

MARKER-ASSISTED BREEDING FOR GUMMY STEM BLIGHT RESISTANCE IN WATERMELON.



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Abstract

Gummy stem blight (GSB) is a major disease in cucurbits caused by three different species of *Stagonosporopsis*: *S. cucurbitacearum*, *S. citrulli*, and *S. caricae*. Cultivated watermelons (*C. lanatus*) are susceptible to GSB, but resistance has been identified in *C. amarus*, a crop wild relative (CWR) of watermelon. Five QTL for *S. citrulli* and *S. cucurbitacearum* resistance have been identified from two different *C. amarus* accessions. Our objective is to pyramid these small-effect QTL into the *C. lanatus* background. In this study, marker-assisted backcrossing (MABC) was carried out using KASP marker assays flanking the target QTL. *C. lanatus* genome recovery is being accelerated by selection for known fruit quality-related domestication traits, including loss of bitterness (*bHLH*), Brix (*CIAGA2*), and red flesh color (*LYCB*). Once QTL introgression is complete, the lines will be evaluated for GSB resistance and horticultural traits. The breeding lines have potential utility in developing resistant cultivars to help watermelon growers reduce the economic losses associated with gummy stem blight.

Introduction

- Previously, five QTL associated with GSB resistance were identified from two different *C. amarus* accessions^{1,4,5,6} (Fig 1).
- Marker-assisted backcrossing (MABC) and selection allows Introgression of GSB resistant QTL from *C. amarus* into *C. lanatus*.

Objectives

- To develop and validate Kompetitive allele-specific PCR (KASP) assays to select for the target QTL, and fruit quality-related domestication traits in watermelon.
- To introgress GSB resistant QTL from PI 482276 into Crimson Sweet, and from PI 189225 into UGA127 (Breeding line) by performing MABC.

Method

- The F_{2:n} lines from two populations, derived from CS x PI 482276⁴ and SB x PI 189225¹, were selected as the donors of GSB resistant QTL..
- The recurrent parent, *C. lanatus* was used as the female due to early flowering and fruit maturity.
- The QTL from PI 189225 (Fig 1) were selected based on flanking markers for *Qgsb5.2*¹, *Qgsb8.1*⁶, and *Qgsb8.2*⁵. One of the markers for *Qgsb8.1* was redesigned.
- The QTL from PI 482276 (Fig 1, green) was selected based on markers closest to and flanking the QTL peak, including a candidate gene within *Qgsb7.1*⁴.
- Additional markers were designed to check for recombination within *Qgsb7.1*.
- Primers were designed to select for fruit quality-related domestication traits in watermelon (Table 1).

Results

- The QTL from PI 482276 and PI 189225 were introgressed into five lines from CS x PI 482276 and four from SB x PI189225, respectively (Table 2).
- Some backcross lines have recovered cultivar-type alleles for domestication genes (Fig. 2).

Table 2: QTL Introgression progress

Population	Line	Gen	QTL Introgressed
CS	9	BC3	<i>Qgsb7.1</i> , <i>Qgsb5.1</i>
	35	BC3	<i>Qgsb7.1</i> , <i>Qgsb5.1</i>
	x	62	<i>Qgsb7.1</i> , <i>Qgsb5.1</i>
	PI 482276	177	<i>Qgsb7.1</i> , <i>Qgsb5.1</i>
SB	262	BC3	<i>Qgsb7.1</i> , <i>Qgsb5.1</i>
	5	BC2	<i>Qgsb5.2</i> , <i>Qgsb8.1</i> , <i>Qgsb8.2</i>
	x	73	<i>Qgsb5.2</i> , <i>Qgsb8.1</i> , <i>Qgsb8.2</i>
	PI 189225	80	<i>Qgsb5.2</i> , <i>Qgsb8.1</i> , <i>Qgsb8.2</i>
	140	BC2	<i>Qgsb5.2</i> , <i>Qgsb8.1</i> , <i>Qgsb8.2</i>

Conclusion

- KASP markers designed for GSB resistant QTL and domestication genes facilitated the selection of desirable alleles.
- Some of the backcross progeny with GSB-associated QTL have recovered cultivar phenotype (Fig 3).
- Selection for the next generations will include background markers.
- Introgressed lines will be phenotyped for GSB resistance in the greenhouse and the field.

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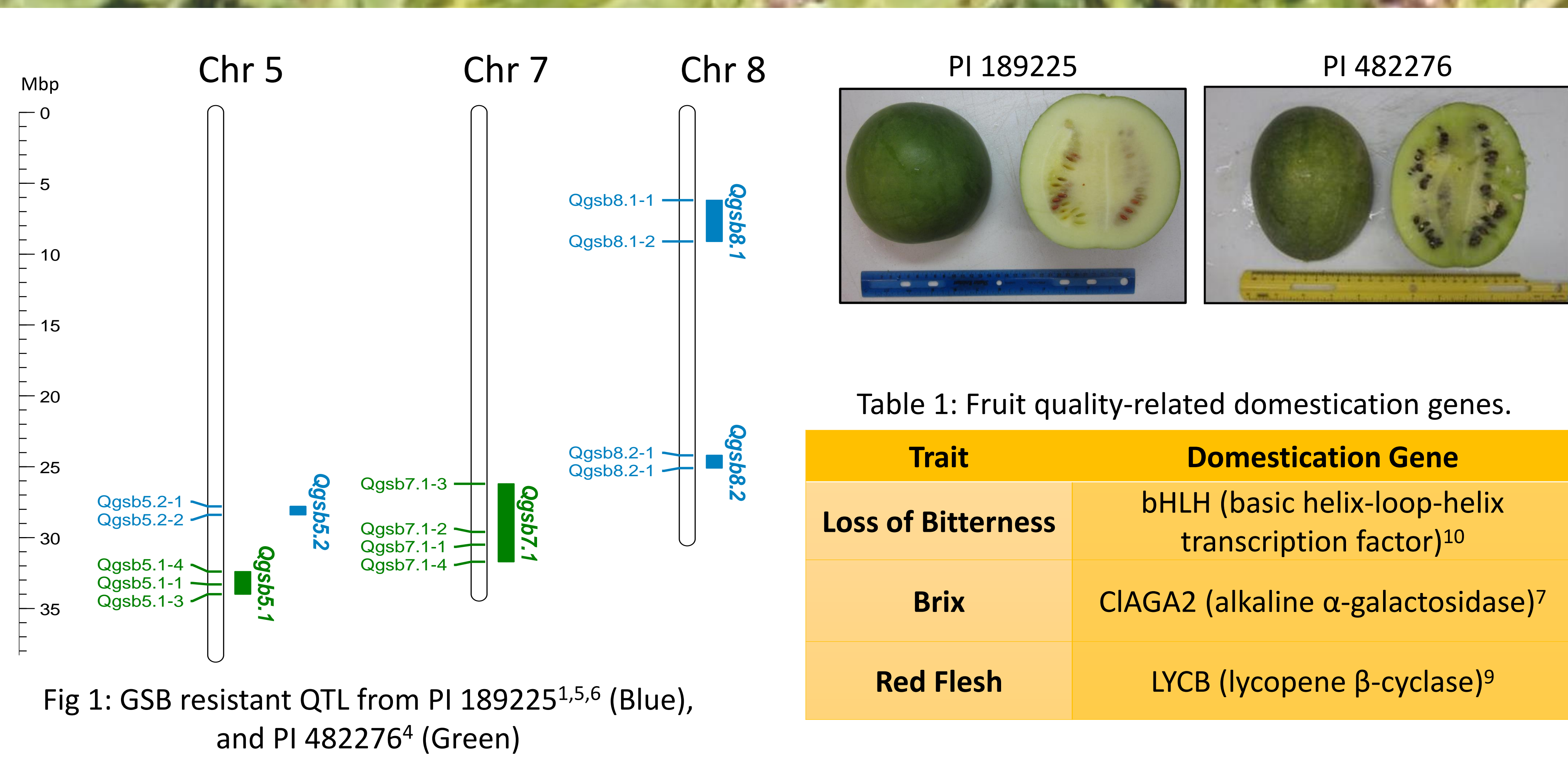


Table 1: Fruit quality-related domestication genes.

Trait	Domestication Gene
Loss of Bitterness	<i>bHLH</i> (basic helix-loop-helix transcription factor) ¹⁰
Brix	<i>CIAGA2</i> (alkaline α-galactosidase) ⁷
Red Flesh	<i>LYCB</i> (lycopene β-cyclase) ⁹

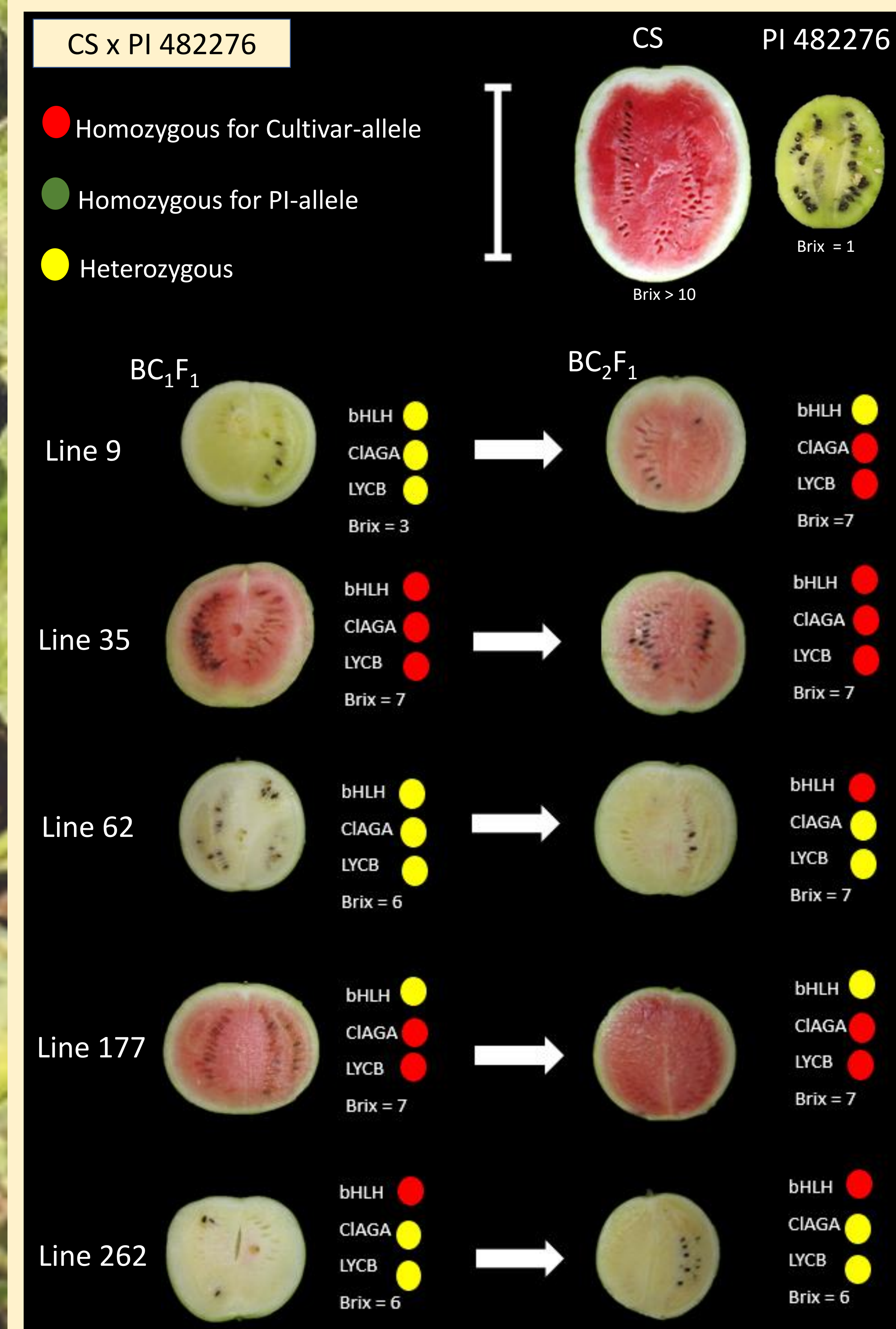


Fig 2: Fruit phenotype, and genotype for domestication genes of the backcross lines that are homozygous for *Qgsb7.1*, and *Qgsb5.1* in BC₁F₁ (left) and BC₂F₁ (right) generations.