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4th International Conference on

Plant Genomics

July 14-15, 2016 Brisbane, Australia

Posters



Plant Genomics 2016

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Selection for forage quality in tall fescue using a dihaploid generation approach

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Within the *Festuca-Lolium* genome complex there is a need for modern breeding approaches that can facilitate the rapid development of improved germplasm or cultivars. Traditional recurrent or mass selection methods for population or synthetic development are labor intensive and time consuming. The recent development of annual ryegrass *Lolium multiflorum* Lam. subsp. *multiflorum* lines, that when hybridized by tall fescue (*Festuca arundinacea* Schreb. (syn.=*Lolium arundinaceum* (Schreb.) Darbysh.), generate F1 hybrids capable of exhibiting genome loss of either the ryegrass tall fescue genome resulting in the recovery of both ryegrass and tall fescue dihaploid (DH) lines. Gamete selection performed at the F1 generation was found to be effective and may have application toward the selection of additional quantitative forage quality or agronomic attributes in tall fescue germplasm. The described gamete selection strategy is applicable to tall fescue (*L. arundinaceum*) and may have applications across the *Lolium/Festuca* genus.

Biography

Bryan Kindiger has completed his PhD from the University of Missouri, Columbia and has been employed with the USDA-ARS for 23 years. He is the lead Researcher for the development of cool-season grass forages at the Grazinglands Research Laboratory. He is presently working on a dihaploid inducement approach for representatives of the *Lolium* and *Festuca* genus.

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Development of molecular markers in order to assess the α -gliadin immunogenic content of an international spelt collection

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Gluten is the water insoluble protein fraction found in the flour of several cereals such as wheat and spelt. Its ingestion is responsible of celiac disease (CD) in genetically predisposed individuals (1-2% of the human population). Alpha-gliadins are a class of proteins of the gluten fraction playing an important role in this pathogenesis with 4 main toxic epitopes recognized by the immune system. In each α -gliadin, the number of toxic epitopes ranges from 0 to 6 since one of them can be duplicated and mutations can alter their composition. Less attention has been paid to spelt than wheat breeding and a high genetic diversity is still held in spelt germplasm collections. A collection of more than 250 spelt accessions from all over the world, including landraces, cultivars and breeding materials was assembled to carry out a genetic diversity study based on their immunogenic profile. Expressed α -gliadins were sequenced and high variations in the epitope composition and occurrence were observed depending on both the accession and the genome (A, B or D) they were expressed from. Thus, we developed PCR markers which specifically target genome-specific motifs. Since the epitope mutated forms lower or suppress the α -gliadin immunogenicity, we are currently developing molecular markers targeting some epitope variants. This will help to investigate the immunogenic content of all the accessions gathered in the spelt collection. This could enable us to highlight toxicity differences among the accessions and thus would be useful in breeding programs to develop safer varieties for CD patients.

Biography

Benjamin Dubois has completed his Bio-Engineering studies in Gembloux Agro-Bio Tech, Belgium. He is currently working on a research project at the Walloon Agricultural Research Center, Belgium since 2014. In parallel, he is pursuing his PhD at the Université Catholique de Louvain, Belgium.

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Acceleration of CRISPR/Cas9 breeding using flowering stimulation and precision lighting

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As a renewable resource, the demand for wood products is expected to continue to increase in the future. Compared to annual crop plants, direct genetic modification of trees species has gained little attention, partially because trees have much longer lifecycles and tight regulations opposing transgenic use in the field. The newly developed gene editing technologies, such as CRISPR/Cas9 increase the potential for the modification of species. CRISPR/Cas9 has several major advantages over previous transgenic based approaches and can work alongside conventional breeding programs by directly improving known yield related loci or genes. In this work, we target reporter genes in *Arabidopsis thaliana* by using a modified CRISPR/Cas9 system and have added a strong ubiquitous CaMV35S promoter, driving the Flowering Locus T (FT) gene. Ectopic expression of FT accelerates sexual development. To regulate the acceleration of flowering time to get viable flowers, we use precision lighting with different ratios of Blue, Red and Far Red light. The CRISPR/Cas9 mutated plants flower earlier than normal as a result of the ectopic FT expression, resulting in fast recovery of the second generation (F2) in *Arabidopsis*. We will use this technology to accelerate breeding in *arboreus* species.

Biography

Juan Pablo Matte has studied both, Forestry Engineering and Biological Science degree in Pontificia Universidad Catolica de Chile. He has completed his PhD in 2013 and Postdoctoral studies in 2015 from The University of Sydney, Australia. Currently he is an Associate Researcher in the Pontificia Universidad Catolica de Chile, under the PAI project number 82140040 from CONICYT.

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Screening of wild oil palm (*Elaeis guineensis*) germplasm for lipase activity

Wong Yun Teng

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A total of 148 *E. guineensis* palms originating from Angola, Cameroon, Guinea Conarky, Nigeria, Senagal, Sierra Leone, Tanzania and Zaire were then screened for lipase activity using the non-radioactive titration method. The analysis revealed genotypes with significantly different lipase activities, indicating that the activity is genotype dependent. Quantitative polymerase chain reaction (PCR) indicated similarity in pattern between gene expression and lipase activity determined by the novel assay. Several low and high lipase genotypes were identified. ANOVA results from this data showed significant differences between countries, populations and families. Heritability for lipase activity was estimated by the variance component of 33 families. The heritability estimate for lipase activity was high, indicating the possibility of selecting for lipase activity at the family level. The findings pave the way for selection and breeding for low lipase genotypes. They are also relevant to genetic marker development for oil quality.

Biography

Wong Yun Teng has completed her PhD from National University of Malaysia and has been working in molecular genetics for ten years, particularly in the oil palm genome. She is currently a Research Officer in Malaysian Palm Oil Board, Malaysia. Besides as a Researcher, she writes regularly and her article is often featured in magazines and newspapers. Her first novel was published in year 2014.

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Molecular cloning and characterization of *BcCSP1*, a Pak choi (*Brassica rapa* ssp. *chinensis*) cold shock protein gene highly co-expressed under ABA and cold stimulation

Feiyi Huang

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Cold shock proteins (CSPs) are a kind of evolutionarily conserved nucleic acid binding protein widely distributed from prokaryotes to eukaryotes. In this study, *BcCSP1*, a novel CSP was isolated from a Pak choi stress induced cDNA library by the rapid amplification of cDNA ends method. This gene had an open reading frame (ORF) of 822 base pairs encoding 273 amino acids. *BcCSP1* contained an N-terminal CSD domain and a glycine rich region interspersed with seven CCHC type zinc fingers at its C-terminus. Multi alignment and phylogenetic analyses showed that *BcCSP1* shared high similarity to AtCSP1 and AtCSP3. Real-time polymerase chain reaction analysis showed that *BcCSP1* was induced and co-expressed under cold stress and abscisic acid treatments. In addition, a *BcCSP1*-YFP fusion protein was localized to the nucleus and cytoplasm. These results indicated that *BcCSP1* plays an important role in responses to cold and ABA treatments in Pak choi. This work may be useful for future functional analysis of other CSP genes in Pak choi.

Biography

Feiyi Huang is currently a PhD student at Nanjing Agricultural University in China majoring in Vegetable Breeding and Molecular Biology. Her research focuses on cold stress and controlling flowering time in non-heading Chinese cabbage. She has published a paper entitled "Molecular cloning and characterization of *BcCSP1*, a Pak-choi (*Brassica rapa* ssp. *chinensis*) cold shock protein gene highly co-expressed under ABA and cold stimulation" in *Acta Physiologiae Plantarum*.

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Marker assisted transfer of drought QTLs and BPH resistance for development of new generation rice varieties

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Rice is the most important cereal food crop of India. Ongoing climate change is predicted to become a major challenge to sustainable rice production in India in the years to come. Among the different rice-producing states in India, the highest average rice yields are obtained in Punjab. Rice is cultivated on around 2.9 million ha in Punjab, with total paddy production of 16.6 million tons and productivity above 5.75 t/ha. The incidence of brown plant hopper has increased tremendously in the past few years causing significant yield losses, furthermore; deteriorating ground table is also a major concern. The situation will worsen with an increase in temperature and deteriorating ground irrigation water scenario. PR 121 is a very popular high yielding bacterial blight resistant variety occupying a large area in the state. It is, however, susceptible to BPH. Attempts are being made to improve this variety for resistance to drought (abiotic stress) and hoppers (biotic stress) through marker assisted selection. Multiple crossing was done to combine drought and BPH resistance in PR 121. IR71033-121-15-B (*Bph20+Bph21*) and IR96321-213-214 (*qDTY1.1, qDTY3.1*) were used as donors. Presently, the material is in BC1F2 generation with about 1050 seeds and will be analyzed for target traits.

Biography

G S Mangat has completed his PhD from Punjab Agricultural University, India. He is the Team Leader of the Rice Research Group, Department of Plant Breeding and Genetics, Punjab Agricultural University, India. He is involved in the development of seventeen high yielding rice varieties using both conventional and marker assisted selection. He is also actively involved in basic and strategic research, teaching and guiding post graduate students. He has published more than 25 papers in reputed journals and has been serving as an Editorial Board Member of repute.

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Whole genome sequencing of ten pathotypes of *Xanthomonas oryzae* pv. *oryzae* using a combination of Illumina and PacBio sequencing chemistries

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Punjab Agricultural University, India

Bacterial blight (BB) of rice caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) is one of the major diseases of rice. The pathogen is highly variable and the current *Xoo* population is classified into ten pathotypes in north western India. The ten pathotypes designated as PbXo-1 to PbXo-10 were differentiated using set of near isogenic lines. None of the genes are effective individually against these pathotypes, thus necessitating pyramiding of genes for durability of resistance to BB. The ten pathotypes have been collected from Punjab state of India, which is less than 1.5% of total area the country and started growing rice on large scale from 1970 onward. DNA from single colony from each of the 10 *Xoo* pathotypes was isolated and sequenced to more 100x coverage using Illumina and PacBio platforms. Hybrid assembly of the Illumina and PacBio reads lead to assemblage of seven pathotypes into single molecule and the remaining three pathotypes assembled into 11-15 contigs. Gene prediction revealed high gene density on both strands with 5500 genes on an average. More than 50 tRNA genes were identified in the *Xoo* pathotypes which is >95% of the reference genome. We are analyzing the data for TAL Effector genes which form the majority of the *avr* genes in *Xoo* as well as for other fitness gene. The comparative analysis of the whole genome sequences of all these ten pathotypes along with the other known reference genomes can provide insights into *Xoo* strain evolution and may help us in finding novel effector genes controlling the disease pathway.

Biography

Jagjeet Singh Lore has completed his PhD in Plant Pathology from Punjab Agricultural University, Ludhiana, India. Presently, he is working as Plant Pathologist (Rice) and actively involved in screening and identification of donors for multiple disease resistance in rice and has identified ten pathotypes of *Xanthomonas oryzae* pv. *oryzae* in Punjab. He has standardized screening protocols for sheath blight and neck blast diseases. He has actively contributed towards the development of high yielding bacterial blight resistant rice varieties occupying a large area in Northern India. He is working in collaboration with International Rice Research Institute. He is also a Co-PI in several ad hoc research projects on rice improvement and has published more than 40 research articles in reputed national and international journals.

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Over-expressing sodium transporters in soybean for salt tolerance improvement

Truyen Quach

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Recent climate change leads to higher temperature and rise in sea level, which results in expanding salinity affected areas and imposes a significant threat to agricultural production in Vietnam and worldwide. A number of genes regulating salinity tolerance have been identified to regulate salt tolerance through export of Na⁺ out of cytoplasm into vacuole and to apoplasm. In this study, we developed transgenic soybean over-expressing individual salinity tolerant genes NHX1, AVP1 and SOS1. These genes were assembled under control of 35S promoter to constitutively drive gene expression throughout life cycle of the soybean plants. The transgenic plants over-expressing individual genes having normal growth with good gene expression will be evaluated for their performance under salinity stress. If results are positive, this investigation will be significant for understanding roles sodium transporters in salt tolerance of soybean.

Biography

Truyen Quach has completed his PhD from University of Missouri. Currently, he is the Head of the Department of Plant Physiology, Biochemistry and Product Quality at Field Crops Research Institute, Vietnam. His lab is focusing on plant genetic engineering to improve plant adaptation to stresses and application of QTL on crop improvement.

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A people-centered system of managing a horticulture training group for service users with mental illness in occupational therapy department in Kwai Chung Hospital

Chan Man-yin

North District Hospital, Hong Kong

Horticulture therapy is the use of plants as a therapeutic medium by a trained professional to achieve a defined goal clinically. The evidence shows horticulture could promote physical, psychological, cognitive, social and economical well-beings. The techniques of horticulture therapy could assist service users to learn new skills or regain from their premorbid situation. Using of horticulture and horticultural-related activities to instill hope for them are very impressive during growth of the plants or even the chance to foster a love to them similarly or for nature at our rooftop garden. Therefore, a new system of work is introduced to an existing horticulture training group with focused learning strategies so as to enrich service performance and outcomes with adequate safety and supervision. Treatment return of the group was reviewed retrospectively from 2011 to 2012. Data was categorized into attendance, new service users to join in, working days, total service users per month, and compliance rate in using of personal protective equipment (P.P.E.) after incorporating biweekly tool box talk with randomly spot checking in the workplace. Discussion group was held among people in-charge of the workshop, related staff and every service users with interactive management style incorporated new initiatives including hourly session for service users from acute admission and sub-acute wards, tool box talk by asking which types of P.P.E. to protect them during work and quarterly reinforcing activities of barbecue and outing. Individual feedback sessions were also held half yearly to gather some qualitative data for continuous improvement. The most reflective data was increased numbers of daily attendance from 3.1 service users of first two quarters in 2011 to 5.6 service users from last two quarters in 2011 to whole year of 2012. The monthly total number of attendees sharply increased from 57.8 service users to 115.4 service users. The compliance rate of P.P.E. was 100% after implementing of tool box talk. All staffs and service users were satisfied with the new management style. The findings gathered support an interactive management style which could enhance performance statistics and satisfaction of service users. The key element of managing a workgroup was to strike a balance between the potential therapeutic value and risk management under the people-centered system.

Biography

Chan Man-yin has completed Bachelor of Science in Occupational Therapy in Hong Kong. She is an Occupational Therapist in Hospital Authority. She is actively involved in Occupational Health and Safety activities in hospital with more than 20 years of working experience in Psychiatric Rehabilitation. She is able to manage many pioneer projects multi-disciplinary within and outside hospital. She has organized several overseas training and attachment before. She is uniquely positioned within the occupational therapy profession. She has authored various publications with ample experience as a conference presenter.

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Differential expression and identification of new adult plant resistance genes to leaf rust in Brazilian wheat cultivar Toropi

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Wheat leaf rust, caused by *Puccinia triticina*, endemic of South America, it is an important wheat disease. The Brazilian wheat cultivar Toropi has proven, durable adult plant resistance (APR) to leaf rust and prehaustorial resistance phenotype. The objective of this study was to identify, characterize and to understand the interaction between *P. triticina* and Toropi by quantitatively evaluating the temporal transcription genes related to infection and defense in wheat. RNA-Seq libraries from the Toropi here produced at 0, 6, 12, 24 hours after inoculation with *P. triticina*. Three replicates of each inoculated and control libraries were sequenced for each time point. A comparison to the Chinese Spring (CS42) transcriptome was performed aiming to identify putative genes unique to Toropi. A total of 58 million bp per library were produced: 10,181 contigs of which 9,156 were common to CS42 and 1,025 were unique to Toropi expressed only in the inoculated libraries. The expression profiles of 15 selected genes varied over time. Classical defense genes, including peroxidases, b-1,3-glucanases and an endochitinase were expressed (pre and post haustorial) over 72 hours infection time course, while induction of transcription of other infection related genes with a potential role in defense, although variable was maintained throughout. These genes had a role in plant lignification, oxidative stress, the regulation of energy supply, water and lipid transport and cell cycle regulation. These Toropi specific sequences could represent new resistance candidate genes to be used in wheat breeding and to guide further functional studies on APR to leaf rust.

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Identification of maize grain Fe and Zn homeostasis-associated QTL in two mapping populations

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Iron (Fe) and zinc (Zn) are essential for plant, animal and human nutrition. Low Fe and Zn in crops and livestock results in their reduced health, which when consumed over prolonged periods can in turn negatively impact the nutrition of human populations. Maize is grown worldwide as a staple crop for some and a valuable commodity for others and has the potential to be a useful tool for targeting the dietary Fe and Zn deficiency among the undernourished poor. Maize's remarkable global spread is largely due to the degree of genetic and phenotypic diversity that can be harnessed into adaptation to local conditions. This study was performed on the Goodman Diversity Panel (GDP) with corresponding analysis of the nested association mapping (NAM) population, to take advantage of greater statistical power and resolution and to perform joint linkage (JL) and genome-wide association (GWAS) analyses of quantitative genetic loci (QTL) across 3 temperate and 2 tropical locations. Previous studies that have used a candidate-gene knockout approach have yielded narrower successes in identifying genetic determinants of ionic homeostasis, whereas the NAM JL-GWAS approach, in this study, has borne significant QTL identification. Currently 227 JL ionic-QTLs have been identified with successive rounds and accompanying GWAS data we anticipate discovery of good QTL for twenty different elements including those for Fe and Zn homeostasis. A web interface for browsing the maize co-expression network has been developed for querying individual genes or large regions of the genome that will shortly become available for public use.

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