

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

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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**  
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Erik SCHWARZBACH, Jiří HARTMANN
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# Line x Tester Analysis for Yield Components in Sunflower (*Helianthus annuus* L.)

Nada HLADNI<sup>1</sup> (✉)

Dragan ŠKORIĆ<sup>1</sup>

Marija KRALJEVIĆ-BALALIĆ<sup>1,2</sup>

Siniša JOCIĆ<sup>1</sup>

Dejan JOVANOVIĆ<sup>1</sup>

## Abstract

The development of new hybrids with a high genetic potential for seed and oil yields based on interspecific hybridization requires information on the mode of inheritance and combining abilities of the newly developed inbred lines for total seed number per head (TSN) and 100 seed mass (100SM). The interdependence between yield components and seed yield (SY) in order to select promising lines to be used subsequently as components of future sunflower hybrids. In the present study, we used seven new divergent (A) cytoplasmically sterile inbred lines obtained by interspecific hybridization, three Rf-restorer lines used as testers, and 21 F1 hybrids developed at the Institute of Field and Vegetable Crops in Novi Sad. The female inbred lines had been developed by interspecific hybridization, while the three male restorer inbreds with good combining abilities were used as testers in the form of fertility restorers. A trial was set up at the Rimski Šančevi Experiment Field of the Institute of Field and Vegetable Crops in Novi Sad using a randomized block design with three replications. The mean values and coefficient of correlation ( $r$ ) as indicators of interdependence between two variables were determined according to Hadživuković (1991). Analysis of combining abilities was done by the line x tester method (Singh and Choudhary, 1976). Significant differences in TSN and 100 SM were found between the A-lines and the Rf-testers and their F1 hybrids. Analysis of combining abilities showed that there were significant differences between the A-lines and Rf-testers in the GCA for both traits under study. Highly significant positive GCA values were found in the A-lines NS-GS-4 and NS-GS-5, while the NS-GS-6 inbred had a highly significant negative value of the GCA for both traits. Among the Rf-testers, highly significant positive GCA values were found in RHA-N-49 for TSN and RHA-R-PL-2/1 for 100 SM. The highest and highly significant positive SCA value for both traits was recorded in the hybrid NS-GS-5 x RHA-R-PL-2/1. The nonadditive component of genetic variance had the main role in the inheritance of TSN and 100 SM, further supporting this was the GCA to SCA ratio in the F1 generation of less than one (0.11, 0.24). The largest average contribution in the expression of TSN was found in the Rf-testers (55.8%), whereas with 100 SM, the contribution of the A-lines was more significant (70.6%). Significant positive interdependence was established between SY and TSN (0.376\*). Between SY and 100 SM, there was highly significant positive interdependence (0.823\*\*).

## Keywords

sunflower, yield components, combining abilities, gene effects, correlations

<sup>1</sup>Institute of Field and Vegetable Crops, Maksima Gorkog 30, 21000 Novi Sad, Serbia

<sup>2</sup>Faculty of Agriculture, Maksima Gorkog 30, 21000 Novi Sad, Serbia

✉ E-mail: nadah@ifvcns.ns.ac.yu

