Genomics Cluster on dicot crops and cultivated plants

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Background:

In recent years the foundation for the genomics of many economically important dicotyledonous plants has been created. Genomics resources available to date comprise DNA and protein databases, cloned genes and ESTs, a wealth of software tools for analysis and many other resources. Whole genome sequencing of several crop plants including tomato and potato (Solanaceae), melon (Cucurbitaceae), apple (Rosaceae), poplar (Salicaceae), but also banana (Musaceae), cotton (Malvaceae), M. truncatula (Fabaceae), and Arabidopsis (Brassicaceae), is well advanced. Many other plants' genomes are in the pipeline to become completely sequenced.

Plant industries already began to utilize these genomics resources and implement them in a variety of applications. This comprises enhanced breeding and selection methods with molecular markers, the production of food, feed and raw materials possessing optimal or new properties and the certification and tracking of varieties, products and food.

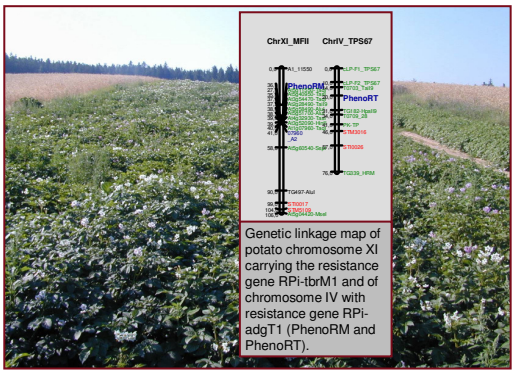
Activities, Methodology

Coordinate, plan, implement and integrate national research on dicot genomics
Develop a national action plan on dicot genomics R&D involving many partners in research and economy
Pursue bi- and multilateral research and development projects among Austrian partners in dicot genomics
Strengthen international cooperation on dicot genomics research

Expected outcomes

Increasing the coordination and integration of national genomics research
Strengthening the significance of national dicot genomics R&D
Strengthening partnerships between industry and research
Focussing dicot genomics research on more, and more innovative topics of national and international relevance
Better mobilization of capacities and resources for dicot genomics research
Increasing the benefits to national industries from dicot genomics research

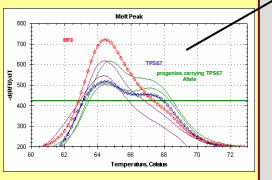
Mapping *Phytophthora infestans* resistance in two Solanum populations



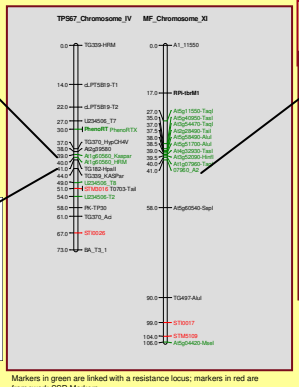
Genetic linkage map of potato chromosome XI carrying the resistance gene RPi-tbrM1 and of chromosome IV with resistance gene RPi-adgT1 (PhenoRM and PhenoRT).

KASPar assay for At1g60560

Genotype	count AlleleT1	count all Alleles	
	End RFUsFAM	End RFUs HEX	Score
MFII	855	1594	0
TPS67	5684	1755	1
1	851	1783	0
2	848	1568	0
3	856	1894	0
4	945	1848	0
5	6241	1836	1
6	5804	1899	1

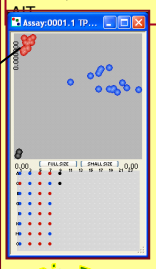


High resolution melting analysis with unlabeled probe



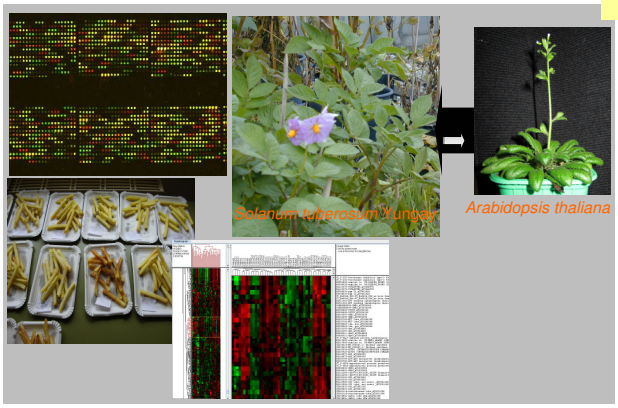
Markers in green are linked with a resistance locus; markers in red are framework SSR Markers

EC Food-CT-2005 513959; "BIOEXPLOIT", AIT



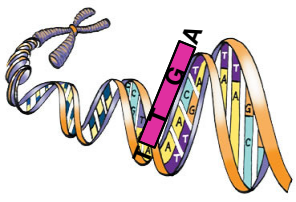
BioExploit

Developing molecular markers for resistance in potato

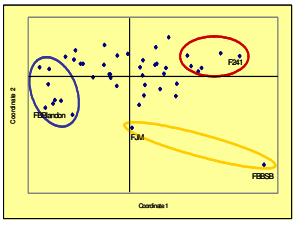


Development of e-Markers for Potato Processing Quality

Niederösterreichische Saatbau Gen NÖS—RWA(VÖSKAP)—AGRANA-Stärke, FFG



Economic aspects of marker assisted selection



NICACAO: Assessment of on-farm diversity and cocoa quality

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