COMPARATIVE STRUCTURAL GENOMICS BETWEEN INCORRUENT WILD POTATO SPECIES


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Wild potato species are an important source of disease resistance genes. Due to sexual incompatibilities with cultivated potato, some of these genes are unavailable for potato improvement. Sequence informations, structural genomics and biotechnology are changing this scenario. To improve access to the wild potato gene pool we have developed linkage maps for two wild potato relatives, Solanum bulbocastanum and S. commersonii using Diversity Array Technology (DArT). These species represent phylogenetically distinct series within the potato tertiary genepool. Here we report details and comparisons of generated linkage maps. To build the map of each species we used F1 mapping populations. Seven hundred fifty and 1000 mappable segregating DArT markers of S. bulbocastanum and S. commersonii have been found, respectively. About 40 common markers have been identified. At LOD score 3, S. commersonii map consisted of 13 linkage groups whereas 14 linkage groups were identified for the S. bulbocastanum map. Length of S. commersonii map was higher than S. bulbocastanum. Resulting maps can be further augmented with other marker sources and this will be the first medium density genome-wide linkage maps for these species. A preliminary bioinformatics study of marker sequences revealed that most of the DArT markers originate from expressed regions. With the ongoing tomato and the cultivated potato genome sequencing projects, sequencing of DArT markers mapped on wild potato will allow comparison of genome-wide structure throughout the genus Solanum.