

# STRUCTURAL GENOMICS OF WILD POTATO SPECIES BASED ON DART ALIGNMENTS

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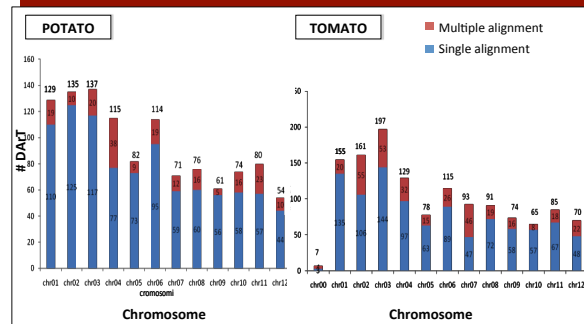
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## Introduction

To improve the access to significant genes of two wild potato species, we are using linkage maps based on DArT markers. Here, bioinformatics and sequencing efforts for potato and tomato genomes were used for structural genomics studies.

**Tab. 1** Blb and cmm DArT alignments on potato and tomato genomes. Blb-cmm indicates DArT markers common between the species.

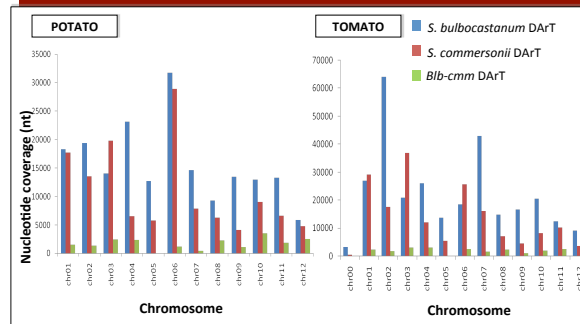
DArT	TOT	POTATO		TOMATO	
		alignment (%)	misalignment (%)	alignment (%)	misalignment (%)
blb	770	70.6	29.4	77.1	22.9
cmm	550	61.5	38.5	81.3	18.7
blb-cmm	103	70.9	29.1	80.6	19.4
TOTAL	1423	70.6	32.8	79.0	21.0



**Fig. 1** DArT chromosome distribution among potato and tomato genomes.

## Results

With a filter of 70% of coverage and score, 70% of DArT markers aligned on the potato and 79% on tomato genome (Tab. 1). Misalignments revealed potentially specific genomic regions of the wild species. DArTs preferentially distributed on chromosomes I, II, III, IV and VI (Fig. 1). The overall nucleotide coverage per chromosome showed a higher value of blb (Fig. 2). Among blb DArT markers aligned to both reference genomes, collinearity as well as correspondence with annotated genes were found (Fig. 3).



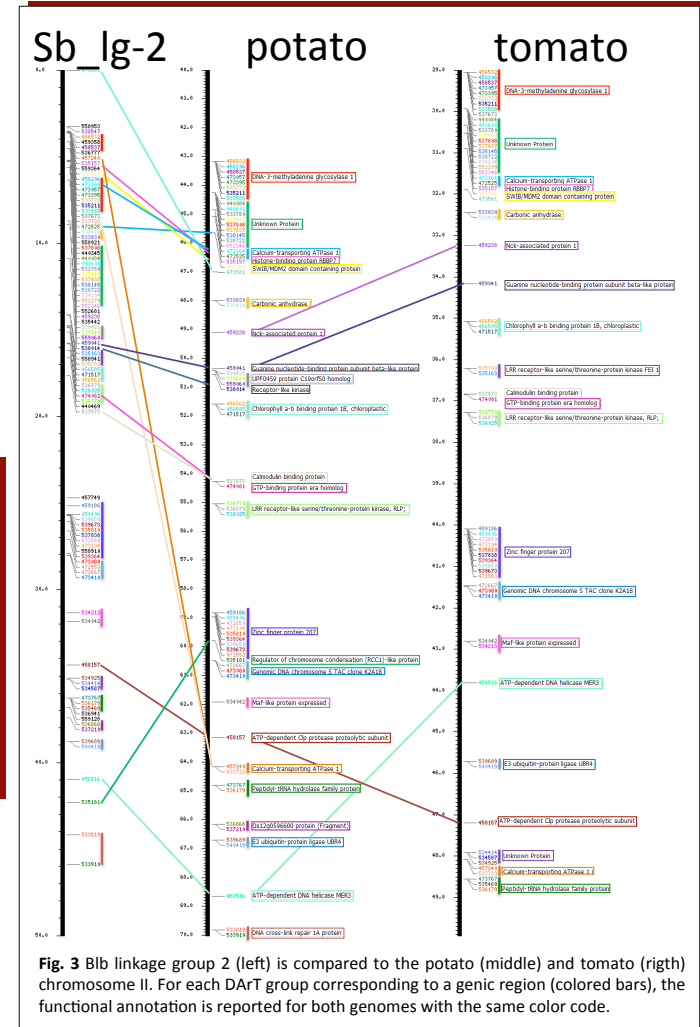
**Fig. 2** DArT nucleotide coverage in potato and tomato genomes.

## Materials & Methods

About 1500 DArT markers, representing the *Solanum bulbocastanum* (blb) and *S. commersonii* (cmm) maps were sequenced. They were aligned using the GenomeThreader software along the chromosome sequences of potato and tomato genomes.

## Conclusions

DArT markers were validated from the bioinformatics standpoint. Structural genome comparisons of the linkage groups analyzed showed marker order conservation and absence of structural and functional differences between tomato and potato.



**Fig. 3** Blb linkage group 2 (left) is compared to the potato (middle) and tomato (right) chromosome II. For each DArT group corresponding to a genic region (colored bars), the functional annotation is reported for both genomes with the same color code.