

COMPREHENSIVE GENOME-WIDE CHARACTERIZATION AND EXPRESSION PROFILING OF NPF AND NRT2 NITROGEN TRANSPORTERS GENE FAMILIES IN DURUM WHEAT

PUCCIO G.*, INGRAFFIA R.*, GIAMBALVO D.*, FREDA S. A.*, HARKESS A.***,
SUNSERI F.****, MERCATI F.**

*) Department of Agricultural, Food and Forestry Sciences, University of
Palermo, Italy

**) Institute of Biosciences and BioResources (IBBR), National Research
Council, Palermo, Italy

***) Hudson Alpha Institute for Biotechnology, 601 Genome Way Northwest,
Huntsville, AL 35806, United States

****) Department of Agriculture, University Mediterranea of Reggio
Calabria, Italy

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Nitrogen (N) is a crucial nutrient for plant growth and development, mainly taken up as Nitrate (NO_3^-). NO_3^- availability in the soil is highly variable and its assimilation is governed by at least two transport systems, depending on soil nitrate concentrations: low affinity nitrate transport (LATS) and high affinity nitrate transport (HATS) systems, responsible for up-taking nitrate at different concentration ranges. LATS is controlled by the nitrate transporter 1/peptide transporter (NPF) family, which includes a different array of membrane transport proteins that can transport a high number of different substrates other than nitrate. HATS is controlled by the NRT2 family, which is more specific to nitrate. The ability of plants to take up nitrogen is directly involved in Nitrogen Use Efficiency (NUE), defined as the total biomass (or yield) per unit of supplied N (Moll et al. 1982, Agronomy J. 74, 562-564).

NPF and NRT2 gene families differ in both their structure and copy number across angiosperms. Compared to bacteria, animals, and algae, land plant genomes exhibit a substantial abundance of NPF/PTR and NRT2 genes.

Moreover, these numbers are even higher in polyploid species when compared to diploid species (Bajgain et al. 2018, Plant Physiol. 160, 906-916). Allopolyploid plant species, such as durum wheat, exhibit a higher abundance of NPF and NRT2 genes, indicating the retention of duplicated genes that may have acquired new functions through neo- or sub-functionalization. These genes may play previously unidentified roles in plants or allow for a more complex and fine-tuned gene expression.

In durum wheat, limited information is available about phylogenesis, evolution, and expression of NPF and NRT2 gene families. We extensively characterized and annotated the NPF and NRT2 families in the durum wheat genome, revealing for the first time 211 NPF and 20 NRT2 genes, respectively. We further provided a comprehensive analysis of their phylogenetic relationships, gene and protein structures and regulatory elements. By using publicly available RNA-seq data from 195 samples covering 9 tissues and 20 cultivars, we deeply characterized the expression profiles and co-expression relationships of both gene families.

Our evidences confirm that the majority of these genes were retained after small-scale duplication events, suggesting a neo- or sub-functionalization of many NPFs and NRT2s in *T. durum*. These findings further suggest that the expansion of the two gene families in wheat may be an important source of variability for the detection of NUE-related genes and potential candidate genes for future breeding programs in the frame of a low impact and sustainable agriculture.