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Abstracts

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CIMMYT – the International Maize and Wheat Improvement Center – is the global leader in publicly-funded maize and wheat research and related farming systems, and the organizer of IDVI (Interdrought 2020). Headquartered near Mexico City, CIMMYT works with hundreds of partners throughout the developing world to sustainably increase the productivity of maize and wheat cropping systems, thus improving global food security and reducing poverty. CIMMYT is a member of the CGIAR System and leads the CGIAR Research Programs on Maize and Wheat and the Excellence in Breeding Platform. The Center receives support from national governments, foundations, development banks and other public and private agencies.

SESSION 1: GLOBAL PERSPECTIVE ON WATER, CROPS, DROUGHT

ID 1182 | Global drought-induced crop losses during 1983-2009

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Droughts are a major climate extreme to reduces crop production. Nonetheless, the historical analysis of global crop losses associated with droughts is poorly investigated so far. In the near future, more severe and more frequent droughts are anticipated under climate change, understanding the vulnerability of crop production to droughts is therefore a key research priority to secure global food security. Here, we estimate the global drought-induced production losses of maize, rice, soy, and wheat during 1983-2009 using a relationship among crop yields, a drought index, and annual precipitation. We find that approximately three-fourths of the global harvested areas—454 million hectares: 161 Mha of wheat (75% of the world's harvested area), 124 Mha of maize (82%), 102 Mha of rice (62%) and 67 Mha of soy (91%)—experienced drought-induced yield losses over this period, and the cumulative production losses correspond to 166 billion U.S. dollars—maize is associated with the largest economic loss ($58 B or 35% of the global total loss), followed by wheat ($47 B or 28%), rice ($37 B or 22%), and soy ($24 B or 14%). Our results also shown that crop production systems display increased vulnerability to drought according to decreases in per capita gross domestic production in the countries with extensive semiarid agricultural areas. This article is available (https://journals.ametsoc.org/doi/full/10.1175/JAMC-D-18-0174.1) as open access in Journal of Applied Meteorology and Climatology, American Meteorological Society.

ID 1262 | Is the importance of water-limited environments to global food supply growing?

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The importance of drought, relative to the many other factors influencing global food security, is not static over time. Understanding how this importance varies with time is useful for deciding, for instance, how much to further invest in improving drought tolerance. In this talk I will review the various factors that increase or decrease the frequency and severity of water limitations to crop growth, and discuss the empirical evidence on net changes over time. Genetic progress, especially over the past decade, has resulted in commercial release of several drought tolerant varieties of major crops. In addition, there is clear evidence that rising CO2 has improved the transpiration efficiency of vegetation. These two factors are reducing the risks of drought for local and global production. At the same time, key aspects of climate such as temperature, rainfall, and humidity continue to change because of greenhouse gas emissions, and management has continued to evolve in order to maximize the productivity of new varieties. Overall, my assessment is that the importance of water-limited environments is generally stable or growing, but evidence in many regions is still sparse.

ID 1326 | Future perspectives - global strategies for crop research in water-limited environments

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The challenge of providing the right amount of water at the right time is as old as rainfed agriculture, but our changing climate brings new urgency to the problem. We anticipate more severe periods of water deficit, water excess, and high temperature. Increased risks will require farmers to adapt their production practices for greater system resilience, and this is especially critical for small-scale producers. Individual components of the system can be improved within the known range of biological feasibility through proven approaches such as improved varieties, suitable soil and fertility management, and effective weed control and belowground pest management. At the Bill and Melinda Gates Foundation(BMGF),our primary investment in crop research for water-limited environments is in support of effective, targeted breeding programs. This is mainly through partnerships with the CGIAR and NARS, with supporting grants such as Excellence in Breeding. For varieties targeted to water-limited environments, high-quality phenotyping under drought stress is essential. Advances in phenotyping technology help, but the primary challenge is to conduct excellent field experiments and to weight environments appropriately. The integration of climate models into the process can identify superior genetics for future environments. There is a need for validated phenotyping techniques for temperature response for breeding programs. Investments in technologies such as transgenes for agronomic traits or protective inputs should be viewed as higher risk and longer term; ex-ante estimation of required effect size can guide prioritization. Research over the past decade has not identified single transgenes that generate large step changes in tolerance to water deficit, with the exception of insecticidal compounds in roots. BMGF is not currently investing in projects to develop specific transgenes for drought, though we do have long-term investments in improving photosynthetic systems and biochemistry that may impact WUE and temperature response. Going forward, synthetic biology may offer promise if temperature optima for key enzymes can be extended or cellular structures can be stabilized.

SESSION 2: OPTIMISING DRYLAND CROP PRODUCTION – CROP DESIGN

ID 1058 | Emerging role of plant available silicon in mitigating drought stress in lentil

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Drought stress is one of the major constraints leading 60% in lentil, one of the most important grain legumes grown in the arid and semi-arid regions across the world. This study investigated the impact of silicon (Si) supplementation on the physiological, biochemical and molecular mechanisms of drought-stressed lentil plants along with the evaluation of nutritional potential and sensory traits of the seeds. Si supplementation studies were conducted on the selected drought susceptible and tolerant lentil genotypes under drought stress and non-drought stress conditions. The results from seed germination studies demonstrated the significant role Si in improving seed germination and alleviating drought stress in lentil seedlings by regulating osmolytes, hydrolytic enzymes and antioxidant defense system. In continuation, further experiments conducted in growth chamber and field provided compelling evidence for the protective mode of action of Si against drought stress through the regulation of photosynthetic mechanism and nitro-oxidative homeostasis in lentil genotypes together with the enhanced growth, development and yield even under control condition, thus suggesting its role as a plant nutrient. Gene expression studies were performed to better understand the molecular regulations and to find out the candidate genes behind Si-mediated drought stress tolerance in lentil plants. The results revealed that numerous differentially expressed genes belonging to photosynthetic, osmoprotective and antioxidant metabolism along with the biosynthesis of hormones and hormone signalling pathways are involved in Si-mediated drought stress tolerance in lentil plants. Non-invasive biometrics from consumers demonstrated that Si supplementation to drought-stressed lentil plants did not have any negative effects on sensory characteristics. Overall, the current results suggest the potential use of Si application as sustainable management strategy to mitigate drought stress in lentil plants, together with the possibility of enhancing nutrient potential and sensory qualities of the seeds.

ID 1082 | Silicon application improves drought and heat stress tolerance through physiological and biochemical mechanisms in wheat

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Drought and heat are the primary abiotic stresses causing wheat yield and grain quality reduction in Australia. The present study investigated the impact of pre-sowing silicon (Si) application on two Australian wheat genotypes RAC875 (tolerant) and Kukri (susceptible) under individual and interactive effects of drought and heat stress. Stress-tolerance efficacy of selected genotypes via Si application was tested against four stress treatments: i) drought (D) with 40%FC for 14 days; ii) heat (H) maintained at 36/22°C for 8/12 hours for 3 days; iii) drought-heat combined (DH) at grain-filling stage; iv) control. A set of physiological and biochemical traits, including plant canopy temperature (Tc) and crop water stress index (CWSI) using infrared thermal imaging were studied to ascertain the Si role for stress mitigation. Results showed that Si application significantly increased the photosynthetic rate under (H) treatment for both genotypes compared to their controls. Chlorophyll fluorescence disruption in RAC875 was reduced by Si supplementation under (D), (H) and (DH) conditions. Si application significantly improved RWC (7.74%), lowered Tc (9.91%) and CWSI (19%) for better adaptation to three stress treatments in both genotypes. Under (D), (H) and (DH), Si application significantly reduced accumulation of compatible solutes (proline) (15.47%, 12.55) as compared to their control in both genotypes, respectively.

Overall, a significant increase in grain yield was observed in response to Si application for the tolerant (29.58%, 17.32%, 4.73%) and susceptible (14.72%, 13.47%, 1.77%) genotypes under (D), (H) and (DH), respectively compared to their controls. The results of the present study showed that Si supplementation has the potential to mitigate (D) and (H) (individually or combined) for the genotypes studied. These findings also provide a foundation for future research to investigate Si adaptation mechanisms in wheat at the molecular level.

ID 1170 | Length and intensity of hydric stress affect the ionome before growth reduction in *Triticum aestivum* and *Brassica napus*

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While plant ionome (i.e. contents of macro, micro and beneficial elements), is usually considered to be strongly regulated, it can nevertheless reveal the physiological state of the plant according to Baxter et al. (2008), taking into account the numerous and complex interactions between nutrients. If many studies have been conducted on the physiological effects of water stress, very few of them explicitly consider the consequences for mineral nutrition of plants. Consequently, a controlled condition experiment was conducted with a winter wheat (*Triticum aestivum*) and a winter oilseed rape (*Brassica napus*), using a high throughput phenotyping platform. One month after sowing, plants were grown under non-limiting mineral nutrient supply and they were kept at 80% field capacity (FC) level (control) while watering was then restricted to reach a FC of about 40 or

20%. They were then kept under the same conditions for about 12 consecutive days, thus providing plants facing different water stress intensity and duration. Plants were sampled by separating different tissues (roots, leaves developed before or during the water stress) and analyzed by different techniques for their ionomic contents. Analysis of 13C discrimination of leaves was used as an integrative indicator of water stress intensity and duration. While growth was only reduced under the longest and the most intensive water stress condition, ionomic analysis revealed that uptake of macronutrients (N, P, K, S, Ca) was significantly lowered before any significant decrease of growth, N being the less affected macronutrient. More surprisingly, the uptake of some micronutrients such as Fe, Cu, Mn, Zn and Mo were even more reduced by water shortage. Overall results suggest that plant resilience to water shortage could be improved using relevant mineral fertilization and will be discussed according to potentially involved regulatory mechanism (specific root uptake systems, hormonal balance).

ID 1195 | Legume crop design for higher water use efficiency: a special case or cause for concern?

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Breeding for higher water use efficiency (WUE) in legumes could increase the sustainable intensification of global agriculture under climate change, requiring fewer water and fertiliser inputs. The reduction of stomatal conductance (gs) through lower stomatal density (SD) is a current target to enhance water use efficiency. This approach is being investigated to improve drought tolerance, particularly in cereal crops. Legume crops, and their associated rhizobial nitrogen fixing capacity, are known to be sensitive to water deficit. However, little is known about the inter-relationships and trade-offs between water loss, fixed carbon for rhizobial symbionts, and the capacity for nitrogen fixation and transport. If, by reducing SD in legume crops we enhance WUE, does it come at the cost of nitrogen fixation and yields? As rhizobial symbiosis is central to legume nitrogen use and WUE, an understanding of the coordination between SD, gs, and root traits including nodulation, is essential if we are to develop novel legume crops for sustainable agriculture. Using a range of legume species and by inhibiting stomatal development pathways, we are beginning to dissect these issues, in the hope of aiding legume crop design for a drier world. Here we discuss our current results and their implications for breeding high WUE 'Climate-Ready' legumes for future food security.

ID 1206 | Higher sowing density of sorghum and pearl millet saves water and increases crop productivity in semi-arid tropics regions.

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In the Sahel and India, sorghum and pearl millet are culturally sown under low to very low densities, and the demographic pressure on agricultural land calls for some sustainable intensification. This raises issues with regards to mineral and water resources. The limitation of water resources is a very constraining factor in semi-arid tropical areas, and raises the question whether intensification is possible in this context. Yet, higher sowing densities have shown positive yield responses in specific crop cultivars, opening an opportunity to make these staple foods more competitive against the riskier maize in dry environments. This work was carried out to measure crop productivity, water use, and water use efficiency in crops cultivars earlier shown to have differences in their response to an increased density. Experiments were done in lysimeters and in the field, at two densities, i.e. 11 and 22 plants/m² (LD, HD). Although the HD treatment in lysimeters used more water, grain and stover productivity was higher and so was water use efficiency. HD plantation had a lower VPD within the canopy. A better ability to intercept light has also been demonstrated in field experiments. The light interception measurement in HD treatment not being total at flowering suggested density could be further increased. In the field the productivity in term of total biomass was also better for HD treatment. Moreover, a higher water status of the soil after harvesting in HD condition also suggested a less water costly cultivation practice. These results should be linked with a lower evaporative demand and a lower exposure of soil to evaporation (Pilloni 2018, master thesis, unpublished). Further works will have to focus on the architectural variations that can possibly explain the different responses.

ID 1241 | Designing sorghum cultivars to fit a water-constrained context and optimize economic return from a sorghum food/feed value-chain

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Post-rainy sorghum is important for 5 M households in South India, where grain and stover residues play an equally important role in this value chain. Post-rainy sorghum production is constrained by water, a limitation that varies over time and space. The project aimed at genetic solutions to this limitation, informed by crop simulation to make better decisions, sound agronomic considerations, and knowledge of end-user demand for grain/residue quality/quantity. Using crop simulation (APSIM), five main stress scenarios were identified and three major sub-regions delimited the target population of environments (TPE). Proof-of-concept stay-green introgressions displayed water-saving traits, i.e. transpiration limitation under high VPD, higher transpiration efficiency (TE), smaller canopy size at anthesis, and also higher capacity to extract water from the soil profile. Stay-green introgression also influenced crop residue quality traits favorably. Stay-green QTLs Stg3A and Stg3B were critical, but their effects were all dependent on the genotypic background. Modelling allowed to predict where underlying functions of staygreen could have the most beneficial effects across the TPE. An ex-ante analysis showed the benefit of the stay-green technology. Using robust modelling outputs rather than subjective informant responses, a revised ex-ante analysis showed a higher benefit from developing two different ideotypes fitted to district-specific end-user demand, rather than a one-fits-all technology. More efforts are now needed to streamline the assessment of quality traits along the breeding pipeline, to operationalize the technologies and approaches developed during the project in breeding programs, and to disseminate seeds of released products of this open-pollinated crop in varied environmental/social contexts.

ID 1263 | Effect of water stress on seed maize production

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The seed maize crops grown in France are almost entirely located in irrigated areas. Irrigation management rules are well described and mastered in the different production sectors. Nevertheless, the intrinsic sensitivity of parental lines to water stress is an important factor to be taken into account in order to obtain optimal yield and the required quality.

A field trial was therefore carry out for three years, aimed at highlighting and explaining the effects of characterized water stress on the physiology (root system, LAI, establishment of reproductive organs and pollination), yield, yield components and quality of seed maize (germination capacity).

By affecting LAI of the male and/or female parents, early stresses can induce disturbances in the pollination period. Similarly, by limiting for females the number of eggs (via the rings number) and the capacity of the eggs to be pollinated, they directly affect the grain number potential. These points show that the starting irrigation is very important in seed maize production. In the following phase, the most sensitive one, the water stress affects pollen emission: reduction in tassel size and pollen potential, and significant reduction in pollen viability. That's why during this phase irrigation must be well managed. Late stresses (post flowering at 50% grain moisture content) were less pronounced in our trial conditions, but nevertheless caused an increase in the number of aborted grains, accelerated foliar senescence, and reduction in grain weight. On the other hand, no effect of water stress has been shown on the germination capacity.

ID 1278 | Comparison of traits relevant to drought resistance of NERICA, Asian rice and African rice and differences in effects of potash and phosphorus fertilizer

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Recently NERICA was developed by a crossing of African rice and Asian rice in West Africa, and is considered to be drought resistant, but drought resistance of NERICA is not clarified enough. In this research, NERICA (three cultivars and three lines), Asian rice (three cultivars and sativa parent of NERICA) and African rice (glaberrima parent of NERICA) were cultivated in the field under drought and traits relevant to drought resistance, stomatal conductance by porometer, soil water content by TDR method, SPAD values by SPAD meter and leaf thickness by micrometer, were measured and compared with dry matter production and yield. Effects of potash and phosphorus fertilizer were also compared among two NERICAs. Glaberrima parent of NERICA showed highest top dry weight but yield was low. One NERICA line, one NERICA cultivar and one Asian rice showed higher top dry weight and yield. Those NERICAs showed high leaf thickness and SPAD values and NERICA line showed high top dry weight maintained high stomatal conductance. In one NERICA line potash increased top dry weight and yield. Cultivar and line differences in yield (ear weight) were significantly correlated with those in stomatal conductance (r=0.537*) and those in leaf thickness (r=0.571*, for NERICA r=0.665*). Cultivar and line differences in stomatal conductance were significantly correlated with those in leaf thickness (r=0.765**, for NERICA r=0.751*). Cultivar and line differences in leaf thickness were significantly correlated with SPAD value (r=0.844**). Importance of maintaining high stomatal conductance and high leaf thickness, and effects of potash fertilizer under drought condition was clarified.

ID 1315 | Comparative multi-crop physiology: relationships between evapotranspiration and yield across multiple crop species

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The optimization of dryland crop production involves the identification of management practices to maximize productivity and water use. Crop species selection is the most fundamental management decision in this regard. Here we present a series of experiments in managed-stress environments designed to evaluate the relationship between evapotranspiration and yield across multiple crop species with special focus on elite materials. The crop species evaluated are: maize, sunflower, sorghum, canola soybean and cotton. Two different genotypes were evaluated for each crop allowing to test for differential S(species)xGxE yield response patterns to different water availability environments. Crops were evaluated in two locations under three levels of water availability. The level of water availability was defined by reapplying 100% (control), 75%, 50%, or 25% (severe drought) of daily evapotranspired water. Numerical and physiological yield components were evaluated across this set of species and genotypes to dissect the species-specific constraints to high productivity in water limited environments. This information is critical for designing cropping systems that optimize water use. Detailed physiological data will also generate useful information for the development of species-agnostic crop simulation models.

SESSION 3: PLANT PRODUCTIVITY UNDER DROUGHT: WATER CAPTURE, TRANSPIRATION, AND TRANSPIRATION EFFICIENCY

ID 1038 | Staying green: Changing how crops use water

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Designer crops for a hotter and drier world are needed to combat climate change. This will involve developing plants with enough plasticity in traits that modulate water supply and demand, such that a range of ideotypes for different environments can be designed. Crop plants need water during grain filling to thrive under drought, so one of the key challenges is to increase access to water at this stage. Adapted genotypes have soil moisture available at that time, resulting in a stay-green phenotype which arises when the supply of water exceeds the demand during grain-filling. We demonstrate how sorghum lines with the stay-green drought adaptation trait can reduce water demand by modifying canopy development and increase water supply by modulating root architecture. Both canopy size and root architecture are partly controlled by members of the PIN family of auxin efflux carriers. The key stay-green region under selection in the Australian sorghum breeding program is Stg3b and SbPIN1 is a strong candidate within this region. SbPIN2 and SbPIN4 are also key candidates in the Stg2 and Stg1 QTLs, respectively. We demonstrated that these PIN genes do regulate expression of stay-green by developing the first sorghums in Australia transformed with key PIN genes in Tx430. Canopy and root traits also impacted the supply/demand balance in wheat and barley under drought. The impact of root traits on grain yield was examined in barley and sorghum trials. These outcomes should help crop improvement programs to develop better adapted genotypes for dry environments.

ID 1042 | Many paths to one goal: A diversity of rice root anatomical responses to drought

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Rice yields are severely affected by drought, and drought-resistant lines are necessary to improve farmer yields. Plants with efficient root systems are a good target for drought-resistance because roots are the main water uptake organ of plants, display wide variation in traits and trait plasticity, and are under-studied in crop improvement efforts. Root anatomical traits are of interest because they affect the plant's ability to access and conduct water to the shoot. Subsets of the Rice Diversity Panel and an IR64 x Azucena RIL set were grown under vegetative-stage drought stress in three locations (greenhouse, rainout shelters) to determine relationships between root anatomy and drought tolerance. The severity of drought stress differed among experiments and impacted the drought responses. Mean biomass reduction ranged from 35-71% in four experiments. Tiller and crown root number reduction was highly correlated with biomass reduction, with larger plants having greater reductions. Under drought treatments with 48% or greater mean biomass reduction, nodal root cross-section, stele, cortex, and mean metaxylem vessel areas were reduced in most individuals. Mean metaxylem area decreased in the greenhouse but increased in rain-out shelters in response to drought. In one location under severe stress, metaxylem vessel number reduction correlated with biomass reduction. Aerenchyma area (%) and root cross-sectional area explained variation in biomass under drought in at least two locations, while stele area and metaxylem vessel area and number were significant in other single locations. K-medoids clustering determined anatomical trait combinations that resulted in high biomass under drought. In most clusters, anatomical traits except metaxylem vessel number were correlated with root cross-sectional area. Some high-performing clusters exhibited few, large metaxylem, while others had numerous, small metaxylem. This data indicates that genotypes exhibit various successful strategies to manage drought stress.

ID 1118 | Transcriptomic Approaches to Uncover the Molecular Mechanisms of Maize Nodal Root Growth during Drought in the Field

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Drought is the most important factor limiting crop production across the globe. Therefore, understanding how plants adapt and survive drought conditions is critical for improving food production with lower water input. One such survival mechanism is the maintenance of root elongation, even in very dry environments. In maize, the nodal root system comprises the majority of the root length of the mature plant, and is therefore critical for sustaining water uptake. The shoot-borne nodal roots have the ability to maintain growth at low water potentials that inhibit growth of other plant organs. Despite the vital nature of this

response to drought survival, the physiological and molecular mechanisms underlying this ability are poorly understood and are the focus of this work. To understand this phenomenon, we are utilizing transcriptomics to explore changes of the maize nodal root growth zone under irrigated and water-limited conditions in two inbred lines, FR697 and B73. These lines have contrasting abilities to maintain nodal root growth under water stress. We are characterizing these changes in both controlled-environment growth chamber conditions and in the field, utilizing a rainout shelter for precise control of drought imposition. This approach allows determination of the molecular and physiological changes during "real world" drought conditions, and to directly compare these changes with those from chamber-grown samples. We have identified potential gene candidates involved in nodal root growth maintenance from data collected during two field seasons and replicated lab experiments. Making use of these datasets, along with additional proteomic and metabolic datasets, we narrowed the gene candidate pool considerably, allowing us to focus our follow up efforts on robust candidates. These candidates are being examined in several genetic backgrounds and in analyses of different whorls of nodal roots to determine whether they are broadly involved in maize nodal root growth regulation during drought.

ID 1129 | Combined studies of advanced high-throughput phenotyping and association mapping reveal the genetic architecture of maize drought tolerance

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Drought is harmful for plant growth and reduces crop yields. Understanding how crops respond to drought will be beneficial for breeding of drought tolerant cultivars. Using a high-throughput phenotyping facility, we detected 2069 image-featured traits (if-traits) for 368 maize inbred lines in drought experiments, of which 67 were from RGB and 2002 were from hyperspectral imaging or CT scanning. Most of these if-traits could be separated between well-watered and drought-stressed conditions based on principle components (PCs). Large variations of these if-traits were detected in response to drought in the populations, suggesting the bio-indicator potential of these traits in drought tolerance. We performed GWAS to these if-traits and identified 3,748 associated genes (or 3,494 QTLs), of which 1612 (~43%) were colocalized with reported genes (based on reported QTLs). Particularly, several well-known genes that were cloned based on traditional traits (survival rates after drought), such as ZmVPP1, ZmNAC111, ZmPP2CA10 and ZmDREB2.7, were identified in our experiments, indicating the reliability of our analyses. The fact that 2136 (~57%) were newly detected genes indicates the advantages of these if-traits over traditional traits in detecting genetic loci in control of maize drought tolerance. As a proof of concept, the roles of two previously unidentified genes PG2 and PPK, encoding phosphoglucomutase 2 and 1-phosphatidylinositol-4-phosphate 5-kinase, respectively, were validated via genetic and molecular studies based on their loss-of-function mutants. We further generated regulatory networks of these genes based on transcriptomic assays of 200 inbred lines (selected from the same 368 inbred lines). A number of hub pathways and key genes were detected. Our study provides a novel approach for genetic dissection and rich genetic resources for maize drought-tolerance breeding.

ID 1137 | Designer roots for future crops

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In 2018 and 2019, farmers in Australia and Europe experienced major yield losses due to severe and widespread drought and heat stress. Improving the root systems of future cultivars could enhance the ability of crops to capture water from deep soil layers, thereby minimizing or avoiding stress. Thus, to enable targeted genetic manipulation of modern crop varieties, understanding the value of different root systems in different environment types, as well as the discovery of key loci underpinning root development, is a high priority for research and pre-breeding programs worldwide. In this seminar, we highlight our recent breakthroughs in understanding the genetic controls of root system architecture and demonstrate the value of specific root architectures in water-limited environments in Australia, drawing on casing studies in bread wheat, durum wheat and barley. We report new breeding approaches that enable efficient modification of root systems by integrating the rapid generation advance technology ‘speed breeding’, high-throughput phenotyping for root proxy traits, and selection for target QTL. We also discuss opportunities to adopt an integrated predictive breeding framework that incorporates root trait information, including field-based canopy proxies for root system architecture. The new approach could be broadly applied across crops, and for the first time, opens the door for incorporating below-ground trait information into the breeding process, thus has potential to increase genetic gain for yield in water-limited environments.

ID 1138 | Emerging effects of root hairs and soil properties on transpiration and leaf water potential under soil drying and increasing VPD

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Understanding the mechanisms that control water use of plants exposed to soil drying and increasing vapour pressure deficit (VPD) has important implications for crop growth in semi-arid regions with low-input agriculture. In particular, the effect of belowground processes on transpiration and stomatal regulation remains controversial. Objective of this study was to understand the role of soil properties and root hairs (as an example of rhizosphere traits) on transpiration and leaf water potential. We hypothesize that root hairs facilitate the water extraction from drying soils, particularly at high VPD, and that this impacts the relation between transpiration rate and leaf water potential. We further hypothesize that stomatal regulation attenuates the drop in leaf water potential when the soil water flow cannot match the transpiration demand and thus emphasizes the importance of root hairs on transpiration rates during soil drying. We compared maize (Zea mays L.) with (wild-type) and without (mutant) root hairs in three different soils (Alfisol, Vertisol and Sandy Soil). Transpiration and leaf water potential were monitored at varying VPD and soil moistures during soil drying. The hairless mutant showed a higher transpiration in wet soils but declined transpiration at greater water contents as compared to the wild-type. Under well-watered conditions, both genotypes had the highest transpiration rates in Vertisol. In Vertisol, both genotypes closed their stomata at relatively higher water content levels. The relation between transpiration and soil moisture strongly varied between soils. No obvious differences between the genotypes were visible in the relationship between leaf water potential and transpiration. This is explained by the prompt closure of stomata. This study provides experimental evidence of the strong link between stomatal regulation and soil-root hydraulic properties.

ID 1190 | Genetic Dissection of Root Architecture in Ethiopian Sorghum (*S. bicolor*, Moench) Germplasm

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The root system architecture (RSA) of plants influences adaptation to water limited conditions and determines the capacity of plants to access soil water. We phenotyped about 2000 sorghum landraces collected from all sorghum growing regions of Ethiopia and varieties/lines using a high throughput root phenotyping platform which consisted of purpose-built root chambers (40 cm high, 35 cm wide and 3 mm thick). A set of 940 selected landraces, representing both narrow and wide nodal angle genotypes were evaluated at two moisture stress sites to evaluate the relationship between root angle and grain yield of genotypes under moisture stress conditions. The same set of genotypes (940) were genotyped using genotyping by sequencing (GBS) to map genomic regions associated with root traits. Significant genetic variation was observed for root number, root angle, root length and root dry weight. Among these traits, wide genetic variation was recorded in nodal root angle among the genotypes, ranging from 16.6° to 26.4°, with high reputability of 78.9%. Root angle was negatively associated with grain yield under moisture stress conditions, indicating narrow root angle genotypes performing better than those genotypes having wide root angle. A total of 22 unique genomic regions associated with root angle, root number, root length and root dry weight were identified with a significant value of p = 8.09x-5 threshold on all chromosomes except chromosome SBI-10. These significant SNP markers were co-localized with 192 previously identified QTLs for drought tolerance traits. Among these, quantitative trait loci for root angle (QERA8.7) and root length (QERL5.4) were co-localized with previously identified QTLs (QRTAN8.1 & QRTLN5.3) on chromosome SBI-8 and SBI-5, respectively. The results of this study suggest that root angle could be used for selection of genotypes for moisture stress tolerance both through conventional and marker-assisted approaches.

ID 1215 | Effect of film antitranspirant application on endogenous ABA concentration and yield components in spring wheat

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Drought stress reduces crop yields in part by causing reproductive sterility, especially of pollen grains. Application of the film antitranspirant, di-1-p-menthene, during reproductive-stage drought has been shown to ameliorate yield loss in wheat but the physiological processes involved are not understood. Using rain shelters to simulate terminal drought, we studied the possibility of a reduced endogenous ABA concentration as the likely mechanism. During two consecutive years, di-1-p-menthene was sprayed on spring wheat plants (cv, Chilham) at seven growth stages (GS33, GS45, GS 51, in 2018 and GS31, GS37, GS43, GS51 and GS65, in 2019) in a randomised block design. Results showed that drought stress reduced stomatal conductance, transpiration and yield components but increased endogenous leaf and spike ABA. The effect of di-1-p-menthene differed depending on growth stage at application. With optimum timing, di-1-p-menthene application reduced the ABA concentration in leaves by 33% and 40% and improved grain yield by 15% and 29% in 2018 and 2019 respectively, averaged over all

times. Grain yield improvement was associated with increased grain number per m2 and increased fertile spike density but not pollen viability. The mechanism of drought stress amelioration with di-1-p-menthene may be related to reduced endogenous ABA, but further work is needed to understand the consequences for yield components.

ID 1216 | Water stress effects on maize and soybean root growth and distribution in the US Corn Belt

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Quantitative measurements of root traits can improve our understanding of the inherent interactions between soils, roots, crops, and weather. Root data is very much needed to improve crop models capacity in simulating root traits. We collected and analyzed 274 deep soil cores (0 to 210 cm depth) across multiple environments in Iowa, which covered 10 soil types, four years weather data (2016–2019), different management practices (rainfed, irrigated, nitrogen fertilizers) and genotypes. Across the soil profile and for every 30 cm increments, we measured root mass, length, carbon and nitrogen contents, and estimated: root length density, specific root length, root to shoot ratio (R:S). These traits were measured over time in 20% of the trails while in the rest of the trails once; at mid-grain filling period. Results indicated a substantial site-year-management-sampling position influence on root traits. Maize root mass ranged from 1.2 to 2.8 Mg ha-1 and soybean from 0.8 to 1.9 Mg ha-1. About 75% of the total root mass was allocated in the top 60 cm soil profile, and its distribution was controlled primarily by soil moisture (water table depth). Maize R:S ratio ranged from 0.04 to 0.13 and soybean from 0.09 to 0.26. In general, our estimates are at the lower end of what is reported in the literature. Drought increased the R:S ratio mostly by decreasing the above-ground biomass. We concluded that water stress (either drought or excess water) first affects the root front velocity and then the dry matter allocation to roots. Prediction of root phenotypes was not possible using a single factor analysis (e.g. soil types or crop biomass). Prediction using simulation modeling (APSIM) is in process.

ID 1217 | Development of an ideal root system architecture for rice adapted to drought conditions

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Global climatic changes have increased the incidence and intensity of drought and the extent of drought-prone regions in the last decade. Adequate root system architecture (RSA) is imperative for the successful production of crops in water-deficient conditions because the root is the primary water uptake organ in most crop plants. Genetic improvement of the RSA should be considered as an option to enhance production in crops under drought stress. We previously demonstrated that altering DRO1, a quantitative trait locus (QTL) for root growth angle, improves drought avoidance in rice. We recently isolated another QTL for root growth angle, qSOR1. We created four different RSA types in rice through QTL pyramiding of functional and non-functional alleles in the DRO1 and qSOR1 genes, indicating that a breeding line with the desired RSA could be developed without phenotypic selection in the field. To demonstrate this concept in the breeding process, we introgressed several root-related QTLs from ‘Kinandang Patong,’ an upland rice with deep RSA, into Colombian lowland varieties with shallow RSA. Preliminary results indicated that several lines selected only by DNA markers showed a deeper RSA than those of the original varieties. The application of root-related QTLs

will facilitate the development of a rice cultivar with wide adaptability in drought-prone regions. However, identification of the root traits critical for crop production under drought stress remains a challenge, primarily because the underground location of the roots inhibits visual analysis. To visualize the root system, we launched a non-destructive 3D root phenotyping platform using X-ray CT imaging. Using this platform, development of a design for an ideal RSA that is robust to drought stress is ongoing.

ID 1222 | Targeting primary root growth to improve drought tolerance in pearl millet [*Pennisetum glaucum* (L) R. Br.]

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In West Africa, global change characterized by extreme temperatures and dry spells reduces cereal yield endangering food security. Selection of varieties with improved drought tolerance and enhanced yield is therefore needed given the high prevalence of undernourishment in this region.

Pearl millet is one of the most important dietary staples in arid and semi-arid regions of WA. As it is well adapted to dry climates, pearl millet is expected to have an increasing importance in the adaptation of agriculture to future climates. However, it lags behind other major cereal crops in its genetic development and its average yields remain low.

Root traits represent potential new targets for breeding new varieties more tolerant to drought stress. Pearl millet root growth is characterized by a fast growth of the primary root after germination. Phenotyping of this trait in a panel of pearl millet inbred lines showed large natural diversity and high heritability. Field trials were conducted to investigate the importance of this root trait for crop establishment and drought stress tolerance after germination. Our recent results reveal a potential adaptive role for primary root growth in pearl millet adaptation to drought stress during early developmental stages. The mechanisms involved are being analysed using a combination of physiology, association genetics, QTL analyses in bi-parental population, and gene expression approaches.

ID 1223 | Genome wide-identification of aquaporins in pearl millet [*Pennisetum glaucum* (L) R. Br.]

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Water absorption from soil to roots and its translocation to different plant organs are of major importance for many physiological processes. Aquaporins (AQP) are water channels that facilitate water flow in and out of cells and critical contributors to water transport. AQP are involved in adjusting plant water balance under different abiotic stresses. Under drought stress, modulation of root hydraulic conductivity (Lpr) through aquaporin function contribute to maintain/adjust transpiration and shoot growth.

Pearl millet is the sixth most important cereal grain but it is a key cereal for food security in arid and semi-arid regions. Although it is well adapted to dry climates, its yield remains low and is drastically affected by drought stress. Recent studies have linked AQP expression to transpiration response under atmospheric drought caused by high pressure deficit in pearl millet (Reddy et al., 2017).

We conducted a genome wide identification of AQP isoforms in this crop. Thirty-two AQP isoforms were identified and annotated. Expression profile of the different isoforms was studied in different organs and a pharmacological approach was used to estimate the contribution of AQP to root Lpr in two pearl millet inbred lines contrasting for transpiration efficiency. Overall, our results reveal diversity in AQP isoforms expression and contribution to Lpr suggesting diverse strategies for AQP regulation in pearl millet.

ID 1225 | Understanding mitigation of drought damage to rapeseed (Brassica napus L.) from sprays of film antitranspirants at different dose rates

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Drought has become the most devastating natural hazard that influences crop growth negatively, particularly in arid and semi-arid regions around the world. A huge loss of crop production in rapeseed (Brassica napus L.) occurs in many regions as a result of water stress. It is reported that film antitranspirants (ATs) have been applied particularly on some ornamental plants. ATs can create a waterproof layer to block the stomata mechanically, and thus reduce water loss through transpiration. There is also increasing evidence that ATs enhance the yield of crops subject to drought when sprayed at the critical stage compared to unsprayed controls. However, the physiological mechanism by which ATs mitigate the drought damage on the yield and yield component of rapeseed is not clear. Therefore, two pot experiments were carried out to investigate the effects of ATs at different dose rates on rapeseed under drought conditions at the flowering stage. Gas exchange including stomatal conductance and CO_2 assimilation rate, as well as yield-related measurements, were taken both on droughted and well-watered plants. The results will be displayed on the poster in detail. Our results show that drought during the flowering stage can lead to a large yield loss of rapeseed. Application of ATs may be considered as a novel crop-management method to help rapeseed under drought reduce water loss and thereby ameliorating plant water stress.

ID 1233 | Plant hydraulic mechanisms underlie greater productivity under drought in grain crops

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Although there has been great interest in plant mechanisms related to crop production under drought, hydraulic mechanisms have rarely been explored. In maize, we find genotypes with the highest yield under drought in the field have the highest maximum hydraulic conductance, and highest maximum diurnal stomatal conductance. These genotypes have large diameter xylem vessels to facilitate this conductance. Interestingly, maize can lose >50% of its conductive capacity each day, resulting from xylem embolization, even under well-watered conditions. However, high yielding genotypes under drought also have greater root flow via root pressure following re-watering. Immediately after stems are cut, there is no root flow from dry plants but after plants are re-watered and given an hour for recovery, there is substantial flow. Measured root pressures in maize can exceed 100 kPa,

which would allow the lifting of water to a height of approximately 10 m in a non-transpiring plant. With extremely low nighttime transpiration and plant heights of approximately 2 m in maize, root pressures measured should effectively pressurize the entire vascular system of the plants and dissolve emboli. In sorghum, maximum root flow after re-watering was also higher in droughted plants than well-watered plants, suggesting an actively-regulated mechanism. We suggest hydraulic mechanisms may be key for maintaining growth of developing grain through reversing stem xylem cavitation, refilling potentially collapsed leaf xylem, and allowing for the resumption of carbon fixation.

ID 1236 | Representing systemic and novel approach to assess drought adaptation in region specific peanut and to accelerate crop improvement program

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Peanut is one of the important legume crops grown in semi-arid tropics of Asia and Africa under rainfed conditions where water stress due to insufficient and/or erratic distribution of rain is one of the major production constraints. Babile and Fedis districts are leading peanut producing areas in Ethiopia. A study was conducted to identity canopy growth traits using high-throughput phenotyping platform (LeasyScan) that can be used in peanut breeding to make selection decisions for adaptation to water-deficit stress. The study on peanut genotypes in field conditions in well-watered (WW) and water-stress (WS) conditions to estimate the yield potential under WW and yield penalty under WS, and canopy growth traits, were studied to understand and identify the canopy growth traits contributing to WS adaptation in peanut that can be of potential use in peanut breeding to make selection decisions using high-throughput phenotyping platfrom. Further the transpiration efficiency and water-use efficiency of peanut genotypes under water-deficit stress was assessed at ICRISAT-Patancheru in Lysimeters. The duration, time and extent of water-stress at Babile and Fedis districts was estimated by using last 31 years of graded weather data of target environments of Ethiopia. Based on this the planting window at Patancheru was decided to mimic the target environments in Ethiopia.

ID 1243 | A Rice RING Type E3 Ubiquitin ligase Oszf1 Enhances The Water Retention Capacity Under Drought Through Ubiquitination And Degradation of OsPIP2

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Water is a key resource for plant growth and survival. The transcellular water movement is facilitated by aquaporins (AQPs) to rapidly and reversibly modify water permeability. This is done by regulating the abundance and activity of aquaporins. The abundance of aquaporins is influenced by the aquaporins synthesis, redistribute, and degradation. The latter contains proteasomal degradation and autophagic degradation. Here we demonstrate a RING zinc finger protein 1 gene, Oszf1, possesses the E3 ligase activity and can modulate the abundance of OsPIP2 to remarkably enhances the drought resistance by reducing the water loss in rice (Oryza sativa). Oszf1 is a candidate gene from a rice drought QTL interval on the long arm of chromosome 4. The expression of Oszf1 was induced by drought. Oszf1 can ubiquitinate OsPIP2 and lead it to be degraded. The

content of OsPIP2 protein was decreased in Oszf1 overexpression (OE) plants. MG132 can inhibit the degradation of OsPIP2. The Oszf1 OE plants, with higher leaf related water content (LRWC) and lower leaf water loss rate (LWLR), exhibit enhanced drought resistance. Whereas, the RNAi plants of Oszf1, with increased LWLR, were more sensitive to drought. These data illustrated that Oszf1 positively regulates the rice drought resistance through promoting the degradation of OsPIP2 protein to enhance water retention capacity.

ID 1247 | Genetic variation in screening upper mid-south soybean lines for a drought tolerant trait: The limited transpiration rate (TRlim)

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Drought conditions in the United States are estimated to result in average annual losses in the range of $10 to $14 billion. Identification and integration of genetic traits enabling increased water conservation in plants could provide increased water availability and plant performance during drought. In the upper mid-south of the U.S., soybean is most often grown under rainfed conditions. Therefore, years in which drought and high evaporative demand occur can result in decreased final seed yield. The objective of this study was to develop a high-throughput protocol for phenotyping for drought-tolerance in soybean in the upper mid-south. An aquaporin inhibitor (i.e., silver nitrate) was used to determine the expression of the limited transpiration (TRlim) trait among soybean lines under high vapor pressure deficit (VPD). The advantage of the TRlim trait is that it allows plant water conservation to increase available soil water during late-season drought. A soybean population of 122 recombinant inbred lines (RIL) derived from crossing of Jackson× KS4895 was tested by applying 200 µM silver nitrate to de-rooted soybean shoots under high VPD (>2.5 kPa). Among 122 RILs, half of the population showed higher sensitivity to silver ion than KS4895 (a parent line). However, several lines showed no or limited changes in water loss with the silver treatment. It appears that the silver screening for RILs population DTR offers the initial capacity for discrimination among the studied soybean lines. Therefore, after initial silver ion screening 26 lines were selected for direct measurement of transpiration rate under varying levels of VPD. Among lines with the low DTR rates, 71% expressed the TRlim, with VPD BP ranging from 1.7 to 2.9 kPa, under high VPD. The soybean RILs expressing low DTR should be studied further under field conditions for evaluation as potential drought tolerant parents in a breeding effort.

ID 1248 | How can we use computational models to extend our understanding of water relations in plants

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In the recent years, many computational tools, such as image analysis, data management, process-based simulation and upscaling tools, were developed to help quantify and understand water flow in the soil-root system, at multiple scales (tissue, organ, plant and population). Several of these tools work together or, at least, are compatible. However, for the un-informed researcher, they might seem disconnected, forming a unclear and disorganised succession of tools. In this presentation, we present how different pieces of work can be further developed by connecting them to analyse soil-root-water relations in a comprehensive and structured network. This explicit network of soil-root computational tools informs the reader about existing tools and help them understand how their data (past and future) might fit within the network. We also demonstrate the novel possibilities of scale-consistent parameterizations made possible by the network with a set of case studies from the literature. Finally, we discuss existing gaps in the network and how we can move forward to fill them.

ID 1255 | Multiple integrated root phenotypes are associated with enhanced drought tolerance in maize

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Drought is a primary limitation for crop productivity worldwide. Multiple root phenes have been identified conferring enhanced performance under water deficit stress. Here, we test the hypothesis that multiple distinct integrated root phenotypes are co-optimizing solutions to crop fitness under drought. Using shovelomics and laser ablation tomography, we phenotyped the root anatomy and architecture of 400 mature maize genotypes under well-watered and water-stressed conditions in the field. We found substantial variation in all 23 root architectural and anatomical phenes measured. A phenotypic bulked segregant analysis revealed that bulks representing the best and worst performers under water stress in the field displayed distinct integrated root phenotypes. In contrast to the bulk of poor performers, the integrated root phenotype of the best-performing bulk under drought consisted of greater cortical aerenchyma formation, more numerous and narrower metaxylem vessels, and thicker nodal roots. Partition against medians (PAM) clustering revealed several clusters of unique root phenotypes related to plant performance under water stress. Clusters associated with improved drought tolerance consisted of phene states that enabled greater soil exploration by reallocating internal resources to greater root construction (increased aerenchyma content, larger cortical cells, fewer cortical cell files), restricted uptake of water to conserve soil moisture (reduced hydraulic conductance, narrow metaxylem vessels), and greater penetrability of hardening, drying soils (thick roots with a larger proportion of stele, smaller distal cortical cells). We propose that integrated root phenotypes associated with improved performance under water stress merit consideration as breeding ideotypes.

ID 1279 | Soil-root hydraulic constraints on transpiration and stomatal regulation in crops

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Although 80 per cent of terrestrial evapotranspiration passes through stomata and transpiration represent by far the largest water flux globally, the fundamental question as to what triggers stomatal closure during drought remains controversial. Droughts is projected to increase in many regions as a results of climate change, yet current models are mainly empirical and hardly capture plant drought responses. It has been shown that closing stomata at high VPD, and hence conserving water early in the season, confer drought tolerance in specific drought scenarios. Thus, we urgently need to improve our understanding of stomatal response to water deficits in soil and atmosphere.

We propose that stomata close when the water potential at the root-soil interface drops and the soil-plant hydraulic conductance starts to decrease. We used a root pressure chamber to measure the relationship between leaf water potential (ψleaf) and transpiration (E) during soil drying in cereals (maize, pearl millet and barley) and herbaceous species (tomato). In wet soils, the relation between ψleaf and E is linear. In dry soils, the relation becomes nonlinear, with ψleaf rapidly and nonlinearly decreasing for small increases in E. We provide experimental evidence that stomata close when dψleaf /dE starts to decrease. Furthermore, we propose possible mechanisms that allow plants to respond to changes in soil-plant hydraulic conductance and to remain in the linear part of the E(ψleaf) relation.

In summary, we show that soil-plant hydraulics constrains transpiration and we provide evidences that stomatal closure and transpiration are primarily triggered by below-ground hydraulic traits, especially those at the soil-root interface. Our results and concepts highlight the coordination between below- and aboveground plant hydraulic conductances and allow to quantify the effect of root traits on the water use economy of crops during drought.

ID 1281 | Root water uptake profiles in response to increasing soil water gradients

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Plant water use is for the most part demand driven but becomes source limited when soils become exceedingly dry. It is often assumed that the soil water potential is the limiting factor in root water uptake (RWU). However, soil water conductivity may also be a limiting factor as this variable reduces more strongly with diminishing soil water contend than does the increase in soil water potential (in absolute terms). Which of the two is more relevant can be addressed by modulating plant transpiration with light intensity. The light dependent RWU profile should not respond to a change of the soil water potential gradient, but is should depend on soil water conductivity heterogeneities when this parameter becomes limiting.

Recently we developed a very precise soil water sensor that can measure changes of local soil water content with a precision of 3.10^(-5) cm^3/cm^3 with 1cm vertical resolution while measuring along a soil column (depth 45cm, diameter 8cm). In combination with a fully controllable LED panel, light induced changes of the transpiration rate can be shown to affect RWU profiles in a distinctive pattern which is not only dependent on root length distribution, but in drying soil also changes with soil water content profiles. Our results clearly illustrate that soil water conductivity is relevant for RWU, without denying the importance of soil water potential.

ID 1295 | Unraveling dynamic belowground phenotypes of cereal crops by focusing on fine root development and function

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Taking up water and nutrients and maintaining contact with the soil microbiota makes the root system irreplaceable for plant growth under suboptimal conditions. We focus on the finer root and hair components of root systems and their ability to flexibly and rapidly respond to soil resources and assimilate supply. Fine cereal lateral roots (branching off other roots; anatomical type-depended specificity; ca. 0.05 to 0.5 mm diameter) and root hairs (epidermis-derived unicellular extensions; ca. 0.02 mm diameter) make up the vast majority of root system surface area, although they are barely visible by eye. Critically, we are discovering wide genetic and environmental responses of cereal fine roots to resource supply and soil conditions. For example, rice genotypes grown in phosphorus-limited solution produced more and longer root hairs as expected. However, in a phosphorus-limited field this phenotype was not expressed and close examination showed that lateral root type was the best predictor of root hair development (Nestler et al. 2016; Kant et al. 2019). Rice genotypes within a diversity panel in a droughted field followed by water resupply elongated leaves and produced roots at different rates (Klein, MSc thesis). We are exploring lateral root and hair longevity and dynamics upon water resupply as a mechanism by which shoot:root allocation varies through selective breeding (Bochmann, MSc thesis). More broadly, phenotyping in rhizoboxes showed wide variation in lateral root proportion to root system length in sorghum and wheat. Fine root development is thus an understudied and exciting opportunity to improve the resource efficiency of cereals, the major source of calories for the global human population.

No ID | Improving Water Use Efficiency through alternation of stomata regulation

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In the U.S. alone the agricultural loss caused by drought annually costs ~$29 billion. Most of the water absorbed by plant roots is lost via transpiration from stomata. However, to capture atmospheric CO_2 during photosynthesis, stomatal pores need to stay open to allow CO_2 to get into the leaf. It is estimated that ~200 water molecules are lost for every carbon atom that is fixed by photosynthesis. The higher the air and surface temperature, the more water plants transpire, which increases the demand for irrigation to secure crop production. One of the solutions to reduce the need for irrigation and secure yield under drought condition is to develop crops that require less water per unit mass of production. Our results collected on tobacco show that increasing, through genetic manipulation, expression of a photosynthesis-related protein of photosystem II subunit S (PsbS) significantly suppresses stomatal opening with little effect on CO_2 uptake and thus increases water use efficiency. The reduction in stomatal opening did not translate into a reduction of CO_2 assimilation although the CO_2 supply was slightly affected. Instead, modified plants showed an increase in photosynthesis capacity through higher maximum carboxylation capacity and the activation stage of RuBisCO. Since PsbS stimulates the thermal dissipation of excitation energy observed as nonphotochemical quenching (NPQ), we predict that increased expression of this protein decreases the chloroplast-derived signal for stomatal opening in response to light and decreases water loss at the leaf level. The PsbS overexpressing lines on average showed a 25% decrease in the amount of water used for each molecule of CO_2 fixed and 27% higher leaf area per water used. Under field conditions that limited wildtype growth, this alteration led to 20% higher biomass.

SESSION 4: PLANT PRODUCTIVITY UNDER DROUGHT: VEGETATIVE AND REPRODUCTIVE GROWTH

ID 1013 | Genotypic variation in whole-plant transpiration efficiency in sorghum only partly aligns with variation in stomatal conductance

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Water scarcity can limit sorghum production in dryland agriculture and increased whole-plant transpiration efficiency (TEwp, biomass production per unit water transpired) could enhance grain yield in such conditions. The objectives of this study were to quantify variation in TEwp for 27 sorghum genotypes and explore linkages of this variation to responses of underpinning leaf-level processes to environmental conditions. Individual plants were grown in large lysimeters in two well-watered experiments. Whole-plant transpiration per unit green leaf area (TGLA) was monitored continuously and stomatal conductance (gsleaf) and maximum photosynthetic capacity were measured during sunny conditions on recently expanded leaves. SPAD leaf chlorophyll measurements of the upper five leaves of the main shoot were conducted during early grain filling. TEwp was determined at harvest. Results showed that diurnal patterns in TGLA were determined by vapour pressure deficit (VPD) and by the response of whole-plant conductance to radiation and VPD. Significant genotypic variation in the response of TGLA to VPD occurred and was related to genotypic differences in gsleaf. However, variation in TGLA explained only part of the variation in TEwp, with some of the residual variation explained by SPAD readings, which were a reflection of photosynthetic capacity. Genotypes with different genetic background often differed in TEwp, TGLA, and leaf chlorophyll, indicating potential differences in photosynthetic capacity among these groups. Observed differences in TEwp and its component traits can affect adaptation to drought stress.

ID 1029 | Osmolyte accumulation plays important roles in the drought priming induced tolerance to post-anthesis drought stress in winter wheat

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Winter wheat were subjected to moderate drought priming before anthesis and then to a severe drought stress after anthesis. The plant morphology, osmolyte accumulation related traits in both leaves and roots were analysed during the priming, the post-anthesis drought stress, and the recovery from the drought stress. The primed plants (PD) showed lower reduction in leaves dry weight and grain yield, higher maximum root length, compared with non-primed plants (CD). The PD maintained lower osmotic potential related to the higher contents of leaf proline and sucrose. The higher proline content could be resulted from the improved activities of Δ1-pyrroline-5-carboxylate synthetase (P5CS) due to the up-regulated expression of P5CS. The higher sucrose content correlated with the up-regulated expression of gene encoding the sucrose-phosphate synthetase. No significant differences between PD and CD in contents of proline and sucrose of root were found. Meanwhile, the PD showed higher activities of antioxidant enzymes, which contributed to lower cell membrane peroxidation level as compared with the CD in both leaves and roots under drought stress. It is concluded that the enhanced tolerance to drought stress in primed plants were related to the enhanced osmolyte accumulation to maintain a better plant water status, which further resulted in relatively higher photosynthesis, lower oxidative stress damage and grain yield under the post-anthesis drought stress.

ID 1030 | Parental drought-priming enhances tolerance to post-anthesis drought in offspring of wheat

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Drought is the major abiotic stress that decreases plant water status, inhibits photosynthesis, induces oxidative stress, restricts growth and finally lead to the reduction of wheat yield. It has been proven that drought priming during vegetative growth stage could enhance tolerance to drought stress at grain filling in wheat. However, whether drought priming imposed at grain filling in parental plants could induce drought tolerance in the offspring is not known. In this study, drought priming was successively applied in the first, the second and the third generation of wheat to obtain the plants of T1 (primed for one generation), T2 (primed for two generations), T3 (primed for three generations). The differently primed plants were then subjected to drought stress during grain filling in the fourth generation. Under drought stress, the parentally primed plants, disregarding the number of generations, showed higher grain yield, leaf photosynthetic rate and antioxidant capacity as well as lower O2.- release rate and contents of H2O2 and MDA than the non-primed plants, suggesting that drought priming induced the transgenerational stress tolerance to drought stress. Moreover, the parentally primed plants showed higher leaf water status, which may result from the higher contents of proline and glycine betaine, and higher activities of Δ1-pyrroline-5-carboxylate synthetase (P5CS) and betaine aldehyde dehydrogenase (BADH), compared with the non-primed plants under drought stress. In addition, there was no significant difference among three generations under drought, and the drought priming in parental generations did not affect the grain yield of the offspring plants under control condition. Collectively, the enhanced accumulation of proline and glycine betaine in the parentally primed plants could have played critical roles in parental priming induced tolerance to drought stress. This research provided a potential approach to improve drought tolerance of offspring plants by priming parental plants.

ID 1143 | Trait targets of the Heat and Drought Wheat Improvement Consortium (HeDWIC)

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Wheat is the most widely grown crop worldwide providing 20% of human calories and protein. It is imperative to build climate resilience into new varieties, which requires innovations in breeding, made possible by recent advances in understanding stress response mechanisms, remote sensing, and genomics. To capitalize on these approaches, CIMMYT and the Wheat Initiative initiated the Heat and Drought Wheat Improvement Consortium (HeDWIC) based on stakeholder consultation. Strategic use of these new technologies combined with proven methods will be applied within 3 main activities of HeDWIC:

1. Applying molecular genetic tools, in conjunction with detailed physiological and molecular characterization of heat/drought adaptive mechanisms, to identify molecular networks, genes and markers that will improve wheat's performance under diverse heat and drought scenarios. This work will be underpinned by the wheat genome sequence and additional genomic resources;
2. High throughput phenotyping -in realistic field environments- of the vast untapped reserve of wheat genetic resources for use in pre-breeding and gene discovery, and validation of trait expression in new germplasm.
3. Augmenting conventional wheat improvement methods using these outputs

In a pilot project, novel lines were developed by selecting for a range of physiological traits in parents and progeny -including more extensive root and the plant ability to store and remobilize stem carbohydrates- through collaboration between breeders and physiologists, resulting in improved varietal performance in heat stressed regions of Pakistan. HeDWIC considers a wide range of physiological traits under two main categories, 1) Resource capture and utilization efficiency; aiming to maximize WUE and RUE; 2) Reproductive growth and resource partitioning; to maximize HI and nutritional quality. HeDWIC will coordinate globally dispersed skills and resources relying on wide consultation of experts to provide new technologies to wheat breeding programs worldwide.

ID 1159 | Integrating aerial hyperspectral reflectance phenotyping and genomic selection for the prediction of wheat grain yield in water-limited environments

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Hyperspectral reflectance phenotyping and genomic selection are two emerging technologies that have the potential to increase plant breeding efficiency for drought-stressed environments by improving grain yield prediction accuracy. Hyperspectral cameras quantify canopy reflectance across a wide range of wavelengths that are responsive to crop water status. Genomic selection models utilize genome-wide marker and/or pedigree information to predict the genetic values of breeding lines. We propose a multi-kernel GBLUP approach to genomic selection that uses genomic marker-, pedigree-, and hyperspectral reflectance-derived relationship matrices to model the genetic main effects and genotype × environment interactions across optimal and drought-stressed environments within a bread wheat (Triticum aestivum L.) breeding program. We utilized an airplane equipped with a hyperspectral camera to phenotype differentially managed well-watered and water-limited yield trials conducted by the Bread Wheat Improvement Program of the International Maize and Wheat Improvement Center (CIMMYT) at Ciudad Obregón, México over four breeding cycles. Multi-kernel models combining marker/pedigree information with hyperspectral reflectance phentoypes had the highest prediction accuracies overall, averaging 0.43. Improvements in accuracy over the single-kernel marker- and pedigree-based models were the greatest for the water-limited treatments, with the addition of hyperspectral data increasing accuracies by 0.13-0.16 on average. However, these improvements were more marginal when correcting for days to heading, with the greatest reductions in accuracy observed for the water-limited treatments. Our results demonstrate the potential of using hyperspectral imaging and genomic selection to predict grain, though there is a need for further study of best practices to account for phenology when using hyperspectral reflectance phenotypes for grain yield prediction in drought-stressed environments.

ID 1164 | Quantifying drought tolerant crop traits using sensing technologies to enhance selection in sorghum breeding trials

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Global food production needs to increase by more than 60% by 2050 to meet the projected demand. At the same time, yield advances have slowed at both a production, as well as, a genetic improvement level. To ensure further progress, a better understanding of the traits that lead to greater yield potential and better adaptation to challenging climatic conditions is needed, which is a major priority in the Australian sorghum pre-breeding program.

However, monitoring and capturing physiological and phenological traits within large breeding trials is time consuming and costly, especially when data has to be collated across various environments. For example, the current method for estimating characteristics like lodging and stay-green involves visually scoring lodging and stay-green across thousands of plots. The advent of sensing technologies, however, has provided avenues to develop tools to assess such traits efficiently and cost-effectively. This study outlines the application and ability of proximal sensing technologies to enhance plant-breeding research outcomes. Specifically, we describe the design of a high-throughput (HTP) software pipeline to capture, manipulate and analyse "BIG DATA" collated from proximal sensors on-board two phenotyping platforms. We discuss analyses and results from the use of high-resolution spatial characterisation of time-sequence data, obtained from multi-spectral sensors and reconstructed point-cloud data. Application of such an approach across breeding fields offers the potential to more accurately and cost effectively determine drought related traits like stay-green and lodging responses among genotypes. The deployment of these new technologies into breeding programs will enable more rapid genetic gain and hence faster delivery of adapted commercial hybrids with improved yield in water limited environments.

ID 1203 | Comparative yield physiology of spring and winter wheat in a semi-arid Mediterranean environment

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In semi-arid southern Australia, average autumn rainfall has been in decline since the early 1990s. As autumn is the optimal establishment period for spring wheat, early sowing has emerged as a management tool to establish wheat outside the period of declining rainfall and increase water-limited potential yield. Winter wheat has a stable flowering time across a range of sowing dates, making it more suited to early sowing than spring wheat, which if sown early flowers during a period of high frost risk. As winter wheat has not been prioritised in breeding programmes in southern Australia, phenotypic determinants of yield are not well understood. This study aimed to determine whether the phenotypic determinants of yield differ in winter and spring wheat sown in a semi-arid environment with Mediterranean rainfall distribution. It was hypothesised that biomass accumulation would explain more yield variation in spring wheat, whereas biomass partitioning traits would explain more yield variation in winter wheat. Following a partially-replicated pilot experiment in 2018, winter and spring lines derived from a Mace/Gauntlet (two high-yielding southern Australian spring cultivars) cross and matched for heading date were sown in a fully replicated field experiment at Birchip, Victoria in 2019. Winter lines were sown earlier to achieve synchronous flowering between the two treatments. 2018 results found no difference in the amount of yield variation explained by traits in winter wheat lines compared to spring wheat. Grain number and dry matter at maturity explained most variation in yield (R = 0.73 and 0.58 respectively). Harvest index and fruiting efficiency were weakly associated with yield (R = 0.16 and 0.10 respectively). Early results from 2019 suggest that biomass accumulation, particularly during vegetative growth, explain yield variation more significantly in spring lines than winter lines.

ID 1207 | Using UAV Measurements to Phenotype Drought and Heat Stress in Wheat

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Wheat is one of the most important crops in the world. However, yields are highly affected by high temperatures in combination with little rainfall. In the future, such drought events are expected to happen more frequently. To meet the food demand of a growing world population, breeding of more drought tolerant wheat varieties is crucial.

To screen and identify wheat varieties with such traits, a multi-year field trial was performed in Bălţi, in the Republic of Moldova. Due to the continental climatic conditions present there the summers are often arid. In the trial 40 wheat varieties were tested, 20 originated from Eastern European countries, 20 from Germany including lines and hybrids. The Eastern European varieties are well adapted to an environment with abiotic stress during summer, and can serve to compare yield levels to what can be achieved with a suitable genetic constitution. German varieties show a higher yield potential under more favorable climate conditions with sufficient precipitation. Phenotyping these varieties under realistic drought conditions, can help to identify and select wheat varieties with a high degree of drought and heat tolerance for future breeding programs.

Thermal and multispectral measurements were conducted from anthesis until harvest, with both handheld devices and a drone. They can provide valuable information about the plants’ water status and nutrient uptake. Additionally, plant samples were cut to corroborate the findings from non-destructive measurements.

Preliminary results showed good correlations between terrestrial and aerial devices. Significant differences between wheat varieties were observed in the grain yield and grain quality as well as in plant surface temperature. Varieties from Germany showed lower yield due to drought stress, and higher temperatures, indicating insufficient water supply. In a next step, the relations and correlations between the single measurements are analyzed and ranking sums are calculated to identify promising varieties.

ID 1264 | Field high-throughput screening of natural genetic variation in photosynthetic traits in durum wheat under drought stress using Light-Induced Fluorescence Transient (LIFT)

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Agriculture often faces multiple stresses. Ensuring food security will require the active release of cultivars with consistent high yield stability and improved resilience to water stress conditions. Field-based high-throughput phenotyping platforms (HTPPs) facilitate the screening of large populations to be able to evaluate and discover meaningful drought-adaptive traits and accelerate the identification of superior genotypes in an accurate and cost-effective manner. For doing so, the HTPPs rely on sensors to characterise either relevant traits or an integrative signal, e.g. photosynthesis, which may serve as a robust selection parameter for crop performance. Chlorophyll fluorescence (ChlF) has become a powerful and widely used non-invasive technique in plant ecophysiology for helping to elucidate the fundamentals of photosynthesis. Even though ChlF has often been proposed as suitable for screening drought, it has not yet been really adopted in breeding programs. This is partially due to the fact that the majority of the existing instruments measure at low-throughput, with limited potential for automation, and are mainly constrained to controlled conditions. Recently the light-induced fluorescence transient (LIFT) sensor has been shown to provide active ChlF data collected at a distance for rapid characterisation of photosynthetic traits, e.g. the operating efficiency of photosystem II (Fq’/Fm’). In the present study, LIFT was mounted on a manually pushed cart to measure over multiple days a large panel of 252 elite accessions of durum wheat subjected to a progressive drought stress in a replicated field trial in Maricopa, Arizona, USA.

Integrating these measurements with high spatiotemporal resolution environmental data, the LIFT sensor helped to interpret the genotype x environment interaction, and to prospect drought-adaptive traits.

ID 1270 | Genotype-specific growth responses of maize nodal roots to water deficit across multiple whorls

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Drought is the leading abiotic stress factor limiting crop productivity worldwide. It has been demonstrated that maize nodal roots have a superior ability to continue elongation under water-limiting conditions relative to other plant organs. Nodal roots originate from multiple stem nodes successively over the course of several weeks and, along with their associated lateral roots, comprise the majority of the mature plant's root system. Maize genotypes with a greater ability to maintain nodal root growth through dry soil will be better able to access water at depth, and thus may have a competitive advantage over genotypes with a weaker nodal root growth response. To identify genotypes that have a greater ability to maintain nodal root growth under water-limiting conditions, a plant growth system was designed that allows for the characterization of nodal root phenotypes across multiple whorls. Several genotypes that were previously shown to have contrasting root system growth responses to water deficit were characterized for their nodal root phenotypes through the first five whorls. Initial data suggest that later-emerging whorls of nodal roots have an increased propensity to maintain growth through dry soil compared to earlier-emerging whorls. Thus, having the capability to study multiple whorls of nodal roots is critical to understanding whole-plant root system growth responses to water deficit. Going forward, genetic mutants will be characterized in hopes of elucidating the molecular mechanism(s) involved in nodal root growth maintenance under water deficit.

ID 1280 | Optical topometry and machine learning for high-throughput phenotyping of stomatal patterning traits applied to QTL mapping in a maize B73xMS71 RIL population

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Stomata are adjustable pores on leaf surfaces that regulate the trade-off of CO2 uptake with water vapor loss, thus having critical roles in controlling photosynthetic carbon gain and plant water use. While key genes with major roles in regulating stomatal development are known, the lack of easy, rapid methods for phenotyping quantitative variation in epidermal cell traits have limited the use of mutant screens and association mapping to discover the genetic basis for variation in stomatal patterning. We present a new high-throughput epidermal cell phenotyping pipeline and demonstrate its utility in quantitative trait loci (QTL) mapping in field-grown maize B73xMS71 recombinant inbred lines (RILs). The boundaries of stomatal complexes and pavement cells on 20X images acquired by an optical-topometer from samples of adult leaves were automatically predicted with high accuracy and precision. Strong correlations were achieved between predicted stomatal complex density (SCD; R2 = 0.97) and stomatal complex area (SCA; R2 = 0.71) compared to expert human measurements. Genetic variation in epidermal traits were strongly correlated across field trials in two years. Interestingly, neither SCD nor SCA showed significant correlations with leaf gas exchange traits. But stomatal complex

width (SCW), stomatal complex length (SCL), stomatal complex length width ratio (SCLWR), pavement cell total area (PTA), stomatal pore area (SPA) and specific leaf area (SLA) did correlate with leaf gas exchange traits. Out of 143 QTLs in total, 36 QTLs were consistently identified for a given trait in both years. And, 24 hotspots of overlapping QTLs for multiple traits were identified. Orthologs of genes known to regulate stomatal patterning in Arabidopsis are located within some, but not all, of these QTL regions. This demonstrates how discovery of the genetic basis for stomatal patterning can be accelerated in maize, which is of considerable agricultural importance but where these processes are poorly understood.

ID 1283 | Understanding legume response to drought: lessons learned and new steps forward

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Global demand for legume crops is increasing, yet production mostly occurs in rainfed systems where yields are low and the rate of yield improvement is stagnating. Therefore, understanding physiological responses to drought is a key priority to increase the productivity of future legume crops. We performed a series of experiments under controlled and field conditions using a panel of common bean (*Phaseolus vulgaris* L.) lines selected for improved adaptation to drought by CIAT. Notably, common bean is one of the most important grain legumes for human consumption and 60% of production is at risk of intermittent or terminal drought. To understand the impact of decreasing source strength on pod development and the effect of drought on seed nutritional content we applied a range of phenotyping techniques and technologies, including nuclear magnetic resonance sensors, gas exchange, stable carbon isotopes and detailed chemical analyses. Despite changes at the whole plant level (reduced photosynthesis, reduced biomass, reduced yield) manipulations of source strength in controlled environments and drought in the field did not influence the development of individual pods or impact on the concentration of key nutrients in the grain. Our results suggest that common bean lines pre-selected for drought adaptation have a degree of resilience in yield development and nutritional content. Understanding the physiological and genetic mechanisms that underpin this response is a high priority. To further advance our knowledge of source-sink dynamics in legume crops, we present a multi-disciplinary research framework integrating legume physiology, crop modelling and genetics. Over the coming years, we anticipate this approach will provide knowledge that will guide plant breeding, improve crop model development and optimise management strategies for farmers to improve yield under drought.

ID 1285 | Developing pearl millet parents and hybrids through integrated high throughput precision Phenotyping Pipelines to increase the genetic gain in highly drought-prone environments (A1 zone)

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The inherent insufficiency of resources (economic cum agricultural) in the Thar dessert region of India coupled with the harsh environments urge the researchers to accelerate development of climate-ready pearl millet cultivars. In the future climate these regions are likely to see increase temperatures and erratic precipitation patterns of the monsoon rains that millions of farmers rely on to raise their crops. One of the interventions

which could alleviate this complex situation would be development of climate-ready cultivars. Despite a lot of novel technologies are in place, the actual deployment in the crop improvement might be challenging. Here, we will demonstrate the strategy to streamline and deploy the novel state-of–the art technologies enabled by the recent decade of research at ICRISAT (i.e. integrate genomics-phenomics-modelling approaches) in order to systematically address the environmental complexity of the pearl millet production regions and so stabilize/increase the crop production in the A1 pearl millet agri-food systems (Rainfall below 400 mm). We will demonstrate how the HTP platform "LeasyScan" could be integrated to access the genetic variability of the current pearl millet breeding material for the physiological traits conferring drought and heat adaptions in the target region. Phenotyping strategized for early generation (F4-F5) of breeding material in hot season as well as in optimal conditions to assess the adaptation and full potential of genotype. In addition to that a weightage selection index is getting streamlined based on phenology, biomass, leaf area, leaf angle, leaf inclination and light penetration for most efficient selection for A1 type of environment.

ID 1287 | A rapid and non-destructive method to modify root architecture in crops

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A challenge for plant researchers and plant breeders is the lack of efficient phenotyping techniques to enable screening and selection for desirable root traits associated with improved crop yield and yield stability under water-limited conditions. New approaches that enable direct selection in crop improvement programs are required. To help to overcome this bottleneck, we have developed an innovative sequential phenotypic screening platform for multiple root traits, where selection can be applied for different configurations of root system architecture (RSA). This is achieved using a "proxy" approach based on measuring two key traits, root angle and root biomass, on the same plants. Visual scoring of traits enables rapid non-destructive phenotyping and plants displaying desirable root trait combinations can be tracked, selected and crossed within the same plant generation. The clear pot method (Richard et al., 2015) has been integrated in the pipeline to measure seminal root angle, along with a semi-hydroponic assay to evaluate root biomass. To validate the approach, we demonstrate that visual scores are highly correlated with actual measures that are destructives. Moreover, speed up selection the rapid generation advance technology 'speed breeding' can be used to advance plant populations and selection accuracy can be improved by incorporating selection for major QTLs using KASP markers. The new approach and toolkit will empower researchers and plant breeders to optimise the belowground components of future wheat varieties to improve productivity in the face of increasing environmental fluctuations.

ID 1290 | Phenomics of Stomata and Water Use Efficiency in C4 Crops

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Water use efficiency (WUE) is a key target for crop improvement. This is because water availability is the primary limitation to crop yield globally and irrigation uses the largest fraction of our limited freshwater supply. The exchange of water and CO2 between a leaf and the atmosphere is regulated by the aperture and pattern of stomata. Mechanistic modeling indicates that stomatal conductance could be reduced or stomatal movements accelerated to improve water use efficiency in important C4 crops such maize and sorghum. While molecular genetics has revealed much about the genes regulating stomatal patterning and kinetics in Arabidopsis, knowledge of the genetic and physiological control of WUE by stomatal traits in C4 crops is still poor. Understanding of natural diversity in stomatal traits is limited by the lack of high-throughput phenotyping methods. Two novel phenotyping platforms were developed. First, a rapid method to assess stomatal patterning in three model C4 species grown in the field – maize, sorghum and setaria has been implemented. The leaf surface is scanned in less than two minutes with an optical tomographer, generating a quantitative measurement of a patch of the leaf surface. An algorithm was designed to automatically detect stomata in 10,000s of these images via training of a neural network approach. Second, a thermal imaging strategy, to rapidly screen the kinetics of stomatal closure in response to light has been developed. We identified genotype to phenotype associations for stomatal patterning, leaf gas exchange and canopy water use through quantitative trait loci and genome wide association studies. Transgenically modified expression of stomatal patterning genes has produced sorghum with greater WUE. These plants were grown in a new field facility for comprehensive evaluation of leaf, root and canopy WUE traits under Midwest growing conditions.

ID 1291 | Abiotic stress on PhénoField platform

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In order to evaluate the impact of water deficit in field conditions, researchers and breeders must set up large experiment networks in very restrictive field environments. Experience shows that half of the field trials are not relevant because of climatic conditions that do not allow the stress scenario to be tested. The PhénoField® platform, part of French Plant Phenotyping Network, named PHENOME-EMPHASIS, is the first field based infrastructure in the European Union to ensure protection against rainfall for a large number of plots, coupled with the non-invasive acquisition of crops' phenotype. In this presentation, we will highlight adaptation strategies of wheat and maize under water deficit conditions using the PhénoField® capabilities. Firstly, PhénoField® automatic mobile rainout shelters allow fine management of rainfall and irrigation. This management is based on micro-meteorological measurements coupled with a simulation of a carbon, water and nitrogen crop balance. Furthermore, high-throughput plant-phenotyping is enabled through phenotyping gantries equipped with various optical sensors. This combined approach provides a particularly interesting model giving access to innovative traits in a dynamic point of view, highlighting plant adaptation strategies to water deficit. The interactions between genotypes and the environment can be deciphered using curve parameters like growth rate, maximum of height, area under curve of vegetative index, senescence kinetics ... All these specificities of the PhénoField® platform open the way to improve various types of crop models and the fine characterization of variety behavior throughout the growth cycle.

ID 1301 | Traits measured in a phenotyping platform account differentially for the genetic variability of yield under heat and drought scenarios

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Phenomics allows dissection of the genetic variability of adaptation traits. However, the relevance of phenotyping under controlled conditions is questioned (Araus et al. 2018). We aimed at testing to what extent a cross-scale analyses allows better understanding of the allelic diversity of traits for drought tolerance understood with a probabilistic approach (Tardieu et al. 2018).

Functional and architectural traits, gene expression and response curves to environmental variables acquired in a phenotyping platform were analyzed by genome-wide association mapping in a panel of 244 maize dent lines crossed with a common flint parent. The resulting set of QTLs was analysed for co-localization with QTLs for grain yield (GY) in 29 fields, clustered in six environmental scenarios combining temperature and soil water status during flowering time as measured in each field (Millet et al. 2016).

35% of QTLs for GY co-localized with traits measured in the phenotyping platform, but with patterns of co-localization depending on the environmental scenario in a studied field. The cumulative effect of trait QTLs accounted for an appreciable proportion of the additive genetic variance for scenario-dependent GY. These results provide insights for understanding the genetic basis of drought tolerance. Furthermore, these genomic regions may be useful for designing maize plants adapted to specific drought-prone European regions.

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Tardieu *et al* (2018). Annual review of plant biology, 69, 733-759.
Millet *et al* (2016). Plant Physiology, 172(2), 749-764.

ID 1313 | Drought and heat stress precision platform for wheat phenotyping

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Precision field-based wheat phenotyping platforms have been developed with the support of the CGIAR WHEAT Program and co-investing national agricultural research institutes, to generate phenotypic data on prioritized traits. Within this network, a new phenotyping platform has been established for the evaluation of drought and heat stress tolerance in wheat, under controlled field conditions and using lysimeter facilities. The platform is placed in a semiarid environment in Central Morocco, at INRA Station in Sidi El Aydi- CRRA Settat. The lysimeter main structure was completed in July 2019, and it is currently under a final round of fine-tuning. The lysimeter is expected to be fully functional in 2020, with capacities for a precise and continuous record of physiological variables. Projects to be soon implemented aim to test night transpiration in wheat lines under high night temperatures and different water stress levels. Previous studies in wheat reported high genetic variability for night transpiration under drought, non-linear responses between day and night transpiration, and differential acclimation strategies between different genotypes. Based on this, primary goals for the platform will be to (i) determine genetic variability in wheat responses to day-night variation on water transpired, (ii) estimate the effect of environmental parameters on night transpiration (in particular, VPD and temperature), (iii) measure the impact of the night transpiration on yield and yield components, (iv) compare field and lysimeter protocols, and (v) identify if any surrogate, such as canopy temperature, can be used to predict night transpiration to identify lines with enhanced drought and heat tolerance. It is expected that the generated information will contribute to rapid advances in breeding for semiarid regions, building on efficiency and capacity for research.

ID 1320 | Ecophysiological screening of cotton genotypes under drought

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Rising incidence of extreme drought and heat events in combination with diminishing freshwater resources associated with climate change threatens the global security of plant-based food, fiber and fuel production. Field-based efforts to unravel the genetic basis of drought response as a path to accelerate breeding are challenged by often-prominent genotype by environment interaction (G x E). It has been suggested that process-based modeling can be utilized as a tool to understand the (context-dependent) mechanisms that could underpin G x E in water-limited scenarios. In order to later leverage these approaches for cultivated upland cotton, *Gossypium hirsutum* L., a pilot field trial was undertaken in Summer 2019 to first assess the extent of genotypic variation in common parameters found in eco-physiological process-based models. We evaluated traits related to photosynthesis, growth and development, and water relations in a drought experiment in four genotypes (DP1549, PD3, VIR Coker, and Tipo Chaco) with different breeding histories at Maricopa Agricultural Center (Maricopa, Arizona, USA). Our results will be used to help parameterize and improve model development of a hydraulics-centric process-based model called Terrestrial Regional Ecosystem Exchange Simulator (TREES) for adaptation to cotton.

No ID | Use of drought tolerance traits within the CIMMYT maize breeding program for stress prone environments in eastern and southern Africa

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At current yield levels, the area of maize cultivation in sub-Saharan Africa must increase by 184% by 2050 to meet future food security needs. Investment in maize breeding for stress prone environments in eastern and southern Africa (ESA) have increased over the past 15 years. The first evaluation of genetic gain for grain yield under abiotic stress in the International Maize and Wheat Improvement Centre (CIMMYT) ESA maize breeding program estimated gains comparable to other regions of the world, however absolute maize yields remain low. There are extensive efforts to increase the rate of genetic gain in yield under stress within the CIMMYT ESA maize breeding program using a range of technologies. Earlier research showed the potential of secondary traits to increase the efficiency of selection for grain yield in maize breeding programs targeting stress prone environments. The CIMMYT ESA maize breeding program operates across a large geographic region and the measurement of secondary traits, particularly at early stages, are time-consuming and costly. Proximal and remote sensing tools provide new avenues to rapidly characterise “breeder preferred traits” at limited cost, while removing the use of qualitative scores. Here we will investigate the use of different approaches to increase selection efficiency in stress breeding in ESA.

SESSION 5: BREEDING FOR WATER-LIMITED ENVIRONMENTS

ID 1002 | Dissecting the genetic variations in control of ABA signal transduction and small RNA expression in maize drought response

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Drought is a major abiotic stress that causes maize yield loss worldwide. ABA is a phytohormone and plays important roles in plant drought tolerance. Small-interference RNAs (sRNAs, 20-24 nt) have broad roles in regulation of plant stress responses. However, the natural variations of ABA signaling and sRNA expression in maize drought response remain elusive. Recently, we performed sRNA-seq and RNA-seq to ~340 maize natural accessions (collected worldwide and with broad genetic diversities) treated with or without drought stress. We detected large amounts of differentially expressed sRNAs and sRNA clusters, whose expression profiles were highly variable in the maize populations in response to drought. We further detected large-scales of eQTLs associated with sRNA/sRNA cluster expression. Through complicated genetic, molecular and transgenic studies, we showed that an eQTL hotspot, TE-IRiC8 (TE-formed inverted-repeat structure in Chr8), regulated maize drought tolerance via sRNA-mediated PTGS. We further demonstrated that IRs were vital genome structures in control of sRNA expression in maize drought response. In other projects, we studied the roles and genome wide variations of 13 ZmPYL genes, encoding ABA receptors, and 13 ZmPP2CA genes, encoding clade A phosphatase and involved in ABA signaling, in maize drought tolerance. Transgenic studies revealed that ZmPYL8, 9, 12 positively, while ZmPP2CA2, A6, A10 negatively regulated maize drought tolerance. Natural variations or haplotypes of these genes in drought tolerance had been discovered. For instance, the deletion allele of -338 in ZmPP2CA10 promoter resulted in the loss of ERSE (endoplasmic reticulum stress response element), and further the reduced ZmPP2CA10 expression and enhanced drought tolerance. These genetic variations have the potential to be used as molecular markers in drought-tolerant maize breeding.

ID 1004 | Wild emmer introgressions reshape root-to-shoot architecture to improve wheat drought tolerance

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Drought is the major environmental factor limiting wheat production and sustainability worldwide. The wild emmer wheat (Triticum turgidum ssp. dicoccoides) genepool harbors a rich allelic repertoire for numerous important traits, including drought tolerance. In the current study, we investigated the potential of wild alleles for enhancing drought tolerance. A set of adapted Near Isogenic Lines (aNIL) was developed by introgression of wild emmer accession Zavitan into elite durum wheat (T. turgidum ssp. durum; cv. Svevo). The NILs were genotyped and anchored to the Zavitan and Svevo genomes. The population was phenotyped using high-throughput image-based phonemics approach and resulted in a wide range of drought adaptive strategies. Cluster analysis of morpho-physiological traits revealed five clusters of drought-responsive strategies, resulted from a shift in plant growth rate, architecture, and water-use-efficiency. In parallel, we tested these NILs under contrasting water availabilities in the field for yield components. Highly productive NIL with enhance drought adaptation was selected for further characterization. Using high-resolution lyzemeters platform we inform the specific physiological changes from the shoot and root-soil water uptake. A significant shift in resources allocation between root and shoot was found, which was supported by enhancing photosynthesis capacity under drought. The identified genetic factors underscore the potential benefit of introducing wild alleles into modern cultivars and is likely to be useful for the selection of drought-adaptive lines in future breeding programs.

ID 1011 | Introgression of wild alleles reshape root to shoot architecture and alters water-stress responsiveness dynamics

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The wild emmer wheat (*Triticum turgidum* ssp. *dicoccoides*) genepool harbors a rich allelic repertoire for numerous important traits, including tolerance to water stress. In the current study we investigated the potential of wild alleles for enhance productivity under water stress. A set of Isogenic Lines (IL) was developed by introgression of alleles from the wild emmer accession Zavitan into elite durum wheat (*T. turgidum* ssp. *durum*) cultivar Svevo. The ILs were genotyped and anchored to the tetraploid wheat genomes and phenotyped using high-throughput image-based phonemics approach. The results highlight a wide range of stress responsiveness dynamics, which were clustered into five morpho-physiological groups. IL20-2 that exhibited plasticity response and high productivity was selected for further physiological characterization. Interestingly, while the IL showed significant reduction in shoot biomass as consequence of water stress, the root biomass increased, as evidence by the high root-shoot ratio. This shift in resources allocation between root and shoot, contribute to enhance photosynthesis capacity under stress. Transcriptional analysis of the roots revealed several candidate root-specific genes, which were enriched metabolic pathways associated with plant adaptations to water stress. The identified genetic factors underscore the potential benefit of introducing wild alleles into modern cultivars shed-light on “left behind” drought-adaptive mechanisms and will serve as basis for future wheat breeding programs.

ID 1032 | To manage the negative impact of the Climate change by redefining the new normal and use of advance tolls in Breeding for crop improvements

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Challenging task for the breeding community is to improve the climate resilient in cultivated plant species for longer sustainability. On a positive note, climate change and cultivar developments move together as every next breeding cycle and selection fall in the changed climate. I believe very strongly, that world will never go hungry if we continue to improve the productivity by genetic gain, reducing harvesting tools, improve plant nutritional use efficiency, and continue improvement in crop diversification and development of new plant type. In this article I have tried to cover all these aspects where we need to challenge ourselves and try to redefine our existing system process in order to increase the efficiency and help world to be out from the fear of food security. Increase in temperature and evapotranspiration can be taken care of very well during the breeding process as the entire breeding nursery planted in open field and generation advancement happen in natural climate. Effect of Drought and water logging condition can be taken care through screening and selection in the targeted conditions. In breeding process, it is important to develop the methodology for root trait selection enabling technology, use of plant physiology in plant breeding, Screening of the early generation material under stream climatic conditions, off season screening, use of weather and climate change information for design the breeding schemes, breeding in targeted ecology and designing nutrients use efficient plant architecture. In this article I have tried to cover all of these aspects where we need to challenge ourselves and try to redefine our existing system process in order to increase the efficiency, continues genetic gain and help world to be out from the fear of food security.

ID 1067 | Genomic Basis of Climatic Adaptation in Sorghum Landraces of Ethiopia

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Sorghum is the most variable of all crops grown in Ethiopia containing tremendous genetic diversity and growing in different agro-ecologies. Exploration of the genome environment association through advanced technology is important to identifying adaptive loci and predicting phenotypic variation. Therefore, the objective of this study was to better understand the genome-environment association of 940 Ethiopian sorghum landraces using SNP markers for adaptive traits (altitude, annual temperature and precipitation variables). The Ethiopian sorghum germplasm was comprising 12 subpopulations (groups) with high levels of admixture (47%). Redundancy analysis indicated that a larger proportion of SNP variation was not explained by either agro-ecology or geographical locations. Only 13% was explained by either agroecology (7 %) or geographical location (3%) with collinearity (3%). Most of the subpopulations belonged to the durra botanical race and none of the subpopulations belonged to the kafir botanical race. Durra sorghum was distributed throughout most of the agroecological zones. Genome-environment association (GEA) study was identified 18 significant SNP markers for adaptive traits. These significant SNP markers were co-located with previously identified drought and cold adaptation QTLs. There was a significant enrichment of GEA SNP markers with a priori candidate QTLs for drought and cold adaptation. Several priority candidate genes were identified around the significant GEA markers (0.7kb to 3.3Mb) which have homologous genes in Oryza sativa Japonica genome with the function of stress tolerance. The associated GEA and candidate genes significantly improve the understand of the genetic control of adaptive traits in sorghum. Therefore, the Ethiopian sorghum germplasm collection could be a source of adaptations to extreme environments (cold and drought) which could be a source of traits for abiotic stresses adaptation for future breeding programs.

ID 1072 | Growth and transpiration response of contrasting sorghum genotypes to progressive soil drying

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Sorghum, a major food crop of the semi-arid tropics, is often exposed to late season drought, and plant traits that allow soil water conservation during the vegetative stage has been hypothesized to increase yield under late season drought stress. In this study, a total of 40 (20 early and 20 medium flowering) genotypes, and among the most contrasting in terms of late season drought tolerance in the field were tested for growth and transpiration response under well watered (WW) and water stress (WS) conditions in a semi-controlled condition. In both groups, shoot growth and total water use under WW conditions were lower in tolerant than in sensitive genotypes; this difference was however largely leveled under WS conditions. In contrast, the variation in root growth did not discriminate tolerant from sensitive genotypes both under WW and WS conditions. Tolerant genotypes also exhibited a decline of transpiration at high fractional transpirable soil water threshold compared to sensitive genotypes in both maturity groups. These results suggest that conservative use of water early in the cropping cycle, explained partly by lower shoot growth

and water use under WW conditions correlate with the late season drought tolerance of sorghum

ID 1073 | Genome-wide association studies for plant production traits under drought in Ethiopian Sorghum (*Sorghum bicolor* L. [Moench]) landraces

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Ethiopia is the center of origin and diversity for sorghum and as such has tremendous variability for a wide range of traits. However, little is known regarding the genetic basis of these traits. Here, 300 Ethiopian sorghum landraces were phenotyped for ten agro-morphological traits at two water limited environments. Subsequently, these accessions were genotyped using genotyping-by-sequencing to obtain a total of 79,754 robust single-nucleotide polymorphisms (SNPs) markers. Principal component analysis and ancestry estimation identified six distinct groups across the Ethiopian landrace collection used for this study. We performed genome-wide association studies (GWAS) to identify loci associated with each trait and understand the genetic interactions between traits. We detected a total of 64 genetic loci associated with these traits, of which seven were shared between at least two traits. The loci identified through GWAS explained ~30 % of the phenotypic variance, on average. When compared with our GWAS results, we observed that there were 10 overlapping regions between our significant SNPs and previously identified QTL for days to flowering (DF), panicle exsertion (PE), grain yield per panicle (GYP) and hundred seed weight (HSW). Most of these SNPs are located near candidate genes with putative functions spread across several categories. In addition, two trait-associated

SNPs showed strong selection signals and loss of genetic diversity. This study provides a fundamental resource for sorghum genetics research and contributes to the characterization of genes and alleles controlling agronomic traits, and will serve as a source of markers for molecular breeding.

ID 1076 | Mapping Quantitative Trait Loci (QTL) for Drought Tolerance in Sorghum [*Sorghum bicolor* (L.) Moench] Using Three Connected F2:3 Mapping Populations

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Identifying quantitative trait loci (QTL) of considerable effects that are expressed in diverse genetic backgrounds of different mapping populations can significantly complement the conventional breeding efforts. However, so far the majority of QTL studies in sorghum were undertaken using individual mapping population with limited marker coverage. The purpose of this study was therefore to map QTL related to drought tolerance using three connected mapping populations of different genetic backgrounds. Three bi-parental populations each with 207 F2:3 lines were evaluated using alpha lattice design with two replications under two moisture stressed environments. QTL for drought tolerance traits were computed separately within each population using composite interval mapping. A total of 106 QTLs were identified from the three individual mapping populations for all traits studied. All the QTLs identified from individual populations

were projected on the combined consensus map for meta QTL analysis. The meta-analysis then reduced the total number of QTLs from 106 to 16 meta QTLs. As a result, 4 mQTL for grain yield per plant, two for days to maturity, one for days to flowering, two for leaf senescence and three for plant height were detected on chromosomes 2, 3, 5, 6 and 9. The consensus map allowed us to map a larger number of markers than possible in any individual map and to obtain a more complete coverage of the sorghum genome. Therefore, the consensus map can be used as a reference resource for genetic studies in different genetic backgrounds and the QTL identified in this study could be used for marker assisted breeding programs in sorghum.

ID 1078 | Breeding drought tolerant maize for Asian tropics - What worked and what need to be fixed?

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About 80% of the maize in Asian tropics is cultivated as rain-fed crop and hence prone to climatic variability and associated weather extremes that leads to deficit moisture (or agricultural drought) at critical crop stages. CIMMYT's Asian regional maize program, based in ICRISAT campus, Hyderabad, India, in partnership with public and private sector maize programs in the region, has been focusing on development of drought tolerant maize germplasm, trait donors and high yielding drought tolerant maize hybrids for current climate, and maintain a germplasm base and product pipe-line to effectively feed the requirement of future climatic situations. The accelerated development and deployment of drought tolerant maize hybrids is based on carefully undertaken field-based precision phenotyping through managed-stress screens, understanding the genetic architecture of the target trait, coupled with application of modern breeding tools, including genome-wide association studies (GWAS), genomic selection (GS), and double haploid (DH) technology, and effective partnerships with committed national programs and seed companies in the region for effective deployment and delivery of drought tolerant cultivars. Good progress has been made and promising drought tolerant hybrids are being licensed to the partners for large scale deployment and scaling-out of drought tolerant hybrids in stress-prone agro-ecologies. However, in view of the climate change mediated weather variability/uncertainty the biggest challenge is to achieve an improved-stable performance across locations/years. This need a further intensified and concerted efforts to minimize genotype x environment interaction effects to develop maize germplasm with improved-stable performance.

ID 1097 | Combining real time transpiration phenotyping to omics: the key to mine biodiversity for water use efficiency?

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Banana responds very early to a reduced water content at root level and/or increased Vapour Pressure Deficit by reducing its transpiration. Once the stomata are closed, root pressure becomes the dominant force supplying water to the shoot. With this reaction banana is able to survive longer periods of water deficit but the disadvantage is that production is very sensitive to water deficit. This mechanism applies across the Musa genetic diversity but we show that there is genetic variability! We phenotyped 32 genotypes. All analyzed ABB genotypes (8) had a lower maximal transpiration rate, kept the maximal transpiration for a shorter time and consumed less water per day (van Wesemael et al., 2019). Stomatal responsivity is key to plant productivity and water use efficiency (WUE). We focused on 5 genotypes and show the impact of the light driven

stomatal conductivity (gs) on photosynthesis (A) and WUE. All genotypes showed a strong coupling of A and gs, confirming the priority of water conservation over CO2 assimilation. However, significant differences in kinetics were observed. By combining phenotyping to transcriptomics and proteomics, we identified in a pilot study allele specific differences (van Wesemael et al., 2018). By analyzing the guards cell proteome and transcriptome (Geilfus et al., 2018; Dittrich et al. 2019) we are currently extending this technology to banana and are identifying key players in stomatal opening and closing and so in WUE. Germplasm collections provide valuable genetic resources. Bioversity International manages a banana collection holding over 1500 accessions. To unravel the true value of this collection, we designed an affordable climate-controlled growth container to simulate certain climates. The container grows 504 plants simultaneously for 6 weeks and enables us to do a fast screening for potential genotypes. Combining phenotyping with omics is a promising strategy to mine the biodiversity for WUE.

ID 1104 | Increasing root biomass production in European winter wheat for improved drought-stress tolerance

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Widespread drought stress affects crop yields in many relevant agricultural regions worldwide. Agriculture, as the biggest global water consumer, therefore faces an enormous challenge to increase water use efficiency, whilst simultaneously maintaining productivity and yield stability under increasingly challenging climate conditions. In this context, there is a great need for a strategic development of varieties that achieve higher yields under erratically occurring drought phenomena. Recently, this has led to a growing interest into the understanding of the root system, as the organ for water and nutrient uptake. However, knowledge about the development of wheat roots and their genetic control is insufficient. This is primarily due to difficulties in measuring of root functions compared to above-ground phenotyping. Reliable molecular makers for relevant root traits can enable breeders to overcome difficulties with underground phenotypic selection. In this study we create near-isogenic lines (NIL) of European elite winter varieties that carry introgressions of a major QTL which confers a larger root system. Backcross progenies are being subjected to foreground selection, using kompetitive allele specific PCR markers (KASP) for the desired QTL alleles. Selection of the elite background is done by the use of genome-wide markers.

We are investigating the relevance of an increased root growth for enhanced water acquisition by the recently established unique phenotyping facility DroughtSpotter XXL. This system allows to track genotype-specific water uptake in 90 cm deep soil filled containers in up to five minutes intervals over the entire lifecycle. Preliminary results show a significant higher water use efficiency of the donor line compared to standard elite varieties. Moreover, field trials integrating different nitrogen fertilizer regimes, contrasting crop rotations and divergent irrigation scenarios allow us to investigate the effect of an altered root system under practical field conditions.

ID 1114 | Manipulating stomatal patterning to improve water use efficiency in wheat

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Stomata mediate the exchange of carbon dioxide and water between plants and the atmosphere. Understanding the control and response of water use efficiency (WUE) - the amount of carbon gain relative to water use - to environmental perturbation is key to understanding future plant function. Manipulating water use efficiency by breeding or biotechnology is a key target for improving crop performance. It has been hypothesized that one way to manipulate water use efficiency is by reducing stomatal density. Previous experiments in Arabidopsis, rice, barley and poplar have supported this hypothesis because stomatal conductance was reduced without a decrease in photosynthetic CO2 assimilation. However, for photosynthesis to be maintained when stomatal conductance is reduced would require some currently unknown mechanism to compensate for reduced CO2 entry to the leaf by increasing photosynthetic capacity or mesophyll conductance. To explore these questions in another major crop, transgenic wheat was designed to alter expression of a gene involved in stomatal development. Using optical topometry, we observed approximately a 20% reduction in stomatal density compared to wildtype. Furthermore, we observed a reduction in stomatal conductance and intercellular [CO2] without any decrease in photosynthesis. Overall, an increase in intrinsic water use efficiency was detected. Detailed mechanistic studies of the processes limiting photosynthesis are now underway.

ID 1146 | Effect of Trait Heritability, Training Population Size and Marker Density on Genomic Prediction Accuracy Estimation in 22 bi-parental Tropical Maize Populations

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Genomic selection is being used increasingly in plant breeding to accelerate genetic gain per unit time. One of the most important applications of genomic selection in maize breeding is to predict and select the best un-phenotyped lines in bi-parental populations based on genomic estimated breeding values. In the present study, 22 bi-parental tropical maize populations genotyped with low density SNPs were used to evaluate the genomic prediction accuracy (rMG) of the six trait-environment combinations under various levels of training population size (TPS) and marker density (MD), and assess the effect of trait heritability (h2), TPS and MD on rMG estimation. Our results showed that: (1) moderate rMG values were obtained for different trait-environment combinations, when 50% of the total genotypes was used as training population and ~200 SNPs were used for

ID 1165 | Marker-Assisted Selection for Drought Tolerance in Wheat

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Marker-assisted backcross breeding was used for transfer of a major grain yield QTL (Qyd.csdh.7AL) that was found to be insensitive to drought after its introgression into each of a number of Indian wheat cultivars (HUW234, HUW468, K307 and DBW17). The donor genotype SQ1was a high abscisic acid expressing breeding line, which also carried desirable attributes other than drought tolerance. Therefore, no marker-assisted background selection was performed, so that desirable attributes other than drought tolerance from both the parents could be brought together and high yielding drought tolerant genotypes could be recovered. The QTL contributed ~20% to the variation for grain yield under drought. Among advanced lines, one line gave 25.5% higher yield relative to the corresponding recipient genotype HUW234 under rainfed condition. Similarly, three lines gave 14.9% to 25.7% higher yield relative to the corresponding recipient genotypes HUW234 and DWB17 under irrigated condition. The high yield in the selected lines was attributed to a number of traits including grains per ear, grain weight, tiller number, biomass and lower canopy temperature.

ID 1166 | Meta-QTLs and Candidate Genes for Drought Tolerance in Wheat

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Meta-QTL analysis for drought tolerance in wheat was conducted utilizing BioMercator V4.2. For this purpose, information about ~374 QTL involving 43 drought-responsive traits was collected from 14 earlier studies conducted in the past using different mapping populations of bread wheat. However, for final analysis, only 62 of the above 374 QTLs were retained by the software due to inadequate information for remaining QTLs. A consensus map with 5,680 markers (SSRs, RFLP and DArT) was prepared using two reference maps available in GrainGenes database. The 62 QTLs were projected onto this consensus map, resulting in the identification of 18 MQTLs (designed as MQTL1 to MQTL18) located on seven different chromosomes (1D, 3B, 4D, 5A, 6D, 7A and 7D). The number of QTL associated with each MQTL ranged from 2 (for MQTL12) to 30 (MQTL 8, 9, 10, 11). Confidence intervals (C.I.) for meta-QTL ranged from 2.07 cM (MQTL10) to 19.46 cM (MQTL12), which are narrower relative to the corresponding intervals carrying the original QTLs, suggesting that MQTLs are relatively robust, and are associated with closely linked markers. Therefore, the MQTL identified during the present study should prove useful in breeding programmes aimed towards development of drought tolerant wheat cultivars. The 18 MQTLs were also used to identify >100 candidate genes, which encoded proteins including glycosyl-hydrolases, protein kinases, zinc finger proteins, the transcription factors, etc. These proteins are known to be involved in abiotic stress tolerance. We propose to validate these candidate genes through qRT-PCR expression analysis in seedlings of drought sensitive wheat cultivars and the corresponding tolerant wheat genotypes grown under moisture stress.

ID 1174 | Introduction of a novel platform for the selection of improved cultivars with increased yield under drought

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Yield increase under water-limiting and/or heat conditions was the ambition for this project. Rather than simply seeking individual lines from a single variety to fulfill our goal, we sought to develop a platform technology that could be used ubiquitously for international wheat improvement programs, if successful. After a five year process, we believe we have successfully developed a novel platform for the discovery of new abiotic stress varieties. This included two back to back years of field trails in the Okanagan Valley, Canada, as well as concurrent controlled greenhouse experiments that have confirmed a 15 to 24% increase in yield depending on the drought/water-limiting conditions imposed.

This means that we can theoretically start with any mutagenized wheat variety, process the M2 population through our platform and find new cultivars with improved yield under water-limiting conditions. This is not accelerated breeding or any other type of technology that would seek to introgress markers from other lines, but rather begins with a forward genetics screen. This screen took us six years to fully elucidate and validate genetically and rather than screen in the field, we conduct our initial screen in the lab. Collaborators involved in the greenhouse testing (and genomics) are Drs. Marcus Samuel (UCalgary), Raju Soolanayakanahally (AAFC), and Sateesh Kagale (NRC).

ID 1187 | Genome-wide association study Identified Genetic Variation in ZmTIP1 Contributes to Maize Root Hair Elongation and Drought Tolerance

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Maize production is frequently threatened by drought stress on a global-scale. Identification of the genetic components underlying the drought tolerance in maize is of great importance. Previously, through a genome-wide association study (GWAS) of maize drought tolerance at the seedling stage, we identified 83 genetic variations which were resolved to 42 candidate genes. Here, we report on comprehensive genetic and functional analysis indicating that ZmTIP1, which encodes a functional S-acyltransferase, plays a positive role in regulating the length of root hairs and the level of drought tolerance in maize. Enhancing ZmTIP1 expression in transgenic Arabidopsis and maize increased root hair length, as well as plant tolerance to water deficit. In contrast, ZmTIP1 transposon-insertional mutants displayed the opposite phenotype. Importantly, a calcium-dependent protein kinase, ZmCPK9, was identified as a substrate protein of ZmTIP1, and that ZmTIP1-mediated-palmitylation of two cysteine residues facilitated the ZmCPK9 PM association. Increasing the level of ZmCPK9 expression consistently enhanced root hair elongation and drought tolerance. Collectively, the results of this research enrich our knowledge about ZmTIP1-mediated protein S-acylation modifications in relation to the regulation of root hair elongation and drought tolerance. Additionally, the identification of a favorable allele of ZmTIP1 also provides a valuable genetic resource or selection target for the genetic improvement of maize.

ID 1192 | Wheat breeding for biotic and abiotic stresses tolerance at ICARDA targeting CWANA and SSA regions

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The wheat breeding program at ICARDA uses conventional and molecular approaches such as the Focused Identification of Germplasm Strategy (FIGS), mega environments, shuttle breeding, doubled haploids, marker-assisted selection, genomic selection, speed breeding and key location phenotyping to develop elite genotypes with high yield potential and resistance to the major biotic and abiotic stresses. Yield levels of the top yielding elite spring bread wheat genotypes ranged up to 6t/ha at Wadmedani station of Sudan under extreme heat stress, 7t/ha at Merchouch station of Morocco under terminal moisture stress (260 -300 mm) and 11 t/ha at Sids station in Egypt under optimum conditions. Genetic gain analysis from 1980 to 2017 showed 2.5, 1.3 and 2.3%year -1 increment at Merchouch, Wadmedani and Sids stations, respectively. Association mapping identified 14 associations related to grain yield on chromosomes 5B (4), 4B (3), 3B (2), 5A (2), 1B, 2B and 7B (1) under moisture stress. Significant MTAs for yield under heat stress have been also identified through genome wide association mapping studies. Wheat genotypes carrying the cytosine base at the wsnp_Ex_c12812_20324622 and wsnp_Ex_c2526_4715978 markers out-yielded the ones carrying the alternative bases

by 15% while genotypes carrying the cytosine base at only one of the two markers increased their yield by 7.9-10%, suggesting the importance of using these markers for MAS in breeding programs to increase yield under heat stress. Pedigree analysis showed that resistance sources for heat and drought tolerance in such elite wheat germplasm were introgressed from synthetic wheats and wild relatives mainly T. dicoccoides. ICARDA distributes yearly more than 400 of such genotypes to its partners through international nurseries. In the last 5 years alone, more than 60 bread wheat varieties of ICARDA origin have been released by National Agricultural Research System (NARS) in the CWANA and SSA regions.

ID 1193 | Discovering favourable gene resources for improving drought tolerance of wheat

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Developing drought-tolerant wheat varieties is an economical and effective strategy to cope with drought stress, which depends on the pyramiding of favourable gene resources. However, the identification of elite genes from a large amount of wheat germplasm resources is a daunting challenge due to its huge and complex hexaploid genome. Here, we take several genes as examples, such as TaSnRK2s, TaPP2A and TaSPLs, which are involved in the regulation of drought tolerance and grain yield. The functions of candidate genes were identified in transgenic plants, and functional markers were further developed based on their sequence polymorphisms in a wheat panel with higher genetic diversity. The favourable alleles of target genes were detected by combining linkage and association analysis, and their contribution and pyramiding effect for phenotypic variations were dissected. Our results demonstrated that a number of favourable alleles of drought-tolerant genes hide in germplasm resources. They have been concentrated in wheat varieties by “unconscious selection” in the history of wheat breeding. However, the frequencies of selection and utilization for different favourable alleles varied remarkably. Therefore, functional marker development and recombination of elite gene alleles will facilitate accurate selection for parental materials and progenies, thereby improving the breeding efficiency.

ID 1197 | Exploiting African rice germplasm to breed for reproductive drought tolerance in upland ecology

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There are two cultivated rice species; *Oryza sativa L.* (Asian rice) and *Oryza glaberrima* (Africa rice). *Oryza glaberrima* was the only rice species cultivated in Africa until the Portuguese introduced O. sativa from Asia. However, *O. glaberrima* is considered as an important rich reservoir of genes for tolerance to various indigenous biotic and abiotic constraints. Thus this specie is highly adaptable to local rice cultivation conditions in Africa. Probably due to such adaptability, *O. glaberrima* is still cultivated in some areas of West Africa. Such resistance to multiple constraints is a highly desirable character for rice cultivated by resource-poor farmers, who cannot afford to adopt intensive agronomic measures against such constraints in the rainfed ecology in Africa. To address the shortage of rice caused by yield reduction, African countries reverted to importation of rice with consequence significant loss of foreign exchange to the tune of 2 billion dollars per year for those countries already indebted. To meet the ever-growing demand for rice by

2030, a significant increase of at least 35% in yield is needed). One of the least expensive alternatives to meet this demand is the development of appropriate drought tolerant cultivars ensured with yield stability and adapted to environmental conditions in the region. During the past five years, the entire O. *glaberrima* accessions (~2500 accessions) of AfricaRice have been screened for reproductive drought tolerance in upland ecology. Six (6) lines with exceptionally high level of tolerance are being identified. They showed at least 30% yield gain over tolerant checks from Asia and Africa under severe reproductive-stage drought. The 6 lines with exceptionally high level of tolerant to drought could be good donors for breeding programs focus on high yielding and drought tolerance.

ID 1198 | Development and evaluation of *Trifolium repens* x *T. occidentale* interspecific hybrids for drought tolerance

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Trifolium repens (white clover) is a natural allotetraploid hybrid between the diploid species T. occidentale and T. pallescens. T. occidentale is adapted to dry, saline coastal habitats and transfer of drought and salt-tolerant traits to white clover could be valuable if interspecific hybridisation can be achieved efficiently and leads to fertile hybrid populations. To achieve hybridisation, 4x plants of T. occidentale were generated through chromosome doubling techniques. Interspecific 4x F1 plants were then produced without embryo rescue, followed by F2 populations and first and second backcross hybrids to white clover. Although male and female fertility were lower than T. repens, they were adequate to produce large amounts of seed from small numbers of inflorescences. Cytological studies on the hybrid plants have shown that chromosome pairing is occurring not only between T. occidentale and T. repens, but also between the ancestral sub-genomes of T. repens. Thus, interspecific hybridization has the potential for major genome recombination and opens the way for introgression of traits from T. occidentale into T. repens.

Forty-five hybrid families, comprising of BC1, BC2 and their inter-crosses, were evaluated in the field and compared with eight commercial T. repens cultivars under three natural summer drought periods. Data were recorded on visual growth and recovery after the dry months. Plants selected based on growth scores were included in an inter-crossing protocol to further reshuffle the interspecific chromosomes for introgression. A set of eight BC2 intercrossed families are currently being evaluated under well-watered versus controlled seasonal drought conditions in a rainout shelter facility for plant traits relevant to improved drought resistance, and variation among families. Traits measured include growth, plant spread, nodal rooting, stolon morphology, and stolon elongation rates. During drought stress leaf samples were taken for relevant biochemical traits including osmolality and 13C discrimination.

ID 1211 | Targeted mining of germplasm banks

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Germplasm banks worldwide are reserves of untapped native genetic variation. Despite this the use of germplasm bank materials by breeders is woefully limited. This is not due to a lack of desire for new variation for crop improvement rather significant challenges related to accession use including linkage drag, photoperiod incompatibility, poor adaptation and lack of useful documentation of germplasm bank resources. The relative affordability of sequence based genotyping has ushered in a new era in germplasm bank exploration. Initiatives in the three major commodities exemplifies this interest. In maize, CIMMYT together with Mexican and international partners has fully characterized the CIMMYT international germplasm bank maize collection using sequence based genotyping. Past and ongoing exploration of this data together with climate and phenotypic data reveals new paradigms and opportunities for variant discovery and allele mining opportunities extending the value of germplasm bank collections not just as resources for novel variation but as test-beds for identification of high value standing variation in elite breeding materials.

Combination of these resources is ushering in a new era of germplasm bank mining and pre-breeding for drought breeding; generating new understanding of high value genetic variants and providing access to novel variants in high quality bridging germplasm for direct breeding application.

ID 1213 | Transcriptomic analysis of photosynthesis related genes regulated by alternate wetting and drying (AWD) irrigation in flag leaves of rice

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Alternate wetting and drying (AWD) irrigation has been widely used to replace continuous flooding (CF), which does not result in yield loss while improving water productivity. However, how this practice affects gene expression to regulate physiology and morphology is largely unknown. In this study, we found that photosynthetic rate (Pn), stomatal conductance (Gs), transpiration rate (Tr) and chlorophyll (Chl) content significantly decreased when soil water potential decreased to -15 kPa in the AWD irrigation regime. We then analyzed the differences between AWD and CF irrigation practices in transcriptomic profiles for flag leaves. Genes were found to be differentially expressed in photosynthesis related pathways namely, Chl biosynthesis, photosynthesis - antenna proteins pathway, photosynthesis process and Abscisic acid (ABA) signal transduction pathway. The study provides important information on the morphological adaptations observed in the flag leaves in response to AWD irrigation, which will act as a basic framework to conduct molecular studies for improving rice cultivation.

ID 1231 | Discovery of germplasm and genomic regions to improve soybean drought tolerance

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Drought stress is the most important abiotic constraint affecting soybean [Glycine max (L.) Merr.] yield in rain-fed production areas. Combating this stress requires soybean plants which possess physiological mechanisms to tolerate episodic drought stress, because less than 10% of U.S. soybean production areas are irrigated. Evaluation of physiological traits that relate to drought tolerance can be used in breeding programs to identify genomic regions associated with the traits and genotypes with favorable combinations of alleles. The objective of this research was to evaluate

drought tolerance related traits in two populations in order to identify germplasm and genetic loci to improve soybean drought tolerance. A panel of over 200 genetically diverse soybean accessions genotyped with the SoySNP50K iSelect BeadChips was phenotyped for canopy wilting, carbon isotope composition (δ13C), nitrogen concentration, nitrogen isotope composition (δ15N), and transpiration response to AgNO3. Additionally, 130 recombinant inbred lines (RILs) derived from 'Hutcheson' × PI 471938 genotyped with the SoySNP6K iSelect BeadChips were evaluated for canopy wilting. Genome-wide association analyses and composite interval mapping revealed genomic regions controlling these drought related traits in soybean, and new soybean accessions were identified with high numbers of beneficial alleles and favorable breeding values for the traits. The germplasm and genomic regions identified through this research are being used to better understand the genetic architecture for these traits and be incorporated into elite germplasm to improve drought tolerance in soybean.

ID 1238 | Selection of drought tolerance lines for water limited environment in maize

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The impact of climate change is affecting the magnitude of rainfall and its distribution, which in turn has adverse effects on crop production. Plants exhibiting high drought tolerance are the most suitable targets of drought-related research and are the most promising sources of drought-related gene and gene regions to be used in the improvement of modern crop varieties. Maize, with its high photosynthetic rates and yields, is a particularly valuable agricultural resources, serving as a food source for human and livestock as well as a biofuel. However, continuously diversifying demands for maize production has led to the constant need for genetic improvement of various agriculturally and economically important traits. In this challenging scenario, molecular approaches offer novel opportunities for the dissection and more targeted manipulation of the genetic and functional basis of yield under drought conditions. In present study, we intend to dissect genetic factors contributing to drought tolerance in maize based on Genome-wide association studies (GWAS). Our objective is to 1) Identify maize genotypes for tolerance to drought stress, 2) Identify genetic regions contributing drought tolerance based on 55K SNP chip. We evaluated 150 maize inbred lines. The germination, survival and recovery rate were measured and we observed a significant difference between genotypes under stress environment. We shortlisted 15 maize inbred accessions categorized based on a) drought tolerant b) moderately tolerant c) drought susceptible. Our further step is to perform a GWAS scan on the shortlisted inbred lines. This will enable us to identify marker-trait association with candidate genes related to traits under drought conditions. Functional annotations of these putative candidate genes will give a valuable insights for maize breeding under drought conditions.

ID 1239 | Drought screening of rice diversity panels and the bridge to breeding

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Genebanks are stewards of the world's crop diversity, and represent large potential for sources of stress tolerance. Using material from the IRRI Genebank, we have characterized diverse sets of rice varieties under drought stress with two aims: 1) to identify new potential sources of drought tolerance that can be used in breeding, and 2) to test hypotheses about inter-relationships among physiological mechanisms. One

example is our work with a panel of ~200 aus genotypes. We identified several genotypes with high and stable yield under reproductive stage drought, we observed that leaf rolling under drought was more related to leaf morphology than to drought tolerance, and we are working on describing how different root traits show stable or plastic responses in the genotypes with highest yield under drought. From these experiences we learned that drought tolerance in rice can be conferred by many different combinations of physiological traits. Furthermore, we learned that the relatively subtle variation across large diversity panels may result in different conclusions than in studies using small numbers of highly contrasting genotypes.

Our next step is to use our physiology datasets on rice diversity panels to contribute to breeding for drought-prone environments. We aim to identify traits/genes/accessions that could improve yield under drought and that are not already present in the elite breeding pool. We are currently comparing our most interesting lines from diversity panels with the elite breeding pool for direct-seeded and rainfed environments with an aim to select accessions that will best complement the existing pool of drought tolerance among elite breeding lines.

ID 1253 | Ratio of kernel Δ13C/δ18O improves the selection potential of bread wheat for increased grain yield under different water regimes: A physiological perspective for direct application in wheat breeding

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A doubled haploid (DH) bread wheat population "B0767&" (Carberry/ AC Cadillac) comprising a set of 208 lines was grown for six years under irrigated and dryland environments to explore the potential of using the ratio of Δ13C/δ18O of mature kernels for selecting wheat germplasm with higher grain yield. Through principal component analysis (PCA) over 50% of variation in grain yield was explained by growing environments, with a major contribution by irrigated environments. PCA biplot analysis was used to select ten DH lines with contrasting grain yield for physiological characterization. Analysis of mature kernels for Δ13C and δ18O for 2016–2018 showed that grain yield was positively correlated with Δ13C under irrigated (R2=0.67) and dryland (R2=0.31) conditions, whereas it was negatively correlated with δ18O under irrigated (R2=0.74) and dryland (R2=0.68) conditions. Use of kernel Δ13C / δ18O ratio to predict grain yield, increased the coefficient of determination value in both irrigated (R2=0.91) and dryland (R2=0.61) environments. The line B0767&AG075 with high Δ13C/δ18O ratio and high grain yield also demonstrated cooler canopy and lower spike temperature, compared to the line B0767&AD028 with low grain yield, under both environments. Flag leaf stomatal conductance (gs) was lower in high yielding lines under dryland conditions showing a linear negative correlation with grain yield, but this relationship was polynomial under irrigated conditions. Our results indicate that the kernel Δ13C/δ18O ratio can reliably select wheat germplasm with high yield potential in both irrigated and dryland environments.

ID 1254 | Multi-environment genome prediction of winter bread wheat in response to French drought stress

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Drought is one of the main abiotic stress limiting wheat (Triticum aestivumL.) growth and productivity around the world. Even if the European temperate climate is supposed to be less subject to severe drought events, recent studies show that water deficit events have led to reduce the yield progression of the last two decades. Furthermore, many studies have been published about the increase of frequency and intensity of this abiotic stress. New high yielding and stress-tolerant cultivars are necessary to help farmers to maintain high productivity and this requires an improved understanding of the basis of physiological and genetic response to drought stress.

In the framework of the Breadwheat Project, a panel of 176 European elite cultivars, mostly French, German and English, has been evaluated in 32 field experiments (combination of years, location and treatment). Physiological traits, yield and yield components have been scored for each trial. A crop model was performed with detailed climatic conditions and soil water status, to identify the timing, intensity and history of stress for each combination of genotype/trial. Four scenarii of water deficit have been identified in this trial network. Tolerance stress index and reaction norms for genotype*environment interaction were calculated for each genotype regarding environment clustering. All cultivars were genotyped with the 420K SNP chip.

By using multi-environment mixt models and bayesian models, we performed genome wide association and genomic prediction studies on tolerance stress index. Several QTLs have been identified and estimation of allele effects shown that some loci are positively correlated with yield potential in drought stress conditions. Models accuracy will be detailed and the use of those results for post-registered varieties characterization or breeding programs will be discussed.

ID 1256 | Characterization of the genetic diversity of Chilean quinoa (*Chenopodium quinoa* Willd) germplasm using genome-wide association analysis

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Quinoa (Chenopodium quinoa Willd) is a pseudo-cereal belonging to the Amaranthaceae family, originating in the Andean region of South America. In recent decades, quinoa has gained global attention for its exceptional nutritional content, including high-quality protein and a range of important vitamins and minerals. Quinoa is well-adapted to marginalized soils and is able to tolerate abiotic stressors such as drought and high salinity, making it an excellent candidate for cultivation in drought-prone regions. While quinoa holds great potential for future food security in the face of climate change, the genetic diversity of this pseudo-cereal remains to be unraveled. Elucidating this diversity and identifying genetic variants related to relevant traits including yield and stress resistance will be crucial for future breeding programs.

This study was performed on a unique and diverse collection of germplasm consisting of local Chilean genotypes belonging to lowland/coastal ecotype which has been developed and is maintained by the Instituto de Investigaciones Agropecuarias (INIA) in Chile. The collection was sequenced and polymorphisms were identified in order to provide insight into adaptations. Genome wide association studies were carried out and the underlying genomic regions were investigated in order to identify potential candidate genes for improved breeding strategies. Significant SNPs were identified for traits including time to maturity and plot yield so that potential candidate genes could be investigated.

Quinoa's high nutritional content coupled with its resilience to abiotic stressors makes it an important crop for achieving global food security. Harnessing the genetic diversity of quinoa is an important step for bringing quinoa into the forefront of modern breeding programs.

ID 1267 | Empirical experience from CIMMYT of molecular marker-assisted breeding for maize drought stress tolerance improvement

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Drought stress has long been recognized as a major constraint to maize yield production in the developing countries, which affects approximately 20% of the tropical and subtropical maize in any given year. In the past several decades, tremendous efforts had been made by CIMMYT in conventional breeding to increase genetic gain for tolerance to drought. However, the generation of multilocation phenotypic data in conventional breeding is expensive and laborious. Modern genotyping technologies have made genotypic data for plant breeding relatively inexpensive, and molecular breeding offers the ability in reducing total breeding cost and improving breeding efficiency. In order to identify environmentally stable QTL under well-watered and drought-stressed conditions to deploy marker-assisted-selection, association mapping was performed in a collection of 300 tropical and subtropical maize inbred lines, and in more than 15 bi-parental populations consisted of more than 2500 genotypes, genetic architecture of grain yield, flowering time, and plant/ear height under well-watered and drought-stressed conditions were revealed. Linkage mapping was applied as well in multiple bi-parental populations developed in eastern and southern Africa and in Latin American. The stable drought-stress tolerance QTL detected in these genetic studies was proposed to deploy into the marker-assisted recurrent selection to enrich the allele frequency for a few desired traits. Empirical evidence showed that marker-assisted recurrent selection and genomic selection have similar performance as phenotypic selection, but at a lower cost, which should be incorporated into maize breeding pipelines to increase breeding program efficiency.

ID 1268 | Overexpression of a Maize Transcription Factor in Maize Increases Grain Yield in the Field

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Increasing maize grain yield has been a major focus of both plant breeding and genetic engineering to meet the global demand for food, feed, and industrial uses. MADS-box transcription factors have been shown to regulate genes involved in controlling numerous plant growth and development characteristics. We have increased and extended the expression of a maize MADS-box transcription factor gene, zmm28, under the control of a moderate-constitutive maize promoter. The resultant transgenic maize plants have increased plant growth, photosynthesis capacity, and nitrogen utilization. Overall, these positive attributes are associated with a significant increase in grain yield relative to wild-type controls that is consistent across years, environments, and elite germplasm backgrounds. We conclude that alteration in expression of a single native maize gene in maize can improve both resource capture and resource utilization, resulting in a significant improvement in grain yield, the ultimate complex quantitative trait.

ID 1271 | The role of cis-regulatory variation in adaptive drought responses in chickpea

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Gene expression regulation is an important component in facilitating plants to mount appropriate responses to environmental stresses like drought. While drought is the most limiting factor to crop production, the relative proportion and importance of cis- and trans¬-regulatory mechanisms in regulating gene expression in drought adaptive responses is a largely unexplored resource in breeding for drought tolerance. F1 hybrids generated from reciprocal crosses between wild (Cicer reticulatum) and cultivated (Cicer arietinum) were grown under unstressed control and declining soil moisture conditions along with parents. Implementing leaf RNASeq and read-backed phasing, binomial tests for deviations from 1:1 haplotypic expression ratio at any F1 locus was used to identify and characterize cis-effects while the difference in the F1 hybrid ratio from the parent 1: parent 2 expression ratio was used to estimate the trans effect per locus. Overall the F1 global hybrid transcriptome was distinct from either parent as estimated by principal component analysis (PCA), recapitulating variations in changes in transpiration rate under increasing drought stress between parents and hybrid progeny. This suggests novel allelic combinations in the hybrids resulting in unique expression profiles with potentially distinctive physiological outcomes. The proportion of this transcriptome differentiation that is due to cis and trans regulation, their expression effect sizes and associated biological pathways will be presented.

ID 1277 | Low-cost, multi-species iSelect XT bead chip array for enhanced scale of physiological and pre-breeding trait research and linkage into breeding programs for in-field impact

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The combination of reference genome assemblies with more ready access to precise phenotyping and genotyping tools operating at larger scale will accelerate the rate of trait dissection and gene discovery underpinning physiological adaptation to environmental stresses. To help assist research communities leverage the power of these genomes and enable integration of research across time and genotyping platforms, an advanced imputation-enabled multispecies Illumina XT 40K SNP chip for wheat and barley has been developed. This chip is based on published reference genome assemblies for each species and comprehensive genotypic datasets created for globally diverse germplasm. We show very high (>95%) accuracy for imputation from XT chip to wheat exome and barley whole genome SNP density, with imputation up to 581 693 wheat and 322 695 barley SNP. The chip also includes SNP content that directly links it to legacy genotyping platforms (e.g. iSelect 90K SNP and Axiom 35K SNP chip in wheat and iSelect 9K SNP chip in barley) plus legacy GWAS/QTL studies. Due to the low unit cost and its' high call rates across diverse germplasm, the imputation-enabled multispecies Illumina XT 40K SNP chip for wheat and barley can be deployed globally on larger populations by physiological and associated pre-breeding researchers working across a wide range of germplasm such as diverse landrace, wild and progenitor germplasm pools. Further, implementation at scale of the low-cost Illumina XT 40K SNP chip at the linkage interface between research and breeding programs will drive genomic enhanced trait introgression. Breeders will then use these traits and genomic tool in recurrent genomic breeding to deliver enhanced impact of research activities in the grower's field as improved varieties. This chip will be made accessible via a third-party agreement to researchers and breeders globally in 2020.

ID 1292 | Responsiveness of introgression lines derived from wild and exotic sorghum germplasm to farmer demands and climate change challenges

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Sorghum is vitally important for food security in semi-arid West Africa. The introgression of wild-and high transpiration efficiency genotypes may contribute genes for abiotic stress tolerance or novel traits. Engaging farmers in the process of varietal evaluation can help researchers to understand farmer's criteria for choosing new varieties and increase the probability of retaining progenies that will eventually be adopted. The objectives are to determine if BC1F5 lines derived from wild sorghum and high transpiration efficiency donors can be identified that outperform their recurrent parent for grain yield in the Sahelian zone and establish if introgressed progenies can be obtained with high farmer appreciation and suitable flowering time for adoption and resilience to climate stress. A total of 104 BC1F4 progenies derived from introgression of two wild parents, 47 from introgression of high transpiration efficiency donors, the farmer preferred landrace varieties used as recurrent parent, CSM63E, and 8 local- and improved check varieties were tested in both on-Station and on-Farm trials in Mali over two years. The rainfall ranging from 600 to 820 mm over the five test environments. A total of 21 progenies were retained by farmers, most of which (17) were derived from introgression of the wild-donors with the remainder (4) from the high transpiration efficiency donors. The five highest-ranking progenies for yield included three wild-introgressed progenies with grain yield ranged from 1110 to 1210 kg/ha followed by the local check with 1070 kg/ha and CSM63E with 1040 kg/ha. The three top yielding progenies combined high farmer appreciation overall and for panicle type, high grain yield, and acceptable flowering time compared the local recurrent-parent CSM63E. These progenies contribute to increasing the diversity of varietal in the context of climate change in the Sahelian zone of West Africa.

ID 1293 | Evaluation of near-isogenic lines of rice introgressed with DEEPER ROOTING 1 and Stele Transversal Area 1 under different water availability and soil compaction

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Deep and thick root systems have been considered to help rice adaptation to drought environment: deep root morphology may help acquisition of soil moisture from deeper layers and thick root linked with thick stele may better conduce water from rhizosphere to shoot. Three sets of experiments have been conducted at Nishitokyo, Japan, for a high yielding indica variety IR64 and its 3 near isogenic lines (NILs) with DEEPER ROOTING 1 (DRO1) and/or Stele Transversal Area 1 (Sta1) (Dro1_NIL, Sta1_NIL, Dro1Sta1_NIL); Exp 1 with all the 3 NILs under 3 different water availability (flooded lowland, water-saving lowland, rainfed upland) in 2013 and 2014, Exp 2 with Dro1_NIL under different soil compaction (none, moderate, hard) in 2013 and 2014, Exp 3 with Sta1_NIL in greenhouse and fields of different water availability (well-water, water deficit) in 2017 and 2018. The main findings are as below. (1) Dro1_NIL had 14% higher yield than IR64 across the 3 water availability due to higher harvest index, aboveground biomass, leaf area index, and number of grains in Exp 1, while Sta1_NIL just had higher harvest index and the combination of DRO1 and Sta1 did not surpass the increment from the effects of DRO1 alone. (2) Proportion of deep roots measured by basket method, which was correlated with root length

density at 30 to 60 cm, was larger in Dro1_NIL than IR64, but the difference was small under hard compaction, with a significant genotype × compaction interaction in Exp 2. (3) Sta1_NIL had larger stele transversal area than IR64 (37,800 vs 35,400 µm2), maintained higher mid-day leaf water potential and showed tendency of higher yield in Exp 3.

ID 1294 | Interactions between stomatal and mesophyll function in wheat with reduced stomatal density

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Stomatal pores control the exchange of carbon dioxide (CO2) and water between plants and the atmosphere, determining plant productivity and water use efficiency (WUE). Reducing stomatal density can lead to greater WUE in wheat. Optimizing increases in WUE without unwanted trade-offs in photosynthetic carbon gain and biomass production would theoretically result from increasing photosynthetic capacity and mesophyll conductance while maintaining low stomatal conductance (gs). But, the interactions between stomatal and mesophyll processes are poorly understood. To explore these questions, transgenic wheat was designed to alter expression of a gene involved in stomatal development. Using optical topometry, we observed approximately a 15-20% reduction in stomatal density compared to wildtype. The decrease in stomatal density translates to a decrease in gs and greater WUE, as in previous reports. Experiments are on-going that combine photosynthetic gas exchange measurements with tunable-diode laser absorption spectroscopy to test for changes in biochemical capacity and conductance to CO2 in the mesophyll.

ID 1300 | Did a common genetic gain across environmental scenarios increase drought tolerance of hybrid maize (1950-2015)?

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Past retrospective studies have shown substantial genetic gain for grain yield in Maize (Zea Mays L.). Within a European context, we quantified grain yield genetic gain in relation to distinct environmental scenarios, and further identified phenotypic changes associated to this genetic progress. Sixty elite maize hybrids released between 1952 and 2015 were tested in a European network of field trials. Experiments were assigned to scenarios of temperature and soil water availability based on environmental conditions measured at field level.

Grain yield genetic gain of 100 Kg.ha-1.year-1 was observed across environmental scenarios, and was associated with an increased grain number. This gain was observed in all scenarios. Delayed male flowering with no associated change in total cycle length was observed across generations, indicating longer vegetative phase duration for more modern hybrids. Crucially, this phenological change was found to account for a third of the increase in grain number observed across generations of maize hybrid release.

Overall, the genetic gain observed for the period 1952 to 2015 is the result of selection on constitutive traits, providing hybrids with a similar yield advantage across diverse environmental scenarios, but no specific advantage under drought conditions.

ID 1302 | Meta-QTL and Candidate Genes for Drought Tolerance in Wheat

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Meta-QTL analysis for drought tolerance in wheat was conducted utilizing BioMercator V4.2. For, information about ~374 QTL involving 43 drought-responsive traits was collected from 14 earlier studies conducted in the past using different mapping populations of bread wheat. However, for final analysis, only 62 of the above 374 QTLs were retained by the software due to inadequate information for remaining QTLs. A consensus map with 5,680 markers (SSRs, RFLP and DArT) was prepared using two reference maps available in GrainGenes database. The 62 QTLs were projected onto this consensus map, resulting in the identification of 18 meta-QTLs (designed as MQTL1 to MQTL18) located on seven different chromosomes. The number of QTLs associated with each MQTL ranged from 2 (for MQTL12) to 30 (MQTL 8, 9, 10, 11). Confidence intervals for meta-QTLs ranged from 2.07 cM (MQTL10) to 19.46 cM (MQTL12), which are narrower relative to the corresponding intervals carrying the original QTLs, suggesting that MQTLs are relatively robust, and are associated with closely linked markers. Therefore, the MQTL identified during the present study should prove useful in breeding programmes aimed towards development of drought tolerant wheat cultivars. The 18 MQTLs were also used to identify >100 candidate genes, which encoded proteins including glycosyl-hydrolases, protein kinases, zinc finger proteins, the transcription factors of WRKY family, cytochrome P450, proline dehydrogenase, etc. These proteins are known to be involved in abiotic stress tolerance. We propose to validate these candidate genes through a study of expression of these genes in seedlings of drought sensitive wheat cultivars and the corresponding tolerant genotypes grown under moisture stress.

ID 1303 | Leveraging information from managed stress trials: Selection indices for breeding for stress-prone environments

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The use of selection indices (SI) is widely established in the animal breeding sector. SI summarize the overall genetic merit (concerning multiple traits) of a selection candidate in a single quantity and thus facilitate an objective ranking. To construct a SI, usually economic weights for each trait have to be defined and the genetic covariance between these traits has to be known approximately. Having defined the weights appropriately, selecting for the SI instead of for individual traits leads to a maximized selection gain in the economic value of the population under selection. The incorporation of estimated genetic covariance among traits enables the optimal use of indirect selection to achieve the highest overall response.

Despite these theoretical advantages and its proven value in animal breeding, the use of SI is less common in plant breeding. Difficulties in assigning economic weights to -for instance- stress resilience or nutrition traits, differences in population structure, and challenges generated by changes in genetic covariance may have limited the implementation of SI in plant breeding.

We use multi-year data of advanced maize hybrid trials of CIMMYT and partners' Southern Africa program to estimate the genetic covariance of yield under optimal conditions, managed low nitrogen stress, managed drought stress and random stress. We discuss difficulties, such as the definition of economic weights or the estimation of genetic covariance, and the potential benefit for accelerating genetic gain when leveraging the different sources of information in a SI. In particular, the formalized indirect selection provided by the incorporation of genetic covariance may make the use of SI attractive for breeding for stress-prone environments.

ID 1305 | Genetic gain in *Sorghum bicolor* (L.) Moench in the US semiarid region

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Sorghum [*Sorghum bicolor* (L.) Moench] is an important staple food and source of animal feed in the semiarid regions of the world. Sustained rates of genetic gain are necessary to supply food and feed to a growing population. However, there are no reports on the rate of genetic gain in commercial breeding programs for sorghum. A five-year study that evaluated 86 genotypes commercialized between the decades of 1960 and 2010 was conducted in nineteen locations within the Sorghum belt of the United States. Yield varied between 3 and 12 Mg/ha. Preliminary results suggest an average rate of genetic gain of 0.024 Mg/ha/yr. However, substantial variation was observed among sites and years. Understanding the causes underpinning the variability in gain among locations and sites can inform the design of breeding programs to accelerate crop improvement.

ID 1307 | Managed-Environments: Taking aim at the Target Population of Environments

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Crop yield is a phenotypic outcome of an interplay of genetics and environment for the developmental, growth, partitioning and adaptation traits that determine crop yield potential and tolerance to biotic and abiotic stresses. Genomic sequences of crops, the ability to identify sequence polymorphisms among individuals and functional genomic technologies have opened up the opportunity for deep investigations of trait genetic architecture within the reference germplasm populations of breeding programs. The Target Population of Environments (TPE) for a breeding program is the environmental complement of trait genetic architecture. The TPE defines the range and biophysical characteristics of environmental conditions that crop genotypes are expected to encounter. In a drought-prone TPE, complex genotype-by-environment (GxE) interactions are commonplace for trait contributions and yield across environments. Therefore, significant research efforts have been invested by many disciplines into the study of trait GxE interactions and into the design of breeding strategies to enhance rates of genetic improvement in the presence of GxE interactions. An important component is the design of Multi-Environment Trials (METs) in which different genotypes are tested and compared across a sample of environments from the TPE. A practical MET design principle is to align the composition of the sample of environments included in the MET with the structure of the expected environmental composition of the TPE. Randomly sampling environments across locations and years can often result in poor MET-TPE alignment. Phenotyping costs and sampling logistics impose significant constraints on the design of METs to achieve the optimal MET-TPE alignment. Managed-Environments have been widely proposed and in some cases successfully used to stratify the sampling of environments and improve the MET-TPE alignment over alternative sampling strategies. The quantitative genetic principles for design of Managed-Environments to enhance MET-TPE alignment are discussed and examples of application of these design principles are reviewed.

ID 1310 | Identification and Mapping of QTLs Associated with Drought-Responsive Traits in a JUG-03 X Valencia-C Peanut Population Measured in the Field and Root Cylinders

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A recombinant inbred line (RIL) population comprising of 286 lines was developed by crossing JUG-03 × Valencia-C for mapping the QTLs and identifying the genomic regions associated with different components of drought tolerance. GBS (Genotyping-by-sequencing) approach was employed to generate genotyping data. A high-resolution genetic map was developed with 1323 SNP loci mapped on 20 linkage groups spanning 2003.13 cM with an average marker density of 1.53 cM. QTL analysis using multi-location phenotyping with a dense genetic map and genotyping data identified 27 major-effect QTLs with phenotypic variation explained (PVE) ranging from 10.9-61.6% for traits measured under field conditions and total 4 QTLs with PVE ranging 5.2-7.4% for the traits measured utilizing root cylinders. Major QTLs were identified for different components of drought, such as haulm yield, protein content, 100 pod weight, test weight, SPAD, palmitic acid, and stearic acid. Only minor QTLs were identified for harvest index, transpiration efficiency, total transpiration, and haulm weight. Identification of QTL regions will uncover important genes and transcription factors shown their involvement in different components of drought tolerance and followed by marker development, which can be deployed to enhance groundnut yield under drought stress.

ID 1312 | A transcriptomics approach to discern molecular differences in distant durum varieties that have been commercially grown in Canada

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Much of Canadian wheat is produced in Saskatchewan, where drought and heat stress during anthesis and grain-filling periods have a significant negative impact on yield. The prevalent practice in varietal development in Canada is influenced by grain quality and agronomic standards that has generally limited sourcing beneficial alleles from wheat lines capable of producing a crop in the short growing season of spring cultivation. Our study is focused on two durum wheat cultivars: Pelissier, an Algerian drought tolerant line that is >100 years old and Strongfield, an elite Canadian cultivar. Pelissier has been a parent at multiple points in the pedigree of Strongfield. Thus, interrogation of the genetic and molecular differences in two cultivars (and their segregating population) is likely to reveal the comparative and contrasting aspects of two distant varieties that have been commercially grown in Canada. Pelissier is known to produce a larger root system in general and this is also true in comparison with Strongfield under both un-stressed and water deficit conditions; it also withstands a drought stress that is detrimental to Strongfield. Pelissier demonstrated photosynthetic stability under water stress as well as heat stress conditions. Given these contrasting phenotypes, flag leaf and root tissue was collected from these cultivars grown in rhizotrons (PVC tubes, 7.5 cm diameter, 120 cm length) under well-watered (95% holding capacity) and drought (30% holding capacity) conditions. The transcriptome revealed differentially

expressed genes. These results were considered in light of the challenge in imposing drought conditions in a phenologically germane manner for the plants to experience stress at or soon after booting. Furthermore, the differential developmental aspects of wheat were also taken into consideration. The results are presented and discussed in light of these critical aspects that are often missed in interpretations of global gene expression profiling.

ID 1322 | Genomic basis of drought adaptation in West African sorghum

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Drought is pervasive in semi-arid regions of West Africa, so increasing yield under drought is a top priority for the region's sorghum breeding programs. Phenotypic selection is stymied by the diversity of drought scenarios encountered, while genotypic selection is limited by our poor understanding of the genetics of drought adaptation. Based on evolutionary models of sorghum in West Africa, we hypothesized that its drought adaptation has an oligogenic basis (few genes of moderate effect) suitable for marker-assisted selection. To test this hypothesis and identify drought-adaptive alleles, we formed a regional collaborative network (breeders, physiologists, geneticists) to conduct a series of genome-wide association studies (GWAS). We established a West African sorghum association panel (landraces and breeding lines), genotyped >400,000 single nucleotide polymorphisms, and phenotyped drought-related traits under managed water stress in field (Senegal) and lysimeters (Niger) over several years. The quality of managed stress phenotyping was evidenced by (i) moderate to high trait heritabilities and (ii) significant crossover genotype-by-environment interactions for canonical pre- and post-flowering drought tolerant lines (Tx7000 and BTx642). GWAS identified marker-trait associations for several putative drought-adaptive traits, including panicle weight under water stress. While the findings are consistent with the oligogenic hypothesis, we continue to consider alternative hypotheses such as confounding population structure and/or polygenic variation. Additional field and modeling experiments are underway to test the hypothesis that off-season managed stress is relevant to rainy-season on-farm conditions. These studies form the foundation of a genomics-enabled breeding network to improve sorghum adaptation in West Africa.

ID 1328 | Breeding for drought tolerance – what have we (not) learnt?

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Drought tolerance is one of the best-researched topics, its analysis spanning decades, yet there is surprising little evidence in which crop improvement programs drought tolerance is systematically being pursued as a breeding goal, and with what benefits. Investments and achievements in augmenting the drought tolerance through breeding seem to be disproportionally less than overall drought research investments. This is concerning given the well-described future impacts of climate change on the frequency of drought, particularly in tropical crop production environments. The complexity of drought tolerance, the large number of genes involved and the likely GxE interactions, seem to take breeders away from combining breeders, physiologists and geneticists insights into applied breeding programs. Breeders have been successful in making systematic yield gains in variable environments, i.e. for the trait “yield” that is likewise determined by many genes and affected by GxE interactions. The same can be true if the highly polygenic nature and GxE interactions are taken as facts when designing drought breeding programs.

CIMMYT's maize breeding program is among the best-documented breeding programs that has made steady progress for improving yields in drought environments. The presentation will summarize insights from environmental, genomic and physiological studies that have guided and further optimized the breeding approach. It encourages crop breeders to make a renewed and rational effort to incorporate drought breeding into their breeding strategy where relevant.

ID 1329 | Genetic analysis of yield in drought-prone areas with a scenario-dependent probabilistic approach

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Yield results from month-long feedback processes, whereas mechanisms of drought response operate over minutes following changes in transpiration demand. Evolution has constrained these mechanisms into strategies for stabilizing the water status of leaves and reproductive organs in rapidly varying environmental conditions. These constraints differ from those maximizing yield because of trade-offs between carbon accumulation and the risk of deleterious plant water status. Breeders successfully selected for high and stable yield across environments, including dry environments, but in doing so they selected for constitutive traits. An analysis of the genetic progress showed that the allelic diversity that governs drought acclimation was left largely unexploited because it results in positive or negative effects on yield depending on drought scenarios. We propose a probabilistic approach where the benefits and risks of alleles combinations are estimated for the most likely drought scenarios in each region, under current or future climates. Integrating

phenomics, modeling and genomic prediction allowed us to identify the combinations of alleles with positive effects on yield in each drought scenario. For this, we identified traits genetically linked to yield in each scenario with experiments in phenotyping platforms and field networks. One third of the yield variance in a given environmental scenario was accounted for by QTLs of traits measured in phenotyping platforms that co-located with yield QTLs. We converted these traits into model parameters, which were in turn predicted based on allelic values for new genotypes, and allowed yield prediction in 100s fields. This strategy may allow exploiting new alleles for yield in dry regions by explicitly taking into account those alleles that optimize adaptive responses in expected environmental scenarios for each region.

ID 1330 | Development of biotechnology tools to improve maize drought stress tolerance

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The Genomics for Climate Change Research Center (GCCRC) is a joint research center created by the State University of Campinas (UNICAMP), and the Brazilian Agricultural Research Corporation (EMBRAPA) devoted to creating biotechnology assets to help developing plants with increased drought tolerance. The GCCRC uses genomics tools for gene discovery and unravels the plant microbiome interaction. Gene editing and transgenesis is used for developing maize plants incorporating novel traits associated with drought tolerance. The GCCRC activities are executed through the biotechnology platform "from gene to trait" that spans from gene discovery to proof of concept under field trial conditions. Unexplored and unknown genes associated with responses to abiotic stresses have been discovered and transformed into sugarcane and in the maize B104 inbred line. Synthetic microbial communities (SynCom) composed of beneficial bacteria isolated from sugarcane has been constructed and evaluated in maize. Inoculation with SynCons has shown a significant impact on maize yield in stressful conditions in both controlled conditions and in the field trials. Sequencing and assembly plant genomes and their associated microbiome of the rupestrian fields are using the discovery of new genes and microbes that help plants adapt to extreme environments.

ID 1333 | Deployment of large-effect drought tolerance QTLs in rice cultivar development at IRRI

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Decades of excellent research has been done in identifying major QTLs contributing to reproductive-stage drought tolerance in rice. Yet the benefit of these loci still remains to be realized in routine breeding operations, with the frequency of most in elite material remaining below 5%. Contributing factors to this are lack of reliable, high-throughput marker systems, lack of availability in elite material, and lack of information on their effectiveness in a diversity of elite backgrounds. Efforts to address these concerns are described, as well as principles to avoid the same situation occurring with future trait development efforts.

SESSION 6: MANAGING CROPPING SYSTEMS FOR ADAPTATION TO WATER-LIMITED ENVIRONMENTS

ID 1017 | Conservation agriculture increases maize production in the dry regions of Mexico

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In the semi-desert areas of Mexico, farmers often produce maize in conditions that are not generally considered suitable for the crop, because it is an essential part of their daily diet and culture. Rainfall in these areas is low and erratic, leading to low yields and high risk of crop failure. Conservation agriculture is a production system based on minimal tillage, soil cover with residues or crops and crop rotation, which has been shown to improve maize yields under rainfed conditions where water is a limiting factor. However, these general principles have to be adapted to the local reality, which can be difficult in low rainfall areas because of low crop residue production. In order to adapt conservation agriculture and other sustainable agriculture practices to the diverse agro-ecological conditions, CIMMYT set up a network of over 60 collaborative trials across Mexico, starting in 2010. Seven of these trials are located in regions that generally receive less than 600 mm of rainfall during the growing season. The results of the trials indicate that conservation agriculture can be adapted to maize production in low rainfall conditions. At all sites, conservation agriculture improved maize yields compared to conventional tillage based systems but the profitability of even the highest yielding treatments remained low. Challenges include providing enough residue cover and finding suitable rotation crops for each region that are competitive with maize.

ID 1048 | Combining eco-physiology, phenomics and crop modeling to enhance daytime and nighttime water-saving in cereal crops

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Under Mediterranean conditions, drought tolerance is often associated with enhanced water availability during seed-fill. Over last 15 years, it has been established that water-saving traits based on transpiration rate (TR) responses to increasing evaporative demand or to decreasing soil moisture could lead to improving water-limited yields. Yet, the extent of natural variation for these response curves remains unknown. In addition, the role of other traits, such as nighttime water-saving by decreasing nocturnal transpiration (TRN) remains unknown and even controversial. Furthermore, information on yield gains arising from such traits is limited, especially for small, food-insecure countries. Here, we describe investigations on wheat and barley describing i) a high-throughput approach for phenotyping TR responses to evaporative demand, revealing substantial diversity among over 100 genotypes and ii) an extensive natural variation in TRN, along with evidence of its circadian control and influence on daytime gas exchange. Evaluating these traits using simulation modeling for Tunisia, where wheat drought tolerance is critical to food security, we identify regions where yield gains could reach 30% dependently on the trait. Critically, even for such a small country, our integrated approach highlighted the need for location-dependent breeding for cultivars equipped with different trait combinations to significantly improve drought tolerance.

ID 1169 | Spectral assessment of chickpea morpho-physiology from space, air and ground

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Chickpea (*Cicer arietinum*) is an important grain legume in semi-arid regions and water-stress is a major constraint to its productivity. There is a growing demand for chickpea grains but climate change toward greater aridity results in higher precipitation instability and risks yields. The ability to assess water potential can support irrigation decisions and may enable more efficient irrigation. We aimed to assess water potential, leaf area index (LAI) and grain yield by spaceborne, airborne and ground spectral sensors. During the growing season of2019, field experiments were conducted in two locations, representing different agro-ecologies in Israel. Five irrigation regimes were applied: 50%, 75%, 100%, 120% and 140% of Penman-Monteith evapotranspiration were implemented. Plants were characterized weekly for water potential and LAI, and grain yield data was obtained at the final harvest. Canopy reflectance was acquired with a VENµS MicroSatellite, a drone mounted multispectral camera and hyperspectral ground level spectrometer. Leaf water potential (LWP), LAI and grain yield values differed between most irrigation treatments. The VENµS data based on partial least squares regression (PLS-R) analysis for water potential, LAI and grain yield resulted in R2 and RMSEV of 0.8 and 0.217 MPa; 0.63

and 0.74 m2m-2; and 0.82 and 0.44 t ha-1, respectively. The PLS-R analysis for hyperspectral data for LWP, LAI and grain yield resulted in R2 and RMSEV of 0.74 and 0.18 MPa; 0.80 and 0.89 m2m-2; and 0.84 and 0.45 t ha-1, respectively. The multispectral 5 bands imagery was used to calculate vegetation indices. The best vegetation index for LWP, LAI and grain yield were OSAVI, NDVI and TCARI, respectively, R2 and RMSE values of, 0.56 and 0.168 Mpa, 0.69 and 0.78 m2m-2, 0.874 and 0.38 t ha-1, respectively. Field experiments during 2020 will serve to assess the repeatability of the predictions and validated the reported correlations.

ID 1191 | Long-term evaluation of tillage methods in fallow season for soil water storage, wheat yield and water use efficiency in semiarid southeast of the Loess Plateau

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Fallow tillage methods play a major role in improving soil water storage and hence wheat yield in Loess Plateau. However, the efficacy and stability of such methods need to be further validated in long-term field observation. A 7-year field experiment (2009–2015) was established in winter wheat fields at Wenxi, semiarid southeast Loess Plateau. The objectives were to determine the responses of soil water storage, and yield to three different tillage methods: including deep ploughing, subsoiling and no-tillage. Results indicated that compared to no-tillage, the soil water storage (0–300 cm) was averagely increased by 7.8% and 6.0% during fallow season, 13.7% and 9.8% in growing season under deep ploughing and subsoiling respectively. Furthermore, the increasing magnitude in soil water due to deep ploughing and subsoiling was, on average, 10.1% and 5.5% higher in dry season than that in wet one. Improved soil water condition under deep ploughing and subsoiling significantly increased the ear number and yield by 20.2% and 15.9%, 30.8% and 25.8% respectively, but did not affect seed number and weight of seed over the experimental seasons. Moreover, yields under deep ploughing and subsoiling were averagely increased by 35.2% and 24.8% in dry season, 28.7% and 20.6% in wet season respectively. Accordingly, WUE and precipitation use efficiency were increased by 12.1% and 31.9% under deep ploughing, 11.1% and 25.0% under subsoiling respectively. Critically, we found that with an increase of 10% water storage efficiency during fallow season, ear number, yield and WUE could be increased by 0.2 million ha−1, 241.1 kg ha−1 and 0.6 kg ha−1mm−1 respectively. Results indicated that deep ploughing in fallow season should be adopted as a promising strategy to retain soil water availability and hence boost wheat productivity in semiarid Loess Plateau.

ID 1194 | Effects of whole soil-plastic mulching with hole-sowing on soil temperature, moisture and yield of buckwheat in arid lands

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To provide a theoretical basis for exploring a high-yield and high-efficiency technique for buckwheat (*Fagopyrum tataricum* [L.] Gaertn.) in semiarid areas of China, we carried out long-term field experiments (2015 to 2017) at the Dingxi Experiment Station of Gansu Academy of Agricultural Sciences in the Loess Plateau of northwestern China. Two planting patterns, namely whole field soil-plastic mulching with hole-sowing (FMS), and hole-sowing on bare soils (CK), were set to investigate the effects of FMS on soil temperature, moisture, yield and water use efficiency（WUE）of buckwheat. Compared

with CK, FMS increased soil water storage (SWS) of 0 to 300 cm layer in normal (2015) and dr years (2016) by 2.91% (16.9 mm) and 5.79% (25.59 mm) ($P < 0.05$). However, no significant difference was found between them in the wet year of 2017. FMS increased average soil temperature (Ts) in 0−25 cm layer by 2.27▮ and 2.20▮ in normal and wet years, respectively. While in dry year with higher temperature, FMS lowered Ts during branching to filling stages. Similarly, FMS appreciably decreased seasonal mean Ts of 0 to 25 cm layer compared with CK. On average, FMS increased crop water consumption in 0 to 300 cm soil layer by 3.89% during the three consecutive years, but the difference was not significant ($P > 0.05$). Nevertheless, FMS increased yield by 7.26% to 95.25%, and WUE by 7.59% to 87.08% ($P < 0.05$). The results demonstrated that the high-yield and high-efficiencyof FMS were more significant during drier years. In conclusion, FMS could increase SWS prior to sowing, decrease Ts during high-temperature periods, prolong filling stage, resulting in the promoted the development of plants, and the significantly enhanced yield and WUE of buckwheat.

ID 1200 | Effects of top dressing with reduced nitrogen fertilizer and density enhance-ment on water use efficiency and growth of potatoes planted in mini-ditch on ridges with plastic mulching

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The optimization of ridge-furrow construction, plant density and fertilizer application are three promising ways to increase rainwater use efficiency, crop yield and water use efficiency. A long–term field experiment was carried out in semi–arid area of northwestern China from 2015 to 2017, using potatoes planted in mini-ditch on ridges with plastic mulching, to explore the effects of fertilizer application and plant density on soil temperature, water consumption at different growth stages, yield and water use effi-ciency. Two plant densities (low density of 49,500 plants ha– 1, and high density of 64,500 plants ha–1) and three fertilization methods (traditional fertilizer application, PM; reduced chemical fertilizer dressing, PMN; and organic fertilizer substitution, PMO) were set up as treatments, using randomized block design with three replications. The high density lowered water consumption in pre-flowering stage, above-ground biomass per plant, and water use efficiency. However, LAI and water consumption were improved in post–flowering stage. Compared with low density treatments, LAI in high density increased by 3.64%–15.01%, and water consumption in tuber bulking period increased by 6.50%–48.52%. PMN and PMO decreased water consump-tion during pre– flowering period, but increased it during post–flowering period, resulting in a 6.95%–49.85% increment in above-ground biomass at bulking stage. On average, PMN increased potato tuber yield and WUE under low density by 9.96%–20.87% and 13.64%–17.61%, 5.46%–20.81% and 13.25%–45.24%, respectively, compared with PM and PMO. Consequently, the increment of plant density did not affect potato tuber yield and WUE. However, PMN and PMO promoted potato water utilization in post–flowering period and increased LAI, resulting in significant incremen of potato tuber yield and WUE, showing an efficient way for fertilization management of potato in semiarid loess plateau of northwestern China.

ID 1201 | Effects of Micro Ridge-Furrow with Plastic Film Mulching and Bunching Seeding on Water Consumption Characteristics and Water Use Efficiency of Winter Wheat at Semiarid Areas of Northwest Loess Plateau

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The precipitation is inadequate in arid and semiarid areas of Northwest Loess Plateau. How to use this part precipitation sufficiently, is the key method to increase the rainfall use efficiency and yield stably of winter wheat in this area. To understand the effect of PRF on soil water storage, water consumption characteristics, yield and water use efficiency of winter wheat. A field experiment has been conducted from 2011 to 2015 on Northwest Loess plateau (104°36′ E, 35°35′ N) . The four-years average soil water storage of PRF at sowing and re-green stage was higher than PMS, SM, CK by 24.3, 38.8, 7.4 mm and 18.2, 26.9, 67.8 mm, respectively. PRF averagely increased wheat evapotranspiration from heading to filling stage by 36.0 mm than PMS. As compared with SM and CK, it increased by 12.1 mm and 16.7 mm, 40.8 mm and 37.6 from re-green to heading and from filling to maturity respectively. The yield of PRF was highest among four treatment, it reached to 4 373.6-4 950.0 kg·hm-2, increased by 2.4%-12.7% than PMS, the significant difference were observed in 2012-2013 and 2014-2015. It significantly higher than SM (except for 2012-2013) and CK (increased by 35.8%-43.8%) in four experimental years. The water use efficiency of PRF increased by 0.4%-12.8% as compared with PMS, the significant difference were observed except for 2013-2014, it also significantly higher than SM (except for 2014-2015) and CK (significantly increased by 8.1% -42.1%) in four experimental years. PRF could increased soil water storage in 0-200 cm profile in sowing and re-green stage, resulted in the increment of grain yield and water use efficiency. Consequently, was the better cropping patterns for high yield and efficiency of winter wheat on semiarid areas of Northwest Loess Plateau.

ID 1204 | Half a world away: How the success of winter wheat in the Pacific Northwest can increase wheat yields in semi-arid southern Australia

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Wheat (*Triticum aestivum* L.) is the most widely-grown crop in the Mediterranean semi-arid (150 – 400 mm) cropping zones of both southern Australia and the inland Pacific Northwest (PNW) of the United States of America (USA). Low precipitation, harsh winters and heat and drought conditions during late spring and summer limit wheat yields in both regions. Due to rising temperatures and reduced autumn rainfall in southern Australia since 1990, cropping conditions in these two environments have grown increasingly similar. This presents the opportunity for southern Australian growers to learn from the experiences of their PNW counterparts. Wheat cultivars with an obligate vernalisation requirement (winter wheat) are an integral part of semi-arid PNW cropping systems, but in Australia are most frequently grown in cool or cold temperate cropping zones that receive high rainfall (> 600 mm p.a.). Despite research showing that early-sown winter wheat cultivars can increase water-limited potential yield in semi-arid southern Australia, there has to date been little breeding effort invested in winter wheat for the region. The genotype x management strategies developed over 120 years of winter wheat agronomy in the PNW highlight the potential advantages early-sown winter wheat offer growers in low-rainfall environments. The increased biomass, stable flowering time and increased late-summer establishment opportunities offered by winter wheat genotypes ensure they achieve higher yields in the PNW compared to later-sown spring wheat. Traits that make winter wheat advantageous in the PNW may also contribute to increased yield when grown in semi-arid southern Australia. Specific traits present in winter wheat genotypes that give them an advantage in semi-arid cropping environments and management practices that best exploit this advantage are also discussed.

ID 1208 | ASALEE, a conception tool for farmer crop rotation concerning water quantity availability

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In France, 1.5 million hectares are irrigated using 3 billion of m3. Climate change increases pressure on water resources for agriculture and risk for farm profitability. Considering this unpredictable context, farmers ask for tool to help them choose crop rotation depending on their soil, climate conditions and risk behaviour. The objective of ASALEE is to compare crop rotations in rainy or irrigated conditions, considering water quantity management, economic and climate variability on technical and economic indicators : net margin, work time, water use... Crop rotations are defined in co-conception meetings with farmers and advisors in order to adapt their management to local issues. ASALEE is built in 2 units, a user interface and a calculation engine coupling:

(1) Irré-LIS®, a water balance with a progressive TAW according to rooting;
(2) Production functions of the form y/Y=f(RET/MET) with y = yield with water stress, Y = yield without water stress, RET = real evapotranspiration and MET = maximal evapotranspiration, to estimate yield losses;
(3) Price variability model (500 scenarios) based on historical references and economic database;

Both units are linked to database for price, climate, crops, soils… Simulations are made on climatic series (20 years). Mean, median, 2nd decile and 8th decile of the indicators are presented in the results. The occurrence to reach the return objective of farmers can be assessed with this analysis. The model has been used for Boutonne area (17), a French watershed in Western France. Farmers wanted to test diversification, integration of high value crops and systems representing complete break with their actual practices (relay cropping, three crops in two years…). The tool can be used as a basis for a group discussion or to produce an operational diagnosis at a farm level. It was developed in collaboration with INRAE, Terres Inovia and Chambre Agriculture 17.

ID 1224 | Effects of mycorrhizal inoculation on drought tolerance of African rice (*Oryza glaberrima*)

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In West Africa, rice is the most consumed crop and countries are developing programs to achieve perennial rice self-sufficiency. However, rapid population growth in the region and global changes associated with uncertainties in rainfalls will inevitably increase the pressure on water resources for agriculture. In that context, it is necessary to adapt rice cultivation to reduced water input and increase its tolerance to drought.

Establishment of symbiosis between rice roots and arbuscular mycorrhizal fungi (AMF) can lead to improved rice drought stress tolerance. Recent evaluation of AMF-inoculation effects in a small panel of rice varieties adapted to different agrosystems suggested a rice genetic control of AMF-symbiosis beneficial effects (Diedhiou et al., 2016). However, the genetic, molecular and physiological determinants controlling improved rice performance after AMF-symbiosis establishment, particularly under drought, remain elusive.

Using a high-throughput phenotyping platform (Cabrera-Bosquet et al., 2016), we quantified drought response in a panel of 150 sequenced *Oryza glaberrima* genotypes after inoculation, or not, by an AMF. Shoot growth and transpiration was followed daily through imaging and weighing, respectively, which allowed estimation of water use efficiency at harvest. Our recent results reveal large variability in AMF-inoculation response. The mechanisms involved are being analyzed using a combination of physiology, association genetics and gene expression.

ID 1242 | Drought adaptation: Insights from species comparison among C4 cereals

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Maize is considered more “drought-sensitive” than sorghum and pearl millet, mostly for its longer duration and larger leaf area, but rigorous trait comparison among these crops is scant. Transpiration efficiency (TE) was compared, across seasons varying in VPD, water regimes, soils, and in plants where reproductive organs were removed. Traits determining water usage – i.e. transpiration response to increasing VPD and soil drying, and canopy development in high/low VPD conditions - were also compared.

Maize had higher TE than sorghum and pearl millet across VPD seasons and water regimes, except under severe stress and high VPD. Under low VPD maize yielded more under stress but water usage was similar among crops, suggesting plant density, rather than water, was limiting sorghum and pearl millet yield. Maize conserved water preferentially by restricting transpiration under high VPD and higher soil moisture, consistent with its higher TE, whereas sorghum and pearl millet conserved water mostly by reducing leaf area and somewhat by restricting transpiration under high VPD. Removing panicles depressed TE in maize and sorghum, but not in pearl millet, suggesting source-sink relationship influenced the control of stomata opening. Soil had a strong effect on TE, depending on VPD and crops: TE differed among soils but only under high VPD, and there, TE differed among soils in maize but not in sorghum and pearl millet. This could be consequences of hydraulic conductivity differences in the soil-plant continuum affecting the transpiration response under high VPD in a crop-specific manner. Based on these results, “less-bred” pearl millet and sorghum should have their sowing density increased, be bred for TE and higher density, and be fitted to soils and VPD conditions that give them a comparative TE advantage over maize.

ID 1249 | Savings of irrigation water and N fertilizer inputs for direct-seeded rice in dry and wet seasons during El Niño period in Central Colombia

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In Colombia where rice is mostly dry-drill seeded without puddling with high input of inorganic nitrogen (N) fertilizers, little quantitative information is available for designing strategies to reduce N fertilizer and irrigation water inputs in different seasons. We conducted on-station field experiments within the framework of SATREPS project between Japan and Colombia (2014-19) to quantify the effects of reduction of N fertilizer and irrigation inputs on grain yield of drill-seeded rice (FEDEARROZ60 variety) on zero-level field in Saldaña in dry (2015) and wet (2016) seasons, which turned out during El Niño, with 5 N levels (220, 180 [two sources], 140, and 0 kgN ha−1) and 3 irrigation strategies (every 3 day water supply [conventional], mild saving with short-extended interval, strong saving with long-extended interval). The main results were (1) mild water saving during the wet season improved water productivity (as calculated per total water supply) without yield penalty but not during the dry season of only 14 mm rainfall from establishment to post-flowering stage with higher evapotranspiration (in spite of similar soil water status), (2) rice crop in the wet season had higher photosynthetic parameters (e.g., stomata conductance, transpiration, carbon isotope discrimination), and agronomic parameters (e.g., water productivity, N recovery, N uptake, radiation use efficiency, grain N concentration), (3) reducing the N application rate from 220 to 140 kgN ha−1 did not reduce yield in either season in all irrigation strategies in spite of slightly reduced N uptake. These results indicate successful water savings depending on seasonal conditions and large potential for improvement of N fertilizer use efficiencies in direct-seeded rice in the tropical lowlands of Colombia. The other achievements in the project are also discussed including root system manipulation for resource acquisition.

ID 1250 | Agroecological characterization of drought-prone rice production in non-system tanks of South India

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Absence of large rivers and uneven seasonal rainfall historically developed “tank irrigation rice ecosystem” in South India. Two non-system tanks with different sizes (28 vs 16 ha of catchment area) in the same rain shadow region in Virudhunagar district, Tamil Nadu (9°N, 78°E), were monitored for 6 years from 2012 to 2017 to assess vulnerability of “samba” rice production which is planted between August and February as a single crop. The historical rainfall after 1985 during the rice growing season was ca. 560 mm, which recently declines (e.g., 246 mm in 2012). Drought caused crop failure in 2 years (i.e., 2016, 2017) out of the 6 years in the smaller tank and 1 year (i.e., 2016) in the larger tank. Field based grain yield was lower in the smaller tank (n=74), with larger spatial and yearly variability, compared with the larger tank (n=106). Shortage of rainfall in 2012 reduced numbers of irrigation from the tank and increased borewell irrigation in both tank, but the small tank depended more on borewell (ca. 60%) than the larger tank (ca. 30%) with more unharvested field numbers (35%) than the larger tank (7%). Yearly and spatial differences in grain yield in the smaller tank (i.e., 1.1- 4.5 t/ha) were associated with N fertilizer application rate (i.e., 90-150 kgN/ha). Carbon isotope discrimination was negatively related with total water use, yield and water productivity in the smaller tank in 2014. Grain yield at the head and middle in the tank ecosystem was higher than the tail in both tanks. Shorter duration ANNA4 and JGL varieties attained higher yield and water productivity than longer duration BPT variety. The variable fragile ecosystems should be strengthened by development of adoptable water-saving technologies.

ID 1258 | Maize grain yield in contrasting production systems of Argentina: drought occurrence and kernel number determination

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Before market release of genetically-modified (GM) insect-tolerant maize (*Zea mays* L.), most part of the Argentine production of this staple was concentrated in an area of ca. 3-4 mill has located in the humid region of the so-called Central Pampas that range between 32-36 ºS and 58-64 ºW. Additionally, most part of those crops were traditionally sown the earliest possible in spring to minimize the risk of summer water deficits around flowering. GM maize allowed to delay sowing, a practice that had three main effects: (i) to place critical periods for kernel set in environmental conditions less prone to water deficits, (ii) to increase the area cropped to maize in sub-humid and semi-arid regions of the country, and (iii) to reduce yield potential in years with no water stress. Currently, temperate maize in the Pampas is sown in an almost 50-50 % distribution between early (ca. mid Sep-mid Oct) and late (late Nov-Dec) sowing dates, including some double-cropping among the latter. These alternatives expose the crop to multiple climatic scenarios, which combined with the broad variation in soil types modify the occurrence and intensity of water deficits along the cycle. In our presentation we will analyze maize response (i.e. grain yield as well as its physiological determinants and numerical components) to water deficits across humid and sub-humid mid-latitude environments of Argentina considering the described management alternatives. Special emphasis will be given to kernel number determination.

ID 1259 | Optimizing genotype x agronomic management interaction to enhance wheat land and water productivity in a Mediterranean rainfed environment

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Wheat is the main staple food crop grown in the Mediterranean rainfed regions in Morocco, but production is unable to meet the demand. The existence of large attainable yield gap shows potentiality to increase wheat yield in the region. However, high variability in inter- and intra-seasonal rainfall presents a big risk for the farmers to invest in best practices. Optimizing genotype selection, seeding time, and crop demand-based water management have the potential to alleviate the risk associated with rainfall variability and enhance the stability of yield. The objective of the study presented here was to explore the best combination of genotype and management practices to enhance yield and water productivity (WP) of wheat in the Mediterranean rainfed environment. Ten advanced durum wheat genotypes were evaluated at two seeding dates (November and December) and two water management - rainfed and crop demand-based irrigation for three growing seasons (2016/17-2018/19). Combining appropriate genotype and management is more effective than solely relying on choice of genotypes. Effect of seeding time on yield and WP was influenced by rainfall amount and distribution. In low rainfall year (270 and 181 mm versus 440 mm long-term average), early sowing enhanced yield and water productivity by 45-100% compared to late seeding. Similarly, in dry year, the application of supplemental irrigation increased yield by 2.1 to 2.5 t ha-1 (72-90%). More than 50% yield variability was explained by variation in rainfall followed by supplemental irrigation (by 14%), and seeding time (by 12%). The contribution of the genotype on yield variability was insignificant. The response of genotype on grain yield and water productivity varied with seeding time and rainfall patterns. Selection of appropriate genotype, adjustment in seeding time, and application of crop demand-based supplemental irrigation help to enhance the stability of yield and WP of wheat under Mediterranean rainfed environment.

ID 1265 | Characterizing abiotic stresses to assist/direct/inform cultivar evaluation and agronomic recommendation – A case study for French winter wheat

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France is a major bread wheat producer, relying on high yields. However, despite mostly favourable conditions, variations in soils characteristics and weather conditions create large yield ranges across the country. Drought is often a major concern for farmers, although significant drought periods are not the only cause of yield loss. It is thus necessary to provide an objective, pluriannual and localized water stress description to provide sound cultivar recommendation to farmers.

We performed a characterisation of water-deficit scenarios and other main abiotic stresses impacting winter wheat. We relied on a similar methodology as Chenu et al (2011), using our own crop models and databases; we sought a dynamic description of water stress, considering potential impact on N uptake, heat stress exposure and potential compensation during grain filling. The typology highlighted several scenarios, differing on the extent of water stress intensity during stem extension and grain filling. Situations with no or limited water stress during the cycle represent almost half of the situations, with large year-to-year differences. Some situations with pre-anthesis water stress appear, with or without end-of-season rainfall and possible compensation. This characterisation becomes a useful tool to describe with similar metrics water-stress scenarios across the country.

We also applied the characterisation process to a set of field trials. It appeared that trial conditions failed to represent homogeneously the various water stress scenarios: some scenarios were frequently under-represented in the trial network. Thus, a precise cultivar characterisation for drought tolerance is difficult without using specific tools such as dedicated platforms. This work indicates that environment characterisation is an easy-to-access tool, valuable for breeders, agronomists and advisors, and can be developed from custom-made crop indicators or simple crop models.

ID 1266 | Results from farmers' fields: technologies developed to improve maize productivity

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Over the past ten years, CIMMYT has been working on innovation in maize- and wheat-based systems in Mexico through hubs that comprise (i) research platforms to develop research-based recommendations for farmers , (ii) modules with side-by-side comparisons in farmers' fields to fine-tune recommendations at the field scale, and (iii) extension areas where farmers apply new technologies. This infrastructure is used to build relationships and feed-back loops among actors and for capacity development with farmers, farm advisors and local researchers. In modules, farmers and farm advisors register data on field operations, costs and yield for the conventional practice and the innovation treatment that the farmer decided to apply. Here, we analyze the yield results of 801 comparisons from modules in areas of Mexico with an average precipitation of less than 600 mm per year and where farmers innovated for at least two years. The innovation treatment included at least the use of an improved variety, conservation agriculture or improved fertilization. Three crops were included: (i) maize with 679 comparisons divided over 20 states, (ii) common bean with 62 comparisons divided over 7 states and (iii) barley with 62 comparisons in three states in Central Mexico (Tlaxcala, Hidalgo and the state of Mexico). Average yields in the conventional practice were 3.81 t/ha for maize, 0.74 t/ha for bean and 2.46 t/ha for barley. The innovation treatment increased maize yields on average 0.83 t/ha or 22% compared to the conventional practice. For beans and barley yield increases were 0.21 t/ha or 28% and 0.14 t/ha or 6%, respectively. Farmers can increase crop yields in dry areas, but more research is needed to help farmers decide on the most cost-efficient option for their conditions.

ID 1284 | Visualization and quantification of nocturnal water fluxes in soil and roots

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Drought is one of the main factors limiting plant growth and food production worldwide. Understanding what processes allows plants to maintain root water uptake and root growth during drought is of paramount importance for designing drought tolerant crops. Hydraulic lift, defined as the transport of water from deep, wet soil layers to dry, upper soil layers through the root system, has been hypothesized to allow plants to maintain root growth and transpiration during drought spells. Although Hydraulic lift is well accepted, its visualization and quantification remains challenging. Here, we used neutron radiography to trace the transport of deuterated water (D2O) from deep, wet soil layers to dry, upper soil layers through the root system of maize plant. The experiments were carried out with maize grown in silty soil in quasi 2-D aluminum slabs. The soil was partitioned in two layers separated by a coarse sand layer that allowed the roots to grow through but limited the water redistribution between the layers. We injected D2O in the bottom soil layers and imaged the root system in the upper soil lays overnight. We found that when the top layer was dry, water was taken up from the deep soil layers and it was released during night by the roots in the upper dry layer. Interestingly, we also found that the hydraulic redistribution within the root system, up to 50% of the water that was taken up from deep soil, enables the growth of new roots in the upper dry soil layers. This information is of fundamental importance to understand how root growth is maintained during drought. In summary, we successfully combined isotope with neutron radiography to visualize and quantify hydraulic lift, redistribution of water within the root system and maintenance of root growth in drying soils.

1286 | Re-designing intensive cereal systems for protecting the blue water in irrigated DryArc

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DryArc is the world’s direst agricultural region consisting of 2 billion hectares of arable land and supports 1.7 billion of human population in nearly 70 countries across Asia and Africa. The region is facing serious multiple challenges of land degradation, water shortages, loss of biodiversity, food insecurity, malnutrition etc which are compounding further due to growing complexity of climate change. Water availability is a major driver of agriculture in any regions but it’s much serious concerns in the DryArc. The irrigated DryArc systems though consists of only 15% acreage (312 mha) of the DryArc region but inhabits over half (0.9billion) population of the region. The growing pressure of population in the irrigated DryArc have already led to serious challenges of depleting ‘Blue Water’ resources in the region. There is a net negative balance in evapo-transpiration by crops and rainfall in the region, thereby more use of the 'Blue Water'. For example, the rice-wheat system of the Indo-Gangetic plains, the key irrigated DryArc system to feed the billions, there are serious sustainability concerns specially related to over use of Blue Water which is prone to be used more intensively with projected climate change scenario. Therefore, technologies and strategies for protecting the blue water in the irrigated DryArc is crucial for future food security and agricultural sustainability. Over past several years, we have been intensively working on 'Re-designing the intensive cereal systems' for protecting the blue water and overall agricultural sustainability. The approaches and practices include, optimizing/re-designing cropping systems using CA-based management and appropriate cultivar choices, layering precision water&nutrient management portfolio in existing and newly designed systems. Synthesis of scientific evidence indicated that redesigning of intensive cereal systems can help in achieving the future food and nutritional security while protecting the blue water, conserving the natural resources and minimizing environmental foot prints.

ID 1298 | Conservation agriculture improves nitrogen use in semi-arid climate in central Mexico

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Nitrogen is a limiting factor in agricultural production in many regions of the world. Fertilization could greatly improve yields, but proper timing and good agronomic management are essential to achieve best use of nitrogen and reduce the risk of leaching. In semi-arid climates, water availability limits nitrogen use efficiency of crops. Conservation agriculture, based on minimum tillage, crop residue retention and crop rotations can significantly improve water availability under such conditions compared to agronomic management with conventional tillage.

An experiment was established at CIMMYT's experimental station El Batan in central Mexico, investigating the effect of different modes of nitrogen application on maize and wheat yields with and without tillage. Data were collected in four years. The experiment was divided into two main blocks consisting of tillage treatments; permanent beds (PB) and conventionally tilled beds (CB). The blocks were subdivided by crop rotations maize-wheat, wheat-maize and wheat monoculture. Four N treatments were applied; (1) control treatment without N fertilization, (2) 80 kg/ha basal banded, (3) 80 kg/ha at first node stage for wheat and at 4-5 leaf stage for maize, (4) 80 kg/ha divided between basal banded and first node/ 4-5 leaf stage.

Maize yields were higher with PB than CB. Nitrogen fertilization improved yields compared to the control treatment under PB. Under CB no yield improvement was observed with any of the fertilized options compared to the control. In wheat the results were similar. Yields were highest with conservation agriculture, followed by yields on PB with monoculture. Fertilization improved yields on PB but not on CB.

Our results suggest that investing in inputs only makes sense when those inputs address the factors most limiting production. In the semi-arid environment studied here, addressing water stress through conservation agriculture had a larger effect on yield than N fertilization.

ID 1304 | Saving important water quantities through water management techniques and physiological thresholds in irrigated potatoes

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Global fresh water is being dramatically reduced by the intensification of anthropogenic activities like agriculture which takes more than 70% of this resource. Thus also, global warming will promote the increase of extreme events raising water scarcity problem in the future. To guarantee sustainable intensification as a part of Climate Smart Agriculture, the growing of important worldwide crops like potato will need to save water through innovative technologies. In this poster, we will summarize two experiences related to water saving agriculture efforts: i) partial root-zone drying (PRD) i.e. the alternated watering of furrows and ii) the use of crop water stress index (CWSI) threshold values to define irrigation timing. Taking experiences from Peru, Ethiopia and China, our results indicated that PRD allows 50% of water saving being more economic and environmentally friendly even than drip irrigation. Irrigation timing when potatoes are close to 0.4 of CWSI allowed 609±29 and 459±31 m3/ha of water saving under furrow and drip irrigation respectively with no yield penalization. It is possible to save an average of 2055±178 m3/ha combining CWSI threshold and drip irrigation with low yield reduction. The scaling the presented technologies need to be addressed in futures studies.

ID 1306 | Physiological basis of genotypic response to management in dryland wheat

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A great majority of dryland wheat producers are reluctant to intensify management due to the assumption that lack of water availability is the most critical factor limiting yield and thus, the response to management intensification would be limited. We conducted on-farm field experiments in Kansas using 21 modern winter wheat genotypes grown under either standard (SM) or intensified management (IM) systems. The goals of this study were to (i) determine whether the SM adopted is adequate to reach achievable yields by farmers in the region and (ii) identify differences in responsiveness to IM among a range of modern genotypes. Across all sites-years and genotypes, the IM increased yield by 0.9 Mg ha-1, outyielding the SM system even in the lowest yielding conditions. As expected, the yield response to IM increased with the achievable yield of the environment and genotype. Across all sources of variation, the yield responsiveness to IM was related to increased biomass rather than harvest index, strongly driven by improvements in grain number (and independent of changes in grain weight), and by improvements in N uptake which resulted from greater biomass and shoot N concentration. Genotypes varied in their response to IM, with major response patterns resulting from the combination of response magnitude (large vs small) and consistency (variable vs consistent). Genotypes with high mean response and high variability in the response to IM across years could offer greater opportunities for producers to maximize yield as those genotypes showed greater yield gain from IM when conditions favored their response. For the background conditions evaluated, intensifying management could improve wheat yield in between c. 0.2 and 1.5 Mg ha-1 depending on genotype.

ID 1321 | Climate resilient Cropping systems for water-limited environments in an acidic Inceptisols of Assam, India

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The North Bank Plains Zone of Assam experiences delay in onset of monsoon, drought, high intensity rainfall, flood etc. thereby affecting production and productivity of winter rice. Significant decrease in trend of monsoon rainfall with increasing rainfall variability in June, September and October might be linked to intermittent dryspells during rice growing season. A drought prone village with 165 households of Lakhimpur district was adopted for implementation of National Innovations on Climate Resilient agriculture project under AICRP for Dryland Agriculture, Biswanath Chariali Centre under CRIDA. The soil of the village belongs to hyperthermic family of Fluventic dystrudepts under land capability class II and III. The village receives average rainfall of 450mm and 1800mm respectively during pre monsoon and monsoon season, which is harvested in 13 nos. of renovated farm ponds (max. capacity: 8000 cub. m) and efficiently used for raising paddy nursery before third week of June and as supplemental irrigation in winter crops. A participatory on farm trial was conducted to find out best suited cropping sequence in upland and medium lands as an adaptive measure during 2014-15, 2015-16 and 2016-17. In upland condition, improved short duration rice cultivars followed by winter crops (potato & toria) were cultivated. Likewise, in medium land situations, medium duration improved winter rice varieties followed by winter crops were cultivated. The results revealed that short duration rice - potato sequence is most profitable with highest Benefit: Cost ratio and RWUE followed by Dishang- rapeseed. In medium land situations, highest ratio and RWUE was observed in winter rice - rapeseed sequence followed by Sali rice - potato.

ID 1324 | Drought-induced nitrogen deficit amplifies the effect of water stress

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Supply of water and nitrogen (N) are critical to crop yield. Multiple interactions between water and N need to be untangled for understanding crop performance in a context of interactions between genotype (G), environment (E) and management (M). We used an allometric framework to quantify the dynamic relationships between crop growth, transpiration and N uptake in annual crops (maize, sorghum) and perennial forages (fescue, alfalfa).

We show a two-fold effect of drought a direct effect whereby crop growth is reduced proportionally to the reduction in transpiration, and an indirect effect mediated by a drought-induced N deficit. Reduction in crop N nutrition by drought can

be assessed as N nutrition index (NNI), the ratio between actual and critical plant N concentration (the minimum plant N concentration for maximum crop mass). The N nutrition of alfalfa was reduced by drought exactly in the same way as tall fescue, indicating that drought affected N2 fixation and N mineral absorption similarly. Sorghum maintained NNI and transpiration efficiency (biomass per unit of transpiration) whereas both NNI and transpiration efficiency declined in drought-stressed maize in comparison to well-watered crops. Nitrogen uptake per unit of transpiration (N/T) appears as a valuable trait for quantifying the combined effect of water and N deficit on water use efficiency (biomass per unit of evapotranspiration, ET). However, as both N/T and crop N concentration decline allometrically with crop biomass, these traits would be biased unless they are scaled by crop mass. Analysis of GxExM interactions on water use efficiency of crops would benefit from consideration of drought-induced N deficit.

ID 1331 | Transformational agronomy: exploiting synergies in management x genotype interactions to increase water productivity in grain production systems

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Past increases in crop water productivity have rarely been attributable to individual innovations in technology or farming practice. Increases have occurred when new and old technologies and practices combine to form improved systems. We argue that focusing research on developing synergistic systems to overcome current and future production constraints will accelerate increases in water productivity whilst meeting the goals of sustainable intensification and challenges of climate change. This will require coordinated effort from multidisciplinary teams, and contrasts to the discipline-focused structure of much current research.

Here we use the grain production systems of south eastern Australia as a case study showing how transformational change can be achieved. In this region, rainfall is low and variable and since 1990 has declined further. Despite this, growers have maintained yields by increasing water productivity.

This has been achieved by implementing synergistic systems consisting of (1) soil water conservation (2) diversity of crops and practices (3) earlier sowing to fit crop lifecycle to seasonal conditions and (4) increased applications of nitrogen fertiliser. For some growers there still exists a yield gap, and water productivity could be further increased through adoption of best practice. Leading growers have closed the exploitable yield gap, and increased water productivity requires an increase in water limited potential yield. Such increases could be achieved by the development of cultivars with stable flowering and improvements in temperature tolerance, allowing growers to respond to variable timing of planting rains by sowing even earlier but maintaining yields at late planting. Collaboration between agronomists and commercial crop breeders has led to development of such cultivars which are in early phases of testing and adoption.

No ID | Genetic diversity of plant responses to environmental constraints for current and future E x M scenarios

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Each genotypic trait/allele associated with tolerance to any constraint can have positive or negative consequences on crop production, depending on the environmental scenario and management practices (G x E x M). It is therefore essential to identify in which specific scenarios a given combination of traits values (ideotype) results in a comparative advantage on crop production. We developed a conceptual framework for predicting the impact of the genetic diversity of adaptive traits in current and future environmental scenarios and management practices, based the coupling between phenotyping and crop modelling. In this talk, I focus on the responses of leaf growth and development to environmental conditions: (i) we developed a phenomic-based model of leaf development and expansion (elongation and widening) for which parameter values can be obtained in phenotyping platforms for hundreds of maize hybrids. (ii) We parametrised 254 maize hybrids maximising the maize genetic diversity (iii) we simulated the optimum crop cycle duration in current and future European environments and (iv) determined ideotypes of leaf growth adapted to the different environmental scenarios. Overall, we provide

elements on “where and when” a combination of trait values can give a comparative advantage on yield, together with the boundary of possibilities within the current genetic diversity.

No ID | Dissecting G×E and QTL×E of maize yield in contrasting scenarios of light, heat and water deficit

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With climate changes, crops will encounter more frequent climatic accidents. Continuing progress in yield requires considering new method to characterize the comparative advantages of varieties under drought and high temperatures. Genomic prediction can assess the performances of thousands of new varieties based on genotypic information, but faces the difficulty of large variations in performance due to the genotype × environment interaction (G×E). The progress of phenomics opens new avenues to tackle the difficulty of dealing with the G×E: the rapid progress of sensor networks and of modelling makes it possible to characterize environmental conditions in any field, and to take them into account in genomic prediction. We have studied maize grain yield in 25 fields over Europe, with irrigated and rainfed treatments in each location. A panel of 246 maize hybrids genotyped with 832K polymorphic SNPs was analysed in these experiments, together with a characterization of phenology in a phenotyping platform. By combining information coming from the field and the platform, we have estimated the responses of yield components to environmental conditions via a regression analysis over the whole dataset. We have identified in this way large effects of temperature and water deficit at flowering time, and of intercepted light during the vegetative stage. The slopes of these responses largely differed between hybrids and were used to predict grain yield of new hybrids in new fields. This work therefore opens new perspectives for plant breeding under climate change.

No ID | Understanding crop environments to adapt management practices and assist breeding

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While abiotic stresses limit crop production in major production regions worldwide, their frequency and intensity is projected to rapidly change with climate change. This will impact genotype × environment interactions that are already impeding progress in plant breeding. Crop modelling can be used to quantitatively characterise the stresses that crops are experiencing in breeding trials and more largely in targeted production environments. They are also valuable to assess how stresses have evolved over time (e.g. shift over the last decades), and how they are projected to change in the near-to-mid future. Understanding the crop environment is an important step to define appropriate strategies to adapt management practices and assist breeding. Example of different case studies will be presented to illustrate the value of envirotyping for crop adaptation.

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