

Comparative structural genomics of disease resistant wild potato species comprising the tertiary gene pool of cultivated potato

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Introduction

The potato tertiary gene pool consists of wild species that are sexually incompatible with cultivated potato (figure 1). These species are rich sources of resistance genes to biotic and abiotic stresses (figure 2), yet remain largely untapped.

Here we report preliminary results toward developing genome-wide linkage maps for potato tertiary gene pool species *Solanum bulbocastanum* and *S. commersonii* using Diversity Array Technology (DART).

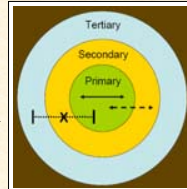


Figure 1. The Gene Pool Concept of Harlan and de Wet (Taxon 20:509) categorizes wild germplasm based on crossability with crop plants. The potato tertiary gene pool includes 20 disease resistant species that cannot be crossed with cultivated potato.

Series*	Species	ERN	Reported Disease Resistances*
I. <i>Macleodiana</i>	<i>S. elaeagnifolium</i>	7	Early blight, PVM, Verticillium
	<i>S. macrodonum</i>	7	
II. <i>Bulbocastanum</i>	<i>S. bulbocastanum</i>	1	Blackleg, Bacterial wilt, Early blight, Late blight, PLRV, PVM, Ring rot, Verticillium, Wart
	<i>S. cardiophyllum</i>	1	Late blight, Ring rot, Verticillium, Wart
III. <i>Pinnatifidum</i>	<i>S. jamaense</i>	1	Blackleg, PLRV, PVY, Ring rot, Verticillium
	<i>S. pinnatifidum</i>	1	Black leg, Early blight, Late blight, PLRV, Ring rot
	<i>S. villosofolium</i>	1	Blackleg, Early blight, Ring rot, Verticillium
	<i>S. torral</i>	1	Late blight, Ring rot
IV. <i>Polyadenia</i>	<i>S. ripifolium</i>	1	Late blight, PLRV, Ring rot, Verticillium
	<i>S. leucifolium</i>	1	Ring rot, Verticillium with
V. <i>Commersoniana</i>	<i>S. polyadenium</i>	1	Blackleg, Late blight, PLRV, PVA, PVM, Ring rot, Verticillium
	<i>S. commersonii</i>	1	Bacterial wilt, Blackleg, Early blight, Ring rot, Verticillium
VI. <i>Circosifolia</i>	<i>S. circosifolium</i>	1	Bacterial wilt, PVM, PVS, Rhizoctonia, Wart
	<i>S. rigidicaule</i>	1	
VII. <i>Agnocaulis</i>	<i>S. agnocaulis</i>	7	Fusarium wilt, Rhizoctonia, Verticillium, Wart
	<i>S. adnigrum</i>	7	
IX. <i>Yunguesana</i>	<i>S. armaritii</i>	2	
	<i>S. chacoense</i>	2	PVA, PVF, PVS, PLRV, Verticillium
	<i>S. amnicolumbense</i>	2	PLRV, Verticillium
	<i>S. narigenae</i>	2	Verticillium
	<i>S. yunguesana</i>	2	

*Classification scheme for supergenus *Solanum* of Hawkes (1998) with modifications after Rodriguez and Spooner (1997), Lara-Cabrera and Spooner (2004), and Spooner et al. (2004).
 *Resistance data from personal experience, published accounts (Austin et al. 1993; Helgason et al. 1998; Michelena et al. 2000; Naves et al. 2000; Song et al. 2003; Vavilov et al. 2003; Vavilov et al. 2005), and USDA Potato Germplasm website.
 Abbreviations: PLRV - Potato Leaf Roll Virus; PVA - Potato Virus A; PVF - Potato Virus F; PVM - Potato Virus M; PVS - Potato Virus S

Figure 2. Tertiary gene pool species are rich sources of biotic/abiotic resistance. The potato tertiary gene pool is phylogenetically unique from cultivated potato and includes 20 species arranged into 9 series. In this study we targeted two species from unique series for genome mapping.

Diversity Array Technique (DART)

DART is a high-throughput microarray-based method yielding an array of clones via genomic representation, a procedure similar to AFLP (Figure 3). We created a community-based DART platform for potato. The potato array has 16,500 features, of which 9,500 are from tertiary gene pool genomes.

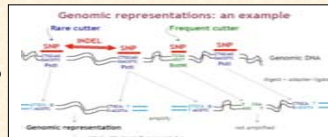


Figure 3. DART: generation of genomic representations (adapted from the DART website: www.diversityarrays.com)

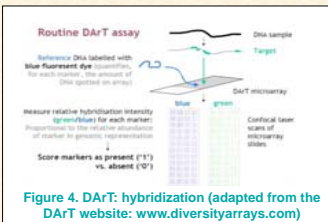


Figure 4. DART: hybridization (adapted from the DART website: www.diversityarrays.com)

Marker profiles for specific genotypes are determined via DNA:DNA hybridization, making DART ideal for cross-taxa comparisons. Hybridizations of mapping progeny targets to individual clones were scored as present (1) or absent (0) (Figure 4).

Reprints of this poster are available at <http://ppg.cfans.umn.edu>

DART markers in tertiary gene pool genomes

Marker data were assigned to segregation classes (χ^2 test, p value = 0.05). The two species yielded consistent marker segregation results.

Table 1. Summary of DART markers generated for two tertiary gene pool species

Species	Segregation Ratio	Number of Markers	Percentage
<i>S. bulbocastanum</i>	1:1	510	79.8%
	3:1	129	20.2%
	Total # markers	639	100%
<i>S. commersonii</i>	1:1	578	78.3%
	3:1	160	21.7%
	Total # markers	738	100%

Genome-wide linkage map construction

The first medium density genome-wide linkage maps were constructed for *S. bulbocastanum* and *S. commersonii* (Table 2). These maps form the basis for future comparisons with other *Solanum* species and serve as a backbone upon which to anchor BAC clones carrying disease resistance genes (see Oral Presentation O-59).

Table 2. DART markers mapped to linkage groups (preliminary results)

	# Linkage groups	Total# markers	Marker redundancy	Map length (cM)	# Markers/cM
<i>S. bulbocastanum</i>	13	467	0.22	574.5	0.81
<i>S. commersonii</i>	17	568	0.26	668	0.85

Comparative genomics: preliminary evidence of synteny

Syntenic conservation of marker order and genome structure and is the basis for comparative genomics. We scanned our preliminary linkage maps for DART markers shared between species; markers 552041 and 557103 are examples.

Assignment of these markers to common linkage groups in *S. bulbocastanum* and *S. commersonii* suggests these species share genome structure (Figure 5). Planned sequencing of mapped DART markers will facilitate comparisons with reference genomes (e.g. tomato and cultivated potato).

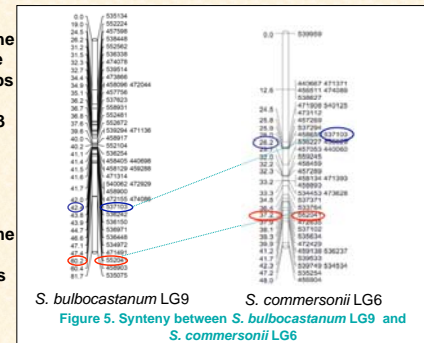


Figure 5. Synteny between *S. bulbocastanum* LG9 and *S. commersonii* LG6

Summary and future perspectives

- We established the first DART based mapping platform for (wild) potato tertiary gene pool species.
- Genome structure comparisons are ongoing projects in our lab.
- Sequencing of DART markers along with whole genome sequencing of potato and tomato will enable detailed comparison between wild potato species and cultivated crops.



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