody>
<tr>
<td>Parental</td>
<td>Dw/Dw x dw/dw</td>
<td>72:0</td>
<td>72:0</td>
</tr>
<tr>
<td>Tall x dwf</td>
<td>0,1-11 x 4,18-7</td>
<td>65:0</td>
<td>65:0</td>
</tr>
<tr>
<td></td>
<td>0,2-3 x 4,20-190</td>
<td>124:0</td>
<td>124:0</td>
</tr>
<tr>
<td></td>
<td>0,2-4 x 4,18-193</td>
<td>72:0</td>
<td>72:0</td>
</tr>
</tbody>
</table>

| Offspring segregation
| dwf/dw |
|---|---|---|
| 72:0 | 72:0 |
| 65:0 | 65:0 |
| 124:0 | 124:0 |

The effect of this outcrossing is to increase slightly the frequency of dwf segre­
gants and decrease slightly the frequency of dbl dwf segregants among their progeny.

Table 1 lists matings designed to test Lammerts’ postulate of a single recessive gene, dw, inducing dwarfism in ‘Chinese Dwarf Mandarin’, a ‘Swatow’ derivative. The genotypes of parents postulated under this model, and the observed and expected seg­
regation among their progeny are also listed in this table. These results support Lammerts postulate of a single recessive gene, dw, in­
ducing brachytic dwarfism in peach. Fur­
ther, they indicate that the recessive gene that induces the dwf phenotype in our breed­ing stock is allelic to Lammert’s dw (6). In our breeding stock, this gene, when homo­
ygous, induces an internode distance of 7.7 ± 2 mm and a stature between 1.37 ± 0.25 during the 6th year.

The dbi dwf phenotype (internode length 4.4 ± 0.8 mm) arose in a number of F2 progeny of F1s that were produced by crossing dwf (internode length of 7.7 ± 2 mm) tall with tall (internode length of 18 ± 3.1 mm) genotypes. The tall parents used in this study comprised both cultivars and advanced se­
lections in the Univ. of California, Davis breeding stock. Were the dbi dwf phenotype under the control of a second recessive gene, dw2, which segregates independently of the recessive gene, dw, then tall phenotypes that yield both dwf and dbi dwf offspring, upon selfing, would have the genotype Dw/dw, Dw2/Dw2. Such phenotypes would yield off­
spring of reduced stature in the ratio of 3 dw/ dw, Dw2/Dw2 : 1 Dw2/Dw2 (dbi dwf) : 1 Dw/dw dw2/Dw2 (unknown phenotype). Contrary to this result, all tall pheno­
types that segregate for both dwf and dbi dwf offspring, upon selfing, yielded ratios that fit a 3 (dwf) : 1 (dbi dwf) model. For example, the progeny of 28 F2 families included tall, dwf, and dbi dwf phenotypes. These families comprised a total of 1660 dwf and 400 dbl dwf F2 offspring. The χ² prob­
ability of this or a better fit to the expectation of a 3:1 ratio (modified by 20% outcrossing) is slightly less than 50%. This result supports

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the postulate that $F_2$ parents that generate tall, dwf, and dbl dwf $F_3$ offspring are of genotype $Dw/dw$, $Dw_2/dw_2$, and that $Dw$ is epistatic over $dw_2$. Were this postulate correct, the $F_2$ dwfs arising in each of the 28 families would comprise two genotypes. Two-thirds of these genotypes would be of genotype $Dw/dw$, $Dw_2/dw_2$. Upon selfing, these genotypes would yield $F_3$ families with no $dbl dwf$s. A wide range of climatic conditions, it is well

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frayed in part by the payment of page charges.

gratefully acknowledge the assistance of N.J. Flickinger and A.D. Bisges, Dept, of Horticul­

ture and research support provided by state and federal

funds appropriated to the Ohio Agricultural Re­

and Development Center, The Ohio State University, Wooster, OH 44691.

would yield $F_3$ families with no $dbl dwf$s. Nine­

eteen $F_2$ families produced by $F_2$ dwfs

selfed, these genotypes would yield $F_3$ families with no $dbl dwf$s. This result is consistent with the prediction that some of the $F_3$ dwfs were of genotype $Dw/dw$, $Dw_2/dw_2$. Upon selfing, these genotypes would yield $F_3$ families with no $dbl dwf$s. Nine­

eteen $F_2$ families produced by $F_2$ dwfs

selfed, these genotypes would yield $F_3$ families with no $dbl dwf$s. This result is consistent with the prediction that some of the $F_3$ dwfs were of genotype $Dw/dw$, $Dw_2/dw_2$.

The above results led to the conclusion that two independently segregating recessive genes control stature; the dominant allele of one gene being epistatic over the recessive allele of the other gene. In the present case $Dw$ appears to be epistatic over $dw_2$. The $F_2$ parents used in this study are true

bred, yielding only $dwf$ progeny (Table 2). Consequently, it can only be concluded that the $dw_2$ allele, expressed in $F_2$ homozygotes came from the tall parents, three of which were the cultivars Red Cal, Kearney, and Fire Red (Table 2).

As in the case with our $dwf$ phenotype, the $dwb$ $dwb$ plant architecture appears to have no significant effect on fruit size and little if any effect on fruit quality. Thus, the results reported here demonstrate that the $dwb$ architecture of tree fruit species can be radically modified by classical Mendelian genetic techniques. They support our earlier contentions that such modifications could be used to effect major increases in productivity, in production efficiency, and in the effectiveness of cultivar improvement programs (4).

Effect of High Temperature on Fruit Set in Tomato Cultivars and Selected Germplasm

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Abstract. Selected $F_2$ and $F_3$ lines of different origin were evaluated at high temperature ($26^\circ$ night and $35^\circ$C day) in the greenhouse along with several known heat-sensitive and heat-tolerant tomato ($Lycopersicon esculentum$ Mill.) cultivars. A number of the selected lines had fruit set comparable to the tolerant cultivars Saladette, Ohio 7663, BL 6807, and Chico III. The expected greater fruit set of the tolerant cultivars vs. that of the sensitive cultivars was observed. High fruit set in this study was not associated with high seed number in the majority of tolerant cultivars evaluated.

Although tomato plants can grow under a wide range of climatic conditions, it is well documented that fruit set is interrupted at temperatures above 26°C/20°C day/night, re-

sp ectively; and is severely interrupted above 35°C/26°C day/night (7). As little as a 4-hr exposure to 40°C in daytime during the reproductive phase prevents fruit set in most cultivars (1–5, 7, 14). Periods of high temperature during the reproductive stage cause interruption in fruit set and split fruit set, leading to yield losses in the temperate growing areas of the world. Harvest of a crop that exhibits split fruit set can result in significant losses, especially with processing cultivars grown for once-over machine har­

vest.

Heat tolerance is regarded as a complex trait (2, 5, 6, 12) with some of the heat toler­

ant genotypes exhibiting significant genotype–environment interaction (14). It is generally accepted that a number of genotypes capable of fruit set at high temperature must be utilized in a breeding program if widely adapted lines are to be developed.

The objective of this study was to deter­

mine whether combinations of fruit set and heat-tolerant characters that occur singly in various heat-tolerant cultivars could provide increased levels of that tolerance.

The experiments were conducted in the greenhouse and the following plant material was used: a) several $F_2$ and $F_3$ selected lines of different origin, derived from a series of crosses involving the heat-tolerant parents ("TH318", ‘Ohio 7663’, ‘UC82’, ‘Saladette’, and ‘BL 6807’); b) standard heat-sen­sitive cultivars (‘C37’, ‘C28’, ‘Ohio 7814’, ‘Ohio 832’, and ‘Ohio 8243’); and c) standard heat-tolerant cultivars (’Ohio 7663’, ‘Chico III’, ‘Saladette’, and ‘BL 6807’). Plants were grown in 30-cm pots containing a soil mix (7 soil : 1 sand : 1 promix­

B.X3). They were fertilized three times a week with a 250-ml application of fertilizer solution containing 7.73 kg of Peters soluble fertili­

izers (20N–8.7P–16.6K) per 76 liters of solution. The high temperature conditions necessitated frequent watering to avoid moisture stress. Standard insecticides were used when necessary.

The cultivars and $F_2$ and $F_3$ lines were evaluated under high temperature in a ran­

domized complete block design with two replications. The experimental unit consisted of two plants. The experiment was carried out in the greenhouse at 26°C ± 2°C night and 35°C ± 4°C day, in a manner similar to the high-temperature screening procedure developed by Stoner and Otto (16). Randomly se­

lected blossoms were tagged at anthesis and self-pollinated through vibration between 18 June and 21 July 1986. The following traits of each cultivar and selected line were recorded: number of fruit set, number of flow­

ers with exserted stigmas, and number of seed per fruit. Percent fruit set and percent

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