

P3.102 - Adaptive changes in pearl millet landraces in Niger revealed by the genetic comparison of their *ex situ* and on-farm genetic resources

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Cultivation of Pearl millet in West Africa is still mainly traditional. During the past decades, important human and climatic changes have occurred in Sahelian countries. In Niger, the cultivated area and human population have doubled in 25 years. Moreover isohyete 400 mm has moved southwards by 200 km in the west and by 100 km in the east of the country. The impact of these changes on genetic diversity and adaptation of pearl millet landraces is still unknown. In this study we analyzed samples of pearl millet landraces collected in the same villages in 1976 (*ex situ* collections) and 2003 (on-farm collections) throughout the entire cultivated area of Niger. The diversity assessed with microsatellite loci did not display significant changes between the 1976 and 2003 collections. We tested the change in allele frequency at the flowering locus *PHYC*. The results suggested a positive selection for the earliness allele, which was consistent with the phenological trends towards earliness observed between the 1976 and 2003 collections by comparing them over three crop seasons in a common garden experiment. In the context of a changing climate, the shortening of the life cycle is an adaptive change in landraces that can cope with climatic change by flowering earlier in drier environments. This study shows how genomics-based diversity studies boost the usefulness of *ex situ* collections of crop genetic resources as baselines to monitor the dynamics of evolutionary changes in agroecosystems, and to identify traits and loci involved in adaptation to changing environmental conditions which can then be targeted by varietal improvement programs.

P3.103 - Genes associated with multiple disease resistance identified through a multivariate mixed model association genetic analysis

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Plants are attacked by pathogens representing diverse taxonomic groups, such that genes providing multiple disease resistance (MDR) would likely be under positive selection pressure. We examined the hypothesis that there is a pleiotropic genetic basis for MDR in maize in the context of naturally occurring genetic variation. To do so, we extended structured association genetic mapping to a multivariate statistical framework. We found high positive genetic correlations between resistances to three different diseases in a public panel of diverse maize inbred lines with linkage disequilibrium that decays over very short physical distances (sometimes within genes). The positive correlations suggested that functional allelic variation at specific genes for MDR do exist in plants. We also used the multivariate approach to test multitrait-marker associations and identified glutathione *S*-transferase as a putative MDR gene. The gene's documented general role in cytoprotection, including defense against pathogen infection, provided biological plausibility for the association in terms of shared aspects of pathogenesis for the pathogens studied. Glutathione *S*-transferases and other proteins involved in detoxification are potentially an important component of quantitative variation in disease resistance.