



2nd International Plant Genetics and Genomics

Symposium - IPGG

October 20 - 22, 2020

Department of Genetics

Faculty of Agriculture, Assiut University

Book of Abstracts

Under Patronage of

Prof .Dr .Tarek Abdalla El-Gammal

President of Assiut University

Prof. Dr. Ahmed El-Minshawy

Vice-President for Graduate Studies and Research

Prof .Dr .Mohamed Hamam Zin Alabdeen

Dean of Faculty of Agriculture

Prof. Dr. Gamal Ibrahim Ahmed

Head of Genetics Department

Organizing committee:

Dr. Ahmed Sallam

Department of Genetics

Associate Professor

amsallam@aun.edu.eg

Mahmoud Sabry Aboud Mohammed

Department of Genetics

Researcher and Teaching Assistant

aboud.s.m@aun.edu.eg

Dr. Elsayed Abdelmonsef Mohamed

Department of Genetics

Associate Professor

eamohamed79@yahoo.com

Abdallah Rafeek

Department of Genetics

Research Assistant

Abdulah011160@agr.au.edu.eg

Dr. Mohamed I. Hassan

Department of Genetics

Associate Professor

m_hassan79@aun.edu.eg

Abdelaal Hamaam Abdelaal Shehata

Department of Plant Pathology

Researcher and Teaching Assistant

abdelaal.hamaam@age.au.edu.eg

Dr. Ameer Efata

Department of Genetics

Associate Professor

aelfarash@aun.edu.eg

Eslam Mohamoud Ahmed Abd-Elhafeez

Department of Food Science and Technology

Researcher and Teaching Assistant

Eslam.mahmoud485@yahoo.com

Citation

2nd International Plant Genetics and Genomics symposium – IPGG, Department of Genetics, Faculty of Agriculture, Assiut University, October 20 - 22, 2020

doi: [10.6084/m9.figshare.13079492](https://doi.org/10.6084/m9.figshare.13079492). <https://pgseminars17.wixsite.com/website>

Table of contents

Content	Page
Introduction	1
Presentation Abstracts	3
1) Germplasm collections – a prerequisite for plant genetics and breeding	4
2) Identification of genes in a collection of historic barley mutants	5
3) Development and application of new genomics platforms for wheat breeding and pre-breeding	6
4) Hybrid Wheat: Looking Ahead	7
5) Prospects of using genomic selection in plant breeding	8
6) Genomic selection and genomics-assisted breeding delivers superior wheat cultivars	9
7) Harnessing genetic diversity in wheat and its wild relatives for disease resistance	10
8) Genomic regions associated with stripe rust resistance against the Egyptian race revealed by genome-wide association study	11
9) CRISPR-Cas toolbox for basic and applied genetics	12
10) Genome editing and metabolic engineering of sugarcane to fuel the emerging bioeconomy	13
11) Expanding plant gene editing scope with highly multiplexable Cas12a systems	14
12) Insight into the genetic contribution of spikelet development in barley under abiotic stress conditions	15
13) Genome-Wide Analysis of mineral concentrations in Wheat Grains	16
14) Isolation and characterization of some new genes in Rye (<i>Secale cereale</i> L.) under Aluminum toxicity conditions	17
15) Harnessing translational research for climate resilience of wheat	18
16) Drought tolerance at the wheat seedling stage: tolerance and survival traits are controlled by two different genetic mechanisms	19
Short Bibliography (keynote speakers)	20

Introduction

- **About the IPGG symposium**

- The symposium is a part of the scientific discussions organized by the Department of Genetics under the title "**Molecular Genetics & Biotechnology Seminars – MGBS**". This symposium focuses on the recent advances in plant genetics and genomics projects. The main objective of the symposium is to exchange ideas and experiences about the new studies published in the field of Plant Genetics and Genomics. Presentations of this symposium are based on research articles that were published in high-profile international journals. The symposium will also include a poster session in which master, Ph.D. students, young researchers, and staff members can present their work in IPGG. The symposium is organized by the Department of Genetics, Faculty of Agriculture, Assiut University, Assiut, Egypt. The expected outcomes of this symposium are:

- 1- Consolidating the scientific cooperation between Assiut University and several universities abroad, as well as among the Egyptian Universities.
- 2- Opening new prospects in the field of Plant Genetics and Genomics especially for young researchers and graduate students.
- 3- To facilitate the process of knowledge transfer among Egyptian Universities and foreign universities in the field of Plant Genetics and Genomics.
- 4- To create a scientific connection among researches in Plant Genetics.

- **About the Faculty of Agriculture, Assiut University**

Vision

Achieving excellence and pioneering in the areas of agricultural education, scientific research, and community services, in compliance with quality and continuous development requirements, within a cultural, research, and ethical environment to achieve sustainable development and meet local and regional job market requirements.

Objectives

- Preparation of qualified individuals in the different disciplines of agricultural activities to meet the needs of society and the job market.
- Provide high-quality education to produce scientists who can assist in the advancement of society.
- Continuous development of the undergraduate and graduate programs to meet scientific advancement.
- Conduct research and applied studies that contribute to solving Upper Egypt's developmental problems.

Organized by Department of Genetics, Faculty of Agriculture, Assiut University, Egypt.

- Enhance the cultural and scientific relations between the faculty and other similar Arab and international faculties through joint mission activities, conferences, joint projects, and exchange of expertise

Mission

To offer high-quality educational programs that prepare qualified graduates capable of working at different fields of agriculture, conducting applied scientific research that can solve the society's problems, and developing natural and human resources within the local environment throughout the adoption of continuous improvement, and developing positive attitudes following Assiut University's mission.

Presentation Abstracts
(Keynote Speakers)

Germplasm collections – a prerequisite for plant genetics and breeding

Börner A.^{*1}, Nagel M.¹, Tarawneh, R.¹, Lohwasser U.¹, Rehman Arif M.A.^{1,2},
Alqudah A.M.¹

¹Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany

²Nuclear Institute of Agriculture and Biology (NIAB), Faisalabad, Pakistan

Email: [*boerner@ipk-gatersleben.de](mailto:boerner@ipk-gatersleben.de)

Abstract

Plant genetic resources for food and agriculture (PGRFA) play a major role in global food security. The most significant and widespread means of conserving PGRFA is *ex situ* conservation. Most conserved accessions are kept in specialized facilities known as genebanks maintained by public or private institutions. World-wide 7.4 million accessions are stored in about 1,750 *ex situ* genebanks.

Plant *ex situ* genebank collections comprise seed genebanks, field genebanks as well as *in vitro* and cryo collections. Species whose seed can be dried, without damage, down to low moisture contents can be conserved in specially designed cold stores. Such “orthodox” seeds can be expected to maintain a high level of vigor and viability for decades. Field genebanks, *in vitro* and cryo storage, are used primarily for species that are either vegetatively propagated or which have non-orthodox seeds that cannot be dried and stored for long periods. Also, perennial species, for example, certain forage species, which produce small quantities of seed, and long-lived plants are maintained this way. It is estimated that worldwide, less than 10% of genebank holdings are stored *in vivo* in the field, and less than 1% are conserved *in vitro*/cryo. Seed storage is the predominant mode of plant genetic resources conservation.

With a total inventory of 150,000 accessions from 3,212 plant species and 776 genera, the ‘Federal *ex situ* Genebank of Germany’ in Gatersleben holds one of the most comprehensive collections worldwide. It comprises wild and primitive forms, landraces as well as old and more recent cultivars of main cereals but also other crops. Starting in the 1920’s material was accumulated systematically. Seed storage is managed in large cold chambers at -18°C. Seeds are kept in glass jars, covered with bags containing silica gel (active collection), and in aluminum bags under vacuum (base collection).

During recent years accessions have been extensively used for genetic studies on various traits, e.g., seed longevity or agronomic and abiotic stress traits mainly in cereals (wheat and barley). Here, we will present several examples of the utilization of germplasm collections for genetic analysis and molecular mapping.

Keywords: plant genetic resources, genetic mapping, seed longevity, abiotic stress

Identification of genes in a collection of historic barley mutants

Mats Hansson

Department of Biology, Lund University, Sölvegatan 35B, 22362 Lund, Sweden.

Email: mats.hansson@biol.lu.se

Abstract

Food production is globally under constant pressure facing an increasing human population under changing climate conditions. At the same time, the agricultural land is desired for energy production and production of biomass. Plant breeding needs to be done to meet the demands. The use of GMO plants could help but regardless they will be legal to use or not, GMO plants will never play an important role as long as they are not accepted by the consumers. In the meantime, traditional mutants induced by eg. X-rays and chemicals have to be explored. The collection of induced barley (*Hordeum vulgare* L.) mutants at NordGen (the Nordic Genetic Resource Center) is one of the largest in the world and a truly unique resource for researchers and breeders who are searching genetic diversity. Several allelic mutants have been kept for each mutant locus, which is important for the identification of the mutated genes as well as for downstream characterization of the gene and its use in plant breeding. Several genes have been identified related to culm length, spike morphology, the timing of flowering, and chlorophyll biosynthesis. A few examples will be given.

Keywords: barley, mutant, gene identification, plant architecture, early flowering, chlorophyll biosynthesis

Development and application of new genomics platforms for wheat breeding and pre-breeding

Awais Rasheed^{1,2}

¹Quaid-i-Azam University, Pakistan

²CIMMYT, China office

Email: arasheed@qau.edu.pk

Abstract

Functional markers (FMs) are the most valuable markers for crop breeding. Low-cost and high-throughput genotyping for FMs could provide an excellent opportunity to effectively practice marker-assisted selection inbreeding. Based on FMs, we developed and validated competitive allele-specific PCR (KASP) assays for genes that underpin economically important traits in bread wheat including adaptability, grain yield, quality, and biotic and abiotic stress resistance. Finally, a KASP platform with a robust marker toolkit for high-throughput and cost-effective screening of 90 functional gene/loci in wheat was developed. It has three advantages: (1) high-throughput, 1536 cultivars can be genotyped with 142 available markers in 2-3 days; (2) low-cost, 9 cents USD per data point including DNA extraction; (3) good quality, highly consistent with normal PCR markers. It has a potential application in wheat breeding to accelerate the characterization of crossing parents and advanced lines for marker-assisted selection of known genes. We also developed new 55K and 15K wheat TraitBreed Affymetrix SNP arrays, and a targeted genotyping-by-sequencing (GBS) platform “*Triticum Geneseizer*”. Such genotyping platforms have significant potential to apply for academic wheat research and applied to breed.

Keywords: Functional markers; Molecular Breeding; KASP markers; SNP chip; NGS

Hybrid Wheat: Looking Ahead

**P. Stephen Baenziger¹, Vikas Belamkar¹, Amanda C. Easterly¹, Nicholas Garst¹,
Hannah Stoll², Amir M.H. Ibrahim³, Bhoja Basnet⁴, Jackie C. Rudd³, and Jean-
Benoit Sarazin⁵**

¹Department of Agronomy and Horticulture, University of Nebraska, USA,

²Department of Agronomy and Plant Genetics, University of Minnesota, USA, ³Texas
AgriLife Institute, Texas A&M University, USA, ⁴CIMMYT, MX, ⁵Asur Plant
Breeding, EstréesSaint-Denis, France

Email: pbaenziger1@unl.edu

Abstract

Wheat (*Triticum* spp.) yields will need to increase by 1.7% per year (from its current increase of 0.9% per year) to feed a larger global population with increasing dietary needs. Hybrid wheat, which is more climate-resilient than pure line wheat, can contribute to achieving this goal. To effectively develop hybrid wheat the following needs to be done: (1) identify heterosis from previously made and predicted wheat hybrids; (2) develop male and female parent lines with the characteristics needed to develop experimental and commercial wheat hybrids in a cost-efficient manner create; (3) Develop heterotic groups or patterns and test multiple mating designs for effectively creating wheat hybrids; and (4) develop cytoplasmic male sterility (CMS) line development and identification and validate restorer genes for wheat hybrids. Recent hybrid wheat research has made great strides in the U.S. and abroad toward developing the tools to foster hybrid wheat development to maximize wheat yield potential. Using an integrated approach involving elite germplasm, chemical hybridizing agents, breeding, phenotyping, genomic selection, and quantitative trait loci mapping it should be possible to help create the scientific and germplasm foundations for successfully launching the hybrid wheat industry in the U.S. and globally. Finally, the research spin-offs from these efforts may have far-reaching improvements in conventional pure line breeding.

Keywords: Heterosis, *Triticum* spp., hybridizing agents, male sterility

Prospects of using genomic selection in plant breeding

Author: Ahmad H. Sallam

Postdoctoral research scientist, University of Minnesota.

495 Borlaug Hall, 1991 Upper Bufford Ave., St. Paul, MN, 55108.

Email: sall0029@umn.edu

Abstract

Fusarium head blight (FHB) is a devastating disease that caused billions of dollars in losses to barley and wheat production in the United States. Deoxynivalenol (DON) is a potent mycotoxin present in fusarium infected grain. Excessive DON levels are a threat to both food safety and end-use quality. Therefore, FHB poses a challenge to barley and wheat breeders. No immunity has been identified in either barley and wheat germplasm, and the resistance is quantitative. Improvement of quantitative traits has relied mainly on a phenotypic selection where the breeding value of each line is estimated from a limited number of phenotypic evaluations. Estimating the breeding value of a line using limited phenotypic evaluations is inaccurate for traits with low heritability. The traditional marker-assisted selection was proposed as an indirect selection method to select individuals based on their marker allele constitution. However, the use of traditional marker-assisted selection has been limited in complex traits because of its low power to detect QTL and bias in the estimated marker effects. Genomic selection can overcome the limitations of traditional marker-assisted selections by using genomewide marker-based predictions to improve and accelerate the breeding process. The genomic selection was found to be an effective breeding approach to reduce FHB severity and DON accumulation for both barley and wheat.

Keywords: marker-assisted selection, genomic selection, disease resistance

Genomic selection and genomics-assisted breeding delivers superior wheat cultivars

Authors: Vikas Belamkar¹, P. Stephen Baenziger¹, Mary Guttieri², Ibrahim El-basyoni^{1,3}, Sarah Blecha^{1,4}, Fang Wang¹, Diego Jarquin¹, and Jesse Poland⁵

¹Department of Agronomy and Horticulture, University of Nebraska-Lincoln, USA,

²USDA, Agricultural Research Service, Center for Grain and Animal Health

Research, Hard Winter Wheat Genetics Research Unit, USA, ³Crop Science

Department, Faculty of Agriculture, Damanhour University, Egypt, ⁴Plant Science

Research Unit, USDA, Agricultural Research Service, USA, ⁵Wheat Genetics

Resource Center, Department of Plant Pathology, Kansas State University, USA

Email: vikas.belamkar@unl.edu

Abstract

The current era is no different from the pre-omics era in terms of the key questions (e.g., increasing yield gain, developing biotic and abiotic resistant cultivars, etc.), but the plant breeding programs now have access to improved and advanced technologies (phenomics, genomics, among others), better experimental designs, and statistical methods that can aid in developing climate-resilient and superior cultivars. The overall goal of this research is to develop novel quantitative genetics methodologies and integrate emerging technologies, such as genomic selection (GS), genomics-assisted breeding, and advanced statistical analyses in the Nebraska wheat breeding program to develop superior cultivars. Cultivar development requires nearly 10 to 12 years and experimental lines are tested in target environments over the years. In the first five to six years of the breeding cycle, the phenotype data are not accurate because lines are evaluated in one location (not representative of all the target environments) with none or minimal replication (due to the limited seed availability), and this also makes them prone to adverse climatic conditions. This main drawback of early generation testing can be overcome by using emerging technologies including GS. This talk will highlight how GS and genomics-assisted breeding using genotyping-by-sequencing derived SNP markers, and advanced phenotypic analyses incorporating spatial variation have substantially increased the selection accuracy in early generation nurseries, observation ($F_{3:5}$), and preliminary ($F_{3:6}$) yield trials, over the last five years. Additionally, practical insights will be presented on lines advanced using these methodologies currently in the final testing nursery as candidates for release as cultivars.

Keywords: Genomic selection, genomics-assisted breeding, *Triticum spp.*, spatial variation.

Harnessing genetic diversity in wheat and its wild relatives for disease resistance

Brande B. H. Wulff

John Innes Centre, Norwich Research Park, Norwich, NR4 7UH, UK

Email: brande.wulff@jic.ac.uk

Abstract

Genetic diversity for disease resistance has been eroded in bread wheat through polyploidization, domestication, and breeding. We have developed sequence-configured panels of wheat and wild progenitors for high-throughput identification of disease resistance genes by association mapping. Cloned resistance genes can speed up resistance breeding through the generation of GM stacks or by conventional marker-assisted selection in combination with speed breeding. We propose an internationally coordinated effort to generate a wheat resistance gene atlas to facilitate more judicious deployment of resistance genes in GM and conventional breeding programs.

Keywords: Wheat, wild wheat, disease resistance, GWAS, GM, speed breeding

Genomic regions associated with stripe rust resistance against the Egyptian race revealed by genome-wide association study

Abou-Zeid A. Mohamed ⁽¹⁾ and Amira M.I. Mourad ^{(2),*}

- ⁽¹⁾ Wheat Disease Research Department, Plant Pathology Research Institute, ARC, Giza, Egypt.
- ⁽²⁾ Department of Agronomy, Faculty of Agriculture, Assiut University, Assiut, Egypt. Email: amira_mourad@aun.edu.eg

Abstract

Wheat stripe rust (caused by *Puccinia striiformis* f. sp. *Tritici*), is a major disease that causes huge yield damage. New pathogen races appeared in the last few years and caused a broke down in the resistant genotypes. In Egypt, some of the resistant genotypes began to be susceptible to stripe rust in recent years. This situation increases the need to produce new genotypes with durable resistance. Besides, looking for a new resistant source from the available wheat genotypes all over the world help in enhancing the breeding programs. In the recent study, a set of 103-spring wheat genotypes from different fourteen countries were evaluated to their field resistant to stripe rust for two years. These genotypes included 17 Egyptian genotypes from the old and new cultivars. The 103-spring wheat genotypes were reported to be well adapted to the Egyptian environmental conditions. Out of the tested genotypes, eight genotypes from four different countries were found to be resistant in both years. Genotyping was carried out using genotyping-by-sequencing and a set of 26,703 SNPs were used in the genome-wide association study. Five SNP markers, located on chromosomes 2A and 4A, were found to be significantly associated with the resistance in both years. Three gene models associated with disease resistance and underlying these significant SNPs were identified. One immune Iranian genotype, with the highest number of different alleles from the most resistant Egyptian genotypes, was detected. The high variation among the tested genotypes in their resistance to the Egyptian stripe rust race confirming the possible improvement of stripe rust resistance in the Egyptian wheat genotypes. The identified five SNPs markers are stable and could be used in marker-assisted selection after validation in different genetic backgrounds. Crossing between the immune Iranian genotype and the Egyptian genotypes will improve stripe rust resistance in Egypt.

Keywords: Genome-wide association study, Single marker analysis, Linkage disequilibrium, gene expression, Coefficient of Infection, Disease severity.

CRISPR-Cas toolbox for basic and applied genetics

Kutubuddin Molla

ICAR-National Rice Research Institute, Cuttack-753006, India, Email:

kutubuddin.molla@icar.gov.in

Abstract

The development of the CRISPR/Cas genome editing system provided us unprecedented ability to manipulate a target genome. Day by day, we are witnessing an explosion of CRISPR/Cas-derived tools for basic and applied research. This rapid advancement has been possible by exploiting the natural diversity of the CRISPR system coupled with protein engineering. The CRISPR-Cas toolbox has too many to offer, including but not limited to conventional targeted gene knockout, gene activation and repression, epigenome editing, single-base alteration, and precise insertion/deletion/replacement with either HDR or prime editing. My talk is intended to present an overview of the spectrum of CRISPR-Cas-derived tools and their mode of action and potential application.

Keywords: CRISPR/Cas9, Orthologous Cas proteins, Base editing, Prime editing, genetic manipulation

Genome editing and metabolic engineering of sugarcane to fuel the emerging bioeconomy

Saroj Parajuli¹, Tufan Mehmet Oz^{1,6}, Ayman Eid^{1,6}, Chakravarthi Mohan¹, Baskaran Kannan^{1,6}, Duoduo Wang^{1,6}, Sara Sanchez^{1,6}, Ratna Karan¹, Aldo Merotto¹, Hui Liu^{2,6}, Eva Garcia-Ruiz³, Deepak Kumar⁴, Vijay Singh^{4,6}, Huimin Zhao^{3,6}, Steve Long^{5,6}, John Shanklin^{2,6}, and Fredy Altpeter^{1,6}

¹Agronomy Department, Plant Molecular and Cellular Biology Program, Genetics Institute, University of Florida, IFAS, Gainesville, FL, USA

²Biosciences Dept., Brookhaven National Lab, Upton, NY, USA

³Department of Chemical and Biomolecular Engineering, the University of Illinois at Urbana-Champaign, Urbana, IL, USA

⁴Department of Agricultural and Biological Engineering, the University of Illinois at Urbana-Champaign, Urbana, IL, USA

⁵Departments of Plant Biology and Crop Sciences, Institute for Genomic Biology, the University of Illinois at Urbana-Champaign, Urbana, IL, USA

⁶DOE Center for Advanced Bioenergy and Bioproducts Innovation, USA

Email: altmeter@ufl.edu

Abstract

Sugarcane is a prime feedstock for commercial production of biofuel and table sugar. We recently demonstrated that metabolic engineering successfully resulted in the accumulation of oil in vegetative sugarcane biomass for increased energy density and the development of advanced biofuel. We are exploring strategies to divert more of the carbon flux from sucrose to triacylglycerol (TAG). This strategy involves the analysis of combinations of gene expression cassettes for metabolic engineering, supporting biosynthesis, and the storage of TAG. Correlations between TAG accumulation and gene combinations and their expression levels will be presented. These data indicate the feasibility of genetically engineering the high biomass crop sugarcane to produce TAG, which can be readily converted to biodiesel transportation fuel. Genome editing tools such as CRISPR/Cas9 have been employed in several crop genomes. They enable precise targeting and introduction of double-stranded DNA breaks in vivo. Subsequent cellular repair mechanisms, predominantly non-homologous end joining (NHEJ), act as critical steps to endogenous gene editing or correction. However, there is very limited control over these mechanisms, which generate an abundance of random insertions and deletions (indels). Frameshift mutations associated with these indels of unspecified size and sequence might result in loss of function phenotypes of agronomic importance. The gain of function mutations, on the other hand, generally require precise nucleotide substitutions in the target locus. This can be accomplished with the aid of a homologous repair template and involves the cellular homology-directed repair (HDR) mechanism. We will present two rapid readout platforms that support the development of efficient multi-allelic NHEJ and HDR mediated precision editing in the highly polyploid sugarcane.

Keywords: Genome editing, metabolic engineering, sugarcane, biofuel

Funding statement:

This material is based upon work supported by the U.S. Department of Energy, Office of Science, Office of Biological and Environmental Research under Pending Award for CABBI (Center for Advanced Bioenergy and Bioproduct Innovation) Proposal Number 0000227119.

Expanding plant gene editing scope with highly multiplexable Cas12a systems

Yiping Qi

Department of Plant Science and Landscape Architecture, University of Maryland,
College Park, MD 20742, USA;

Email: yiping@umd.edu

Abstract

CRISPR-Cas12a is a promising genome editing system for targeting AT-rich genomic regions. Compared to Cas9, Cas12a has shown higher targeting specificity in plants. Unlike Cas9 that usually generates small deletions, Cas12a cleavage generates staggered ends resulting in larger deletions, making it a suitable nuclease for gene knockout. Moreover, Cas12a only requires a short CRISPR RNA (crRNA) for each target and possesses RNase activity for crRNA array processing, making it an ideal platform for multiplexed editing. Cas12a has been widely applied in plants and achieved high editing efficiencies for single-gene targets. However, comprehensive genome engineering using CRISPR usually requires simultaneous targeting of multiple genes at defined locations, which cannot be achieved easily and efficiently with current Cas12a systems, due to their strict PAM (protospacer adjacent motif) requirements and limited multiplex capacity. To expand the targeting scope of Cas12a, we screened nine new Cas12a orthologs and identified six that possess high editing activity and specificity in rice. Among them, Mb2Cas12a stands out with high editing efficiency, relaxed PAM requirements, and tolerance to low temperatures. Engineered Mb2Cas12a can also target altered PAMs. These new Cas12a systems have greatly expanded the targeting scope of Cas12a in major crops (rice, maize, and wheat). To further enable large-scale genome engineering, we compared 12 multiplexed Cas12a systems and identified a potent system that exhibited nearly 100% biallelic editing efficiency with the ability to target as many as 14 sites in rice. This is the highest level of multiplex edits in plants to date using Cas12a. Two compact single transcript unit CRISPR-Cas12a interference systems were also developed for multi-gene repression in plants. This study has greatly expanded the targeting scope of Cas12a for crop genome engineering.

Keywords: CRISPR-Cas12a, PAM, multiplexed editing, plant gene editing

Insight into the genetic contribution of spikelet development in barley under abiotic stress conditions

Alqudah A. M. and Börner A.

Resources Genetics and Reproduction, Department Genebank, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Corrensstr. 3, OT Gatersleben D-06466 Stadt Seeland, Germany, Email: alqudah@ipk-gatersleben.de

Abstract

Spikelet numbers per spike dramatically reduce during the late reproductive phase that represents half of the maximum yield potential. The molecular genetics of spikelet development and how to keep them alive are not yet studied in barley. Therefore, we studied the developmental process of spikelets and genetic contribution controlling alive spikelet related traits. We characterized 184 diverse barley accessions under field conditions through the developmental process and performed genetic analysis. We developed a phenotyping approach to better understand such traits by separating developed and undeveloped spikelets at different developmental stages using a portable USB Digital Microscope. We used state-of-the-art technologies such as Genotyping-By-Sequencing (GBS) for mapping the novel loci underlying the studied traits. We could use more than 125K SNPs in barley for genome-wide association study and such a high dense map had never been used in barley. We also applied the latest bioinformatics approaches e.g. SNP-phenotype network (for the first time in barley), and RNA-Seq expression analysis to detect the most important SNPs and putative candidate genes.

Here, we provided the first report about genetic factors controlling spikelet development and its abortion, i.e., novel genomic regions, e.g., on chromosome 7HS. Current work demonstrated the pivotal role of sucrose and phytohormones in spikelet development and keeping them alive. Our findings shed light on the genetic control of alive spikelets that serve as a source of marker-assisted breeding, and a resource for future molecular and genetic validation. We proposed a novel genetic network between spikelet development-related traits and the determinants of boosting grain yield.

Keywords: alive spikelet; spikelet development; maximum yield potential; GWAS; barley; candidate genes; sugar-related genes; phytohormones

Genome-Wide Analysis of mineral concentrations in Wheat Grains

Dalia Z. Alomari; Marion S. Röder

Plant breeding department /Gene and genome mapping, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany, Email:
alomari@ipk-gatersleben.de

Abstract

After the green revolution and improving crop yield production, the nutritional qualities were dropped down. Therefore, improving the nutritional quality became an imperative need particularly in the developing countries where malnutrition is spreading and one of the important crops in the world is wheat. Discovering the genetic factors underlying the natural variation of minerals in wheat (*Triticum aestivum* L.) is the main goal of the project. A genome-wide association study (GWAS) of calcium (Ca) iron (Fe) and zinc (Zn) concentrations in wheat grains using a European wheat diversity panel of 369 varieties and phenotypic data based on three years of field experiments has been used. Inductively coupled plasma optical emission spectrometry (ICP-OES) was used to measure the mineral concentrations in wheat grains. High genotyping densities of single-nucleotide polymorphism (SNP) markers were obtained from the application of the 90k select ILLUMINA array and 35k Affymetrix array resulting in 15,523 polymorphic markers and additionally, a subpanel of 183 genotypes was analyzed with a novel 135k Affymetrix marker array including 28,710 polymorphic SNPs. Best linear unbiased estimates (BLUEs) for Ca, Fe, and Zn were calculated across the years and ranged from 288.20 to 647.50 $\mu\text{g}\cdot\text{g}^{-1}$, 24.42 to 52.42 $\mu\text{g}\cdot\text{g}^{-1}$, and 25.05 to 52.67 $\mu\text{g}\cdot\text{g}^{-1}$ respectively with a high heritability value for Ca and moderate value for both of Fe and Zn.

A total of 485 SNP marker-trait associations (MTAs) were detected incomplete panel data obtained from grains cultivated in both of the two years and BLUE values by considering associations with a $-\log_{10}(P\text{-value}) \geq 3.0$. The most significant association was located on chromosome 5A (114.5 cM) and was linked to a gene encoding cation/sugar symporter activity as a potential candidate gene.

GWAS revealed 41 and 40 significant SNPs for Fe and Zn respectively in the complete panel whereas the number of significant SNPs was increased to 137 and 161 in the subpanel. The most significant association was located on chromosome 2A (763,689,738-765,710,113 bp) and within this region, we detected candidate genes that were associated with Fe uptake or transportation such as NAC transcription factors and transmembrane proteins. The most significant and consistent associations for Zn were located on chromosomes 3B (723,504,241-723,611,488 bp) and 5A (462,763,758-466,582,184 bp) and within this genomic region we found candidate genes involved in Zn uptake and transport or represent bZIP and mitogen-activated protein kinase genes.

These findings provide insight into the genetic basis for understanding the background of mineral accumulations in wheat grains by highlighting potential candidate genes that in turn may help breeders to select high Ca, Fe, and Zn-containing genotypes to improve human health and grain quality.

Keywords: wheat, calcium, iron, zinc, GWAS, SNP, MTAs, candidate genes.

Organized by Department of Genetics, Faculty of Agriculture, Assuit University, Egypt.

Isolation and characterization of some new genes in Rye (*Secale cereale* L.) under Aluminum toxicity conditions

Diaa Abd El Moneim

Department of Plant Production, (Genetic Branch), Faculty of Agricultural and Environmental Sciences, Arish University, El- Arish, 45511 Egypt

Email: dabdelmoniem@Aru.edu.eg. ORCID identifier: - 0000-0003-3285-0563

Abstract

Aluminum is the most abundant metal and the third most common element in the earth's crust. Many of the soils used for agriculture, particularly those in developing countries where forests have been cleared, are considered sufficiently acidic that they restrict the growth of many susceptible plant species. Al tolerance is an important component of an overall acid soil management strategy that will increase crop productivity on acid soils and also minimize further soil acidification. With the advent of molecular techniques, it is now possible to identify the genotypes having a high level of Al tolerance at the early stage of growth, without the masking effect of the environment. Rye (*Secale cereale* L.) has great importance due to its broad tolerance to biotic and abiotic stress, a feature generally lacking in other temperate cereals. Compared to other cereals, rye has the best overwintering ability and the highest tolerance to drought, salt, or aluminum stress among all small-grain cereals. Several potential genes could be involved in the processes of plant defense against aluminum stress. In this study, five different novel genes (MDH1, MDH2, CS, FUM, and PME) were isolated and characterized. Moreover, the chromosomal location has been determined. The full cDNA and genomic DNA in four different Rye cultivars (three cultivars tolerant and sensitive inbred line) were isolated. Also, genes variability within *Secale cereale*, by comparing the cDNA sequences of the three cultivars tolerant and sensitive, and the variability between different species of Poaceae was investigated. To confirm the role of the studied genes in aluminum tolerance, the expression of messenger RNAs encoded by studied genes in roots and leaves for tolerant cultivar and sensitive line, produced by treatment with Al at different exposure times and different concentrations were studied. Gene expression analysis for *ScMDH1*, *ScMDH2*, *ScCS*, and *ScFUM* indicates that these genes are expressed more intensely in the roots than in leaves. While in all cases, the amount of messenger RNAs is greater intolerant cultivar than sensitive.

Keywords: Rye (*Secale cereale* L.). Aluminum tolerance, Gene expression

Harnessing translational research for climate resilience of wheat

Matthew Reynolds

CIMMYT, Km 45, Carretera Mexico-Veracruz, El Batan, Texcoco 56237, EdoMex, Mexico. Email: m.reynolds@cgiar.org

Abstract

Despite being the world's most widely grown crop, investments in wheat research fall behind those in other staple crops. The current annual rate of yield gains for wheat is only about 40% of that needed to meet 2050 consumer demand, and climate stresses will increasingly challenge future yield gains. However, there is promising evidence that the research gaps needed to boost heat and drought tolerance of wheat can be filled through the translation of new ideas into novel breeding technologies using powerful new tools in genetics, and remote sensing for example. Such technologies can also be applied to identify new climate resilience traits from among the vast and largely untapped reserve of wheat genetic resources available in collections around the world. Several research opportunities exist which together are expected to boost genetic gains in wheat under drought and heat stress. Specifically, improving crop design targets using big data approaches, development of phenomics tools for field-based screening and research, application of genomic technologies to elucidate genetic bases of climate resilience traits, and the application of these outputs in developing next-generation breeding methods. The global impact of these outputs will be scaled out through the International Wheat Improvement Network (IWIN), a global germplasm development and testing system that contributes key productivity traits as well as new cultivars to well over half of the global wheat growing area.

Keywords: pre-breeding, physiology, genetic resources, big data, gene discovery

Drought tolerance at the wheat seedling stage: tolerance and survival traits are controlled by two different genetic mechanisms

Ahmed Sallan^{1*}, Shams Eltaher², Vikas Belamkar³, Waseem Hussain⁴, Ahamed. M. Alqudah⁵ and P. Stephen Baenziger³

¹Department of Genetics, Faculty of Agriculture, Assiut University, Egypt

²Genetic Engineering and Biotechnology Research Institute, University of Sadat City, Egypt

³Department of Agronomy & Horticulture, University of Nebraska-Lincoln, USA

⁴ International Rice Research Institute, Los Baños, Laguna 403, Philippines

⁵ Resources Genetics and Reproduction, Department Genebank, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany

Email: *amsallam@aun.edu.eg

Abstract

Drought stress is one of the most severe abiotic stresses that limit wheat growth and its development. Breeding for drought tolerance at the seedling stage is very important for the wheat plant to continue its growth cycle especially if the drought occurs at this stage. To improve drought tolerance and select the most promising drought-tolerant genotypes, we developed a new protocol for breeding drought tolerance in seedling winter wheat. Two different genetic backgrounds were used in this study; biparental population (BPP, N=147) and diverse population (DP = 160). The genotypes in both populations were evaluated in a greenhouse under controlled conditions. Each population was evaluated in three replications with a randomized complete block design. Two types of traits were scored namely (1) tolerance traits include days to wilting, leaf wilting, and stay green and (2) recovery traits which included days to regrowth, shoot regrowth, drought survival rate, and leaf recovery. Three selection indices were calculated; (1) tolerance index (TI), recovery index (RI), and drought tolerance index (DTI) including TI and RI. A high genetic variation was found among genotypes in both populations for all traits. The heritability estimates were higher in GP (0.77 – 0.95) than in BPP (0.53 – 0.90). In both populations, no or very weak correlation was found between tolerance and recovery traits. The TI and RI had the same trend of correlation in BPP ($r = 0.03$) and GP ($r = 0.04$). The drought tolerance index had high significant phenotypic and genotypic correlations with all traits in both populations. Both populations were genotyped using genotyping-by-sequencing. Linkage mapping was performed on BPP, while GWAS was performed on GP to detect genomic regions and alleles associated with tolerance and recovery traits. In both populations, no common QTL were shared in both types of traits. In conclusion, recovery and tolerance traits are controlled by different genetic mechanisms. Drought selection index (including RI and TI) facilitated selecting the most promising genotypes in both populations. One genomic region on chromosome 2B was found to control survival traits in both populations. The results of this study helped in understanding some complexity of drought tolerance in wheat

Keywords: GWAS, QTL mapping, Drought, Heritability, Recovery index, Tolerance index

IPGG 2020
Speakers Bibliography



Priv.-Doz. Dr. Dr. h.c. Andreas Börner, Leibniz Institute for Plant Genetics and Crop Plant Research, Gatersleben, Germany, boerner@ipk-gatersleben.de

Andreas Börner received his Ph.D. in Plant Breeding and Plant Genetics from the Martin-Luther-University, Halle-Wittenberg in 1988. Between 1990 and 1996 he was head of the research group Wheat Genetics of the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK). He joined the Genebank of the IPK as the head of research group Resources Genetics and Reproduction in 1997. Since 2005 he has served as the head of program Management and Evaluation, which is responsible for the long-term maintenance of the IPK Genebank collection of cultivated plants and their wild relatives. The Genebank is a major player in the global ex-situ plant conservation effort, housing a wide spectrum of accessions representing most of the temperate crop species. In addition to his responsibility for the optimization of the management of the collection, he runs an active research program focused on the investigation of seed longevity, the study of the genetic integrity and genetic diversity as well as a comprehensive phenotypic (phenomic) and genetic description of materials related to the major temperate cereal crops. In close co-operation with many external partners, segregation and association mapping populations are exploited to detect genes (QTLs) responsible for agronomic characters of interest.

For research topics and publications see:

<http://www.ipk-gatersleben.de/en/genebank/resources-genetics-and-reproduction/>



Mats Hansson, Department of Biology, Natural Science Faculty, Lund University, Sweden, mats.hansson@biol.lu.se

Ph.D., Department of Microbiology, Lund University
Postdoc, Carlsberg Laboratory, Copenhagen, Denmark
Professor, Department of Biology, Lund University
Interested in barley genetics



Awais Rasheed, Quaid-i-Azam University, Pakistan, CIMMYT, China office, arasheed@qau.edu.pk

MS and Ph.D. (Quaid-i-Azam University, Islamabad, Pakistan). Currently, I am working as Assistant Professor at Quaid-i-Azam University (Pakistan) and Adjunct Associate Scientist in International Maize and Wheat Improvement Center (CIMMYT) based in Beijing. My expertise is wheat genomics and my main responsibilities are developing a new genotyping platform for wheat breeding and allele discovery.



P. Stephen Baenziger, Department of Agronomy, University of Nebraska, Lincoln, Nebraska 68583-0915, Email: pbaenziger1@unl.edu

PRESENT ACADEMIC RANK: Nebraska Wheat Growers Presidential Chair and Professor

Education

B.A. *magna cum laude*, 1972, Harvard University (Biochemical Sciences)

M.S. 1975, Purdue University (Plant Breeding and Genetics)

Ph.D. 1975, Purdue University (Plant Breeding and Genetics)

Teaching Interests

Is the primary instructor for Agronomy 815A, and B, two of three modules that comprise Introduction to Plant Breeding. These modules are the first graduate-level courses that many plant breeding students will take and maybe the only course that students in collateral fields will take. The instructor is keenly interested in using web-based technology to teach his course in traditional and nontraditional ways.

Research Interests

Is the primary small grains breeder (winter wheat, triticale, and barley) for Nebraska. Cultivar and germplasm development are the main goals of the program. Developing improved breeding methodology, emphasizing biotic and abiotic stress tolerance, hybrid wheat, and the use of biotechnology are three of his basic research goals.



Ahmad H. Sallam, Ph.D. Department of Plant Pathology / Department of Agronomy and Plant Genetics, University of Minnesota-Twin Cities, USA: sall0029@umn.edu

Position: Postdoctoral research scientist

Education: P h.D. in Plant breeding and quantitative genetics, University of Minnesota, USA.

M.S. in Plant breeding and quantitative genetics, University of Minnesota. The USA.

Research interests:

- Breeding wheat and barley to improve tolerance to biotic and abiotic stresses
- Exploiting genetic diversity in germplasm collections to identify novel genetic variants



Vikas Belamkar, Research Assistant Professor, Department of Agronomy and Horticulture, University of Nebraska – Lincoln, Lincoln, Nebraska, USA, vikas.belamkar@unl.edu

B.E., Biotechnology, Sir M. Visvesvaraya Institute of Technology, Bangalore, India, 2007. M.S., Biotechnology, Texas Tech University, Lubbock, Texas, USA, 2010. PH.D., Genetics, Iowa State University, Ames, Iowa, USA, 2015. Postdoctoral research associate., Genomics and Bioinformatics, University of Nebraska-Lincoln, Lincoln, Nebraska, USA, 2015-2016

Summary:

My current interests are in the areas of exploring innovative ways of connecting genome to phenome at different biological levels, understanding genetic mechanisms and architecture of traits important for pure line and hybrid cultivars, abiotic stress tolerance, predictive analytics, and data-driven research for building healthy agricultural systems.

Major Project Activities:

- Conduct research in the areas of quantitative genetics, bioinformatics, and plant breeding.
- Lead the efforts on optimization and deployment of genomic selection, marker-assisted selection, and other uses of molecular marker information for improving winter wheat.
- Design and analyses of field trials (single and multi-environment) using mixed linear models incorporating spatial adjustments to generate best estimates of the phenotypic data.
- Coordinate genotyping-by-sequencing (GBS) efforts, perform single-nucleotide-polymorphism (SNP) calls, and work in collaboration with the small grains breeder, and national and international collaborators on genomic selection and predictions for the hybrid wheat.
- Work closely with the small grains breeder to translate the information generated into timely decision making for advancements in the breeding program.
- Assist with the small grains breeding program management and graduate student mentoring in the area of bioinformatics, statistics, and quantitative genetics.



Brande Wulff – Crop Genetics, John Innes Centre, Norwich Research Park, Norwich, UK, brande.wulff@jic.ac.uk

Molecular cloning of genes underpinning genetic variation opens up novel precision-deployment possibilities via marker-assisted selection, gene editing, and transgenesis. However, large genomes, extensive regions of suppressed recombination, and long generation times, often impose significant barriers to gene cloning in crops and

their wild relatives. Faced with these challenges, we have developed fast, new and efficient methods for gene discovery and cloning which use mutant and natural populations followed by sequence alignment to locate genes [1-5]. We also developed a method for halving the generation time of wheat and other crops, in a controlled environment, dramatically speeding up capabilities for research and breeding purposes [6-7]. Our focus is on wheat and major diseases of wheat, including the rusts, blast, and Septoria. Our long-term aim is to use conventional genetics or transgenesis to engineer pyramids of resistance genes for more durable resistance against major diseases of wheat [8-9].

1. Steuernagel et al (2016). NLR-parser: a tool to rapidly annotate the NLR complement from sequenced plant genomes. *Bioinformatics* 15;31(10):1665-7.
2. Steuernagel et al (2016). Rapid cloning of disease-resistance genes in plants using mutagenesis and sequence capture. *Nature Biotechnology* 34:652-5.
3. Sánchez-Martín et al (2016). Rapid gene isolation in barley and wheat by mutant chromosome sequencing. *Genome Biology* 17(1):221.
4. Arora et al (2019) Resistance gene cloning from a wild crop relative by sequence capture and association genetics. *Nature Biotechnology* 37:139-143.
5. Steuernagel et al (2020) NLR-Annotator enables annotation of the intracellular immune receptor repertoire. *Plant Physiology*, DOI: <https://doi.org/10.1104/pp.19.01273>
6. Watson et al (2018). Speed breeding is a powerful tool to accelerate crop research and breeding. *Nature Plants* 4:23-29.
7. Ghosh et al (2018). Speed breeding in growth chambers and glasshouses for crop breeding and model plant research. *Nature Protocols* 13:2944-2963.
8. Dhugga and Wulff (2018) Wheat, the cereal abandoned by GM. *Science* 361:451-452.
9. Wulff and Jones (2020). Breeding a fungal gene into wheat. *Science* 368:822-823.



Dr. Amira Mourad, Department of Agronomy, Faculty of Agriculture, Assiut University, Assiut, amira_mourad@aun.edu.eg

Dr. Amira is an Assistant Professor at the Department of Agronomy, Assiut University. She got her BSc and MSc from the Department of Agronomy. Then, she awarded a joint supervision fellowship to complete her Ph.D. at the University of Nebraska-Lincoln, the USA under the supervision of Prof. Dr. Peter Stephen Baenziger. She has been nominated to be a member of the Honor Society of Agriculture, USA from 2017 to now. Dr. Amira published in international journals such as BMC Plant Biology, Frontiers in Plant Sciences, BMC genomics, and Nature Scientific Reports. Amira's research aims to genetically improve cereals to diseases resistance such as common bunt, rust diseases, blight diseases, etc. and to identify new genes associated with disease resistance using genome-association mapping and QTL mapping.



Kutubuddin Molla, Crop Improvement Division, ICAR-National Rice Research Institute, Cuttack, India,
kutubuddin.molla@icar.gov.in

Kutubuddin A. Molla is a faculty scientist at the ICAR-National Rice Research Institute, Cuttack, India. He obtained his MSc and Ph.D. degrees from the University of Calcutta, Kolkata, India. He is a recipient of the prestigious Fulbright fellowship. Dr. Molla has done his post-doctoral research at the Pennsylvania State University, USA, from 2017 to 2019. Dr. Molla is an expert in plant genetic engineering and genome editing. Dr. Molla is interested in precise genome editing in crop plants and uses CRISPR/Cas and other advanced editing techniques for crop improvement. Besides the Fulbright fellowship, Dr. Molla bagged many prestigious awards, including

- The Young Scientist Award by Indian Science Congress Association,
- Jawaharlal Nehru best Ph.D. thesis award by Indian Council of Agricultural Research,
- Early Career Research Award by Department of Science and Technology, Govt. of India.
- He is also the recipient of the AAAS/Science Program for Excellence in Science from the American Association for the Advancement of Science (AAAS), Washington D.C.
- He won two outreach lecture funds from the Institute of International Education (IIE), Washington D.C, USA.
- Won 11th Post Doc Research Exhibition Award from Pennsylvania State University, USA

Dr. Molla is currently serving as the editorial board member of Frontiers in Genome Editing and PlosOne Journal. He has recently edited a Springer book on ‘CRISPR-Cas Methods’.

Besides his research activities, Dr. Molla is passionate about science communication.



Fredy Altpeter, Agronomy Department, Plant Molecular and Cellular Biology Program, Genetics Institute, University of Florida, IFAS, Gainesville, FL, USA, altpeter@ufl.edu

Fredy Altpeter is a faculty member of the Agronomy Department at the Institute for Food and Agricultural Sciences of the University of Florida in Gainesville, FL, USA since 2001 and was promoted to Professor in 2012. In 2013 and again in 2018 he was awarded the University of Florida Research Foundation Professorship in recognition of his distinguished research program in biotechnology and the breeding of grasses. He received a vocational degree in farm management from the chamber of agriculture in Saarbrücken, Germany, a Dipl. Ing. Agr. degree (MS equivalent) in Crop Science and a Dr. sc. Agr. degree (PhD. equivalent) in Plant Breeding and Biotechnology from the University of Hohenheim in Germany. He did a postdoc with Indra Vasil at the University of Florida on the genetic transformation of wheat from 1994 to 1997 and was a group leader at the Plant Genome Resource Center at the IPK Gatersleben, Germany from 1997 to 2001. His

Organized by Department of Genetics, Faculty of Agriculture, Assuit University, Egypt.

research program integrates traditional plant breeding, translational genomics, biotechnology, and genome editing to identify critical heredity units and develop genetically improved cereals, turf, and biomass/bioenergy grasses. Fredy's teaching activities include graduate courses in Molecular Genetics, Plant Molecular and Cellular Biology, and Plant Breeding. He is very active in mentoring undergraduate and graduate students and visiting scientists. Fredy serves/served as associate editor of Scientific Research; The Plant Genome; Plant Cell Tissue and Organ Culture; Plant Breeding; Crop Science. He is currently the chair of the C7 division of the Crop Science Society of America and served on the board of directors for the Society for In Vitro Biology from 2011 to 2019, received the SIVB Distinguished Service award in 2012, the SIVB Distinguished Scientist award in 2020 and was elected Fellow in 2018. He can be reached by email at altpeter@ufl.edu.



Yiping Qi, Department of Plant Science and Landscape Architecture, University of Maryland, College Park, MD 20742, USA, yiping@umd.edu

Dr. Yiping Qi received a Ph.D. degree from the University of Minnesota, Twin Cities. He is currently an Associate Professor at the Department of Plant Science and Landscape Architecture at the University of Maryland, College Park. He is interested in developing genome engineering and synthetic biology tools to boost plant fundamental and translational research. Since 2009, he has made contributions to the development of plant genome editing systems based on Zinc Finger Nucleases (ZFNs) and Transcription activator-like effector nucleases (TALENs). In recent years, his lab has developed CRISPR-Cas9, Cas12a, and Cas12b systems for plant genome editing and transcriptional regulation. Dr. Qi has over 40 publications on plant genome engineering and he is a recipient of the SIVB 2020 Young Scientist Award.



Ahmad M. Alqudah, Resources Genetics and Reproduction Department Genebank, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Corrensstr. 3, OT Gatersleben D-06466 Stadt Seeland, Germany, alqudah@ipk-gatersleben.de

Ahmad Alqudah is a young scientist with extensive expertise in agronomy, plant breeding, genetics, and bioinformatics. He received BSc in 2005 and then MSc in Field Crops Production focused on abiotic stress physiology from Jordan University of Science and Technology(Jordan) in 2007. In 2015, he completed his Ph.D. in Plant Breeding and Genetics at the Martin-Luther-University Halle-Wittenberg (Germany). Since then, he is a postdoctoral research scientist at IPK Gatersleben(Germany) as a Cereal Geneticist aims to understand the underlying molecular genetic factors of agronomic, developmental, adaptive, and grain yield-related traits in wheat and barley. He is using a recently developed next-Generation Sequencing (NGS) technologies such as Genotyping-by-Sequencing and RNA-Seq with his outstanding bioinformatics skills to discover QTL or genes throughout QTL mapping, GWAS in addition to genomic prediction.

Organized by Department of Genetics, Faculty of Agriculture, Assuit University, Egypt.



Dalia Z. Alomari, Plant breeding department /Gene and genome mapping, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany, alomari@ipk-gatersleben.de

Dalia Alomari is a Postdoctoral research scientist (2019-present) at IPK Gatersleben (Germany). She earned her Ph.D. in 2019 in Plant Breeding and Genetics at the Martin-Luther-University Halle-Wittenberg (Germany). She did her Bachelor's and master studies in the field of Nutrition and Food Technology Science at Jordan University of Science and Technology (JUST), Jordan. Her research interest is improving the grain nutritional quality to improve human health based on genetic analysis.



Diaa Abd El Moneim, Associate Professor of genetics, Faculty of Environmental Agricultural Sciences, Arish University, dabdelmoniem@aru.edu.eg

Diaa Abd El Moneim received his Ph.D. in plant molecular genetics from Complutense University of Madrid- Spain in 2012. Between 2012 till 2014 he worked as a postdoctoral researcher in the national center of biotechnology – Madrid –Spain. He joined Deanship of preparatory year –Jouf University – K.S.A. as Assistant professor of Biology. Since 2020 he has served as Associate professor of genetics at Arish University, which is responsible for Lecturing about advanced applications for plant molecular genetic; Organizing meetings and building relationships with national and international institutes; Supervised graduate/undergraduate researchers, and leading research projects in assessing cereals crops under different abiotic stress. During his Ph.D. and postdoctoral studies, he skilled with advanced molecular genetics techniques which are helped him to study molecular breeding of cereal crops, particularly for abiotic stress tolerance. Generally, his research interests focused on the isolation and characterization of abiotic stress-responsive genes and proteins, physiological and molecular mechanisms of the abiotic stress response, and tolerance. Also, study intracellular signaling pathways that are required for plants to coordinate stress responses under a variety of abiotic stresses



Matthew Reynolds, CIMMYT, Km 45, Carretera Mexico-Veracruz, El Batán, Texcoco 56237, EdoMex, Mexico, m.reynolds@cgiar.org

Is Distinguished Scientist at the International Maize and Wheat Improvement Centre (CIMMYT). He received a BA in Botany from Oxford University in 1983, an M.Sc. in Agricultural Botany from Reading University in 1984, and a Ph.D. in Horticultural Science from Cornell University in 1989. He currently holds the position of Head of Wheat Physiology at CIMMYT and serves on the management committee of the CGIAR Platform for Big Data in Agriculture, as well as Leader of the Community of Practice Organized by Department of Genetics, Faculty of Agriculture, Assuit University, Egypt.

for Crop Modelling for the platform. He has honorary positions at the University of Nottingham, Texas A&M, and Oklahoma State Universities and is a board member of the Global Plant Council ([GPC board](#)). He was appointed to the Mexican Academy of Science in 2018. He has published widely in the areas of crop physiology, genomics, and pre-breeding and was included in the top 1%, of the world's researchers in 2018 and 2019, across 21 research fields, by Web of Science. He has been active in developing global collaborations to tap into the expertise of plant scientists worldwide –such as the International Wheat Yield Partnership [IWYP site](#)- and the Heat and Drought Wheat Improvement Consortium [HeDWIC site](#)



Dr. Ahmed Sallam, Department of Genetics, Faculty of Agriculture, Assiut University, Assiut, amsallam@aun.edu.eg

Dr. Ahmed Sallam is an Associate Professor (promoted by Scientific Excellence Track, 2019) in the Department of Genetics at Assiut University, Egypt. He earned his scientific degrees from the Department of Genetics, Assiut University, Egypt (BSc and MSc) and Division of Plant Breeding, University of Goettingen, Germany (Ph.D.). After that, he worked as a postdoctoral Scientist for two years at the University of Nebraska-Lincoln, USA. Dr. Sallam received a Ph.D. award from the German Academic Exchange Service (DAAD). He received recognition of high scholarship and outstanding achievement from the Honor Society of Agriculture (Gamma Sigma Delta foundation), USA. Dr. Sallam published in high-profile international journals such as Scientific Reports, BMC Plant Biology, Frontiers in Plant Sciences, Frontiers in Genetics, International Journal of Molecular Scientists. He also a reviewer in some international journals such as the Journal of Advanced Research, Theoretical Applied Genetics, PLOS one, Frontiers in Plant Sciences, etc. His research interest is improving abiotic and biotic stress tolerance in cereals and legumes using QTL mapping, genome-wide association study, and genomic selection