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MULTI-ENVIRONMENTAL ANALYSIS OF 49 TRIALS CONDUCTED IN THE MEDITERRANEAN BASIN AND MEXICO FOR THE DISSECTION OF THE GENETIC BASIS OF GRAIN YIELD IN *TRITICUM DURUM* DESF.

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The dissection of the genetic basis of grain yield (GY) is one of the major challenges the scientific community is facing to guarantee a sustainable and safe agricultural system. One of the strategy breeders and scientists have adopted to tackle such a challenge is the set up and analysis of multi-environment trials in order to identify the main trait and thus genes involved in the adaptation to different environmental conditions. In this study we present the analysis of 49 trials conducted in just as many pheno-environments. The core vegetal material was the UniBo durum wheat association panel, a fully genetically characterized collection of 189 elite and advanced breeding lines chosen from the main breeding programs and suitable for genome wide association study (GWAS). The experiments were conducted in 13 years mainly in the Mediterranean basin and Mexico. Grain yield and heading/flowering time were collected in all the experiments while yield components (grains/spike, spike/m^2 and TKW) in most of the experiments. Different morpho-physiological traits were collected in different experiments. Data analysis is ongoing. A dendrogram of environments was produced on the base of the Ward's distance of the correlation of GY. GWAS was performed on best linear unbiased estimators calculated on mega-environment representing different branches of the environments dendrogram from k=2 to k=12. The accurate characterization of mega-environments on the base of available climatic and soil properties data, jointly with the study of penetrance of the effect of QTL in such mega-environments will allow us to spot the main genomic regions involved in durum wheat adaptation and GY control.

ABSTRACT