



Short Communication

NJ cluster analysis of the *SnRK2*, *PYR/PYL/RCAR*, and *ABF* genes in Tibetan hulless barley

H.J. Yuan^{1,2}, Y.L. Wang^{1,2}, Z.X. Wei¹, Q.J. Xu^{1,2}, X.Q. Zeng^{1,2}, Y.W. Tang^{1,2}
and T.S. Nyima^{1,2}

¹Tibet Academy of Agricultural and Animal Husbandry Sciences, Lhasa, China

²Barley Improvement and Yak Breeding Key Laboratory of Tibet Autonomous Region, Lhasa, China

Corresponding author: T.S. Nyima

E-mail: nima_zhaxi@sina.com

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ABSTRACT. The abscisic acid (ABA) signaling pathway is known as one of the most important signaling pathways in plants and is mediated by multiple regulators. The genes *SnRK2*, *PYR/PYL/RCAR*, and *ABF* are relevant to both ABA-dependent and -independent signaling pathways. To elucidate the profile of these genes from Tibetan hulless barley (*Hordeum vulgare* L. var. *nudum* Hook. f.), we collected available sequences from RNA-Seq data, together with NCBI data from five other model plant species (*Arabidopsis thaliana*, *Brachypodium distachyon*, *Oryza sativa*, *Populus trichocarpa*, and *Sorghum bicolor*). Gene trees of *SnRK2*, *PYR/PYL/RCAR*, and *ABF* were constructed using a neighbor joining (NJ) method. For all genes, we identified a dominant group in which all six species were represented. Three, four, and five groups were found in the NJ trees of *SnRK2*, *PYR/PYL/RCAR*, and *ABF*,

respectively. For each gene, Tibetan hulless barley was divided into three groups. Our analyses indicated that Tibetan hulless barley was associated with *B. distachyon*. The NJ cluster analysis also suggested that Tibetan hulless barley was affiliated with *S. bicolor* (*SnRK2*), *A. thaliana* (*PYR/PYL/RCAR*), and *O. sativa* (*ABF*). These results illustrate a diverse expression of genes *SnRK2*, *PYR/PYL/RCAR*, and *ABF*, and suggest a relationship among the six species studied. Collectively, our characterization of the three components of the ABA signaling pathway may contribute to improve stress tolerance in Tibetan hulless barley.

Key words: *Hordeum vulgare*; Drought-responsive genes; Neighbor-joining tree