Can the analysis of the genetic diversity of stress responses challenge the consensus on the relative performance of maize and sorghum under drought scenarios?

Boris Parent (boris.parent@inrae.fr)

LEPSE, INRAE, Montpellier, France

After a record drought in summer 2022 in Europe, both the population and public authorities expect a strong response from agriculture to use less water in the very near future. In this context, increasing sorghum acreage appears to be an alternative to maïze. Indeed, it is widely believed that maize is better suited to optimal conditions and sorghum to rainfed conditions. However, this reputation is based on few studies and few genotypes, which would ideally represent THE maize and THE sorghum as species. There is a great pool of genetic diversity in each species and thus potentially wide ranges of «drought or temperature resistance». It should therefore be possible to find sorghums and/or maize adapted to each specific environmental scenario. For example, there is a wide range of earliness available in each species. Earliness has a major role, positive in avoiding late drought but negative under moderate or chronic drought. It is therefore essential to identify in which specific scenarios a given combination of trait values (ideotype) results in a comparative advantage on plant production. In this talk, dealing here with maize, I will show how we have developed a conceptual framework to predict the impact of the genetic diversity, based on the coupling between phenotyping and crop modeling: (i) the development of a model of leaf development and expansion for which parameter values can be obtained in phenotyping platforms (ii) the parameterization of 254 hybrids that maximize the maize genetic diversity; (iii) and the determination of ideotypes of cycle length, leaf growth and sensitivity to water deficit and radiation, in current and future European environments. Overall, we provide evidence on «where and when» a combination of trait values can give a comparative yield advantage, as well as the limit of possibilities in current genetic diversity.

Table of contents