

Facilitating the fishing in the gene pool of the wild eggplant relative *Solanum incanum* by developing introgression lines



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Despite the economic importance of eggplant (*Solanum melongena*), breeders have made little use of the genepool of cultivated and wild relatives, even though fully fertile hybrids are obtained with some of them (1) (Fig. 1).



Figure 1. Wild (*S.linneanum* and *S.incanum*) and cultivated (*S.aethiopicum* L. and *S. macrocarpon*) specieses closely related to eggplant

Solanum incanum is a wild close relative of eggplant naturally occurring in dry areas from northern Kenya to Pakistan (2). It presents resistance to drought, cold, and to some diseases, as well as high levels of bioactive phenolic compounds, in particular chlorogenic acid. However, *S. incanum* also presents many undesirable characteristics typical of wild species. Development of introgression lines (ILs) facilitate the use of genes from wild species by breeders (3). In order to develop a set of ILs of *S. incanum* in the genetic background of *S. melongena* we obtained the interspecific hybrid, which was highly fertile, very vigorous, and proved to be an excellent rootstock for eggplant. This interspecific hybrid was backcrossed with the *S. melongena* parent to obtain the BC1 generation (Fig. 2).



Figure 2. BC1 population from the interspecific hybrid *S. incanum* x *S. melongena* to *S. melongena*

A genetic map in which markers were distributed in 12 linkage groups (LGs), which matches the haploid chromosome number of eggplant, was developed from the BC1 generation.

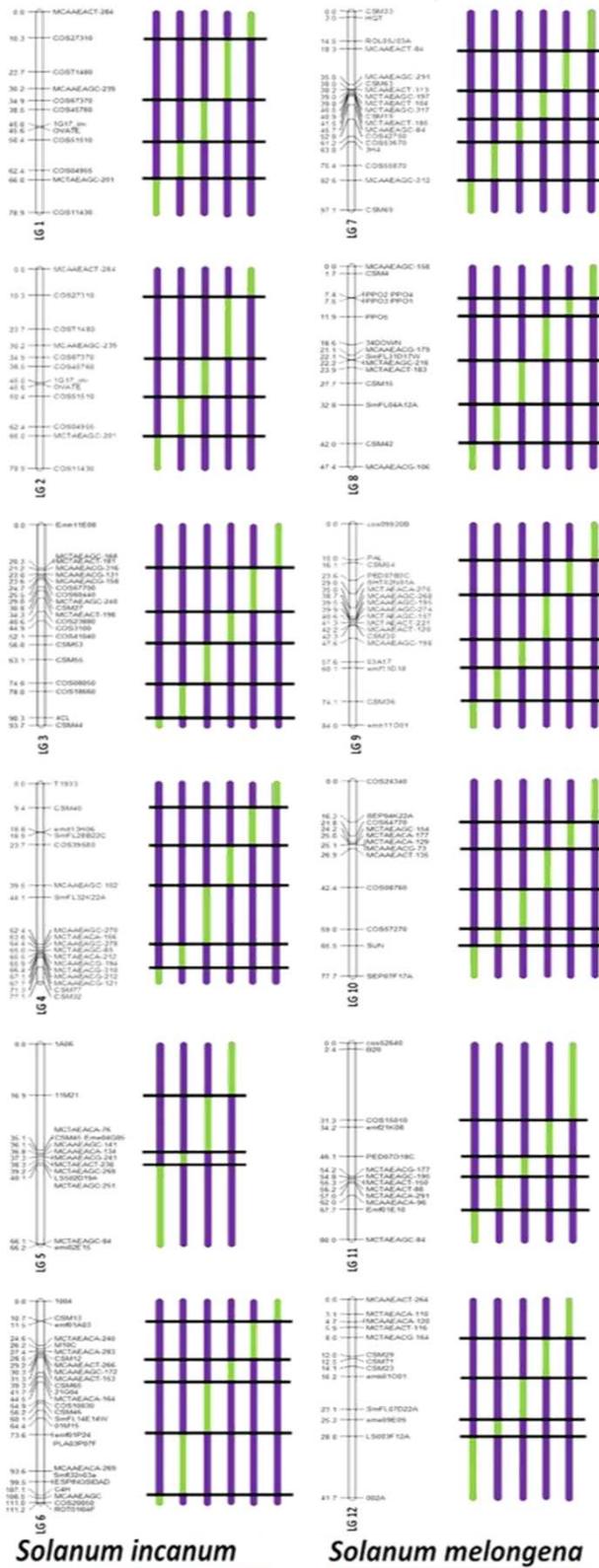


Figure 4. Set of ILs covering the whole *S. incanum* genome in the *S. melongena* genetic background

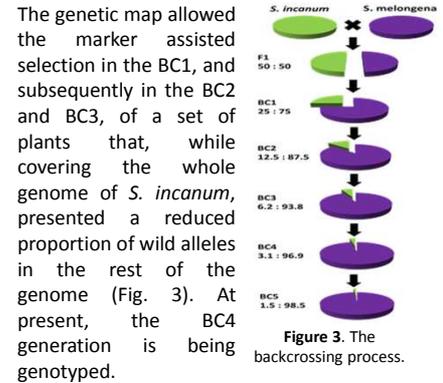


Figure 3. The backcrossing process.

The genetic map allowed the marker assisted selection in the BC1, and subsequently in the BC2 and BC3, of a set of plants that, while covering the whole genome of *S. incanum*, presented a reduced proportion of wild alleles in the rest of the genome (Fig. 3). At present, the BC4 generation is being genotyped.

The results obtained up to now show that with one or two additional BC generations followed by fixation by means of selfing, a set of 60-80 ILs (with five to eight ILs per LG) covering the whole *S. incanum* genome in the *S. melongena* genetic background, will be obtained (Fig. 4). We have also been able to map six genes involved in the chlorogenic acid (CGA) synthesis pathway, and a set of seven BC3 plants, each of which is carrying the *S. incanum* allele for a different CGA pathway gene, has been identified.

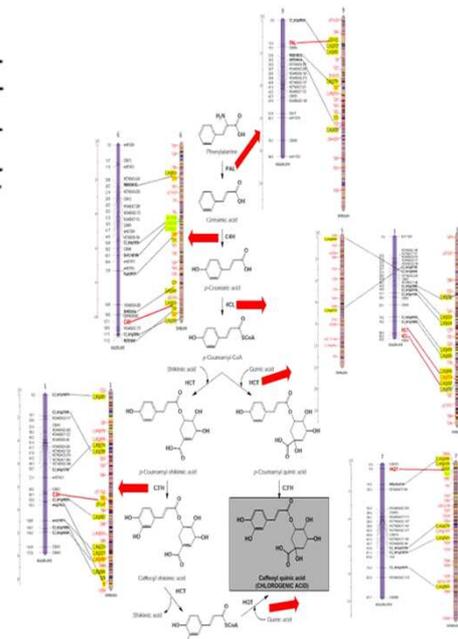


Figure 5. Candidate genes mapped in the chlorogenic acid pathway.

The set of ILs will be of great utility for eggplant breeders and will allow the ready use of genes of interest from *S. incanum* in developing new eggplant cultivars with new characteristics and adapted to present and future needs (1).

REFERENCES

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