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A DATA-DRIVEN APPROACH HARNESSING GENOMIC, PHENOTYPIC, AND BIOCLIMATIC DIVERSITY REVEALS CLIMATE-DRIVEN GENOMIC OFFSET IN A COLLECTION OF ETHIOPIAN TEFF

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Climate change has dramatic impacts on the agroecosystems of the global South and threatens food security of millions of smallholder farmers. In these settings, the increasing food demand must be met with the sustainable intensification of crop production using climate ready varieties. These challenges can be addressed by transdisciplinary research efforts joining genomics, climate science, and participatory varietal selection targeted to challenging cropping environments.

Here, we report a case study characterizing the genomic vulnerability of teff (*Eragrostis tef*) in a changing climate. Teff is a staple crop in the Horn of Africa, used for traditional food preparations, such as enjera in Ethiopia and Eritrea, and recently regarded as super-food in western markets. After an initial evaluation of 3850 Ethiopian landraces, we selected and genotyped a representative subset of 321 georeferenced accessions, using ddRAD sequencing. We then derived historical and projected climate data of the studied area, including sampling locations, from publicly available databases. The core collection was phenotyped at two locations with the involvement of local female and male farmers providing genotype appreciation scores.

Using a machine-learning regression tree-based approach —where 12,153 SNPs were used as response variables and derived bioclimatic variables as predictors — we computed the importance of each environmental predictor in

the change of allele frequencies on the landscape. With this information, we built a model able to predict teff genetic composition across geography and climate. We then measured the genomic vulnerability of teff as consequence of climate change at the 2070 horizon by measuring the mismatch between current and predicted genetic-climate combinations. We merged this information with a genome-wide association study (GWAS) targeting associations between SNPs and phenotypes of agronomic relevance, uncorrelated climatic variables, and farmers' preferences.

Results indicate that predicted genomic vulnerability differs in extent among different climate change scenarios yet allows to consistently identify geographic regions with highest predicted genomic offset of teff. The GWAS identified 213 significant associations targeting plant morphology, yield components and farmers' preferences. Together with results of the machine-learning regression tree-based approach we were able to prioritize loci for breeding and with potential for adaptation. This integrative approach may drive the improvement of crops in challenging environments, providing a valuable framework for climate-smart germplasm management and sustainable intensification of smallholder farming.