

A LARGE NESTED ASSOCIATION MAPPING (NAM) POPULATION FOR BREEDING AND QTL MAPPING IN ETHIOPIAN DURUM WHEAT

DELL'ACQUA M.*, KIDANE Y.******, ALEM C.*****, NIGIR B.*, MENGISTU D.*****, FADDA C.**, PÈ M.E.*

*) Institute of Life Sciences, Scuola Superiore Sant'Anna, Pisa, 56127 (Italy)

**) Bioversity International, Addis Abeba (Ethiopia)

***) Amhara Agricultural Research Center, Bahir Dar (Ethiopia)

****) Mekelle University, Mekelle (Ethiopia)

QTL mapping, multiparental populations, disease resistance, pre-breeding, landraces

Having thoroughly characterized the phenotypic and molecular uniqueness of Ethiopian durum wheat landraces, we produced a large nested association mapping (NAM) population harnessing their untapped diversity in a structured set of recombinant inbred lines (RIL). The NAM was established choosing 50 landraces providing traits of interest (*e.g.* resistance to pests) and maximizing molecular diversity. Each selected landrace was crossed to a durum wheat line with an international background (Asassa), establishing independent bi-parental families interconnected through the presence of Asassa alleles. The recombinant families underwent single seed descent, yielded altogether 6,280 RILs currently in F₈. The NAM population design provides superior power in quantitative trait loci (QTL) mapping, as increases the number of recombination events and segregating alleles as compared to a classic bi-parental crossing design. Owing to the recurrent presence of Asassa, the 50 NAM families can be either individually analyzed or joined in any combination of interest to provide insights in the molecular mechanisms underlying durum wheat QTL. The Ethiopian NAM aims at a dual objective. The first objective of the population is indeed to provide the durum wheat scientific community with a powerful QTL mapping tool that will side the increasing availability of genomic tools in wheat towards high-throughput candidate genes identification. At the same time, the Ethiopian NAM is the first systematic effort in incorporating the genetic diversity of Ethiopian landraces in a pre-breeding panel closing the gap between local and international material, eventually transferring landrace traits in an improved genetic background. Here we discuss the molecular and phenotypic characterization of twelve NAM families, represented by 100 RILs each. The 1,200 NAM RIL showed elevated molecular variation, and a genetic structure reminiscent of the breeding design followed. The NAM RILs were phenotyped for ten agronomic and five disease traits in two locations in the Ethiopian highlands, for a total of 4,800 plots. Farmers' appreciation of NAM RILs was also recorded in a quantitative manner in the two phenotyping locations, allowing the characterization of the RIL breeding potential to address the needs of local agriculture.