SRM College of Agricultural Sciences

SRM Institute of Science and Technology

Baburayanpettai,Chengalpattu, Tamil Nadu - 603 201

NATIONAL SEMINAR on

"Recent Strides in Deciphering Gene(s) in Plants"

RSDGP'24

SOUVENIR

(A Book of Abstracts)

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Genetics and plant breeding played a pivotal role in the Green Revolution in India by increasing crop yield and there by making country self-sufficient in food grain production. Plant Breeders develop high yielding varieties of wheat, Rice and other crops. Professor M. S. Swaminathan, the "Father of Green Revolution", created high yielding wheat varieties Breeders incorporated semi-dwarfing genes in to Wheat and Rice crops, to evolve shorter, stronger genotypes with higher yield potential. Rice breeders evolved basmati strains of Rice that produce heavy grains, while still standing tall. Breeders bred wheat, rice crops to create new varieties (Kalyan sona and Sonalika in wheat) use of improved fertilizers and irrigation techniques have also contributed to the Green Revolution. Green Revolution led to a significant increase in a crop yield between 1969-70. For example in India wheat production doubled in four crop seasons.

Oflate, with the invention of male sterile lines, hybrid breeding was successful in pearl millet, Sorghum, Sun flower and other mandate crops. The development of hybrids and realization of higher yield, forms the second Green Revolution. I hope that the application of biotechnological techniques in crop plants will bring about "Ever Green Revolution." In this context, the understanding about the gene(s) would be useful in manipulating the genes in crop improvement programme. I wish the organiser to get great grand success in conducting the said National Seminar on "Recent Strides in Deciphering Gene(s) in Plants".

Wish you all the best

Dr. N. Asoka Raja
Associate Dean
SRM College of Agricultural Science
Baburayanpettai

Variation is spring of life. Any successful crop improvement programme through gene manipulation depends upon the amount of variability available in the reference population. Variations are brought out by heritable changes and also ofcourse through environmental factors. Heritable variations are important in effecting a sound crop improvement programme, through gene manipulation. Heritable variation arise either through recombination and / or through mutations. Smallest unit capable of recombinant is recon and smallest unit capable of mutation is muton. The smallest unit of DNA capable of coding one polypeptide is cistron. Our understanding about gene(S) is improving depending upon our resolving power. The factor (genes) as suggested by Mendel has modified and evolved into cistron of Benzer.

Gene manipulations are done by three different ways like, 1. Pollen mediator gene transfer, 2. Chromosome mediator gene transfer and 3. DNA mediator gene transfer

Pollen mediator gene transfer technique have proved its mettle in evolving high yielding varieties and hybrids. Chromosomal engineering techniques have been successful in evolving rust resistant wheat. DNA mediator gene transfer techniques stand for merit consideration, as it's useful in evolving transgenic resistant plant with inbuilt tolerance to biotic as well as abiotic stresses.

The population in India is about 1.45 billion. The present food production is 332 million tonnes. It's expected that it will reach 1.67 billion by 2050 for which requirement of food will be 400 million tonnes. This can be achieved by increasing production and productivity by gene manipulation. In this context, the National seminar entitled as "Recent Strides in Deciphering Gene(s) in Plants" is useful in unrevealing the properties of the genetic material, as well as in tailoring potential genotypes with efficiency by all means. I believe this seminar outcome is very interesting and significant in the field of Genetics and Plant Breeding.

I wish you all the best

Dr. S.Thirugnana kumar
Professor and Head
Department of Genetics and Plant Breeding
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Baburayanpettai

As the days move and years spring, an array of innovative techniques, which essentially touches upon the frontiers in modern biological sciences, are available to the Plant Breeders. Professor M.S. Swaminathen, has optly stated that "Man has become the Bharma" -the God of creation. Infact, it is evident from the fact that breeders has evolved new crops (Triticale and Raphanobrassica) that were not available in nature.

The early attempts made towards the understanding of the mechanism of hereditary were full of pitfalls and ideas. The Austrian Priest, Gregor Johann Mendel, 1866, was the first to make comprehensive and scientific approach, to unravel the mechanism of hereditary. It formed the first mile stone in Genetics. Hackle (1866) established that nucleus of the cell stores and transmits hereditary units. The decisive contribution to the problem of gene action has come from Garrod (1908). Haldane (1930), propounded the one gene – metabolic step hypothesis. Beadle and Tatum (1945) propounded the one gene- one enzyme hypothesis.

Ingram (1950s) proposed one gene-one polypeptide hypothesis. Benzer (1956) refined it as one cistron-one polypeptide hypothesis. These hypothesis solved the problem of, how genes exert their effects on the characters. Muller's (1922) definition of genes form the second millstone of Genetics. Muller gave the brilliant answer about the three fate full properties of the genetic material (Transcription and Translation, Replication, and Mutation). Muller qualities himself as the founder of Molecular Genetics. Muller's ideas forms the second millstone in Genetics.

James Watson and Francis Crick (1953) proposed the double helical structure of DNA. It completely vindicated Muller's pioneer model of genes. The contribution made by Watson and Crick is illuminating as the 3rd major millstone in Genetics. The chemical nature of the genetic

material was brought out with the experiments of Avery et al. (1940). They have demonstrated that the transforming principle in *Pneumococcus* was DNA. Pauling (1948) found out that the two strands of DNA are complementary to each other, so that each can serve as a replica of each other. Watson and Crick also proposed the replication of DNA is semi-conservative. Watson also proposed the "central dogma", which explains the flow of genetic information transfer from DNA to RNA and Protein.

Nirenberg and Khorana written the complete dictionary of genetic code. Khorana and his co-workers (1970) deduced yeast alanine tRNA gene and artificially synthesised it for the first time. It formed the fourth milestone in Genetics. Jacob and Monod (1961) proposed the operon model to explain the regulation of gene expression in prokaryotes. Arber, Nathan and Smith (1970) found out the restriction enzymes (molecular scissors). That opened the flood gate in Genetic analyse and recombinant DNA techniques. It formed the fifth milestone to understand the genes.

Fraley *et al* (1983) first time reported about the expression of bacterial genes in plants. The natural gene transfer mechanism namely, transformation (Griffiths 1925), conjugation (Lederberg and Tatum 1946) and transduction (Zinder and Lederberg 1952) remains as natural model for artificial gene transfer.

The understanding about the genes become perfect depending upon our resolving techniques. In this contact, I whole heartedly congratulate the organizing secretary for having organised a National Seminar on "Recent Strides in Deciphering gene(s) in Plants". It is a need of the day. I wish all the best.

Dr.A.Chandrasekar
Organizing Secretary
Assistant Professor (Plant Biotechnology)
Department of Genetics and Plant Breeding
SRM College of Agricultural Science
Baburayanpettai

It gives me immense pleasure that the Department of Genetics and Plant Breeding, SRM College of Agricultural Science, Baburayanpettai is organizing the 2th National Seminar on "Recent Strides in Deciphering Gene(s) in Plants" on 30.09.2024. The National Seminar is organized jointly by the section of Biotechnology, Genetics and Plant Breeding and Seed Science and Technology of SRM College of Agricultural Sciences. Thus, it is designed to provide an innovative and comprehensive overview of Biotechnology, Genetics and Plant Breeding as well as Seed Science and Technology with focus given to major research advances including genome editing, genetic engineering, Marker-assisted Selection, Genomics and Plant Breeding approaches.

The purpose of this National seminar is to bring together researchers from various fields in different disciplines to share knowledge and experience, as well as to stimulate new ideas for future Research and Development. The delegates from various parts of the Tamil Nadu as well as from Kerala, Manipur and Andre Pradesh are delivering their innovative research finding which would definitely help to initiate the future collaborative research among the scientists.

I appreciate the attitude of the organizer and the various team members for selecting such a useful title for the National Seminar. I extend my congratulation to all the organizers and I wish the National Seminar a great grand success.

Effect of gamma irradiation on seed germination and seedling growth of *Vigna radiata* (L.Hepper)

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Abstract

Mungbean seeds were treated with various doses of gamma irradiation (100 to 500 GY) to study seed germination and seedling growth. The sensitivity of gamma irradiation was observed on different germination and growth parameters such as germination rate (%), seedling height (shoot length), root length, and number of lateral branches per primary root. The results showed that depressive effects were increased with increasing radiation dosages. A 50 percent reduction in germination and seedling size (injury) was observed at 400 GY of gamma-ray irradiated seedlings. It was considered as LD 50 value (optimum dose) for gamma-ray in mungbean variety Vamban 3.

Keywords: Mungbean, gamma ray, sensitivity index

An Economic Analysis of Red Gram Production Technology's Effect on Farm Income and Productivity in Tamil Nadu's Karur District

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Abstract:

In India, red gram is a significant pulse crop. Approximately 20 percent of the nation's total pulse production comprises red grams. The current study tried to assess the degree of increased production technology adoption, the yield gap, the effect of red gram technologies on employment and income patterns, and the contribution of technology to red gram crop yield. The human labor usage was mainly for irrigation, weeding, and harvesting. The utilization of labor revealed that among the sample farms, the usage of human labor was maximum in the case of semi-medium farms (25.31 man-days/ha). The average machine labor usage at the district level was 6.85 hrs/ha. The average seed rate adopted by sample farmers for Red gram cultivation was 6 kg/ha and small farms used more quantity of seeds (8 kg/ha) compared to other farm size categories. Among the fertilizers, maximum usage of MOP was noticed (114.51 kg/ha), followed by urea (94.45 kg/ha), complex (93.27), and DAP (90.16 kg/ha). For the control of pests quinalphos (0.62 lit/ha) was applied by the sample farmers. The average productivity of Red gram at the district level was 7.6 q/ha and the maximum yield was obtained by medium farms at the rate of 8 q/ha. The gross returns from the Red gram cultivation in the district was Rs. 43366.3 /ha. The net returns from Red gram cultivation were Rs. 12639.5 /ha and it was maximum for small farms (Rs. 18118.7/ha), followed by medium farms (Rs. 15473.6/ha).

Keywords: Red gram, Technology, Gene

Combining ability analysis over environments in Diallel crosses of Maize (*Zea mays* L.)

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Abstract:

A study was conducted in maize to assess General Combining Ability (GCA), Specific Combining Ability (SCA), and their interactions across three different environments. Nine inbred maize lines were crossed in all possible combinations, including reciprocal crosses, using a 9 × 9 diallel method. The resulting single-cross hybrids, along with their parental lines, were analyzed for their combining ability in various environments. Both GCA and SCA showed highly significant variances across all traits, including days to physiological maturity, plant height, cob length, cob girth, cob weight, 100-grain weight, and grain yield per plant. This highlights the importance of both additive and non-additive gene actions in these traits. The ratio of additive to non-additive variance was greater than 1 for most traits, except for cob length, cob girth, cob weight, and grain yield. This suggests that additive gene effects predominantly influence traits such as days to physiological maturity, plant height, and 100-grain weight, indicating that these traits could be improved effectively through simple selection. The hybrid UMI79 × UMI176 excelled in grain yield, cob weight, cob girth, and early maturity. For reduced plant height, UMI176 × UMI467 was identified as the best-performing hybrid across all environments. UMI176 × UMI13 was the top hybrid for cob weight and cob girth. Hybrids UMI79 × UMI57, UMI79 × UMI285, and UMI432 × UMI936 (W) stood out for cob length. This investigation underscores the importance of both GCA and SCA in maize breeding and points to promising hybrid combinations for improving key traits such as yield, cob dimensions, and early maturity across various environments.

Induced Chemical Mutagenesis on Sunnhemp (*Crotalaria juncea* L.) to determine the lethality, germination, and seedling survivability.

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Abstract

Sunnhemp, (*Crotalaria juncea* L.), is a member of the Fabaceae family and is used extensively in industry as a green manure, fiber crop, and fodder crop. The seed was exposed to ethyl methane sulphonate (EMS), diethyl sulfate (DES), and sodium azide (SA) in this study. Ethyl methane sulphonate (EMS), diethyl sulfate (DES), and sodium azide (SA) at concentrations of 5 mM, 10 mM, 15 mM, 20 mM, 25 mM, 30 mM, 35 mM, 40 mM, 45 mM, and 50 mM were applied to the seeds. The untreated seeds were used as a control. In this investigation, increasing mutagen concentrations in M1 generation reduced seed germination, seedling survival, and lethal dosage LD50. The seed germinated on the 15th day, and the seedlings survived until the 30th day. The LD50 value is based on 50% germination. The LD50 values were set at 35 mM for EMS, 30 mM for DES, and 25 mM for SA. The maximum seed germination value measured was 05 mM, while the minimum value was 50 mM. So, it was discovered that mutagens at lower doses caused less biological damage and may be useful for causing beneficial mutations in Sunnhemp.

Keywords: EMS, DES, and SA, LD50 value, Sunnhemp, seed germination, survivability.

Genetic Transformation in Mulberry (*Morus* sp.)

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Abstract

Mulberry (*Morus* sp.) a multipurpose agroforestry tree belongs to the family Moraceae. It has been exploited commercially in the sericulture industry as the foliage forms the chief food source of the silkworm *Bombyx mori* L. The trees are quite tolerant to drought, pollution, and poor soil. Being nutritious and palatable the leaves are said to increase milk yield in dairy animals. The fruits are a major ingredient of a particularly seductive drink known as mulberry wine and wood is valued for sporting goods. Conventional breeding of woody plants is slow and difficult due to high levels of heterozygosity and long generation cycles. This makes them an ideal target for gene transfer technologies that have the potential to hasten the production of new genotypes and broaden the available gene pool. Genetic transformation provides an alternative means for elucidating gene function and for making targeted single-trait improvements in clonally propagated plants. Two requirements for successful plant transformation are the ability to introduce desirable genes into the genome and the capacity to regenerate plants from the transformed cells. Genetic transformation is one of the attractive means of introducing desired traits to pre-existing genotypes within a short period. The availability of efficient transformation and different regeneration systems opens the way for transferring desirable genes against diseases and stresses into commercially important mulberry clones. The biotic assay with transgenic plants proved that these transgenic plants have no deleterious effect on silkworm rearing and feeding. Therefore, these improved mulberry plants can be used for rearing silkworms in the future. Furthermore, the application of some resistant genes, such as resistance to pests or adverse conditions in mulberry is necessary to realize the goal of improving mulberry quality efficiently by genetic transformation techniques. Hence, these resources are essential for the successful application

of the genetic transformation tools in mulberry to enhance its productivity and adaptability for sustaining a vibrant sericulture industry in India.

Keywords: Mulberry, Genetic transformation, transgenic plants, silkworm

Yielding and Red Rot-Resistant Sugarcane Variety CoC 25, Suitable for Early Season of Tamil Nadu

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Abstract:

Production and productivity of sugarcane are governed by varieties, seasons, and agronomic package of practices besides balanced nutrition. Among the components, varieties play a paramount role in sugar mills. Hence it is imperative to identify new sugarcane varieties to replace the deteriorating commercial varieties through which the overall productivity could be stabilized. Therefore, to meet the immediate needs of the sugarcane farming community and sugar factory, there is a need for more early maturing, high sugar varieties having high tonnage, and good ratooning ability to meet the challenges for improving sugar recovery and productivity. In this regard, the high-yielding and early-duration sugarcane variety CoC 25 was released by Tamil Nadu Agricultural University in 2017 for Tamil Nadu. The CoC 25 was evolved through hybridization and selection involving two high-yielding and high-quality parents of Co 85002 x HR 83-144 at Sugarcane Research Station, Cuddalore. This clone is characterized by thickness, and tall, and it is a good ratooner. It is a quick-growing cane with cylindrical internodes and round-shaped medium-sized buds. It matures in 300-330 days. It is moderately resistant to red rot disease and less susceptible to shoot borers. Performance of the proposed sugarcane clone C 260628 was tested in the station trials at Sugarcane Research Station, Cuddalore, different centers in advanced varietal trials under All India Coordinated Research Project on Sugarcane in East Coast Zone and different factory farms or farmers fields under Adaptive Research Trials in Tamil Nadu. Due to high and stable yield performance over locations of Tamil Nadu and Puducherry and moderate resistance to red rot disease, tolerance to shoot borers and drought, the early maturing sugarcane clone C 260628 was released as "Sugarcane CoC 25" by the State Variety Release Committee (SVRC) for commercial cultivation of Tamil Nadu and Puducherry.

Genome-wide association studies (GWAS) to identify novel genomic regions associated with leaf rust resistance in bread wheat (*Triticum aestivum* L.)

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Abstract

Leaf rust is one of the important diseases of wheat limiting production and productivity. To identify quantitative trait nucleotides (QTNs) or genomic regions associated with seedling and adult plant leaf rust resistance, multilocus genome-wide association studies (ML-GWAS) were performed on a panel of 400 diverse wheat genotypes using 35K single-nucleotide polymorphism (SNP) genotyping assays and phenotypic trait data of leaf rust resistance. Association analyses using six multi-locus GWAS models revealed a set of 201 significantly associated QTNs for seedlings and 65 QTNs for adult plant resistance (APR), explaining 1.98-31.72% of the phenotypic variation for leaf rust. Among these QTNs, 51 reliable QTNs for seedling and 15 QTNs for APR were consistently detected in at least two GWAS models and were considered reliable QTNs. Three genomic regions were pleiotropic, each controlling two to three pathotype-specific seedling resistances to leaf rust. We also identified candidate genes, such as leucine-rich repeat receptor-like (LRR) protein kinases, P-loop containing nucleoside triphosphate hydrolase, and serine-threonine/tyrosine-protein kinases (STPK), which have a role in pathogen recognition and disease resistance linked to the significantly associated genomic regions. The QTNs identified in this study can prove useful

in wheat molecular breeding programs aimed at enhancing resistance to leaf rust and developing next-generation leaf rust-resistant varieties.

Keywords: Leaf rust; seedling and adult plant resistance; quantitative trait nucleotides; ML-GWAS

Cowpea Speed Breeding using regulated growth chamber conditions

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Abstract:

Cowpea (Vigna unguiculata) is a vital crop for dryland farming and food security. It is widely consumed as a protein source and used as fodder for livestock. Cowpea breeding is utilizing advances in plant improvement technology such as marker-assisted selection and genome editing. However, traditional breeding methods are slow, producing only one generation per year due to the seasonal nature of cowpea cultivation. The speed breeding aims to develop and validate a speed breeding protocol for Cowpea, where it plays an important role in food security. Speed breeding is a technique used to accelerate breeding cycles and has been successfully applied to crops like wheat, soybean, and chickpea. The protocol is designed to facilitate multiple breeding generations per year, potentially accommodating up to eight generations. The protocol uses regulated growth chambers and seeds from oven-dried immature pods. Carbon dioxide supplementation was tested but no significant effect was shown. Key conditions such as temperature, light intensity, and humidity were optimized for plant growth, cross-pollination, and seed maturation. Using the optimized speed breeding technique, Cowpeas can be produced in seven to eight generations annually instead of the conventional one generation under field circumstances. Seeds of immature pods, when oven-dried at 39°C for two days reduced the time between pollination and the next sowing by 62%, without negatively affecting plant development. The speed breeding protocol developed is simple, cost-effective, and can be applied in any standard growth chamber, significantly accelerating cowpea breeding programs.

Keywords: Cowpea, Speed breeding, Carbon dioxide Supplementation, Regulated growth chambers

In vitro Evaluation of different plant extracts, micronutrients, and oil cake amendment for management of dry root rot of black gram caused by *Macrophomina phaseolina*

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Abstract:

The present study was planned to evaluate the efficacy of various plant extracts, micronutrients, and oil cake amendments against *Macrophomina phaseolina* causing dry root rot of black gram. The effectiveness of eight different plant extracts was evaluated by different concentrations. All the plant extracts reduced the growth of the fungus significantly at different concentrations. Among the eight plant extracts, the neem leaf extract showed maximum inhibition of mycelial growth (61.11 %) at 10% concentration followed by Prosopis leaf extract (46.67%) and notch (37.78%). However, calotropis (22.22%) and bougainvillea (25.56%) were found to be the least effective in inhibiting the growth of the fungus. Among micronutrients, zinc sulfate exhibited maximum inhibition (65.6%) followed by ammonium sulfate (50%). However, sodium silicate (17.8%) was found to be the least effective in inhibiting the growth of the fungus. All the oil cakes namely coconut, neem, gingelly, groundnut, cashew nut, and pungam tested at 5 and 10 percent concentration *in vitro* inhibited the mycelial growth of *M. phaseolina* under *in vitro* conditions. Neem cake extract was the most effective in reducing the mycelial growth of (66.67%) *M. phaseolina* at 10 percent concentration by recording as compared with control. Coconut oil cake extract also effectively inhibited the growth of the fungus at a 10 percent concentration by recording a 51.11 percent reduction. On the other hand, Pungam oil cake (22.22%) was found to be the least effective in inhibiting mycelial growth. The findings of our study may help in the development of sustainable management strategies against DRR thus minimizing its yield consequences in black gram. However, there is a need to further strengthen the investigations on this aspect based on a thorough understanding of the biology of the pathogen and host-plant-environment interaction especially under field conditions.

Keywords: Black gram, *Macrophomina phaseolina,* Plant extracts, Micronutrients, Oil cake amendment, Dry root rot (DRR)

Genome editing for engineering drought and salinity tolerance traits in crops using the CRISPR system

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Abstract

Extended periods of drought, brought about by climate change, hinder plant growth and lead to substantial annual agricultural losses. In addition to drought, salinity represents a significant abiotic stressor that severely impacts crop health and agricultural productivity. When plants encounter drought and salinity, they engage in a series of complex processes that unfold over time and space. These processes encompass stress detection, recognition, epigenetic adjustments, genetic transcription, post-transcriptional processing, translation, and post-translational modifications. As a result, the ability of plants to tolerate drought and salinity stress is determined by numerous genes and their interactions with the environment, rendering it a polygenic trait. An optimal approach to address these challenges involves the development of crop varieties that yield high outputs and possess enhanced stress resilience, complemented by advancements in agricultural techniques. Recently, genome-editing technologies, notably the Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) tools, have proven effective in uncovering how plants respond to drought and saline conditions, indicating the concurrent utilization of CRISPR-based genome editing tools and contemporary genomic-assisted breeding strategies is gaining momentum in uncovering the genetic factors that underlie complex traits for crop enhancement. Furthermore, it highlights recent advancements in CRISPR-based tools and their application in comprehending the intricate nature of plant adaptations to drought and salinity stress at multiple levels. Integrating CRISPR techniques with modern breeding approaches represents an ideal means of identifying the genetic elements governing plant stress responses and facilitating the incorporation of advantageous traits to cultivate stress-resistant crops.

Keywords: CRISPR-Cas, genome editing, drought and salinity stress, polygenic trait and trait introgression

Vein architecture modification in rice (*Oryza sativa*) crop improvement

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Abstract :

Rice (*Oryza sativa* L.) is a major source of energy than any other crops for the human population. Grain yield per hectare of rice needs to be increased against the negative effects of climate change. Rice is an inefficient photosynthesizing plant since it has C_3 mode and which is losing up to 25% of previously fixed carbon during photorespiration. If the temperature exceeds 30°C, the rate of photosynthetic efficiency of C_3 plants reduces by up to 40%, especially in rice. Also, the elevated CO_2 concentration limits the stomatal conductance in rice. Leaf veins are inevitable for physiological responses in the lamina. The reduced interveinal density (IVD), or high vein density (HVD), characteristic is thought to be one of the earliest steps in the evolution of C_4 photosynthesis. The leaf venation is tightly linked with photosynthesis since CO_2 enters the plant via the stomata during transpiration. The photosynthate is being transported away from the leaf via the phloem. The three-to-four-fold increase in vein density during early angiosperm evolution increased the photosynthetic capacity of the plant in the absence of C_4 traits. Thus, a good vascular network, optimal ratio of mesophyll (M) and bundle sheath (BS) cells along with close contact ensures the rapid exchange of photosynthates. The C_4 plants with reduced M: BS ratio which reduces the path length of photosynthesis and facilitates rapid intercellular diffusion of metabolites. Hence, modification of the C_3 cycle and its related traits are the finest way to increase the photosynthetic ability of rice as an alternative to the C_4 cycle introduction. Recently, researchers deciphered *OsWOX9A*, *SHR/SCR,* and *LVPA4* genes for vein architecture modifications in rice.

CRISPR-CAS system: Revolutionizing plant defence mechanism

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Abstract

Emerging targeted genome editing technologies are becoming vital in studying plant diseases. Following the identification of CRISPR in the adaptive immune systems of prokaryotes, this technology and its related proteins have been effectively utilized for genome modification. The CRISPR/Cas system functions *via* three key processes: adaptation, biogenesis, and target interference. This subject's remarkable efficiency, straightforwardness, and adaptability have garnered considerable attention from the scientific community. CRISPR/Cas has been applied to address plant diseases induced by bacterial pathogens such as *Pectobacterium* (responsible for soft rot), viral agents like TMV and CMV, and fungal threats like *Fusarium* (which leads to wilt). The CRISPR/Cas system has significantly improved tissue culture methods for the regeneration of plants. This review examines different CRISPR/Cas systems, their related tools, and their applications in studying plant diseases.

Keywords: CRISPR Cas, defense, *Fusarium*, *Tobacco mosaic virus,* and target interference

Developmental Advances in Sorghum (*Sorghum bicolor* L.) for Enhanced Nutritional Performance

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Abstract

Sorghum (*Sorghum bicolor* L.) is an incredibly versatile and resilient crop, primarily cultivated in semi-arid regions where its ability to thrive under challenging conditions makes it a vital source of food security. Recent advancements in sorghum breeding, genomics, and biotechnology have focused on enhancing agronomic traits and nutritional quality to address the challenges of climate change and malnutrition. Emphasis has been placed on increasing yield potential, improving drought and heat tolerance, and bolstering resistance to pests and diseases. The use of marker-assisted and genome-wide selection has significantly expedited the identification and incorporation of beneficial alleles for these traits. Additionally, efforts have been concentrated on enriching the nutritional value of sorghum, particularly its protein quality and micronutrient levels through biofortification, including iron, zinc, and provitamin A. Key genes, such as the kafirin genes (e.g., kafirin1), have been manipulated to improve protein digestibility and lysine content. For biofortification, Yellow Stripe-Like Transporter (YSL) genes, like YSL1 and YSL2, enhance iron and zinc accumulation, while Phytoene Synthase (PSY) genes boost provitamin A content. Molecular tools like CRISPR/Cas9 have enabled precise genetic modifications to optimize sorghum's physiological and biochemical pathways for improved adaptation and nutritional benefits. The advancements make it a crucial crop for sustainable agriculture, capable of contributing to global food security amidst environmental challenges. Ongoing research and innovation in sorghum development will be vital in meeting the demands of a rapidly changing world.

Keywords: Sorghum, Genomics, Nutritional quality, drought, heat, Resistance, Biofortification, Sustainable, Kafirin

CRISPR-Cas9 genome editing in *Oryza sativa*

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Abstract:

Rice, a global staple food, faces increasing demands for improved yields and grain quality. While traditional breeding has achieved high yields, it often compromises grain quality. The CRISPR-Cas9 genome editing system offers a powerful tool to address these challenges. CRISPR-Cas9 allows precise modifications to the rice genome, enabling the development of varieties with enhanced tolerance to biotic and abiotic stresses, herbicide resistance, and improved yield. The availability of the rice genome sequence and the development of CRISPR-Cas9 have significantly advanced our understanding of the genetic mechanisms underlying grain quality. This knowledge, coupled with the precision of CRISPR-Cas9, opens new avenues for developing rice varieties that meet both yield and quality standards, ensuring food security and consumer satisfaction and this research used CRISPR-Cas9 technology to create a new type of rice that is good for people with diabetes and kidney problems. The CRISPR Cas9 tool-based edits in the rice enhanced the tolerance to abiotic stresses such as drought (OsPUB7, OsERA1), salinity (OsRR22, OsDSG1), heat stress (OsRHS, PGL10), cold stress (OsPIN5b, GS3, OsMYB30, OsCS511) and biotic stresses such as rice blast (OsSULRT3, Osa-miR827, Bsr-d1) and bacterial blight (OsSWEET14, OsSWEET13, OsPUB9). This technology has been successfully applied to improve grain quality; a complex trait influenced by numerous genes. Researchers have utilized CRISPR-Cas9 to target genes responsible for various aspects of grain quality, including its size, shape, texture, and nutritional content. Editing of the gene SBEIIb modifies the starch structure in the rice endosperm. Mutation in SBEIIb resulted in the enhancement of RS (Resistant Starch) content in the rice endosperm which is important for reducing the glycemic index of the rice starch. Mutants with high yield and enhanced aroma by simultaneously editing three cytochrome P450 homologs (Os03g0603100, Os03g0568400, and GL3.2) and OsBADH2 using the CRISPR/Cas9 system. The mutants showed increased grain size, higher 2-acetyl-1-

pyrroline (2AP) content, and increased grain cell numbers, with no significant changes in other agronomic traits. Besides, editing in the OsNIP 3:1 gene reduced the Arsenic accumulation in the rice grain.

Improving Abiotic Stress Tolerance in Sorghum: Focus on the Nutrient Transporters and Marker-Assisted Breeding

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Abstract:

Sorghum is a vital cereal crop for food and energy security in semi-arid regions, particularly under the challenges posed by climate change and low-input agricultural systems in developing countries. This review highlights the necessity for improving sorghum's resilience to abiotic stresses such as drought, salinity, cold, and nutrient deficiencies (low phosphate and nitrogen) by application of marker-assisted breeding and nutrient transporters. We focus on the potential of marker-assisted breeding and the characterization of nutrient transporters to enhance sorghum's stress tolerance. Key nutrient transporter families, including nitrate (NRT), phosphate (PHT), and sulfate (SULTR) transporters, have been identified for their roles in mitigating low nutrient stress. Although several quantitative trait loci (QTL) have been linked to drought, salinity, and cold resistance, research into QTL and transporters for low nitrogen and phosphorus stresses remains limited. Furthermore, the application of marker-assisted techniques and nutrient transporter studies in addressing macro- and micro-nutrient stresses is still largely unexplored. As sorghum has a small genome size, this makes it a model species for genetic and genomic studies, to develop tolerant species. This review aims to emphasize the critical need for further research in these areas to bolster sorghum production, thereby supporting plant breeders and biotechnologists about the importance of sorghum and the need to conduct studies on marker-assisted breeding and nutrient transporters under low nutrient stresses to improve the sorghum production.

Keywords: Sorghum stress tolerances; Food security and energy security; Nutrients transporters; Marker-assisted breeding; Production.

Leveraging Tomato Genetic Diversity for Enhancing Abiotic Stress Tolerance

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Abstract

Tomato (*Solanum lycopersicum*) is a key crop with diverse applications in global agriculture and food industries. Its genetic diversity is essential for breeding programs aimed at improving resilience to biotic and abiotic stresses. Understanding this diversity is crucial for developing varieties with enhanced resistance to environmental challenges, such as cold and drought tolerance, which are increasingly significant in the context of climate change. One of the main breeding objectives of cold and drought tolerance, improving fruit quality and increasing yield stability under stress conditions. By assessing the genetic mechanisms underlying these traits, the study provides valuable resources for breeding programs. Through genotyping and phenotyping, key genes such as DREB1 and CBF have been identified as vital components in the cold tolerance response, while P5CS and NCED are highlighted for their roles in drought tolerance. These genes are involved in hormonal regulation, osmotic balance, and cellular stress response pathways, providing a strong foundation for developing stress-resistant varieties. Wild species like *Solanum pimpinellifolium* and *Solanum peruvianum*, have been integrated into breeding programs due to their natural resilience to abiotic stresses. These wild species offer untapped genetic diversity that enhances the potential to develop tomato cultivars with improved tolerance to environmental extremes. By leveraging the genetic diversity present in this germplasm collection, the study underscores the potential of breeding for stress tolerance to ensure sustainable production and food security. The incorporation of genetic resources from wild species and traditional landraces into modern breeding programs offers promising avenues for addressing the agricultural challenges posed by climate change.

Keywords: Genetic diversity, Abiotic stress resistance, drought tolerance, cold tolerance, germplasm collection, and sustainable agriculture.

Bioagents for Biotic Stress Management in Bush Pepper

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Abstract

Black pepper (*Piper nigrum* L.) is the most important and most widely used spice in the world. Lateral shoots of black pepper used as propagating material for pepper production grow like bush-like appearance called bush pepper. Nowadays, bush peppers are gaining much importance among farmers, since these plants do not need any supporting material for growing. The low productivity and crop loss due to pests and diseases have been identified as a major constraint in the production of bush pepper. The major disease identified in bush pepper is 'slow wilt' caused by root-knot nematode *Meloidogyne incognita* present in pepper growing parts of Tamil Nadu along with fungal disease. The present study was made for the management of nematode and fungal disease complex under field conditions bioagents was conducted in the existing popular black pepper variety 'Panniyur 1' at Horticultural Research Station, Pechiparai. *Pseudomonas fluorescens*, *Bacillus subtilis*, and *Trichoderma viridian* AM fungi are used for fungal disease complex management in bush pepper. The study revealed that all the bioagents were found to have the potential to increase significant plant growth and reduce the nematode population and disease incidence. The lowest percent wilt disease incidence (9%) was recorded in AM fungi followed by *B. subtilis* when compared to untreated control. The population of root-knot nematode *Meloidogyne incognita* in soil and roots was significantly lower in all biological agents treated bush peppers than in untreated control. The percent reduction in nematode population in the soil, egg mass/g, and adult female nematode/g was maximum in AM fungi with 67.73, 67.85.2, and 53.33 percent

respectively over untreated control. Maximum green pepper yield was recorded in Am fungi-treated plants compared to untreated control.

Keywords: bush pepper, biological agents, root-knot nematode, wilt disease

Ecofriendly Management of Nematode in Tuberose

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Abstract

Plant parasitic nematodes are one of the major limiting factors in the production of tuberose. Among the nematodes, root-knot nematode *Meloidogyne incognita* is important which causes 40 percent of yield loss. A field experiment for the management of root-knot nematode in tuberose was conducted during 2015-2016 at ADAC&RI, Trichy. Application of *Paecilomyceslilacinus, Pochoniachlamydosporia* (commercial formulation), marigold, and neem cake along with carbofuran 3G @ (33 kg/ha) as the standard check was taken up in a nematode sick field. Along with untreated control. Observation on several flowers/spikes, average weight of 10 flowers (g), spike length, and flower yield during the study period were recorded. At the time of termination of the experiment, the soil samples were collected from the tuberose field and processed in the laboratory for the final nematode population in the soil. Results showed that the application of *P. chlamydospores* (bulb treatment @1 kg/ha) effectively reduced the nematode population in soil (43.9 percent) compared with untreated control. Similarly, the lowest nematode gall index (1) was recorded in bulb and soil treated with *P.chlamydosporia*. Also, enhanced flower yield (43.3 percent) and spike length 62 cm (11.8 %) were recorded when compared to untreated control (54.7 cm). This study concluded that the application of *P. chlamydosporia* (bulb treatment @1 kg/ha) effectively controls the nematode population in soil and plant root systems.

Keywords: Tube rose, biological agent, *Pochoniachlamydosporia*, *Meloidogyne incognita*

Awareness Creation on Nutritional Security through Demo on Barnyard Millet ATL I Variety

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Abstract

To create awareness on Barnyard millet ATL I in Trichy since it is a healthy alternative to cereal grains like rice, and is a good source of vitamins, fiber, calcium, and phosphorus. At this juncture, Frontline demonstrations were conducted in Trichy dt on ATL I Barnyard millet variety at five locations, and 2 kg of variety was distributed to the farmer in Aryambatti village for raising in one acre. The treatment imposed was Seeds 2kg, 2000, Azophos, ZnSo4, and the **Yield obtained** 21.00 **(q/ha) which is** a 17% increase over the farmer practice and the BCR 1.55 whereas the Local variety yield was only 18.00 **(q/ha) and the BCR is** 1.45. It's for people with celiac disease or gluten intolerance. Here's some more information about barnyard millet: The soil type is Irrigated upland red sandy loam and the special features of the variety are Drought tolerant; non-lodging, long compact, cylindrical panicle. Resistant to stem and shoot borer. The Promotion of small millets with ICM practices is the sole objective to ensure nutritional security. This variety of barnyard millet has high levels of total phenols and flavonoids. Health benefits of Barnyard millet may help with diabetes, cardiovascular disease, obesity, skin problems, cancer, and celiac disease. , it's grown as a substitute crop when rice fails. Storage box away from moisture and heat, and consume it within six months of the manufacturing date. The farmer nourished well with the grain obtained and fed the stalk to the cattle.

KEYWORDS: Barnyard millet -Health benefits- nutritional security

Proteomics as a Tool for Bioactive Compound Identification in Vegetables

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Abstract

Proteomics, the comprehensive analysis of proteins, is becoming recognized as an essential method for discovering bioactive chemicals in plants. These molecules, including phytochemicals like flavonoids, alkaloids, and glucosinolates, are linked to many health advantages, *viz.,* antioxidant, anti-inflammatory, and anticancer effects. Conventional approaches for identifying these chemicals, like chromatography and mass spectrometry, possess inherent limits; yet, the progression of proteomic methodologies offers a more thorough comprehension of the protein profiles in vegetables. Research may examine post-translational modifications and protein-protein interactions critical for the synthesis and regulation of bioactive compounds using methods such as two-dimensional gel electrophoresis and mass spectrometry. Moreover, proteomics may elucidate the diversity of these chemicals across various vegetable species, cultivars, and growing circumstances, which is crucial for agricultural biotechnology and breeding initiatives focused on improving health-promoting attributes in crops. The advancement of proteomics in discovering bioactive chemicals offers a viable avenue for enhancing human health via nutrition. Future studies need to concentrate on the integration of proteomics with other omics technologies, including metabolomics and genomics, to get a comprehensive knowledge of the molecular pathways governing bioactive chemicals in vegetables. This interdisciplinary approach may facilitate the creation of functional foods and nutraceuticals with targeted health advantages, hence fostering a more health-conscious society. By using proteomics innovatively, we may harness the potential of vegetables as sources of bioactive substances that enhance health and prevent illnesses.

Key Words: *Proteomics, bioactive compounds, vegetables, phytochemicals, health benefits.*

Estimation of genetic variability in different f_2 crosses in blackgram for mungbean yellow mosaic virus.

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Abstract

Black gram is being cultivated in an area of 4.3lakh hectares with a production of 3.11 lakh tones and productivity of 723 kg/ha In Tamil Nadu. It is highly prone to Mungbean Yellow Mosaic Virus (MYMV) disease belonging to the genus *Begomovirus* which affects its production and productivity. Although there are many strategies for managing YMV disease like vector management, modifying cultural practices are not more effective. Therefore there is a need to develop resistant varieties as a better method of management. Seven advanced F_1 cultures (Viz., VBN8 x LBG652; Vamban3 x VNB8; Vamban3 x VBN6; MDU1 x VBN6; CO5 x Mash 1008; CO5 x Mash114; and CO5x VBN6) were raised during the summer season of 2019 to study the pattern of inheritance and segregation of disease resistant in Blackgram. Significant variation was observed for all the traits according to the observed mean. A wide range of variation was observed for plant height, number of pods per plant, and seed yield per ha. GCV was lower in VBN8 X LBG652 for Plant height (1.88%) and highest in MDU1 x VBN6 for several pods per plant (56.45%) showing a high genotypic influence in these traits. High heritability coupled with the genetic advance in days to 50% flowering and several pods stated the crosses followed the genetic inheritance of the traits. Vamban 3 x VNB 8 is observed with a wide range, high heritability, and genetic advance showed, this particular cross has more scope for exploring the variability for future breeding of work for Mung bean yellow mosaic virus resistance.

Groundnut BreedingAgainst Biotic and Abiotic Stress - Retrospect of Chances and Challenges

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Abstract

Groundnut (*Arachis hypogea* L.), is an important legume cash crop for tropical farmers and its seeds contain high amounts of edible oil (43–55%) and protein (25–28%). The average yield of groundnut per hectare in India is around 1300-1400 kg. India has the largest groundnut area of about 6 million hectares (24% of the world), producing about 8 million tonnes of pod accounting for only 20% of the world's groundnut production. China with around 18% area under groundnut contributes 39% of the world's production due to better drought and nutrient management practices. Anyhow, a combination of improved genotypes and best agronomic practices recorded more than 6000 kg/ ha. Biotic constraints like insect pests, diseases, and weeds tend to affect yield in groundnuts. The locally grown cultivars have only a poor yield potential and also lack resistance to diseases and insects. Aflatoxin production in groundnuts can affect pod development before harvest and also at post-harvest stages when harvested pods are not dried or stored properly. Under abiotic stress, drought or water deficiency in arid cultivation remains a major constraint for groundnut farming. The breeding programs in groundnuts follow an empirical approach to drought resistance breeding, largely based on kernel yield and traits of local adaptation, resulting in slow progress. Recent advances in the use of easily measurable surrogates for complex physiological traits associated with drought tolerance encouraged breeders to integrate these into their selection schemes.

Keywords: Breeding, Groundnut, Yield, Biotic and Abiotic Stress

Enhancing Rust Resistance in Indian Bread Wheat (*Triticum aestivum* L.) through Marker-Assisted Selection of Stem and Leaf Rust Resistance Gene (*Lr19/Sr25*)

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Abstract:

Wheat, one of the earliest cultivated crops, has served as a dietary staple food since ancient times. Its global demand continues to rise annually, driven by its high-yield potential. However, wheat is greatly affected by abiotic and biotic stresses, particularly fungal diseases like leaf and stem rust caused by *Puccinia triticina* and *Puccinia graminis* f. sp. *tritici* respectively, which can lead to yield losses of up to 100%. Genetic resistance is the most economical, reliable, and sustainable way to control rust diseases in wheat. In this study, the linked leaf and stem rust resistance gene *Lr19/Sr25* was introduced in the background of two Indian wheat cultivars, Lok-1 and WH147 through a marker-assisted backcross approach. The linked *SSR* marker, *Gb* (*Lr19/Sr25*) was used for foreground selection to select genotypes carrying the respective gene. The stable lines were selected at BC_2F_4 generation and subjected to phenotypic evaluation at both seedling and adult plant stages to assess their resistance to leaf and stem rust pathotypes. Compared to the recipient parent, the introgressed lines of Lok-1 and WH147 displayed significant resistance to leaf and stem rust, and their agronomic performance was as good as, or even marginally better than that of the recipient parent. This study sheds light on the use of marker-assisted selection (MAS) in shortening the breeding cycle, improving biotic stress resistance, and sustaining the yield potential of selected wheat varieties.

Keywords: Bread wheat, leaf rust, stem rust, molecular markers and MAS

"Investigating the OsGA2ox8 gene provides insights into its mechanisms for conferring osmotic stress tolerance in rice"

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Abstract

Osmotic stress is a big problem for rice farming. It can hurt both how much rice we grow & the quality of the rice, too. Gibberellin 2-oxidase plays an important role in breaking down gibberellin (GA). But, it's still a bit foggy how gibberellin 2-oxidase genes help plants handle stress from the environment. This study digs into how OsGA2ox8 rice can deal with stress. It looks closely at how it keeps gibberellin balanced & what this means for other plant responses. We used gene expression analysis, and transgenic methods, & looked at physical changes under osmotic stress. When OsGA2ox8 activity was increased, the transgenic rice plants exhibited improved tolerance to osmotic stress. They managed this by increasing levels of osmotic regulators & antioxidants. It's interesting to note that plants with higher OsGA2ox8 levels had shorter shoots and roots when they were seedlings. But when they reached the heading stage, there was no big difference in overall height. This might come from how OsGA2ox8 works together with OsGA20ox1. It hints at a complex feedback system in rice plants regarding GA production & breakdown.

Keywords: Osmotic stress tolerance, Gibberellin 2- oxidase gene

Small RNAs and their Roles in Plant Development

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Abstract

Small RNAs (sRNAs) are tiny RNAs of 20-30 nucleotides and guide regulatory processes at the DNA or RNA level in a wide range of eukaryotic organisms. Many, although not all, small RNAs are processed from double-stranded RNAs or single-stranded RNAs with local hairpin structures by RNase III enzymes and are loaded into argonaute-protein-containing effector complexes. Many eukaryotic organisms have evolved multiple members of RNase III and the argonaute family of proteins to accommodate different classes of small RNAs *viz.,* short interfering RNAs (siRNAs), microRNAs (miRNAs), small nuclear RNAs (snRNAs) and small nucleolar RNA (snoRNAs) with specialized molecular functions. Some sRNAs cause transcriptional gene silencing by guiding heterochromatin formation at homologous loci, whereas others lead to posttranscriptional gene silencing through mRNA degradation or translational inhibition. Small RNAs are not only made from and target foreign nucleic acids such as viruses and transgenes, but are also derived from endogenous loci and regulate a multitude of developmental and physiological processes. A multitude of sRNAs accumulate in plant tissues. Although heterogeneous in size, sequence, genomic distribution, biogenesis, and action, most of these molecules mediate repressive gene regulation through RNA silencing. Besides their roles in developmental patterning and maintenance of genome integrity, sRNAs are also integral components of plant responses to adverse environmental conditions, including biotic stress.

Keywords: RNA, Nucleotide, Enzyme, Transgene

Unveiling Genetic Resources for Higher Grain Protein Content in Rice

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Abstract:

Rice (*Oryza sativa* L.) is the sole crop among cereals containing a storage protein called "*Oryzenin*" which has more balanced amino-acid profiling when compared to the prolamin-rich storage protein. Approximately one-third of the global population is currently suffering from protein malnutrition. As rice is consumed in bulk quantities, enhancing the protein content in the grains, there is ample scope to enhance protein nutrition through rice consumption even for underprivileged populations. Keeping this line an experiment was conducted using 169 rice accessions, which included landraces, improved lines, and commercial varieties in three different environments *viz*., Paddy Breeding Station (PBS), Coimbatore; Regional Research Station (RRS), Paiyur and Tamil Nadu Rice Research Institute (TRRI), Aduthurain. The rice grains were threshed, cleaned, dehulled manually, and ground to a fine powder, and 0.5 to 1g of each sample was subjected to the NIR ZEUTEC spectra Analyzer^{TM} instrument. The study identified a few promising and stable genotypes with grain protein content exceeding 10% across all three locations, including IG74, *Gandhasala, Ponkambi samba, Purple puttu,* and *Burma kavuni*. Hence these genotypes could be used as a better source to meet nutritional security. In the subsequent phase of the study, six parent rice varieties were chosen based on the genetic distance and the stable genotypes identified from the G × E interaction for grain protein content. Further developed into subsequent generations (F_2) to determine the superior recombinants based on their grain protein content and yield. Bulked Segregant Analysis (BSA) performed for grain protein content in the F_2 population resulted in co-segregation of markers RM243 on chromosome 1, RM264 on chromosome 8, and RM420 on chromosome 7 between the parents and the high and low protein bulks. Further validation of the new marker RM420 in different genetic backgrounds showed that the marker has been significantly associated with grain protein

content. Thereby, the obtained information, the grain protein donor accessions, markers associated with traits, and breeding stocks will prove valuable in the upcoming rice breeding program with the target of enhancing the grain yield potential together with grain protein content, ultimately contributing to nutritional security in a breeding program.

lpa genes and phytic acid content in rice grains

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Abstract:

Rice (Oryza sativa L.) is the most important cereal crop and staple food of over half the world's population. 'Rice is life' for human beings, especially in the Asian subcontinent, where 90 percent of the world's rice is grown and consumed by 60 percent of the population and two-thirds of the world's poor live. Despite being a major cereal globally, rice grain is not the most suitable cereal grain for the poor and affluent in developing countries due to the less bioavailability of micronutrients due to phytic acid. Phytic acid, myo-inositol 1, 2, 3, 4, 5, 6 – hexakisphosphate (IP 6) is the major storage compound of phosphorous (P) in plants. In cereal, phytic acid typically represents about 75% of the P and inorganic P is about 5% of the total P of the seed. Since Phytic acid acts as a strong chelator of metal cations, it binds them to form phytate, a salt of InsP6, and drastically reduces the bioavailability of mineral cations viz., Zn2+, Cu2+, Mn2+, Ca2+, and Fe3+. Alleleic segregation analysis of mutants showed that the recessive allele lpa1-3 at the OsLpa1 locus (Os02g0819400) was responsible for a noteworthy reduction in seed phytic acid content. The SNP change C623T in the fourth exon of the lpa1-3 gene resulted in threonine (Thr) to isoleucine (Ile) amino acid substitution at position 208 (Thr208Ile). Hence, Thr208Ile substitution in lpa1-3 reduced Lpa1 enzyme activity, resulting in reduced PA biosynthesis. The reduction in phytic acid P in rice lpa1-1 led to a 5- to 10fold increase in grain inorganic P. Phytic acid P was also reduced by 45% in bran obtained from lpa1-1 grain, and this was complemented by a 10-fold increase in inorganic P. There was no effect on Zn concentration. These studies suggest that developing low-phytate rice might improve the nutritional quality of the whole grain, milled polished rice, and the bran produced during milling. Rice low phytic acid 1 (lpa1) mutant was identified using a forward genetics approach.

Molecular Breeding for Nutritionally Enriched Maize

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Abstract

Malnutrition affects millions worldwide, exacerbating poverty and hindering economic development in sub-Saharan Africa (SSA), Latin America, and the Caribbean. Plant breeding offers a sustainable solution to enhance micronutrient content in crops, ensuring nutritional security. Especially protein deficiency affects millions worldwide, particularly in developing regions. Plant breeding offers a viable solution to enhance protein content in crops, ensuring nutritional security. Maize is a major source of food security and economic development as it is among Asia's top three cereal crops. Yet, maize is deficient in certain essential amino acids, vitamins, and minerals. Biofortified maize cultivars enriched with vital minerals and vitamins could be particularly impactful in rural areas with limited access to diversified diets, dietary supplements, and fortified foods. Significant progress has been made in developing, testing, and deploying maize cultivars biofortified with quality protein maize (QPM), provitamin A, and kernel zinc. In this review, we outline the status and prospects of developing nutritionally enriched maize by successfully harnessing conventional and molecular marker-assisted breeding, highlighting the need for intensification of efforts to create greater impacts on malnutrition in maize-consuming populations, especially in low- and middle-income countries. Molecular marker-assisted selection methods are particularly useful for improving nutritional traits since conventional breeding methods are relatively constrained by the cost and throughput of nutritional trait phenotyping.

Keywords: biofortification, quality protein maize, provitamin A, kernel zinc, vitamin E

Effects of Mutagens on Various Traits in Mung bean (*Vigna radiata*)

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Abstract

Pulses play a vital role in global agriculture because of their high protein content, abundance of key amino acids, and capacity to fix atmospheric nitrogen. One of India's main pulse crops is green gram (Vigna radiata L. Wilczek), commonly referred to as mung beans. According to Grover (2011), it is India's third-most significant pulse crop. Its origin is South Asia. It is a member of the family Fabaceae and subfamily Papilionaceae. It is an inexpensive source of protein (24%) and carbohydrates (38–40%). Genetic diversity is one of the conditions for crop enhancement. A variety of biotic and abiotic factors influence mung bean grain production. Because of the minimal genetic variability, conventional breeding techniques do not contribute to increased productivity. Therefore, we can increase the yield by modifying the genetic composition and adding the stress resistance genes. The yield can be increased by enhancing the current genotypes through mutations and other cutting-edge breeding techniques. Mutation breeding has become more popular than traditional breeding because mung bean variability is minimal. Inducing the desired variability of genetics so appears to be best achieved by induced mutagenesis. Due to the extremely low frequency of natural mutations, mung bean genetic diversity is improved by inducing artificial mutations. The generation and restoration of biodiversity may be aided by induced mutations. Enhancing conventional crops like mung bean could be greatly aided by mutation breeding, especially induced mutation.

KEYWORDS

Mung bean, Variability, Mutations, Mutagens

Molecular Breeding for Nutritionally Enriched Maize

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Abstract

Maize is a crucial food source and driver of economic development in regions like sub-Saharan Africa, Latin America, and parts of Asia. However, it lacks some essential amino acids, vitamins, and minerals. Biofortified maize cultivars enriched with these nutrients can significantly benefit rural populations with limited access to diverse diets and supplements. This process aims to enhance the levels of essential nutrients such as vitamins, minerals, and proteins in maize to address malnutrition and improve human health. Recent advancements in developing quality protein maize (QPM), provitamin A, and kernel zinc have shown promise. Biofortification shows the current status and prospects of nutritionally enriched maize, emphasizing the importance of intensifying efforts to combat malnutrition, especially in low- and middle-income countries.

Researchers utilize molecular tools to identify and manipulate specific genes responsible for the synthesis of key nutrients in maize. Molecular marker-assisted selection is highlighted as an effective approach for improving nutritional traits, overcoming the limitations of traditional breeding methods, which often struggle with the high costs and challenges of phenotyping nutritional traits. Enhanced breeding strategies can lead to more impactful solutions for populations reliant on maize as a staple food.

Scientists can selectively breed maize varieties with higher levels of desired nutrients, by understanding the genetic basis of nutrient accumulation. For example, biofortified maize varieties can be developed to contain increased levels of vitamin A, iron, zinc, or essential amino acids. By harnessing the power of genetics and breeding, scientists can create maize varieties that not only provide essential macronutrients but also address specific micronutrient deficiencies prevalent in certain countries. This approach offers a sustainable solution to combat malnutrition and improve food security throughout the world.

Keywords: Biofortification, quality protein maize, provitamin A, kernel zinc, vitamin E.

Quality Protein Maize for Nutritional Food Security

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Abstract

Maize is a staple food for billions of people and its rich in dietary fibres and other nutrients. It is also used as feed for livestock. Malnutrition has emerged as one of the most serious health problems worldwide. A deficiency of essential micronutrients in the diet leads to abnormal growth and development in humans. Quality Protein Maize (QPM) is that ensures the nutritional security of maize-dependent communities. Maize protein has low nutritional significance to humans due to the reduced content of essential amino acids like lysine (0.52%) and tryptophan (0.13%). QPM is described as nutritionally superior maize with high lysine, tryptophan, and leucine contents along with high biological value and high protein intake. Opaque2 is a recessive gene used for improving quality protein in maize. The two genes responsible for grain hardness have been mapped in the long arm of chromosome 7 and the other is located near the gamma zein gene *gzr1*. The advanced molecular methods that accelerate the development of maize are Marker-Assisted Selection (MAS), CRISPR, and Genome Editing. The breeding programs are also focused on bio-fortification, which involves improving both micronutrient and protein content in maize. High-protein maize hybrids are being developed that aim to combine bio-fortification with enhanced protein content and quality.

Keywords: Protein, QPM, Opaque2, Zein, Marker-assisted selection, CRISPR

Decoding the Genomic Database of Ornamental Plants: Current Status & Prospects

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Abstract

The database integrated according to families/clade orientation places greater emphasis on the integration and unification of disparate plant data than the single species database does. After decades of development, the Genome Database for Rosaceae (GDR, https://www.rosaceae.org) was first established in 2003 and has since greatly increased data and functionality related to plant-plant interactions in the Rosaceae family. The Rosaceae Trait Ontology, which is closely related to the Plant Trait Ontology (TO), was created by the GDR team using the precise data on reported trait loci in Rosaceae that are contained in GDR. Apart from this, QTL in GDR also consists of published symbols, trait names, taxa, trait descriptions, screening techniques, map locations, linked markers, statistical values, datasets, contact details, and references. Curators additionally assign labels to QTLs. As of right now, 24 crops, including apricot, apple, and strawberry, as well as five ornamental plants - *Cerasus* × *yedoensis*, *Malus baccata*, *Rosa multiflora*, *Rosa chinensis*, and *Prunus persica*-have their genome assemblies and annotation data included in GDR. The genome information for Phalaenopsis Aphrodite and Dendrobium officinale is absent from OrchidBase. Two cultivars, "Tunisia" and "Dabenzi," are absent from the pomegranate genome according to the Hardwood Genomics Project. Numerous extensive plant databases have been created; the majority of the published plant genome data may be found in Phytozome, PGDD, PLAZA, and Ensembl plants, which are among the more representative ones. The genetic diversity and genomic structure of crops today have been significantly influenced by domestication and evolution. Understanding and identifying the wild ancestral species of ornamental plants, as well as figuring out when and where domestication occurred and whether it resulted from single or multiple domestication events, as well as comprehending the genetic underpinnings of the differences in morphological, physiological, and biochemical traits between ornamental plants and their ancestral species, can all be accomplished through a thorough investigation

and study of the genetic mechanism of crop domestication. Analyzing the reasons and changes in crop populations' genetic makeup about their ancestral species. A growing number of decorative plants now have their genome data thanks to recent advancements in genome sequencing technology, however, this still represents a small percentage of the resources available for ornamental plant germplasm. Modern ornamental plant researchers face many challenges, including the need to safeguard and use valuable genetic resources, sequence ornamental plants in an organized and acceptable manner, and do in-depth mining. Therefore, to reduce the bottleneck of current variety innovation and utilization, breeders must fully utilize genomic theories and methods (such as molecular markers, whole genome selection, genome editing, and synthetic biology), analyze the genetic regulation mechanism of significant ornamental characteristics, establish an effective biological breeding technology system, and carry out variety creation.

Keywords: Ornamental plants, genomics, QTLs, morphological, physiological and biochemical traits.

Marker-based Genetic Diversityof Rice Genotypes for Salinity Tolerance at Panicle Initiation Stage

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Abstract

The study was designed to evaluate salinity tolerance at the panicle initiation stage and characterize the genetic diversity in a set of rice genotypes with different adaptations to saline soil using microsatellite markers (SSR markers). In the evaluation for salinity tolerance, the landraces Nona okra and Pokkali showed high tolerance at 6 EC DSM^{-1}(Electrical Conductivity) levels. In the panicle initiation stage followed by FL 478 and CSR 36 with moderate tolerance. For diversity analysis, a total of 70 SSR primers across the 12 chromosomes were used. Of these, 34 were polymorphic among the selected genotypes. The diversity analysis grouped the 13 genotypes into six clusters. Cluster I consisted of three varieties *viz.,* ADT37, ADT 47, and TRY(R)3. Cluster II was the biggest cluster having six varieties viz., ADT42, ADT43, AD09225, FL478, CSR10, and CSR36. Cluster III consisted of a mono cluster of TNAU RiceADT49 and Cluster IV consisted of TRY(R)2. Cluster V consisted of a monocluster of Pokkali and cluster VI consisted of Nonabokra which is highly salt tolerant. The maximum similarity value was 0.828 and the minimum similarity value was 0.502. The genetic distance was ranged between 0.172 to 0.489. The lower genetic distance of 0.172 was observed between FL478 and AD09225, and the higher genetic distance was observed between Nona okra and ADT47 (0.489) followed by TRY(R) 2 and Pokkali. The Polymorphism information content ranged from 0.138 to 0.705. The highest PIC value was observed in RM493 (0.705) followed by RM 3412 (0.638) and RM 412(0.591). The lowest PIC value was observed in RM5933 (0.118), RM 240 (0.142), and RM 287 (0.138). Hence parental selection based on genetic diversity is highly essential to developing a good variety. In the future utilizing the highly genetically divergent parents of ADT(R) 47 and Nonabokra may help to develop high-yielding salt-tolerant varieties.

Keywords : Rice; Microsatellite markers; Cluster; Similarity value; Genetic distance

Strategies of Plant Breeding for Enhanced Nutritional Security

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Abstract:

Breeders began employing nutrient profiles, metabolites, genotypes, and omics technology to create desired genotypes as research evolved. It is common practice to transfer desired genes to the target genotype by both vertical and horizontal gene transfer. Crop breeding makes a significant contribution to improving human health, and the environment and secures nutrition. Plant breeding has been very successful and has delivered today's highly productive crop varieties, the rate of genetic improvement must double to meet the projected future demands. One of the major bottlenecks of plant breeding is the time it takes to develop an improved crop variety. Traditionally, it can take one or two decades because of the many steps of crossing, selection, and testing required. Therefore, plant breeders and researchers around the world are developing new technologies and approaches to help speed up the efficiency of crop breeding. On farms, the adoption of poor or suboptimal management practices results in a yield 'gap', where the potential of crop yields is not realized. This gap exists even in developed countries but is often largest in developing countries where machinery and other equipment and supplies, along with agronomy advice, are not readily available. Closing the yield gap is considered a challenging, yet high-priority, goal for enhancing productivity and global food security. Apart from traditional breeding, the progress in biotechnology and omics technologies has effectively recognized multiple potential genes for environmental and nutritional security. With the effective introduction of these genes into target crops, poverty, starvation, and environmental pollution have all been eradicated, and the ecosystem as a whole including human health. The strategies for improving nutritional security include Biofortification wherein breeding crops increase their levels of essential vitamins and minerals through biotechnological tools like marker-assisted selection by utilizing genetic markers for the quick identification of desirable traits for transfer. Further, introducing genes from other species to enhance nutrient content or stress tolerance as a part

of transgenic approaches and moving towards more precise techniques like CRISPR and Gene editing for the improvement of nutrient profiles. Moreover integrating breeding with practices that support ecosystem health, such as organic farming and conservation agriculture along with the factors that contribute to soil fertility and resilience, supports long-term agricultural sustainability. In conclusion, modern plant breeding, enhanced by biotechnology and omics technologies, is essential for addressing global challenges such as food security, nutritional deficiencies, and environmental sustainability. By accelerating the development of improved crop varieties and closing the yield gap, especially in developing countries, breeders can significantly contribute to human health and ecosystem resilience. Innovative strategies, including biofortification, genetic engineering, and sustainable farming practices are crucial for creating nutrient-rich crops and ensuring that diverse populations have access to essential food sources. Overall, the future of agricultural productivity and nutritional security relies on the integration of advanced breeding techniques and sustainable agricultural practices.

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Antifungal Potential of Macroalgae and their Effective Strategies for Twister Blight (*Colletotrichum gloeosporioides*) of Onion Management and Plant Growth Enhancement

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Abstract:

Seaweed extracts from *Sargassum cristaefolium* and *Kappaphycusalvarezii* at 10% concentrations, effectively inhibited the mycelial growth of *Colletotrichum gloeosporioides*. GC-MS analysis identified various compounds in these extracts with antifungal, antibacterial, and antioxidant properties. In both pot culture experiments and field conditions, where seaweed extracts were applied as bulb treatment, soil drench, and foliar spray, a significant reduction in twister blight disease incidence was observed. Among the treatments, Treatment three, involving bulb treatment with *Sargassum cristaefolium* at a 10% concentration, soil drench with the same seaweed at a 10% concentration, and foliar application of *Sargassum cristaefolium* at a 10% concentration, demonstrated a remarkable 69.39% reduction in twister blight, showcasing efficacy comparable to biocontrol agents and chemical fungicides. In pot culture conditions, enhanced activities of peroxidase, polyphenol oxidase, and phenylalanine ammonia-lyase were noted, indicating a role in boosting disease resistance. Histopathological examinations further revealed reduced tissue damage in treated plants. The positive impact of seaweed extracts extended to various plant growth parameters, including increased plant height, bulb weight, bulb diameter, and the number of bulbs per plant. Additionally, protein content in both leaves and bulbs exhibited an increase in treated plants. This comprehensive study not only underscores the potential of seaweed extracts as effective bio-stimulants for disease management but also highlights their positive influence on overall plant health and productivity.

Keywords: Defense mechanism, GCMS analysis, Histopathology, Onion twister blight and Seaweeds

Genetic Improvement for Fruit Trees through DNA Isolation Protocols

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Abstract

Fruit trees such as *Emblica officinalis, Aegle marmelos, Ziziphus mauritiana, Buchanania lanzan, and Carissa grandiflora* are highly adaptable to arid, semiarid India and play a vital role in the rural economy with the dual benefit of fruits as food and nutritional security of the country. The availability of quality planting materials with the ability to bear the present climate variability is a major hurdle towards their integration under different agroforestry systems. Analysis of DNA is an influential tool for the genetic improvement of long-rotation tree species. To hasten the selection of high-yield and climate resilience genotypes/varieties, many of the modern PCR techniques can be applied with a prerequisite of quality genomic DNA. Isolation of high-quality DNA from these trees needs standard protocols due to the presence of high levels of polysaccharides, polyphenols, tannins, etc., which interfere with the extraction and purification of DNA. To standardize the species-specific DNA isolation protocols, experiments were conducted at Tree Improvement Laboratory, National Research Centre for Agroforestry, Jhansi in 2013 by the three DNA isolation methods *viz.,* CTAB method, modified CTAB method, and

SDS method. The yield and purity of genomic DNA were checked by the absorbance ratios at 260nm and 280nm respectively by using the Thermo Scientific NanoDrop™ 1000 Spectrophotometer. To know the extent of shearing of the genomic DNA, the quality was estimated by agarose gel electrophoresis. In this study, the DNA concentration and quality for *Emblica officinalis* were as high as 1074 ng/µl under the Modified CTAB method whereas the lowest 110 ng/µl concentration was observed in the CTAB method. In the case of *Aegle marmelos, Buchanania lanzan,* and *Carissa grandiflora* DNA concentration and quality were recorded as high as 508 ng/µl, 1106.6 ng/µl, and 474 ng/µl respectively under the CTAB method. The SDS method was more suitable for *Ziziphus mauritiana* due to the higher DNA concentration (1159.6 ng/µl) and purity ratio of 1.6 (A260/A280). These standardized species-specific DNA isolation protocols are recommended to exploit further the productivity augmentation of the species by molecular approaches, biotic and abiotic stress resistance selection/breeding, etc.

Keywords: DNA isolation, purity, protocol, molecular analysis, and genetic improvement.

Chemical characterization of Leaf dye of Axle wood

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Abstract:

Anogeissus latifolia (DC.) is a medium-sized deciduous tree belonging to the family Combretaceae and it is commonly known as Tahiti. It attains a height of about 30-40 feet. The present study was undertaken to investigate the standardization of the dye extraction procedure from *Anogeissus latifolia* leaves. Pigment from leaves, fruits, seeds, wood, and roots was used as dyestuff for textiles and as paint in art and craft. Natural dyes are environmentally friendly, hygienic, user friendly, and more permanent than other colorants. The replacement of natural dyes could happen until the introduction of synthetic dyes due to the feasible coloring properties of natural dyes the materials used and the methods followed in different experiments concerned with the study are furnished. *Anogeissus latifolia* leaves were collected from Nilgiris and Anamalais, Studies were conducted with variables like Temperature (70◦C, 80◦C, 90 ◦C, 100◦C,), Ratio (1:3,1:5,1:7 w/v), pH (3.2± 0.2 to 4.1± 0.2), Duration of soaking (1,2 and 3 days), Between the two sources leaves collected from Nilgiris shows higher dye content on 3rd day of soaking at 80◦C Temperature, Ratio 1:5, pH value is 3.5± 0.3, Absorbance value is 1.985± 0.02, Transmittance value is 1.062, leaves collected

from Anamalais shows higher dye content on 2nd day of soaking at 90◦C Temperature, Ratio 1:3, pH value is 3.3±0.3, Absorbance value is 1.976± 0.01, Transmittance value is 1.058, Hence Dye content on Nilgiris shows higher than Anamalais sample.

Keywords: *Anogeissus latifolia,* Nilgiris, Anamalais, Temperature

Marker-Assisted Selection of Leaf and Stem Rust Resistance Genes (*Sr24/Lr24*) In Bread Wheat (*Triticum Aestivum* L.)

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Abstract

Bread wheat (*Triticum aestivum* L.), is one of the most widely consumed food grains. The requirement for wheat is predicted to increase by 60% by the year 2050, with the demand growing at a rate of 1.6% per year. Same time, the production of wheat is constantly challenged by various biotic and abiotic factors. Among the biotic factors, fungal disease, leaf (caused by *Puccinia triticina*), and stem rust (caused by *Puccinia graminis*) create a significant threat, leading to substantial yield losses even up to 100%. Selection of two or more genes in a single genotype can be difficult using a conventional selection system. Under these circumstances, phenotype-neutral selection through marker-trait association becomes essential. Through marker-assisted backcross breeding, the linked leaf and stem rust resistance gene *Sr24/Lr24* was introduced into the recipient parent's viz., Lok-1 and WH147. Advanced lines (BC_3F_5) were phenotyped at the seedling and adult plant stages to assess their resistance to predominant leaf and stem rust pathotypes. The presence of the rust resistance genes was further carried out using molecular marker *Sr24#12* (*Sr24/Lr24*) in the backcross derivatives. The incorporation of *Sr24/Lr24* genes has markedly strengthened the resistance of wheat lines to leaf and stem rust, leading to greater yield stability.

Keywords: MAS, stem rust, leaf rust, markers

A Nutrient-Rich Green Gram Culture Suitable for Sustainable Nutrient Security

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Abstract

Green gram also known as mungbean or moong is widely used in Indian cuisines and no meal is complete without the addition of days. Green gram dal is touted as a superfood as it is one of the richest sources of plant-based protein in the world. It is widely grown in Southeast Asia, the Indian subcontinent, and East Asia. In India, it has been cultivated since ancient times and it is the largest producer of this legume. It is imbued with essential amino acids including phenylalanine, leucine, isoleucine, valine, lysine, and arginine. It helps to meet daily protein needs without increasing fat intake. Furthermore, it also contains profuse amounts of essential nutrients like manganese, magnesium, potassium, copper, phosphorus, zinc, and vitamins B1, B2, B3, B5 and B6. Whole mung beans are taken as sprouts and it is observed that sprouting changes the nutritional composition. Sprouted green beans are low on calories, and contain notable amounts of amino acids and antioxidants than normal ones. It is endowed with a rich array of antioxidants like phenolic acid, flavonoids, caffeic acid, and cinnamic acid. Moreover, sprouting green beans reduces the levels of phytic acid, which is an antinutrient that lowers the absorption of minerals like zinc, magnesium, and calcium. With the view of the above, the green gram culture VGG 18-002 was developed from the cross between EC 496839 × IPM 409-4. It is an early maturing (65-70 days) bold seed (5.5 to 6.0 grams). Sprouted seeds of the culture produce a higher quantity of Vitamin C (18.17 mg/100g sprouted grains) than the check variety CO 7 (12.25 (mg/100g). The culture gives an average yield of 900 kg/ha in 132 locations, which is a 13.9, 16.4, and 14.8 *percent* increased yield over the check varieties CO8 (790 kg/ha) CO7 (773 kg/ha) and VBN 4 (784 kg/ha) respectively. The special features of this culture are high yielding (900kg/ha – average yield; 1754kg/ha – potential yield), early duration, bold seeds, synchronized maturity, amenable for single harvest, non-shattering, and suitable for snacks, savories, and value addition. It is

moderately resistant to the Mungbean Yellow Mosaic Virus (MYMV), powdery mildew, and Urdbean Leaf Crinkle Virus diseases.

Keywords: green gram, high yield, bold seed, sprouted grain, high nutrient, value addition.

Crispr/Cas9-Mediated Gene Editing to Confer Turnip Mosaic Virus (Tumv) Resistance in Chinese Cabbage (Brassica Rapa)

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Abstract

Genome editing approaches, particularly the CRISPR/Cas9 technology, are becoming state-of-the-art for trait development in numerous breeding programs. Significant advances in improving plant traits are enabled by this influential tool, especially for disease resistance, compared to traditional breeding. One of the potyviruses, the turnip mosaic virus (TuMV), is the most widespread and damaging virus that infects Brassica spp. Worldwide. We generated the targeted mutation at the eIF (iso)4E gene in the TuMV-susceptible cultivar "Seoul" using CRISPR/Cas9 to develop TuMV-resistant Chinese cabbage. We detected several heritable indel mutations in the edited T0 plants and developed T1 through generational progression. It was indicated in the sequence analysis of the eIF(iso)4E-edited T1 plants that the mutations were transferred to succeeding generations. These edited T1 plants conferred resistance to TuMV. It was shown with ELISA analysis the lack of accumulation of viral particles. Furthermore, we found a strong negative correlation ($r = -0.938$) between TuMV resistance and the genome editing frequency of eIF(iso)4E. Consequently, it was revealed in this study that the CRISPR/Cas9 technique can expedite the breeding process to improve traits in Chinese cabbage plants.

Keywords

CRISPR/Cas9, turnip mosaic virus, disease resistance, breeding, genome editing, Chinese cabbage.

Improvement of ornamental Crops through CRISPR Genome Editing Technology

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Abstract:

The clustered regularly interspaced short palindromic repeats (CRISPR)/CRISPR-associated protein (Cas) system has recently emerged as a powerful genome-editing tool for accurately changing DNA sequences at specific locations. Nowadays, the floriculture industry needs additional and more cultivars with superior characteristics such as flowering promotion, both by increasing the number of flowers and changing flowering time, floral longevity, color spectrum, aromas, and creation of innovation in flower structure. CRISPR/Cas9 gene editing provides excellent means of genetically improving floricultural crops including improvement in flowering traits such as color modification, prolonging the shelf life of flowers, flower initiation, and development, and changes in the color of ornamental foliage by genome editing. It has been successfully employed to create gene knockouts in ornamental plants to induce genetic alterations in *Petunia inflate, Petunia hybrid, Chrysanthemum morifolium, Dendrobium officinale, Torenia, Ipomoea, Lilium longiflorum and Lilium pumilum, and Phalaenopsis equestris*. Commercialization of genetically engineered ornamentals is subject to many legal concerns worldwide very much like other GM crops. However, GE using CRISPR/Cas9 will lead to transgene-free non-GM ornamental plants which may be more easily acceptable for commercialization than GM ornamentals ectopically expressing genes.

Keywords: CRISPR, Ornamental crops, flower traits, Gene expression, genetic improvement

CRISPR-Cas9 Genome Editing in Crop Breeding for Climate Change Resilience

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Abstract:

Abiotic stresses such as drought, high temperature, cold, salinity, and soils with heavy metals are challenging factors that are reducing agricultural production. To mitigate the risks of environmental changes, traditional and molecular breeding approaches are used in crop improvement programs. The duration of the crop breeding program is longer while using the traditional breeding approaches. The CRISPR Cas9 tool in crop improvement programs is highly useful in the development of new traits in the crop through targeted gene editing protocols. The gene *SIMAPK3* regulates the heat stress tolerance mechanism negatively and editing of these genes conferred increased heat sensitivity in the mutant when compared to the wild. Also, it was observed that this gene regulated the HSPs and HSF genes in tomato crops. In rice, *OsCNGC14* and *OsCNGC16* gene editing improved the heat tolerance with altered expression of HSPs and HSF genes. Generation of mutant alleles in the *drought and salt tolerance* (*DST*) gene using CRISPR-Cas9 in *indica* rice cv. MTU1010 caused the formation of broader leaf width with less number of stomata which caused enhanced water retention. Besides, the functional mutation in the *DST* gene caused the downregulation of stomatal developmental genes *SPCH1*, *MUTE,* and *ICE1*. Also, *dst* mutants showed moderate levels of tolerance to osmotic stress and high levels of salt stress in the seedling stage in MTU1010 rice. CRISPR Cas9-induced mutations in *OsPYL9* conferred drought tolerance in rice through increasing enzymatic activities, wax accumulation, and upregulating proteins related to abiotic stress, circadian rhythm, and ROS activities. The creation of allelic forms in *OsRR22* through the CRISPR Cas9 tool improved salt tolerance without affecting agronomic traits. Hence, the CRISPR Cas9 tool is currently generating novel allelic forms in the genes in a targeted manner in the crop plants for the development of climate resilience genotypes to manage unpredictable climate change and its adverse effect on crop production.

Genomic Editing in Rice

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ABSTRACT

Plant breeding has been transformed by genome editing technologies, especially CRISPR/Cas9. These technologies allow for precise adjustments to be made to the genomes of crops. Using genome editing to improve rice (Oryza sativa), a staple meal for more than half of the world's population, has the potential to significantly increase yield, disease resistance, and environmental adaptability. This study examines the developments in rice genome editing applications, emphasizing effective changes meant to enhance nutritional quality and agronomic characteristics. We also go over the regulatory environment and public attitudes on genetically modified crops, highlighting the importance of open communication in promoting acceptance. Future directions in rice genome editing are also discussed, such as the application of multi-omics techniques and the possibility of gene stacking to create climate-resilient rice variants.

Advances in Integrating Rice Disease Resistance and Breeding for Sustainable Production

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Abstract

Rice, one of the world's most important staple crops, faces severe threats from various diseases. The development of rice varieties that are resistant to diseases like rice blast, bacterial blight, and sheath blight is crucial for protecting global rice production from the harmful effects of these pathogens. Integrating plant pathology with advanced breeding techniques has opened new pathways to developing rice varieties that can withstand evolving diseases. Traditional breeding methods have been enhanced through molecular approaches, such as marker-assisted selection (MAS), which has significantly accelerated the incorporation of disease-resistance genes, especially against rice blasts. Novel genetic insights into pathogen-host interactions have further facilitated the precise introduction of resistance genes from wild relatives into elite rice cultivars. Moreover, CRISPR/Cas9 and other gene-editing tools offer unprecedented control over the genetic architecture of rice, providing breeders with the ability to target specific disease-resistance genes and rapidly deploy them into rice varieties. This interdisciplinary approach, integrating advanced breeding strategies with an in-depth understanding of rice disease dynamics, is critical for achieving long-lasting resistance. Ultimately, these efforts contribute to safeguarding rice yields and ensuring global food security in the face of climate change and the emergence of new pathogen strains.

Keywords: Rice disease, resistance breeding, molecular approaches, rice blast, bacterial blight

Marker-assisted Selection for Gall Midge Stress Tolerance in Rice

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Abstract

Rice has a special importance in Asia, where about 80 % of the rice is produced and consumed as a stable food. Considering the increasing demand, because of population increase on the one hand and decreasing land and water resources available for rice cultivation. Hybrid rice is a fast-growing technology in India that holds the promise of breaking the yield plateau to food for the ever-growing population. The present study was carried out to improve CO 43 a popular variety of Tamil Nadu for GM resistance through marker-assisted backcross breeding. A set of genes *Gm1* and *Gm4* for gall midge resistance were used for this study. A total of 136 plants in the BC_3F_4 generation were genotyped with SSR markers RM1328, and RM22550, for the genes *Gm1, and Gm4,* respectively. Gall midge screening was conducted in the field condition. The lines selected for gall midge resistance genes recorded a higher level of resistance than the recurrent parent CO43.

Keywords: Rice, Marker-assisted selection, Gall Midge, SSR marker

Current Trends and Advancements in Next-Generation Sequencing Technology

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Abstract

Next-generation sequencing (NGS) has revolutionized genomics, expanding our knowledge of genome structure, function, and dynamics. This groundbreaking technology has enabled extensive research and allowed scientists to explore the complexities of genetic information in unprecedented ways. With its high-throughput capacity and cost-effectiveness, NGS has become a fundamental tool for researchers across diverse disciplines, from basic biology to clinical diagnostics. The advent of next-generation sequencing (NGS) has brought about a paradigm shift in genomics research, offering unparalleled capabilities for analyzing DNA and RNA molecules in a high-throughput and cost-effective manner. This transformative technology has swiftly propelled genomics advancements across diverse domains. NGS allows for the rapid sequencing of millions of DNA fragments simultaneously, providing comprehensive insights into genome structure, genetic variations, gene expression profiles, and epigenetic modifications. The versatility of NGS platforms has expanded the scope of genomics research, facilitating studies on rare genetic diseases, cancer genomics, microbiome analysis, infectious diseases, and population genetics. Moreover, NGS has enabled the development of targeted therapies, precision medicine approaches, and improved diagnostic methods. This review provides an insightful overview of the current trends and recent advancements in NGS technology, highlighting its potential impact on diverse areas of genomic research. Moreover, the review delves into the challenges encountered and future directions of NGS technology, including endeavors to enhance the accuracy and sensitivity of sequencing data, the development of novel algorithms for data analysis, and the pursuit of more efficient, scalable, and cost-effective solutions that lie ahead.

Keywords: next-generation sequencing, genomics, microbiome, molecular diagnostics, bioinformatics, Nanopore, PacBio, Illumina, pyrosequencing.

Seed Development and Maturation Studies in Pigeon Pea

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ABSTRACT

Seed maturation is a genetically controlled process that comprises a series of morphological and physiological changes that range from fertilization to absolute independence from the mother plant. Pigeonpea is an important legume crop that meets greater demand. Hence, this study was carried out to determine the physiological maturity of pigeonpea with good emergence (%). The crop was raised and seeds were harvested from 18 DAA to 35 DAA and evaluated for different parameters. The results revealed that even immature seeds harvested 24 DAA emerged with 90%. Higher emergence was recorded in seeds harvested at 29 DAA. Maximum parameters were increased up to 29 DAA and thereafter there was a decline.

Keywords: Redgram, seed development, maturation, germination.

Detoxification of Cassava using CRISPR/Cas9 – A Review

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ABSTRACT

Cassava (Manihot esculenta) is a starchy tuber root crop that is a staple food of Africa. This plant produces cyanogenic glucosides like Linamarin and Lotaustralin. The first and limiting step of cyanogen biosynthesis in cassava is catalyzed by the enzymes CYP79D1 and CYP79D2, which are derived from valine and isoleucine, respectively, and are synthesized in the leaves and shoot tips before being transported to the storage roots. By deleting the CYP79D genes through CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats)-Cas9 (CRISPR-associated protein 9) mutagenesis, cassava cyanogenesis can be avoided. It precisely cuts the target DNA using the Cas9 protein and a guide RNA (sgRNA). It enables faster genetic modification than other methods due to its ease of use, effectiveness, affordability, and ability to target multiple genes.

Keywords: CRISPR, Linamarin, Lotaustralin, cyanogenesis

Zinc Finger Nuclease -A Review

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ABSTRACT

Genome editing allows a researcher to precisely modify plant DNA and introduce new traits to improve crop yields. Zinc finger nucleases (ZFN) are artificially made proteins that can be used to edit genomes by making Double-stranded breaks (DSB) in DNA. It consists of a chimeric programmable nuclease containing a DNA-binding zinc finger domain and a nonspecific FOKI endonuclease domain. ZNF is applied in fields where targeted genome editing is needed, by generating double-stranded nick on target DNA to create an indel for disrupting the gene function. The binding of those ZFNs with the target DNA gives rise to dimerization and DNA breaking to remove the functions of genes, creating gene knockouts. Due to the requirement for the joining of two proteins which brings about dimerization, the ZFN method has more specificity to the target sequence.

Keywords: genome editing, ZFNs, FokI, gene knockout, new traits

Induction of Salinity Tolerance Using Bio-Chips

(Integrating Genomics with Stress Tolerance)

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ABSTRACT

Salinity is one of the detrimental abiotic stresses that lower the productivity and quality of crops. As India shares a coastline boundary of more than 7500 km, salinity would be a common problem in many regions. The salt stress causes alterations in osmotic potential and ionic toxicity. The Salt Overlay Synthesis pathway is a major signaling pathway for salt stress and protects the plants. The SOS pathway has three components viz., SOS-1, SOS-2, and SOS-3 that act as signaling components. DNA chip technology can be used to activate this pathway. DNA chip/Bio-chip/DNA microarray technology in genomics is used to study the extent to which certain genes are turned on and off in the cells. This technology can detect mutation in the gene. The microarray is prepared by hybridizing the cDNA probes. Bio-chip technology is easier than the DNA sequencing protocols. Parallelism, miniaturization, speed, automation, and multiplexing are the characteristics of DNA chips. Sensing genes, signaling genes, regulatory genes, and functional genes responsible for various salinity tolerance mechanisms can be activated and regulated by this technology. At the molecular level, ionic toxicity (Na+, K+) can be detected using this novel approach. Bio-chips have wide applications in gene expression profiling, drug discovery, etc., Yet, DNA chip technology is more expensive and complex. Perhaps, integrating the genomics approach with stress response would enhance the tolerance mechanisms and build resilience in crop production.

Keywords: DNA chip, microarray, osmotic potential, cDNA probe, SOS pathway, ionic toxicity, salinity tolerance

Biofortified Nutri-Cereals for Ensuring Nutritional Security

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ABSTRACT

Millets, also known as Nutri-cereals are a group of small-grained cereals that are highly tolerant to drought and other extreme weather conditions. To address societal lacuna like malnutrition, imbalanced nutrition, and hidden hunger, Scientists have developed a new-fangled approach to 'Biofortification'. Biofortification is the process of adding nutritional value to the crop. The bioavailability of nutrients can be increased by eliminating the anti-nutritional factors such as trypsin inhibitors, and HCN content etc., this can be achieved by conventional breeding methods or through genetic engineering techniques. The conventional breeding approach allows the crossing of varieties over the years, for countable generations to get a plant with desirable nutritive traits and improved yield. Which, conventional breeding is widely followed in India. Indian Council of Agricultural Research (ICAR) has released biofortified millet varieties. It can be obtained using advanced breeding lines and by Marker Assisted Selection. The pure line varieties in Finger millet CFMV-1 are rich in iron and calcium. CLMV-1 is the iron and zinc-fortified little millet variety released. Hybridization technique is used in developing zinc and iron biofortified Pearl millet. On the other hand, genetic variation among the varieties remains minimal and the initial cost of biofortification is hefty. The addition of micronutrients is very limited, even after biofortification. With proper genetic enhancements, the bioavailability of desired nutrients can be increased manifold. This novel method can be employed to enhance the nutritive traits in minor and underutilized millets, to encounter food and nutrition insecurity.

Keywords: Biofortification, nutraceutical properties, hidden hunger, anti-nutritional factors, genetic enhancements.

Marker Assisted Selection –A Smart Biotechnological Strategy for Modern Plant Breeding - Review

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Abstract:

Molecular marker-assisted selection, or MAS, is a helpful method used by geneticists and plant breeders to quicken the breeding cycle and increase the efficiency of selection. Phenotypic selection may not always be as efficient, effective, or trustworthy as MAS. Molecular markers are helpful in quickly identifying the economically significant features in the breeding population for further manipulation. Improved responses from selection are possible with marker-assisted selection since markers can be applied at the seedling stage, guaranteeing great precision at a lower cost. Selection moves more quickly use of DNA-level polymorphism. Microsatellite markers, SSR (Simple Sequence Repeats) markers, and RFLP (Restriction Fragment Length Polymorphism) markers are examples of dominant markers that are mostly used.

Breeding Transgenic Rice for Plant-Based Milk: A Substitute for Breastmilk

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Abstract

Globally, only 48% of infants under six months of age are exclusively breastfed. Breastmilk is the perfect source of nutrients for a baby and offers protection against infections, allergies, diseases, and Sudden Infant Death Syndrome (SIDS). Breastfeeding is crucial during the first six months of life, during which pneumonia and diarrhea, the major causes of infant mortality, can be prevented. Also, sufficient breastfeeding can reduce the risks of breast and ovarian cancer in mothers.

However, a huge proportion of newborns receive supplementary foods early, which is influenced by various factors. This is a cause for concern.

Protein Hydrolyzation in rice is a process of glutelin extraction and alkaline hydrolyzation that increases the functionality of the formulation. Two transgenic High Free Lysine (HFL) lines of rice containing approximately 25 times higher lysine content are self-bred to obtain rice with increased serotonin biosynthesis. This fortified crop can be used in producing rice hydrolysate formulations, which are important substitutes to breastmilk for infants with cow's milk allergy. Globally 595,379 deaths in childhood are attributed to not breastfeeding annually. This is primarily due to the failure of alternative nutrition sources to supply the necessary nutrients critical to the infants' growth. Thus, the development of fortified plant-based milk that is rich in proteins and easily digestible is the need of the hour.

Keywords: SIDS, High Free Lysine, biosynthesis, rice hydrolysate, breastmilk

Improvements using CRISPR/Cas Genome Editing in Tomato

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ABSTRACT

Tomatoes have a limited genetic base, which makes breeding extremely difficult. Thus, quick and effective tomato breeding is now feasible thanks to the development of clustered regularly interspaced short palindromic repeat (CRISPR)-associated protein9 (CRISPR/Cas9) genome editing. CRISPR/Cas9 has been used to edit and functionally characterize a wide range of tomato traits, including plant architecture and flower characters (e.g., leaf, stem, flower, male sterility, fruit, parthenocarpy), fruit ripening, quality, and nutrition (e.g., lycopene, carotenoid, GABA, TSS, anthocyanin, shelf-life), disease resistance (e.g., TYLCV, powdery mildew, late blight), abiotic stress tolerance (e.g., heat, drought, salinity), C-N metabolism, and herbicide resistance. It has been demonstrated that CRISPR/Cas9 may introduce de novo domestication of elite features from wild relatives to cultivated tomatoes and vice versa. Advances in CRISPR/Cas enable the use of online tools for single guide RNA design and multiplexing, cloning (e.g., Golden Gate cloning, GoldenBraid, and BioBrick technology), sturdy CRISPR/Cas constructs, effective transformation protocols like Agrobacterium, and DNA-free protoplast method for Cas9-gRNAs ribonucleoproteins (RNPs) complex, Cas9 variants like PAM-free Cas12a and Cas9-NG/XNG-Cas9, homologous recombination (HR)-based gene knock-in (HKI) by geminivirus replicon, and base/prime editing (Target-AID technology). Consequently, CRISPR/Cas research is advancing currently to enable quick and effective tomato breeding.

Keywords

Abiotic stress, biotic stress, CRISPR/Cas9, plant architecture, flower, fruit quality, genome editing, and tomato.

Genome Editing in Tomato Crop

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Abstract:

In response to biotic and abiotic stressors, plants frequently encounter shifting climatic conditions. In many crop plants, abiotic stressors are the main factors limiting crop output and nutritional quality. The ability to employ genome editing tools for the functional characterization of several genes important for crop development has been made possible by advancements in genome sequencing and high-throughput methodologies. CRISPR/Cas9 has been demonstrated in many food crops including tomatoes. Tomato (*Solanum lycopersicum) i*s both a food crop and a model plant that has been used for many years to study gene function, especially fruit biology. This dual purpose plus available resources (mutant populations, genome sequence, and transformation method) makes tomatoes a perfect candidate for gene editing. Tomato has a narrow genetic base which poses a big challenge in breeding. So, with the advent of the clustered regularly interspaced short palindromic repeat (CRISPR)-associated protein9 (CRISPR/Cas9) genome editing, fast breeding is now possible in tomato breeding. Many traits have been edited and functionally Characterized using CRISPR/Cas9 in tomatoes such as plant architecture and flower Characters (e.g. leaf, stem, flower, male sterility, fruit, parthenocarpy), fruit ripening, quality and nutrition (e.g. lycopene, carotenoid, GABA, TSS, anthocyanin, shelf-life), disease resistance (e.g. TYLCV, powdery mildew, late blight), abiotic Stress tolerance (e.g. heat, drought, salinity), C-N metabolism and herbicide resistance. This paper focuses on the methods to modify the genome to improve various tomato traits such as yield, quality, disease resistance, and nutritional content. Using RNAi, insertional mutagenesis, and CRISPR/Cas9, many candidate genes conferring tolerance to abiotic stresses like heat, cold, drought, and salinity stress have been edited. In this context, fast and efficient genome editing tools like CRISPR/Cas9 can be used to explore genetic

resources for improving the nutritional content and stress tolerance of tomatoes and other crops. Examples of gene editing that has given tomatoes both biotic and abiotic stressors at the same time are shown in this review. The primary goal of this research is to implement this powerful technology to enhance the nutritional traits, production, and quality of fruit from tomato plants. Last but not least, the advantages and disadvantages of genome editing are discussed, along with tomatoes' political and public acceptability.

Keywords: Biotic stress, abiotic stress, trait improvement, tomato, CRISPR/Cas9, genome editing.

Effective CRISPR/Cas9 Editing of the CSLD2 Orthologue Affects the Cell Morphogenesis of Spinach Root Hair

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Abstract

The CRISPR/Cas9 system is a useful tool that has been widely used to alter plant genes. However, spinach, a significant crop of leafy vegetables, has not benefited from the application of CRISPR/Cas9. Here, we used the CRISPR/Cas9 system to precisely alter two cellulose synthase-like D (CSLD) genes implicated in the development of root hair in spinach hairy roots, namely Spo23361 and Spo10340. There were four different types of alterations that were found: replacement, insertion, deletion, and combination mutations. Of these, deletions accounted for the bulk, or roughly 64.1%. Mutation rates differed largely among different targets. Seven homozygous/bi-allelic and eight heterozygous/chimeric mutant lines of Spo23361 were produced from 15 independent transgenic hairy root lines. The bulking and short root hairs seen in all seven homozygous/biallelic lines were indicative of Arabidopsis csld2 mutant traits. From 15 different transgenic hairy root lines, 13 heterozygous/chimeric mutant lines of Spo10340 were obtained; however, no homozygous/bi-allelic lines were found. All of the lines displayed a comparable phenotype of root hair with normal hairy roots. The transcriptome study also showed that several genes involved in membrane trafficking and cell wall regulation had aberrant expressions, which may explain why root hair growth in Spo23361 mutants is reportedly inhibited. The results we find suggest that CRISPR/Cas9-mediated transformation by Agrobacterium rhizogenes is a quick and effective method for modifying the spinach genome. It creates a strong basis for the eventual large-scale genome editing of spinach.

Keywords

CRISPR/Cas9, cellulose synthase-like D (CSLD) gene, spinach, hairy root, root hair, transcriptomic analysis.

Genome Evolution and Diversity of Wild and Cultivated Potatoes

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ABSTRACT

The potato (Solanum tuberosum L.) is the world's most important non-cereal food crop, with the vast majority of commercial cultivars being highly heterozygous tetraploids. Advances in diploid hybrid breeding from true seeds have the potential to transform future potato breeding and production. So far, few studies have investigated the genome evolution and diversity of wild and cultivated landrace potatoes, limiting the use of their diversity in potato breeding. We assemble 44 high-quality diploid potato genomes from 24 wild and 20 cultivated accessions representing Solanum section Petota, the tuber-bearing clade, as well as two genomes from the neighboring section Tuberosum. When compared to closely relate seed-propagated solanaceous crops, it has a larger repertoire of disease-resistance genes, indicating that tuber-based propagation strategies have an impact on potato genome evolution. We identify a transcription factor that regulates tuber identity and interacts with the mobile tuberization inductive signal SP6A. We also identify 561,433 high-confidence structural variants and create a map of large inversions, which provides insights for improving inbred lines and avoiding potential linkage drag, as evidenced by a 5.8-Mb inversion linked to carotenoid content in tubers. This research will speed up hybrid potato breeding and improve our understanding of the evolution and biology of potatoes, a global staple food crop.

Keywords

Diploid Hybrid Breeding, Disease Resistance, Mobile Tuberization, Genome Editing, Potato.

Genome editing of Targeted point Mutations in the Brassica oleracea var. botrytis genome via a modified CRISPR/Cas9 system

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ABSTRACT

In this study, we used the modified CRISPR/Cas9 system to produce targeted point mutations in cauliflower. Acetolactate synthase (ALS) and Centromere-specific histone H3 variant (CENH3) genes were selected as the base-editing targets and hypocotyls of cauliflower were used as explants. For the ALS gene, a C-to-T conversion in the Pro182 codon (CCT) can alter the encoded amino acid, likely resulting in herbicide resistance, and a C-to-T mutation in the Leu133 codon (CTT) in the CENH3 gene may produce a haploid inducer. Results indicated that the transformation efficiency was 1.8%–4.5% and the mutation efficiencies for the ALS and CENH3 genes were approximately 22% and 87%, respectively. The ALS mutant cauliflower showed strong herbicide resistance, with possible immediate implications for broadleaf weed control in cauliflower fields.

Keywords

Cauliflower; Targeted point mutations; Base-editing; CRISPR/Cas9; ALS; CENH3.

Functional characterization of BoGL5 by an efficient CRISPR/Cas9 genome editing system in Broccoli

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ABSTRACT

CRISPR/Cas9 has been widely used for precise and efficient genome editing in several organisms, notably in major crops, for gene function characterization and trait improvement. However, the application of this genome editing tool is very limited in Brassica oleracea, especially in broccoli (Brassica oleracea var. italica). Here, we report that the genome of broccoli, a worldwide important Brassicaceae vegetable, can also be precisely edited by a CRISPR/Cas9 system with multiple single-guide RNA-expressing cassettes. The gene BoGL5, previously identified as a candidate for the glossy green mutant, was chosen as the target gene. We generated 14 T0 transgenic plants, among which 14.3% and 50% produced mutations at the expected position in targeted regions 1 and 2, respectively. Two of them with a 100% mutation rate showed a glossy green phenotype and dramatically reduced cuticular wax load. These results indicate that CRISPR/Cas9 can be used as a promising technique for gene functional verification and trait improvement in broccoli.

Keywords

Abiotic stress, biotic stress, CRISPR/Cas9, plant architecture, flower, fruit quality, genome editing, Broccoli.

Optimization of Seed Coating Formulation for Seed Quality Enhancement in Coriander

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ABSTRACT

Coriander (*Coriandrum sativum L.*), often referred to as cilantro or Chinese parsley, is an essential vegetable and spice crop known for its nutritional and medicinal properties. Seeds with good quality and germination potential are crucial factors for crop production. The germination potential is improved by seed quality enhancement techniques. These techniques reduce seedling emergence time, increase uniform establishment, and facilitate good crop stand in many field and horticultural crops. They include seed dormancy-breaking treatments like seed leaching, seed priming, and seed coating, etc., these enhancement technologies are key players in the seed industry. Seed coating involves modifying the physical properties of seeds by applying certain physical, chemical, or biological compounds to the natural surface of the seed coat. Seed coating improves germination, accelerates phenological events, enhances physiological and morphological attributes, and increases yield. This study aimed to standardize the dosage of hormone-based seed coating formulations to enhance germination and seedling growth in coriander seeds. Coriander seeds were coated with different concentrations of seed-coating polymer and a germination study was conducted in the laboratory using rolled towel method with four replications. The hormone-based seed coating formulation has recorded significantly higher germination% (69%), root length (16.75 cm), shoot length (7.9 cm), dry matter production (0.058 g/10 seedlings), Vigour Index I (1706), and II (3.9) at 10 g polymer/kg of seed and 290 mL of water. Seed Coating with 10 seed coating formulation dissolved in 290 mL of water enhanced the seed germination and seedling growth.

Keywords: Coriandrum sativum, Seed coating, Dosage, Germination, Vigour

CRISPR/Cas9-mediated editing of Phytoene Desaturase gene in onion (Allium cepa L.)

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ABSTRACT:-

Clustered regularly interspaced short palindromic repeats (CRISPR)/ CRISPR-associated protein 9 (Cas9) is a precise genome editing tool used to introduce genetic modifications in a wide range of crop species. Thus far, there is no report of CRISPR/Cas9-mediated genome editing in onions (Allium cepa L.).In the present study, we targeted two exons of the gene coding for Phytoene desaturase (AcPDS) in onion cv. Bhima Super. The sgRNA-carrying constructs were co-cultivated with 8-week-old embryogenic calli using an Agrobacterium-mediated transformation protocol and incubated of the media without hygromycin B selection. Out of the total 617 co-cultivated calli, 21 (3.4%) regenerated shoots exhibited three distinct phenotypes: albino, chimeric, and pale green; in comparison to the wild-type non-transformed regenerated shoots. Total chlorophyll content was drastically reduced in albino shoots and significantly decreased in chimeric shoots. Out of the six Cas9 gene PCR-confirmed regenerated shoots, two exhibited the albino phenotype due to insertions/deletions (InDels) and substitution-based mutations in and around the AcPDS target sites. Deep amplicon sequencing revealed a significantly variable InDel frequency between two sgRNAs, ranging from 1.2% to 63.4%, along with a 53.4% substitution frequency. The mutation of the AcPDS gene generated a visually detectable albino phenotype, thus confirming the successful editing of the AcPDS gene. This is the first time a CRISPR/Cas9-mediated genome editing protocol has been successfully established in onion, with the AcPDS gene serving as an example. This study will provide the necessary momentum for researchers to further basic and applied research on onions.

KEYWORDS:-

PDS, onion transformation, CRISPR/Cas9, genome editing, chlorophyll.

Genome-Wide Analysis of the SAUR Gene Family and Its Expression Profiles in Response to Salt Stress in *Santalum Album*

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The SAUR (small auxin-up RNA) family constitutes a category of genes that promptly respond to the hormone auxin and play a pivotal role in diverse biological processes encompassing plant growth and the response to abiotic stress. *Santalum album L.*, a semi-parasitic evergreen tree, is renowned for its economically valuable essential oils, positioning it among the most prized tree species. In this study, a meticulous identification and comprehensive analysis of 43 SAUR genes was conducted within the *S. album*. Based on phylogenetic relationships, the SaSAUR genes were systematically categorized into five groups. A collinearity analysis revealed intriguing insights, disclosing 14 segmental duplications and 9 tandem duplications within the SaSAUR genes, emphasizing the pivotal role of duplication in the expansion of this gene family. Noteworthy variations in the expression levels of SaSAUR genes were observed by delving into the SaSAUR transcriptome data from various tissues, including leaves, roots, and heartwood, as well as under salt-stress conditions. Notably, SaSAUR08 and SaSAUR13 were significantly upregulated in heartwood compared with roots and leaves, while SaSAUR18 was markedly more expressed in roots compared with heartwood and leaves. Furthermore, SaSAUR27 and SaSAUR28 were found to respond closely to salt stress, hinting at their potential involvement in the salt-stress response mechanism. This research offers a comprehensive investigation of SAUR genes in S. album and establishes a foundation for future exploration of the SAUR gene family, particularly its relation to growth and salt-stress responses.

Keywords: SAUR gene family; *Santalum album*; transcriptome analysis; salt stress; RT-qPCR

Speed Breeding: A Sign of Hope for Food Security

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Abstract

Farmers will need to boost food production by 60–80% by 2050 to feed the projected 9 billion people due to the world's population growth. Another major concern that comes up is the need for breeding programs to adapt to the changing climate. Speed breeding (SB) is the best approach to get quick results in both of these areas. Reducing crop cycle times through rapid generation advancement technology is the goal of speed breeding, which is being hailed as the future of plant breeding. Crop plants typically have long life cycles that are greatly shortened by this novel method. For crops that don't react to light, speed breeding can produce up to 6 generations annually, while other crops can only produce 2 to 3 generations. Managing photoperiodic conditions to achieve maximum light exposure for faster growth is essential to speed breeding. Furthermore, this method is a useful way to control the temperature needs of crops grown in greenhouses or playhouses. Speed breeding speeds up the breeding process and makes it easier to develop new varieties by creating an ideal environment for crop growth. Furthermore, speed breeding complements other cutting-edge technologies like high-throughput genotyping and genome editing platforms. By combining these tools, speed breeding accelerates and scales variety development. A viable approach to attaining climate resilience, long-term yield, and nutritional security is speed breeding, which modifies temperature, light duration, and intensity to hasten plant development. Speed breeding has a wide range of uses, from improving transgenic and CRISPR pipelines to expedited breeding programs. Speed breeding also makes it possible to study physiological traits in plant species and to apply genomic selection strategies more quickly. Essentially, speed breeding is a revolutionary method of plant breeding that promises previously unheard-of levels of variety development agility and efficiency while also providing hope for the continent's food security.

Keywords: Speed breeding, crop improvement, food security

Recent Resistant Genotypes in Black gram (*Vigna mungo* L.) for Root rot Diseases

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Black gram (*Vigna mungo* L.) is a nutritious legume primarily cultivated in South and Southeast Asia, with India being the largest producer. However, the crop faces numerous biotic and abiotic challenges that result in considerable yield reductions. Achieving the goal involves creating varieties that are resistant to significant diseases such as yellow mosaic disease, leaf crinkle virus, leaf spot, anthracnose, and root rot, as well as pests like whiteflies, cowpea aphids, thrips, stem flies, and bruchids. In addition to enhancing on-farm yields, integrating traits that are favored in the market is crucial for the successful adoption of these improved varieties. However, black gram breeding programs often depend on a limited selection of parental lines, resulting in a narrow genetic base for the varieties developed. *Macrophomina phaseolina* leads to various issues such as root rot, collar rot, seedling blight, stem rot, leaf blight, and pod and stem blight. This is a polyphagous necrotroph that can survive in the soil for several years, complicating disease management plants often develop localized dark brown lesions at the soil line, which eventually encircle the stem. Sclerotial bodies can also be seen on the outer tissues of the stems and roots. *Macrophomina phaseolina* in black gram, and a study screened 41 black gram genotypes for resistance to this disease. The research also characterized the morphological traits and internal transcribed sequence regions of the nuclear rDNA operon to identify *M. phaseolina* in black gram. Using the paper towel technique, two genotypes, CO-5 and IPU 07-3, were found to be resistant to dry root rot (disease scores ≤3), while 18 showed moderate resistance (disease scores >3 to ≤5). Five genotypes with disease scores below 4.0 and two susceptible ones were re-evaluated, confirming moderate resistance in CO-5, IPU 07-3, and MASH 1-1. Additional testing in a greenhouse with the sick pot assay further validated the resistance of these three genotypes. Compared to the susceptible check (VO 2135-B-BL), CO-5 demonstrated the best survival rate with a disease incidence of 13.4%, followed by IPU 07-3 at 16.7% and MASH 1-1 at 19.9%. These findings suggest that CO-5, IPU 07-3, and MASH 1-1 can be valuable parents for breeding black gram cultivars with enhanced resistance to dry root rot.

Applications and Major Achievements of Genome Editing in Watermelon

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ABSTRACT

In plants, genome editing is an attractive method to alter gene functions to generate improved crop varieties. Genome editing is thought to be simple to use and has a lower risk of off-target effects compared to classical mutation breeding. Genome editing can be applied directly to crops that contain complex genomes and/or are not easily bred using traditional methods. Watermelon (Citrullus lanatus), which belongs to the Cucurbitaceae family, is a rich source of citrulline, vitamins, and lycopene. CRISPR-Cas9-mediated mutations in the phytoene desaturase (ClPDS) gene, encoding a key enzyme of carotenoid synthesis, caused the expected albino phenotype in watermelon plants. The CRISPR-Cas9-mediated base editing system was also utilized to achieve single-nucleotide conversion at the acetolactate synthase (ClALS) gene in watermelon. Watermelon plants possessing C to T mutations in the codon of Pro 190 (CCG) at the ClALS gene have become resistant to all sulfonylurea herbicides without compromising fruit and seed size, and seed yield. In addition, the CRISPR-Cas9 system was used to generate the knockout mutation of the phytosulfokine1 (ClPSK1) gene responsible for the infection by Fusarium oxysporum f. sp. niveum (FON). The loss-of-function mutation of ClPSK1 rendered watermelon seedlings more resistant to infection by FON. Recently, it was reported that the ClWIP1, a homolog of CsWIP1 and CmWIP1 in cucumber and melon, respectively, acts as the gynoecium (gy) gene in watermelon. The ClWIP1 is specifically expressed in carpel primordia in male floral buds and is also linked to the abortion of carpel primordia in early floral development. Artificial gynoecious watermelon lines have been generated using the CRISPR-Cas9 system targeting the ClWIP1.

Keywords

CRISPR-Cas application, genome-editing, mutation, resistant varieties, watermelon