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## Genome-wide identification and characterization of phosphate transporters from wheat with their possible role during grain development

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Phosphorus (P) is poorly available for plants due to its assimilation by microbes and strong interaction with most of the cations within the soil. Under P-limiting environments, plant exploits selective high- and low-affinity phosphate transporters (PHTs) to enhance their ability of Inorganic phosphate (Pi) uptake into roots, translocation to shoots and remobilization into developing sink tissues. Cereal grains accumulate high amounts of Pi during seed development either as free Pi or bound form (~80% is phytic acid). Although, seed is a major 'sink' for Pi utilization, not many reports addressing the importance of the Pi homeostasis and phytic acid accumulation in seeds. This warrants detailed investigation of Pi homeostasis and transport functions in developing seed tissues. The current study aims to identify seed-specific wheat (Triticum aestivum) PHTs and evaluate their importance during wheat grain development. Genome wide survey, EST analysis and phylogeny revealed 23 putative TaPHTs in wheat, mainly distributed into four sub-families, including PHT1 (1-14), PHT2, PHT3 (1-3), PHT4 (1-6). Genomic coordinates were ascertained for all the identified TaPHTs and their location on the chromosomes was also confirmed. qRT-PCR analysis resulted in identification of wheat PHTs those were highly expressed in seeds. Co-relation studies were performed on the seed tissue between gene expression and accumulation of Pi. Our result suggested enhanced expression of certain wheat PHTs in specific seed tissues as compared to other seed parts. Interestingly, phosphate homeostasis related genes (PHO-pathway) were also differentially expressed in seed tissues. Future works are directed to functionally characterize the identified high affinity PHTs from wheat. The above work will help in understanding of relevant signaling networks empowering phosphate accumulation in developing cereal grains.

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## Identification of *Arabidopsis* candidate genes in response to biotic and abiotic stresses using comparative microarrays

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**P**lants have evolved with intricate mechanisms to cope with multiple environmental stresses. To adapt with biotic and abiotic stresses, plant responses involve changes at the cellular and molecular levels. We investigated the role of cyclopentenones in mediating plant responses to environmental stress through TGA (TGACG motif-binding factor) transcription factor, independently from jasmonic acid. Candidate genes were identified by comparing plants inoculated with *Botrytis cinerea* or treated with heat, salt or osmotic stress with non-inoculated or non-treated tissues. About 2.5% heat, 19% salinity and 41% osmotic stress-induced genes were commonly up-regulated by *B. Cinerea* treatment and 7.6%, 19% and 48% of genes were commonly down regulated by *B. Cinerea* treatment, respectively. Our results indicate that plant responses to biotic and abiotic stresses are mediated by several common regulatory genes. Comparisons between transcriptome data from *Arabidopsis* stressed-plants support our hypothesis that some molecular and biological processes involved in biotic and abiotic stress response are conserved. Thirteen of the common regulated genes to abiotic and biotic stresses were studied in detail to determine their role in plant resistance to *B. cinerea*. Moreover, a T-DNA insertion mutant of the Responsive to Dehydration gene (rd20), encoding for a member of the caleosin (lipid surface protein) family, showed an enhanced sensitivity to *B. Cinerea* infection and drought. Future research directions towards a better dissection of the potential crosstalk between *B. cinerea*, abiotic stress and oxylipin signaling are of our particular interest.

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