



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.1.09

GENOMIC SCAN IN DURUM WHEAT REVEALS REGIONS CONTROLLING ADAPTATION TO THE HEAT-PRONE CONDITIONS OF THE SENEGAL RIVER

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Wheat is a major food crop in West Africa, but its production is significantly affected by severe heat. Unfortunately, these types of high temperatures are also becoming frequent in other regions where wheat is commonly grown. In an attempt to improve durum wheat tolerance to heat, a collection of 287 elite breeding lines, including several from both ICARDA and CIMMYT, was assessed for response to heat stress in two irrigated sites along the Senegal River: Fanaye, Senegal and Kaedi, Mauritania during 2014-2015, and 2015-2016 winter seasons. The maximum recorded grain yield was 6 t ha⁻¹, which was achieved after just 90 days from sowing to harvesting. Phenological traits (heading, maturity and grain filling period) and yield components (1000-kernel weight, spike density and biomass) had also large phenotypic variation and a significant effect on grain yield performance. This panel was genotyped by 35K Axiom to generate 8,173 polymorphic SNPs. GWAS identified a total of 32 stable QTLs for phenological traits, grain yield and its components across all 14 chromosomes. Seven QTLs were linked to grain yield *per se* on Chromosomes 1A, 3A, 4A, 4B, 6A, 6B and 7A; seventeen QTLs controlling grain yield components and eight QTLs were related to phenological adaptation. Identification of these genomic regions can now be used to design targeted crosses to pyramid heat tolerance quantitative trait loci (QTL), while the SNPs underlying these QTL can be deployed to accelerate selection process facilitated by DNA-aided breeding.

Keys words: GWAS, QTL, SNP, heat tolerance, durum wheat, West Africa.

ABSTRACT