



# Genome-wide analysis and identification of KT/HAK/KUP potassium transporter gene family in peach (*Prunus persica*)

Z.Z. Song, R.J. Ma and M.L. Yu

Institute of Horticulture, Jiangsu Academy of Agricultural Sciences, Nanjing, China

Corresponding author: M.L. Yu  
E-mail: mly1008@aliyun.com

Genet. Mol. Res. 14 (1): 774-787 (2015)  
Received January 14, 2014  
Accepted April 3, 2014  
Published January 30, 2015  
DOI <http://dx.doi.org/10.4238/2015.January.30.21>

**ABSTRACT.** The KT/HAK/KUP family members encoding high-affinity potassium ( $K^+$ ) transporters mediate  $K^+$  transport across the plasma membranes of plant cells to maintain plant normal growth and metabolic activities. In this paper, we identified 16 potassium transporter genes in the peach (*Prunus persica*) using the Hidden Markov model scanning strategy and searching the peach genome database. Utilizing the *Arabidopsis* KT/HAK/KUP family as a reference, phylogenetic analysis indicates that the KT/HAK/KUP family in the peach can be classified into 3 groups. Genomic localization indicated that 16 KT/HAK/KUP family genes were well distributed on 7 scaffolds. Gene structure analysis showed that the KT/HAK/KUP family genes have 6-9 introns. In addition, all of the KT/HAK/KUP family members were hydrophobic proteins; they exhibited similar secondary structure patterns and homologous tertiary structures. Putative *cis*-elements involved in abiotic stress adaption,  $Ca^{2+}$  response, light and circadian rhythm regulation, and seed development were observed in the promoters of the KT/HAK/KUP family genes. Subcellular localization prediction indicated that the KT/HAK/KUP members were mainly

located in the plasma membrane. Expression levels of the KT/HAK/KUP family genes were much higher in the fruit and flower than those in the other 7 tissues examined, indicating that the KT/HAK/KUP family genes may have important roles in K<sup>+</sup> uptake and transport, which mainly contribute to flower formation and fruit development in the peach.

**Key words:** *Prunus persica*; Potassium transporter; KT/HAK/KUP family; Genome-wide analysis