

# Comparative structural analysis of the drought responsive dehydrin and aquaporin gene families in *Brachypodium*

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## INTRODUCTION

Dehydrins (DHNs) belong to the group 2 LEA (Late Embryogenesis Abundant) protein genes and play an important role in the response of the plant to abiotic stress, mainly heat, salinity and drought stresses. Under these stresses, DHNs accumulate to a large extent in maturing seeds and in all vegetative tissues. As many studies reveal, there is a positive correlation between DHN gene expression (creation of DHN proteins) and plant stress tolerance. Aquaporins (AQPs) belong to the major intrinsic protein (MIP) superfamily of membrane proteins conserved in plants and animals as well as bacteria. Supporting evidence suggests that AQPs have an important role in stomatal closure and circadian regulation. There are more than 150 MIPs identified and, although some of them are constitutively expressed, others are regulated in response to drought and salinity.

## HOMEOLOGY ACROSS GENERA

Biomart data has been used to retrieve *Brachypodium* homeolog genes from other related crops. Some genes in *Hordeum*, like those in chr 6, are related to different *Brachypodium* chromosomes (in chrs 1, 3, 4 and 5). The opposite happens in *Zea*, where genes from of *Brachypodium* chromosome 1 have homeologs in chrs 5 and 7. Interestingly, these genes have homeologs in all species but *Sorghum* and *Oryza*. Finally, a DHN coded in *Brachypodium* chromosome 4 is shared only with *Hordeum* and *Triticum*; while another from chr 3 is shared only with *Sorghum* and *Oryza*.

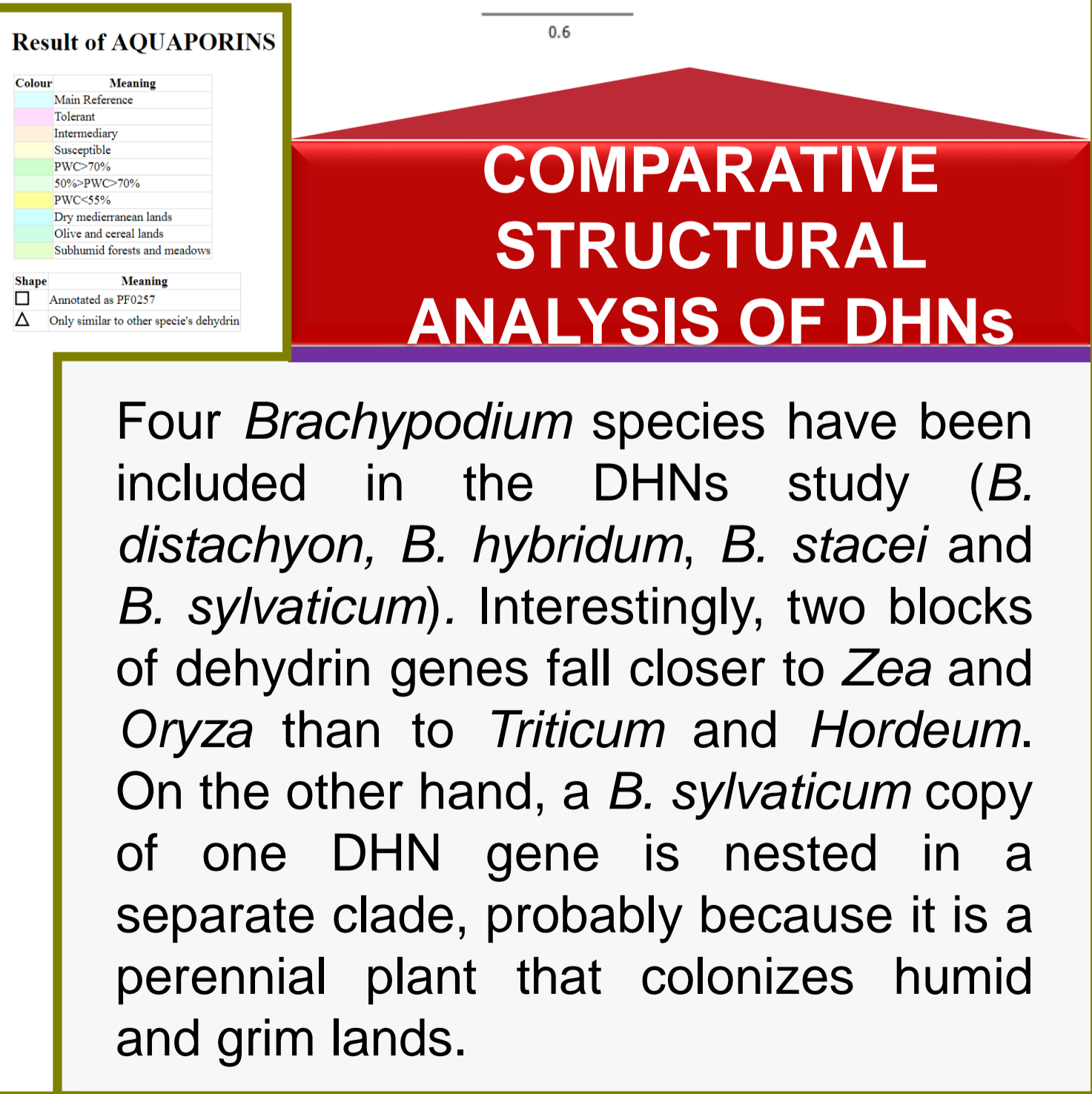
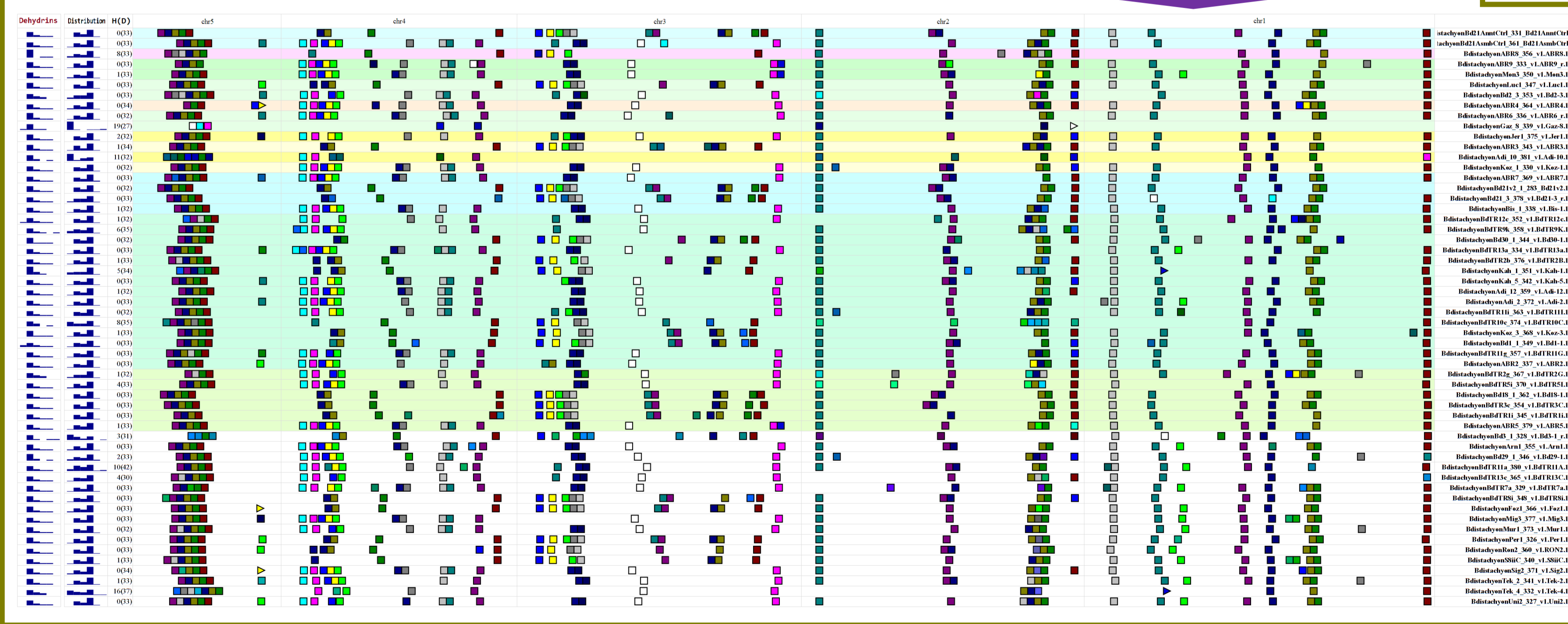
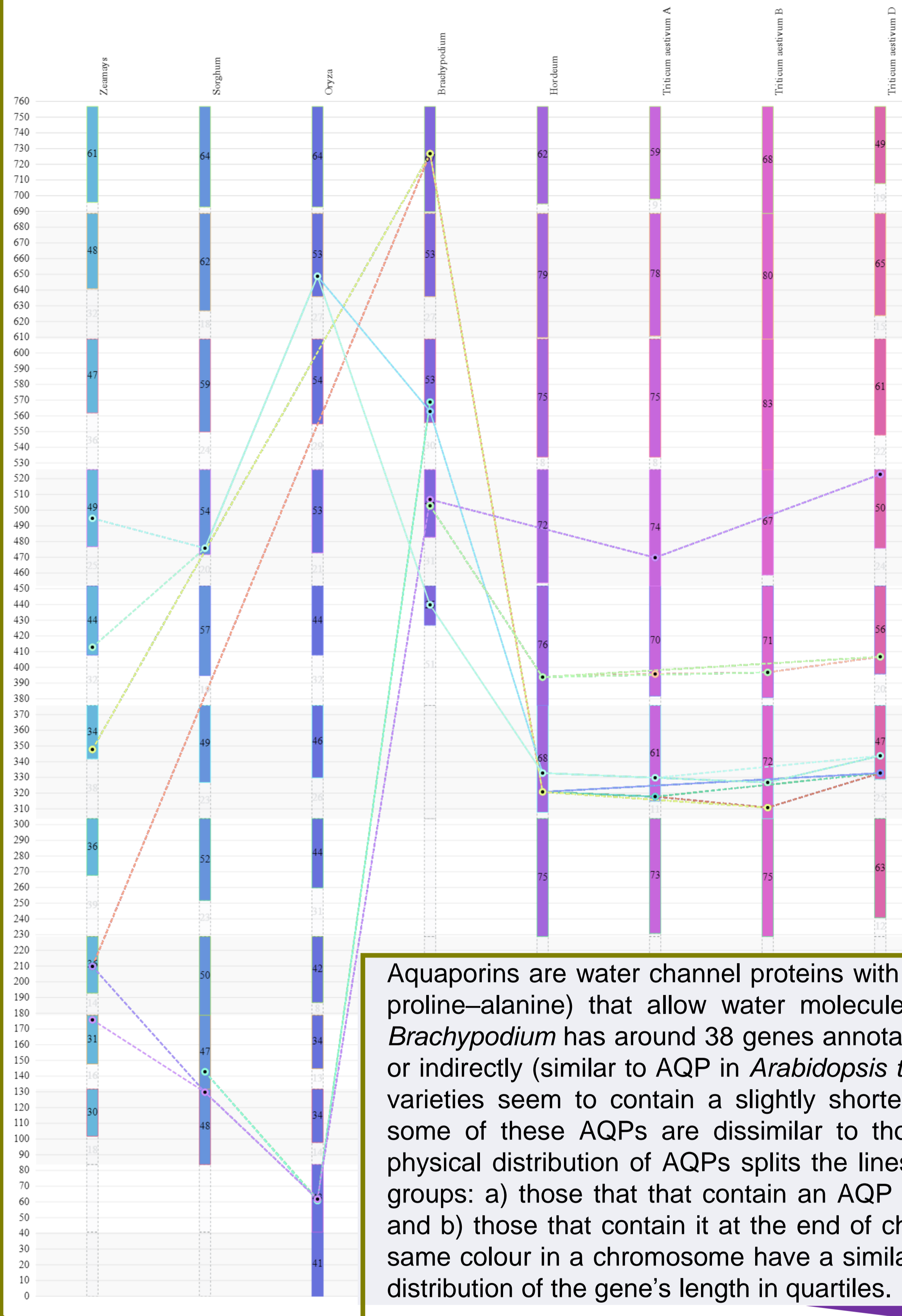
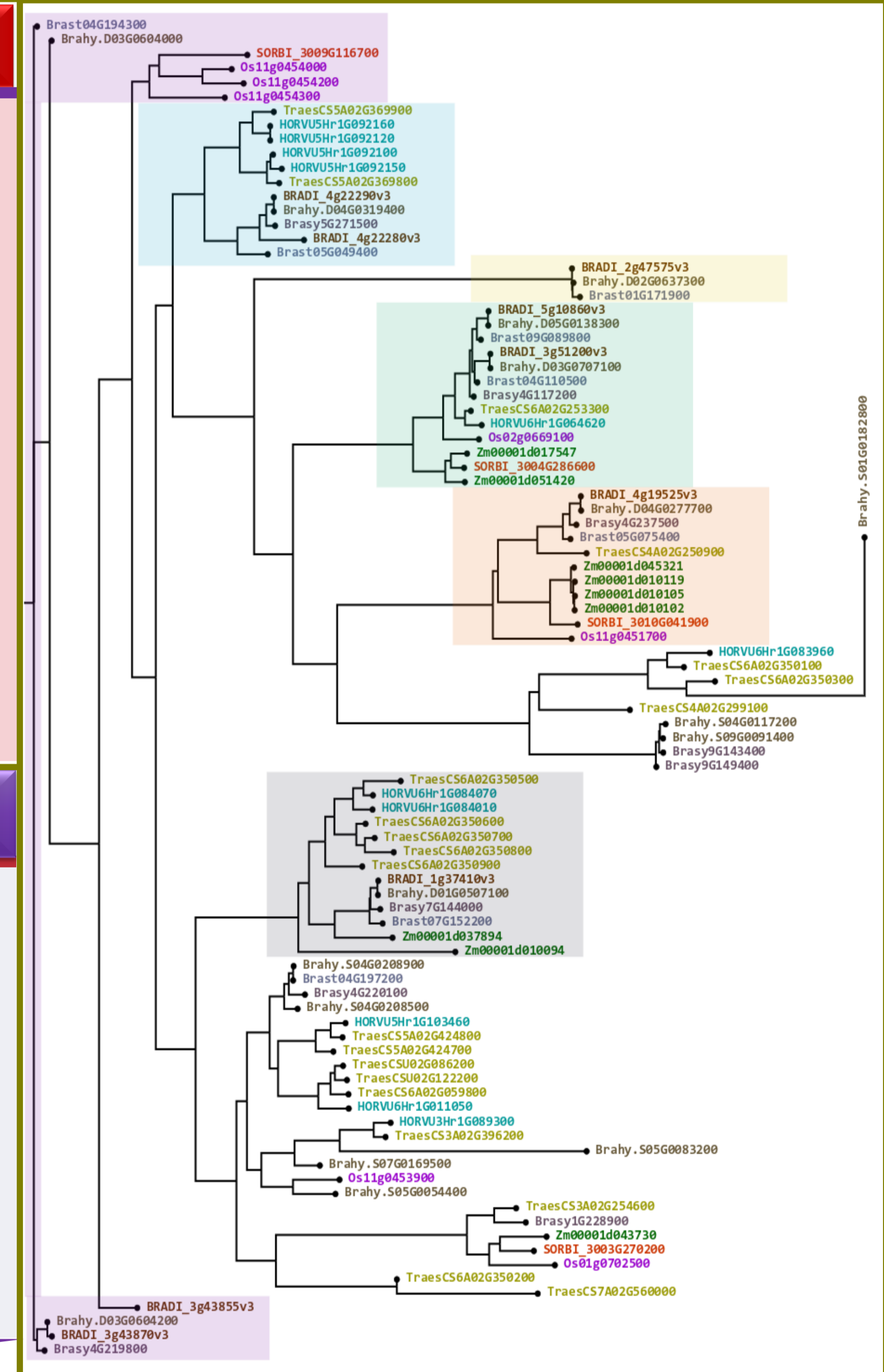
## DEHYDRINS

Classification of dehydrins is based on their structural conserved motifs, designated as Y, S and K segments. All the annotated dehydrins of the *Brachypodium* lines analysed in this work contain the most specific K-segment.

*Brachypodium* dehydrins have been compared to other grass DHNs using two different approaches: i) homeology and chromosome distribution; and ii) secondary structure similarity.

## AQUAPORINS

Aquaporins are water channel proteins with two NPA segments (asparagine–proline–alanine) that allow water molecules to pass through one by one. *Brachypodium* has around 38 genes annotated as AQPs directly (PFAM 230) or indirectly (similar to AQP in *Arabidopsis thaliana* or *Oryza sativa*). Tolerant varieties seem to contain a slightly shorter aquaporins and dehydrins and some of these AQPs are dissimilar to those of the rest of varieties. The physical distribution of AQPs splits the lines of *Brachypodium* into two main groups: a) those that contain an AQP gene cluster at the end of chr3; and b) those that contain it at the end of chr 4. In the figure, genes with the same colour in a chromosome have a similarity >95%; left columns show the distribution of the gene's length in quartiles.



## COMPARATIVE STRUCTURAL ANALYSIS OF DHNs

Four *Brachypodium* species have been included in the DHNs study (*B. distachyon*, *B. hybridum*, *B. stacei* and *B. sylvaticum*). Interestingly, two blocks of dehydrin genes fall closer to *Zea* and *Oryza* than to *Triticum* and *Hordeum*. On the other hand, a *B. sylvaticum* copy of one DHN gene is nested in a separate clade, probably because it is a perennial plant that colonizes humid and grim lands.

## REFERENCES

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