Phenotypic characterization of a sorghum association panel for salinity stress tolerance: Key input for GWAS analysis

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Introduction

Salinity and alkalinity in soils represent a major problem worldwide due to their adverse effect on agriculture, in terms of productivity and sustainability. Moreover, this problem is projected to worsen because of climate change. According to FAO-UNESCO Argentina is the third country with the largest area of soil affected by halomorphism in the world, after Russia and Australia.

Sorghum is a staple food in semi-arid regions of low-level development countries, is key for achieving the objective of food security due to its high potential for marginal soils.

Sorghum genetic improvement for tolerance to salinity and or alkalinity has lagged with respect to tolerance to biotic stresses; possibly because salinity/alkalinity tolerance is a complex trait both physiologically and genetically (quantitative inheritance), controlled by numerous QTL. One of the studies to address this type of genetic trait is genome-wide association mapping (GWAS), whose advantage lies in a higher resolution for the identification of causal genes. The general objective of this work is to contribute to the genetic improvement of sorghum for the extension of its cultivation to areas affected by salinity and alkalinity, accelerating the times of traditional improvement. To move forward in this regard, we phenotypically characterized the Sorghum Association Panel (SAP) composed of 325 sorghum genotypes, which largely covers the natural genotypic variability of this species and has extensive genotypic information available (~ 260,000 SNP markers). This information, and the use of bioinformatics tools, will allow the identification of genomic regions associated with tolerance to salinity, alkalinity, and their combination.

Material and methods

Four trials were carried out in a greenhouse, using a hydroponics system with automatic irrigation. Hoagland 0.5X complete nutrient solution was used for the control condition. The same solution was used for the saline treatment plus the addition of 150 mM NaCl. The salinity treatment was imposed when the plants fully developed in their second leaf. Once the development of the fourth leaf was reached, physiological variables were measured using a portable fluorometer (leaf temperature, chlorophyll content, and its fluorescence), and growth (plant dry weight, height, and thickness of leaves) was measured.
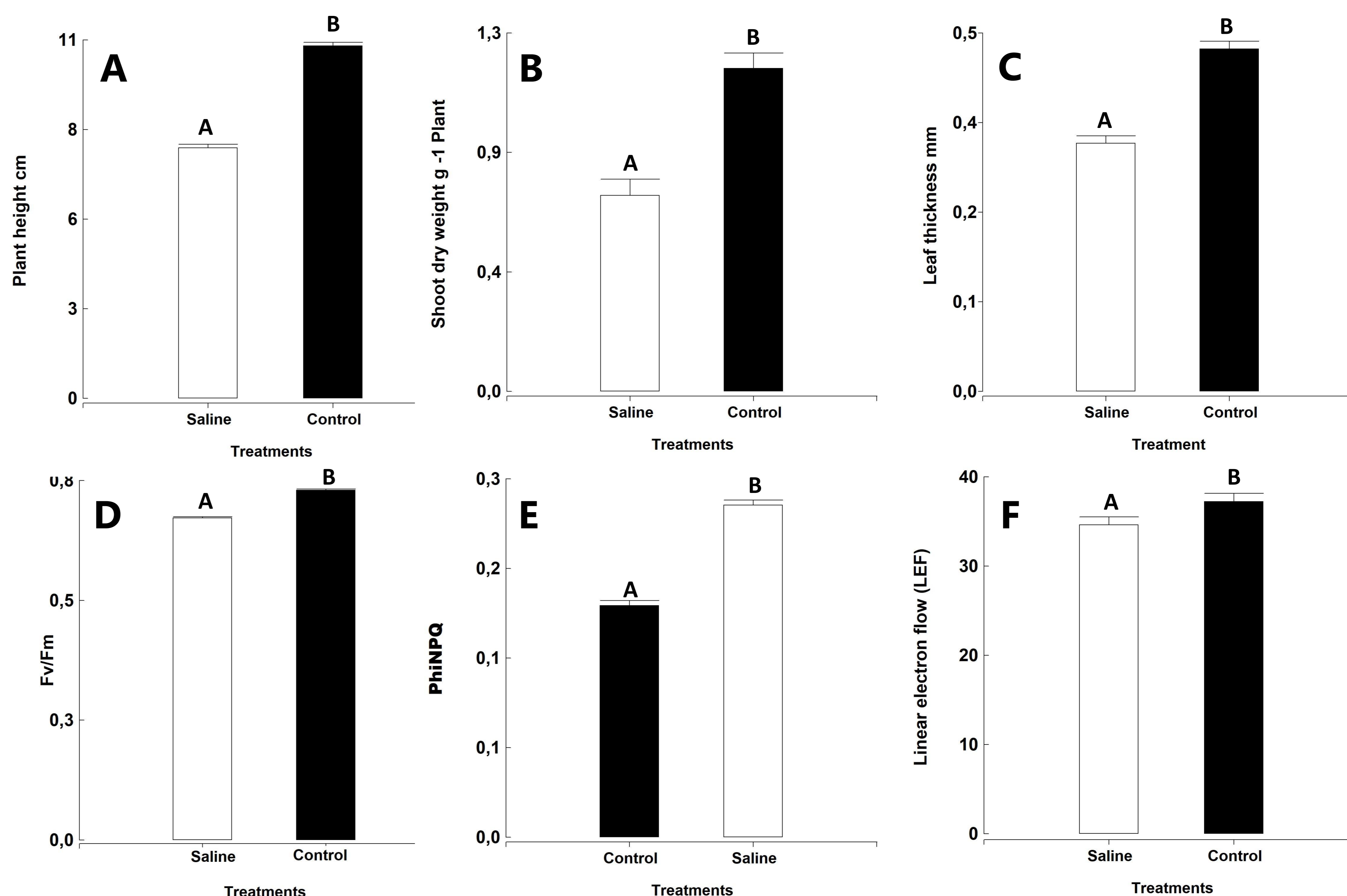

Hidroponics greenhouse experiments

Photosynthetic variables measurements

Results

Salinity significantly affected the plant growth: height (29%, panel A), dry weight (39%, panel B), and leaf thickness (27%, panel C) in the 325 sorghum genotypes. In addition, salinity affected some physiological variables such as the quantum yield of photosystem II (Fv'/Fm', by 9%, panel D) the proportion of light that goes to non-photochemical quenching (φNPQ, increased by 47%, panel E) and the linear electron flow (LEF, dropped 7%, panel F).

Conclusion

Salinity affected the physiological and growth variables of the Sorghum Association Panel (SAP). The results of this phenotyping, together with the use of bioinformatics tools, will serve as a basis for the location of new molecular markers (SNPs) and the identification of candidate genes responsible for tolerance to salinity stress. Knowledge of the phenotypic and genotypic variability of sorghum, as well as the response variables of crops to salt stress conditions, will contribute to the selection and potential improvement of materials with increased tolerance to this stress.