

STRUCTURAL GENOMICS OF WILD POTATO SPECIES BASED ON DArT ALIGNMENTS

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To improve the access to resistance and agronomically significant genes of *Solanum bulbocastanum* and *S. commersonii*, two wild potato species, we had previously developed their first genetic linkage map based on DArT markers. In this study, bioinformatics and ongoing sequencing efforts for the potato (*Solanum phureja*) and tomato (*Solanum lycopersicum*) genomes were useful to select DArT markers associated with interesting genes. About 1500 DArT markers, representing the *S. bulbocastanum* and *S. commersonii* maps, were sequenced by BigDye™ Terminator ABI PRISM® 310 Genetic Analyzer. Then, they were aligned using the GenomeThreader software along the chromosome sequences of both potato (<http://www.potatogenome.net>) and tomato (<http://solgenomics.net>) genomes. Although a filter of 70% of coverage and score was considered, most of alignments showed a quality higher than 90%. Ninety-two % of DArT markers aligned on the potato genome, while 79% of them aligned to tomato. In particular, only the 5% of markers aligned to neither genome, thus revealing makers potentially specific to genomic regions of the wild potato species. As expected, DArT markers showed better correspondences with the potato. Interestingly, in both genomes DArT markers were preferentially distributed on chromosomes I, II, III, IV and VI. Among DArT markers belonging to linkage groups and aligned to both the potato and the tomato genomes, collinearity as well as correspondence with annotated genes were found. Moreover, the chromosome association of the linkage groups analyzed was considered. Results are discussed from evolutionary and breeding standpoints.