



Providing genomic tools to improve phenotype prediction for complex traits

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► To cite this version:

Maryse Nicolaï, Nurudeen Adeniyi Alimi, Anne-Marie Sage-Palloix, Ghislaine Nemouchi, Bruno Savio, et al.. Providing genomic tools to improve phenotype prediction for complex traits. International Conference, Feb 2010, Vienne, Austria. hal-02757361

HAL Id: hal-02757361

<https://hal.inrae.fr/hal-02757361>

Submitted on 4 Jun 2020

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MOLECULAR ASPECTS OF PLANT DEVELOPMENT

**International Conference
February 23-26 2010, Vienna, Austria**



**MOLECULAR ASPECTS OF
PLANT DEVELOPMENT 2010**

Programme and Abstracts

N 59. Providing Genomic Tools to Improve Phenotype Prediction for Complex Traits

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The EU project ‘Smart tools for Prediction and Improvement of CropYield’ (KBBE-2008-211347), or SPICY, aims at the development of genotype-to-phenotype models that fully integrate genetic, genomic, physiological and environmental information to achieve accurate phenotypic predictions across a wide variety of genetic and environmental configurations. Molecular markers of the Quantitative Trait Loci (QTLs) for yield related traits and for model parameters are needed for phenotype prediction. To improve the estimation of allelic values, complex and correlated traits will be reduce to expected causal components through multivariate and mixed model analyses and QTLs will be mapped for these components. Functional markers will further be searched for the QTL, improving the accuracy of phenotype prediction from genetic information. The genomic part of this project explores functions underlying QTLs by quantitative genomics using both *a priori* (genes reported in literature as playing an important role in growth responses) and global gene expression polymorphism (genes that are differentially expressed in the RIL population, eQTL). The genes of interest will be mapped in pepper genome by SNPlex. SNP positions will be confronted with positions of eQTLs and trait/ model parameter QTLs. Colocalization of a structural gene (SNP), a trait QTL and an eQTL will argue in favour of causal relationships between the identified gene and the trait. Validation will be attempted through genetic association in the pepper germplasm collection. Successful candidate genes will provide potential allelic values for phenotype prediction.