

## Interaction of Cucurbitacin Genes

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The *Bt* gene of *Cucumis sativus* L. has been reported to produce bitter fruits (1). We found that the bitterness is due to a quantitative, but not a qualitative change in cucurbitacin content. Fruits of *Bt* plants are high in cucurbitacin C (Cuc C), the same cucurbitacin compound present in normal cucumbers (Table 1). Plants heterozygous for *Bt* had fruits with an intermediate content of Cuc C.

The F<sub>2</sub> progeny of 'Eversweet' x PI 173889 was analyzed for Cuc C content in cotyledons by thin layer chromatography (2) to study the interaction of *Bt* and *bi*. If *Bt* were epistatic to *bi*, a ratio of 15 with to 1 without Cuc C would be expected, while a 3:1 ratio would be expected if *bi* is epistatic to *Bt*. The observed segregation of 48 with Cuc C to 16 free of Cuc C conformed precisely to that expected on the basis of epistasis of *bi*. Bimodal segregation occurred among the F<sub>2</sub> plants having Cuc C, with peaks at 0.25 and 0.40 mg Cuc C/g. Dividing the F<sub>2</sub> population into three groups (0.31-1.00, 0.10-0.30, and 0 mg Cuc C/g) resulted in a ratio of 34:14:16, in close agreement (p = 0.7-0.8) with the 9:3:4 ratio expected.

Additional evidence on the epistasis of *bi* to *Bt* was obtained when fruits of 'Spartan Salad' (+/+ *bi/bi*) x PI 173889 (*Bt/Bt* +/+) was analyzed for Cuc C. The ratio of 31 bitter (>0.01 mg Cuc c/g): 11 normal (0.01 Cuc C): 23 nonbitter (no Cuc C) agreed (p = 0.1-0.2) with the 9:3:4 ratio expected on the basis of epistasis of *bi*, and differed (p = < .001) with the 12:3:1 ratio expected if *Bt* were epistatic.

Serious problems have been encountered with some commercial seed lots of summer squash due to the presence of a gene for bitter and highly toxic cucurbitacin compounds that is believed to have resulted from cross-pollination with an ornamental gourd (3). The bitterness of the fruits of some ornamental gourds (*C. pepo* var. *ovifera*) and the closely related *C. texana* is due to a single dominant gene. Since this gene is analogous to the *Bt* gene of cucumber, a nonbitter gene in squash that is similar to the *bi* gene of cucumber would have value; it might protect a squash cultivar, through epistasis, from producing bitter fruits after gene introgression from an outcross.

A single gene, *cu*, of *Cucurbita pepo* is known to govern cucurbitacin B content of cotyledons (4). We confirmed this, and found that *cu* determines cotyledon content of cucurbitacins D, E, and I as well as cucurbitacin B. Classification for *cu* can be made by tasting cotyledons. Cultivars such as 'Scallop' and 'Straightneck' that are recessive for *cu* have nonbitter cotyledons, whereas 'Zucchini' and other cultivars dominant for *cu* have bitter cotyledons. In this respect, the *cu* gene of *Cucurbita pepo* is similar to the *bi* gene of *Cucumis sativus*, since both produce a phenotype of nonbitter cotyledons. They differ, however, in gene action. Cucumber gene *bi* completely blocked cucurbitacin biosynthesis, while squash gene *cu* reduced but did not eliminate cucurbitacin formation. Another fundamental difference between *Cucurbita* gene *cu* and *Cucumis* gene *bi* is that *cu* is not epistatic to the dominant gene in the species for bitter fruits. The F<sub>2</sub> of *C. pepo* cv. Early Prolific Straightneck x *C. texana* segregated 3 bitter fruits: 1 nonbitter, not in the 9:7 ratio that would be expected if *cu* were epistatic.

Table 1. Cucurbitacin content of cucumber fruits of different genotypes.

<u>Line</u>	<u>Genotype</u>	<u>Phenotype</u>	<u>Cuc C content mg/g fr. wt.</u>
Spartan Salad	+/+ <i>bi/bi</i>	nonbitter	0.00
Wisconsin SMR 18	+/+ +/+	normal	0.01
PI 173889	<i>Bt/Bt</i> +/+	very bitter	0.58
(Spartan Salad X PI 173889) F <sub>1</sub>	<i>Bt/+ bi/+</i>	bitter	0.26

#### Literature Cited

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