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► To cite this version:

Claude Welcker, Emilie Millet, Santiago Alvarez Prado, Aude Coupel-Ledru, Tsu Wei Chen, et al.. A genome-wide approach combining field and platform phenotyping to investigate plant responses to drought and high temperatures. Interdrought V, Feb 2017, Hyderabad, India. 2017. hal-01607348

HAL Id: hal-01607348

<https://hal.science/hal-01607348>

Submitted on 2 Jun 2020

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Development of drought tolerant wheat cultivars using wide hybridization, genomics and molecular breeding approaches

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More than 50% of the global wheat area is affected by periodic drought while 66% of the irrigated area receives only limited irrigation. The water stress during grain-filling period leads to reduced yield due to accelerated leaf senescence, oxidative damage to photo-assimilation and reduced grain-filling period, carbon assimilation, seed set and development. Some of the mechanisms for drought avoidance are early flowering and rapid grain filling and tolerance due to osmotic adjustment by compatible solutes, anti-oxidative defense, improved root architecture, translocation of reserves, and hormonal regulation. The landraces and related wild species constitute a reservoir of useful variability for breeding for drought tolerance. A spontaneous translocation of 1RS of *Secale cereale* in wheat possesses several QTLs, especially on its terminal region for root architecture, better can-

opy temperature, higher CID and increased stomatal conductance leading to 20% higher grain yield of wheat cultivars under limited water regimes. A region with three candidate genes for lateral root development and higher root and shoot biomass under water stress have also been identified on 7DL.7EL translocation in wheat. Genomic regions of a pre-Green Revolution drought-tolerant variety C306 have been identified using two different mapping populations. Combinations of suitable alleles of vernalization and photoperiod genes can be used to develop wheat cultivars for drought tolerance for different agro-climatic regions. All the above genes and other for drought tolerance on the syntenic genomic regions of other cereals can be explored in wheat germplasm and used for marker assisted breeding for drought tolerance.

A genome-wide approach combining field and platform phenotyping to investigate plant responses to drought and high temperatures

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Natural genetic resources need to be fully explored for designing novel genotypes able to cope with climate change, with special emphasis on identification of traits and allelic sources of adaptation to drought and high temperature. We base our approach on a combination of methods involving genetic analyses in phenotyping platforms and in the field. The rationale is that a given trait or allele confers advantages for yield in specific scenarios of water deficit or high temperature, but most often not in all of these scenarios. We have explored, in a network of field experiments, a series of environmental scenarios for identifying the scenarios where a given allele has positive, negative or no effect on yield. We have then dissected these effects into responses

to specific environmental conditions and their genetic variability. The latter step involves phenotyping in an automated phenotyping platform, allowing one to infer traits that are impossible to measure in the field, such as radiation use efficiency, sensitivity of growth to water deficit or stomatal control. We have applied this strategy to a panel of 250 maize hybrids allowing a multi-scale multi environment whole-genome association study. Resulting pattern of QTL effects expressed as function of environmental variables and traits can be used for assessing the performance of genotypes and the contribution of genomic regions under current and future stress situations, and for accelerating the breeding for drought-prone environments.