



# BOOK OF ABSTRACTS

**2015** EAPR Breeding and Varietal Assessment  
Section and EUCARPIA Section Potatoes

## **18<sup>TH</sup> JOINT MEETING**

*Vico Equense, Italy - November 15th – 18th, 2015*

*Local organising committee:* Riccardo Aversano, Amalia Barone, Maria Raffaella Ercolano, Edgardo Filippone, Luigi Frusciante (University of Naples Federico II, Dept. Agricultural Sciences)

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## P15 Development of symptoms in diploid and tetraploid potato after inoculation with highly aggressive strain of *Dickeya solani*

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Pectinolytic bacteria *Dickeya solani* is spreading in potato crops in Europe. The highly aggressive strain of *D. solani*, IFB0099 (syn. IPO2276), has been used for inoculation of potato tubers and potato plants. The plant material consisted of cultivars and diploid interspecific hybrids of *Solanum*, originated beside *Solanum tuberosum* from wild and primitive cultivated potato species. The temperature 26° C was chosen, for testing tuber resistance, based on the results of tuber maceration of four cultivars, Irys, Glada, Gandawa, Sonda, in four different temperatures: 20° C, 23° C, 26° C and 30°C. The tuber resistance of 24 diploid clones did not differ significantly from the highly resistant standard of resistance to *Pectobacterium*, the somatic hybrid of *S. brevidens* (+) *S. tuberosum*, USA 249, and was significantly higher than the resistance of cvs Glada, and Irys, medium resistant and susceptible to *Pectobacterium* spp., respectively. The best cultivar in this experiment was cv. Mieszko, originated from the double backcross of the highly resistant to *Pectobacterium atrosepticum* diploid clone DG 88-9. The plant resistance was evaluated after inoculation with bacteria of the bases of stems of potato pot-plants grown in a greenhouse. Plants were covered with transparent foil after inoculation to provide high humidity. Due to high temperature in a greenhouse the symptoms of the stem base rotting were observed after few days post inoculation. In the repeated experiment the symptoms were observed mostly as leaf necroses and wilting than the rotting of stems. In general, potato cultivars showed symptoms of infection with bacteria *D. solani* on higher number of plants than the diploid clones. Thus the diploid hybrids might be used for improving potato resistance to bacteria *D. solani*.

## P16 Use of the reference potato genome sequence to improve tetraploid genetic maps of chromosome IX

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The reference potato sequence is a useful resource to develop new markers in regions of interest. Using genetic mapping, we identified, a region of chromosome IX responsible for a significant variation of late blight resistance in two tetraploid mapping families. Our aim was to improve the accuracy of the maps. We used SolCAP SNP then developed SSR markers in the 7,1 Mbp region of the V4.03 reference genome previously determined using Blast of primers genetically mapped in a ~25 cM interval.

Three full-sib tetraploid families (150 or 280 individuals) were used to test then map the markers.

12/138 SolCAP SNP located in the region were chosen on the basis of their distribution along the pseudomolecule, position into gene related to resistance pathways and costs estimates. They were revealed using KASPar technology (LGC Genomics) 148 primers pairs were selected in 3434 unilocus primers pairs designed with Primer3 around the 5940 microsatellite motifs detected in the region using a local tool. The selection criteria were: 4bp repeat length, ~150kbp between the markers, molecular weight between 200 and 400bp. Before mapping the entire families, the informativeness of the primers was checked using both parents and 8 individuals of three full-sib families. PCR products were separated using an ABI PRISM® 3100 Genetic Analyzer.

7/12 SNP showed polymorphism in the 3 families. 4 SNP were polymorphic in only 2 families and the remaining SNP was polymorphic in only one family. Level of polymorphism varied from 2 to 5 clusters depending on the dosage and the parental configurations.

43/48 markers amplified 1 to 5 alleles. 43 to 50 alleles were polymorphic in each family, among them, 15 alleles were common to all. 13 markers were chosen on the basis of the origin of the polymorphism, the number of alleles revealed and their intensity.

Mapping on the entire families is underway.