

## EARLY GIBBERELLIN RESPONSES ASSOCIATED WITH STAMENS DEVELOPMENT IN SUNFLOWER

*Angela PORT*

*Moldova State University, Center of Functional Genetics, Republic of Moldova*

E-mail: [portang@yahoo.com](mailto:portang@yahoo.com)

Different stresses induced by the climatic changes reorganize the cellular signaling pathways, resulting in new gene expression profiles and metabolome that ensure the plant adaptive responses. The microsporogenesis, compared to other stages of development, is highly regulated reproductive processes, much more susceptible to environmental and endogenous inputs.

Male sterile phenotype could be a result of inappropriate perception and transduction of gibberellins signals, the hormone known to promotes the reproductive development through multiple interacting pathways in regulating gene transcription. The comparative transcriptomic data of different physiological states facilitates the understanding of the importance of GA action on flowering plant fertility and the triggers of the defective anthers / pollen development.

Two genetic models, CMS-Rf system (Drofa F<sub>1</sub> and their parental lines) and near-isonuclear lines (fertile SW501 line and its CMS-PET1 analogue) of which plants was treated with GA<sub>3</sub> at developing inflorescence buds stage (to induce male sterile phenotype) were analyzed. The inflorescence buds 2, 4, 8, 24, 36 hours following hormonal treatment and stamens at different stages of microsporogenesis were subjected to microscopically and Real-time PCR analyses of genes/ESTs involved in meiosis, oxidative systems, cell signaling, energetic and hormonal metabolism, mitochondrial functionality, apoptosis.

The Real-time PCR experiments that were aimed to identify early GA-regulated genes by comparative analyzing the gene expression profile in different fertile genotypes and with cytoplasmic male sterility in the presence or absence of GA treatment allowed us to identify differential changes in transcripts accumulation starting 2 hours following hormonal treatment. The differential expression of genes induced by gibberellin in inflorescence bud in premeiosis is analyzed in association with the assays of pollen development that revealed 80-90% of meiocytes disrupted in pachytene and arrested during following meiotic divisions in CMS anthers and various abnormalities, chromosome aberrations (delayed chromosomes, chromosome bridges, chromosome laggards, micronuclei, stickiness chromosomes) in microsporogenesis stages of plants with induced sterility.

The obtained data revealed various genes expression profiles related to sterility type and genetic background. Many of the studied genes/ESTs are gibberellin responsive from the first hours after exogenous treatment. Reported evidences may lead to new investigations to gain further understanding in this field.

*This study was funded by the project of the State Program 20.80009.5107.01 - Genetico-molecular and biotechnological studies of the sunflower in the context of sustainable management of agricultural ecosystems.*