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## BOOK OF ABSTRACTS

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ORGANIZATION SUPPORT:



## Using high-throughput technologies to improve stress tolerance characteristics in sunflower

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Sunflower (*Helianthus annuus* L.) is one of the most relevant crops as a source of edible oil. Advances in sunflower genomics have greatly enhanced the development and application of new tools for crop improvement, and promoted the expansion of sunflower uses to new markets like biofuels, biolubricants and biopharma. In this context, the power of throughput technologies allow us to bring new insights into the genomic information that would become a key tool to afford an efficient system for molecular breeding.

Gene expression chip was designed specifically for sunflower. After its validation, microarray analysis has been performed concerning various stress situations: water deficit as a physiological event that induces senescence, resistance to sclerotinia, application of root-modifying treatments (jasmonic acid, ibuprofen) and application of endogenous transcription factors. Blast2GO [1] has been used to generate the functional annotation and the suite of tools, Babelomics [2], allowed us to analyze microarray data.

RNA-seq assays will include a study of quantification of expression (Illumina) and an observational study with standard libraries (454) to build a catalog of transcripts which will be used to assemble a reference genome for the mapping. The first study will be on different levels of resistance to sclerotinia.

This work generated the first custom sunflower oligonucleotide-based microarray under Agilent technology, validated for its application to transcriptional studies of sunflower subjected to different growth and/or developmental conditions.

The use of high-throughput technologies allow us functional genomic characterization of sunflower. This information is useful to improve the characteristics of tolerance to biotic and abiotic stress.

[1] Babelomics: an integrative platform for the analysis of transcriptomics, proteomics and genomic data with advanced functional profiling. Ignacio Medina et al. NAR-00461-Web-B (2010).

[2] Blast2GO: a universal tool for annotation, visualization and analysis in functional genomics research. Ana Conesa et al. *Bioinformatics*, **21**, pp. 3674-3676 (2005).