P.1.01

FINE-MAPPING OF *QSBM.UBO-2BS*, A MAJOR QTL FOR RESISTANCE TO SOIL-BORNE CEREAL MOSAIC VIRUS (SBCMV)

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QSbm.ubo-2BS, a major QTL responsible for SBCMV (Soil-borne cereal mosaic virus) response in durum wheat, was characterized in Meridiano (resistant) x Claudio (moderately susceptible) Recombinant Inbred Lines (RILs). *QSbm.ubo-2BS* was mapped as a unique major QTL ($R^2 = 88.5\%$) within a 2 cM-wide interval (LOD-2) in the distal region of chromosome arm 2BS, with *wPt-2106* (DarT®) as the closest marker. The Illumina 90K SNPs array allowed to map 36 gene-associated SNP markers in the region containing the mendelized QTL. Five SNPs from the Illumina 90K and ten SNPs from the Affimetrix 420K wheat array were converted to KASP™ markers. High resolution mapping was constructed using KASP™ markers flanking the QTL interval on ~2000 RILs Svevo (resistant) x Ciccio (moderately susceptible) developed by UNIBA. In total, 330 recombinant RILs were identified and characterized for SBCMV response in an inoculated field. Symptom severity was scored on a 0 to 5 scale and screened with five KASP™ markers distributed along the QTL interval confirming its presence. Based on the markers physical position, the gene space of *Qsbm.ubo-2BS* was defined. On a total of 43 genes, 12 could be described as candidates of resistance response. As to future perspectives, exome capture analysis will be conducted to identify allelic variants among the candidate resistant genes. Moreover, an RNAseq experiment was performed on two groups of five susceptible and five resistant haplotypes each. Two large recombinant populations obtained by crossing resistant and susceptible parents, produced and advanced at F_4 generation, are being analyzed to identify new informative recombinants and heterozygotes to obtain $F_{4:6}$ contrasting genetic stocks. The research was supported by FSOV (*Le Fonds de soutien à l'obtention végétale*): *Développement d'outils phénotipyque et génotypique pour améliorer la sélection de la résistance du blé dur à deux virus des mosaïques du blé*.

P.1.02

THE ANCIENT MEDITERRANEAN DURUM WHEAT QUALITY QTLOME ASSESSED BY DARTSEQ-SNP MARKERS

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Durum wheat (*Triticum turgidum* L. var. *durum*) was originated in the Fertile Crescent and spread over the Mediterranean Basin developing into local landraces specifically adapted to their growing regions. The wide genetic diversity and the high level of polymorphism in quality genes of landraces can be used as a source of genetic variation for agronomical and quality traits in breeding programs. The aim of this study is the identification of molecular markers linked to quality traits in a set of 161 durum wheat Mediterranean landraces by association mapping (AM).

Experiments were carried out during the 2007, 2008 and 2009 harvesting seasons in north-eastern Spain, under rainfed conditions. Quality analysis were performed for the following traits: grain protein content (GPC; %), gluten strength (GS; ml), yellow colour index (YI) and test weight (TW; kg/hl). Phenotypic data was fitted to a linear mixed model to produce the best linear unbiased predictors (BLUPs). High through-put genotyping was conducted using DArTseq Technology at Diversity Arrays Technology Pty Ltd (Canberra, Australia) and 5212 DArTseq single nucleotide polymorphism (SNPs) were used for mapping purposes. Association mapping (AM) was performed using a Mixed Linear Model and marker trait associations (MTA) were considered significant using a threshold of $-\log10(P) > 3$.

A total of 85 marker trait associations (MTAs) involving 70 SNPs were significant for the 4 traits in the 3 years and across years. Twenty-eight markers were located in genome A and 42 in genome B. Test weight was the trait with the highest number of associations (54), followed by YI (16), GS (8) and GPC (7).

P.1.03

MICRO RNA RESPONSE TO CHRONIC AND SHORT-TERM NITROGEN DEPRIVATION IN DURUM WHEAT SEEDLINGS

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Nitrogen (N) is an important macronutrient for crop productivity; its availability is essential from the seedling stage since N is also a major component of chlorophyll. In durum wheat, phenotypic traits and yield are negatively influenced by N deficiency. MiRNAs are small non-coding RNA molecules that can regulate key genes in response to stress, thus contributing to environmental adaptation of plants.

In the present work, durum wheat cultivars Ciccio e Svevo were grown in standard and in N starvation conditions, and leaves and roots were collected at the seedling stage (Z14). Eight small RNA libraries were obtained and sequenced. After bioinformatics analyses, 294 miRNAs were detected, including 7 newly identified. Using quantitative qPCR, expression levels of selected miRNAs and corresponding target genes were evaluated in durum wheat seedlings subjected to chronic or short-term (6-48 hours) N stress conditions.

Some miRNAs showed an immediate response to N stress, others exhibited a gradual up- or downregulation during the short-term stress, which was either maintained or not during a longer (chronic) stress period. One of the newly identified miRNAs, ttu-novel-106, showed to be immediately downregulated after nitrogen starvation conditions, while MYB-A, its putative target gene, was straightaway upregulated. These results were validated using 5′ RACE assay that allowed the identification of the ttu-novel-106 putative cleavage site in the *MYB-A* gene sequence. Additionally, the *PHOSPHATE 2* (*PHO2*) gene showed an opposite expression trend compared to its regulatory miRNA ttu-miR399b. Identification of putative ttu-miR399 binding sites at the 5′ UTR region of *TtPHO2* and cleavage validation were carried out for this gene.

This work provides novel insights into the activation mode of durum wheat miRNAs in response to N deprivation, confirming the importance of miRNAs in the adaptation of seedlings to N stress, and opens new perspectives for the use of miRNAs in breeding programs.

P.1.04

MOLECULAR CHARACTERIZATION OF ITALIAN DURUM WHEAT LANDRACES

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Durum wheat (Triticum durum spp.) is an allotetraploid crop widely grown in the Mediterranean region, especially in Italy, where with bread wheat, it represents the main source of carbohydrates that characterize the local diet. Modern breeding programs have greatly improved yield and technological quality of this plant sometimes resulting in a reduction of genetic variability and potentially making crops more vulnerable to disease and climate change. Therefore novel sources of genetic variability are needed to be employed in future breeding programs. Collections of old varieties and landraces may hold novel variability not present in modern varieties, therefore evaluation of the genetic variation within collections and local landraces is crucial. In this study, nearly 130 old Italian landraces and 20 modern varieties of durum wheat were genotyped using the Axiom® Wheat breeder's Array with 35 K features. One plant from each accession, grown in a peat based soil inside a glasshouse, was chosen and its Genomic DNA was isolated from the third leaf using a Phenol-Chloroform extraction method treated with RNase-A. Plants were then grown until the ripening of the ear and the seeds produced were collected and will be used as single seed descent lines for the future work. Samples were genotyped with Affymetrix GeneTitan® system and SNP callings were assigned using the software package GTC developed by the same company. SNP data were elaborated to analyze the genetic relationship between the different lines, then a Population structure analysis was inferred with a Bayesian model-based clustering method. Our results show that landraces contain a substantial amount of novel genetic diversity that should be considered in the current breeding program. Collection of old varieties and landraces represent a potentially important source of variability that should be characterized and conserved.

P.1.05

THE EXPLOITATION OF GENETIC RESOURCES AND NEXT GENERATION BREEDING MAY OPEN NEW PERSPECTIVES TO INCREASE DURUM WHEAT ADAPTATION TO DROUGHT STRESS

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The Mediterranean region is one of the main region affected by the impact of global climate change (GCC) with strong drawbacks on agricultural productions and thus on food security. Durum wheat (Triticum turgidum L. var. durum) is a rain-fed crop mainly cultivated in the Mediterranean basin, which despite being able to survive various environmental stresses, is threatened by GCC. In particular drought stress (DS) is one of the major constraints that can negatively affect crops growth and yield. Identifying genotypes with higher adaptability to DS is thus a primary goal for researchers and breeders. In this research, we focused on a set of genes, known to be involved in DS response in other crop species, and characterise them at genomic and expression level. To better elucidate their involvement in DS response, a reverse genetic strategy was followed taking advantage of the wheat TILLING database (www.wheat-tilling.com, John Innes Centre, Norwich, UK). Several mutant lines carrying SNPs that should lead to a functional knock-out of each selected genes (both A and B alleles) were selected. The double mutants have been produced following a classical breeding scheme combined with the use of KASP markers. In parallel, an allele mining approach has been performed, with the aim to identify the presence of natural alleles of the selected genes within a durum wheat germplasm collection representative of the durum wheat Mediterranean cultivation area developed at IBBR-CNR Bari. The phenotypic effects of each mutation (both induced and natural) will be evaluated by using the high-throughput phenotyping platform held by ALSIA (Metaponto, Italy).

P.1.06

ASSOCIATION MAPPING FOR QUALITY TRAITS IN A DURUM WHEAT COLLECTION

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Grain protein content and gluten strength are major targets in durum wheat breeding programs (*Triticum turgidum* L. var. *durum*). Six experiments were conducted in the south of the province of Buenos Aires (Argentina) using a world-wide durum wheat germplasm collection (170 entries) in order to analyzed grain protein content, thousand kernel weight and gluten strength. This collection was genotyped with the Breeders' 35K Axiom® array and four major genes markers. The population structure was assessed by using a subset of 1,000 SNPs in low linkage disequilibrium and association mapping (AM) was performed for all the phenotypic traits using 3,745 markers. It was possible to find associations between the three phenotypic traits and the molecular markers used, confirming previously reported chromosomal regions and in some cases, detecting novel QTLs. Seven SNPs on 2A, 2B, 3B and 7B chromosomes were associated with thousand kernel weight in three environments, some of them were previously reported in similar genome regions in bread and durum wheat panels. Six markers located on chromosomes 2B and 4A were associated with grain protein content in two environments. Additional marker-trait associations (MTA) for protein content were considered unsatisfactory showing low environmental stability. Several MTA were detected on 1B (7.46 - 36.42 cM) for gluten strength. AM was effective to detect several of the QTLs previously reported on the same chromosomal regions through biparental mapping. These results suggest that AM is a suitable tool to identify genomic regions for traits that are routinely measured in wheat breeding programs.

P.1.07

GENOME WIDE ASSOCIATION STUDY REVEALS NOVEL QUANTITATIVE LOCI FOR OSMOTIC ADJUSTMENT UNDER DROUGHT STRESS IN DURUM WHEAT

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Drought is one of the most devastating stressors limiting crop survival and adaptability, thereby affecting yield loss. Osmotic adjustment (OA) is one of the major components of drought resistance in crops thanks to an active accumulation of solutes in response to a water potential reduction, thereby maintaining turgor. Although yield differences in wheat yield have been correlated to OA capacity, the genetic basis of this trait is unknown.

This work reports the first Genome Wide Association Study (GWAS) in durum wheat for OA as well as for relative water content (RWC), osmotic potential (ψs) and dry biomass (DB) under full and deficit irrigation conditions. In the field trial in 2018 at the Maricopa Agricultural Center (AZ), 248 durum wheat elite lines and cultivars from worldwide (Durum Panel) were evaluated according to a randomized block design with two replicates. Leaf samples were first collected at flowering under well-irrigated conditions and 10 days later under severe water-stressed conditions. To analyze OA, eight fully expanded flag leaves were sampled from each plot, re-hydrated to full turgor for 8 hours and stored in freezer. The extracted leaf sap was collected for measuring ψs using an osmometer. The resulting osmolality (mosmol kg^{-1}) was converted to osmolarity (MPa) to evaluate OA as ψs (control) - ψs (water-stressed).

The genetic characterization of the Durum Panel was carried out with the Illumina iSelect wheat 90K SNP assay. A Mixed Linear Model (MLM) for GWAS was performed in Tassel in order to identify the genetic intervals harboring loci controlling OA, RWC, ψs and DB. Two major QTL hotspots on chromosomes 6AS and 6AL were found to concurrently affect OA, RWC and DB with a positive effect of OA on both RWC and DB. These results support OA as a prime drought-stress adaptive trait in support of plant production under water-stressed conditions in durum wheat.

P.1.08

CHLOROPHYLL FLUORESCENCE AS A PROXY TO IDENTIFY QTLS FOR HEAT-STRESS TOLERANCE IN DURUM WHEAT

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Heat stress (HS) is one of the main constrains to durum wheat (Triticum turgidum L. var. durum Desf.) production worldwide, particularly in Mediterranean countries. Furthermore, it is a complex quantitative trait quite laborious to evaluate. Chlorophyll fluorescence (CF) measured as photochemical efficiency ratio (Fv/Fm) has been used as a proxy to evaluate HS tolerance in wheat. This genome-wide association study (GWAS) was performed in order to identify QTLs for CF under both normal and heat-stressed conditions and verify their coincidence with QTLs for HS tolerance. A panel of 183 cultivars of T. durum elite cultivars suitable for GWAS was evaluated in greenhouse based on a randomized block design with three reps. Each experimental unit (3-L pot) included 12 plants. All pots were kept in well-watered conditions at 23/20 °C (168 h light/dark). The HS treatments (5 and 7 days at 38/28 °C in 16/8 h light/dark) were applied at the 4-leaves unfolded stage (Zadoks, 1974). After that, stressed plants were returned to control conditions for recovery (3 days). Chlorophyll fluorescence was measured with the Light-Induced Fluorescence Technique device, on both control and HS plants (i) 5 and 7 days after the start of the HS treatment, and (ii) 3 days after the end of the HS treatment. GWAS analysis based upon the Illumina iSelect wheat 90K SNP assay identified 21 main loci with significant effects (-log10 > 3.0) on Fv'/Fm'. GWAS confirmed a highly significant region on Chr. 6B which was highlighted in all experimental conditions, hence suggesting the likely presence of a constitutively expressed QTL. In the same way, one QTL on chr. 3B region was detected in all stressed conditions suggesting the presence of a major QTL affecting HS tolerance in durum wheat.

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P.1.09

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

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

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

P.2.10

TETRAPLOID WILD SPECIES IN IMPROVEMENT BREAD AND DURUM WHEAT

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Rising interest in natural and organic products led to the reopening of ancient wheat as a source of grain for healthy nutrition. Several wheat species are used and further adapted to cultivation in industrial scale, e.g., *Khorasan*, *T.spelta*, *T.compactum*.

The most nutritionally favorable ratio of calcium to phosphorus is characteristic of species; T.turgidum (1:6,0); T.persicum (1:5,7); with the maximum of 1:19 (T.compactum.) and 1:16,0 (T.spelta).

By the ratio of calcium to magnesium, the most balanced are among tetraploids - *T.turgidum* and *T.persicum* (1:2.1).

Among the introgressive spring wheat samples the following samples with the maximum content have been selected: Kazakhstan 10 x *T.dicoccum* — for *K, P, Ca, Mg*; Kazakhstan 10 x *T.timopheevii* — for *N, S, Fe, Zn, Mg, Mn*; Kazakhstan early ripening x *T.timopheevii* — for *F, S*.

For tetraploid wheat, the protein content varied from 15.8% for *T.turgidum* to 23.6% for *T.militinae*. Level of 19.0% and higher was in the grain of *T.aephiopicum*; *T.dicoccoides*; *T.monococcum* and *T.persicum*. Among the hexaploid species, the maximum protein content is noted in the *T.kiharae*.

The protein content in the grain of various species was formed due to the predominance of different protein fractions: globulin in grain of *T.militinae*; due to gliadin in *T.dicoccoides*, *T.dicoccum* and *T.timopheevi*. Introgressive winter forms are characterized by mainly glutenin fraction content in grain from 30% for genotype (Bezostaya1 x*T.militinae*)x*T.militinae* to 34% for genotype Erythrospermum350x*T.kiharae*.

Two forms are characterized by equal amounts of glutelin and globulin or the prevalence of globulin fraction (29% and 28%): Erythrospermum350x*T.militinae* and Steklovidnaya24x*Ae.cylindrica* (28% and 26%).

Wild relatives were characterized by an amylose content in the range of: *T.timopheevi* (31,5%) > *T.dicoccoides*; *T.macha*; *T.persicum* > *T.spelta* > *T.militinae*, *T.spharacoccum* (26.4%).

In addition, transitional form is the most optimal approach for the evaluation and subsequent transfer of unique wheat genes for alleles from its wild relatives.

P.2.11

GENETIC ARCHITECTURE OF SEMOLINA YIELD AND OF ITS COMPONENTS IN DURUM WHEAT (*TRITICUM TURGIDUM* SPP. *DURUM*)

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During durum wheat domestication and selection process, successive genetic bottlenecks occurred and induced a strong reduction of genetic diversity in *Triticum turgidum ssp durum* compared to its progenitors. To enlarge genetic diversity available for breeding, we founded in 1997, the Evolutionary Prebreeding pOpulation (EPO) including a great diversity of wild, primitive and modern forms of *T. turgidum.* We maintained an allogamous rate of about 20 % in this population thanks to the presence of male sterile plants. After 17 generations of intermating coupled with a mild selection for architectural trait values, we derived an inbred line panel to study relationships between genotypes and phenotypes.

During 2 years, we measured phenotypic variability of 181 lines for semolina yield (SY), which quantify the performance of the genotype at the first step of industrial process, and its most important components. Thousand Kernel Weight TKW, Specific Weight SW, Grain Protein Content GPC, were estimated by near infrared spectroscopy according our own calibrations ($0.89 < R^2 < 0.95$). Phenotypic variance, heritability and correlation patterns have been carried out underlying the importance of the annual effect; inter annual broad sense heritability varied from 0.3 (GPC) to 0.45 (TKW). EPO lines were genotyped for 420 k array developed for the BreedWheat project and we used about 168 000 SNPs with high quality resolution and physically mapped on Zavitan reference. After correction of the phenotypic data for the spatial variation, GWAS analysis was performed, allowing us to identify genomic regions explaining from 8 to 18 % of SY, TKW, GPC and SW variation. The major TKW QTL mapped on the 2AS co-localized with the SY QTL. We discuss the potential of this panel to decipher genetic architecture of traits and the complementary between this panel and EPO to precise the highlighted locus.

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P.2.12

MAPPING OF QTLS FOR RESISTANCE TO STEM RUST IN TETRAPLOID WHEATS

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The recent emergence of new widely virulent and aggressive strains of Stem Rust (SR, *Puccinia graminis*) is threatening world as well as Italian durum wheat production, especially under the trend of higher temperature and humidity. A big effort has been undertaken to explore the genetic variability for resistance to this fungal pathogen and discovering novel resistance genes. As large untapped sources of genetic diversity, panels of tetraploid wheat lines provided of several thousands of SNP markers were used for association mapping. This large collection consisted of a group of durum wheat cultivars, produced by the last century breeding, a collection of wild emmer wheats (*T. dicoccoides*), and lines belonging to other wild and domesticated tetraploid subspecies. In a tight cooperation with the University of Minnesota, this collection was evaluated for reaction to several SR races, including the known Ug99 and the recently emerged TTTTF, in controlled greenhouse and field conditions. Among the genotypes belonging to the collection are parents of two segregating populations (Cirillo x Neodur, Latino x MG5323) that were used for the validation of mapping results. Novel resistance loci were identified, that can be incorporated into new durum varieties through breeding programs. The QTLs found in this study, together with those available in literature, were projected to the recently sequenced durum wheat reference genome (cv Svevo) in order to define more precisely the chromosome regions and candidate genes involved in resistance to rusts. Lines which were resistant to multiple races of rust pathogens were also found among both *T. dicoccoides* and durum wheat cultivars as a source of resistance genes whose cloning will be undertaken based on the results here obtained.

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P.2.13

GENETIC MARKERS ASSOCIATED TO ARBUSCULAR MYCORRHIZAL COLONIZATION IN DURUM WHEAT

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The arbuscular mycorrhizal (AM) symbiosis between soil fungi and plant roots is ecologically and agriculturally important, given its functional role in plant nutrition. The genetic basis of susceptibility to mycorrhizal colonization in wheat sub-species (*Triticum* spp.) has been investigated. The mycorrhizal status of wild, domesticated and cultivated tetraploid wheat accessions, differing for selection history, origin and/or year of release, inoculated with the AM species *Funneliformis mosseae*, was evaluated. In order to detect genetic markers in linkage with chromosome regions involved in AM root colonization, a genome wide association analysis was carried out on 108 durum wheat varieties and two AM fungal species (*F. mosseae* and *Rhizoglomus irregulare*). Our findings showed that a century of breeding on durum wheat and the introgression of *Reduced height* (*Rht*) genes associated with increased wheat grain yields did not select against AM symbiosis in durum wheat. Moreover, mycorrhizal colonization ranged from 2 to 45% depending on environmental conditions, symbiont identity and wheat accession. Seven putative Quantitative Trait Loci (QTLs) linked with durum wheat mycorrhizal susceptibility in both experiments, located on chromosomes 1A, 2B, 5A, 6A, 7A and 7B, were detected. The individual QTL effects (r^2) ranged from 7 to 16%, suggesting a genetic basis for this trait. Marker functional analysis has been carried out to find candidate genes. In conclusion, the genetic mapping of QTLs associated with mycorrhizal colonization will allow a more effective breeding for the development of new genetic material and a start point for further research.

P.2.14

ASSESSMENT OF SOME QUALITY AND YIELD COMPONENTS TRAITS IN OLD AND MODERN TUNISIAN DURUM WHEAT VARIETIES UNDER RAINFED CONDITION

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Durum wheat grain quality has become, in recent years, one of the main breeding goals, due to the increase in market demand for good durum's quality despite many biotic and abiotic constraints. This work aims to evaluate some grain quality traits and yield components of 27 tunisian durum wheat old cultivars, 5 tunisian improved varieties and 7 ICARDA inbred lines, under rained conditions in Mornag station (Tunisia), for 2 years 2015 and 2016. Results showed that yellow index (b* value) has the highest heritability across the environments (0.9) followed by grain protein content (Gpr) ranging from 0.87 to 0.96 and gluten strength (SDS) with a range of 0.82 to 0.9, respectively. However, all the other traits related to yield components showed a medium heritability. Furthermore person's correlation between the 12 traits demonstrated a very strong significant positive correlation between GY (grain yield) and NS (number of spikes/m2) 61.30%, between NGS (number of grains/spike) and TFT (total fertile tillers) 64.27%. The b value is highly influenced by TFT (total fertile tillers) 46.12%, TA (Seed total area) 41. 5% and NGS (number of grains/spike) 34.58%. Whereas, for Gpr we observed a significant positive correlation with BY (biological yield) 40.19% and a significant negative correlation with TW (test weight) - 43.14%. Clustering analysis based on mean values of all the traits across the environments classified the collection into 3 main groups; the first group includes the genotypes with high yellow index, high gluten strength and high grain yield; the second groups is composed of genotypes with high total seed area and high test weight and the last group is formed with genotypes with high biological yield and high protein content. This study allowed us to screen from the old varieties the genotype with a desirable trait that could be used for further breeding programs.

P.2.15

DISCRIMINATION OF WHEAT VARIETIES IN THE FIELD BY HYPERSPECTRAL IMAGING ON CANOPIES.

Presenting Author Martin Ecarnot

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Issues about crop systems durability, environment protection, and input reduction are in the center of the discussions concerning future agro-systems. In this context, variety mixtures, arouses a growing interest. To date, studies of varietal mixtures have only remained descriptive and post-harvest made, making it impossible to predict mixing effects of given varietal mixtures. Thus, the development of varietal mixtures having both relevant properties for the development of a more sustainable agriculture and interesting agronomic performances requires to be able to disentangle the mechanisms driving interactions between genotypes. To clarify the contribution to each genotype in a given mixture, nondestructive and noninvasive methods are highly desirable. Hyperspectral images (NEO HySpex VNIR-1024, 400-1000 nm, 216 bands) have been acquired in the field, 1 meter above wheat plots that were constituted by either a single variety or varietal mixture at several growing stages. The purpose is to discriminate the pixels of vegetation according to its variety thanks to its spectrum. After filtering out the soil pixels, the discrimination was carried out on leaves pixels by means of an original combination of Partial Least Squares – Discriminant Analyze (PLS-DA) and Support Vector Machine (SVM). Different pre-treatment and strategies of Calibration-Validation sampling are tested. In some conditions, the pixels of the validation set were classified in the correct variety up to 90%. The spatial distribution of the quality of prediction is investigated. Our work also showed that the discrimination model works better with the most illuminated leaves.

These results show promising performances which could lead to a use of this methodology to quantify biomass production of variety mixtures. This plants characterization tool could be used in plant improvement programs and research on variety mixtures.

P.2.16

A CANDIDATE GENE ANALYSIS OF QTLS FOR ROOT GROWTH ANGLE IN DURUM WHEAT

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Optimization of root system architecture (RSA) traits is an important objective for modern wheat breeding. Durum wheat *Triticum turgidum* L. var. *durum* Desf.), germplasm, including two recombinant inbred line populations and one association mapping panel of 183 elite cultivars was searched for RSA QTLs. Seven QTLs were selected for investigation of gene content in the QTL confidence interval based on the Chinese Spring *T. aestivum* IWGSC1.0+POPSEQ (Mayer et al, 2014, Chapman et al. 2015) as well as based on the golden standard wheat genome assemblies of *T. dicoccoides* accession Zavitan (Avni et al, 2017), *T. durum* cultivar Svevo (Maccaferri et al, unpublished) and *T. aestivum* IWGSC RefSeq v1.0 (IWGSC, 2018). The TriAnnot v4.3 pipeline was used for gene prediction and annotation. Candidate genes were prioritized based on annotation, expression analysis, evidence mining for association to auxin response/signaling, root hair formation/elongation, gravitropism and root meristem (KnetMiner). Candidate genes were functionally validated in orthologs. The QTL confidence intervals ranged from 1.8 to 14.0 Mb and contained 4 from to 37 candidate genes. Candidate genes were involved in MYB transcription factor, auxin response factors (ARF) family, PIN-formed (PIN) protein family of auxin transporters, zink finger protein family and other candidates. All these gene families have been shown to be involved in controlling RGA in both rice and *Arabidopsis*. The tissue expression of candidate genes was investigated in 13 varieties of durum wheat and in wheat expression databases expVIP (Borrill et al, 2016), WheatExp (Pearce et al, 2015). The most promising candidate genes will be validated by re-sequencing the alleles from the relevant parents/representative cultivars, investigating of their transcriptome profiles and identification of TILLING mutants in Kronos collection.

P.2.17

WHOLE PLANT PHENOTYPING TO SELECT CLIMATE-READY DURUM WHEAT GENETIC RESOURCES

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Durum wheat is an important crop for agriculture and the economy of Mediterranean countries where more than half of the crop is cultivated. The upcoming climate change, and especially the shortage of water in the Mediterranean area is going to strongly affect wheat production and quality. While genomic tools are in place for adapting major crop species to environmental stresses, fast selection and quantification of phenotypic traits or components remains challenging. Traditional phenotyping is a labor intensive and time consuming procedure based mainly on destructive methods that greatly limit its application. The use of phenotyping automated platforms may overcome these limitations, collecting large data sets high-throughput and non-destructively. In this study, high-throughput phenotyping was used to characterize a selection of 40 durum wheat landraces held by CNR-IBBR institute. Shoot and root wheat morphology were investigated to dissect mechanisms underlying wheat resistance and resilience to drought. In a first experiment, image in different spectral ranges was used to examine the dynamic phenotypic response to reduced water availability, in association with stress indicators (plant biomass and biovolume, water use efficiency and the plant stress index). The root system architecture of each landrace was also investigated to select those more useful for plants drought adptation. Root phenotyping was carried out using the GROWSCREEN-Page platform at the IBG-2, Forschungszentrum Julich GmbH, Germany, which allows the acquisition of time series of the developing root system, and quantification of short-term variations. Most traits showed a large variation within the genotypes. In general, root length traits contributed more than shape and branching related traits on the overall variability of the root system architecture among genotypes. This approach allowed to select, on the basis of the whole plant phenotypic traits, a set of durum wheat landraces, potentially more adaptable to the upcoming climate change.

P.2.18

RESTORATION CONSERVATION AND CHARACTERIZATION OF LOST GENETIC DIVERSITY OF WHEAT LANDRACES FROM ISRAEL AND PALESTINE

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Key words: Landrace, wheat, genetic diversity, conservation

During the 20th century, the worldwide genetic diversity of wheat was sharply eroded by continual selection for high yields and industry demands for particular standardized qualities. Wheat landraces cultivated in Israel and Palestine demonstrate high genetic diversity, and accumulation of adaptive imprints to various environments . While most of the local Israeli-Palstenian wheat landraces were lost in the transition to Green Revolution varieties, some germplasm collections made at the beginning of the 20th century have survived in genebanks worldwide (VIR, USDA, CGN etc.) and in private collections. The current status, poor conservation and lack of knowledge put this unique genetic resource in high risk of erosion and in urgent conservation priority.

The overall long-term goal of this project is to restore, conserve, study and characterize an exhaustive collection of Israeli and Palestine landraces (IPLR) (n=794). Herein, we focus on characterizing the IPLR tetraploid sub-collection, which include Triticum durum (n=575), T. dicoccum (n=17), T. polonicum (n=7) and a reference panel of elite Israeli cultivars (n=51). Characterization is based on detailed passport data, morphological and phenotypic field based assessment and genetic profiling. Lines were genotyped based on 84 SNP markers distributed evenly across the wheat A and B genomes [*Kaspar* Durum World Reference Collection (DWRC) assay]. SNP data show high genetic diversity in the IPLR-durum collection compared to modern cultivars. Likewise, variable preliminary phenotypic data show the high potential of this exotic germplasm. A core collection of 96 durum lines was constructed based on the genetic distances between accessions of the durum IPLR sub collection and was added as an associated panel to the DWRC, and genotyped using the iSelect 90K bead chip array. This will enable comparisons of the diversity of the two collections and other regional collections.

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P.3.19

REGISTRATION OF “HAMMADI” A NEW MOROCCAN DURUM WHEAT VARIETY

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Durum wheat is the third important cereal in morocco. It is cultivated on more than 1 million hectare annually. However, durum wheat production faces many constraints; mainly drought and diseases. Since 2005, INRA wheat breeding program started focusing its strategy in developing new germplasm with good grain quality like protein content and high yellow index. Indeed, the Moroccan national program released three new varieties with relatively high protein and yellow pigment, in addition to good diseases resistance. These varieties are ‘Louiza‘,‘Hammadi‘ and ‘Itri‘. In the current paper, we will focus on the variety ‘Itri‘.

‘Itri’ (PM9) is spring durum wheat (*Triticum turgidum*), developed by the National Institute of Agricultural Research (INRA) Morocco in 2016. Itri was released based on its high grain yield, moderate resistance to septoria and leaf and yellow rust. PM9 is more adapted to arid and semi-arid regions. The variety was developed from a cross between an ICARDA line (RISSA/GAN//POHO_1/3/ PLATA_3//CREX/ALLA/) and the best cultivated Moroccan cultivar (Karim).

Itri showed good agronomic performance under drought conditions and wide adaptation for the Moroccan arid and semi-arid environments. During the years of evaluation in replicated yield trials in few experimental stations, the variety showed relatively higher yield than all other lines. It showed also a good protein content and good yellow index when compared to all old Moroccan varieties

Keywords: *‘Itri’, PM9, Variety, durum wheat, leaf and rust, septoria, protein content, yellow index, yield and grain quality*

P.3.20

IDÉOTYPE SUD – IDEA AND APPROACH. FRANCE AND PORTUGAL COLLABORATES FOR THE CHARACTERIZATION OF WHEAT VARIETIES MORE TOLERANT TO WATER AND HEAT STRESS

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In order to progress on the characterization of wheat varieties more tolerant to climate change, which is already particularly sensitive in the Mediterranean climate, Arvalis - Institut du Végétal in France and the Portuguese Institute for Agrarian and Veterinary Research (INIAV) and the Portuguese cereal producers (ANPOC) in Portugal have developed a collaboration based on a original method, multidisciplinary (genetics, agronomy, ecophysiology) and with a multi-actors approach: farmers, researchers and field advisers.

In order to save time, both on the study of wheat performance under different possible climate scenarios, and on assisting to progress to choose more tolerant bread and durum wheat varieties, a solid collaboration was started in 2011 between Arvalis Gréoux and the Portuguese Institute for Agrarian and Veterinary Research (INIAV), based at Elvas (wheat breeding team), with a common research programme called Ideotype Sud, to reinforce the effectiveness of this work.

This collaboration is based on a common remark and goal: the southern cereals producers see their yields stagnate or even regress. The chaotic climate frequently defeats their technical efforts. On one hand, an effort should be done to better use the possibilities of genetics to characterize the varieties' aptitudes and, on the other hand, to help producers to manage their crops according to the climate of the year, in Portugal and France.

Ideotype SUD takes the form of an identical trial comprising a selection of Portuguese and French/Italian bread and durum wheat varieties, tolerant or sensitive to water stress and heat stress, conducted in rainfed and irrigated conditions, and followed on a common protocol including measures of yield components, stress indicators, and characterization of the environment. Therefore the stress scenario lived each year is well characterized, and these trials since 2011 allowed to scan many types of stressful climatic scenarios.

P.3.21

ENVIRONMENTAL INFLUENCE ON QUALITY PARAMETERS OF SOME DURUM WHEAT VARIETIES GROWN IN ALGERIA.

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Durum wheat (*Triticum turgidum* L. ssp. *durum* Desf.) is one of the most important cereal crops in the Mediterranean region in terms of cultivated area and per capita consumption. However, durum wheat cultivation generally suffer from insufficient yield stability due to changes of environmental conditions and annual and seasonal climatic fluctuations.

Two different studies were undertaken, the first aim is to evaluate the effect of environmental factors on quality parameters of 21 durum wheat varieties grown under three Algerian locations conditions during two cropping seasons (2013 to 2015). The other study performed under rainfed conditions in 2016/2017 cropping season at Elkhroub experimental aimed an assessment of fourty old local and new durum wheat varieties for their technological, biochemical parameters and grain yield.

In the first study, there is a strong influence of location and growing season on all quality parameters of grain. During the two cropping years, the influence of rainfall amount was low but statistically significant correlations with protein content and yellow index only at El-Khroub. Negative but not significant correlations were observed with brown, yellow berry indeces and black point rate. Among sites, El-Khroub offered the best rainfed conditions for the production of high-quality durum wheat grain.

Results showed in the second study an important genetic variability among the genotypes for all considered traits (quality and yield). Differences were highly significant for total protein content (9,4% to 15,4%), Thousand kernel weight (33,5g to 54,75g), grain moisture (9,55 to 10,93%), wet and dry gluten (6,93 to 12,3g and 2,56 to 5,1g), wellow berry (1,6 to 10,37%), black point (2,85 to 11,45%) and grain yield (2,34 to 4,8t/ha). Old local varieties were globally lower in grain yield than all the new ones but exhibited a higher TKW and total protein levels. The biochemical analysis contributed also to caracterize the different genotypes studied and showed an important polymorphism.

Key words : durum wheat, quality traits, grain yield, old and new varieties, genetic variability.

P.3.22

IDÉOTYPE SUD – RESULTS. FRANCE AND PORTUGAL COLLABORATES FOR THE CHARACTERIZATION OF WHEAT VARIETIES MORE TOLERANT TO WATER AND HEAT STRESS

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To fight against yield stagnation in bread and durum wheat, ARVALIS-Institut du végétal (France) and National Institute for Agrarian and Veterinarian Research (INIAV), Portugal, lead since 2012 variety trials reinforced on two stations: Gréoux (Paca region), France and Elvas, Portugal, subjected to important climatic constraints.

The extensive range of climatic conditions experienced since 2012 and the routine use of the Phénomobile, since 2016 in Gréoux, also made possible to use these trials as supports for methodological advances at the interface between broadband phenotyping, varieties and agronomic models. The complementarity of these agronomic and genetic innovative approaches opens the way to potential valorisation both in selection and in advice to producers on the choice of varieties in their environments.

A more refined characterization of the varietal characteristics related to the stress response was done. Senescence dynamics of the top leaves was evaluated by a portable equipment (greenseeker) or by phenomobile tool (NDVI). Results shows that yield performance of the varieties is strongly correlated with the date of the point of inflection of the senescence curve, either in rainfed or irrigated conditions.

Today, the precision of the achievements made by the Phénomobile makes possible to consider fine-tuning wheat development models by variety, through the varietal adjustment of the parameters used in the crop models (model ARVALIS CHN) and by realizing this, to phenotype on active variables in the CHN model more directly involved in wheat agronomic performance. Thus it is designed to refine the ideotype by mobilizing these resources.

As part of a future research program, the extension to other countries of the Mediterranean basin is envisaged with a start of collaboration with Tunisia, and partnerships in Italy.

Beyond breeder knowledge of the varieties (yield components, precocity, foliar port), the access to the hidden functional parameters of CHN allows to better know the varieties for adaptation to stress, to better advise, refining the varietal bouquet by environment, according to climatic scenarios.

P.3.23

FIRST DURUM WHEAT CULTIVAR FOR DRY LAND AREAS IN CHILE?

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In Chile, the wheat area reached 240,000 ha, about 10% of production is durum wheat associated in irrigated situation opposite to the rest of the world where the great proportion is of dry land conditions, where the Mediterranean climate prevails with a strong water stress and high temperatures during the grain filling. Coastal dryland is defined as the agroclimatic zone located on the western slope of the Coastal Range between the Coquimbo (29º53’ S) and Los Lagos Regions (40º 35’ S). Rainfall occurs mainly between April and September.

Investigates during the years 2015-2017, the effect of high temperatures in two sites of Mediterranean area: Hidango (Dry land) (36º 06’ 48’’S; 71º 47’ 52’’ West; 269 m.a.l.s) and Santa Rosa (Irrigated) (36° 31’34 “S, 71 ° 54’40”.), in both sites the temperature during grain filling exceeds 32°C. We evaluated in both sites twenty five durum wheat varieties included Llareta-INIA, Lleuque-INIA, Queule-INIA and Waha. Traits evaluated include: Yield (t ha-1), hectoliter weight (kg hL-1), protein content (%), plant height (cm), (%), sedimentation value (cc) and diseases resistance to rust days phenology, color b, grain vitreousness, grain black point, susceptibility and resistance to leaf rust (P.triticina), yellow rust (P.striiformis) and stem rust (P. graminis), powdery mildew (B. graminis), and BYDV. The best performance is CIMMYT line: SORA/2*PLATA_12/3/SORA/2*PLATA_12//SOMAT_3/4/AJAIA_13/YAZI//DIPPER_2/BUSHE N_3, selected in 2009 in Obregon, México and evaluate in Chile in contrast environment previously described.

P.3.24

LOSSES IN GRAIN YIELD AND QUALITY OF CHILEAN *TRITICUM DURUM* PRODUCTION. IMPACT OF CLIMATE CHANGE?

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In season 2016/17 in Chile, the national area cultivated with durum wheat was 28,178 hectares, concentrated between 32º55’S and 37º28’S, with some planting in 38º40’S y 40º51ºS. Until 2015/16 the national production of durum wheat kept a sustained growth increasing from 98,690 Tons in 2011/2012 to 200,929 Tons the season 2015/16. Nevertheless, the seasons 2015/16 and 2016/17 the production suffered important losses 36% of grain yield and a quality decay reflected in a decrease of semoline color.

This study investigates, the effect of climate fluctuations, temperatures and precipitations, registered along the growth period of crop, in three representative sites of Mediterranean area: Hidango (34º 11’ 00’’S; 71º 46’ 00’’ West; 269 m.a.l.s), Chillan (36° 36’ 00’’South; 72° 07’ 00’’West; 124 m.a.s.l.), and Los Angeles (37º28’S 72º21’W; 139 m.a.s.l), where the temperature during grain filling exceeded 32°C, during 2016/17 and 2017/18. We evaluate duration of vegetative and reproductive phases, plant height, hectoliter weight, semoline color, vitreous, protein content and grain yield in four national durum wheat varieties Llareta-INIA, Corcolén-INIA, Lleuque-INIA and Queule-INIA.

Considering that the climate projections to the Chilean production area, indicate important temperature increases and decreases in rainfall during crop growth, the study proposed is important to formulate new strategies associated to the breeding process that allow obtain varieties that have good grain yield and quality, under abiotic stress conditions.

P.3.25

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

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

P.3.26

IRRIGATION EFFECTS ON QUALITY CHARACTERISTICS OF DURUM WHEAT IN TUNISIA

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Durum wheat accounts for more than 50% of the total wheat-growing area in the Mediterranean region, where it is used for the preparation of diverse food products such as pasta, couscous and bread. Water stress is a major limiting factor for a maximum wheat yield potential. Durum wheat is grown under supplemental irrigation in central Tunisia. Kairouan accounts for more than 30% of irrigated wheat. However, the region's insufficient water resources force farmers to use irrigation. The purpose of this study was to determine the effect of irrigation on durum wheat technological quality. Sixteen advanced lines and seven durum wheat varieties from the national breeding program were tested under two water regimes: full irrigation (100% ETP) and reduced irrigation (50% ETP) during 2016-2017 cropping season. The trial was lead out in a complete randomly design. the following quality traits were determined on harvested grain: yield grain, grain protein content, 1000 Kernel weight, test weight, moisture content, sedimentation volume, gluten index and semolina yellowness. The results showed that water regime have differentially affected the quality parameters. Grain yield, test weight, 1000 kernel weight and gluten strength increased with irrigation. However, the protein content and yellow pigment content among the pasta making quality characteristics have been found to be at the highest levels for all varieties and advanced lines in deficit irrigation. Under both regimes, highly significant correlations were found between grain yield and protein content (r=- 0, 51), between gluten strength and the grain protein content (r=0, 57) and between test weight and yield (r=0, 6). Thus it could be suggested that in order to combine acceptable quality characteristics with the highest grain yield in the region, a supplemental irrigation exceeding the level of 50% ETP should be applied.

P.3.27

GENETIC DISSECTION OF ROOT ARCHITECTURAL TRAITS AND THEIR ASSOCIATION WITH DROUGHT ADAPTATION IN DURUM WHEAT

Presenting Author Khaoula EL Hassouni
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Durum wheat (Triticum durum Desf.) is one of the most important crops of the world but its growth and production are often hampered by limited water availability. Roots play an important role in water acquisition and use. Therefore, a better characterization of the root system architecture is critical to crop improvement and should represent a strategic insight to design new cultivars capable of capturing soil moisture more efficiently. The genetics modulating root system architecture are still not well understood. In the present study, a panel of 100 durum wheat genotypes originating from different countries were investigated for the genetic variability in root architecture and growth traits. Two protocols were used, a 'clear pot' protocol for seminal root characterization and 'pasta strainer' for mature root evaluation. To examine whether genotypes change their root system architecture depending on water availability, the genotypes were assessed for their rooting pattern under water-limited and well-watered treatments in near field conditions. This study revealed that water treatment effect was not significant for root architecture, indicating a strong genetic control of this trait. A significant genetic variability for root angle was found and two main categories of root types were identified: genotypes with (i) superficial and (ii) deep rooting systems. Then, the two classes were tested in the field yield trials with different water regimes to assess impact on yield. A significant advantage for grain yield was shown by deep rooted genotypes in the environments with terminal reduced moisture. The complete set was genotyped and a genome scan using 8173 SNPs markers developed by 35K Axiom array allowed to identify the genomic regions influencing drought adaptation mechanisms and their relationship with yield. The use of this genomic regions could lead to an improved resilience to climate change and increase durum wheat productivity in drought-prone areas.

P.3.28

GENETIC DISSECTION OF FUSARIUM HEAD BLIGHT RESISTANCE IN DURUM WHEAT (*TRITICUM TURGIDUM SSP. DURUM*)

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Fusarium Head Blight (FHB) represents a worldwide threat for many grain crops leading to severe yield and quality losses while threatening human and animal health due to mycotoxin accumulation. *Triticum turgidum* ssp. *durum*, the most important tetraploid wheat in the world, is notoriously highly susceptible to FHB.

With the aim to provide a most accurate inventory of Quantitative Trait Loci (QTLs) for FHB in durum wheat, we performed a genetic characterization of 130 elite accessions (Fusarium Panel) and 165 F6 RILs from the population Simeto × Levante. The Fusarium Panel was evaluated in three artificially inoculated nurseries and in three years while the inoculation was carried out with *Fusarium graminearum* and *Fusarium culmorum*. The RIL population was evaluated in greenhouse in Tulln (Austria) in two years and inoculated with *F. graminearum*.

Custom R scripts were used to produce best linear unbiased prediction (BLUP) values for the following traits: AUDPC incidence, AUDPC gravity, AUDPC Fusarium index, deoxynivalenol (DON) and Fusarium Damaged Kernels (FDK). A genetic characterization of RILs and Fusarium Panel was carried out using the Infinium wheat SNP 90K iSelect assay and the genotype scores were used to conduct a Genome Wide Association Study (GWAS) in Tassel v.5.2.7 (for Fusarium Panel) and a QTL analysis based on single-marker and multiple interval mapping (MIM) in Windows QTL Cartographer (for RILs). A remarkable number of QTL hotspots were detected in the following chromosomes: 1BL, 2AL, 3AL, 3BS, 3BL, 4AL, 5AL, 5BL and 6AL. Then conserved linkage blocks were investigated in major QTL/gene regions and their related effects. Tag-SNPs and haplotypes identified in this study will be used for marker-assisted selection (MAS) programs in order to accelerate new breeding strategies for FHB-resistant wheat cultivars.

P.3.29

GENETIC CHARACTERISTICS OF HETEROSIS OF WHEAT (*TRITICUM* L.)

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A comprehensive assessment of the changes in the nucleic acid content of individual structural elements of cell, nuclei, mitochondria and chloroplasts, in hybrids of wheat, performing heterosis, were carried in comparison with their parental forms.

It was reveled that, the content of DNA in per cells of leaf tissue of the heterosis hybrids plants was higher than those of their parents. Thus, reduction of the cell numbers for per unit area and increasing of cells' size were observed in hybrids. Hybrids were also characterized by increased DNA content in the nucleus of leaf cells, which associated with the new classes of ploidy level (2c– 4c) in the heterosis hybrids of wheat, that explained by the amplification and also differential replications of DNA.

Activation of DNA synthesis in heterosis hybrids was not observed by the same fraction of DNA in all cases. High levels of total DNA content in the leaves of heterosis hybrids was due to the increased labile DNA fraction in many cases, while in some cases both labile and stable fractions. At the same time, there was redistribution in favor of the fractional composition of euchromatin fractions. Increasing of the labile and stable fractions of DNA, presumably, was on account of the formation of numerous endoploid cells in the hybrids, while increasing of the individual fractions through the gene amplification.

A total increased energy supply of cells in heterosis hybrids may contribute by mitochondrial and chloroplast systems. Obviously, in the case of nuclear DNA and plasmogen function with an increased load the hybrids gets more energy to enhance the biosynthesis of necessary substances and this may appear as a high heterosis effect.

P.3.30

"INDIAN DURUM WHEAT – ITS IMPORTANCE AND POTENTIAL FOR PASTA INDUSTRY"

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In India, an estimated of 1.5 to 2.0 million tonnes of durum wheat is produced annually. Dry and hot environment of central and peninsular parts of India viz., Madhya Pradesh, Gujarat, Maharashtra, Karnataka and Southern Rajasthan are suitable for durum cultivation. Best quality durum wheat with excellent appearance, good hecto-litre weight, high protein and less yellow berry incidence is predominantly produced in the Malwa plateau of Madhya Pradesh due to longer grain filling period and short vegetative growth in the region. Its grain density, combined with high protein content (>12.5%), <10% yellow berry incidence and >7.0 ppm ß-carotene content and gluten strength, make durum the wheat of choice for producing premium semolina, which is being used in making Indian recipes viz., rava-dosa/macaroni/ noodles/snack foods etc. With the rising demand for speciality foods like pasta in India and other countries, the market for durum wheat is growing at an exponential rate. Intensive research and development efforts made by Regional Research Station, Indore of ICAR-Indian Agricultural Research Institute brought the durum wheat back into cultivation in Central India with very high yield potential. With intensive popularization of newly evolved high yielding and rust resistant *durum* varieties viz., HI 8627, HI 8663, HI 8713, HI 8737 and HI 8759 etc., with a yield potential of > 50 q/ha and their "low-cost cultivation technology", durum wheat production in Madhya Pradesh improved significantly leading to the declaration of the state as "Agri-Export Zone (AEZ)" for durum wheat also. Recently, multi-national food companies in India are utilizing Indian durum wheat, which is comparable with its Canadian and Australian counterparts in terms of quality for processing rather than depending on the imports. The pasta industries are looking for more hectolitre weight & hardness to have better extraction rate (~ 68-72%), high protein (~13%), less black tip and dark crease, freedom from yellow berry and Karnal bunt for good finishing of pasta products. Compared to bread wheat, higher heat tolerance of durums ensures higher yields with lesser irrigation. Modern durum varieties are generally resistant to currently prevalent and bread wheat virulent rust pathotypes, and thus, have been contributing to arrest the spread of wheat rusts in the country. Thus, it is an ideal wheat to be grown in Central and Peninsular parts of the country for "ensuring food and nutritional security", increasing employment opportunities through fast food industry and sustainability. Increasing global demand, value addition potential, resistance to diseases, better market price are some of the key factors which make Indian durum wheat an export commodity as well as capable of catering to Indian market. It has an export potential similar to basamati rice. The potential markets for Indian durum can possibly be countries in Middle East, Mediterranean region and Africa after catering the huge demand in Indian markets. An awareness campaign is, therefore, urgently required for the growers, traders and consumers about the importance of durum wheat as high economical crop and for use as "Health Food".

P.4.31

DIVERSITY AND CORRELATION ANALYSIS IN DURUM WHEAT (*TRITICUM AESTIVUM* L) GERMPLASM

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Genetic diversity was confirmed by measuring different morphological traits i.e. seed traits and other genomic traits. In In present study, genetic diversity based on DNA markers and seed morphological traits was assessed in a set of 20 wheat accessions. Variance and association study of desirable traits determine the genotypic differences among the wheat germplasm. Seed thickness has positive correlation with seed length and seed length width ratio (r= 0.166**, r=0.340**). On the other hand, seed thickness also showed positive significant association with seed width and 1000-grain weight (0.274^{**}, 0.180^{**}, respectively). After screening genetic diversity of potential wheat lines were studied to check the polymorphism by using 15 SSR markers. DNA was extracted and PCR analyses were done to study PIC values and allelic diversity of the genotypes. Minimum (0.404) and maximum (0.833) PIC values were observed from primers 'WMC15' and 'WMC24', respectively. For molecular diversity analysis data from 15 polymorphic SSR primer pairs were used to determine total number of alleles (4.53), polymorphic alleles (4.40), polymorphism% (96.5) and polymorphic information content (0.636). The main objective of this study is to screen out the genotypes on the basis of various genotypic and phenotypic traits for further use in breeding research programme for improving wheat yield.

Keywords: Wheat, Morphological Traits, Germplasm, Association, Genetic Diversity

P.4.32

GPDUR PROJECT : GENETIC AND PHENOTYPIC EVALUATION OF DURUM WHEAT FOR SIMULTANEOUS IMPROVEMENT OF GRAIN YIELD AND PROTEIN CONTENT

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In France, cultivated area of durum wheat has dramatically decreased in few years, since 2010. The government decided to launch a large recovery plan in order to stimulate all the sector (from breeding to transformation). One of the major issue is the negative correlation between yield and protein content. Results of last registration year show that yield is improved to the detriment of protein content. This last trait is major for market accessibility, genetic progress for yield is then accessory. However, wheakness in yield improvement penalizes durum wheat competitivity regarding others crops which are included in the rotation.

Negative relation yield-proteins is not a durum wheat specificity. In bread wheat, recents studies on GPD (Grain Protein deviation) have shown that it is possible to broke this relation. And the determinism linked to nitrogen post-flowering starts to be known.

Our project propose to evaluate, with genetic and phenotypic approaches, a panel of lines selected to represent a large genetic diversity : french lines, international elites lines (from P. Tuberosa), EPO population (Evolution Pre-Breeding Population). All the lines have been genotyped with SNPs from TaBW280K chip from the french Breedwheat project.

The panel has been tested for disease resistance and for quality and it will be phenotyped in a multi-local network for GPD and specifically on 2 high throughput phenotyping platforms at field level (Mauguio, Gréoux) in order to try to understand and validate hypothesis for GPD determinism established in bread wheat. Phenotypic and genetic data will be used for association mapping analysis in order to identify molecular markers linked to GPD and compare the genetic architecture of this trait to what is known in bread wheat. At the end of the project, breeders will have access to genetic information that can be implemented in their breeding programs to improve the selection of progenitors advantageous for GPD.

P.4.33

TITLE: PHENOTYPIC AND GENOTYPIC DIVERSITY IN AN ARGENTINIAN DURUM WHEAT (TRITICUM TURGIDUM L. VAR DURUM) PANEL

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Durum wheat (Triticum turgidum L. var. durum) is the quintessential raw material needed to produce pasta, an important component of human diet. Argentina is one of main producers of pasta in the world, taking the eighth place. The aim of this work was to evaluate the genotypic and phenotypic variability of 61 Argentinean cultivars and breeding lines. Three experiments were performed in contrasting environments across the durum wheat production area. The analysis of the genetic diversity and the population structure was performed using 1,000 selected SNPs from the Axion 35K array in low linkage disequilibrium ($r<0.5$). Yield (kg/ha) and 19 yield-related traits were evaluated from either 4.2-5.5m2 plots. The effect of SNP markers on major genes (Rht-B1, Ppd-A1 and Vrn-A1) was evaluated in the collection. Cultivars carrying Rht-B1b showed the highest yield associated with increased spike fertility, harvest index, grain number and grain weight per plant. Cultivars with the allele Vrn-A1b exhibited lower yields related to a lower harvest index and spike fertility while Ppd-A1a was associated with higher yields and grain numbers. The analysis of population structure showed two main groups (K=2), one consisting of old cultivars carrying the wild type allele Rht-B1a and the other of the modern cultivars. Cluster analysis (UPGMA) clearly differentiated one winter cultivar and one cultivar with partial cold requirement from the others. In addition, the genotypes from each breeding program were mainly clustered together. Phenotypic analysis showed significant differences between genotypes for all of the evaluated traits. Moreover, in the case of yield highly significant differences between environments and genotype by environment interactions were detected. Harvest index, spike fertility and grain number per spike showed positive high and highly significant correlations with yield. Harvest index showed the highest correlation coefficients with values over 0.65 for two of the locations considered.

P.4.34

VARIETAL INVESTIGATIONOF DURUM WHEAT TARGETING INDUSTRIAL PRODUCTION OF SEMOLINA AND PASTA IN NEPAL[1]

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Introduction and testing of durum wheat from CIMMYT-Mexico was initiated in 2007 by Agriculture Botany Division of NARC at Regional Agriculture Research Station, Khajura and its command areas for establishing durum wheat as industrial crop suitable for mid and far western plain regions of Nepal. The current research involved introduction, testing and selection of genotypes from CIMMYT's IDSN, IDYN nurseries and their advance into National trials, DWAVTs and Participatory Variety Selection (PVS) for variety recommendation. For identifying superior genotypes, yield and yield attributing traits of 94 durum wheat genotypes were evaluatedat Khajura from 2011/12 to 2016/17. Throughout all trials, days to heading and maturity varied from 71 to 105 days and 105 to 135 days after sowing, respectively.Grain yield varied from 1.35 to 6.86t ha^{-1}, plant height from 59 to 108 cm; number of tillers per m^{2}from 84 to 497, number of grains per spike from 25 to 74; grain weight per spike from 0.62 to 3.50 g and thousand grain weights varied from 12.7 to 82.4 g. Based on Best Linear Unbiased Prediction (BLUP), DWK26, DWK98, DWK38, DWK94 and DWK135 showed the best performance. Correlation among yield attributing traits and clustering of genotypes were performed based on both least square means and BLUP values, providing us a distinct association of traits with yield and superior clusters for precise selectionof superior genotypes. For the first time, two durum varieties: DWK26 (6.22 tha^{-1}) and DWK38 (6.72 t ha^{-1}) has been released in 2017 named as Khajura Durum 1 and Khajura Durum 2 respectively. Seed production of these varieties is going on targeting 1,000 hectares in Nepal. Coordination of stakeholders for durum varietal improvement with end-use production and consumption is of great importance. Establishment of the crop at industrial scale is crucial for the economic enhancement of farmers and food security.

P.4.35

ENHANCING GRAIN YIELD BY KNOCK DOWN GRAIN WEIGHT 2 GENES IN DURUM WHEAT

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Grain Weight 2 (*GW2*) has been identified as a key gene for yield in several crop species. In durum wheat two homeoalleles (*GW2-A1* and *-B1*) have been identified and located on the short arm of chromosomes 6A and 6B. In the present study an RNA interference approach permitted to down regulate the *GW2* genes in the durum wheat cultivar Svevo. The gene expression analysis on immature (21 DPA) T_4 seeds highlighted a drastic reduction (>75%) of *GW2* transcript in the GW2-RNAi lines compared to wild type (cv Svevo). Significant differences were detected for parameters related to yield and grain morphology. In particular, total starch (determined on single kernel), grain width and grain area were increased in all the transgenic lines in the range 10-40%, 4-13% and 3-5%, respectively. In addition, a transcriptional analysis was performed on target genes whose expression was found to be modulated by the knock down of *TaGW2-A1* in previous studies. qRT-PCR analysis highlighted that the transcript abundance of the cytokinin dehydrogenase 1 (*CKX1*) and the large subunit of ADP-glucose pyrophosphorylase (*AGPL*) were strongly up-regulated in the three transgenic lines compared to the control, whereas a different transcriptional behavior was observed for the cytokinin dehydrogenase 2 (*CKX2*) and the gibberellin 3-oxidase (*GA3-ox*), that were less expressed in the transgenic lines. A comparative proteomic study, performed on the metabolic fraction extracted from mature kernels, allowed to detect some differentially expressed proteins (DEPs) involved or potentially involved in the cell wall development.

P.4.36

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

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

P.4.37

WHEAT RUST SURVEILLANCE AND MONITORING IN SICILY 2016-2018

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Severe and widespread attacks of stem rust (Sr) and yellow (stripe) rust (Yr) were observed in Sicily in 2016. Since then, extensive surveillance and monitoring have been carried out in the region during 2017 and 2018, in farmers' fields and in breeding trials. In total, 82 Yr and 62 Sr isolates from Italy (approx. 90% from Sicily) were analysed at the GRRC for race phenotyping and SSR genotyping. The dominating race of stem rust in 2016 and 2017 was TTRTF, also found in mainland Italy. TTRTF was found on 25 different durum wheat varieties and breeding lines including the most grown varieties in Sicily. Another race, TKKTF, was found in Sardinia in 2017. Sr genotyping and race phenotyping for 2018 is on-going. The test of Yr isolates from 2016 to 2018 resulted in the identification of four races, i.e., "Warrior (-)", "Triticale 2015" "PstS14" and "Triticale2006". Triticale2015 dominated in 2017 and Triticale2006 were the most wide-spread race in 2018. In this study, the majority of commercial durum cultivars were susceptibly to both stem and yellow rust. Some varieties were susceptibility to more than one race of yellow rust. In Sicily, the majority of farmers do not protect their wheat crops with fungicides, and the durum wheat community needs tools and services for rusts disease surveillance and pathogen monitoring supplemented by new resistant germplasm to be included in breeding programs. All results regarding disease surveillance and pathogen monitoring is available in the Wheat Rust Toolbox and on wheat rust information platforms e.g. the GRRC website and RustTracker. Sicily is also included as a case study region in the H2020 project called RustWatch, a new European early-warning system for wheat rust diseases. Surveillance tools and services as well as updated results on disease surveillance and pathogen monitoring in Sicily will be presented.

P.4.38

EFFECT OF SILICON ON DURUM WHEAT GROWTH AND DROUGHT STRESS TOLERANCE

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Silicon (Si) has beneficial effects on durum wheat, mainly under biotic and abiotic stress. Silicon can affect biochemical, physiological, and photosynthetic processes and, consequently, reduce drought stress. In this study, the effect of silicon fertilization on the growth and drought tolerance of eleven varieties of durum wheat under water stress induced by polyethylene glycol (PEG). Experimental trial were conducted in hydroponic culture with four treatments (T1: non-stress, T2: non-stress + 150 mg / l (Si), T3: stress (200 g / l PEG) and T4: l PEG) + 150 mg / l (Si)). and chlorophyll index (SPAD), cell membrane stability (SMC), relative water content (RWC), fresh seedling weight (SW), vigueur Index (VI) and dry weight (DW) were determined. The results obtained revealed that the addition of silicon significantly improved ($p < 0.001$) the majority of traits measured on durum wheat, particularly in high concentrations (15 and 20 mg / l). Silicon increased SW, DW and VI by 25%, 21.42% and 143.12% when the Si concentration increased from 0 mg / l to 20 mg / l respectively. Thus, Silicon increased the SPAD values by 25.80% and decreased the electrical conductivity by 6.97%. In general, the results showed the positive effect of silicon on germination and the growth of durum wheat under water stress conditions.

Keywords: *durum wheat, silicon, water stress*

P.4.39

MONSANTO'S BEACHELL-BORLAUG INTERNATIONAL SCHOLARS PROGRAM

Edward Runge* and David Baltensperger

Corn, wheat and rice are the world's 3 most important cereal crops. Corn yields are growing faster than world population but wheat and rice are not, and are putting millions of people on a collision course with hunger. These facts led the late Dr. Norman Borlaug to ask Monsanto executives to boost research into wheat and rice breeding.

The Monsanto Beachell-Borlaug International Scholars Program is named after Monsanto and the greatest wheat and rice breeders of the 20th century, and was established on Dr. Borlaug's 95th birthday on March 25, 2009. It is directed by Dr. Ed Runge and administered by Texas AgriLife Research of Texas A&M University and was guided by a distinguished judging panel from around the world.

Since the program's inception 89 scholars, from 30 different countries, were selected for support with the $13 million provided by Monsanto over 8 years. They were selected from 432 applicants. Scholars include 35 women and 54 men, 37 in rice breeding and 52 in wheat breeding. Twenty-two scholars are still completing their Ph.D. programs. These scholars represent the best of the best entering the plant breeding profession. Scholars were expected to seek employment in public institutions if possible.

Conclusions – MBBISP

1. Has greatly increased research in rice and wheat breeding.
2. Was unique as Scholars conducted research during their PhD program in both developed and in developing/transition countries. The MBBISP enhanced interaction between professors and scientists in developed and developing/transition countries.
3. Concluded that Scholars needed additional leadership training and established a 40 hour leadership and development course taught by TERO International Staff (Clive, Iowa). Scholars took the leadership course during the first 2 years (20 hours each year) of their PhD program, before attending Monsanto Day at Ankeny or Huxley, Iowa, and the World Food Prize. The leadership course was well received.
4. Scholars will impact food security for many generations through their leadership.

In 2017 Monsanto established the "Ted Crosbie MBBISP Impact Award" to begin recognizing notable contributions. Scholar impact is just beginning to be recognized since the earliest graduates have been employed for less than 6 years. Dr. Bhoja Basnet, who is in charge of CIMMYT's hybrid wheat breeding program, was selected to receive the Ted Crosbie MBBISP Impact Award for 2017.

P.5.40

PAVING THE PATH OF DURUM WHEAT HYBRID: IDENTIFICATION OF HETEROTIC COMBINATIONS AND FLOWERING GENES.

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The combined challenge of population growth and climate change has been forecasted to exert tremendous pressure on global food supply. To meet this challenge, a paradigm shift is required in our approach to continuously generate more productive technologies using novel approaches. One such approach is to tap the hybrid technology. The present study examined the magnitude of heterosis in durum wheat through evaluation of 18 parents along with 53 F_1 hybrids. The hybrids along with their parents were also evaluated in precision phenotyping platform (Lemnatec) at different levels of water stress and in near-field condition. Combining ability analysis suggested predominance of non-additive gene action as underlying principle in the expression of heterosis for grain yield and its components in durum wheat. The results showed >13% best-parent heterosis, indicating the scope for exploitation of heterosis in durum wheat. Among the hybrid combinations, Valnova x Miki followed by Iride x Miki, Svevo x Miki and Valnova x Svevo were the best for all the traits studied. However, there was no correlation between genetic similarity of different sub-populations and heterosis. Another aspect of hybrid technology is to ensure adequate pollination between heterotic parents which require overlapping flowering time. To understand the genetic control of flowering time, a genome wide association study (GWAS) was conducted to identify genomic regions associated with the control of flowering time in durum wheat. A total of 384 landraces and modern germplasm were assessed in 13 environments to determine five pheno-environments based on temperatures, day length and other climatic variables. Genotyping was conducted with 35K Axiom array to generate 7,740 polymorphic SNPs. In total, 14 significant QTLs for landraces and 26 QTLs for modern germplasm were identified for flowering time consistently across the environments. Some QTLs had strong association with previously identified genes at defined confidence interval. The results obtained from these experiments indicated sufficient heterosis and few heterotic combinations could be exploited for hybrid breeding program in durum wheat.

Keywords: *durum, heterosis, heterotic combination, flowering time.*

P.5.41

STATE OF RESEARCH ON WHEAT AS A STRATEGIC CROP IN THE SENEGAL RIVER VALLEY

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Abstract: Due to its multiple uses (bread, couscous and pasta, starch and animal feed), Senegal wheat imports has hugely increased in 15 years from 216 465 t in 2000 to 573 435 t in 2016 for a value exceeding 250 million US$.

Whilst it is clear that bread wheat was of particularly interesting for our country, it should be kept in mind that the consumption of durum wheat made product as pasta, couscous, and biscuits, are becoming more and more important in our consumption habits.

Wheat cultivation has the potential to significantly increase the cultural intensity of the Senegal River Valley (SRV) with cold dry season wheat plantings that are expected to partially satisfy domestic demand for durum and bread wheat without hindering rice production and while gaining market part for durum wheat by specifically exploiting the particular seasonality that favors the maturity of wheat in the SRV when supply to the world market is sharply declining.

Studies in the 1970s and 1980s had demonstrated the possibility of wheat production in the SRV and pre-extension of wheat cultivation had even started in 1973 in Savoigne and Dagana in 1975. However despite water and land availability, favorable climate and research results of the period, the economic and strategic plans of the time did not favor wheat cropping extension over large areas.

However, acquired knowledge during these years gave important data whose exploration and updating would help in saving time for new research interest.

Under the auspices of the Senegalese Institute for Agricultural Research (ISRA), significant achievements and progress have been achieved since the beginning of the 2000s with partners from different countries (Morocco, Mali, Egypt) and international institutions (ICARDA , CIMMYT). This paper highlights achievements during the last 10 years as well as prospects for the next years.

Keyword: Senegal river valley, wheat

P.5.42

EMPHASIS ON THE NETWORK OF EUROPEAN PLANT PHENOTYPING INFRASTRUCTURES AND ON ITS ITALIAN NODE PHEN-ITALY

EMPHASIS*,** , PHEN-ITALY***, ****.

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EMPHASIS (European Infrastructure for Multi-scale Plant Phenotyping And Simulation for Food and Security in Changing Climate) is a pan-European distributed infrastructure of the ESFRI (European Strategy Forum on Research Infrastructures) Roadmap. EMPHASIS aims at exploiting, through high-throughput phenotyping, the genetic diversity required for the enhancement of plant productivity, the resistance to biotic and abiotic stresses, and, in general, progresses in plant breeding. The infrastructure will enable diverse users to quantify relevant plant traits and to precisely analyze genotype performance in current and future agro-climatic scenarios. EMPHASIS will furthermore establish links between big data acquisition and management, and models at single plant and crop level, achieving reliable simulations of performances (from genotypes to whole crops) in different environmental scenarios. State of the art facilities will be accessible to users from academia, the industry and relevant stakeholders, delivering scientific breakthrough and innovation, and maintaining Europeans leadership in plant phenotyping. At the Italian level, Phen-Italy the national node of the preparatory phase of the ESFRI Project EMPHASIS-PREP, is co-coordinated by CNR and ALSIA, and is structured in a Joint Research Unit (JRU) that is participated by 11 more universities and research entities, contributing to the development and successful exploitation of plant phenotyping in the Mediterranean area.

P.5.43

IMPROVED SEPTORIA TRITICI BLOTCH DISEASE CONTROL USING VARIETY MIXTURES

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Septoria tritici blotch (STB), caused by *Zymoseptoria tritici* is a serious threat to durum wheat in the Mediterranean Basin. Frequent virulence changes, slow release of resistant varieties and insufficient crop rotations lead to recurrent Septoria disease epidemics in Tunisia. Hence, variety mixtures is a promising method to improve the disease management. Field experiment conducted at the Septoria Phenotyping Platform at Kodia station (Tunisia) using three durum wheat varieties with different levels of resistance to STB were assessed in 2017/2018 cropping season to examine the effect of mixtures on disease levels. The wheat varieties included Karim, by far the most widely grown variety in Tunisia, which is susceptible to STB, and Salim and Monastir, the two newly released varieties with high levels of disease resistance. Pure stands along with two-way mixtures and three-way mixtures of different proportions were planted in three replicates in a randomized complete block design.

F-1 and flag leaves were collected at two time points late in the season. Disease incidence was assessed visually and conditional severity was measured as the percentage of leaf area covered by lesions as well as the density of pycnidia within lesions with the help of the automated digital image analysis. The two measures of conditional severity in each leaf were multiplied by the incidence of the respective plotto estimate the full severity. Separate comparisons were conducted for the two time points. Preliminary results suggest that STB is efficiently controlled by adding a proportion of resistant variety to a susceptible variety. Karim in the pure stand showed the highest disease levels and adding only 25% of a resistant variety in two-way or three-way mixtures decreased the disease levels to a level comparable to pure stands of the resistant varieties.

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GENOMIC REGIONS INFLUENCING YIELD STABILITY IN DURUM

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Durum wheat (*Triticum durum* Desf.) is a major stable crop and it represents a base of the Mediterranean diet. This region is subject to a Mediterranean climate, which is extremely unpredictable with severe changes in moisture and temperature occurring each crop season. This unpredictability is summarized by breeders as GxE and the identification of traits controlling this interaction is quintessential to ensure stability in production season after season. To study the genetics of yield stability, four RILs populations derived from elite x elite crosses were assessed for yield and 1,000-kernel weights across five diverging environments in Morocco and Lebanon These 550 RILs were characterized with 4,909polymorphic SNPs via genotyping by sequencing. A consensus map was derived by merging the individual genetic maps of each population. Finally, imputation was used to fill all the missing haplotypes and reach a reduction of missing data to below 8%. Several significant QTLs were identified to be linked to TKW, grain yield and a stability index, namely AMMI wide adaptation index (AWAI). A second approach to identify loci controlling stability was the use of a global panel of 288 elites, accessions and landraces tested in 15 diverging environment. Multi-locations data were compiled via GxE models to derive the AWAI stability index. In addition, this panel was characterized with 8,173 polymorphic SNPs via Axiom 35K array. Significant associations were identified for all traits, including QTLs unique to AWAI. The sum of the identified QTLs can now be pyramid via marker assisted selectionand molecular designed crosses in order to obtain very stable cultivars.

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P.6.45

GLUTEN FORMING CAPACITY OF ARGENTINEAN DURUM WHEAT GENOTYPES (*TRITICUM DURUM* DESF.) IS RELATED TO CULTIVAR´S INTRINSIC GLUTEN STRENGTH AND PROTEIN LEVELS.

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For the *durum* wheat-pasta chain, grain protein (PROT), and hence, gluten content of semolina (WGC), are key factors associated with superior pasta texture and cooking quality. Both attributes have proved to be closely related, and predominantly influenced by environment. However, cultivars can differ significantly in WGC even at similar PROT levels, revealing the existence of genotypic differences in their gluten forming capacity (GFC), represented by means of the WGC/PROT ratio. Although this fact could give rise to controversy during grain or semolina trading, it still remains under investigated for the set of cultivars grown in Argentina. To shed light on this topic, a multi-environmental study was conducted over a three year period in representative sites of Southern Buenos Aires province, to investigate the response of five genotypes sown in ten environments, concerning their GFC and WGC. As expected, WGC of genotypes were closely associated to PROT levels (between 11,7% and 18,4%), varying from a minimum of 28,6% to a maximum 47,4% (r= 0,89, P≤0,0001). GFC also varied broadly, within the range of WGC/PROT between 2,20 and 2,82, depending on genotypes´ gluten strength (r= -0,47, P≤0,0001) and protein levels (r= -0,31, P≤0,05). Thus, weak and moderate-to-weak gluten strength genotypes (Gluten Index < 70) exhibited their highest GFC in the lower range of PROT levels, experiencing a significant decline in the upper ones (WG/PROT from 2,81 to 2,35). Instead, moderate-to-strong and strong gluten cultivars (Gluten Index > 70) showed inferior GFC at low PROT levels, leading to WGC below those observed for weak or moderate-to-weak cultivars. However, the latter behaved more stable, or even raised their GFC with increasing protein levels (WG/PROT from 2,24 to 2,82), resulting in WGC comparable, or still higher to those measured in weak or moderate-to-weak cultivars.

P.6.46

DEVELOPMENT OF FUNCTIONAL DURUM WHEAT PASTA DERIVED BY WASTE MATERIAL FROM THE BREWING PROCESS

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Currently, the re-use of by-products from agro-food processes is one of the main circular economy strategies. Brewer spent grain (BSG), the major by-product of the brewing industry, has desirable nutritional and functional properties and can be an interesting supplement for human consumption to provide health benefits. The incorporation of spent grain as ingredient in the formulation of food products has been limited to a smallscale production of high-fibre bakery stuff. Dry pasta is considered an optimal, economic and easy-to-use vehicle for health promoting phytochemicals since it comes widely and frequently in Western countries' diet. In this work, BSG from barley was used in addition to durum wheat semolina to develop pasta with an increased nutritional value. Three different concentrations of BSG (5, 10, 20%) were added to semolina. Barley spent grain enriched pasta have been compared with traditional durum wheat pasta for ash, proteins, β-glucans, total starch and total dietary fibre content and for total antioxidant capacity (TAC) level. Protein content resulted to be similar in traditional and spent grain enriched pasta whereas the last showed an increase in total starch content up to 4%, in TAC up to 22%, in β -glucans up to 86% and in fibre up to 184%. Results relative to ash content in BSG enriched pasta revealed a gradual increment staying, however, largely within Italian legal limits for whole grain pasta. A rise of bulkiness and stickiness along with a decrease of firmness of cooked spaghetti was observed with the increase in the percentage of BSG added. This study can help to develop new functional and innovative food products that, starting from waste materials, can respond to different needs in terms of quality, sustainable development and efficiency in the use of resources.

P.6.47

DEOXYNIVALENOL CONTENT IN LESS REFINED MILLING FRACTIONS OF DURUM WHEAT EMPLOYING AN INNOVATIVE TECHNOLOGY

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The consumption of fiber-rich foods is currently recommended as an important strategy to adopt an healthy diet. Durum wheat (*Triticum durum* Desf.), such as other cereals, contains many bioactive compounds of great interest with regard to the biological and nutritional aspects and mainly found in the coating structures of the kernel. As a result of the traditional milling process these structures form byproducts fractions (e.g.: bran) which tend to concentrate the organic contaminants such as deoxynivalenol (DON), the most widespread *Fusarium* toxin in wheat within the temperate regions of the world.
The aim of the work was to apply an innovative milling technology by employment of micronization and turbo-separation to obtain less refined milling fractions characterized by a good quality with regard to the technological use and hygienic-sanitary aspects suitable for the production of semi-integral finished products (pasta, bread, etc.). The preliminary results obtained allowed to identify one fraction (F1 250) obtained by the turbo-separation process as the best compromise between a good yield of milling transformation and a marked reduction in the content of deoxynivalenol (16%) in comparison with the whole milled sample. Therefore, the objective was to find out the most suitable process conditions to obtain less refined fractions rich in bran showing both a good reduction of the deoxynivalenol content and useful to manufacture end products enriched by nutritional point of view. Finally, the analysis on durum wheat samples grown in different cultivation areas confirmed the marked influence of the environmental factor on the concentration the same mycotoxin in samples assayed in this work.

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Keywords: deoxynivalenol; micronizator, turbo-separator.

P.6.48

THE EFFECT OF ACORN (*QUERCUS ILEX*) FLOUR ADDITION TO PASTA QUALITY

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The aim of the present study was to evaluate the effect of Tunisian *Quercus ilex* acorn flour incorporation on pasta quality. Durum wheat semolina was substituted with 10, 20 and 30 g/100 g of acorn flour. Cooking quality including optimal cooking time, swelling index and cooking loss of pastas were evaluated. Proximal analysis and sensory evaluations were performed on the produced pastas and acorn flour. In this regard, the obtained results on acorn flour characterization showed that acorn flour was a rich source of carbohydrates (46%), lipids (10 %) and proteins (8 %). Also, acorn flour had high total phenolic and total flavonoid contents (232.56 mg GAE/g DM and 7.08 mg CE/g DM, respectively).Moreover, methanolic extracts of acorn flour exhibited remarkable DPPH radical scavenging activity with IC_{50} values (296 µg/ml). The results demonstrated that pasta with acorn flour had decreased cooking time, increased cooking loss percentage and luminosity value compared with semolina control pasta (0% acorn flour). Pasta with 30% acorn flour demonstrated the lowest gluten content and the highest ash content. In conclusion, the addition of acorn flour has proved to increase the functional benefits of the pasta.

Keywords: Acorn flour, durum wheat semolina, cooking quality, DPPH radical scavenging activity.

P.6.49

THE ORGANIC TREATMENTS ON COMMODITIES AND ENVIRONMENT: THE EFFICACY OF THE NATURAL PYRETHRUM.

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The stored grain quantities worldwide are showing approximately a 10 - 25% annual losses as a consequence of the stored-product insects. It is indeed estimated that, depending on the area considered, the direct and indirect losses of grains and grain-based products fluctuate from about 10% in temperate regions to almost 25% in humid tropical areas.

Residual insecticides are widely used to protect the stored cereal grain against the insect's attack and, in particular, the contact insecticides admixture is the main solution chosen in many major countries.

The necessity of new effective choices compared to the conventional insecticides still in use, arise from the up growing organic productions.

In Italy from 2010 until now, for example, the agricultural land dedicated to the organic production is improving every year up to a 30% total, and it is still increasing.

Given the higher complexity in protecting the organic foodstuff, compared to the conventional treatments on commodities, the stockers are called to achieve an higher hygiene standards in the storage warehouses.

The most part of treatments on grains and on storage environments involve the employ of highly residual insecticides, such as the Organophosphate and Pyrethroids.

Pyrethrum is a natural insecticide derived from the dry flowers of Chrysanthemum cinerariaefolium, which contains 1–2% pyrethrum extract by weigh, with a major production in Kenya, Rwanda and Tanzania, Tasmania, China and Papua New Guinea.

Natural Pyrethrum is a mixture of 6 closely related different components (Pyrethrin I and II, Cinerin I and II, and Jasmolin I and II) called Natural Pyrethrins, with a neurotoxic activity, which affect the sodium channel of the insects.

The six components of pyrethrum show a knockdown and insecticidal action, with pyrethrins showing a more effective activity than Cinerins and Jasmolins. In particular, Pyrethrin I is associated with a greater killing activity and Pyrethrin II with a faster knockdown effect.

Despite the similarity in the structural formula of the components, the effects on the nerve impulses of the insects are different.

We are testing our product on the durum wheat and the response is positive.

P.7.50

CHARACTERIZATION OF THE SEED PROTEOME OF TRITICUM DURUM VARIETIES SELECTED FOR THEIR DIFFERENT IMMUNOGENIC POTENTIAL.

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The wheat gluten proteins are studied, not only for their technological properties for the production of pasta and bread, but also because they are involved in an autoimmune disease, the celiac disease, which affects genetically predisposed individuals. Previous *in vitro* digestion studies showed that different quantities of immunogenic peptides originate from different wheat varieties, and that environmental factors can influence the content of these peptides in the same variety. In this research, two durum wheat cultivars, Saragolla and Cappelli, were studied to compare the reserve proteome, the embryo proteome and the immunogenic peptides amount, with the aim to characterize not only the nutritional and technological characteristics, but also their immunogenic potential. Gliadins were separated by 2D-PAGE and quantified by densitometric analyses, as they contribute to the production of immunogenic peptides. *In vitro* digestion of the gliadin fraction revealed that the two cultivars have different immunogenic potential which can be partially explained with the difference observed in the gliadin composition.

The embryo proteome was also analyzed by 2D-PAGE to identify any differences in the enzyme and metabolic component of the seed proteome, which could eventually influence the quantity of gluten proteins in the endosperm. A higher abundance of antioxidant enzymes and stress response proteins has been observed in Saragolla respect to Cappelli. Furthermore, the total phenolic content, the antioxidant capacity, and the aminoacidic composition of wheat flours were analyzed in both cultivars. The differences observed at proteomic level were confirmed by the antioxidant activity measured in flours.

P.7.51

EFFECTS OF OPUNTIA FICUS-INDICA CLADODES IN FUNCTIONAL BREAD MADE WITH SICILIAN DURUM WHEAT LANDRACES

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In Mediterranean countries, durum wheat is also used for production of handmade traditional breads. Specific interest was aroused by the use of some old durum wheat landraces that represent a valuable source of biodiversity. Some of these genotypes are still used in Sicily for the production of typical breads. Recently, the growing consumer interest in qualitative aspects of food products has driven the market towards healthier and nutrient-rich products. In Sicily, prickly pear (Opuntia ficus-indica (L.) Mill.), a succulent plant belonging to the family Cactaceae, native to Mexico but naturalized throughout the Mediterranean basin, is located. This plant produces cladodes which over the years have been the subject of numerous scientific studies that have contributed to characterize both the bioactive component content and their biological effects, associated with reduced risk of chronic diseases. The aim of this study is to obtain a typical Sicilian bread but enriched with Opuntia ficus-indica cladodes, used as a new functional ingredient for enhancing nutraceutical properties of durum wheat bread. In this work, two durum wheat Sicilian landraces (Timilia e Perciasacchi), compared with one commercial semolina, and Opuntia cladodes harvested in Sicily were investigated. In the caryopsis of durum wheat genotypes, the grain storage proteins were characterized by SDS-PAGE electrophoretic patterns of low molecular weight (LMW) and high molecular weight (HMW) glutenin subunits. In cladodes of Opuntia, total phenolic and DPPH scavenging activity (%) were detected. Each durum wheat genotype and the mixture of each of them with cladodes powder were evaluated for rheological and technological parameters and breadmaking test was performed. The results of the electrophoretic characterization showed variability among studied genotypes. Cladodes of Opuntia showed a good total polyphenol content linked to the DPPH scavenging activity. The experimental breads, obtained with 5% cladodes powder, subjected to sensory analysis, has been pleasant to taste.

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PHENOTYPING OF OLD AND MODERN DURUM WHEAT GENOTYPES FOR GLIADIN COMPOSITION IN RELATION TO HEALTH QUALITY

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The selection of durum wheat genotypes during the last decade led to the release of varieties with higher grain yield and better technological properties. Grain storage proteins account for 60–80% of total grain proteins. Glutenin proteins (HMW-GS, LMW-GS) are mainly responsible for dough strength, while gliadins contribute to the viscous properties. Furthermore in prolamins some epitopes were found to be relevant for gluten related disorders, such as celiac disease and wheat allergy. Gluten improvement for pasta quality was due to both a favourable allelic composition [1] and different sub-fraction expression [2]. The impact of breeding on gliadin composition has been little investigated. Changes in protein composition due to breeding appear in a reduction of the glia/glut ratio and in the proportion of ω-gliadins, both in terms of expression and number of isoforms [2]. In this study some durum wheat genotypes with different release date were investigated for prolamin composition, in particular gliadins, in relation to health aspects. 2DE SDS-PAGE showed differences in gliadin protein spots in either ω- or α-/β and γ-type gliadin gel regions. The characterization of these spots by a dedicated enzymatic digestion, high resolution mass spectrometry analysis and database search using a manually curated database (GluPro V1.0) [3] is in progress. Though preliminary, the first results of the proteomic approach allowed the reliable identification of the ω-gliadins, including isoforms up to date not represented in the databases, responsible for the differences observed in 2D-PAGE profiles. Investigation by enzyme-linked immunosorbent assay (ELISA), by a monoclonal antibody raised against the 33-mer α-gliadin peptide (QPQLPY) was performed (G12 AgraQuant, RomerLabs). Genetic differences were found in gliadin composition, especially in relation to gluten-related disorders. This will led useful information to deep insight into the effect of breeding on gluten composition also in relation to gluten related disorders.

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P.8.53

AE. TAUSCHII INTROGRESSION INTO DURUM WHEAT

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The D-genome represents an important source of genes for disease resistance and quality traits in wheat. *Ae. tauschii*, the D-genome donor of wheat, has frequently been used in bread wheat improvement. However, very little work has focussed on the use of the D-genome in durum wheat improvement. In an attempt to create a panel of different D-genome introgression segments into a durum wheat back-ground, an accession of *Ae. tauschii* was crossed to the Langdon disomic 5D/5B substitution line (which lacks the *Ph1* locus). In the absence of the *Ph1* locus on the long arm of chromosome 5B, homoeologous recombination can occur, potentially leading to the introgression of D-chromosome segments into the A or B-genome chromosomes. Viable F_1 seeds were crossed and back crossed to the durum wheat genotype “Om Rabiaa 5”. Cytogenetic analysis of 80 BC_1F_2 lines via multicolour-genomic *in situ* hybridisation (GISH) allowed the identification of eight lines showing D-genome segments introgressed into the A and B genome chromosomes. Four of these lines are tetraploid (28 chromosomes). The B-D translocations identified are of a Robertsonian type, while the A-D translocations are telomeric. In addition 18 BC_1F_2 lines were found to be monosomic or disomic addition/substitutions for at least one or two D-chromosomes. The introgressions, addition and substitution lines were characterised using a set of 21 D-genome specific SSR markers and multicolour-fluorescent *in situ* hybridisation (mc-FISH). All of the introgressed D genome segments were derived from either 5DL or 5DS with either the A-or the B-genome. The D chromosomes present in the addition and the substitution lines were mainly derived from chromosome 5D. It was also observed that introgression was not restricted to the gametes of the $F_{1,}$ i.e., introgressions were generated in the BC_1F_1 in the presence of a single copy of the *Ph1* locus. This work is one of several strategies that we have used to transfer D genome segments into durum wheat. Once stable homozygous lines have been generated they will be made available, free of IP, for exploitation in breeding programmes and for research.

P.8.54

FROM KAZAKHSTAN BASED ON MICROSATELLITE MARKERS

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Durum wheat (*Triticum durum* Desf.) is an important crop both in the world and in Kazakhstan. Effective breeding strategies require knowledge of the genetic diversity level of local cultivars. Polymorphism of the 92 durum accessions, including 29 local accessions, was analyzed using 10 microsatellite markers. The average polymorphic information content (PIC) values for studied DNA markers was 0.3658 and ranged from 0.1267 in Xgwm219 to 0.5457 in Xgwm247. The average genetic diversity indices of Shannon and Nei were equal to 0.7174, 0.4243, respectively. The level of genetic diversity of local accessions was relatively high in comparison to the rest of the studied samples. The genetic distance between cultivars was calculated. Also, with the help of microsatellite markers, a cluster analysis of the studied cultivars was conducted. Polymorphic markers were selected for future studies on the durum genetic diversity. The obtained information will be used in local breeding programs.

P.8.55

FROM PLANT BREEDING TO INDUSTRIAL PROCESS: INTEGRATED DATA MANAGEMENT BASED ON A RESEARCH RESOURCE PLANNING.

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Modern breeding techniques such as genome-scale marker assisted selection and high throughput phenotyping are huge generators of great potential data along with the now easily accessible sensor and environmental data. Combined with the needs of the market, generated by an integrated chain of return of experience from the food industry and from end-consumers, it makes data management a real challenge to make this information a source of improvement in breeding.

Before using Research Resource Planning[1] (RRP), breeding organizations were lacking tools to analyse and get concrete indicators out of genotypic, phenotypic and processing data altogether, with restricted time and resources. Most of the historical data handling and analysis solutions combined various software or solutions implying complexity and difficulties for global, multidimensional analysis.

In the case of wheat, with its diverse uses, including complex end chain processes for seed transformation, integrated approaches can be particularly beneficial for breeding organizations.

Indeed, possible combination of metadata and data from every step of the breeding process in an integrated data management system for all campaigns would help wheat commercial breeders fit the changing pasta quality standards accentuated by the consumer expectations.

Besides, integrated data management and analysis approaches, based on a RRP, will also support innovative long-term processes such as hybrid wheat breeding, genomic selection, and further pedigree studies implying specific and complex analysis algorithms (e.g. evaluating parents combining ability).

This presentation discusses the possibilities offered by an RRP such as RnDExperience® by Doriane® to integrate data management tool for wheat breeders, and the benefits provided in terms of integrated analysis and decision making focusing on processing information and consumers expectations into breeding strategies.

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[1] A Research Resource Planning is collaborative software based on relational database allowing users to manage multiple research processes of an organization