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Performance of phenomic selection in sorghum : Exploring population structure and GXE effects on prediction accuracy

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The concept of phenomic selection has been formalized by Rincent et al. (2018) based on the idea that spectral information (Near Infra Red Spectroscopy (NIRS), Hyperspectral Imaging…) acquired from animal or plant tissues contains genetic information that can be used to predict the genetic values of candidates to selection. Together with this genetic information, spectra also captures information linked to the environment and genotype by environment interaction effects, that can also prove to be useful to optimize the prediction of individual's performances in different environmental contexts. Furthermore, because spectral information corresponds to intermediate phenotype (endophenotypes) located between the genome and phenotypes of interest, it can also capture interaction effects between genes that are typically difficult to obtain from DNA polymorphism information. This novel approach of phenomic prediction has proven to be relevant in several plant species, achieving higher genetic gains in a variety of contexts than with classical phenotypic or genomic selection approaches. In this study, we explored the relevance of phenomic selection to predict various traits of agronomic interest in two sorghum population's types. First, a broad-based population (GWAS) that has been evaluated across more than ten environments on which near infrared spectra were acquired on grains (1 environment) and stems (5 environments) was used. In addition, a large multi-reference Back-Cross Nested Association Mapping population, based on 3 recurrent parents and more than 20 donor parents (Garin et al., 2023), including more than 3900 BC1F4 families characterized in diverse conditions and for which NIRS spectra have been acquired on grains (1 to 2 sites maximum depending on the families) was also mobilized. Based on these populations, two questions were addressed, the effect of population structure on the prediction accuracies of genomic and phenomic selection and the definition of strategies to capture GXE effects to maximize prediction accuracies.

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