The role of homeodomain-leucine zipper class I transcription factors in the drought response of wheat

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Abstract

Traditional breeding for increased yield under water limiting conditions has been hampered by the complexity of the polygenic plant response and the unpredictability of seasonal conditions. This has made it difficult to observe the hereditability of a selected trait. Given these difficulties, breeders have been selecting for yield improvement under water deficit by phenotyping methods rather than by genetic association. Hence, an improvement in yield under water limited conditions is often seen under well-watered conditions and so selection has been for yield increase and not “drought tolerance”. Understanding the plant drought response at the molecular level will aid efforts to increase yield under water limited conditions. An approach to reveal the molecular mechanisms of the plant drought response is to study the role of transcription factors which act as global regulators of gene expression.

Members of the homeodomain-leucine zipper class I (HD-Zip I) γ-clade TFs show drought and ABA inducible expression and are believed to act in plant adaptation to abiotic stress. It was therefore considered that, HD-Zip I γ-clade TFs pose good candidates for studying a part of the drought response mechanism. To this end three wheat γ-clade HD-Zip I TFs were isolated, *TaHDZipI-3*, *TaHDZipI-4* and *TaHDZipI-5*, and studies of their function were performed.

Studies were performed to confirm the relationship of the isolated γ-clade TFs with homologues. The three wheat γ-clade HD-Zip I TFs show patterns of induction by abiotic stresses and interaction with the putative HD-Zip I *cis* element that suggests differences exist between dicot and monocot homologues.

Transgenic wheat and barley plants constitutively over-expressing wheat γ-clade HD-Zip I TFs have been produced. Investigations were made to analyse any role of HD Zip I TFs in stem development and the regulation of lignin deposition in anther development. Wheat constitutively over-expressing *TaHDZipI-4* displayed no differences in stem length contrary to other reported observations made on γ-clade HD-Zip I TFs. However, a stem developmental series showed that there is an increase in endogenous expression correlating with internode maturity and a developmentally specific spike in expression in the entire stem. Analysis of lignin deposition was performed using barley expressing *TaHDZipI-3*, *TaHDZipI-4*, and *ZmHDZip1* under the 35S promoter. Results suggest that no differences in anther lignin deposition have occurred.

Transgenic wheat was grown under two different drought scenarios, sustained water deficit or cyclic drought, to assess the effect of γ-clade HD-Zip I TFs under the regulation of a strong drought inducible promoter. No improvement in yield under water deficit was observed.

It appears that wheat HD-Zip I γ-clade TFs have diversified from known dicot homologues in their expression characters and role as transcription factors. Hence, the mechanisms of action of these TFs in monocots may be different from that in Arabidopsis. Despite the efforts and analyses presented here as part of the PhD project, the role of γ-clade HD-Zip I TFs in the plant drought response remains elusive.

Statement of authorship

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- Harris JC, Hrmova M, Lopato S, Langridge P. 2011. Modulation of plant growth by HD-Zip class I and II transcription factors in response to environmental stimuli. New Phytologist 190: 823-837.

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Acknowledgments

To my wife, Nady Harris, thank you for staying on the rollercoaster.

Frequently used abbreviations

ACPFG	Australian Centre for Plant Functional Genomics
ABA	abscisic acid
ABRE	ABA responsive element
cDNA	complimentary DNA
DRE	drought responsive element
DREB	DRE binding factor
gDNA	genomic DNA
HD	homeodomain
HD-Zip I	homeodomain-leucine zipper class I
LZ	leucine zipper
nt	nucleotide
PCR	polymerase chain reaction
QPCR	quantitative PCR
RT-PCR	reverse transcriptase PCR
Ta	*Triticum aestivum*
Td	*Triticum durum*
TFs	transcription factors
Tx	transgenic
WT	wild type