



International Conference

FROM SEED TO PASTA III

A SUSTAINABLE DURUM WHEAT CHAIN
FOR FOOD SECURITY AND HEALTHY LIVES



Bologna - Italy, 19-21 September 2018

P.3.25

GENOMIC SELECTION AND GENOME SCAN TO IDENTIFY VALUABLE DURUM WHEAT GERMLASM FOR HEAT STRESS

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Durum wheat production is globally important, but grain yield has been stagnating in recent decades. In order to ensure that its production maintains the pace with increasing demand, breeding for high grain yield must be supported by molecular-based methods. Genomic estimated breeding values (GEBV) for selection and genome scan were assessed as molecular tools holding maximum potential for durum wheat breeding. Four recombinant inbred line populations bred by inter-mating elite germplasm were sown in yield trials at five sites. All progenies were characterized using “genotyping by sequencing” method. A consensus map was developed, and missing genotypes were imputed using a Hidden Markov model to reach a total of 1987 polymorphic markers. Bayesian ridge regression with models accounting for genotype \times environment interactions, were used to determine the predicted values and their relative accuracy in several combinations. The prediction was conducted testing full-sibs and half-sibs as training population for grain yield and 1000 kernel weight. “Full sibs” gave better accuracies within and across sites. The high level of accuracy achieved suggests that GEBV for selection holds great potential for durum wheat breeding, as long as full-sibs are used as training populations. In order to test the exploitability of genome scan to guide breeding crosses. A separate genome-wide association study was conducted. A total of 288 elite lines were sown in the south of Morocco and at two sites along the Senegal River for two years. These sites are separated by 16° latitude and show a temperature differential of 10°C. Implementing a G \times E model facilitated identifying the most heat tolerant among the tested entries. In addition, 8,173 polymorphic SNPs were inquired, and several associations could be identified between markers and the ability to withstand the heat gradient. Hence, GWAS holds great potential to increase genetic gain in breeding via increased accuracy in determining the crosses to be made, and the deployment of marker-aided breeding for target traits.

ABSTRACT