

Breeding the Tomato Micro-Tom Model System for Ornamental Value

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Keywords: *Lycopersicon*, *Solanum*, mutants, fruit color, fruit shape

Abstract

Taking advantage of its small size (8 cm tall) and short life cycle (70 days), the ornamental tomato cv. Micro-Tom (MT) was proposed as a model system for tomato genetics. Ever since, MT has been used for large scale mutagenesis and the introgression of allelic variation already known in other cultivars and tomato wild species. Such new genotypes could also be used to improve its value as an ornamental. Here we report the introgression, through successive backcrosses, of various mutations affecting fruit color and morphology into the MT background. Various true type genotypes combining reduced plant size and fruit color variation were obtained upon introgression of the mutations *Del*, *old gold (og)*, *Beta (B)*, *green stripe (gs)*, *pink fruit (y)*, *yellow flesh (r)*, *tangerine (t)*, *apricot (at)* and *green flesh (gf)*. Four mutations affecting fruit format, i.e. *ovate (o)*, *fasciated (f)*, *sun* and *fs8.1*, were also introgressed into MT. These mutations and the combination of them greatly extends the value of MT as an ornamental and introduces the possibility of exploring the large diversity of induced and natural mutations in tomato for this purpose.

INTRODUCTION

Micro-Tom (MT) is a miniature dwarf determinate cultivar of tomato (*Solanum lycopersicum* L. Syn. *Lycopersicon esculentum* Mill.), originally bred for home gardening purposes (Scott and Harbaugh, 1989). It differs from standard tomato cultivars primarily by two recessive genes: *dwarf*, and probably, *miniature* (Meissner et al., 1997; Lima et al., 2004; Martí et al., 2006). The determinate phenotype of MT is caused by a mutation in the *SP* gene (Martí et al., 2006). MT has been put forward as a model system for tomato genetics (Meissner et al., 1997) being amenable for large scale mutagenesis (Meissner et al., 1997; Watanabe et al., 2007; Matsukura et al., 2007) and introgression of alleles present in other cultivars and wild species (Lima et al., 2004). Thus, MT is now being used to address research topics from fleshy fruit development (Serrani et al., 2007), and mycorrhizae formation (Zsögön et al., 2008) to stress tolerance (Malacrida et al., 2006; Gratão et al., 2008a, b). Since novelty is highly valuable for ornamentals, some of the new mutations and allelic variation in MT may also be useful for this propose. Here we report the introgression, through successive backcrosses, of various mutations affecting tomato fruit shape and color (Stevens and Rick, 1986) into the MT background. These mutations and the combination of them greatly extend the ornamental value of MT.

MATERIALS AND METHODS

The genotypes harboring the mutations described in Table 1 were used as pollen donors for crosses with MT. The F₁ plants were selfed to obtain a recombinant F₂ population which was selected for small size, as described in Lima et al. (2004), and the mutation of interest. The selected plants were backcrossed with MT up to the sixth generation (BC₆), with selfing every second generation to screen for homozygous recessive alleles (Fig. 1). Plants were grown in a greenhouse under automatic irrigation (four times/day to field capacity), mean temperature of 28°C, 11.5 h/13 h (winter/summer) photoperiod, and 250 to 350 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$ PAR irradiance obtained by reduction of natural radiation with a reflecting mesh (Aluminet, Polysack Industrias Ltda, Itápolis, Brazil). Mutant seed was sown in trays containing a 1:1 mixture of commercial mix (Plantmax HT, Eucatex, Brazil) and expanded vermiculite, supplemented with 1 g L⁻¹

10:10:10 NPK and 4 g L⁻¹ lime. Ten days after germinations, plants were transferred to 150 ml (MT) or 10 L (donor cultivars) pots containing the aforementioned soil mix. After each crossing, mature fruit was harvested and the seed was cleaned of the pulp by fermenting for 12 h with bread yeast (*Saccharomyces cerevisiae*, Fermix, Brazil). Seeds were then washed and air-dried in the shade.

RESULTS AND DISCUSSION

Here, successive backcrosses were made using MT as a recurrent parental (Fig. 1) in order to introgress mutations affecting fruit shape and color (Table 1). This is a less labor-intensive approach than mutagenesis, which would require a large structure and the screening of a large amount of plants to create an equivalent mutant collection. Further, for some loci, particularly those which are probably already knocked-out in MT (e.g. *Del* and *B*), introgression may be the only way to produce the desired allelic variation. Hence, 14 new mutants were obtained in the MT background in a short period of time and within limited growth facilities. The ornamental value of the genotypes created stands on their reduced plant size and diversity of fruit shape and color (Fig. 2). The collection presented here could be also used as a founder of new fruit shapes and colors, through the combination of mutations such as *y + r*, which creates white fruits, and *ovate + sun*, which produces extreme elongated fruits as in the cv. Long John. Since some of the mutations now near isogenic to MT are also the subject of intense research (Ronen et al., 2000; Isaacson et al., 2002; Liu et al., 2002), their availability in a plant with reduced size and short life cycle will greatly facilitate such studies. Moreover, the ornamental MT collection presented here may also be helpful as a tool for preliminary genetic mapping of new mutations, since the mutations introgressed are easy to score and cover almost all tomato chromosomes (Table 1).

ACKNOWLEDGMENTS

We thank the Fundação de Amparo a Pesquisa do Estado de São Paulo (FAPESP) for financial support (grant 02/00329-8 and 07/07175-0).

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Tables

Table 1. Mutations affecting fruit color and shape introgressed into Micro-Tom.

Mutant	Chrom. ¹	Morphology	Parental ²
<i>Delta (Del)</i>	12	Reddish-orange colored fruits due to delta-carotene accumulation.	LA4099
<i>Old gold (og)</i>	6	Crimson colored fruits due to high lycopene accumulation. Corolla tawny orange.	cv. Ouro Velho
<i>Beta (B)</i>	6	Orange colored fruits due to beta carotene accumulation.	LA1401
<i>Green stripe (gs)</i>	7	Longitudinal green stripes in epidermis of unripe fruits. Stripes become yellow in ripe fruits.	LA2514
<i>Colorless epidermis (y)</i>	1	Pink fruit color due to the lack of pigments in the epidermis.	LA2514
<i>Yellow flesh (r)</i>	3	Yellow fruit color due to reduced phytoene accumulation. Pale yellow corolla.	cv. MsK
<i>Tangerine (t)</i>	10	Orange fruit color due to reduced lycopene accumulation. Pale orange corolla.	LA0159
<i>Apricot (at)</i>	5	Yellow fruit color with pinkish blush. Corolla nearly white.	LA2514
<i>Green flesh (gf)</i>	8	Purplish-brown fruit color and green seed gel due to chlorophyll persistence	LA1797
<i>Ovate (o)</i>	2	Ovate or pear shaped fruits.	cv. Long John
<i>Fasciated (f)</i>	11	Increased number of locules, petals, sepals and stamens. Large and flattened fruits.	cv. Caqui
<i>Sun</i>	7	Elongated fruit format.	cv. Long John
<i>Clausa (clau)</i>	4	Flattened and cleistogamous fruits.	LA3583
<i>Fruit shape (fs8.1)</i>	8	Blocky fruit format.	cv. Roma

¹Chromosome position of the mutation.

²The LA parents refer to genotypes obtained and described in the Tomato Genetics Resource Center (<http://tgrc.ucdavis.edu>).

Figures

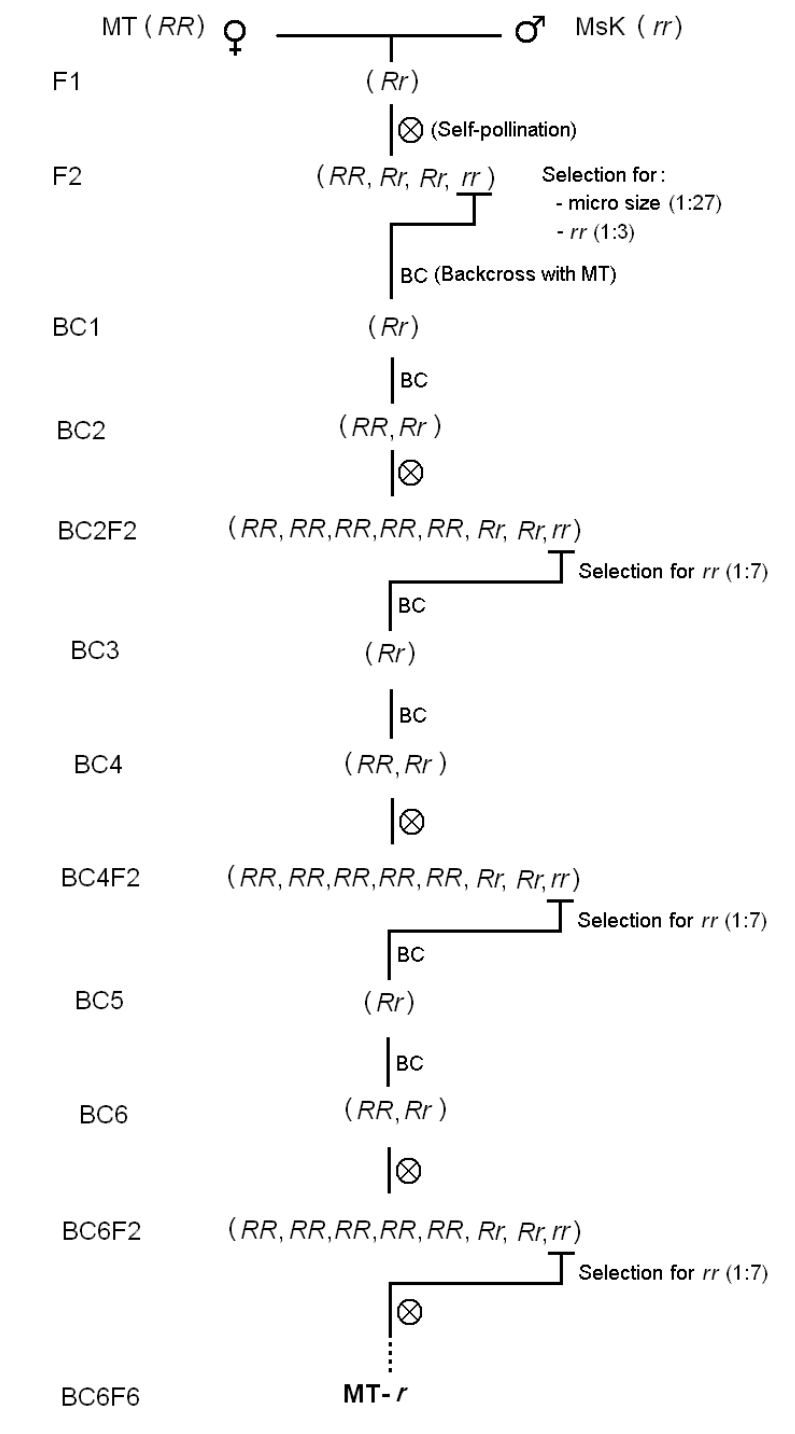


Fig. 1. Scheme of the introgression process. Mutations affecting fruit color or shape, represented here by *yellow flesh* (r), were introgressed into the Micro-Tom (MT) background through a series of six backcrosses (BCs) and selfings (BCnF2). The selected BC6F2 genotype was considered near isogenic to MT and after additional six self-pollinations (BC6F6) the true type genotype was named MT- r .

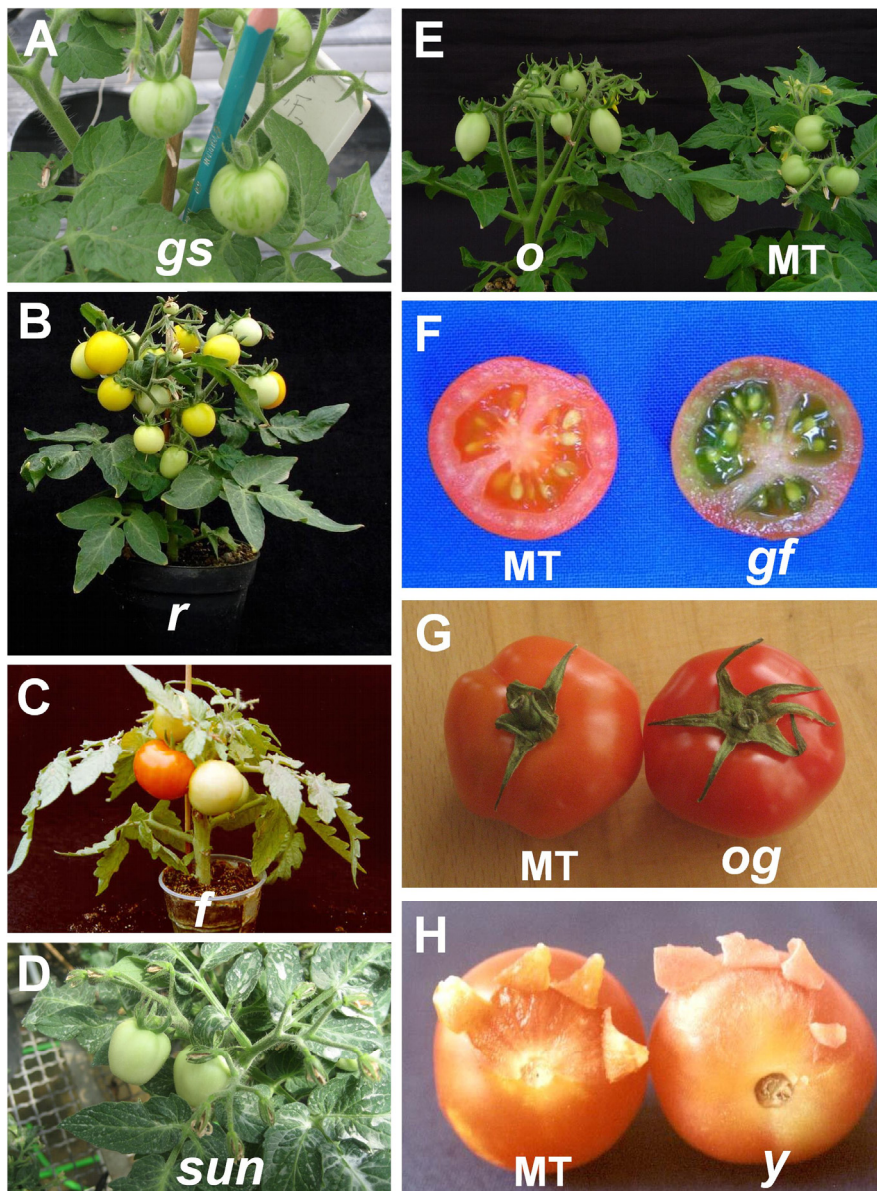


Fig. 2. Phenotypes of Micro-Tom (MT) plants harboring mutant alleles for fruit color and shape. A. Fruits with irregular longitudinal green stripes in epidermis due to the *green stripe* (*gs*) allele; B. Yellow fruits in a plant harboring the *yellow flesh* (*r*) allele; C. Flattened and large fruits due to the increased number of locules (not shown) in the *fasciated fruit* (*f*) allele; D. Elongated fruit shape due to the *sun* allele; E. Ovate (sometimes pear shaped) fruits as a result of the *ovate* (*o*) allele; F. Persistent chlorophyll giving ripe fruits purplish-brown color and green gel due to the *green flesh* (*gf*) allele; G. Intense pigmentation of the fruit as a result of high lycopene accumulation due to the *old gold* (*og*) allele; and H. Pink fruits due to the lack of normal yellow pigmentation in epidermis as a result of the *colorless fruit epidermis* (*y*) allele.