

# Identification and Transcriptional Profile of Selected Phosphate Responsive Genes during Phosphate Deprived Condition in Maize

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**Abstract**—The post green revolution agriculture is based on generous application of fertilizers and new cereal genotypes that are suited for such high input regimes. Cereals, like maize (*Zea mays* L.) are capable of utilizing less than 10% of the applied inorganic phosphate (Pi) - a non-renewable fertilizer resource. A greater understanding of the molecular mechanism underlying the acquisition, transportation and utilization of Pi may lead to strategies to enhance phosphate use efficiency (PUE). In this study, we have identified 12 maize phosphate responsive genes based on sequence similarity and functional domain analysis with *Arabidopsis* phosphate responsive genes. The comparative expression of these 12 genes in root and shoot tissues of hydroponically grown maize inbred HKI-163 under sufficient (10mM  $\text{KH}_2\text{PO}_4$ ) and low Pi (5 $\mu\text{M}$   $\text{KH}_2\text{PO}_4$ ) condition was validated by semi quantitative Reverse Transcriptase and Real Time polymerase chain reaction assays. The Real Time expression of 11 out of 12 genes in phosphate deficient condition were significantly up or down regulated as expected. The expression pattern of two putative transcription factors *ZmHPR1* and *ZmZAT6* were more or less same in shoot tissue whereas in root tissue *ZmPHT1* was found more expressive (11.49 fold up regulated) as compared to *ZmZAT6* (0.57 fold down regulated). The putative acid phosphatase- *ZmACP5* expression was up regulated by 162.81 and 74.40 fold in both root and shoot tissues respectively. The RNase, *ZmRNS1* showed 115 fold up regulation in roots under phosphate deprivation. Among the two putative high affinity Pi transporter (*ZmPht1;4* and *ZmPht2*), *ZmPht1;4* was found specific to root whereas *ZmPht2* was found up regulated in both root and shoot tissues (196.56 and 30.40 fold respectively). Therefore, *Pht1;4* might be involved in Pi acquisition from soil and *ZmPht2* might be involved in phosphate remobilization within plants. The genes involved in phosphate homeostasis pathway (*ZmSIZ1*, *SPX1* and *Pho2*) were up regulated in root and shoots. *ZmCHS* involved in metabolic pathway was also up regulated in roots. These genes can be useful for further characterization and might be useful for engineering high PUE in the maize crop.

**Acknowledgement:** This research was funded by a grant from National Agricultural Science Fund (NASF 1007070) to PY