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**Transcriptome - Proteomic and markers co-profiling offers approaches associated with resistance in wheat to cereal cyst nematodes and common root rot diseases****Mehdi Nasr- Esfahani***Esfahan Agriculture and Natural Resource Research and Education Center, Iran*

Improvement of disease resistance in crops has a great potential to increase productivity by preventing the huge losses caused by the plant pathogens. Cereal cyst nematodes (CCN), *Heterodera filipjevi* (Madzhidov) Stelter, and common root rot (CRR), *Bipolaris sorokiniana* (Sacc.) are the destructive diseases on cereal crops globally. Limited information on CCN-CRR infection, epidemiology and lack of adequate resistant cultivars is hampering their management significantly. Thus, in this-study, the reaction of resistant and susceptible wheat, *Triticum aestivum* L., cultivars out of 33 irrigated wheat genotypes screened for resistance to *H. filipjevi* and *B. sorokiniana* was investigated to determine the changes in the expression of markers gene, Cre3, PRX-groups (TaPrx111 and TaPrx112), EDS1, LTP5, PGIP, PR-1, PIEP1, TLP, UGT, Stb6 and PFT, using real-time quantitative PCR (qPCR) analysis at various time intervals. In addition, the activities of defense-related enzymes; peroxidase (POX), superoxide dismutase (SOD), polyphenol oxidase (PPO), catalase (CAT), phenylalanine ammonia-lyase (PAL),  $\beta$ -1,3-glucanase (GLU) and chitinase (CHI), as well as total phenol content (TPC) were analyzed accordingly. Subsequently, the genetic variability of the entire germplasm, 33 wheat cultivars using seven simple sequence repeat (SSR) primer pairs was analyzed. Five out of seven used SSR primers produced a total of 20 polymorphic bands, of which the number of alleles in each gene locus varied within 3–7 bands. The cluster diagram divided the wheat genotypes into four separate groups i.e., resistant, partially resistant, susceptible and highly susceptible accordingly. Surprisingly, PRX gene marker, basically resistant to abiotic-stresses such as high-salinity and drought, also regulating the ROS-balance in plants, similarly modulates-immunity against-*H. filipjevi*. Similarly, Cre3, a resistance gene to cereal cyst nematode *H. filipjevi*, was regulated in cultivars resistant to *B. sorokiniana*. Similar results were obtained for Stb6, a gene resistant to *Septoria tritici blotch*, EDS1 resistant to powdery mildew, *Blumeria graminis*, and the genes PR-1 and UGT resistant to leaf rust, *Puccinia triticina*. Antioxidant enzyme activity also showed the highest increases in resistant genotypes.

Integrated transcriptome-proteomic analysis identified key expansion genes associated with resistant wheat to Cereal cyst nematodes and common root rot.

**Biography**

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