

# WRKY33 MODULATES THE RESPONSES TO LOW NITROGEN SUPPLY OF CONTRASTING N-USE EFFICIENT EGGPLANTS

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## Abstract

Nitrogen use efficiency (NUE) is an important and complex crops trait and its improvement represents a strategy to maintain high yield reducing N-supply. We report the genome-wide transcriptomic analysis of four eggplants contrasting for NUE to identify key genes related to the NUE pathway, after short- and long-term low-N exposure, in both root and shoot. Co-expression Gene Networks (CGN) analysis permitted to identify up-regulated differential expressed genes (DEGs) involved in the light reaction pathway, the biological processes response to inorganic substance, abiotic stimulus and cellular response to nitrogen starvation in high NUE genotypes. Some transcription factor (TF) were up-regulated in the N-use efficient genotypes, in particular, WRKY33 showed a significant up-regulation triggering the higher expression of 21 genes cluster including other TFs, many of which associated to N-metabolism. To validate our results, an independent de novo experiment including two other NUE-contrasting genotypes, at both low and high N supply, was carried out. Interestingly, the high significant WRKY33 expression and its cluster were confirmed in the high NUE genotypes at low-N supply. Moreover, the WRKY33 role was confirmed in Arabidopsis as the 35S::AtWRKY33 over expressing line showed a more competitive root system able to uptake more efficiently N from the soil.

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