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| Abstract theme | Green Biotechnology |
| Title: | Novel Somatic Hybrids and Autotetraploid Breeding Parents for Citrus Scion Improvement |
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| Abstract | Citrus breeders and growers are concentrating their efforts to develop climate smart varieties. However, narrow genetic base in Citrus germplasm, along with the quantitative nature of majority of agronomic traits, polyembryony, pollen-ovule sterility, sexual and graft incompatibilities, and extended juvenility have made conventional breeding time consuming and expensive, which compromises its efficacy as a strategy for citrus cultivar development. Citrus improvement program is based primarily on stacking of suitable traits, which is best achieved via interspecific hybridization of complementary parents. Among various existing biotechnological advancements, Somatic hybridization via protoplast fusion, offers a viable alternative to traditional approaches of citrus improvement. Somatic hybridization and cybridization have become an integral part of citrus variety improvement programs worldwide. The main goal of citrus scion and rootstock improvement based on somatic hybridization is to create allotetraploid somatic hybrids between parents that possess complementary characteristics. Present research reports on protoplast fusion of two mandarin cultivars, W Murcott (<i>C. reticulata</i> Blanco x <i>C. sinensis</i> Osbeck) + Snack mandarin (<i>C. reticulata</i> Blanco x <i>C. sinensis</i> Osbeck) via PEG- mediated method in different parental combinations. Out of 2000 somatic embryos recovered from W Murcott + Snack fusion combination; 655 single shoots were regenerated and 56 out of these produced rooted plantlets. The ploidy evaluation of these putative somatic hybrids was carried out through Flow cytometry. The EST-SSR markers were used to evaluate their parental source. Seven EST-SSR primers viz; CX6F06, CX6F07, CX6F09, CX6F10, CX6F14, CX6F17, and CX6F19 confirmed fourteen out of 56 putative somatic hybrids as autotetraploid somatic hybrids. These hybrids exhibited morphology similar to that of W Murcott, with potential to thrive under arid conditions of Pakistan. Their breeding with Kinnow can produce triploid crop of an intermediate season. These hybrids will add new germplasm to the citrus scion breeding program addressing the HLB problem in Pakistan. |
| Keywords: | Protoplasts, Cybrids, EST SSRs, Somatic Hybrids, Polyembryony |
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Abstract theme

Green Biotechnology

Title:

Development of SNP Based High Throughput Molecular Assay for Gene(s) Conferring High Grain Yield in Wheat

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Abstract text

Bread wheat is among the four major food and cash crops of South Asia and used as a staple grain, mainly in Pakistan. Wheat faces severe challenges in the face of climate change. Drought, salinity, and abrupt temperature fluctuations are the important stress factors having adverse impact on agricultural productivity in the region. Among various abiotic stresses drought stress (DS) significantly impact on grain yield. Plant-specific serine/threonine kinase, Sucrose non-fermenting 1-Related Protein-Kinase-2 and Cytokinin oxidases/dehydrogenases play essential role wheat growth and development. It has been well established that *SnRK2* and *CKX* involved in response to abiotic stresses and play their part to ensure higher thousand kernel weight (TKW) in wheat under drought conditions as well. Characterization of these gene families, exploration of sequence polymorphism followed by association of these allelic variation with grain yield related attributes and development of high throughput functional markers is the going forward to fully utilize these genes in marker assisted breeding. In present study, we developed novel functional marker for the two genes conferring drought tolerance and higher grain yield in common wheat. In total, four assays (CAPS and KASP based) for *TaSnRK2.4* and *TaSnRK2.9* were developed in current work and two previously reported CAPS assays for *TaCKXs* were employed for their use in wheat selection breeding. We examined specific alleles associated with drought tolerance causing and higher grain yield in 153 Pakistani wheat cultivars released in last ~60 years. Favorable allelic variations of *TaSnRK2.9* were predominant in the local wheat germplasm demonstrating unconscious gene pyramiding and selection pressure during conventional wheat breeding. *TaCKXs* showed moderate to low selection frequency of superior allelic variation among the studied germplasm. No polymorphism was detected for *TaSnRK2.4* in Pakistani wheat germplasm. A historical set of 153 Pakistani wheat genotypes, was also phenotype based on days-to-heading, number of productive tillers plant⁻¹, spike length (cm), number of grains spike⁻¹, plant height (cm), thousand grain weight (g) and Normalize Difference Vegetative Index (NDVI) via Green-Seeker. Marker trait association (MTA) studies was conducted on the data obtained from this historical wheat set. We anticipate that MTAs for target genes will be instrumental in future wheat breeding of Pakistan.

Keywords:

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| Abstract theme | Green Biotechnology |
| Title: | Present status of the biotechnological advancement in Bangladesh |
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| Affiliation | ¹ Director General Bangladesh Rice Research Institute Gazipur 1701, Bangladesh ² Biotechnology Division Bangladesh Rice Research Institute, Gazipur-1701 |
| Abstract text | Variety development using biotechnological tools is one of the ways to ensure food and nutritional security of the ever-growing population of Bangladesh. Realizing its importance, biotechnological research was initiated in the late 1970s involving only tissue culture. Due to its unbounded success, multiple biotechnological techniques such as embryo rescue, marker assisted selection (MAS), gene pyramiding, QTL identification, DNA fingerprinting, gene cloning, genetic transformation and CRISPR/Cas9 genome editing have been widely used to improve crop varieties. BRRI has released ten high yielding rice varieties using different biotechnological techniques among which BRRI dhan86 and BRRI dhan88 are most noteworthy for their protein enrichment. Through the MAS, two (Xa4 & Xa21) and three (Xa4, xa13 & Xa21) bacterial blight resistance gene were pyramided in BRRI dhan29 and BRRI dhan28, respectively. Heat tolerant BRRI dhan28 and BRRI dhan29 were developed by the introgression of spikelet fertility QTLs (qSF4.1 & qSF4.2) through MAB. Two major QTLs for yield contributing trait were identified in a mapping population BRRI dhan28/Oryza rufipogon. QTL conferring Arsenic phytotoxicity tolerance and |

genes that confer tolerance to abiotic stress factors such as drought, extreme temperatures, and soil salinity is one of the strategies for developing climate-resilient crops. Therefore, mining genes from stress response pathways for abiotic stress tolerance is a way forward to develop climate-resilient cultivars. This typically involves identifying genes in model plant species using molecular biology techniques. Once these genes have been identified, genetic engineering techniques can be used to introduce them to different plants. Virus-induced gene silencing (VIGS), a rapid and effective transient technique to evaluate gene function, was developed to assist high-throughput functional genomics on a large scale. The *Spindly* (*SPY*) gene is a negative regulator of drought stress in cotton. The current study was designed to silence the *SPY* gene through VIGS using binary vector pYL156 (TRV RNA2) in cotton. The *SPY* homolog in cotton was designed, cloned and put into the vector. The agroinfiltration method was used to introduce VIGS vectors in plant leaves. Drought stress was applied to trigger the expression of stress-responsive genes. The gene expression was quantified through qPCR in both stressed and normal plants. Low gene expression was observed from 7-14 days post infiltration (dpi). The study could help in the functional analysis of the *SPY* gene and will explore its role in drought responsiveness in upland cotton that can be further exploited to develop drought-tolerant varieties. Thus, food security can be ensured by promoting sustainable agriculture techniques, promoting crop diversification, bolstering safety nets, and confronting climate change.

Keywords: Abiotic stress, climate resilient breeding, Food security, functional genomics, VIGS

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| Abstract theme | Green Biotechnology |
| Title: | Upscaling plant breeding from traditional to genomic selection in Kazakhstan |
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| Abstract text | <p>Kazakhstan occupies 272 M hectares, which makes it ninth largest country across the world. The country has a huge agricultural capacity, but unfortunately is not being deployed properly. Nevertheless, wheat cultivation and productivity remain on top agenda of the country's agriculture. Almost half of the arable land, ~12 million hectares, produces 15-20 M tonnes of wheat, half of which is exported. Despite large production areas, an average wheat yield of ~1 t/ha remained constant since 1960s. The crop improvement programs majorly rely on traditional breeding methods in the country. There is a need to manipulate final grain quality and yield by improving genetic potential and resilience to stress using advanced breeding approaches. Bread wheat (<i>Triticum aestivum</i>) is one of the most adaptable and widely grown cereal crop across the world for food as well as feed. Global wheat production and yield increased, did, significantly in the last decade, despite the decline of its grown area. However, the trend has not changed in Kazakhstan since 1990s. The average wheat yield in the country could reach 1.6 t/ha, reaching a minimum of 0.5 t/ha in worst scenario compared with global average. As Kazakhstan is one of the main wheat grain provider globally, volatile wheat production poses a significant threat to the global as well as regional food security. Despite unstable grain production, Kazakhstan plays a significant role in contributing to current and future global food security and is known as one of the major high quality wheat suppliers in the world. Kazakhstan's share in global wheat exports among top exporters accounted for about 1.5% at the minimum and 3.2% at the maximum with the mean of ~2.35%, depending on the season, in a last decade. Thus, long-term systematic wheat breeding programs with the use of current advanced technologies and techniques may assist to overcome the existing problems.</p> |
| Keywords: | Kazakhstan, wheat, genomics |
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| Abstract theme | Green Biotechnology |
| Title: | Biotechnological solutions to address climate change in Pakistan |
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| Abstract | Climate change has significant effects on Pakistan's agriculture sector, posing several challenges and threats to crop yield and food security. These threats include drought, alterations in temperature regimes & monsoon patterns, disease dynamics etc. To address these challenges, it is crucial to implement adaptation and mitigation strategies in Pakistan's agriculture sector. These strategies may include the adoption of climate-resilient crop varieties, efficient irrigation techniques etc. Aside other solutions, biotechnology can play a significant role to address the challenges of climate change in Pakistan's agriculture sector. Using the biotechnological and genetic engineering tools, the issues of climate change can be address by the development of drought and heat tolerant GM crops, disease and pest resistance, carbon sequestration, improved crop productivity etc. Plant tissue culture is another tool of biotechnology that can help to develop the disease free somaclones and micropropagation of valuable plants. Furthermore, genomics and DNA based Marker Assisted Selection (MAS) also offering the screening of desired plants very accurately at early generations. In combination with conventional breeding tools, genomics and MAS also helping the scientist to pyramid the multiple desired genes in one plant. In case of wheat, research is mainly focused on development of rust resistant, good quality and drought tolerant plants using genomic and molecular breeding approaches. Development of BLB resistant rice variety i.e. Super Gold is the one of the major success stories of AARI which was developed by using linked DNA markers and to pyramid the 05 BLB resistant genes from coarse rice to basmati rice. In case of cotton, climate-smart high yielding Bt. varieties i.e. FH-333 and FH-Tristar are also the example of application of genetic engineering and molecular breeding tools. Work for the development of high yielding, drought & heat tolerance, good quality etc. in maize and red rot resistance in sugarcane also successfully completed using tissue culture and Marker assisted breeding technology. Genetic diversity analysis, DNA fingerprinting for the development of varietal identification key and molecular verification of approved transgenic events of newly developed crop varieties are the routine activity. AARI is also regularly |

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| | working on the strengthen of its research capabilities and seeking the collaborations not only at national level but also at international levels with top agricultural research and development organizations, universities and institutes. The main focus of this collaboration are the exchange of germplasm, technologies, capacity building of scientists on the latest technologies and Joint venture on R&D initiatives. |
| Keywords: | Climate Change, Biotechnology, Agriculture, Marker Assisted Breeding, Tissue Culture, Genetic Engineering |
| Bibliography | Muhammad Akhter, Sajid-ur-Rahman, Saeed-ur-Rehman and Obaid Ullah Khan. 2023. Biotechnological solutions to address climate change in Pakistan. 2nd International Forum for Agri-Biotechnology 4-5 July 2023, Astana, Kazakhstan. |
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| Abstract theme | Green Biotechnology |
| Title: | Development of Disease Resistance in Plants Using CRISPR/Cas Technology: A Step Forward to Ensuring Food Security |
| Authors | ZULQURNAIN KHAN ^{1,*} , CAIXIA GAO ² , SULTAN HABIBULLAH KHAN ^{3,4} , AFTAB AHMAD ³ , MUHAMMAD SALMAN MUBARIK ⁴ , FURQAN AHMAD ^{3,5} , ZULFIQAR ALI ¹ , ASIF ALI KHAN ¹ |
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| Abstract text | After ensuring food security for several decades, the green revolution has gained its potential and reaching its biological boundaries which is reflected by the stagnation in yield. Meeting the growing food demands of the masses, due to increasing population, is the biggest challenge for plant scientists. CRISPR-edited crops hold tremendous potential for food security and global agriculture. CRISPR technology has become a new face of genome editing with rapidly increasing applications in academic research (functional genomics and reverse genetics) as well as applied research for developing crop varieties with new or improved traits. After successful deployment of gene editing technology to modify simple traits, more ambitious ventures to combat food security challenges in the wake of growing world population with changing climate are in progress. CRISPR may be used in several ways to develop resistance in plants; targeting host susceptibility genes/factors, inserting resistance genes, activating host immunity, breaking host-pathogen cross-talk/interaction etc. We have used CRISPR system against bacterial and viral disease and found promising results. In case of bacterial disease, bacterial leaf spot, we targeted susceptibility gene with CRISPR to enhance plant immunity against the disease in tomato, while in case of viral diseases (caused by begomoviruses), we targeted several viral genes to develop resistance. It was found that targeting multiple genes simultaneously may provide resistance up to 70-80%. Moreover, delay in |

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| | symptoms, low virus titer and attenuated symptoms were observed on the CRISPR plants. Initially, we screened all gRNAs in the model plants; <i>Arabidopsis</i> and <i>Nicotiana benthamiana</i> . Later, we expressed selected gRNAs-CRISPR, transient and stable expression, in tomato and cotton. CRISPR technology has a potential to be used for genetic improvement of plants to ensure food security and safety. Moreover, producing DNA-free, non-GMO plants with CRISPR is an attractive approach for breeders of all regions of the world. |
| Keywords: | Plants Diseases, CRISPR/Cas, GMO, New breeding techniques, Climate-smart crops, Diseases Resistance, Food Security |
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| Abstract theme | Green Biotechnology |
| Title: | Biocontrol of <i>Pectobacterium carotovorum</i> subsp. <i>carotovorum</i> using bacterial strains isolated from the potato microbiome |
| Authors | SBAl NISRINE ¹ , MAJDOULI KARIMA ¹ , AIT DADA IMANE ¹ , CHAHBOUNI MAROUANE ¹ , AMINE ABDESSAMAD ¹ |
| Affiliation | ¹ Biochemistry, Environment and Agri-food laboratory, University of Hassan 2, Casablanca, Morocco |
| Abstract text | <p>The potato (<i>Solanum tuberosum</i> L.) is among the staple crops. Morocco, with a production of about 2 million tons, is the 6th main producer in Africa. However, the yield remains low compared to the potentiality of this culture. The causes are multiple; we mention among others the attack of bacterial diseases. Pectolytic enterobacteria (<i>Pectobacterium</i>) are among the most common pathogens that cause soft rot and black leg of potatoes. This pathogenic species has a wide spectrum; it has been reported as pathogenic for half of the angiosperms.</p> <p>Chemical bactericides have been widely employed in the past to control soft rot disease caused by <i>Pectobacterium carotovorum</i> subsp. <i>carotovorum</i>, a bacterium that affects various vegetable crops, including potatoes in Morocco. However, their use has been restricted due to the adverse effects on human health and the environment. Consequently, biocontrol methods have gained attention as an alternative approach to manage plant pathogens. In this study, we aimed to investigate the antagonistic effects of different bacterial strains isolated from the potato microbiome. Bacterial isolates were recovered from various plant tissues and geographical origins, and those exhibiting the strongest ability to reduce soft rot symptoms in vivo and display remarkable in vitro antagonistic activity against <i>Pectobacterium carotovorum</i> subsp. <i>carotovorum</i> were selected. Forty strains were isolated exclusively from tubers, all demonstrating the ability to inhibit the pathogen's growth on potato slices. The symptom suppression observed for these strains on potato slices exceeded 50%. Among the forty isolates, ten exhibited symptom suppression rates exceeding 90%. In vitro assays confirmed the antagonistic activity of these ten strains through the formation of inhibitions zones on agar media.</p> |
| Keywords: | <i>Pectobacterium carotovorum</i> subsp. <i>carotovorum</i> , soft rot disease, biocontrol, bacterial strains, green biotechnologie. |

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| Abstract theme | Microbial Biotechnology |
| Title: | Unlocking the Potential of Biofilm-forming Plant Growth-promoting Bacteria for Growth and Yield Enhancement in Wheat |
| Authors | MUHAMMAD NAVEED |
| Affiliation | ¹ Institute of Soil and Environmental Sciences, University of Agriculture, Faisalabad-38040, Pakistan |
| Abstract | <p>This study explores the untapped potential of biofilm-forming plant growth promoting bacteria (PGPB) in improving the growth and productivity of wheat crop under greenhouse and natural field conditions. Wheat (<i>Triticum aestivum</i> L.) is one of the most essential cereal crops, providing a significant portion of the global human diet. As the world's population continues to grow, there is an increasing demand for sustainable agricultural practices to enhance crop productivity. Wheat, being a major staple crop worldwide, faces numerous challenges such as nutrient deficiency, soil salinity & drought, and environmental stresses (biotic and a-biotic). Traditional agricultural practices often rely on chemical fertilizers and pesticides, which can have detrimental effects on the environment and human health. Therefore, alternative strategies utilizing beneficial microorganisms like PGPB have gained attention. Harnessing the beneficial interactions between wheat plants and PGPB can offer sustainable and eco-friendly solutions to address these challenges. It highlights key findings on the effectiveness of specific PGPB strains and their application methods in enhancing wheat growth and productivity under greenhouse and field conditions. Previously, we examined the various application methods for PGPB, including seed inoculation, foliar application, and fertigation by soil amendments, to optimize their effectiveness in enhancing wheat productivity. Similarly, we also examined the various strains of PGPB, including rhizobacteria and endophytes for their effectiveness in enhancing wheat growth parameters, such as plant height, root development, biomass accumulation, and grain yield. Furthermore, the study explores potential challenges and limitations associated with the practical implementation of PGPB-based strategies in wheat cultivation. The findings of this research will contribute to the development of sustainable agricultural practices, aiming to improve wheat productivity, reduce chemical fertilizer dependency, and ensure food security in a changing global environment. By unlocking the potential of PGPB, farmers can adopt eco-friendly approaches that promote sustainable crop production, reduce environmental impacts, and enhance soil health.</p> |
| Keywords: | Biofilm, PGPB, Inoculation, Food Security, Wheat |

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| Abstract theme | Microbial Biotechnology |
| Title: | Biotechnology and Modification of Biological Climatic Based Insecticides to Cope With Changes |
| Authors | ¹ HESHAM ELSHESHTAWY |
| Affiliation | ¹ Agricultural Genetic Engineering Research Institute (AGERI), Giza 12619, Egypt |
| Corresponding author detail | Hesham Elsheshtawy |
| Abstract text | <p>Food security is defined by the Food and Agriculture Organization as "food security exists when all people, at all times, have physical or economic access to sufficient, safe, and nutritious food to meet their dietary needs and food preferences for an active and healthy life" (<i>FAO, 1996</i>). If climate change occurs at the rate which is predicted by current global circulation models, it could have wide-ranging implications for all diseases. Although most scientists agree that changes in global temperature will have an impact on infectious disease transmission patterns, the magnitude of the impact is undetermined. The global climate will probably shift as a result of increasing levels of certain "greenhouse gases." Although there will be overall net global warming, its distribution will not be uniform across all regions. Temperature, rainfall, and other climatic variables will vary significantly by region. One of the most serious threats to agriculture is the insane expansion in population without reserves, which is causing an increase in the demand of agricultural resources such as medicine and food, considering they will number approximately 9.8 billion by 2050, we will need to increase production by a minimum of 2.2 times from 1970 to 2020 (2.5 billion tons) (<i>FAO, 2017</i>). This global fight is made even more terrible by crop production losses caused by plant infections, notably fungal pathogens, which destroy 33% of food crops (<i>Fisher et al., 2012</i>). Using microorganisms as a biological control to prevent plant diseases caused by phytopathogenic fungi and insect pests provides a reliable alternative to common strategies, particularly chemical fungicides, which have raised serious concerns about food contamination and environmental pollution; however, we must prepare for any expected changes in the climate so that the killing power of this bio insecticide is not compromised. The most difficult issue in plant protection is locating alternate sources of chemicals having pesticide action. Renewable resources play an essential role in overcoming resource constraints and environmental damage. In addition to plants as a source of bioactive chemicals, the utilization of various forms of trash as a medium for microbial growth is an important source of biopesticides. This could also help to solve the problem of growing trash production. Although substantial progress has been made in the development of formulations and methods of application, more study on the use of biopesticides in plant protection is required. This is primarily intended to address the need for a legislative framework to govern nanomaterials placed on the food market. In the future, studies will focus on improving procedures and doing multidisciplinary research to develop good, safe, effective, and economical plant protection solutions.</p> |
| Keywords: | |
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| Abstract theme | Microbial Biotechnology |
| Title: | Harnessing the Plant Microbiome to Combat Climate Change |
| Authors | SHAHID MUKHTAR ¹ |
| Affiliation | ¹ Department of Biology, University of Alabama at Birmingham (UAB) |
| Abstract text | <p>According to the United Nations, “climate change is a global emergency, and it is a race we are losing, but it is a race we can win”. This global temperature change has far-reaching consequences that are accelerating environmental breakdowns including severe heat and drought conditions. Drought alone constitutes a serious threat to animals and crops by affecting up to 45% of the agricultural areas globally, which is home to 38% of the world's population. In the US, drought is increasingly common, currently costing an average of \$9.6B per year. Heat waves can further exacerbate drought. Thus, heat and drought are considered one of the most critical economic problems and natural threats to the planet. Addressing this impact requires beneficial plant microbiome to building resilient ecosystems facing global environmental challenges. Metagenomic studies will facilitate understanding and further engineering the microbial community associated with drought and heat stress tolerance. This grant proposal focuses on investigating the impact of plant microbiome under heat and stress conditions. Using model system <i>Arabidopsis thaliana</i> (<i>Arabidopsis</i> hereafter), we aim to characterize the diversity and composition of the endophytic microbiome by employing metagenomics and leveraging the expertise of Microbiome Institutional Research Core. Changes in the endophytic community structure and function will be assessed to understand the role of specific microbial taxa in plant stress responses. Functional analyses will evaluate the contribution of endophytes to stress tolerance mechanisms in <i>Arabidopsis</i>. Physiological and morphological traits will be measured to assess the impact of endophytes on plant growth and performance under heat and drought stresses. <i>In vitro</i> assays will explore stress-related metabolite and enzyme production by select endophytic strains. Synthetic communities (SynComs) will be made after performing compatibility assays. Co-transcriptomics will be performed to study gene expression patterns in both <i>Arabidopsis</i> and bacteria. In summary, this study aims to provide insights into the impact of plant endophytes on stress resilience and growth, contributing to our understanding of plant-microbe interactions. The findings will inform strategies for enhancing stress tolerance in crop plants through microbial manipulation, potentially revolutionizing agricultural practices for sustainable and resilient crop production.</p> |
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| Abstract theme | Microbial Biotechnology |
| Title: | Transforming plant growth and disease management using microbiome technologies |
| Authors | AMALIA MOHD HASHIM ^{1,2} , ZUHAIRI ABDUL MALEK ² , NURNADIA NABILAH MOHD BASRI ¹ , NOOR BAITY SAIDI ³ , MOHD TERMIZI YUSOF ¹ , NURFADHILAH KHAIRIL MOKHTAR ² , MOHD HAFIS YUSWAN MOHD YUSOF ¹ , DZARIFAH ZULPERI ⁴ , MOHD FAIZAL ABU BAKAR ⁵ |
| Affiliation | ¹ Department of Microbiology, Faculty of Biotechnology and Biomolecular Sciences, Universiti Putra Malaysia, 43400 UPM Serdang Selangor, Malaysia ² Halal Products Research Institute, Universiti Putra Malaysia, 43400 UPM Serdang Selangor, Malaysia ³ Department of Biology Cell and Molecule, Faculty of Biotechnology and Biomolecular Sciences, Universiti Putra Malaysia, 43400 UPM Serdang Selangor, Malaysia ⁴ Department of Plant Protection, Faculty of Agriculture, Universiti Putra Malaysia, 43400 UPM Serdang Selangor, Malaysia ⁵ Malaysia Genome and Vaccine Institute, Jalan Bangi, 43000 Kajang, Selangor, Malaysia |
| Abstract text | <p>This project focuses on utilizing data-driven microbiome technologies to create SynCom (synthetic microbial community) for transforming conventional agricultural strategies in managing plant growth and disease, by taking Bacterial Leaf Blight infecting rice plant as a case study. Combination of reductionist and holistic approaches and employment of artificial intelligence that escape the laborious, unguided, and time-consuming random selection processes are highlighted. The methodology involves acquiring the core microbiota metagenome-assembled genomes of rice phyllosphere from the NCBI database, constructing co-occurrence networks, and developing machine learning models for growth promotion or pathogenic strain prediction. Microbiota from rice fields and other sources are then isolated, tested, categorized based on selected properties, subjected to longitudinal stability monitoring by co-culturing and amplicon sequencing analysis. Their genomes have been partially acquired through whole genome sequencing (WGS) and analyzed. The selected strains are then evaluated in vitro and in vivo as a SynCom for disease suppression ability. Future work includes WGS analysis of the remaining strains to enhance prediction, metatranscriptomics to elucidate the SynCom's mechanistic action in suppressing disease, and metabolic modeling to determine the optimal media for increased efficacy and further upscaling. The Design-Build-Test-Learn (DBTL) framework will be implemented for enhanced performance. To broaden the application of SynCom, the potential of SynCom technology in marker-assisted breeding is proposed, where selected microbial consortia can be incorporated into breeding programs to enhance desired traits. Analyzing SynCom composition and dynamics will allow identification of key microbial strains and genetic markers associated with positive plant characteristics. The contributions of CRISPR, microfluidics, imaging and spectral-based phenotyping, and phenomics in SynCom development are also discussed. These tools enable gene editing, controlled microenvironment analysis, comprehensive phenotypic trait assessment, and enhanced understanding of SynCom behavior, respectively. Plant-microbe relationships are emphasized as sustainable solutions for crop production and protection. These relationships enhance nutrient availability, suppress diseases, improve stress tolerance, promote soil health, and contribute to bioremediation. Collaboration among stakeholders is necessary to scale up SynCom technology in OIC countries. Governments can provide financial incentives and create policies for its adoption. Research and development organizations drive innovation, while entrepreneurs translate advancements into practical applications. Knowledge-sharing platforms facilitate the development and deployment of SynCom technology. In conclusion, the adaptable SynCom technology offers a sustainable approach to crop improvement, customizable for specific agricultural conditions in OIC countries. Engaging youth, addressing challenges, leveraging innovation, and strengthening collaborations are vital to achieving food security and building resilient food systems.</p> |
| Keywords: | SynCom, Metabolic modelling, Omics, Plant growth promotion, Plant disease management, Machine learning, DBTL framework |
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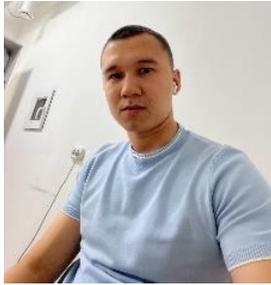
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| Abstract theme | Microbial Biotechnology |
| Title: | Microbial Intervention to the Agriculture for Climate-Resilience and Food Security |
| Authors | ASMA IMRAN ¹ |
| Affiliation | ¹ National Institute for Biotechnology and Genetic Engineering, NIBGE, Faisalabad |
| Abstract text | Global food security is under pressure due to increasing population, demand of quality food, adverse impacts of climatic, biotic and abiotic stress and low per acer yields. This opens up new perspectives to promote new agricultural system based on sustainability, climate resilience with a special focus on increasing the use efficiency of the resources e.g., the fertilizers or water. Crop growth is the function of temperature, soil fertility, and water status; all at optimum satisfaction. Microbes being the key inhabitants of soil are in direct contact with the plants and exert significant impact on plant growth and productivity. A precise management of the rhizosphere microbial population can stimulate plant growth, increase its tolerance to different biotic and abiotic stresses and decrease plant dependence on chemical fertilizers. Generally, these microbes colonize plant roots and influence plant growth either directly or indirectly. They provide unavailable air/soil nutrients to plants and produce growth hormones for regulating plant growth hence reduce dependence on chemical fertilizers, making the entire system more-ecofriendly and less-polluted. Microbes also produce enzymes and secondary metabolites which enable plants to withstand against heat, drought, salt or pathogen attack which increase plant resilience and reduce dependence on pesticides. The microbes also increase the use efficiency of chemical fertilizers in plants. Microbial biotechnology has become one of the most dynamic and expanding fields of research and the production, formulation and application of microbes as biofertilizers and biocontrol agents are being done commercially. Further, at the interface of microbiology and nanotechnology, hybrid fertilizers have also been developed that combines the benefit of nanoparticles and microbes for fulfilling the nutrient demand of crops at reduced chemical fertilizer applications. The microbial intervention to the rhizosphere is ecologically safe, and economically viable to get higher agricultural yields with promised climate-resilience and food security. |

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| Keywords: | Microbes, Fertilizer use efficiency, Biofertilizers, environmental pollution, fertilizer crises, Climate-smart Agriculture |
| Bibliography | <p>1. Marghoob U.M., Nawaz A, Ahmad M, Waheed M. Q., Khan M. H, Imtiaz M., Islam E, Imran A, Mubeen F, 2023. Assessment of halotolerant bacterial and fungal consortium for augmentation of wheat in saline soils. <i>Frontiers In Microbiology</i> (in Press). (IF=6.064)</p> <p>2. Mahreen N., Yasmin, S., Asif, M., Yahya, M., Ejaz, K., Mehboob-ur-Rahman, Yousaf, S., Amin, I., Zulfiqar, S., Imran, A., Khaliq, S., Arif, M., 2023. Mitigation of water scarcity with sustained growth of Rice by plant growth promoting bacteria. <i>Frontiers in Plant Science</i>. DOI: 10.3389/fpls.2023.1081537 (IF=6.627)</p> <p>9. Imran A*, Sardar F, Khaliq Z, Nawaz MS, Shehzad A, Ahmad M, Yasmin S, Hakim S, Mirza B.S., Mubeen F, Mirza MS. 2022. Tailored bioactive compost from agri-waste improves the growth and yield of chili pepper and tomato. <i>Frontiers in Bioengineering and Biotechnology</i>, 9: 787764 (IF=6.064)</p> <p>13. Imran A*, Hakim S., Tariq M, Nawaz MS, Laraib I, Gulzar U, Hanif MK, Siddique M J, Hayat M, Faraz A., Ahmad M. 2021. Diazotrophs for lowering nitrogen pollution crises; looking deep into the roots. <i>Frontiers in Microbiology</i> Doi: 10.3389/fmicb.2021.637815 (IF=6.064) cit: 8</p> |
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| Abstract theme | Microbial Biotechnology |
| Title: | Effects of plant growth-promoting rhizobacterium (PGPR) on growth and antioxidant enzyme activities in salt-stressed durum wheat (<i>Triticum durum</i>) |
| Authors | HIMISSI IMEN ¹ , HACHANA AMIRA ¹ , ARFAOUI HANEN ¹ , ANNABI MOHAMED ¹ |
| Affiliation | ¹ National Institute of Agronomic Research of Tunisia |
| Abstract text | <p>Current crop production systems are a major reason for changing global climate through diminishing biodiversity, physical and chemical soil degradation, and water pollution. The over application of fertilizers and pesticides contribute to climate change through greenhouse gas emissions (GHG) and toxic soil depositions. At this crucial time, there is pressing need to transition to more sustainable crop production practices, ones that concentrate more on promoting sustainable mechanisms, which enable crop to grow well in resource limited and environmentally challenging environments, and also develop crop with greater resource use efficiency that have optimum sustainable yields across a wider array of environmental conditions. One potential way to decrease negative environmental impacts resulting from continued use of a chemical fertilizer is inoculation with plant growth promoting rhizobacteria (PGPR). These rhizobacteria plays an important role in enhancing plant growth through a wide variety of mechanisms. The use of PGPR for improving plant nutrition and thus partially compensating the need of chemical fertilizers is becoming a popular strategy for sustainable agriculture. In this study we aimed to investigate the effects of plant-growth-promoting rhizobacteria (PGPR) on durum wheat variety under saline conditions. Two strains S14 (<i>Pseudomonas</i> sp.) and S7 (<i>Bacillus</i> sp.) were used as bio-inoculants. Under stress and non-stress conditions, bacterial isolates had significant positive effect on the recorded biochemical and physiological parameters of wheat. The results stated that inoculated plants showed a significant increase in growth traits (shoot length, root length, shoot fresh weight and root fresh weight) and chlorophyll content and a significant decrease in H₂O₂ and MDA content compared with non inoculated controls. This indicates the effectiveness of S7 and S14 strains in mitigating the effect of salt stress in durum wheat. From the results it may be concluded that, indicated a positive effect of applied bacterial treatments on the resistance of wheat plant to the salinity stress and due to the relative susceptibility of wheat to salinity, pre-treatment of the plant using of the desired microbes is recommended before planting in soil areas susceptible to salinity.</p> |
| Keywords: | Durum wheat, Salt stress, Inoculation, PGPR, antioxidant enzymes |
| Bibliography | |

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| Abstract theme | Animal Biotechnology |
| Title: | Development of The PCR Real Time Method and Identification of Staphylococcus Aureus in the Objects of Veterinary Sanitary Supervision in the Conditions of Northern Kazakhstan |
| Authors | CHUZHEBAEVA GULZHAGAN DZHAMBULOVNA ¹ , BAYMENOV BAKHIT MURATOVICH ² , ALIYEVA GULNUR KOZYEVA ³ , MUKANOV TAMERLAN, MARATOVICH ⁴ , SERIKBAIOV ORAZBEK NURLIBAYUGLI ⁵ |
| Affiliation | ¹ Chuzhebaeva Gulzhagan Dzhambulovna ² Baymenov Bakhit Muratovich ³ Aliyeva Gulnur Kozyevna ⁴ Mukanov Tamerlan Maratovich ⁵ Serikbaiov Orazbek Nurlibayugli |
| Abstract text | The purpose of this investigation is to select primers and probe for identification of staphylococcus aureus in the objects of veterinary-sanitary supervision in PCR REAL TIME format based on Staphylococcus aureus-specific thermally-stable nuclease gene (nuc). The performed work resulted in selection of the following primers and probe: forward primer 5'-GGTTGATACACCTGAAACAAAGCA -3'; reverse primer 5'- ATACGCTAAGCCACGTCCAT -3'; probe TGGTCCTGAAGCAAGTGCATTTACG; product length – 160 base pairs. When optimizing the temperature regime for annealing of primers and probes, a temperature gradient with vertical temperature difference from 63°C to 65°C was used, where the optimum annealing temperature of primers was 65°C. This result was confirmed in the experiment with construction of calibration graphs for different indicators of genome equivalents in a temperature gradient from 63°C to 67°C. To determine the diagnostic specificity, 67 isolates collected from swabs, animal biomaterial, and products of animal and plant origin, as well as isolates obtained from the Republican collection of microorganisms (Republic of Kazakhstan) were randomly selected and analyzed. The diagnostic specificity was 100%, and allows to detect Staphylococcus aureus with a low risk of false positive and false negative results to a high degree of reliability. The detection limit for the target gene was 22 copies/μl. of DNA of Staphylococcus aureus which is equal to 6.71-5 ng/μl. Staphylococcus aureus is one of the most common pathogens causing intramammary infections in cattle. Staphylococcus aureus is responsible for significant quality and economic losses in worldwide dairy production [1, 2, 3, 4]. Staphylococcus aureus is one of the main causes of food poisoning outbreaks around the world. Raw milk may be directly contaminated with Staphylococcus aureus from infected dairy animals. Also, contamination of milk and dairy products may be due to poor hygiene during production, retail sale and storage of food products, or indirectly to human carriers of microorganisms [5, 6, 7, 8]. Food products such as dairy products and processed meat may be contaminated with enterotoxigenic strains of S. aureus |
| Keywords: | Staphylococcus aureus, nuc gene, PCR REAL TIME |
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| | |
|-----------------------|--|
| Abstract theme | Animal Biotechnology |
| Title: | Veterinary and sanitary assessment of the quality and safety of fish in WKR reservoirs |
| Authors | ASKHAT ZHUMABAYEV ¹ , ZHENIS KUSHMUKHANOV ² , ZHANGELDY USSENOV ³ |
| Affiliation | |
| Abstract text | <p>Control of the quality and safety of food products by the relevant authorities is not carried out in full, limited only by organoleptic studies and physical and chemical safety indicators. These indicators do not indicate the complete biosafety of food products in the regions of the Republic of Kazakhstan. To fully guarantee the biosafety of food products, it is necessary to carry out organoleptic, physicochemical, parasitological studies of water bodies in our country. Also, together with parasitological studies, we investigated fish products for the content of heavy metal salts and antibiotics. In WKR, the risk of the spread of parasitic fish diseases that are dangerous to human health remains. At the same time, the regional features of the environmental hazard, as well as the epizootic process in parasitic diseases of fish, are not well understood, which significantly reduces the effectiveness of the safety of using fish and fish products in solving the country's food problem. The significance of the problem on a national and international scale; opisthorchiasis, anisakiasis of fish causes significant harm to the health of the population and carnivores. The economic damage is made up of the culling of infected fish and the diagnosis and treatment of these diseases in humans. To achieve sustainable growth rates of aquaculture in the Republic of Kazakhstan, it is necessary to ensure the veterinary well-being of the ichthyofauna. Infectious and parasitic diseases reduce the safety of fish during their cultivation and do not allow to obtain maximum productivity indicators. In addition, parasitic diseases contribute to a decrease in the quality of fish products. Sick fish lags behind in growth, through the development of clinical signs of helminthic lesions, it loses its presentation and it is not recommended to use it for food for people and animals without special neutralization. The use of fish products increases the risk of infecting people with dangerous invasive diseases, the pathogens of which use fish as an intermediate host. Thus, a number of researchers point to the focus of opisthorchiasis in Northern and Western Kazakhstan with an annual incidence of people up to 1-150 cases. The impact of the obtained results on the development of science and technology and the expected social and economic effect, during the implementation of the program, monitoring of the epizootic situation on the main dangerous zoonoses of fish in various environmental objects and the implementation of preventive measures will be carried out. There is also information from the sanitary and epidemiological station on cases of human and animal diseases with invasive diseases that were transmitted through fish and other representatives of the ichthyofauna in the reservoirs of the region.</p> |
| Keywords: | Safety fish and fish product |
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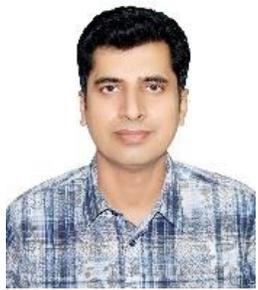


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| Abstract theme | Animal Biotechnology |
| Title: | Lab Grown Biotech or Natural Meat: Choices in the Perspectives of Climate Change and One Health |
| Authors | QAMAR SHAKIL ¹ , KHALID HUSSAIN ² , MUHAMMAD UMER FAROOQ ¹ , ZOHAB ASIF ³ , RASHID MINHAS ⁴ , NAEEM KHALID ⁵ |
| Affiliation | ¹ Fodder Research Sub Station, Ayub Agricultural Research Institute Faisalabad ² Department of Agrometeorology, University of Agriculture Faisalabad ³ FC College, Department of Biotechnology, Lahore, Pakistan ⁴ Agriculture Research Station, Bahawalpur, Pakistan ⁵ Food Technology, Post-harvest Institute, Ayub Agricultural Research Institute Faisalabad, Pakistan |
| Abstract text | The global population is growing at an unprecedented rate, and with it, the demand for meat is surging. However, meat production methods contribute significantly to climate change and public health issues. In response, lab-grown biotech meat, also known as clean meat, has emerged as a new alternative approach and have certain impact. Clean meat offers numerous benefits but the residual impact have certain health drawbacks and needs further research. Natural meat is an enriching nutritious diet on the other hand and the consequences of it are well documented. Livestock production efficiency can be improved through proper feeding availability which can fulfill the meat demand naturally. This can be improved through advance fodders (Alfalfa, Sorghum) and forages production to ensure the maximum natural meat production and utilization. This report provides a detailed overview of the technology and benefits of clean meat, as well as its implications for climate change and public health. Additionally, we explore alternative feed sources, feeding management systems, and their potential to mitigate the environmental impact of livestock production system. By examining these issues from the perspectives of One Health, which encompasses the interconnections between human, animal, and environment, we hope to provide a comprehensive understanding of the challenges and opportunities associated with meat sources. Green fodder is an economic source of nutrients for the dairy animals. It is highly palatable and digestible. Micro-organisms present in green fodder help in improving digestibility of crop residues under mixed feeding system. It also helps in maintaining good health and improving breeding efficiency of animals. Fodder crops like alfalfa (Perennial forage, N-fixation, highly palatable, digestible and nutritious, drought tolerant and frost tolerant) provide natural habitat too many insects' spp. and minerals to soils as it has 7-9 m deep root system. Other fodder crops for irrigated conditions, increases soil fertility (N-fixation) and have potential to improve average green fodder yield to OIC countries. |
| Keywords: | Clean meat, Natural meat, Nutritious Fodders, Environmental impacts, Economic globalization |
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| | |
|-----------------------|---|
| Abstract theme | Food Biotechnology |
| Title: | Enabling Policy Environment to Promote Adoption of New Technologies for Food Security |
| Authors | MUHAMMAD ASI KAMRAN ¹ , NEHAL AHMAD KHAN ¹ , IQRAR AHMAD KHAN ¹ |
| Affiliation | ¹ University of Agriculture Faisalabad, Pakistan |
| Abstract text | Despite widespread success of the Green Revolution (GR) since 1960s in terms of high yield of wheat followed by gains in yield of other crops due to spillover effects, many parts of the world remained deprived of the opportunity mainly due to non-compatibility of the policy environment. International public good institutions like CGIAR system were instrumental to bring about the success in providing germplasm and elite lines for development of high yielding crops varieties. The GR success was not without its unintended negative consequences mainly due to policies that promoted rapid intensification resulted in micronutrients deficient food mix, increased inequality, loss of soil fertility, loss of ecosystem services, lack of adoption of technologies for the marginal environments, and reduced crops diversification. These externalities have huge sustainability implications. With advances in agricultural biotechnology, precision agriculture, internet of things (IOTs), data science, artificial intelligence (AI) and blockchains etc, (what may be called as GR 2.0); a new set of policies and regulatory environment is needed to harness benefits form the new revolution. The paper is focused on enabling policy environment and approaches to take advantage of technological innovation in GR 2.0 for climate smart, food secure and sustainable future. The possible role of inter-governmental organization like IOFS for possible collaboration among the member states and crafting policies for benefits of the member states is also highlighted. The paper highlights policy implications of provision of public goods in general and agricultural biotechnology products in particular with rle of interdisciplinary and trans-disciplinary approaches in provision and dissemination of public R&D. |
| Keywords: | agriculture innovations, digital agriculture; enabling policy environment; green revolution 2.0; public goods provision |
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Abstract theme

Food Biotechnology

Title:

Development and Implementation of RNA-Interference-Based Technology to Confer Antiviral Resistance in Crop Species

Authors

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Abstract text

Phytopathogenic viruses cause enormous damage to agriculture and the economy. The existing methods of counteracting viruses are reduced to obtaining virus-free seed material, but this method is not always effective, since a new strain of viral infection appears every season, and obtaining virus-free planting material is a very expensive, laborious and lengthy process. In this regard, the work on the timely diagnosis of infectious plant diseases and the development of new strategies to counteracting viruses are especially relevant. One of the potential tools for increasing plant resistance to viruses is RNA interference (RNA-i). An essential feature of the protective mechanism of RNA interference is the presence of short double-stranded interfering RNA (siRNA, short interfering RNA) with a length of 21-23 nucleotides, which are powerful modulators of RNA interference. When the RNA-i process is triggered, the viral double-stranded RNA (dsRNA) is fragmented by the DISER enzyme (ribonuclease from the RNase III family) into complementary short interfering RNAs (siRNA) of the viral RNA, which are further involved in the endoribonuclease effector complex RISC (RNA-induced silencing complex) and are directly involved in the recognition and subsequent degradation of viral RNA targets. The helper component-proteinase (HC-Pro) is a multifunctional suppressor protein synthesized by Potato virus Y (PVY). It has the ability to neutralize the protective mechanisms of RNA interference (RNAi) in potato plants, thereby causing systemic infection in the host plant and significant damage to tuber material. This technology demonstrates how one of the key functions of HC-Pro, the capture and retention of short interfering RNAs (siRNAs) with a size of 21-23 bp, can be utilized to create in vitro virus-resistant potato. The proposed method is based on the selective dissociation of the HC-Pro/siRNA complex from PVY-infected plants and siRNA-priming in healthy plants. Purified preparations of PVY-specific siRNA were obtained using column gel filtration followed by immunoprecipitation and phenol-chloroform extraction. Injections of siRNA into the leaf tissues of PVY-free micropropagated potato plants, specifically Kazakhstani cultivars, resulted in reduced accumulation of viral particles in the cytoplasm of inoculated plants and the development of resistance to PVY throughout the entire vegetation period.

Keywords:

Solanum tuberosum, HC-Pro, PVY, RISC, siRNA, RNA interference

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| | |
|-----------------------|--|
| Abstract theme | Food Biotechnology |
| Title: | The Use of Recombinant Proteins in The Development of Diagnostic Test For the Detection of Campylobacter Jejuni |
| Authors | ALFIRA ZHAKHINA ¹ , SERGEY BOROVIKOV ¹ |
| Affiliation | ¹ NCJSC S.Seifullin Kazakh Agro Technical Research University |
| Abstract text | <p>Campylobacteriosis is an infectious disease of many animal species, as well as humans, caused by pathogenic microorganisms of the genus <i>Campylobacter</i>, and is defined by its intensity, severity levels, and polymorphism of symptoms. In recent years, campylobacteriosis has become increasingly important as a food poisoning infection in humans. It also has been registered in many countries around the world. Infected animals and animal products are the primary sources of infection. Food safety is negatively impacted by bacteriological diagnostic methods with insufficient sensitivity and efficacy. Modern immunochemical methods, such as ELISA and LFT, effectively solve the problems that exist in the diagnosis of intestinal infections. However, these diagnostic methods require the use of highly specific and highly active antigens and antibodies. Our goal was to obtain recombinant <i>C. jejuni</i> Omp18 and MOMP antigens and evaluate their usefulness in disease diagnosis and obtaining specific mAbs.</p> <p>The sequences of the Omp18 and MOMP genes of <i>C. jejuni</i> antigens were synthesized de novo. The synthesized genes were cloned into the pET32 expression vector to produce recombinant antigens. Protein purification and refolding was performed using metal affinity chromatography on HisTrap columns. The properties of the recombinant proteins were studied using western blotting, LC-MS/MS spectrometry, and ELISA. Two bacterial strains, producing recombinant <i>C. jejuni</i> Omp18 and MOMP antigens with molecular weights of 36 and 64 kDa, respectively were obtained. The resulting proteins reacted with specific antibodies. Comparative analysis of the amino acid sequence of the recombinant antigens showed complete similarity with the reference sequences presented in the PubMed NCBI database. In western blot and ELISA with positive control sera, an active reaction of sera with proteins of molecular weight 36 and 64 kDa was observed. Statistical analysis of ELISA results with 94 bovine sera showed the diagnostic performance of recombinant antigens with a high percentage of certainty. High titers of specific antibodies were found when laboratory animals were immunized with recombinant proteins. Hybrid cell lines producing mAbs to recombinant antigens were obtained by fusing myeloma cells and splenocytes from immunized Balb/c mice. The obtained mAbs to recombinant antigens Omp18 and MOMP will be used in the development of a rapid test for the detection of <i>C. jejuni</i> in animal products. The recombinant Omp18 and MOMP antigens are able to detect antibodies in the serum of infected or recovered animals. The recombinant Omp18 and MOMP antigens have also been shown to be suitable for producing specific mAbs.</p> |
| Keywords: | campylobacteriosis, <i>Campylobacter jejuni</i> , monoclonal antibodies, outer membrane proteins, recombinant antigens. |
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| Abstract theme | Food Biotechnology |
| Title: | Designing a LF Test for the Detection of Antibiotics in Livestock Products |
| Authors | FARIZA ZHAGIPAR ¹ , ASSEM JANGULOVA ¹ |
| Affiliation | ¹ Faculty of Veterinary and Livestock Technology |
| Abstract text | <p>Currently, in animal husbandry practice, milk producers mainly rely on the use of antibiotics and medicines for the treatment of mastitis and other infectious diseases, and also use them as growth stimulants. Uncontrolled use of antibiotics can lead to the formation of a residual amount of drugs in animal products, which disrupts the normal functioning of the intestine, the development of allergic reactions, the development of antimicrobial resistance and other side effects. In this regard, it is very important not only to regulate, but also to control the use of antibiotics in animal husbandry and veterinary medicine. The developed immunochromatographic analysis method conjugated with colloidal gold nanoparticles was used to design the LFT. Serological, immunochemical, biotechnological, and statistical research methods were performed in this study. The results of the studies showed that the test line applied to the nitrocellulose membrane was not stained when using samples where the concentration was equal to or higher than the maximum permissible concentration (MPC): STR 400 and 200 mcg/ml, OTC 15 and 10 mcg/ml, HAF 0.6 and 0.3 mcg/ml. The samples were added to the sample cushion, the antibiotics present in the sample were bound to the antibodies. The result of the reaction was the staining of the test and control strips below the MPC of antibiotics streptomycin 100 mcg/ml, oxytetracycline 5 mcg/ml, chloramphenicol 0.15 mcg/ml. No cross-reactions with concentrations below MPC were observed in any case. For the reference analysis of the sensitivity and specificity of the developed LFT, milk and meat samples were tested in comparison with commercial kits. This analysis showed an analytical sensitivity almost equivalent to the results of the ELISA test. The sensitivity of the LFT on the STR and OTC was 90%, and on the HAF – 88.3%. Specificity was studied by analyzing samples obtained from healthy herds, where all the claimed samples showed a negative result using two methods. The measured specificity was 100%. Thus, optimal concentrations of antibodies have been established for the formation of the test and control bands of the NCM for the determination of streptomycin, oxytetracycline and chloramphenicol antibiotics. The specificity of the immunochromatographic test when compared with a commercial analogue is below the maximum permissible concentration, which ensures maximum analytical sensitivity of the test system when determining antibiotics in the studied meat and milk samples.</p> |
| Keywords: | antibiotic, enzyme linked immunosorbent assay, maximum permissible concentration, lateral flow assay. |
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| Abstract theme | Food Biotechnology |
| Title: | New Approaches of Camel and Bovine Chymosins in Cheesemaking |
| Authors | ZHIGER AKISHEV ¹ |
| Affiliation | ¹ National Center for Biotechnology, 13/5 Korgalzhyn Road, Astana, 010000 |
| Abstract text | <p>In 2021, worldwide milk production reached 918 million metric tons, an 11% increase from 2016 and more than double the quantity produced in 2000. Approximately 96 percent of total cow and buffalo milk production remains stable (cow and buffalo milk accounted for 81 percent and 15.2 percent of world milk production, respectively). In 2021, goat, sheep, and camel milk accounted for 2.3%, 1.2%, and 0.4% of total global production, respectively. The agriculture of the Mediterranean, Western, and South-Eastern Asian regions rely heavily on this milk. Milk from deer, donkeys, and mares is not generally consumed, but it is culturally significant for some nations and ethnic groups. Other types of milk have recently been the subject of intense research due to their possible health benefits and prospective usage in infant formula due to their hypoallergenic characteristics, despite the prevalence of cow's milk.</p> <p>Currently, coagulants of animal, plant, and microbial origin are used to curdle milk in the cheese-making process, but traditionally, rennet, produced by the glandular cells of the fourth stomach section of ruminants, is utilized. The greatest amounts of rennet are produced during the early milking period of calves, goats, and lambs, and rennet is therefore only produced in young animals (3–10 days old). Rennet is a combination of the two endopeptidases: pepsin and chymosin, which are often known as renin. Chymosin content in renin ranges from 10% to 90%, and a preparation containing mostly or purely chymosin is of the highest use in cheesemaking since its composition has a major influence on the organoleptic and taste properties of cheese. Bactrian camel (<i>Camelus bactrianus</i>) chymosin has a milk-clotting activity higher than that of calf chymosin for cow's, goat's, ewes', mare's and camel's milk. Submerged fermentation by a recombinant yeast (<i>Pichia pastoris</i> GS115/pGAPZαA/ProchymCB) was implemented in a 50 L bioreactor, and the recombinant camel chymosin was prepared successfully. The activity of BacChym in yeast culture was 174.5 U/mL. The chymosin was concentrated 5.6-fold by cross-flow ultrafiltration and was purified by ion exchange chromatography. The activity of the purified BacChym was 4700 U/mL. The BacChym powder was obtained with an activity of 36,000 U/g. By means of this chymosin, cheese was prepared from cow's, goat's, ewes', camel's and mare's milk with a yield of 18%, 17.3%, 15.9%, 10.4% and 3%, respectively. BacChym could be a prospective milk-clotting enzyme for different types of milk and their mixtures.</p> |
| Keywords: | Recombinant chymosin, <i>Camelus bactrianus</i> , cheese making, milk-clotting enzyme, fermentation |
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| Abstract theme | Food Biotechnology |
| Title: | Diagnostic Markers for Authenticity and Quality of Animal Products |
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| Abstract text | Increasing demands for high-quality animal protein drives the global milk and meat industry to augment their potential productivity, while reducing carbon footprints and waste excretion. To attain this goal, there has been tremendously progress in animal biotechnology over the past 40 years to produce recombinant proteins and organic nutrients, clones of elite individuals, and genetically modified animals for agricultural and biomedical purposes. Obviously, the efficiency of livestock production has been improved significantly due to advances achieved in animal breeding, management, and nutrition during the past few decades. However, there is still room for improvement in quantity and quality of animal products through the application of modern biotechnology techniques. Identification of animal products offered for sale and public consumption is necessary for consumer preference and regulatory surveillance. Nowadays, biotechnology provides a wide variety of valuable, quick and effective tests to trace the product origin and authentication in favor of sanitary and health of consumers. Adulteration of animal products, including meat and milk, may be precisely detected using real-time polymerase chain reaction (qPCR). |
| Keywords: | |
| Bibliography | |
| Bio photograph | |



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| Abstract theme | Food Biotechnology |
| Title: | Genetically Engineered Enzyme Preparations for the Processing of Plant Carbohydrates |
| Authors | ASSEL KIRIBAYEVA ¹ |
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| Abstract text | Amylases are known enzymes that hydrolyze starch. The high efficiency of amylolytic enzymes allows them to compete in industry with the technology of chemical hydrolysis of starch. Hemicellulose and cellulose are the main heterogeneous polysaccharides of plant biomass. Hemicelluloses composed of β -D-xylose residues are xylans, which are the main component of hemicellulose. Xylanases are endoenzymes that hydrolyze homopolymers to release xylooligomers, and β -glycosidases hydrolyze xylooligomers to xylose. Xylanases are being researched intensively because they are used in the food and feed industries, in the bleaching of pulp and paper, and in textile and biofuel production. The amylolytic strain T5 was isolated from the soil and identified as <i>Bacillus licheniformis</i> . The α -amylase gene from <i>B. licheniformis</i> T5 has been cloned and expressed in <i>Escherichia coli</i> (rAmyT5-E) and <i>Pichia pastoris</i> (rAmyT5-P). The recombinant α -amylases rAmyT5-E and rAmyT5-P are maximally active at pH 6.0 and 70 °C and 80 °C, respectively. More than 80% of rAmyT5-E activity is retained after incubation in the pH range 5-9, rAmyT5-P after incubation at pH 6-9. The activity of recombinant α -amylases at high temperatures of 50-90°C and pH range 6-9 may recommend α -amylase from <i>B.licheniformis</i> T5 for use in the industrial processing of starch-containing raw materials. Here, a strain having xylanolytic activity and identified as <i>Bacillus sonorensis</i> T6 was isolated from soil. The xylanase gene of <i>Bacillus sonorensis</i> T6 was cloned and expressed in <i>Escherichia coli</i> and in <i>Pichia pastoris</i> . The recombinant xylanases were found to have optimal activity at 47–55°C and pH 6.0–7.0. The recombinant xylanases retained |

100% of activity after 10 h incubation in the pH range 3–11 and 68% of activity after 1 h at pH 2.0. The good stability in a wide range of pH and moderate temperatures may make the xylanase from *Bacillus sonorensis* T6 useful for various biotechnological applications.

Keywords:

Bibliography

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Abstract theme Food Biotechnology

Title: Bio-fortification: A natural strategy to combat malnutrition

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Abstract text The food security is a fundamental right of every individual and it is the duty of the nations to ensure access of every individual to nutritious and safe food. The world population is increasing day by day and accordingly the challenges of food and nutritional security are also increasing. This food and nutritional insecurity is leading towards malnutrition. The South Asian region has the highest prevalence of malnutrition in the world and about 336 million people are reported to be hungered in the region. The prevalence of child malnutrition is estimated at over 46 percent of children in the age group 0-5 years. Deficiencies of minerals (iron, zinc and folate) are more prevalent in many parts of the world where cereal based foods are recognized as staple foods. Current interventions, such as supplementation or fortification, are being practiced with varying success to overcome this malnutrition but at the same time these also have some limitations for availability, economy, toxicity and increased risk of overdosing. For the mentioned reasons, it is of great significance to find ways to naturally fortify foods with micronutrients, and to increase the bioavailability of the naturally present minerals in the foods to cope with the problems related to mineral deficiencies. This can be achieved through biofortification which include the approaches or processes of improving the nutritional value of edible crops through selective conventional breeding, mineral fertilization, advanced transgenic approaches or fermentation. As a case study, we used fermentation technology to combat mineral malnutrition and it was observed that there was a significant increment in mineral contents of the fermented food products as compared to the non-fermented products (Bread and Cake). From studies it was concluded that the fermentation technology can be used as a biofortification technique to combat malnutrition but the mechanism is culture/strain dependent.

Keywords: Biofortification, Hunger, Malnutrition, Fermentation

Bibliography

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