



Use of translational genomics to indentify genes important for pea seed development and composition

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► To cite this version:

Mélanie Noguero, Christine Le Signor, Vanessa Vernoud, Isabelle d'Erfurth, Jérôme Verdier, et al..
Use of translational genomics to indentify genes important for pea seed development and composition.
Mendel's legacy - 150 years of the genius of genetics, Sep 2015, Brno, Czech Republic. hal-01812827

HAL Id: hal-01812827

<https://hal.science/hal-01812827v1>

Submitted on 5 Jun 2020

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Mendel's legacy
150 years
of the genius of genetics

RESEARCH IN PLANT GENETICS (FROM MENDEL'S PEAS TO THE PRESENT)

Date: 7th-11th September 2015

Venue: Mendel Museum of Masaryk University, Brno, Czech Republic

Abstracts for poster section

Venue: Mendel Museum of Masaryk University, Brno, Czech Republic
Mendlovo nám. 1a, 603 00, Brno
www.mendel.museum
info@mendelmuseum.muni.cz

This conference is dedicated to the legacy of RTDr. Vítězslav Orel, DrSc., the tireless promoter of Mendel's work.

ANNOTATION

In 1865 G. J. Mendel presented the results of his experiments with the heredity of plants, garden pea in particular. His manuscript "Experiments in Plant Hybridization" establishes him as the founder of genetics.

The aim of this conference is to celebrate the 150th anniversary of Mendel's discovery by presenting broad range of current plant genetics as well as to show the progress made on Mendel's experimental model species.

The abstracts for poster section are also available on CD included to the book of abstracts.

THE EVOLUTION OF DEFENSE MECHANISMS AGAINST HERBIVORES IN THE SUBFAMILY CARDUOIDEAE

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In this study, we are investigating correlation of ecological traits with phylogeny of 31 genera of subfamily Carduoideae to understand how defence mechanisms are shaped in evolution. To answer this question, we reconstructed phylogenetic relationships of *Arctium*, *Carduus*, *Carlina*, *Centaurea*, *Cirsium*, *Colymbada*, *Echinops*, *Onopordum* and *Serratula* genera by using sequences chloroplast *trnL* gene, *trnL-trnF* noncoding regions and sequences of the nuclear ribosomal internal transcribed spacer (ITS1-5.8S-ITS2). Phylogeny was established based on Bayesian and maximum likelihood approaches. Plant defence ability and attractivity for herbivores was described by a range of traits including leaf toughness, spinosity and hairiness, specific leaf area, and content of carbon, nitrogen and phosphorus in the leaves and of carbohydrates and polysaccharides in the receptacles. Currently we are also studying traits related to content of secondary metabolites. Finally, we also use data on observed interaction between the plants and herbivores using data on leaf and flower head damage. To understand the genetic background of some of the traits, we study expression of 34 protein coding genes, which are involved in cell wall construction. We use Bayesian approach and D statistics to study the relationship between all these traits and species phylogeny.

USE OF TRANSLATIONAL GENOMICS TO IDENTIFY GENES IMPORTANT FOR PEA SEED DEVELOPMENT AND COMPOSITION

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We have been using genomics approaches with *Medicago truncatula* as a tool to identify key genes determining seed yield and composition in closely related legumes of agricultural importance including pea. By separating the developing seed tissues we have shown extensive compartmentalization of gene expression and metabolic activities at different stages of development (Gallardo et al, 2007). Putative regulatory genes specific for each seed tissue have been identified using a TF (Transcription Factor) qRT-PCR platform (Verdier et al., 2008), the Affymetrix Gene Chip (Benedito et al, 2008), and more recently, Nimblegen arrays (Buitink et al. submitted). By cluster analysis, putative target genes of selected TFs could also be identified. The genetic map positions of genes of interest have been compared with QTLs in *M. truncatula* for protein quantities and other seed phenotypes, and a number of the loci fell within QTL intervals. In several cases, similar QTLs have been mapped at syntenic positions in pea. Using this approach, putative roles were assigned to two genes, both specifically expressed in the developing endosperms of *M. truncatula* and pea. One encodes a DOF class transcription factor, whose mutant phenotype severely affects endosperm development (Noguero et al, 2015). The second gene encodes an endosperm-specific subtilase (SBT1.1), which affects final seed weight in both *M. truncatula* and pea (D'Erfurth et al, 2012). The analysis of further genes affecting seed composition is ongoing, using the same strategy.

The research leading to these results has received funding from the European Community FP7 grant agreements FP7 KBBE-613551, LEGATO, and FP7 KBBE-289562, ABSTRESS, from the French National Research Agency (QualityLegSeed and GenoPea), and from the Burgundy Regional Council. We thank Julia Buitink (INRA Angers) for pre-publication access to Nimblegen array data.