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Whole-genome identification and expression analysis of *GmKEA* and *GmNHX* members under abiotic stresses in soybean

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Soybean (*Glycine max* [L.] Merr.) is cultivated under a wide range of environments, and is exposed to environmental stresses, soil salinity is the major abiotic stress limiting soybean planting. Soil salinity play a significant negative effect on soybean growth, and improving salt tolerance is an important goal of breeding programs in soybean. In salt stress condition, the sodium ion ( $\text{Na}^+$ ) is harmful for plants, whereas

$\text{K}^+$  is essential. Sodium toxicity and potassium insufficient are important factors affecting the growth and development of soybean under salt stress. As the capacity of plants to maintain a high cytosolic  $\text{K}^+/\text{Na}^+$  ratio is the key determinant of tolerance under salt stress. This study was focused on identification of  $\text{K}^+$  efflux antiporter (KEA) and  $\text{Na}^+/\text{H}^+$  antiporter (NHX) family members in soybean. Expression patterns of the two gene family members were also analyzed under abiotic stresses. As a result, we identified twelve soybean *GmKEAs* and ten soybean *GmNHXs* in soybean whole genome. Interestingly, the novel KEA member *Glyma16g32821*, which encoding 11 transmembrane domains, were extremely up regulated and remained high level in root after the excessive potassium treatment and lack of potassium treatment, respectively. The novel NHX member *Glyma09g02130*, which encoding ten transmembrane domains, were extremely up regulated and remained high level until in root under NaCl stress. *Glyma09g02130* and *Glyma16g32821* were confirmed as plasma membrane proteins using subcellular localization method. Integrated analysis showed that the new genes *Glyma09g02130* and *Glyma16g32821* all belong to the cation/hydrogen antiporter family.