PROTEOME AND TRANSCRIPTOME ANALYSIS OF OROBANCHE CUMANA WITH DIFFERENT LEVELOF VIRULENCE

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Abstract

Since 1970, when a new broomrape race, called Moldovan race or race C, was identified on the territory of Moldova, the aggressiveness of the parasite increased significantly and new, highly virulent races appeared very quickly. Actually, all the known races of *Orobanche cumana* Wallr. have been detected in our country and the areas affected by these parasitic plants expanded considerably across the territory of Moldova.

Taking into account that studies of the relation between host and pathogen are focused in particular on the plant response to the parasite and less on the molecular basis of infection process and virulence of the supposed races, the aim of this paper is the comparative analysis of transcriptomic profile of genes encoding enzymes involved in host invasion (PME, PGU, PRX and CHS) and proteomic profile of germinated broomrape seeds with different virulence.

For the comparative analysis two populations of *O. cumana*, one belonging to race E or less virulent than E and one from highly virulent race H, collected from sunflower fields located in the Central part of the Republic of Moldova were used.

The study of the relative expression of genes *PRX*, *PME*, *PG* and *CHS* at the different developmental stage (tubercle, underground and aerial shoots) of angiosperm *O. cumana* has revealed the correlation between the transcription level and virulence of parasite. Thus, all the genes were up-regulated in the most virulent population comparative to the less virulent.

To analyses differentially expressed proteins two-dimensional difference gel electrophoresis (2D-DIGE) and mass spectrometry (MALDI-TOF MS) were used. The comparative analysis of the proteome revealed 19 DEPs. A number of these have been identified as enzymes of the respiratory system, as well as stress-related proteins. Also, a variety of transporting, regulatory or synthetic proteins have been identified, including some proteins with unknown function that can be co-expressed at various parasitic stages and may be important in the development of haustorium. Among the proteins were also identified cell wall modifying enzymes and proteins known to be involved in the invasion of the parasite.

Keywords: broomrape, two-dimensional difference gel electrophoresis, gene expression