PROJECT TITLE

Metabolic adaptation to ammonium nutrition: learning from natural variation in Brachypodium distachyon

CONSORTIUM

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SUMMARY OF THE REPORT

The use of ammonium fertilizers, in combination with nitrification inhibitors, has been demonstrated efficient to mitigate some of the detrimental effects of excessive nitrogen fertilization such as NO_3^- leaching or N_2O emission (Ruser and Schulz, 2015; Coskun *et al*., 2017). However, ammonium nutrition may represent a stressful situation for crops. Although great progress has been done in understanding how plants deal with ammonium stress, the metabolic adaptation of plants is not completely understood and very few molecular components with plants ammonium tolerance have been identified (Li *et al*., 2014; Liu and von Wirén, 2017). In this context, the general objective of this work is to gain knowledge on plants response to ammonium nutrition using genetic and metabolic natural variation as a tool.

To do so, we have characterized the metabolic adaptation of a large panel of 52 *de novo* sequenced *Brachypodium distachyon* natural accessions, already shown as genetically diverse (Gordon *et al*., 2017). Moreover, we studied two close relative species of *B. distachyon*: *B. stacei* and *B. hybridum* (Catalan *et al.,* 2012). Plants were grown in the University of the Basque Country UPV/EHU (Spain) in aerated hydroponic tanks under exclusive nitrate or ammonium nutrition.

The metabolic characterization of the accessions was performed in the HiTMe Platform (INRA Bordeaux, France) and consisted in the quantification of key metabolites and enzyme activities for primary metabolism. Briefly, determined the content of chlorophyll, NO_3^-, NH_4^+, amino acids, organic acids, sugars and the activity of 10 enzymes of nitrogen and carbon metabolism. Marlon de la Peña, PhD student in the UPV/EHU, spent two periods of three months, six months in total, in the platform to perform these analyses.

The obtained results represent to our knowledge the most complete metabolic database for *B. distachyon* in relation with mineral nutrition and will be extremely helpful for our research group looking to understand plants adaptation to ammonium nutrition. The results will also be of great utility for the growing research community working with *B. distachyon*. The obtained phenotypic data will also be used to try to identify genes associated with the different traits by the use of Genome Wide Association Studies (GWAS). Besides, within the collection to be studied, accessions with available RIL populations are included and their future study will be another approach to find QTLs associated with ammonium nutrition