

eucarpia

XIII EUCARPIA Biometrics in Plant Breeding Section Meeting

30 August :: 1 September 2006

Zagreb :: Croatia

Book of Abstracts



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30 August - 1 September 2006 :: Zagreb :: Croatia

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Dear Colleagues,

Organizing Committee welcomes you to the XIII meeting of the EUCARPIA Biometrics in Plant Breeding Section, in Zagreb, Croatia.

It was a great pleasure to find out that joint effort of Scientific and Organizing Committee invested in preparation of the meeting yielded widespread interest. Therefore, we expect more than 100 participants from 30 countries. We have received abstracts of 66 contributions in addition to 7 invited lectures. All the abstracts have been thoroughly reviewed by the members of Scientific Committee and hereby we thank them for their time and efforts. They have selected 22 abstracts for oral presentations, while remainder will be presented as posters. Furthermore, 11 posters were selected for short (oral) presentations. As an outcome, we can expect that the Meeting will further contribute to the development of biometrical methods and models to be used in plant breeding and related plant sciences.

The meeting is hosted by Faculty of Agriculture of the University of Zagreb. Its Department of Plant Breeding, Genetics and Biometrics was founded in 1920. The first textbook for the course of Biometrics was published back in 1946, written by Alois Tavčar who was the Head of the Department for more than 50 years.

This Book of Abstracts has been published as a supplement to the journal *Agriculturae Conspectus Scientificus* (ACS), the oldest and the most prominent journal in the field of agriculture in Croatia. ACS publishes original scientific papers, scientific reviews and preliminary communications in the field of agricultural and related sciences. The journal is fully available at [www.agr.hr/smotra](http://www.agr.hr/smotra).

And last but not least, the Organizing Committee greatly appreciates support from the sponsors. Without their help the task of organizing this meeting would become extremely taunting.

We wish you all a very fruitful meeting and the pleasant stay in Zagreb.

Jerko Gunjača

On Behalf of the Organizing Committee

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**Session 1: Linkage and LD based QTL mapping methodology I**

- | 01 **A Ruby in the Rubbish: Searching for Signatures of Selection Using Molecular Data**  
Bruce WALSH
- | 02 **Linkage Analysis and QTL Mapping in Blackcurrant (*Ribes nigrum* L.) Using a Population of Full Sib and Selfed Offspring**  
Christine A. HACKETT, Rex BRENNAN, Linzi JORGENSEN, Joanne RUSSELL
- | 03 **Development of LD Mapping System for *Oryza sativa* L. Germplasm**  
Hiroyoshi IWATA, Daisuke HORYU, Hiroyuki KANAMORI, Nobukazu NAMIKI, Yusaku UGA, Shuichi FUKUOKA, Kaworu EBANA
- | 04 **Adjusting for Population Structure in Genetic Association Studies**  
David BALDING
- | 05 **Association Mapping of Key Traits in UK Barley Recommended List Trials**  
Malcolm MACAULAY, Joanne RUSSELL, Luke RAMSAY, David F. MARSHALL, Robbie WAUGH, William (Bill) T.B. THOMAS
- | 06 **Association Mapping in Potato (*Solanum tuberosum* L.)**  
Björn D'HOOP, M. João PAULO, Ben VOSMAN, Herman VAN ECK, Richard VISSER, Rolf MANK, Fred A. VAN EEUWIJK
- | 07 **Neutral Mutation and the Mechanism of Adaptation**  
Krunoslav BRČIĆ-KOSTIĆ

**Session 2: Linkage and LD based QTL mapping methodology II**

- | 08 **QTL by Genetic Background Interaction: Application to Predicting Progeny Value**  
Jean-Luc JANNINK
- | 09 **QTL Detection and Marker-assisted Selection in a Multiparental Maize Design**  
Guylaine BLANC, Alain CHARCOSSET, André GALLAIS, Laurence MOREAU
- | 10 **Changes of Heterotic Pattern and Allele Frequencies in the M3S Maize Population after Two Cycles of Selfed Progeny Recurrent Selection Revealed by SSR Markers**  
Hrvoje ŠARČEVIĆ, Ivan PEJIĆ, Marijana BARIĆ, Vinko KOZUMPLIK
- | 11 **Analysis of Quantitative Traits in an F4 Population Derived from Crossing Four Accessions of *Arabidopsis thaliana***  
M. João PAULO, Xueqing HUANG, Fred A. VAN EEUWIJK, Maarten KOORNNEEF
- | 12 **Use of Haplotype Relationships in Genome-wide LD-mapping Methods**  
Jaap B. BUNTJER, Anker P. SØRENSEN, Johan D. PELEMAN
- | 13 **Bayesian Analysis of Complex Traits in Pedigreed Plant Populations**  
Marco C.A.M. BINK, Cajo J.F. TER BRAAK, Martin P. BOER, Johannes JANSEN
- | 14 **Searching for Interacting QTL in Pedigree-related Populations of an Outbreeding Species**  
Johannes JANSEN, Eric W. VAN DE WEG, Martin P. BOER, Marco C.A.M. BINK
- | 15 **Identification of QTLs Underlying Resistance to Soybean Cyst Nematode Races 3 and 5 in Soybean PI 494182**  
Mohsen EBRAHIMI, Prakash R. ARELLI, Yiwu CHEN, Dechun WANG, Mohammad Reza GHANADHA, Abas Ali ZALI, Bahman YAZDI-SAMADI, Hasan ZEINALI

**Session 3 | Computer science, bioinformatics and analysis of large data sets**

- | 16 **The Importance of GCA and SCA in a Context of Gene Expression**  
Marnik VUYLSTEKE
- | 17 **Support Vector Machine Regression for Hybrid Prediction**  
Steven MAENHOUT, Geert HAESAERT, Bernard DE BAETS
- | 18 **Population Genetical Simulation and Data Analysis with Plabsoft**  
Hans Peter MAURER, Albrecht E. MELCHINGER, Matthias FRISCH
- | 19 **Optimization of DH-line Based Recurrent Selection Procedures in Maize**  
Hartwig H. GEIGER, Gerardo Andres GORDILLO
- | 20 **MBP: A Software Package to Optimize Hybrid Maize Breeding Procedures**  
Gerardo Andres GORDILLO, Hartwig H. GEIGER
- | 21 **Comparison of Tree Architecture Using a Tree Edit Distance: Application to 2-year-old Apple Hybrids**  
Vincent SEGURA, Aïda OUANGRAOUA, Pascal FERRARO, Evelyne COSTES
- | 22 **Design a Marker-based Pedigree Selection Strategy for Parent Building in Barley Using Computer Simulation**  
Guoyou YE, David MOODY, Livinus EMEBIRI, Maarten VAN GINKEL
- | 23 **Parental Selection in Self-pollinating Crops Using Best Linear Unbiased Prediction (BLUP)**  
Andrea Michaela BAUER, Jens LÉON
- | 24 **Discriminating Maize Inbred Lines Using Molecular and DUS Data**  
Jerko GUNJAČA, Ivica BUHINIČEK, Mirko JUKIĆ, Hrvoje ŠARČEVIĆ,  
Antun VRAGOLOVIĆ, Zdravko KOZIĆ, Antun JAMBROVIĆ, Ivan PEJIĆ
- | 25 **A Comprehensive Database Management System for Integrating Phenotypic and Genomic Data in Scientific and Applied Plant Breeding Programs**  
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Hans Peter MAURER, Matthias FRISCH
- | 26 **Quantifying Tomato Flavour and its Metabolic Basis**  
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Garnt DIJKSTERHUIS, Yuri TIKUNOV, Arnaud DE BOVY, Fien MEIJER-DEKENS,  
Pim LINDHOUT, Fred A. VAN EEUWIJK

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Scott CHAPMAN
- | 28 **Modelling Nitrogen Stress with Probe Genotypes to Assess Genetics Parameters in Winter Wheat**  
Maryse BRANCOURT-HULMEL, Anne LAPERCHE, Jacques LE GOUIS
- | 29 **Multiplicative Cultivar Effects in Trial Series in Different Environments**  
Erik SCHWARZBACH, Jiří HARTMANN
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Martin P. BOER, Fred A. VAN EEUWIJK, Marcos MALOSETTI



- | 31 **Assessing the Importance of Genotype x Environment Interaction for Root Traits in Rice Using QTL Analysis by Mixed Models**  
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- | 32 **Multi-trait QTL Mixed Modelling with an Application to Drought Stress in Maize**  
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José CROSSA, Fred A. VAN EEUWIJK
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Rose TAKUSEWANYA, Richard SSEKABEMBE, Frank BAGAZONZYA
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Fien MEIJER-DEKENS, Pim LINDHOUT, Fred A. VAN EEUWIJK
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## Use of Additive-Dominant Model in Genetic Analysis of some Quantitative Characteristics in Sunflower

Dejan JOVANOVIĆ (✉)

Radovan MARINKOVIĆ

### Abstract

A simple link between the expected means of quantitative traits of different generations (progenies) can be established if the mean values are dependant exclusively on additive and dominant gene effects. This study aims to prove the correctness of the hypothesis that progeny means depend solely on additive and dominant genes, which can be tested in several ways, one of which is the applied tests. Seven  $F_1$  hybrids obtained by crossing five sunflower inbred lines were used to analyze the impact of genes with additive and dominant effects and their interactions on the inheritance of plant height, leaf number per plant and head diameter. The linkage among the expected progeny means was tested using the scaling tests method, while the estimates of gene effects and mode of inheritance were made by Generation Mean Analysis. The additive-dominant model proved adequate only for leaf number per plant in crosses  $C_5$  and  $C_7$ . Besides the main gene effects (additive and dominant), epistatic gene effects were also of great importance in the inheritance of all three traits. In the inheritance of plant height, duplicate epistasis between dominant increasers was found in  $C_2$ , while  $C_1$ ,  $C_4$  and  $C_7$  had duplicate epistasis between dominant decreaseers. In the case of leaf number per plant, we only found duplicate epistasis between dominant decreaseers in  $C_1$ ,  $C_3$  and  $C_6$ , while in the inheritance of head diameter both types of duplicate epistasis were found, namely duplicate epistasis between dominant decreaseers in  $C_1$  and duplicate epistasis between dominant increasers in  $C_2$ . It can be concluded that the additive-dominance model was not adequate in explaining the differences between various generation means. In addition to of additive and dominance gene effect, digenic epistatic effects were also found to be important in the inheritance of the characters studied. Therefore, geneticists and breeders working on sunflower should make provisions for the occurrence of epistatic gene effects in their research programs.

### Keywords

sunflower, quantitative traits, genetic analysis, additive-dominant model

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