18th *Sunflower International Conference*

PROGRAM

MAR DEL PLATA & BALCARCE . ARGENTINA
Sheraton Mar del Plata Hotel
February 27 . March 1 / 2012

February, Wednesday 29th

Session 8 - Oil and meal quality, other applications.Chair Guillermo Pozzi, Co Chair Martin Cantore

08.30 – LS - From the lab to the market: new challenges for sunflower oil quality research. Leonardo Velasco, Instituto de Agricultura Sostenible, CSIC, Córdoba, Spain.

09.05 – IS – Association mapping approach for analysis of QTL determining fatty acid composition and oil content in sunflower seeds. Andrés Zambelli, Center for Biotechnology Research, Advanta Semillas, Argentina.

09.25 – IS – Tocopherol mutations in sunflower. Yakov Demurin. Genetics Laboratory, VNIIMK, Russia.

09.45 – IS – Identification and Characterization of Genes Conferring Reduced Saturate Oil in Sunflower (Helianthus annuus L.). J.T. Gerdes, Global Sunflower Breeding Leader, Dow AgroSciences/Mycogen Seeds.

10.05 - 10.15 – SOP - Germination of sunflower genotypes with modified fatty acid composition. Raul González Belo, INTA Balcarce, Argentina.

Session 9 – Genomics. Chair Ruth Heinz, Co Chair Joel Piquemal

10.15 - Draft Assembly of The Sunflower Genome. Loren Rieseberg, Botany Department, University of British Columbia, Vancouver, Canada.

10.45 – Coffee break

11.15 – LS – On the Origin of Sunflowers: Fossils, Genes, Genomes, and Hybridization. Loren Rieseberg, Botany Department, University of British Columbia, Vancouver, Canada.

11.50 – LS - SNP diversity, genome mapping, and association genetics in sunflower. John Burke, Department of Plant Biology, University of Georgia, Athens, GA, US.

12.30 - lunch

14.00 – 16.00 – Poster Session Day 3

16.00 – SOP
- Development and validation of a high density sunflower microarray for functional studies on biotic and abiotic stresses. Paula Fernández, CICVyA, INTA Castelar, Argentina.

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· The identification of candidate genes underlying agronomically important traits represents a key strategy for molecular breeding applications. Different transcriptional strategies can be addressed, taking into consideration the target species and molecular tools available. In the case of sunflower, the lack of availability of a commercial oligonucleotide-based chip has limited transcriptional studies. Besides, transcriptional analyses based on RNA-seq technology are still limited in species lacking full genome sequences as sunflower. The goals of this study were the development of comprehensive unigene collection of H. annuus, its functional annotation and the design and validation of a custom sunflower oligonucleotide-based microarray for identification of concerted transcriptional responses associated to leaf senescence and fungal pathogen infections. · A large scale EST (> 130,000 ESTs) cleaning, assembly and sequence annotation was done using Blast2GO (www.blast2go.de). The resulting unigene collection was used to design the first custom sunflower oligonucleotide-based microarray under Agilent technology. Pre-processing and differential expression analysis of Agilent microarrays was performed using functions implemented in the limma package, available from the open source Bioconductor platform (http://www.bioconductor.org/). Gene set analysis was based on Gene Ontology information using FatiScan software integrated in Babelomics suite (http://babelomics.bioinfo. The microarray performance was evaluated under two experimental assays to study the response of sunflower to water deficit, as a physiological event that induces senescence, and the response to the necrotrophic fungal pathogen Sclerotinia sclerotiorum. Factorial experiment designs were applied and statistical analysis based on mixed-models was followed. The selected differential genes were further validated by qPCR, using reference genes previously characterized for sunflower. · The final EST assembly comprises 41,013 putative transcripts (12,924 contigs and 28,089 singletons). The resulting microarray includes a total number of 42,326 features: 1,417 Agilent controls, 74 control probes for sunflower 10 times replicated (740 controls) and 40,169 different non-control probes representing the Sunflower Unigen Resource (SUR version 1.0). The evaluation assays allowed the detection of 558 differentially expressed genes between water stress and control conditions from which ten genes were further validates by qPCR. Regarding the response to S. sclerotiorum, 33 genes were identified to be involved in the response to S. sclerotiorum ($p<0.001$). Thirteen of them were directly related to the response to the infection regardless of the sunflower time course and 20 were differentially expressed depending on the time course and/or showed interaction effect. · The developed unigene collection used to generate the oligonucleotide microarray, gathers nearly all of the known functional sequences from cultivated sunflower. The global analysis of gene expression, validated under two stress conditions showed that the H. annuus microarray is suitable for a wide range of functional genomics analyses, showing a precise and accurate level of trustability along different gene expression profiles. This work generated a curated and trustable sunflower unigene collection which resulted in the first custom sunflower oligonucleotide-based microarray under Agilent technology. The work presented here gives the sunflower community a trustable microarray to use under different transcriptional applications. Key words: microarray ? transcriptomics ? bioinformatics ? unigene ? sunflower