QTL detection and Marker Assisted Selection for the Resistance to Phytophthora Palmivora using a F2 Theobroma Cacao L. progeny

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Background. Obtain sustainable varieties resistant to disease is one of the main goals of genetic improvement of cocoa. In partnership between CEPLAC (Comissão Executiva do Plano da Lavoura Cacauiero) and CIRAD (Centre International de Recherche Agronomique pour le Développement), studies to detect and characterize QTLs for resistance to witches’ broom (Moniliophthora perniciosa) and to pod rot (Phytophthora palmivora), are conducted. QTL detection for resistance to Phytophthora palmivora, were carried out from a segregating F2 progeny (172 ind) resulting from the cross between Scavina-6 (resistant Forastero clone) and ICS1 (susceptible Trinitario clone). Phenotic symptoms were revealed seven days after inoculation by a P. palmivora strain (CEPLAC phytopathology laboratory collection). A drop of 0.2ml of a concentrated solution of zoospores was deposited on leaf discs. Phenotypic analyses on necrosis severity (note 0 :without penetration point until note 5 :total necrosis) were obtained from sixty discs per genotype. QTL analyses were carried out using a genetic map established with 202 markers (SNPs and SSRs). The remaining par of the F2 population (972 individuals excluding plants used for the QTL analysis), was genotyped with the SSR markers associated with QTLs detected. The 972 genotypes were classified according to the presence of favorable QTL-allele or unfavorable QTL-allele. Phenotypic analyses on necrosis severity were carried under the same conditions as for the QTL analysis and two sets of thirty seven selected genotypes with favorable QTLs and unfavorable QTLs, were inoculated.

Results. The remaining par of the F2 population (972 individuals) was genotyped with the SSR markers : mTcCIR91, mTcCIR175 et mTcCIR430, respectively associated with the three QTLs detected in the linkage groups 10, 3 and 2, explaining 25% of the total variation. Statistical analysis results presented here, show a significative difference between both sets of plants, showing a very efficiency selection for Phytophthora resistance only with these markers close to QTLs.

Conclusion. Scavina-6 is also an important source of resistance to witches' broom (Moniliophthora perniciosa). The same approach using this same F2 population Scavina-6 by ICS1, is underway to select resistant plants.


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The book of abstracts

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Program

Thursday 19/05/11

8h30-9h00 Registration

9h00-9h30 Opening and Introduction

Session 1. Methods for QTL detection and Genetic Architecture Analysis (1/4)
Chair: Tomasz Strabel

9h30-10h10 A Hidden Markov Model Combining Linkage and Linkage Disequilibrium Information for Haplotype Reconstruction and Quantitative Trait Locus Fine Mapping (invited) Tom Druet

10h10-10h25 Inferring haplotypes and parental genotypes in larger full sib-ships and other pedigrees with missing genotype data Carl Nettelblad

10h25-10h40 Genome-wide analysis in a Chinese x Western chicken F2 intercross Zheya Sheng

10h40-10h55 Transcriptome profiling reveals interaction between two QTL for fatness in chicken Yuna Blum

COFFEE BREAK

Session 1. Methods for QTL detection and Genetic Architecture Analysis (2/4)
Chair: Suzanne Rowe

11h25-12h05 Genetic dissection of susceptibility for Crohn’s disease (invited) Jean-Pierre Hugot

12h05-12h20 QTL detection for survival related traits in atlantic salmon Francois Besnier

12h20-12h35 Genetic and genomic study of the rainbow trout Oncorhynchus Mykiss response to a salinity change Yvan Lebras

12h35-12h50 A comparison of regression models for testing QTL/eQTL co location Xiaoqiang Wang

12h50-13h05 A simulation-based approach for controlling the false positive rate in genome-wide association studies Marcin Kierczak

LUNCH

Session 1. Methods for QTL detection and Genetic Architecture Analysis (3/4)
Chair: Francois Besnier

14h15-14h30 Mapping QTL from QTL-MAS workshop data using four methods Naveen Kumar Kadri
Bayesian Variable Selection to identify QTL affecting a simulated quantitative trait

Estimation of breeding values and detection of QTL in QTL-MAS 2011 dataset using GBLUP and Bayesian approaches

Genomic Breeding Value Prediction and QTL Mapping of QTLMAS2011 Data Using Bayesian Methods

COFFEE BREAK

Session 1. Methods for QTL detection and Genetic Architecture Analysis (4/4)

Chair: Jean Pierre Bidanel

Variance Controlling Genes: Significant Contributors to The Missing Genetic Variation for Complex Traits

Use of planes in genotype space to detect high order epistasis

A problem of locating multiple interacting QTL by logic regression

qtl.outbred: Interfacing outbred line cross data with the R/qtl mapping software

AnnotQTL: a new tool to gather functional and comparative information on a genomic region

GPU accelerated QTLMap

Departure for Rennes City Center

Cocktail at Rennes City Hall offered by Rennes Métropole

Visit of the Brittany Parliament (4 groups)

Dinner at the “Taverne de la Marine”, Place de Bretagne
Friday 20/05/11

Session 2 . Methods for Genomic Evaluation (1/2)
Chair : Rodolfo Cantet

9h00-9h40 Strategies to improve the accuracy of genomic predictions (invited) Dorian Garrick
9h40-9h55 Could genomic selection methods be efficient to detect QTL? Carine Colombani
9h55-10h10 Linear models for breeding values prediction in haplotype-assisted selection Anna Mucha
10h10-10h25 Effect of the prior distribution of SNP effects on the estimation of total breeding value Valentina Riggio
10h25-10h40 Approximate Bayesian prediction of genomic breeding values and variances using INLA Patrik Waldmann

COFFEE BREAK

Session 2 . Methods for Genomic Evaluation (2/2)
Chair : Frédéric Hospital

11h10-11h50 Genomic selection: implementation in dairy cattle (invited) Vincent Ducrocq
11h50-12h05 A simple two step Bayesian approach for genomic prediction of breeding values Mohammad Shariati
12h05-12h20 Genomic Analyses for the common dataset of the 15th QTL-MAS Workshop Chonglong Wang
12h20-12h35 Alternative strategies for selecting subsets of predicting SNPs by LASSO-LARS procedure Graziano Usai
12h35-12h50 Genomic selection using regularized linear regression models: ridge regression, lasso and elastic net and their extensions Joseph O Ogutu
12h50-13h15 Poster session

LUNCH

Session 3 . Comparative analysis of submitted QTLMAS2011 Results
Chair : Olivier Filangi

14h15-14h35 All the truth about the QTLMAS2011 Data Jean Michel Elsen
14h35-14h55 Comparison of submitted methods for QTL identification in the QTLMAS2011 Data set Olivier Demeure
14h55-15h15 Comparison of submitted methods for GEBV estimation from QTLMAS2011 Data set Pascale Le Roy
15h15-15h45 Closing Remarks