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The complete chloroplast genome sequences of eight Fagopyrum species: insights into genome evolution and phylogenetic relationships

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Buckwheat (Fagopyrum genus, Polygonaceae), is an annual or perennial, herbaceous or semi-shrub dicotyledonous plant. There are mainly three cultivated buckwheat species, common buckwheat (F. esculentum) is widely cultivated in Asia, Europe, and America, while Tartary buckwheat (F. tataricum) and F. cymosum (also known as F. dibotrys) are mainly cultivated in China. The genus Fagopyrum is taxonomically confusing due to the complex phenotypes of different Fagopyrum species. In this study, the chloroplast (cp) genomes of three Fagopyrum species, F. longistylum, F. leptopodum, F. urophyllum, were sequenced, and five published cp genomes of Fagopyrum were retrieved for comparative analyses. We determined the sequence differentiation, repeated sequences of the cp genomes, and the phylogeny of Fagopyrum species. The eight cp genomes ranged, gene number, gene order, and GC content were presented. Most of variations of Fagopyrum species cp genomes existed in the LSC and SSC regions. Among eight Fagopyrum chloroplast genomes, six variable regions (ndhF-rpl32, trnS-trnG, trnC, trnE-trnT, psbD and trnV) were detected as promising DNA barcodes. In addition, a total of 66 different SSR (simple sequence repeats) types were found in the eight Fagopyrum species, ranging from 8 to 16 bp. Interestingly, many SSRs showed significant differences especially in some photosystem genes, which provided valuable information for understanding the differences in light adaptation among different Fagopyrum species. Genus Fagopyrum has shown a typical branch that is distinguished from the Rumex, Rheum, and Reynoutria, which supports the unique taxonomic status in Fagopyrum among the Polygonaceae. In addition, phylogenetic analysis based on the cp genomes strongly supported the division of eight Fagopyrum species into two independent evolutionary directions, suggesting that the separation of cymosum group and urophyllum group may be earlier than the flower type differentiation in Fagopyrum plants.

Speaker Biography

Yu fan is studying the doctoral program of joint training in the Institute of crop science of Chinese Academy of Agricultural Sciences and Guizhou University. He has long been engaged in plant evolution, population genomics and the collection and protection of crop germplasm resources. At present, he has collected thousands of buckwheat germplasm resources and participated in the publication of a new species and a subspecies in fagopyrum plants.

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The effects of molecular hydrogen seed priming on the germination of legumes

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Plant life is essential for human existence and increasing demands for nutritional produce in the current unstable climate inspires researchers to find novel and sustainable solutions to protect and enhance plant vitality and stimulate growth. Seed priming is used within the agri-food industry to control and enhance the germination of seeds. Such processes allow for more uniform and better germination of the treated seeds. Seed priming can enhance germination over wide-ranging temperatures, can augment cellular responses to numerous abiotic stresses and reduce incidence of disease in seeds.

Molecular hydrogen (H2) is now well documented as having anti-oxidant and cellular protective effects in numerous eukaryotic species, including plants and seeds. H2 is an electrochemically neutral, non-polar, diatomic molecule with a low molecular weight (2.016 g/mol). These important characteristics make H2 highly favourable for use as a seed priming agent allowing the molecule to diffuse through structural components of seed cells and membranes that occur around organelles, such as the nucleus and mitochondria. The distribution of H2 across cellular walls and membranes, is not affected by electrochemical gradients and the H2 molecule can readily pass through the hydrophobic phase of phospholipid bilayers. This allows molecular hydrogen to influence cytosolic reactions as well as fundamental organelle biochemistry and there is a growing body of scientific evidence that describes a myriad of cellular protective qualities of importance for the agri-food industry is that H2 is non-toxic and can be readily dissolved into an aqueous medium and applied to seeds, seedlings and mature plants, making it an effective, sustainable and inexpensive means of treatment.

Speaker Biography

Grace Russell is a PhD researcher in the dept. of applied science, at the University of the West of England, Bristol, UK. She lives and works in Somerset, UK, where she has been researching, writing and presenting her work throughout the recent pandemic. Her research interests centre around new and emerging restorative gases, molecular and oxy-hydrogen. Much of her academic focus has involved investigating the intricate molecular mechanisms, and downstream cellular effects associated with these gaseous compounds. Her recent work has culminated in numerous peer-reviewed journal publications, and a book: Molecular Hydrogen – an Ongoing Academic Journey.

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Genome-wide identification and expression profile analysis of trihelix transcription factor family genes in response to abiotic stress in Sorghum [Sorghum bicolor (L.) Moench]

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Transcription factors, including trihelix transcription factors, play vital roles in various growth and developmental processes and in abiotic stress responses in plants. The trihelix gene has been systematically studied in some dicots and monocots, including Arabidopsis, tomato, chrysanthemum, soybean, wheat, corn, rice, and buckwheat. However, there are no related studies on sorghum. In this study, a total of 40 *Sorghum trihelix* (SbTH) genes were identified based on the sorghum genome, among which 34 were located in the nucleus, 5 in the chloroplast, 1 (SbTH38) in the cytoplasm, and 1 (SbTH23) in the extracellular membrane. Phylogenetic analysis of the SbTH genes and Arabidopsis and rice trihelix genes indicated that the genes were clustered into seven subfamilies: SIP1, GTγ, GT1, GT2, SH4, GTSb8, and orphan genes. The SbTH genes were located in nine chromosomes and none on chromosome 10. One pair of tandem duplication gene and seven pairs of segmental duplication genes were identified in the SbTH gene family. By qPCR, the expression of 14 SbTH members in different plant tissues and in plants exposed to six abiotic stresses at the seedling stage were quantified. Except for the leaves in which the genes were upregulated after only 2 h exposure to high temperature, the 12 SbTH genes were significantly upregulated in the stems of sorghum seedlings after 24 h under the other abiotic stress conditions. Among the selected genes, SbTH10/37/39 were significantly upregulated, whereas SbTH32 was significantly downregulated under different stress conditions.In this study, we identified 40 trihelix genes in sorghum and found that gene duplication was the main force driving trihelix gene evolution in Sorghum. The findings of our study serve as a basis for further investigation of the functions of SbTH genes and providing candidate genes for stress-resistant sorghum breeding programmes and increasing sorghum yield.

Speaker Biography

Li Kui Yin has been teaching and conducting research in crop cultivation at Anshun University since graduating from Guizhou University in 2008 with a master's degree. He has successfully passed various examinations to enter the PhD program in crop science at Guizhou University in 2019 to pursue his PhD in crop genetic breeding, and his research interests are in the molecular study of genes related to starch synthesis in brewing Sorghum seeds.

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Comparative performance of Entomopathogen infecting rice bug in region 8

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The study was to emphasizing entomopathogens in pest management of rice crop over chemical pesticides. Biological control with pathogenic fungi might provide long lasting insect control without damage to the environment or non-target organisms. Metarhizium anisopliae SPW and Beauveria bassiana are two of several natural agents for controlling a broad range of insects by direct penetration of the host cuticle. Percent infection of rice bug depends on number of spores and timing of application. Rice bug showed infection three days after application with 75.83% for M. anisopliae SPW while 55% for B. bassiana under laboratory infection using 1x108 spore count. In pot experiment, it showed that increasing its spore count from 1x106 to 1x108 can increased its effectiveness. However, after applying of entomopathogens in the field, it showed that heavy rains (615mm-788.6mm) may affect its effectiveness to the insect. On 1st trial, only B. bassiana showed promising effect to the insect. Infected insects were found in all treatments with highest infection of 44.26% however, M. anisopliae SPW only infects other rice pest. On 2nd trial, M. anisopliae SPW (29.83%) showed its effectiveness higher than B. bassiana (12.1%). Infection occurrence can last up to the harvesting of the crops.

Speaker Biography

Brenda Balbarino-Almeroda is a science research specialist II in the department of agriculture-RFO8, Abuyog experiment station, Leyte, Philippines. Currently, she is the unit head of on-station research and off-station collaboration unit in Abuyog experiment station. She is also a training coordinator for on-the-job training and occupational internship program. She is a technical expert in pest management on jackfruit, rice, corn and banana. She has participated in various international conferences and received awards for her contribution. She also has membership in various association/organization in Philippines.

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Impact and challenges of digital agricultural marketing initiative of the government in India: A case of E-NAM

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The present agricultural marketing system in India is posed with several challenges for marketing of agricultural produce such as fragmentation of state into multiple marketing areas, each area is administered by separate APMC, multiple levy of market fees, requirement for multiple licenses for trading in different APMCs and states, licensing barriers leading to conditions of monopoly, poor quality of infrastructure in the APMCs, low usage of technology, asymmetric information, etc. So integration of agriculture markets across the country through e-NAM platform is seen as an important measure for overcoming these challenges. In 2016, the Government of India introduced new online platform to bring transparency in marketing of agriculture produce called as e-NAM. The e-NAM is supposed to be a game changer in the agricultural marketing ecosystem of the country. The study tries to analyse the impact of e-NAM on prices and arrivals of major agricultural commodities, and the challenges faced by various stakeholders in implementation of e-NAM in the state of Haryana in India. The study was conducted in 8 APMCs in Haryana and 400 farmers, 80 traders and 8 e-NAM officials were interviewed for the study. The results of the study revealed that the quantity of commodities traded through e-NAM platform has increased by 55.71 percent in Haryana. Except Sirsa APMC, there was a significant increase in quantity arrivals in the remaining seven APMCs during the past five years. Except Sorghum, there was a substantial increase in prices of the eight agricultural commodities ranging from 24.88 percent to 77.16 percent from 2015-16 to 2020-21. The study highlights the various problems faced by the farmers, traders and e-NAM officials in implementation of e-NAM and suggests suitable strategies for strengthening of e-NAM in the country.

Speaker Biography

Chidanand Patil completed his MBA and Ph.D in the field of "Agribusiness Management" from University of Agricultural Sciences (UAS), Bangalore and UAS, Dharwad respectively. Later he worked as a post-doctoral associate at Indian Institute of Management, Bangalore in University of Glasgow (United Kingdom) sponsored project entitled "information, market creation and agricultural growth". He worked on an international project in Thailand on "ICT initiatives in agriculture for boosting the farmers' income – lessons from Thailand" sponsored by Indian council of social science research (ICSSR), New Delhi and National research council of thailand (NRCT). Currently, he is working on ICSSR-IMPRESS project entitled "Performance of regulated APMCs in Haryana under new agricultural marketing reforms (e-NAM) regime" sponsored by the Ministry of human resource development. He has supervised 23 agribusiness project reports and published more than 22 research papers in various journals. He has been awarded with the Jawaharlal nehru scholarship for doctoral studies (2012); Manthan – business plan presentation competition 2012 award" organized by FKCCI (Federation of Karnataka Chambers of Commerce and Industry); selected for ICSSR doctoral studies fellowship; selected for SRF (senior research fellowship) for doctoral studies sponsored by Indian council of agricultural research. He has presented research paper on "ICT in agriculture for improving farmers' income – A study of India and Thailand" during the 13th ICSSR-NRCT joint seminar sponsored Chiang Rai, Thailand (2019). He has delivered a talk on "Agri-entrepreneurship opportunities and ICT in agriculture" at Pridi Banomyong International College, Thammasat University, Thailand (2019). His research interest is in the area of agricultural marketing, food and agriculture policy and agripreneurship development.

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Genome wide association analysis to enhance seed and nutrition quality traits in pigeonpea

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Pigeonpea is an important legume crop with high protein content and nutritional attributes for more than a billion-people living in South Asia. Ever-increasing pigeonpea consumption as a major source of protein necessitates the improvement of varieties for more efficient production. The nutritional value enrichment of pigeopea is very much essential to reduce malnutrition of developing countries in the post green revolution era. To utilize its potential, a coordinated and comprehensive evaluation of germplasm is required. Identification of potential genes/alleles governing complex traits of seed quality and nutritional content such as seed weight, seed colour, total protein content (TPC), amino acid and resistance starch are essential in marker-assisted breeding for quality trait improvement of pigeonpea. The current gain in knowledge on the seed quality and nutritional value related genes and QTLs will help into develop desired genotypes for the humankind. The availability of gene-based markers and advanced tool will assist breeders to accumulate specific alleles of genes known to play a role in nutritional grain quality traits in pigeonpea. Therefore, the present study on the profiling for the first-time to understand these complex genetic architectures of qualitative and quantitative traits in pigeonpea. For GWAS (genome-wide association study), high-throughput genotyping information of 62K SNP “CcSNPnks” genic chip genome-based SNPs discovered from 45 diverse varieties of pigeonpea utilized. The chip comprises total 62,053 SNPs from 9629 genes belonging to five different categories, including 4314 single-copy genes unique to pigeonpea, 4328 single-copy genes conserved between soybean and pigeonpea, 156 homologs of agronomically important cloned genes, 746 disease resistance and defense response genes and 85 multi-copy genes of pigeonpea. Our analysis revealed that the average protein content carrying genotypes are DG(RG)45, AKPR -324, MC-99, UP-73 and BRG-2 (16.8, 19.3, 21.5, 24.7, 30.3 gm). This led to identification of most effective genomic loci (genes) associated with seed quality and nutritional content in pigeonpea from diverse sets of wild and cultivated genetic backgrounds. The informative functionally relevant molecular tags scaled down essentially have potential to accelerate marker assisted genetic improvement by developing seed quality and nutritionally rich pigeonpea cultivars.

Speaker Biography

Nisha Singh is working as an assistant professor (bioinformatics), department of bioinformatics, COABT, Guru Angad Dev Veterinary and Animal Sciences University, Ludhiana and DST-INSPIRE faculty at ICAR-National institute for plant biotechnology, New Delhi, India. She has completed her PhD in plant genomics from ICAR-NIPB, New Delhi, India and postdoctoral studies from Cornell University, Ithaca, New York, USA. She has rich expertise in crop genomics, proteomics and bioinformatics and well recognized national and international level. She has published more than 50 papers in reputed international journals and has been serving as an editorial board member and reviewer of reputed journals.

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Methods to reduce grain chalkiness in rice by overexpressing OsMADS29 under seed-specific promoters

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Rice is a staple food crop for more than half of the world's population. Various grain characteristics like grain length, aroma, and texture have varied likings or dislikings in different cultures. However, one universally undesirable trait is grain chalkiness. The chalkiness is caused by suboptimal starch accumulation during the final stages of grain filling, causing a disordered cellular structure, rounder amyloplasts, and more air spaces than head rice. Chalky grains are more brittle than non-chalky grains and can break more easily during milling. The MADS29 (M29) gene is a primary regulator of seed development in rice. Our earlier experiments have also demonstrated that the mere expression of M29 enhances starch accumulation in a completely heterologous system of tobacco BY-2 cells, suggesting that M29 could be the master regulator of starch biosynthesis. Therefore, to augment the starch biosynthesis machinery in the center of the endosperm, we planned to express M29 under the control of two seed storage protein promoters, namely, P26 (2062 bp) and O18 (1249 bp). This intervention reduces grain chalkiness by up to 90% and increases grain width, length, and grain weight by up to 6%, 16%, and 23%, respectively. Thus, we can improve grain quality by expressing M29 outside its expression domain, in the center of the endosperm.

Speaker Biography

Vibha Verma completed her Ph.D. in 2019 from the faculty of interdisciplinary and applied sciences, the University of Delhi, from the laboratory of Prof. Sanjay Kapoor in the department of plant molecular biology. Her focus has been on post-transcriptional regulation of a MADS-box transcription factor which seems to be one of the master regulators of rice seed development and grain filling. She has also used heterologous systems like tobacco BY-2 cells and Physcomitrella patens to elucidate the role of this transcription factor in influencing auxin: cytokinin homeostasis and its downstream effects on plastid biogenesis and starch synthesis. She has also been exploring avenues of biotechnological applications of M29 by altering its expression in different cell types of rice.

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Effect of organic nitrogen on the performance of potato in organic farming

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Crops grown under organic systems may suffer from insufficient nitrogen due to the mismatch between the N bioavailability and its demand dynamics by the plant. This work investigates the response of three potato varieties to a combination of organic fertilizers (compost and fish meal) for a nitrogen supply at the rates of 0, 30, 70, 90, 110, 130 and 180 kg ha-1. In addition, about 100 kg ha-1 of nitrogen was supplied from inherent soil organic matter mineralization. Field trials were conducted during two cropping seasons on two plots left fallow for several years according to the requirements of organic farming. The results obtained show that the contribution of increasing doses of nitrogen has a significant effect on total dry matter, tubers dry matter, total nitrogen uptake, tubers nitrogen uptake, nutritional and morphological quality parameters and tuber yield. Tuber yield ranged from 34 t ha-1 (control) to 52 t ha-1 (230 kg ha-1 of nitrogen). Moreover, the different cultivars have a significant effect on all the parameters studied apart from the yield and the nitrate content of tubers. The dose of 230-250 kg ha-1 of nitrogen is recommended to achieve satisfactory yield (about 50 t ha-1) of the organic potato while producing good tuber quality under similar conditions.

Speaker Biography

Ahmed Harraq have completed his PhD at the age of 49 years. He is a professor at National School of Agriculture of Meknes, department of agronomy and plant breeding, Morocco. His area of research is organic farming. He has several publications that deal with the mineralization of organic fertilizers and its effects on crops. Currently, he is conducting several green manure trials in organic farming.

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3D Root: A root phenotyping toolkit for 3D scans by X-Ray Computed Tomography

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University of Salamanca, Spain

Breakthrough imaging technologies may challenge the plant phenotyping bottleneck regarding marker-assisted breeding and genetic mapping. In this context, X-Ray CT (computed tomography) technology can accurately obtain the digital twin of root system architecture (RSA) but computational methods to quantify RSA traits and analyze their changes over time are limited. RSA traits extremely affect agricultural productivity. We develop a spatial–temporal root architectural modeling toolkit called 3D Root based on 4D data from X-ray CT by cylindrical fitting. This novel approach is optimized for high- throughput phenotyping considering the cost-effective time to process the data and the accuracy and robustness of the results. As a consequence, significant root architectural traits and its distribution, including number, length, growth angle, height, diameter, branching map, and volume of axial and lateral roots, are fully automatically extracted. As 3D scans from X-ray CT become a standard data to non-invasively digitize RSA in lab conditions, we envision 3D Root will contribute moving the next generation of root phenotyping forward.

Speaker Biography

Monica Herrero-Huerta did her civil engineering with a PhD entitled 'Close-range photogrammetry applied to agroforestry engineering' from the department of cartographic and land engineering, University of Salamanca (SP, 2016). She completed her postdoctoral studies from Delft University of Technology (The Netherlands) in the department of geosciences and remote sensing (2015-2018). She is a research staff member at Purdue University for the Institute for plant science, College of agriculture (IN, USA). Currently, she is a distinguished researcher at the University of Salamanca (SP) and active member from TIDOP research group (Geomatic technologies for the 3D digitization and modeling of complex objects) (SP). Her research interests to date have been focused primarily on close-range hyper spectral photogrammetry and LiDAR by alternative platforms and specifically in computer vision and deep learning analysis by multi-sensor data fusion applied to plant science.

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