

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 Cacaueira) 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). Phenotypic 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 part 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 part 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.

G. M. Tahi, G. M. Tahi, B. I. Kébé, A. Sangare, F. Mondeil, C. Cilas and A. B. Eskes (2006). Foliar resistance of cacao (*Theobroma cacao*) to *Phytophthora palmivora* as an indicator of pod resistance in the field: interaction of cacao genotype, leaf age and duration of incubation. *Plant Pathology* 55, 776–782.

C. Lanaud, O. Fouet, D. Clément, M. Boccara, A. M. Risterucci, S. Surujdeo-Maharaj, T. Legavre, X. Argout (2009). A meta-QTL analysis of disease resistance traits of *Theobroma cacao* L. *Mol Breeding* DOI 10.1007/s11032-009-9297-4.



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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 <i>Oncorhynchus Mykiss</i> 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

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

14h15-14h30	Mapping QTL from QTL-MAS workshop data using four methods	Naveen Kumar Kadri
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14h30-14h45	Bayesian Variable Selection to identify QTL affecting a simulated quantitative trait	Anouk Schurink
14h45-15h00	Estimation of breeding values and detection of QTL in QTL-MAS 2011 dataset using GBLUP and Bayesian approaches	Marcin Pszczola
15h00-15h15	Genomic Breeding Value Prediction and QTL Mapping of QTLMAS2011 Data Using Bayesian Methods	Dorian Garrick

COFFEE BREAK

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

Chair : Jean Pierre Bidanel

15h45-16h00	Variance Controlling Genes: Significant Contributors to The Missing Genetic Variation for Complex Traits	Xia Shen
16h00-16h15	Use of planes in genotype space to detect high order epistasis	Mats Pettersson
16h15-16h30	A problem of locating multiple interacting QTL by logic regression	Magdalena Malina
16h30-16h45	qtl.outbred: Interfacing outbred line cross data with the R/qtl mapping software	Ronald M. Nelson
16h45-17h00	AnnotQTL: a new tool to gather functional and comparative information on a genomic region	Olivier Demeure
17h00-17h15	GPU accelerated QTLMap	Guillaume Chapuis

17h30

Departure for Rennes City Center

18h00

Cocktail at Rennes City Hall offered by Rennes Métropole

19h00-20h45

Visit of the Brittany Parliament (4 groups)

21h00

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	<i>Poster session</i>	

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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	