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Involvement of miRNAs in the short-term response of pine roots to ammonium nutrition.

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Post-transcriptional gene regulation is an essential control point regarding gene expression programs. A class of small non-coding RNAs, microRNAs (miRNAs) play important roles during this process. They act on target mRNAs through post-transcriptional gene silencing, either by endonuclease mediated transcript cleavage or by translational repression of targeted mRNAs (Pattanayak et al., 2013). Thus, miRNAs are involved in the regulation mechanisms of important plant processes, including the regulation of the processes related to nitrogen nutrition (Gutiérrez, 2012).

In the present work, maritime pine (*Pinus pinaster* Aiton) was used to study the role of miRNAs regarding NH_4^+ nutrition in conifers, a group of plants that exhibits tolerance to NH_4^+ nutrition compared to NO_3^- nutrition specially during seedling stage (Ortigosa et al., 2022). This fact is of high interest since numerous NH_4^+ nutrition can negatively affect the growth and development of different crops.

The global miRNA expression has been characterized in the roots of maritime pine seedlings after 2 h and 24 h from fertilization with two levels of NH_4^+ solutions (0.1 mM and 3 mM). The miRNA-seq analysis revealed 271 new miRNAs with an identified precursor although only 4 were differentially expressed.

Gutiérrez RA. 2012. *Science*, 336:1673-1675.

Ortigosa F, et al. 2022. *Plant Cell and Environment*, 45,915-935.

Pattanayak D, et al. 2013. *Plant Molecular Biology Reporter*, 31, 493-506.

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