

Genotypes of commercial sweet corn F₁ hybrids

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Abstract

Sweet corns are enjoyed worldwide as processed products and fresh ears. Types of sweet corn are based on the gene(s) involved. The oldest sweet corn type has a gene called “*sugary* (*su*)”. *Sugary*-based sweet corn was typically named “sweet corn”. With its relatively short shelf life and the discovery of a complementary gene, “*sugary enhanced* (*se*)”, the sweet corn (*su* only) was rapidly replaced with another type of sweet corns, *sugary enhanced* sweet corn, which has recessive homozygous *su/su*, *se/se* genotype. With the incorporation of *se/se* genotype into existing *su/su* genotype, *sugary enhanced* sweet corn has better shelf life and increased sweetness while maintaining its creamy texture due to high level of water soluble polysaccharide, phytoglycogen. Super sweet corn as the name implies has higher level of sweetness and better shelf life than *sugary enhanced* sweet corn due to “*shrunk2* (*sh2*)” gene although there’s no creamy texture of *su*-based sweet corns. Distinction between *sh2/sh2* and *su/su* genotypes in seeds is phenotypically possible. The involvement of *se/se* genotype under *su/su* genotype, however, is visually impossible. The genotype *sh2/sh2* is also phenotypically epistatic to *su/su* genotype when both genotypes are present in an individual, meaning the seed shape for double recessive *sh2/sh2 su/su* genotype is much the same as *sh2/sh2 +/+* genotype. Hence, identifying the double and triple recessive homozygous genotypes from *su*, *se* and *sh2* genes involves a testcross to single recessive genotype, chemical analysis or DNA-based marker development. For these reasons, sweetcorn breeders were hastened to put them together into one cultivar. This, however, appears to be no longer the case. Sweet corn companies began to sell their sweet corn hybrids with different combinations of abovementioned three genes under a few different trademarks or genetic codes, i.g. Sweet Breed™, Sweet Gene™, Synergistic corn, Augmented Supersweet corn. A total of 49 commercial sweet corn F₁ hybrids with B73 as a check were genotyped using DNA-based markers. The genotype of field corn inbred B73 was *+/+ +/+ +/+* for *su*, *se* and *sh2* as expected. All twelve *sugary enhanced* sweet corn hybrids had the genotype of *su/su se/se +/+*. Of sixteen synergistic hybrids, thirteen cultivars had *su/su se/se sh2/+* genotype while the genotype of two hybrids and the remaining one hybrid was *su/su se/+ sh2/+*, and *su/su +/+ sh2/+*, respectively. The synergistic hybrids all were recessive homozygous for *su* gene and heterozygous for *sh2* gene. Among the fifteen augmented supersweet hybrids, only one hybrid was triple recessive homozygous (*su/su se/se sh2/sh2*). All the other hybrids had *su/su se/+ sh2/sh2* for one hybrid, *su/su +/+ sh2/sh2* for three hybrids, *su/+ se/se sh2/sh2* for three hybrids, *su/+ se/+ sh2/sh2* for four hybrids, and *su/+ +/+ sh2/sh2* for three hybrids, respectively. What was believed to be a classic super sweet corn hybrids also had various genotypic combination. There were only two hybrids that turned out to be single recessive *sh2* homozygous (*+/+ +/+ sh2/sh2*) while all the other five hybrids could be classified as one of augmented supersweet genotypes. Implication of the results for extension service and sweet corn breeding will be discussed.

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