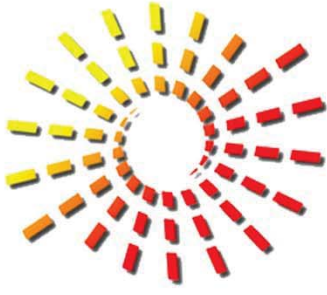


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A strategy for broadening the genetic base of eggplant using wild relatives as donors of variation

Prohens J^a, Fonseka H^b, Kouassi A^c, Plazas M^a, Fonseka R^d, Kouassi AB^c, Gramazio P^a, Welegama T^b, Kouassi B^c, Herraiz FJ^a, Ranil R^d, Rodríguez-Burruezo A^a, Niran L^c, Fita A^a and Vilanova S^a

^a *Instituto de Conservación y Mejora de la Agrodiversidad Valenciana, Universitat Politècnica de València, Valencia, Spain;*

^b *Horticultural Crop Research and Development Institute, Peradeniya, Sri Lanka;* ^c *Laboratory of Genetics, Félix*

Houphouët-Boigny University; ^d *Department of Crop Science, University of Peradeniya, Sri Lanka;* ^e *Agriculture Research Station, Girandurukotte, Sri Lanka*

Like many domesticates, common eggplant (*Solanum melongena*) has a narrow genetic base when compared with its wild relatives. Unlike other important vegetable crops, up to now few efforts have been made to use wild species for developing new eggplant varieties. We have initiated a project funded by Global Crop Diversity Trust aimed at using a comprehensive and systematic strategy to broaden the genetic base of eggplant, in particular for adaptation to climate change, by exploiting genetic resources of its wild relatives. We are in the process of developing a set of introgression lines based on backcross generations to eggplant of a hybrid between *S. melongena* and the drought tolerant wild species *S. incanum*. Several types of molecular markers, including SSRs and SNPs have been used in the backcross process. *Solanum incanum* introgression lines are being crossed to local varieties from Southeast Asia and West Africa, areas highly vulnerable to climate change, in order to develop drought tolerant materials. Also, eggplant interspecific hybridization has been used to obtain interspecific hybrids with 9 wild species of the primary and secondary gene pools. In addition, by using embryo rescue techniques, interspecific hybrids have been obtained with tertiary gene pool species *S. torvum*. New crosses recently performed have also allowed recovering putative hybrids with three other species of the secondary gene pool and with tertiary gene pool species *S. elaeagnifolium*, which is highly tolerant to drought. Interspecific hybrids are being backcrossed to the cultivated *S. melongena* and successful backcrosses have been obtained up to now for six wild species. Screening for drought will be performed in these materials. In addition, new sets of introgression lines will be obtained. The strategy we are using will allow broadening the genetic base of eggplant, which will ultimately result in new varieties with greater resilience to stresses resulting from climate change.

De novo transcriptome sequencing in four non-model species in genus *Solanum* (*S. incanum*, *S. aethiopicum*, *S. muricatum* and *S. caripense*): Analysis and molecular markers detection for breeding purposes

Gramazio P, Herraiz FJ, Blanca J, Ziarsolo P, Plazas M, Prohens J and Vilanova S

Instituto de Conservación y Mejora de la Agrodiversidad Valenciana, Universitat Politècnica de València, Camino de Vera 14, 46022 Valencia, Spain

Transcriptome sequencing has become an essential tool to generate genomic data in species where genomic resources are sparse. Here we present the results of transcriptome sequencing of four *Solanum* species (*S. incanum*, *S. aethiopicum*, *S. muricatum* and *S. caripense*) using Illumina HiSeq 2000 platform, the comprehensive analysis of their de novo assembly and molecular marker discovery. *S. incanum* is considered as the wild ancestor of common eggplant (*S. melongena* L.), exhibiting a great amount of phenolics and tolerance at drought. Scarlet eggplant (*S. aethiopicum*) is a cultivated African eggplant, showing resistance at some biotic stresses and is used also as rootstock for common eggplant (*S. melongena*). Pepino (*S. muricatum*) is a neglected herbaceous domesticate native to the Andean region grown for its juicy fruit and is phylogenetically close to potato and tomato. *Solanum caripense* is a wild relative of pepino showing high levels of soluble solid content and phenolic acids and resistance to Tomato Mosaic Virus and to *Phytophthora infestans*. More than 100 million raw reads were obtained for all species which were assembled with Trinity software. We obtained 83,905 unigenes for *S. incanum*, 87,084 for *S. aethiopicum* and 75,832 for *S. muricatum*. As *S. caripense* is phylogenetically very close to pepino we mapped its reads against the pepino assembled transcriptome instead of assembling them separately. All unigenes were functionally and structurally annotated to identify potentially encoding proteins and orthologs, to assign GO terms, EC number and KEGG pathway, and to predict ORFs and introns. More than 1000 EST-SSRs were discovered in each transcriptome as well as tens of thousands of intraspecific and interspecific SNVs (SNPs and INDELS). The genomic information and markers generated in this study will be extremely useful in the breeding programs of eggplant and pepino, as well as for tomato and potato and to perform marker-trait association and QTL analysis studies.