

A COMMON ANCHORED MAP BASED ON A FRAMEWORK OF COSII MARKERS FOR POTATO AND A SET OF TOMATO “EXOTIC LIBRARIES”

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Genome mapping results and their recent applications have demonstrated that the genetic diversity stored in germplasm banks can be utilized much more efficiently than before. Therefore, a major objective in modern breeding is to return to natural biodiversity resources, in the form of wild species or old varieties, and employ some of the diversity that was lost during domestication and breeding for the improvement of the agricultural performance of modern varieties. In this respect, “exotic libraries”, which consist of sets of segmental introgression lines (ILs), each carrying a single marker-defined genomic region that derives from a donor wild species in an otherwise uniform elite genetic background, have proven to be very efficient tools for plant breeders. Comparative mapping has also shown extensive genome colinearity among plant species of the same family. Therefore, in order to enhance the rate of progress of breeding based on wild species resources, and to facilitate comparisons between function maps of tomato and potato, “exotic libraries” of tomato from a diverse selection of accessions (including *S. pennelii* LA0716, *S. habrochaites* LA1777, *S. chmielewskii* LA1840, *S. neorickii* LA2133) and a diploid mapping population of potato are being anchored using a common set of Conserved Ortholog Set II (COSII) markers (http://www.sgn.cornell.edu/markers/cosii_markers.pl). This work is being conducted within the framework of the EU-SOL project (<http://www.eu-sol.net/>). The construction of a common PCR-based marker framework, which links the tomato and potato maps, the genetic infrastructure of tomato “exotic libraries”, along with the numerous qualitative and quantitative traits mapped in both species, should facilitate quantitative trait locus (QTL) identification, additional mapping, cloning of the underlying genes and the use of the novel variation in marker-assisted breeding.