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Bioinformatics analysis of Pinus pinaster Aiton transcriptome in response to ammoniacal nutrition

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Conifers have a great economic and environmental value[1]. Nitrogen is an important limiting factor for the development of plants[2]. Conifers are well adapted to ammonium nutrition since it is the main source of inorganic nitrogen in the ecosystems that they live[3].

The present work is based on the study of ammonium uptake and management by maritime pine (*Pinus pinaster* Aiton) and its implication in the production of plant biomass. This conifer is present in western Mediterranean area and it is used for reforestation soil stabilization and industry. Due to its importance in this region maritime pine has been used as model conifer tree which has led to different omics studies and resources[45].

For this purpose we have developed several experiments using pine seedlings subjected to different levels of ammonium at the short and long term using the latest biotechnological and bioinformatic advances. The studies of RNA-seq allow us to obtain a large amount of transcriptomic information of mRNA lncRNA and miRNA level in the roots under ammonium nutrition. These data need different bioinformatic workflows to extract expression results with reliability and biological context. Parallel to these studies we have performed direct RNA sequencing using the Minion device of Oxford Nanopore Technologies (ONT). Thanks to this kind of technology we have been able to identify epitranscriptomics changes in our samples under ammonium nutrition. With this aim we have had to develop a new bioinformatic workflow. The characteristics of this new kind of sequencing allow us to analyze the RNA-seq studies from another perspective.

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