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DIFFERENTIAL GENES EXPRESSION UNDER ANTERO- AND RETROGRADE CONTROL IN SUNFLOWER MICROSPOROGENESIS

Port Angela
Center of Functional Genetics, Moldova State University, Chisinau, Republic of Moldova
E-mail: portang@yahoo.com

Nowadays, sunflower is among the leading crops of major importance for global food security. The economic interest of sunflower breeding is mainly determined by the production of seeds, whose biological yield can be increased by exhaustive knowledge of reproductive development. The control of pollen fertility is essential for germplasm diversification, hybrids with a high degree of heterosis obtaining and, more recently, ensuring the biosecurity of the introduction of transgenic plants into culture, as well as for the numerous researches of male gametophyte in various physiological or changeable environmental conditions. Of particular interest are the peculiarities of male gametophyte development in plants with gibberellin-induced male sterility (GA_3-IMS), a phenomenon that is not based on dysfunctions generated by the different genomic interactions. Thus, fertile inbred lines with androsterile analogs, fertility restorer lines and progeny (F_1) with restored fertility form an excellent model for research of cell communication, and being associated with AG3-IMS may elucidate the antero- and retrograde signaling processes of male gametogenesis under the gibberellins action. Previously, was provided the first evidence that sunflower with GA_3 induced male sterility is associated with a similar transcript to mitochondrial orfH522 characteristic for PET1 cytotype. Taking into account that the GA_3-IMS phenotype is not the result of nucleocytoplasmic incompatibility it was concluded that meiosis cell division, mtDNA replication and mitogenome maintenance are not reliable. Thus, candidate genes involved in the mentioned events during sunflower microsporogenesis were assessed by RT- qPCR. In these investigations were used near-isonuclear lines, fertile SW501 with the *H. annuus L.* cytoplasm and male sterile SW501CMS with *H. petiolaris* cytoplasm, Drofa F_1 hybrid and its parents. The plants were exogenously treated with GA_3 solution by spraying on developing inflorescence buds. The florets from inflorescence buds (R1-R3) were subjected to microscopical, physiological and molecular analyses. The model of additive/nonadditive genes expression was used to compare transcripts profiles between F1 hybrid and its parents. Sterility of sunflower anthers as GA-induced response resulted from the perturbation of the endogen hormone concentration, as well as from the ability of cells to perceive this perturbation and activate the subsequent transduction pathways of cellular signals. It was ascertained various genes expression profiles related to sterility type, genetic background and stage of pollen development. All studied sunflower transcripts are gibberellin responsive and showed high degree level of co-expression. Several genes differentially expressed in sterile anthers (CMS and GA-IMS) were down-regulated, suggesting on DNA damage-responsive cell - cycle arrest, an important mechanism for the preservation of genomic stability. Also, the transcriptomic data showed more non-additive gene expression patterns in hybrids than additive revealing, often, microsporogenesis stage specificity. It is suggested that those genes whose expression changes in F_1 hybrids (non-additively) can be associated with heterosis, being involved in specific signaling pathways that could be targeted regulated. The fact that researches on the mechanism of heterosis continue to be essential as part of enhancing food production, there is considerable incentive to investigate the genomic consequences of heterotic gene pool development.

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