NATIONAL SYMPOSIUM ON

RECENT TRENDS IN BIOINFORMATICS STRATEGY FOR DISEASE MECHANISM AND BIOMEDICINE

November 24, 2018

SOUVENIR & ABSTRACTS

(BTIBNS – 2018)

Organized by

BIOINFORMATICS TECHNOLOGIES OF INDIA
(Discover the Science of Life)
Munshinagar Gate, Near ICAR-CARI Campus, Bareilly, India

Venue
Rotary Bhawan, Chaupla Road, Civil lines, Bareilly, Uttar Pradesh, India
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National Symposium on

Recent Trends in Bioinformatics Strategy for Disease Mechanism and Biomedicine

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Message

Dr. Bashah J. Khan
Director

I am delighted to say that the Bioinformatics Technologies of India is organizing the National Symposium on Recent Trends in Bioinformatics Strategy for Disease Mechanism and Biomedicine on 24th November, 2018.

Bioinformatics is an important field now a days, developed with efforts of basic biology, information technology and statistics. It has implications in various interdisciplinary domains of science which have to deal with major disease researches and their drug studies.

As I understand, the aim of National Symposium is to provide a platform for stimulating discussion on different aspects of disease mechanism, drug designing, cheminformatics studies etc. for better understanding of the targeted disease problems.

I wish the National Symposium 2018 which held at Bareilly a great success.

Dr. Bashah J. Khan

Regd. no. : 386/17-18

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Message

Dr. Kuldeep Kumar
Executive Director Research

On behalf of the Organizing Committee, I am extremely delighted to invite all the eminent speakers, invitees, delegates and our dear students to the National Symposium on Recent Trends in Bioinformatics Strategy for Disease Mechanism and Biomedicine on 24th November, 2018.

Bioinformatics innovation is a complex creative process that harnesses the application of knowledge and creativity for discovering, developing and bringing to clinical use, new medicinal products that extend or improve the lives of patients. We are going through a period of very stringent regulatory guidelines for drug discovery & development, which are undoubtedly essential to ensure the consumer health, but have severe effects on cost and time of new drug discovery and development. There is a need for paradigm shift in the approaches to new drug discovery and its development. This conference will provide an open forum to have an opportunity to interact with the leading scientists from across the globe and to enrich their knowledge in the area of bioinformatics and its regulatory requirements. Let us join our hands together to share our knowledge and experience that will go a very long way in helping to build up the healthy, prosperous and developed nation. As I Understand, the aim of National Symposium is to provide a platform for stimulating discussion on different aspects of disease mechanism, drug designing, cheminformatics studies etc for better understanding of the targeted disease problems.

I would like to convey thanks to all our plenary and session speakers as well as delegates for their valuable contribution. Attempts at all levels is being made by organizing committee to make your stay enriching, contended and amiable. I also kindly request you to pardon us for any inadequacies experienced by you.

We will greatly appreciate your active participation and ensure that you carry rich remembrances of this event with you.

Looking forward to meet you all.

Dr. Kuldeep Kumar

NATIONAL SYMPOSIUM
ON
“RECENT TRENDS IN BIOINFORMATICS STRATEGY FOR DISEASE MECHANISM AND BIOMEDICINE”
(November 24, 2018)

Programme Schedule

08:30 – 09:30 AM	**Registration**
09:30 – 10:30 AM	**Inaugural Session**
10:30 – 11:00 AM	**Keynote Lecture**
11:00 – 11:30 AM	**High Tea**
11:30 AM – 01:15 PM	**Technical Session – 1**
01:15 PM – 02:00 PM	**Lunch**
02:00 PM – 03:30 PM	**Technical Session – 2**
03:30 PM – 04:30 PM	**Poster Session**
04:30 PM – 05:00 PM	**Valedictory Session**

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ABSTRACTS

Xenogenic acellular periosteum along with epoxy-K wire external fixator augments the healing in large segmental bone defects in canine

Khangembam Sangeeta Devi and Anil Kumar Gangwar

Department of Veterinary Surgery and Radiology, College of Veterinary Science and Animal Husbandry, Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad (U.P.)
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Abstract

The present study was conducted on a client-owned three mongrel dogs (one having tumor of radius and other two cases with massive traumatic bone loss). The native periosteum of buffalo fetal origin was decellularised by treatment with 1% sodium dodecyl sulfate (SDS) for 18 hours under constant agitation. The bone defects in all the cases were transplanted with xenogenic decellularized periosteum scaffolds. Thereafter the bones were stabilized by epoxy K-wire external fixator. Postoperatively the animals were assessed by clinical (weight bearing on the affected limb, presence of discharge/infection at the site and overall functional recovery) and radiographic examination. Oxidant and antioxidant status of the patients was also determined. Soon after fixation weight bearing was good (grade 2-3). Almost full weight bearing (grade 3) was observed within 6 weeks. On day 7 the level of MDA decreased significantly. The level of SOD decreased significantly ($P<0.05$) up to day 7 thereafter the values increased significantly ($P<0.05$) on day 30. Significant ($P<0.05$) increase in the level of catalase was noted up to 30 days. Oxidative stress factor (OSF) was significantly ($P<0.05$) decreased up to day 7. At 6 weeks interval, the acellular periosteal scaffold was replaced by a narrow vital callus and the fracture gap was completely filled by bridging callus. Functional outcome was good to very good. Xenogenic acellular periosteal scaffolds were found biocompatible and it was concluded that these scaffolds along with epoxy-pin fixation can be used for the treatment of segmental bone defect in canines.

In-vitro expression profile of *HSP 70.1* and *HSP 90.1* genes in Peripheral Blood Mononuclear Cells of Indian native Tharparkar and crossbred Vrindavani cattle

Lakshya Veer Singh, G. Ravi Kumar, Shishir Kumar Gupta, Smita Gupta, Pragya Singh, Shweta Sharma, Aditya Prasad Sahoo, A. K. Tiwari

Molecular Biology Laboratory, Division of Veterinary Biotechnology, ICAR-Indian Veterinary Research Institute, Izatnagar, Bareilly, Uttar Pradesh, India[1]; Email: lakshyaveer@gmail.com

Abstract

Circulating peripheral blood mononuclear cells (PBMCs) can be used as an effective model to understand the heat stress response of different cattle types and buffaloes. Environmental temperature is one of the significant abiotic influences that impact the normal biological function and productive performance of dairy cattle. This investigation was undertaken to determine the temporal profile of HSPs (HSP70.1 and HSP90.1) expression in circulating PBMCs isolated from Tharparkar and crossbred (Vrindavani) cattle in response to lethal heat shocks at T40, T41 and T42 °C for 13 hours. The qRT-PCR expression data showed significant increase in mRNA levels of the both HSPs genes in heat stressed PBMCs. Out of two HSPs, HSP 90 was relatively more expressed followed by HSP70 in these two cattle types, indicating its prominent role as molecular chaperone to stabilize the native conformation of proteins. Also, the response elicited was different for both the cattle as the level of expression of HSPs throughout the time period of heat stress was higher in crossbred cattle than in Tharparkar. Results indicated that PBMCs from crossbred Vrindavani cattle are less tolerant to heat exposure than those from Indian native Tharparkar cattle, which is associated with higher expression levels of HSP70 and HSP90 genes.

New insights on microalgal biomass from biofuel production as a new generation of animal feed

Santosh Kumar, Sanjeev Porwal, Manish Sachan

Department of Botany, Government Girls Degree College, Kurawali, Mainpuri, U.P.
Department of Chemistry, Government Girls Degree College, Kurawali, Mainpuri, U.P.
Department of Zoology, Government Girls Degree College, Kurawali, Mainpuri, U.P.

Abstract

The continual rise in global population has led to a necessary exploration of alternative energy and food sources. Because corn and soybean meal are staple foods crops for humans and animals, their common inclusion in animal diets as the main sources of energy and protein directly competes with their allocation for human consumption. Alternatively, marine microalgae and its biomass from biofuel production demonstrate consistent viability as unconventional agricultural animal feed additives, owing to their lipidrich and well-balanced amino acid profiles. For biofuel production, certain algae species cultivated for lipid extraction are enriched in essential polyunsaturated fatty acids, including docohexaenoic acid and eicosapentaenoic acid, which lay claim to a broad spectrum of beneficial health effects. The biomass leftover may be incorporated into animal diets, and has shown to generate animal products like meat, milk, and eggs that are similarly fortifed with polyunsaturated fatty acids. Because of this, the incorporation of microalgal biomass into animal feeds is well-matched to alleviate food insecurity for both humans and animals, provide an alternative energy source in the form of biodiesel, promote more sustainable animal agriculture, contribute to reductions in environmental pollution through carbon sequestration, and procure additional value-added, nutrient-enriched animal products for human consumption.

Pharmacological and nutritive potential of *Euphorbia granulata*

Manish Sachan, Santosh Kumar, Sanjeev Porwal

Department of Zoology, Government Girls Degree College, Kurawali, Mainpuri, U.P.
Department of Botany, Government Girls Degree College, Kurawali, Mainpuri, U.P.
Department of Chemistry, Government Girls Degree College, Kurawali, Mainpuri, U.P.

Abstract

Background Euphorbia granulata is herb of family Euphorbiaceae having several traditional uses. Methods The papers on nutritional and medicinal value of E. granulata are collected from electronic search engines (Google Scholar, PubMed). Synonyms are confirmed from "The plant List." Results Pharmacological studies suggest that the extracts of E. granulata possess antioxidant, antibacterial, antifungal, diuretic, antiulcerative colitis and spasmolytic properties. Moreover, it is rich with nutritive components such as carbohydrates, lipid contents (saturated and unsaturated fatty acids), minerals and protein (amino acids). Toxicological data of E. granulata showed that it may be poisonous and toxic at higher doses. Conclusion Research studies suggest that E. granulata has sufficient pharmacological potential against several diseases including infections, gastric ulcers, anuria, oliguria and spasmodic disorders; however, more research is required to confirm its pharmacological potential. Moreover, dose fixation studies should be carried out to avoid its toxicity.

Graphene-based nanocomposites: synthesis and their theranostic applications

Sanjeev Porwal, Santosh Kumar, Manish Sachan

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Department of Zoology, Government Girls Degree College, Kurawali, Mainpuri, U.P.

Abstract

Graphene, the mother of all carbon materials, has unlocked a new era of biomedical nanomaterials due to its exceptional biocompatibility, physicochemical and mechanical properties. It is a single atom thick, nanosized, two-dimensional structure and provides high surface area with adjustable surface chemistry to form hybrids. The present article provides a comprehensive review of ever-expanding application of graphene nanomaterials with different inorganic and organic materials in drug delivery and theranostics. Methods of preparation of nanomaterials are elaborated and biological and physicochemical characteristics of biomedical relevance are also discussed. Graphene form nanomaterials with metallic nanoparticles offer multiscale application. First, graphene act as a platform to attach nanoparticles and provide excellent mechanical strength. Second, graphene improves efficacy of metallic nanoparticles in diagnostic, biosensing, therapeutic and drug delivery application. Graphene-based polymeric nanocomposites find wider application in drug delivery with flexibility to incorporate hydrophilic, hydrophobic, sensitive and macromolecules. In addition, grapheme quantum dots and graphene hybrids with inorganic nanocrystal and carbon nanotubes hybrids have shown interesting properties for diagnosis and therapy. Finally, we have pointed out research trends that may be more common in future for graphene-based nanomaterials.

Molecular gene cloning of Cyclophilin A (*CypA*) from *Triticum aestivum*

Ankita Gupta[1*], **Sanjeev Duby**[1]

1. Department of biotechnology, Govt. Model Science College, Rewa MP.
* Email: ankikeshari19@gmail.com

Abstract

Cyclophilin A (*CypA*), like protein conserved in all genera, is known to have good regulatory responses of various intra and extracellular processes including stress tolerance. Cyclophilin A (*CypA*) is a ubiquitously distributed intracellular protein belonging to the immunophilin family, which is recognised as the cell receptor for the potent immunosuppressive drug cyclosporine A. Interestingly; *CypA* has a crucial role as peptidyl-prolyl cis-trans isomerases (PPIases). Our target to make a gene clone of Cyclophilin A from the wheat plant and analysed the gene sequence with the database. In our recent report, we make a 781 bp long gene clone of Cyclophilins –A from wheat. Here, we make a cyclophilin-A gene clone from *Triticum aestivum* which is responsible for abiotic stress tolerance in wheat.

The retrieved sequence data analysis suggested that gene; the *CypA* sequence showed about 100% -99% with other Cyclophilin A gene sequence. The conclusion of this study conclusively indicates that *CypA* gene of wheat is highly conserved in most of the wheat *spp.* as analogous to patterns of other plants.

Production and Optimization of an Alkaline Protease from *Bacillus subtilis* Isolated from Soil Samples

Krishna Ash and Sushma

Department of Biochemistry & Biochemical Engineering, JIBB, Sam Higginbottom University of Agriculture, Technology and Sciences (SHUATS), Allahabad, Uttar Pradesh, India

Abstract

Protease enzymes have immense commercial value and play a pivotal role in application of various industrial sectors. Microbial proteases are one of the important groups of industrially and commercially produced enzymes which have several applications. In this study 148 bacterial strains were isolated from 50 different soil samples of slaughter house, fish market and sewage wastes of Lucknow, Uttar Pradesh, India. Out of which thirty eight strains competent of secreting extracellular alkaline protease. In preliminary screening the isolate SSB3 showed highest ability to hydrolyzed casein and skimmed milk which was done on skim milk agar media. Based on biochemical test the isolate showed positive for casein, starch, catalase and negative for gram staining, indole, methyl red, voges-proskauer, gelatin, urea, oxidase, hemolysis and triple sugar iron test and found to be non motile. Strain SSB3 with the maximum yield alkaline protease was identified as *Bacillus subtilis* based on nucleotide homology and phyogenetic analysis (16S rDNA sequencing). Protease production was enhanced by optimizing the culture conditions. Many physical parameters were studied to optimize the maximum yield of alkaline protease. The maximum enzyme activity were observed with optimum incubation time, temperature, pH, carbon, nitrogen sources, NaCl and metallic ions were determined as 36 h, 37°C, pH 11.0, 1% glucose, 1% yeast extract, 1M NaCl, and 1mM Zn^{2+}, respectively for protease production. The study revealed that the strain of *Bacillus subtilis* is a potent source of alkaline protease. In consequence, such additions can supplement alkaline protease production and their application in various industries.

Lysozyme - An good quality biomolecule to understand Protein Mass Spectrometry

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Abstract

Mass spectrometry (MS) plays a fundamental position in identifying number one structures of proteins and their post-translational changes. The study performed to recognise the current MS strategies in protein characterisation and a bottom-up approach for protein identification. We used hen lysozyme as protein biomolecule and carried out numerous strategies like direct MS and LC-MS/MS. ESI mass spectra of lysozyme recorded in advantageous ion polarity using ion trap and orbitrap. The spectrum has proven multiple protonated adducts of lysozyme while the high resolution offered by orbitrap is absolutely obtrusive from the observation of isotope peaks corresponding to [M+10H] 10+. The reduced-alkylated lysozyme becomes subjected to proteolysis by trypsin digestion. The digested product was separated by reverse phase chromatography (attached with mass spectrometric), then characterised via LC-ESI-MS/MS. In LC-ESI-MS full spectrum, the peaks at m/z 838.40 and 902.45 had been recognised to be due to tryptic peptides as a consequence of reduced-alkylated lysozyme. Means of the bottom-up proteomic technique showed the sequences of these peptides. The study concluded that the chicken lysozyme is one of the appropriate molecules to study protein Mass Spectrometry.

Production of Extracellular laccase from Bacterial Strain *Pseudomonas putida* using different Parameter

Sarvesh Kumar Mishra and Shailendra Kumar Srivastava

Department of Biochemistry & Biochemical Engineering, JIBB, SHUATS, Allahabad, India

Abstract

Laccase is the model enzymes for multi-copper oxidases can be used in bioremediation, beverage processing, ascorbic acid determination, baking, as a biosensor and to improve food sensory factors. An effort was made to screen, optimize and production of laccase enzyme produced by the consortium of laccase producing *Pseudomonas putida*. Up to the present time, laccases connect mostly been unaided and characterized from flora and fauna and fungi, and unaided fungal laccases are used currently in biotechnological applications. In contrast, little is known just approximately bacterial laccases, although recent immediate assume ahead in the combined genome analysis suggests that the enzymes are widespread in bacteria. Since bacterial genetic tools and biotechnological processes are skillfully conventional, therefore developing bacterial laccases would be significantly important. Laccase activity was determined by measuring the oxidation of guaiacol at 530 nm. Laccase activity was maximum when manage at the following conditions, 60 hr. incubation, 40 °C temperature, and pH-8, 2 % nitrogen sources, 3 % peptone and beef extract and 2 % carbon sources, glucose and sucrose in the production medium. This research summarizes the distribution of laccases among bacteria, and able to producing maximum laccases at the most advantageous conditions.

A perspective on management of *Helicoverpa armigera* (hubner)

Santosh K. Bisen

Deptt. Of zoology Govt S.S.P college Waraseoni Distt Balaghat

Abstract

Helicoverpa armigera is a major pest of agriculture, horticulture and floriculture throughout the old world and recently invaded parts of the new world. We overview of the evolution in thinking about the applications of the area wide approaches to assist with its control by the cotton and agriculture approaches are highlight important lessons and future and challenges to achieving the same in the new world. An over reliance of broad spectrum insecticides lead to Helicoverpa spp. in Indian gram crop rapidly become to resistant to DDT, synthetic pyrethroids, organophosphate carbonates and endosulphan. Voluntary strategies were developed to show the development of insecticide resistance, which included rotating chemistries and basing spray decisions on threshold. Despite adoption of these practices, insecticide resistance continued to develop until the introduction of genetically modified cotton provided a platform for augmenting integrated pest management in the gram crops. Compliance with mandatory resistance management plans for gram crop necessitated a shift from pest control at the level of individual fields or farms towards a coordinated area wide landscape approach. Our take home message for control of H. armigera is that resistance management is essential in genetically modified crops and must be season long and area wide to effective.

Novel Drug delivery in Mucoadhesive Polymers

P. Bhavesh, P. Arun, D. Nilesh, P. Shailendra

Abstract

Mucoadhesive drug delivery systems, are gaining popularity day by day in the global pharma industry and a burning area of further research and development. Extensive research efforts throughout the world have resulted in significant advances in understanding the various aspects of mucoadhesion. The research on mucoadhesives, however, is still in its early stage, and further advances need to be made for the successful translation of the concept into practical application in controlled drug delivery system (CDDS). There is no doubt that mucoadhesion has moved into a new area with these new specific targeting compounds (lectins, thiomers, etc.) with researchers and drug companies looking further into potential involvement of more smaller complex molecules, proteins and peptides, and DNA for future technological advancement in the ever-evolving drug delivery arena The current article focuses on polymers used in mucosal delivery of therapeutic agents. The mucoadhesive drug delivery system is a popular novel drug delivery method because mucous membranes are relatively permeable, allowing for the rapid uptake of a drug into the systemic circulation and avoiding the first pass metabolism. Mucoadhesive polymers have been utilized in many different dosage forms in efforts to achieve systemic delivery of drugs through the different mucosa.

Current Scenario Prevalence of Bovine Tuberculosis in India

Sanjeev Kumar Shukla[1], **Shubhra Shukla**[2]

Bioinformatics Technologies of India, Bareilly, U.P., India[1,2]

Abstract

Bovine tuberculosis (bTB) is a chronic disease of cattle that impacts productivity and represents a major public health threat. Despite the considerable economic costs and zoonotic risk consequences associated with the disease, accurate estimates of bTB prevalence are lacking in many countries, including India, where national control programmes are not yet implemented and the disease is considered endemic. To address this critical knowledge gap, we performed a systematic review of the literature and a meta-analysis to estimate bTB prevalence in cattle in India and provide a foundation for the future formulation of rational disease control strategies and the accurate assessment of economic and health impact risks.The analyses further suggest that production system, species, breed, study location, diagnostic technique, sample size and study period are likely moderators of bTB prevalence in India and need to be considered when developing future disease surveillance and control programmes. Taken together with the projected increase in intensification of dairy production and the subsequent increase in the likelihood of zoonotic transmission, the results of our study suggest that attempts to eliminate tuberculosis from humans will require simultaneous consideration of bTB control in cattle population in countries such as India.

Recent Update of *Mycobacterium marinum* in India

Shubhra Shukla[1], **Sanjeev Kumar Shukla**[2]

Bioinformatics Technologies of India, Bareilly, U.P., India[1,2]

Abstract

Mycobacterium marinum is a well-known pathogenic mycobacterium for skin and soft tissue infections and is associated with fishes and water. Among nontuberculous mycobacteria (NTM), it is the leading cause of extrarespiratory human infections worldwide. In addition, there is a specific scientific interest in *M. marinum* because of its genetic relatedness to Mycobacterium tuberculosis and because experimental infection of *M. marinum* in fishes mimics tuberculosis pathogenesis. Microbiological characteristics include the fact that it grows in 7 to 14 days with photochromogenic colonies and is difficult to differentiate from Mycobacterium ulcerans and other mycolactone-producing NTM on a molecular basis. The diagnosis is highly suspected by the mode of infection, which is related to the hobby of fishkeeping, professional handling of marine shells, or swimming in nonchlorinated pools. Clinics distinguished skin and soft tissue lesions (typically sporotrichoid or subacute hand nodules) and lesions disseminated to joint and bone, often related with the local use of corticosteroids. In clinical microbiology, microscopy and culture are often negative because growth requires low temperature (30°C) and several weeks to succeed in primary cultivation. The treatment is not standardized, and no randomized control trials have been done. Therapy is a combination of surgery and antimicrobial agents such as cyclines and rifampin, with successful outcome in most of the skin diseases but less frequently in deep tissue infections. Prevention can be useful with hand protection recommendations for professionals and all persons manipulating fishes or fish tank water and use of alcohol disinfection after contact.

Prevalence of *Listeria* in fruit juices as well as fruits

K.K. Meena, K. Kumar, G. Gupta and D. Shrivastav

School of Life Sciences, Jaipur National University, Khorebariyan, Jagatpura, Jaipur, Rajasthan, India

Abstract

Listeria monocytogene is an important food associated pathogens. Human listeriosis ranks among the most frequent cases of death due to foodborne illness. The ability to persist in food processing environments and multiple under refrigeration temperature makes *L. monocytogenes* a significant threat to public health. Fruits form an important component of human diets of healthy as well as sick and convalescing human of all age. Since fruits are consumed raw, it may be a source of infection. But little is known with respect to presence of pathogens such as *Listeria* in fresh and raw fruits. In the present study, an attempt was made to find out prevalence of *Listeria* fruits and fruit juices.

A total of 217 samples of fruits and fruit juices were collected from different city, which consisted Litchi (37), Aalubukhara (50), Mango juice (55) and Orange juice (75) and examined bacteriologically for presence of *Listeria*. Out of these 217 samples, *Listeria* could be isolated from 10 (4.60%) of the samples, 8 and 2 of which were from fruits and fruit juices, respectively. All the 8 isolates from fruits were recovered from Litchi. One of the 2 isolates from fruit juice was recovered from Orange juice while one was from Mango juice. Antibiotic sensitivity of the *Listeria* isolates was studied against 24 antibiotics. All the *L. monocytogene* isolates were resistant to ceftazidin, methicillin, nalidixic acid, penicillin-G and ticarcillin. These were highly sensitive to gentamycin and tetracycline while 2 isolates of *L. monocytogenes* were sensitive to amphicillin, cephalexin, chloramphenicol, ciprofloxacin, ofloxacin and trimetthoprin. The isolation of *Listeria* from fruits and fruit juices through low, indicate the public health problem which may arise because of consumption of these.

Prevalence and Molecular Characterization of *Salmonella* isolated from in Meat products from Retail Outlets of India

Kuldeep Kumar and P.C. Lakhera

Department of Biotechnology, HNB Garhwal Central University, Srinagar Garhwal, Uttarakhand

Abstract

The present study was aimed to investigate and characterize Salmonella in meat sold in retail outlets of Uttar Pradesh, India. A total of 300 samples including 100 samples each of chicken, mutton and beef were collected over a 2-year period and examined for the presence of Salmonella. Based on cultural characterization, the overall prevalence of Salmonella was 4 % (12/300) and the prevalence of Salmonella in Chicken, mutton and beef were 1% (1/100), 4% (4/100) and 7% (7/100) respectively. Serotyping results indicated that of the 12 confirmed Salmonella isolates, 3 (25%) belonged to S. Typhimurium, 5 (41.66%) to S. Virchow and remaining one (8.33%) each of S. Heidelberg, S. Hato, S. Bsilla and Salmonella rough strain. Molecular detection of Salmonella based on invA gene revealed that 12 of the tested sample to be positive with specific amplification of a 284 bp fragment.

Molecular characterization and its expression pattern in the Mung bean

Mukul Kumar

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Abstract

Mung bean is the most important legume pulse crops in the world, it is well known for its high content of good quality seed protein for food. Mung bean grow best in full sun in well-drained sandy loam soil with moderately dry conditions. The olive-green mung beans should be harvested in the field after their pods have dried. In mung bean genotypes,variation in protein (20.6 to 24.1%), starch (45.8 - 49.5%), soluble sugar (7.1 to 8.9%) and crude fiber content (2.9 to 4.3%) with low fat content (below 2.3%).The appropriate water supply method for heterotrophic cultivation and the present study was to evaluate the heterotrophic growth behaviour of mung beans cultivated. Oxygen uptake and carbon dioxide evolution rates were calculated using a growth curve, and the changes in oxygen and carbon dioxide concentrations in a mung bean sprout bed. The growth in heterotrophic cultivation can be classified into three stages by growth status change in growth rate. Manipulation of the key enzymes of phytic acid biosynthesis pathway can be a probable approach for generating low phytate mung.The phytic acid biosynthetic pathway reveals the terminal enzyme Inositol pentakisphosphate 2-kinase (IPK1) to be one the most important enzyme controlling the metabolic flux of phytate generation. Amino acid sequence of GmIPK1 showed much similarity with that of *Glycine max* and Cicer arietinum. It also showed the presence of the characteristic Ins_P5_2-kinase domain required for catalytic activity Multiple alignment of the selected amino acid sequences of the homologs of IPK1 from different plants were performed using Clustal Omega program. phylogeny of homologs of IPK1 illustrated a high degree of divergence of legume IPK1s and with that of other plants and only there was conservation of catalytic domains in the IPK1 homologs. This study provides an initial idea on the molecular characterization of GmIPK1 enzyme for its further in detailed study and subsequent utilization in generating low phyate mung with enhanced mineral bioavailability.

Phytochemical Screening and *In vitro* anti-cancer activity of methanolic leaves extracts of *M. Esculenta* (kafal) and *Cardamom* (Elaichi grass) against heLa cell lines

Manoj Kalakoti, Pragya Pandey, Mahesh Kumar

Institute of Biotechnology, G.B. Pant University of Agriculture & Technology, Patwadangar, Nainital, Uttarakhand

Abstract

To investigate the phytochemical constituents and *in vitro* anticancer properties of methanolic leaves extract of *M. esculenta*(kafal) and *Cardamom*(Elaichi grass). Methanol solvent was used for the preparation of the crude leave extract of both the plants and phytochemical analysis test were performed. The plants have been used for very long times in traditional system of medicine as anti inflammatory agent and in wound healing. The anticancer activities of the extracts of two plants were determined by MTT assay against HeLa cell lines at concentration of 100 mg/ml. As per phytochemical study, methanolic extract of *M. esculenta* (kafal) leave contain alkaloid, phenol & tannins, flavanoids content and various other secondary metabolities**.** Screening also confirm the presence of alkaloids, steroid and carbohydrates, tannins, lignins and reducing sugar inmethanolic leaves extract of *Cardamom* (elaichi). Results of MTT assay concluded that the leaves extract of *M. esculenta* (kafal) showed effective activity against HeLa cell lines with the percent cell growth inhibition (49.76±1.26%) at the concentration dose of 100 mg/ml. The methanolic leaves extract of *Cardamom* (elaichi) revealed moderate effects on cancer cells with cell growth inhibition (25.16±1.55%). Based on this study, result provides some evidence for anticancer activities of these plants which could be useful for developing new anticancer therapies.

In-vitro anti-cancer activity and phytochemical Screening of *Cinnamomum virum* (Dalcheeni) bark extract of methanol against heLa cells

Manoj Kalakoti, Pragya Pandey, Mahesh Kumar

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Abstract

Cinnamomum virum (Dalcheeni) bark methanolic extract was used to evaluate the phytochemical constituents and *in vitro* anticancer properties by using MTT assay against HeLa cell lines. Active phytoconstituents of methanolic bark extract alkaloid, tannins, flavanoid, saponins, glycosides and trace amount of tannins**.** MTT assay result showed effective cytotoxity activity of bark extract against HeLa cell lines at the concentration 100 mg/ml with the percent cell growth inhibition (47.94±0.21%) after 24 hrs. This study concludes that the present phytochemicals of *Cinnamomum virum* bark extract have significant anticancer activity on Hela cells.

To evaluate *In-vitro* Anti-Cancer activity and phytochemical analysis of *Dactylorhiza hatagirea* plant root extracts against cancer cells

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Abstract

Cancer had always been the most serious disease in humans around the world due to its high morbidity and mortality. The objective of the present study was to investigate the *in vitro* anticancer properties of plants *Dactylorhiza hatagirea* (Salam punja) roots extract extracted from methanol, aqua-methanol and aqueous solvent. Due to its high medicinal and edible value and also its rare availability, the species has great demand in national and international market. The MTT assay test results were used to evaluate the anti-cancerous activity of the root extracts of plant against HeLa cell line. The analysis of phytochemical confirmed that the alkaloid, phenol& tannins, flavanoids content with various phytoconstituents were found to be more active in aqueous root extract of *D. hatagirea*. Less amount of secondary metabolites were revealed in the methanolic root extract of plant. Results obtained from the assay indicates the effectiveness ofaqueous root extract of plant with per cent cell growthinhibition 59.89±1.34% of cancer cell line at the concentration of 100 mg/ml. Least activity was noticed in methanol extract with cell growth inhibition 29.16±0.98% at the concentration dose of 100 mg/ml. The effectiveness of the plant could be due to the presence of secondary metabolites, which can be used as valuable information for further studies and investigation on *in vivo* animals for possible development of anticancer drug.

Expressway for identification of viral suppressor of RNA silencing

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Abstract

Resistance to pathogen infection in plants is defined through a spectrum ranging from reduced susceptibility, moderate susceptibility to hypersensitive response (complete resistance). Several OMICs tools have emerged, along with genomics, to elucidate resistance mechanisms of plants to pathogens. Amongst these RNA silencing plays an important role in shielding plants from viral infections by restricting its replication and systemic spread in the host. Suppressors of RNA silencing (RSS) act in the counter-defense for viruses by restricting the silencing pathways at different steps of the biogenesis or function of the small RNA. The suppressor functions have been acquired by already existing viral proteins so they do not share any evolutionary homology or pattern. They are diverse not only in sequence but also in the ways they suppress the silencing machinery. These facts pose a challenge to the scientific community to identify suppressor molecules and understand the mechanism of virus infection to design effective strategies to counter the viral attacks. Small circular ssDNA satellites encode a βC1 gene associated with Chilli leaf curl virus (ChiLCuV) which is positionally and functionally conserved. The precise function of betasatellite and its encoded βc1 protein in pathogenesis is unknown, even though it has been suggested that DNA β may play a direct or an indirect role in replication, facilitating movement or countering host defense response. The ability of the Chilli leaf curl virus betasatellite (ChiLCuβ) encoded βc1 to suppress PTGS was investigated by using Nicotiana benthamiana hairpin line harbouring a post transcriptionally silenced green fluorescent protein (hp-GFP) transgene. Inoculation of hp-GFP plants with a recombinant pCAMBIA 1302 vector carrying ChiLCuβ- βc1 resulted in restoration of GFP expression. RT-PCR analysis confirmed that the observed GFP fluorescence was associated with GFP mRNA transcript accumulation. Inoculation with recombinant pCAMBIA 1302 vector carrying ChiLCuβ- βc1to naturally GFP silenced line, were similarly shown to result in hp-GFP silenced plants with restored GFP expression indicating that betasatellites are involved in overcoming host defense. Here we present a simple, quick and reliable strategy to identify a suppressor activity of ChiLCuβ- βc1 through the GFP based in-planta reversal of silencing assay. This strategy can be used to measure the suppressor activity as well as strength of suppressors of any viral protein which provide useful biological insight for new avenues in RNA Silencing.

Effect of herbal liver stimulants on growth and performance of broiler chicks

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Abstract

The study was carried out to evaluate the effect of herbal liver stimulants on growth and performance of broiler chicks. Hundred-day old commercial broiler chicks were randomly selected and were divided into four groups (G1, G2, G3, and G4) comprising of 25 chicks in each group. Treatment groups G2, G3, and G4 were provided 3ml, 6ml and 9 ml herbal liquid liver stimulant in drinking water per 25 chicks per day for 0-3 weeks on starter ration and 6ml, 9ml and 12ml herbal liquid liver stimulant per 25 chicks per day on finisher ration respectively, In the control group G1 no addition feed supplement given for 0-3 and 3-5 weeks. The body wt. at five weeks of age was 1210.0, 1255.0, 1278.0 and 1290.0 gm in group G1, G2, G3, and G4, respectively. Feed conversion efficiency upto fifth week in group G1, G2, G3, and G4 was 1.90, 1.89, 1.88 and 1.87, respectively. The dressing percent was 73.44, 74.66, 74.91 and 75.81, respectively in all the groups. It was observed from the study that growth rate, feed conversion efficiency and dressing percentage were significantly higher in herbal liver stimulant feed supplemented groups compare to control. This indicates incorporation of herbal liver stimulant feed supplement in broiler ration level @ 9 ml/100 broiler chicks/day upto 0-3 weeks of age and @12 ml/100 broiler chicks/day 3-5 weeks of age is profitable in broiler production.

Myxobolus nobilisii sp. nov. (Myxosporea: Myxozoa) causing severe gill disease in *Hypophthalmichthys nobilis* in Ranjit Sagar Wetland, Punjab (India)

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Abstract

The Indian major carp, *Hypophthalmichthys nobilis* (Hamilton, 1822) is a tropical freshwater cyprinid fish native to inland waters in Asia. During the present study, a novel myxosporean parasite was found infecting the gill lamellae of *H. nobilis* from Ranjit Sagar Wetland in Punjab, India. Myxospores were pyriform with elongated anterior end and round posterior end; length 9.66± 0.09 µm, width 5.0± 0.01 µm. There were two polar capsules of un-equal length, length of larger polar capsule 4.31± 0.07 µm, width 2.31± 0.02 µm, length of smaller polar capsule 4.0± 0.05 µm, width 2.10± 0.03 µm with 8-11 turns of the polar filament. The 440 bp 18S rDNA sequence was up to 97% similar to *M. catlae* from other cyprinid fishes in India. Histopathology was also studied which showed the plasmodia of *M. nobilisii* sp. nov. to be located in the the gill lamellae of *Hypophthalmichthys nobilis* and were typed as 'Intralamellar-vascular type, LV2'. This type of plasmodia leads to deformation of whole of the infected gill lamellae, therefore causing maximum loss of respiratory surface. In having, unique myxospore morphology, histopathology and 18S rDNA sequence, we propose *Myxobolus nobilisii* as new to science.

Myco-fabrication of metal nanoparticles: An approach towards sustainable agriculture

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Abstract

Variable properties of atoms and molecules at nanoscales in contrary to their bulk counterparts have been captivating and draws the attention towards the surplus roles of these minute particles in solving the plethora of problems specially addressing the agricultural sector in the 21st century. The present era of research and commercialization are making an approach towards more ecofriendly fabrication of such nanomaterials. The current study adds on to one such strategy and focuses on the application of fungi as biofactories. Apart from intensively studied fungi like Fusarium, Aspergillus, Verticillium, and Penicillium Several other genera specially soil mycota needs to be explored for formation of different nanoparticles and their characterization for future implementation required to be focused on. we drive our interest onto Trichoderma - a common soil fungi possessing extreme metal tolerating capacity and also well known for its myriad of extra cellular secretomes. Different species of the fungi will be screened for various metal nanoparticles and their characterization will be ensured by TEM, SEM, X-ray crystallography and spectroscopic techniques. We hope to get more monodispersed particles by controlling the physical reaction measures like pH, temperature, incubation time etc. and also draw a specific relation between these parameters and shape, size of the nanoparticles so produced.

In silico Studies of Pharmacokinetic Properties of Noval Drug Molecules docked on Il-6 leads to Drug Discovery and Design

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Abstract

Pharmacokinetic (PK) includes the study of mechanisms of absorption and distribution of an administered drug. Pharmacokinetic literally means the movement of drugs. It is more commonly defined as “what the body does to the drug”. PK study is split into four process: Absorption, Distribution, Metabolism, Excretion (ADME). Many of the failure of drug candidates in development programs are attributed to their undesirable pharmacokinetic properties such as poor absorption and extensive first-pass metabolism. To ensure the success of a drug candidate it is essential that a drug has good bioavailability and desirable T1/2.Therefore, an accurate estimate of the PK data and good understanding of factors that affect the PK guide drug design. Drug discovery and development is an intense, lengthy and an interdisciplinary endeavor. The use of computers and computational methods parameters all aspects of drug discovery today and forms the core of structure-based drug design. High-performance computing, data management software and internet are facilitating the access of huge amount of data generated and transforming the massive complex biological data into workable knowledge in modern day drug discovery process. Today, the process of drug discovery has been revolutionized with the advent of genomics, proteomics, bioinformatics and efficient technologies like, combinatorial chemistry, high throughput screening (HTS), virtual screening, *de novo* design, *in vitro, in silico* ADME/T screening and structure-based drug design. This study includes a discussion of PK and the importance of PK in drug discovery.

TOXICOLOGICAL EFFECT OF MERCURIC CHLORIDE ON THE REPRODUCTIVE CYCLE OF THE TELEOST FISH (*Channa punctatus*)

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Abstract

It is well known fact that the synthetic chemical insecticides and peesticides have caused severe environmental damage before and after their use. Before their use, chemical factories spread pollutiion during their production and after their use, they are toxic to non-target organisms. Non-degradability, bioccumulations and bio-magnifications cause them highly toxic to nature. Some plant species produces secondary metabolites. They are found in leaves, fruits, seeds, barks and roots of plant species. Chemically, secondary metabolites are Anthrocyanins, Anthroquinones, Carotenoids, Chalcones, Alkalanoids, Coumestanes, Deoxyflavones, Flavanoids, Litnnoids Tannins, Steroids and Rotenoids. Many secondary metabolites have been reported to be insecticidal or pesticidal effects by many scientists and workers. Plant origin chemicals are biodegradable and break down into non-toxic substance in a short time period. Present paper deals with some local plant origin chemicals as ecofriendly green chemicals to reduce synthetic chemicals and pollutions. It is need of the day.

Antibiotic Resistance Pattern of *Salmonella* Typhimurium

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Abstract

Antimicrobial resistance pattern of 104 isolates of *Salmonella* Typhimurium identified over last three decade at the National Salmonella Centre (Vet.) revealed 83 antibiotic resistance patterns. One of the isolates showed resistance to as many as 12 drugs and similarly another isolate showed resistance to 10 drugs. There were 27 isolates which showed resistance to 5 to 9 antibiotics. Furthermore, resistance to 4 antibiotics was shown by 8 isolates.

Highest resistance was observed with doxycycline hydrochloride (36.53%), and tetracycline (36.53%), followed by neomycin (33.65%), kanamycin (32.69%), amoxicillin/clavulanic acid (29.80%), furazolidone (25.96%), tri-methoprime (22.11%), chloramphenicol (22.11%) and amikacin (19.23%). On the other hand *Salmonella* Typhimurium were found to be the most sensitive to gentamicin (92.31%), cefoperazone (86.53%), ceftazadime (83.65%), ciprofloxacin (83.65%), streptomycin (85.57%), ceftazidime (83.65%), ceftriaxone (81.73%), and cephotaxime (78.84%). The study of antibiotic drug resistance pattern according to source indicated that the poultry isolates showed maximum (26) resistance pattern followed by isolates from mare (6), mice (6), rabbit (5), guinea pig (5), pig (5), chick (8), dairy product (5) sewage (4), calf (3), duck (3), monkey (3), lizard (2), goat (2), buffalo meat (2), dog (1), fish (1), (1), human (1), and food products (1).

The results also indicated that there was marked increase in resistance to most of the antibiotics tested after the year 1980 with variations in between. However, some of the antibiotics such as cefoperazone, gentamicin, ciprofloxacin, streptomycin, and chloramphenicol did not show much change in resistance pattern over the years.

Occurrence of Multi-drug Resistance *Salmonella* and *E. coli* in Vegetables

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Abstract

An increasing association between fresh vegetables and foodborne infection outbreaks has led to concern about contamination of vegetables with fecal pathogenic bacteria in the agricultural environment. In our study two hundred samples of foods of plant were screened for *Salmonella* and *E. coli* including 50 each of Mint, Coriander, Cucumber and Green Chilli. Samples collected from the retail market/ road side venders in and around Bareilly were studied for their antimicrobial resistance pattern against 16 antimicrobial agents. From 200 samples no any isolate of *Salmonella* found and on the other hand 41 isolates of *E coli* have found. Maximum resistance was encountered with amoxyclav (75.60%) followed by nitrofurantoin (70.73%), co-trimazine (63.41%), co- trimoxazole (43.90%), nalidixic acid (43.90%), cephalorodine (41.46%), amphicillin (39.02%), colistin (21.95%). The resistance percentages of other drugs like streptomycin, cephalexin, ciprofloxacin, nitrofloxacin, chloramphenicol, cephotaxim and amikacin are 19.51%, 17.07%, 14.63%, 14.63%, 12.19%, 17.31% and 4.87% respectively. Among the 41 strains of *E. coli,* 34 resistance patterns were observed. One of the isolates showed resistant to as many as 10 drugs and 4 isolates showed resistance to 9 drugs. There were 18 isolates which showed resistance to 5 to 8 antibiotics and remaining isolates were resistant to 1-4 drugs.

Due to the Adonistration of Vitamin A to First Pregnant Cattle changes in Weight and Harmones

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Abstract

Reproduction being a luxury function, nutrition plays a primary role for its optimum expression. Apart from energy and protein intake, the micronutrients (vitamins and minerals) are highly essential for better reproductive efficiency. Though these micronutrients are required in very minute quantities, they are considered indispensable for normal cellular metabolism, growth and maintenance including reproduction. The beneficial effects of vitamin A in controlling various maladies causing reproductive failure have been well documented. The aim of this study was to determine the weight and hormonal changes through the administration of vitamin A to pregnant for the first time in growing beef cattle. A total of 28 Korean cattle used for this aim. The cattle were allocated to two groups as pregnant (n=14) and nonpregnant (n=14). Body weight increased of the vitamin A treated animals. Progesterone level was higher from 5-7 months during pregnancy in the animal treated with vitamin A which is similar the slandered concentration. In conclusion nvitamin A supplementation could improve growth and development of cattle with fertility impairment.

Food: Nutraceutical Aspect

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Abstract

An apple a day keeps the doctor away means that eating nutritious food will make you healthier. The health and wellness of human beings is largely dictated by the consumption of nutritious foods. Consumption of biologically active ingredients in fruits and vegetables has been linked to help combat diseases such as cancer, cardiovascular diseases, obesity, and gastrointestinal tract disorders. Nutraceutical can be defined as a food or part of food or nutrient that provides health benefits including the prevention and treatment of a disease. Nutraceuticals may offer many benefits: May increase the health value of our diet, May help us live longer, May help us to avoid particular medical conditions, May have a psychological benefit from doing something for oneself, May be perceived to be more "natural" than traditional medicine and less likely to produce unpleasant side-effects. Food products used as Nutraceuticals are categorized as Prebiotics, Dietary fibre, Omega 3 fatty acid and Antioxidant. All therapeutic areas such as anti-arthritic, painkillers, cold and cough, sleeping disorders, digestion and prevention of certain cancers, osteoporosis, blood pressure, cholesterol, depression and diabetes have been covered by nutraceuticals. Methods to enhance active components in foods by manipulating the diet to get maximum level of active components are Combination of food ingredients rich in Nutraceutical, Fortifying food with active ingredients, by fermentation of food products and changing food habits to natural type of diet. Diet rich in Nutraceutical along with regular exercise, stress reduction and maintenance of healthy body weight will maximize health and reduce disease risk.

PEPTIDE VACCINES AND THEIR USES IN DISEASE PREVENTION

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Abstract

Peptide vaccine contains specific epitopes of an antigen are usually composed of 20–30 amino acids. As these peptide vaccine constructs can be considered proteins on the basis of their size, the use of protein engineering techniques is feasible for their synthesis. These vaccines have been shown effective in preventing animal infection in some instances, and various formulations are under evaluation for their potential clinical use in humans. Peptide vaccine have several advantages over conventional vaccine because of its easy synthesis with low cost, increased safety and relatively safe. Promising results have been obtained with hepatitis B virus, respiratory syncytial virus, human papillomaviruses, bovine leukemia virus, feline immunodeficiency virus and hepatitis C virus. In the case of the Human Immunodeficiency Virus type-1 (HIV-1) infection peptide vaccine is useful because virus neutralize humoral responses because of presence gp41 transmembrane subunit on membrane-proximal external region (MPER). Identification of linear B-epitope that embodies an HIV vulnerability site was useful for focusing humoral responses to MPER by peptide-based immunogens is a pursued goal in HIV vaccine development. Peptides vaccines are more advanced than conventional vaccine.

PROSPECT OF *AZOLLA* IN KOSHI REGION OF BIHAR

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Abstract

To meet the present and future demands of the growing human population, certain new strategies are to be adopted to meet the input requirement for production of crop, livestock and their by-product. The search for alternatives to green manure, feed and fodder for different species of plants and animals, a wonderful plant called "*Azolla*". Despite was introduced and popularize since the early 1990's, it has not been a lot for farmers of *koshi* region of Bihar, who used *Azolla* plant for his farming. In fact, the benefit of aquatics plants this one quite a lot. *Azolla* an aquatic floating fern is an excellent biofertilizer used as green manure in rice cultivation, feed for livestock and employed as bioremediation of polluted soil and water bodies and reclamation of saline soil. The ability of this fern is to fix atmospheric nitrogen at a faster rate due to the presence of heterocystus cyanobacterium Anabaena-Azollae. It is also a very rich source of proteins, essentials amino acids, vitamins, growth promoter and minerals because of high nutritional quality it becomes as an ideal feed for livestock. Azolla suppresses tender weed growth and minimize evaporation losses of soil water. As a green manure azolla influences soil physical, chemical and biological property of soil. Basal application of azolla green manure @ 10-12 tones ha^{-1} increases soil nitrogen by 50-60 kg ha^{-1} and reduces 30-35 kg of nitrogenous requirement of rice crop. Azolla may be used for the production of hydrogen fuel and biogas, control of weeds and mosquitoes and reduction of ammonia volatilization. Azolla can be multiplied in nursery plots, ponds, ditches, concrete tanks and polythene limed ditches. So, the attention is required in *koshi* region of Bihar to addresses certain key issue in azolla for its exploitation and better employment in agriculture and allied sectors.

Impact of water hyacinth compost, vermicompost and inorganic fertilizers on soil enzyme activity and microbiological properties of a Typic Ustifluvents

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Abstract

A field experiment was conducted during *rabi* 2014-15 in sandy loam soil of Agro-climatic Zone-II of Bihar at Mandan Bharti Agriculture College, Agwanpur, Saharsa to examine the effect of soil enzyme urease and microbial population under organic and inorganic farming practices in wheat. The experiment was designed in split plot design with NPK levels in main plot and organic sources in sub-plot. Wheat (*variety* DBW-14) was grown for present investigation. The organic fertilizer used was compost made from water hyacinth, vermicompost while on the other hand for inorganic fertilizer, a mixture of urea, single super phosphate and muriate of potash was used. Total bacterial population was counted by soil dilution and plating techniques using Asperagine-Mannitol Agar medium whereas fungal counted on Rose Bengal Streptomycin Agar medium by pour plate techniques. Population of actinomycetes was enumerated using KenKnight and Munaieer's medium by pour plate method. There was considerable increase in the population of bacteria, fungi, actinomycetes as well as urease activity with application of chemical fertilizer and organic manure alone or incombination. The population of bacteria, fungi, actinomycetes as well as soil urease enzyme activity increased significantly in the organic manure treated soil compared with the chemical fertilizer treated soil.

Introgressions of gene for tomato leaf curl virus [ToLCV] resistance/ tolerance in tomato (*Solanum lycopersicum* L.)

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Abstract

Tomato (*Solanum lycopersicum* L.) belongs to the family Solanaceae and is the fourth most economically important crop in the world: after rice, wheat, and soybean (Nowicki *et al.*, 2013). China is the world's leading tomato producing country with 30.7 per cent share followed by India with 11.5 per cent share (Anonymous, 2014). At present the hybrid cultivars were getting boon in tomato all over the world for higher yield, quality and disease resistance. Therefore, the present investigation were carried out with entitled "introgression of gene for tomato leaf curl virus [ToLCV] resistance/ tolerance in tomato (*Solanum lycopersicum* L.)." was carried out at the Vegetable Research Farm, Department of Horticulture (Vegetable & Floriculture), Bihar Agricultural University, Bhagalpur, Bihar to know the extent of heterosis, assessing combining ability and generating information on gene action for tomato leaf curl virus [ToLCV] resistance/ tolerance in tomato. In this respect sixteen diverse parents (12 lines and 4 testers) were selected and intermated in a line x tester fashion and in the next year forty-eight crosses along with 16 parents were evaluated in RBD. Analysis of variance showed significant differences among all the genotypes for all the characters under study. The genotypes, IC-395457 and *Solanum peruvianum* among parents while H-86 × *Solanum peruvianum* and Arka Meghali × IC-395461 among cross combinations were found superior for earliness. Heterobeltiosis for fruit yield and quality traits was recorded significantly positive in LA-3948 × Pusa Rohini, H-86 × *Solanum peruvianum* and LA-3967 × IC-395461. Maximum negative heterosis for ToLCV incidence was observed in LA-3948 × Pusa Rohini, H-86 × *Solanum peruvianum* and LA-3952 × *Solanum peruvianum*. For yield and quality traits LA-3930 and *Solanum peruvianum* was good general combiner. H-86 × *Solanum peruvianum*, LA-3948 × Pusa Rohini and LA-3952 × IC-395457 were good specific combiners for number of fruits per plant, harvest duration and fruit yield traits. Cross combinations *viz.* H-88-78-5 × IC-395457, Pant-T-5 × *Solanum peruvianum* and LA-3952 × IC-395461 were good specific combiners for all quality traits. LA-3976 was good general combiner for tomato leaf curl virus infestation. According to scaling test and generation mean analysis, epistasis (non-allelic interactions) and both additive and non-additive gene actions were found operating in the inheritance of almost all characters. Variance ratio was also found less than one for all the character except number of fruit per plants and phenol content, again it confirmed the predominant role of non-additive gene action for controlling almost all the characters. On the basis of investigation, H-86 × *Solanum peruvianum*, LA-3948 × Pusa Rohini and H-86 × Pusa Rohini were found most promising hybrids for yield and ToLCV tolerance in tomato and can be used in future breeding programme.

Prevalence and correlation of Keratometry, Axial Length and Post-Operative IOL Power measures in cataract surgery

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Abstract

PURPOSE: To describe prevalence and correlation of Keratometry, Axial Length and Post Operative IOL Power measures in cataract surgery for different age group population. **Methodology:** Prospective and Interventional Randomized study concluding Sample size of 200. $K_{average}$ readings, Axial Length readings and IOL power calculation are taken by Optical Coherence Biometry (AL-Scan). The observation made on different age groups and different parameters groups. **Results**: 200 eyes observed among them 105 are male and 95 are females, ranging in between 40 to 70 years with the male: female ratio of 1: 0.90. The mean ± st.dev of age is 61.97 ± 8.57. The mean ± st.dev of Keratometry is 44.57±1.59. The A.L. observed for the inclusion criteria of 21-25 m.m. in accordance to the Optical Coherence Biometry, the Mean ± St dev is 23.16 ± 0.78. The IOL Power observed for same sample size with the Mean ± St dev of 20.88 ± 1.59. The maximum frequencies according to 61-70 years of age group cases are 131 (65.50%) among three groups and are with the most affected type of cataract is Nuclear Sclerosis with Posterior Sub Capsular cataract having total count of 88 (44.00%). The maximum frequencies of Keratometric reading is 185 (46.25%) among five groups, in the group range of 44.01D-46 D. The maximum frequencies for axial length are 79 (39.50%), in the group range of 22.01-23.00 mm among four groups. The IOL Power groups sub divided into six groups, the group 20.50 to 22.00 D showing maximum frequencies of 96 (48.00%).

Conclusion: The prevalence for Keratometry is 44.57 D; for axial length 22.63mm; for IOL Power is 21.23 D and for cataract, 61-70 year of age, males are prone to nuclear and PSC type of cataract. Correlation between IOL Power to AL reading shows linear inverse relation but AL and IOL Power with K reading does not show linear relation.

THE COMPARATIVE STUDY OF APPLANATION AND OPTICAL COHERENCE BIOMETRY METHODS FOR THE INTRA OCULAR LENS POWER CALCULATION

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Abstract

Purpose: To compare applanation biometry (A-Scan) and optical coherence biometry (AL-Scan) methods for IOL power calculation based on Axial Length and post operative refractive outcome. **Methodology:** Prospective and Interventional Randomized Comparative Study, Sample size of 400, studied under two sub groups, for Axial Length readings and IOL power calculation by A-Scan (Biomedix) and AL-Scan (Nidek). Keratometry readings are taken only by AL-Scan. **Results**: Mean ± St. dev. of A.L. measured by App. Biometry was low (22.79 ± 0.9 mm) than Opt. Coh. Biometry (23.16 ± 0.78 mm) to be significant (P= <.0001). Mean ± St. dev. IOL power was higher (21.75 ± 2.1D) than App. Biometry (20.88 ± 1.59 D) to be significant (P= <0.0001). Mean ± St. dev. of refractive status for Myopia is higher -0.97 ± 0.53 by App. Biometry than Opt. Coh. Biometry -0.5 ± 0.19, to be significant (P= <0.0001) and Mean ± St.dev. for Hyperopia is higher 0.98 ± 0.59 by App. Biometry than Opt. Coh. Biometry 0.46 ± 0.18, to be significant (P= <0.0001). Bland–Altman plots showed perfect agreement between both methods regarding A.L. and calculated IOL power. Further subgroup analysis revealed a statistically significant difference in different age groups and types of cataract for Posterior Sub capsular cataract alone and Nuclear Sclerosis with Posterior Sub capsular cataract (P= <0.001). **Conclusion:** There is significant difference between App. and Opt. Coh. Biometry; however, certain situations of Cataract is demanding mandatory role of App. Biometry.

Ivermectin Toxicity occurring in *German shephered (puppy) male dog*: A Case Study

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Abstract

A 3-month-old german shepered male puppy weight 10 kg was coming to pratap clinic of veterinary and veterinary medicine Manipuri Uttar Pradesh, for treatment. Earlier puppy was treated for tick infestation as per the owner told by given about 100mg of ivermectin tablet orally. Owner observed some clinical sign after 8 to 10 medication. Clinical examination revealed hypothermia (101.2°F), tremors, ataxia, partial blindness, dilated pupil, weakness, incardination, no responsiveness, unable in defecation and behavioural changes. Therapeutic management was done by the administration of avil 1ml , neurokind 1.5ml, RL 100ml, NS 150ml, manitol 1-2ml/kg BW IV stat, vetacept 1ml/day, lasix 1.5ml repeated 10 hourly and dexamethasone @ 0.25-0.5mg/kg BW IM BID, rectal enema for passing feaces to withdrawal ivermectin on first day and with infusion of 150ml dextrose (5%) IV. The dog recovered uneventfully after treatment.

Evaluation of recombinant CFPs based cocktail ELISA vis a vis Indigenous ELISA to differentiate infected from vaccinated population of domestic livestock

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Abstract

Johne disease (JD) is endemic in the domestic livestock population and bio-load of *Mycobacterium avium* subspecies *paratuberculosis* (MAP) is increasing rapidly in the absence of control programs in the country. We at CIRG, have developed a very effective 'therapeutic vaccine' using this vaccine, several cases of advance to very advance cases of JD have recovered. In the present study, we identified six important MAP specific culture filterate proteins viz. MAP 1693c, MAP 2168c, MAP ModD, MAP 85c, Pep AN and Pep AC, having greater sero-reactivity than other cellular proteins. These CFPs were successfully cloned, expressed and purified as a His-tag fusion protein exhibiting approx 20, 22, 50, 55, 18 and 23 kDA molecular masses, respectively. Immuno-blotting showed high sero-reactivity with control polyclonal sera of infected animals from respective species. Characteristics of these recombinant CFPs were evaluated by cocktail ELISA to detect antibody against MAP, as well as to assess their diagnostic potential as accompanying marker assay, which is able to differentiate Healthy, Infected and Vaccinated animals. Native semi-purified protoplasmic antigen (sPPA) based Indigenous ELISA and the CFPs based Indigenous cocktail ELISA were compared. Both the tests showed comparable results in the detection of anti-MAP antibodies. However, recombinant CFPs based cocktail ELISA showed improved sensitivity and high specificity. Serum samples from negative, healthy and vaccinated animals (goats, sheep, cattle and buffaloes) were used for the optimization of assay. We have screened more than 200 serum samples from each species (goats and cattle) where, optimized recombinant CFPs based cocktail ELISA successfully discriminate healthy, infected and vaccinated animals. These results depict that serological tests may be improved by using CFPs instead of whole cell sonicated sPPA. Cocktail of CFPs can be potentially targeted for developing diagnostics with improved sensitivity and high specificity in the early or subclinical stages of the MAP infection.

Epidemiology and bio-type profile of *Mycobacterium avium subsp. paratuberculosis* recovered from domestic ruminants, wild animals and commercial milk and milk products in India

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Abstract

Samples from domestic ruminants, wild animals and Raw, commercial milk and milk products of 8 places of 7 states were screened to estimate the bio-incidence of MAP using multiple tests; Screening (Fecal, milk and tissue microscopy; serum and milk ELISA) and confirmatory tests (culture, IS*900* PCR and IS*1311* PCR_RE). State and animal species-wise bio-incidence was;

I. Uttar Pradesh

A. Goats: Breed wise bio-incidence was 81.5, 92.0, 80.9 and 55.0% in clinically affected goats from Jakhrana, Jamunapari, Barbari and Sirohi breed of CIRG, Mathura using f-microscopy, respectively. Using i-ELISA, bio-incidence was 81.25% in clinically suspected goats from barbari herds endemic for Johne's disease, respectively. Using f-microscopy and i-ELISA the bio-incidence was 70.0 and 75.0% in other farm herds.

B. Sheep: Bio-incidence was 73.3% (33/45) and 50% (10/20) in clinically suspected sheep from UP using f-microscopy and i-ELISA, respectively. In other farm flocks, bio-incidence was estimated using f-microscopy, i-ELISA and f-PCR was 40.0, 17.5 and 2.5%, respectively.

C. Cattle and Buffaloes: In farmer's cattle and buffaloes herds, MAP bio-incidence was 66.6 and 75.0% using f-microscopy and 25.0 and 33.3% using m-microscopy, respectively.

D. Milk and Milk Products: Sampling and screening of 1605 Raw milk, 133 commercial milk and 276 commercial milk products of different brands was done.

Raw milk: 1605 Raw milk samples were screened by seven tests combinations and bio-presence of MAP were estimated using iELISA, microscopy, iFAT, IS*900* PCR, dELISA and LAT and Culture, the 46.8, 13.6, 47.5, 61.2, 57.4, 52.0 and 12.3%, respectively.

Commercial pasteurized milk: 133 commercial milk (liquid milk, flavoured milk and millk powder) samples were screened by six tests combinations and 63.1% (84/133) were positive (in one or more than one tests) for bio-presence of MAP. Screening using iELISA, microscopy, iFAT, IS*900* PCR, dELISA and LAT, the 22.4, 41.3, 39.8, 7.9, 33.3 and 23.1% milk samples were detected positive, respectively. Of 22 PCR positive samples 16 were genotyped where all were bison-type. Commercial milk samples were cultured where only one samples came positive. Culture results for other samples are awaited.

Commercial pasteurized milk products: 276 commercial milk products (Curd, Butter milk, Ice cream, Lassi, Butter, Cheese, Matka Kulfi, Cream, Coffee milk shakes, Fruit Yoghurt, Makhana Kheer, Rabdi) samples were screened by six tests combinations using iELISA, microscopy, iFAT, IS*900* PCR, dELISA and LAT, the 27.0, 42.8, 58.6, 9.0, 49.6 and 42.8% milk samples were detected positive, respectively. Of 8 PCR positive samples were genotyped where all were bison-type. Commercial milk products were cultured where only one samples came positive from milk products. Culture results for other samples are awaited.

II. Jammu & Kashmir: Bio-incidence was 44.5, 56.7 and 48.57% in clinically affected sheep from three Govt. farms (SRS Suhama, Gaubal, Ladhakh), using f-microscopy, i-ELISA, f-PCR, respectively. In 3 unorganized farms of Jammu and Kashmir, bio-incidence was 32.9, 61.5 and 25.0% by f-microscopy, i-ELISA, f-PCR, respectively.

III. Punjab: Bio-incidence was estimated in wild carnivores, wild herbivores and domestic ruminants. Bio-incidence was 46.5 and 6.89% in wild carnivores; 55.3 and 0.0% in wild herbivores; and 53.1 and 1.45% in domestic ruminants using f-microscopy and f-PCR respectively.

IV. Karnataka:

A. **Sheep:** 28 Fecal, 85 serum and 29 tissues (intestines and MLN) were screened by f-microscopy, t-microscopy, i-ELISA, IDEAXX ELISA, t-PCR and t-QPCR. Bio-incidence of MAP was 42.8, 13.7, 28.5, 100.0, 27.5 and 51.7%, respectively.

B. **Elephant:** Domesticated Elephant in Karnataka was also screened for MAP infection by f-microscopy and f-PCR where, bio-incidence was 50.0 and 0.0%, respectively.

C. **Other studies:** Of 5 goats, 79 sheep were screened using i-ELISA, 100.0% goats and 24.0% sheep were positive; of 16 cattle, 11 sheep and 1 horse were screened by f-microscopy, 31.2, 63.6 and 0.0% were positive.

V. Odisha: Goats from 4 farms were screened to know the JD status. Bio-incidence was 47.6, 94.7 and 8.94% using f-microscopy, i-ELISA, f-PCR, respectively. In another study 22 goat serums were screened by i-ELISA where bio-incidence was 68.1%. In commercial milk and milk products, bio-incidence was 0.0% by all tests (m-microscopy, m-ELISA, m-PCR).

VI. Tamilnadu: Of 306 cattle, 221 goats and 147 sheep serums were screened for JD status where bio-incidence was 70.2, 49.7 and 87.7% by i-ELISA.

VII. Madhya Pradesh:

A. Slaughtered Buffaloes: Fecal (141), blood (17), serum (205) and tissues (intestines near ICJ and MLN) (20) were screened by t-microscopy, i-ELISA, t-FAT, dot-ELISA and b-PCR. Bio-incidence of MAP was 85.1, 75.1, 100.0, 56.4 and 58.8%, respectively.

B. Goats, Cattle and Buffaloes:

Study A: Fecal (58), milk (15), serum (17) were collected from goats, cattle and buffaloes screened by f-microscopy, m-microscopy, i-ELISA, f-PCR, m-PCR and bio-incidence of MAP was 67.2, 100.0, 70.5, 0.0 and 0.0%, respectively.

Study B: Of 80 cattle, 191 goat serums were screened by i-ELISA, bio-incidence was 61.2 and 65.4%, respectively. Bio-incidence was in 62 cattle and 10 goats was 69.3 and 20.0% by f-microscopy. Of 43 cattle screened by f-PCR, bio-incidence was 9.3%.

Goats: Of 559 goats serum samples from Bhopal were screened by i-ELISA where bio-incidence was estimated 65.4%.

Effect of spacing and periodical staggered nipping on *Botrytis* disease incidence and quality of castor (*Ricinus communis* L.)

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Abstract

The field experiment was conducted during the *kharif* seasons of 2013 and 2015 at ZARS, University of Agricultural Sciences, Gandhi Krishi Vigyan Kendra, Bengaluru on red sandy clay loam soil to know the influence of periodical staggered nipping and spacing on *Botrytis* disease infestation and quality of castor. Nipping and different spacings in castor significantly influenced the disease incidence and castor oil yield. Periodical staggered nipping leaving one spike in each branch recorded lower *Botrytis* disease scoring (2.71) and chaffiness (6.43 %) as compared to non-nipping treatments. This treatment also recorded significantly higher oil content (44.34 %) and oil yield (7.75 q ha^{-1}). Among the different spacing levels lower *Botrytis* disease scoring (3.17), chaffiness (11.61 %) and significantly higher oil content (44.29 %) were noticed with the spacing of 120 x 45 cm. Whereas, significantly higher oil yield was recorded in the spacing of 90 x 45 cm (6.91 q ha^{-1}). Interaction effects between periodical staggered nipping and spacing were not significant.

COMPARATIVE STUDY OF REFRACTIVE ERRORS IN DIFFERENT AGE GROUPS IN ASSOCIATION WITH ANTERIOR CHAMBER DEPTH AND AXIAL LENGTH

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Abstract

To determine the axial length and anterior chamber depth and play an important role on refractive status of the eye in different age groups. Randomized Prospective Observational Cross-Sectional Study with Sample size of 400 and studied under two sub groups. The axial length and anterior chamber depth readings are measured by immersion biometry by A-Scan (Alcon) and Refraction under cycloplegia by streak Retinoscope and Post mydriatic test.

The sample size of 400 is observed in two sub groups. The Mean ± St. dev. Of Axial Length of Group A, is Emmetropic (23.39 ± 0.47), Hypermetropic (21.64 ± 0.95) and Myopic (24.34 ± 1.04). Myopic eyes have higher axial length compare to emmetropic and hypermetropic its strongly significant (*P*= <.0001) and the Mean ± St. dev. of Anterior Chamber Depth is Emmeropic (3.74 ± 0.18), Hypermetropic (3.43 ± 0.24) and Myopic (3.88 ± 0.25). Myopic eyes have higher anterior chamber depth compare to emmetropic and hypermetropic its strongly significant (*P*= <.0001). The Mean ± St. dev. Of Sph. Equivalent is Emmetropic (0 ± 0), Hypermetropic (+2.67 ± 1.88) and Myopic (-3.0 ± 1.20). Myopic eyes have higher Sph Equivalent compare to emmetropic and hypermetropic its strongly significant (*P*= <.0001).

The Mean ± St. dev. Of Axial Length of Group B, is Emmetropic (22.96 ± 1.12), Hypermetropic (22.56 ± 0.69) and Myopic (24.73 ± 0.78). Myopic eyes have higher axial length compare to emmetropic and hypermetropic its strongly significant (*P*= <.0001) and the Mean ± St. dev. of Anterior Chamber Depth is Emmeropic (3.37 ± 0.31), Hypermetropic (3.28 ± 0.35) and Myopic (3.94 ± 0.30). Myopic eyes have higher anterior chamber depth compare to emmetropic and hypermetropic its strongly significant (*P*= <.0001). The Mean ± St. dev. Of Sph. Equivalent is Emmetropic (0 ± 0), Hypermetropic (+1.39 ± 0.82) and Myopic (-2.71 ± 1.12). Myopic eyes have higher Sph Equivalent compare to emmetropic and hypermetropic its strongly significant (*P*= <.0001). In this study, it was found that hypermetropic eyes tend to have shorter axil length and myopic eyes tend to have longer axial length compare to emmetropic eyes in certain age group. Also, it was observed in our study that eyeball (axial length) tends to grow up to 18 years of age. Then after it cease to enlarge.

Effect of SO_2 on biochemical components of *Brassica juncea* cv. Pusa Bold

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Abstract

The effect of SO_2 on biochemical in (*Brassica juncea [L.] Pusa Bold*). In exposed seedlings SO_2 concentration ranging (653, 1306, 2612&3918 µg m^{-3} SO_2). Resulted accumulation of metabolites especially ascorbic acid is the adaptive mechanisms that operate in plants and shows Appreciable decrease due to SO_2 was observed in ascorbic acid content of *Brassica juncea [L.] Pusa Bold* plants. Carbohydrate level in plant is also influenced by SO_2 exposures, the possible reason for decreased sugar content in plants under SO_2 stress. All four concentrations of SO_2 caused reduction in carbohydrate in both crops except at 653 µg m^{-3} of SO_2 where a rise in carbohydrate level was seen. A perusal of literature suggests that SO_2 had a marked impact on protein content of leaves and seeds. They reported that protein degradation under SO_2 stress was either due to decreased photosynthesis or due to inhibition of protein synthesis. Appreciable decrease due to 653 µg m^{-3} and 3918 µg m^{-3} of SO_2 was observed in the protein content of leaves as well as seeds. A marked decline found in the nitrogen& phosphorus content of SO_2 fumigated plants. Minerals like nitrogen and phosphorus in leaves of *Brassica juncea* were recorded to be substantially reduced following the long-term exposures of 653, 1306, 2612 and 3918 µg m^{-3} of SO_2. SO_2 caused more decline in leaf nitrogen content of *Brassica juncea*. The experimental crops, on exposure to SO_2 had shown decline in their phosphorus content. The reductions in carbohydrate, protein and mineral content were directly related to decline in chlorophyll content of treated seedlings. Results indicate that calcium hydroxide treatments afforded protective effects against $SO_{2.}$ The effect of SO_2 on biochemical breakdown and rate of photosynthesis was due mostly to the specific direct action of SO_2 and was not a function of increased acidity.

After analysing the response of growth, yield and biochemical components in crop fumigated with 653, 1306, 2612 and 3918 µg m^{-3} of SO_2 *Brassica juncea* was more tolerant to various levels of SO_2 pollution and, therefore, could perform comparatively better growth in the presence of SO_2.

Integrated nutrient management on growth and yield of groundnut at Coastal zone of Karnataka

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Abstract

At 80 DAS recommended nutrient practice + 50 per cent RDN through vermicompost applied treatment resulted in significantly higher number of nodules (61.13) followed by POP + 50 per cent RDN (recommended dose of nitrogen) through poultry manure (60.37). At 90 DAS, POP + 50 per cent RDN through poultry manure recorded significantly higher leaf area per plant (2089 cm^2) followed by POP + 50 per cent RDN through vermicompost (1921 cm^2) as compared to other treatments. Recommended nutrient practice + 50 per cent RDN through poultry manure recorded significantly higher dry matter production (88.36 g $plant^{-1}$), followed by POP + 50 per cent RDN through vermicompost (85.88, g $plant^{-1}$). During 90 DAS to at harvest, treatments of POP + 50 per cent RDN through poultry manure recorded significantly higher values of CGR *viz.,* 0.0057 g cm^{-2} day^{-1} and followed by POP + 50 per cent RDN through vermicompost (0.0056 g cm^{-2} day^{-1}). Whereas, at 90 DAS to harvest higher NAR values of 0.00239 and 0.00226 g cm^{-2} day^{-1} were registered in POP + 50 per cent RDN through vermicompost and poultry manure treatments, respectively. Pod yield was significantly superior in POP + 50 per cent RDN through poultry manure (2272 kg ha^{-1}) followed by POP + 50 per cent RDN through vermicompost (2162 kg ha^{-1}) and POP + 50 per cent RDN through goat manure (2018 kg ha^{-1}).

OPTIMIZATION OF SPACING FOR PIGEONPEA (*Cajanus cajan* (L.) Millsp.) UNDER PROTECTIVE IRRIGATION

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Abstract

A field experiment entitled “Optimization of spacing for pigeonpea (*Cajanus cajan* (L.) Millsp.) under protective irrigation” was conducted during *kharif*, 2011 at Zonal Agricultural Research Station, Gandhi Krishi Vignana Kendra, Bengaluru. The experiment was conducted on sandy clay loam soil by giving protective irrigation at critical stages (flowering, pod initiation and maturity) of crop. The soil was medium in available nitrogen, phosphorus and potassium. The experiment consisting of nine treatments on spacings (90 x 30, 90 x 45, 90 x 60, 120 x 30, 120 x 45, 120 x 60 , 144 x 30, 144 x 45 and 144 x 60 cm), it was laid out in randomized complete block design with three replications.

Significantly higher yield components like number of pods and pod weight per plant were obtained at wider spacing of 144 x 60 cm (442.73 and 257.18 g plant-^{1}, respectively) when compared to closer spacing of 90 x 30 cm (336.40 and 189.97 g plant-^{1}, respectively). Significantly higher seed yield of pigeonpea was obtained with a spacing of 90 x 30 cm (2266 kg ha^{-1}) when compared to wider spacing of 144 x 60 cm (938 kg ha^{-1}). Although the individual plant performance was better under wider spacing, the productivity per unit area was higher at 90 x 30 cm spacing due to the higher plant population (37,037 plants ha^{-1}). Similarly 90 x 30 cm recorded higher gross returns (₹80,310 ha^{-1}), net returns (₹63,310 ha^{-1}) and benefit cost ratio (3.72).

Yield, uptake and soil nutrient status of secondary nutrients and microbial activity of groundnut as influenced by integrated nutrient management at Coastal zone of Karnataka

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Abstract

Pod yield was significantly superior in POP + 50 per cent RDN (recommended dose of nitrogen) through poultry manure (2272 kg ha^{-1}) followed by POP + 50 per cent RDN through vermicompost (2162 kg ha^{-1}) and POP + 50 per cent RDN through goat manure (2018 kg ha^{-1}). Higher uptake of calcium resulted in POP + 50 per cent RDN through poultry manure followed by POP + 50 per cent RDN through vermicompost (32.50 and 30.95 kg ha^{-1}, respectively). The highest total uptake of magnesium (14.92 kg ha^{-1}) was recorded in POP +50 per cent RDN through goat manure, followed by POP + 50 per cent RDN through vermicompost (12.98 kg ha^{-1}). Significantly higher sulphur uptake (15.17 kg ha^{-1}) resulted in POP + 50 per cent RDN through poultry manure, followed by POP + 50 per cent RDN through vermicompost (13.60 kg ha^{-1}). Higher bacteria, fungi and actinomycetes population (37.27 cfu x 10^5, 41.92 cfu x 10^3 and 13.73 cfu x 10^4 g^{-1} of soil, respectively) were found by the application of recommended dose of nutrients (POP) + 50 per cent RDN through vermicompost.

Integrated nutrient management on yield and nutrient status of soil in paddy at Coastal zone of Karnataka

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Abstract

A field experiment was carried out during *kharif* 2014 at Zonal Agricultural & Horticultural Research Station, Brahmavar, Udupi, Karnataka. Significantly higher grain yield (5159 kg ha^{-1}) of paddy was recorded in package of practice (POP- FYM 5 t + 60:30:45 kg N:P_2O_5:K_2O ha^{-1}) +50 per cent RDN through vermicompost, followed by POP + 50 per cent RDN through poultry manure (5101 kg ha^{-1}) as compared to package of practice (4425 kg ha^{-1}, respectively). Significantly higher total nitrogen and phosphorus uptake was observed in package of practice (POP) + 50 per cent RDN through vermicompost (109.85 and 45.51 kg ha^{-1}, respectively). Total potassium uptake was recorded highest in POP + 50 per cent RDN through eupatorium (60.23 kg ha^{-1}). Maximum available nitrogen (375.90 kg ha^{-1}) was observed in POP + 50 per cent RDN through gliricidia followed by POP + 50 per cent RDN through eupatorium (375.03 kg ha^{-1}). Available P_2O_5 (74.60 kg ha^{-1}) was more with POP + 50 per cent N through poultry manure followed by POP + 50 per cent RDN through goat manure (73.26 kg ha^{-1}). Application of recommended dose of nutrients POP (FYM 5 t + 60:30:45 kg N:P_2O_5:K_2O ha^{-1}) + 50 per cent RDN through eupatorium and POP + 50 per cent RDN through vermicompost resulted in higher available K_2O (135.43 and 134.13 kg ha^{-1}, respectively).

Population Dynamics and management against Budfly *Dasyneura lini* Barnes in Linseed (*Linum usitatissimum* Linn.)

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Abstract

The population dynamics of budfly *Dasyneura lini* was experimented during rabi season 2012-13 at the Student's Instructional Farm of Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad (U.P.). The incidence of budfly was recorded on variety Neelum at weekly intervals from germination till the harvest of the crop. There were eight treatments, namely Imidacloprid 17.8 SL @ 0.005%, Nimbicidine 0.25%, NSKE 5%, Neem leaf extract 5%, Green chilli extract 0.5%, Garlic extract 5%, Tulsi leaf extract 5% and Control. While application of Imidacloprid (17.8 SL @ 0.005 %) was found most effective followed by Nimbicidine @ 0.25 %, NSKE @ 5 % was found as the least effective in controlling of bud fly infestation. On the basis of yield, the highest yield was obtained from Imidacloprid 17.8 SL @ 0.005 % (16.22 q ha^{-1}) followed by (14.29 q/ha^{-1}) with Nimbicidine @ 0.25 %. On the basis of overall performance of all the eight treatments Imidacloprid was isolated as the most effective treatment for the control of linseed budfly.

Studies on Population Dynamics of major insect-pests in Linseed (*Linum usitatissimum* Linn.)

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Abstract

The field experiment was carried out at the student instructional farm of Narendra Deva University of Agriculture & Technology, Narendra Nagar (Kumarganj), Faizabad. The site is located at 42 km away from the district head quarter, Faizabad on Faizabad-Raibareily road. The incidence of insect-pests were recorded on variety Neelum on weekly interval from germination to harvest of the crop.Weekly observations of different insect-pests were recorded on 20 randomly selected plants in the plot of 10×10 Sqm. Namely, leaf minor (*Chromatomyia horticola*) and Semilooper (*Plusia aurichalcea*) recorded from early vegetative to maturity of the crop. Linseed budfly (*Dasyneura lini*) were recorded from initiation of flowering to maturity of the crop. First appearance of leaf miner was recorded in the second week of December on the variety of Neelum during *Rabi* 2012-13. Initially, the damage was 0.49 %, which peaked to its maximum 12.30 % .The incidence of Semilooper was recorded in the first week of December during *Rabi* 2012-13. Initially, the population fluctuated from 0.30 per plant to 1.18, 0.31 per plant in third week of February, respectively. The incidence of budfly was recorded as bud damage from second week of January and continued till last week of March during the year 2012-13 in variety Neelum. The bud damage varied from 0.51 % to 10.10 % during *Rabi* 2012-13.

Pesticides use in Agriculture and Livestock with their Impacts on Environment: A growing threat to sustainable food and animal production

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Abstract

Pesticides are extensively used in insects/ pests management in agricultural and forestry sectors, and they can also be used at home and at work to eradicate household pests to increase agricultural production tremendously. The main use of pesticides in India is for cotton crops followed by paddy and wheat. A vast majority of the population in India is engaged in agriculture and is therefore highly exposed to the pesticides used in agriculture. Exposure to pesticides both occupationally and environmentally causes a range of human health problems. Indiscriminate and repeated application of pesticides leads to loss of biodiversity, pest-resistance and other ecological imbalance. Many pesticides are not easily degradable, they persist in soil, leach to groundwater and surface water and contaminate wide environment.

In India, the use of pesticides remains the cornerstone of controlling ticks, lice and other ecto-parasites from the livestock animals. In the absence of an effective alternative method of control, reliance on chemicals is bound to increase, which exerts selection pressure on the target organism resulting into the development of resistance. The persistence nature of pesticides led to their accumulation in animal tissues and subsequently causes human dietary exposure through consumption of animal products viz. meat, milk, eggs and sea foods. Low dose but long-term exposure of pesticides can cause serious health hazards to human health and environment as well. The reports on occurrence of pesticides residues in animal products manufactured in India are fragmentary, but provide confirmation to the fact Indian consumers do get dietary exposure to these pesticides. Thus, the intensive pesticide application results in several adverse effects in the environment and human health that cannot be ignored.

Bioinformatics for Crop Breeding and Sustainable Agriculture

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Abstract

Bioinformatics deals with computer aided study of plant species. It includes gene mapping, gene sequencing, varietal information data base, plant genetic resources (PGRs) data base. It also deals with the study of genomics, proteomics and metabolomics in various plant species. It can be further divided as agricultural bioinformatics, horticultural bioinformatics, medicinal plants bioinformatics, forest plants bioinformatics, etc. The goal of modern crop breeding is to understand the genetic and molecular basis of all biological processes in plants that are relevant to the specie. This understanding is fundamental to allow efficient exploitation of plants as biological resources in the development of new cultivars with improved quality, resistant to various biotic and abiotic stresses and reduced economic and environmental costs. Thus, the key objectives for plant bioinformatics include: to encourage the submission of all sequence data into the public domain, through repositories, to provide rational annotation of genes, proteins and phenotypes, and to elaborate relationships both within the plants' data and between plants and other organisms. Bioinformatic studies are useful in pedigree analysis of various cultivars and hybrids. Information about the parentage of cultivars and hybrids is entered into the computer memory which can be retrieved any time. International Plant Genetic Resources Institute (IPGRI), Rome Italy has developed descriptors and descriptor states for various crop plants. Such descriptors help in uniform recording of observations on germplasm of crop plants all over the world. Thus huge data is collected on crop genetic resources for several years which can be used for further crop improvement programme. Bioinformatics plays an important role in systematic management of this huge data.

Role of Bioinformatics in Agricultural Science for Sustainable Development

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Abstract

Bioinformatics is the study of biological data using information tools. It is an interdisciplinary science emerging from interaction of computer, statistics, biology and mathematics to analyze genome arrangement and contents, biological sequence data, predict the structure and function of macromolecules that use in interpreting and decoding plant genome. The broad amounts of data produced in agricultural sciences resulted to the evolution and development of bioinformatics. Bioinformatics has a number of applications in animal as well as in plant biology.Bioinformatics develops software, algorithms, databases and tools of data analysis to make discoveries and infer the information. Thus it will help to improve the plant quality based on health care disease diagnosis. Bioinformatics approaches (databases and tools) in agricultural science and implication of next generation sequencing technology on crop breeding. In agricultural science, these tools are helpful in improving crop, improving nutrition quality. It helps in improving the quality of crop plants and traditional medicinal material. Bioinformatics is also very useful to identfy various resestant genes in the organisms which are very improtant for the crop improvement. Plants are made resistant to insects by incorporating desire gene to the plant. The first resistant plant was made by incorporating the cry gene from Bacillus thuringiensis (Bt). It is bacterial species which increases the soil fertility and protect the plant from pests. The genes of the Bt can be incorporated into the plant gene. Therefore, bioinformatics has very significant role in agricultural as well as envoronmental science for sustainable development.

Utilizing wild *Oryza* species for improving Phosphorus uptake

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Abstract

For efficient plant metabolism, root growth and yield, phosphorus is an element of unequivocal importance. Limited availability of P in the soil is identified as a major limiting factor for growth and productivity across Asian, African and South American countries. Further, the native soil P reserves are limited and exhaustible under intensive agriculture. In earlier studies, *P*hosphorus *S*tarvation *Tol*erance *1* (*PSTOL1*), a protein kinase gene, was cloned in *aus* type rice variety Kasalath acting as an enhancer of early root growth whose expression is up-regulated under phosphorus-deficient conditions that enable the plant to acquire more P and other nutrients and enhances grain yield. Sixty-seven representative accessions of *O. rufipogon* and Vandana as a positive control were sequence characterized for *PSTOL1* gene at School of Agricultural Biotechnology, PAU Ludhiana. These accessions were then classified into 17 haplotypes. Four accessions of *Oryza rufipogon* namely IRGC81989 (H11 haplotype), IRGC93216 (H2), IRGC 104395 (H2) and IRGC104852 (H1) were screened along with the checks PR114, Vandana and Rasi under three different phosphorous levels of soil (0%, 50% and 100% of GRD). The observations of the experiment revealed accession IRGC 104852 showing a considerable level of tolerance in terms of the development of panicles under deficient conditions of soil, although it showed a slight reduction in height, whereas IRGC 81989 was not able to withstand deficient conditions and IRGC 104395 showing comparable performance under all three conditions of soil. The recipient parent PR114 showed a considerable level of reduction in plant height and panicle number under deficient soil conditions as compared with control conditions. Using these results crosses has been attempted between the donor and recipient parent for transfer of phosphorous deficiency tolerance trait into present day cultivar.

Morphological characterization of aromatic rice (*Oryza sativa* L.) germplasm of India

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Abstract

The present study was conducted with an objective to characterize DUS traits in aromatic rice germplasm of India. The material comprising of a core set of 73 genotypes representing aromatic rice germplasm was grown in a complete randomized block design along with five checks viz. Pusa Basmati 1, PB1121, Tarori Basmati, Badshah Bhog, and Sugandhmati in two replications. The data for ten DUS traits were collected which included days to 50% flowering, plant height, tillers per plant, spikelet per panicle, fertile grain per panicle, sterile grain per panicle, decorticated grain length, decorticated grain width, 100 grain weight, and plot yield. The highest plant height (172cm) was observed for the genotype Basmati 11 while minimum plant height (64.6cm) was reported in Sathi. The number of tillers per plant ranged from 6 to 35, where the genotype Yamini (Basmati CSR 30) was detected with the highest number of tillers per plant. Further, spikelet numbers per panicle of the aromatic germplasm lines RAU 3043, Kapoor Kranti, Dhanaprasad, Binirhen, Longku Labat, JGL 1798 (Jagithyal Sannalu), and Badshah Bhog were significantly higher than the mean values of spikelet numbers per panicle of the checks. Moreover, genotype JGL 1798 (Jagithyal Sannalu) was also observed carrying the maximum number of fertile grains per panicle (265) and had only 6 sterile grains per panicle. Furthermore, the decorticated grain length of the genotype UPR 3565-10-1-1 (9.06) was found more than the all the five checks under study. The decorticated grain width of only two of the genotypes (Co ACC 167 and Bindi) fell in the medium grain length category (2.0-2.5 mm) while the rest of the genotypes were falling in the narrow grain width category (<2.0 mm). The 100 grain weight values of Sathi, Guinata, and Niaw Hawn Mali were significantly higher in comparison to the checks. However, the genotypes IR 841-85-1-1-2 (39.09 kg/acre) and Hung-mi-hsiang-ma-tsan (30.47kg/acre) had significantly higher plot yields in comparison to the checks. The study indicated that the aromatic rice genotypes can be distinguished and identified on the basis of plant and seed morphological traits. Moreover, the genotypes identified with high yield potential and other important traits can be further utilized in the breeding programs to improve the elite cultivars.

Bioinformatics and its application in Agricultural Entomology

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Abstract

Bioinformatics has emerged as an effective tool to facilitate biological discoveries more than a decade ago. Bioinformatics is a new field of science but it is making progress in every field of agriculture very rapidly. The information provided about the genes by the tools makes the scientists to produce enhanced species of plants which have drought, herbicide, and pesticide resistance in them. So many plants have been made insect resistant by incorporating the desired genes. *Bacillus thuringiensis* is a bacterial species which increases the soil fertility and protects the plants against pests. The researchers mapped its genome, they used its genes to incorporate into the plant to make it resistant against insects. For example, corn, cotton and potatoes have been made insect resistant so far. By having the genes of bacteria in the plants genome, when insects eat the plants, the bacteria enter in their bloodstream and make them starved, ultimately they die. Bt corn is one species of food plants which have been modified by inserting bacterial genes in it. It is effective against insects by developing resistance against them. The use of Bt genes in the plants genome has made the agriculturists to use the insecticides in very little amount. As a result, the productivity and nutritional value of plants will also increase and will be beneficent for human health. Therefore, it can be concluded that the bioinformatics has very significant advantages in the field of agricultural sciences as well as other branches of science and hopefully it will be more advantageous in upcoming years.

Impact of water hyacinth compost, vermicompost and inorganic fertilizers on soil enzyme activity and microbiological properties of a Typic Ustifluvents

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Abstract

A field experiment was conducted during *rabi* 2014-15 in sandy loam soil of Agro-climatic Zone-II of Bihar at Mandan Bharti Agriculture College, Agwanpur, Saharsa to examine the effect of soil enzyme urease and microbial population under organic and inorganic farming practices in wheat. The experiment was designed in split plot design with NPK levels in main plot and organic sources in sub-plot. Wheat (*variety* DBW-14) was grown for present investigation. The organic fertilizer used was compost made from water hyacinth, vermicompost while on the other hand for inorganic fertilizer, a mixture of urea, single super phosphate and muriate of potash was used. Total bacterial population was counted by soil dilution and plating techniques using Asperagine-Mannitol Agar medium whereas fungal counted on Rose Bengal Streptomycin Agar medium by pour plate techniques. Population of actinomycetes was enumerated using KenKnight and Munaieer's medium by pour plate method. There was considerable increase in the population of bacteria, fungi, actinomycetes as well as urease activity with application of chemical fertilizer and organic manure alone or incombination. The population of bacteria, fungi, actinomycetes as well as soil urease enzyme activity increased significantly in the organic manure treated soil compared with the chemical fertilizer treated soil.

DEVELOPMENT OF TOPICAL FORMULATION FOR THE TREATMENT OF DIABETIC WOUND HEALING

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Abstract

Diabetes has become a global public health issue and burdens our health care system especially in urban areas of India. As the diabetes epidemic grows vigorously, secondary complications of diabetes, such as impaired wound healing, are increasing disproportionately. Impaired wound healing is among the leading causes in diabetic patients and is the major reason of amputation. The main objective of this research work is to develop topical formulation containing anti-inflammatory drugs to be applied in the treatment of skin wounds and study their comparative effects. Hydrogels are one of the most popular types of wound dressings which are in use nowadays. Moreover, hydrogels have been found to promote fibroblast proliferation by minimizing the fluid loss from the wound area and protect the wound for rapid healing. There are so many synthetic drugs available for the treatment of wounds but hydrogels are preferred due to economic and eco-friendly nature. Carbopol based hydrogels were selected as delivery system for wound treatment. Among the formulations and different dressings to be useful on damaged skin, carbopol based hydrogels is leading as they can provide a moist environment for the wound and at the same time deliver the induced drug to the wound. Carbopol hydrogels have proven good bio adhesive properties on the skin surface as it is widely in cosmetics. Now on the other hand, macrophages are essential immune cells necessary for regulated inflammation during wound healing. Macrophages, the major inflammatory cells present in wounds, have two phenotypes: M1 and M2. M2 macrophages are necessary for angiogenesis and wound healing. Thus, we detected the expression of M1 and M2 macrophages and whether they are getting polarized or not. Rapid healing of diabetic skin wounds can be detected by promoting granulation tissue formation, angiogenesis, extracellular matrix secretion, wound contraction, and re-epithelialization.

USE OF BIOINFORMATICS IN WOUND HEALING

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Abstract

Most of the therapeutic interventions came late in the pathological process. Many studies have been done in the complex field of wounds and wound healing. In that way the use of bioinformatics holds the promise of improving our basic approach to understand the process. Transcriptional and proteomic profiling of different wound areas, different wound types in animal model and human subject are some of the bioinformatics approach which are in use nowadays. These kind pf approaches are valuable steps in elucidating the underlying molecular pathways which maybe aberrant, particularly in chronic diabetic wound. Such studies can also be helpful for comparisons between different wound subtypes and other phenotypically different disease to identify opportunities for adapting existing therapies. Use of Laverne (a bioinformatic tool) is a very good option to help facilitate scientific exploration of related genes, disease and pathways based on co-citation. Moreover, the development of MAVIS system, which is able to automatically measure the dimensions of skin wound is a great achievement in wound healing study. Overall these models is a step towards constructing an integrative system biology model of human wound healing. It is feasible to create predictive, multiscale network models of disease by merging genotype, gene expression, clinical traits, and other multiscale measures using causal network inference methods. This can validate the identification of the ''key drivers'' of pathology, which may represent novel therapeutic targets that play a more direct role in the analysis of disease.

Prediction of Molecular Activity Sites in Root Specific Gene MIC-3 After Root Knot Nematode Infection Approaching to Drug Designing

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Abstract

The Nematodes are simple organism. Comprised of approximately 1000 somatic cells in the adult stage, these worm-like organisms are an example of functional and anatomical economy lacking eye, appendages and true segmentation. Their size typically 0.40-1.0 mm in length. Nematode cause various diseases in human as well as in plant also here we discuss about the Root Knot disease which is caused by Nematode in plant roots. Root Knot disease is caused by the various species of Meloidogyne. These Nematodes burrow into the soft tissues of root tips and young roots, and cause the nearby root cells to divide and enlarge. The Root Knot disease plant show following signs of attack: slow growth, yellowing in leaves collapse of individual plant, severe infected seed lings produce few roots and usually die rapidly. Heavy infection of older plant cause the plant dies off early, swelling organs developed on the root of infected plant. Here we find out the active molecular sites of cotton plant protein Meloidogyne induced protein MIC-3 by the use of molecular activity finding software. This helps us to predict the active or functional amino acid sites of protein that we use.

Prediction of Putative T-cell Epitope from Indian Groups on Mycobacterium tuberculosis Structural Proteins

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Abstract

Tuberculosis is an airborne disease caused by the bacterium, mycobacterium tuberculosis. M. tuberculosis organisms are also called tubercle bacilli. Tuberculosis usually affects the lungs, but it can also affect other parts of the body such as the brain, the kidneys or the spine. A person with TB can die if they do not get treated. Immunoinformatics the aim of this field is to convert the immunological data into computational problem, solve these problem using mathematical and computational approaches and then convert these results into immunologically meaningful interpretations. It is based on similar concepts and tools. Such as sequence alignment and protein structure prediction tools. Immunoinformatics combines, immunology with computer science, mathematics, chemistry and biochemistry for large scale analysis of immune system function. They immune system plays an important role in the development of personalized vaccines for a variety of diseases including: Infectious disease, autoimmune diseases and cancer. Globally, BCG remains one of the most widely used vaccines against TB. However, reports on its efficacy to prevent pulmonary TB have been variable and in some instances conflicting (59) new and improved vaccines against TB are critically needed, M. tuberculosis and BCG- specific immune responses and comparative analysis of mycobacterial genomes, novel vaccine design strategies and candidates have been distributed. BCG provide incomplete protection against tuberculosis in infants. A new vaccine modified Vaccinea. Proteins antigens and their specific epitopes are formulation targets for epitope based vaccine the identification of T-cell epitopes from immune relevant antigens of M. tuberculosis is a critical step in the development of a vaccine covering diverse populations. Proteins of M. tuberculosis for stimulation of specific host immune response, in different cell types like T-cells, macrophases in the pathogenesis of the disease. Therefore the identification of T-cells epitope from the set of proteins may serve to define candidate antigens with vaccine potential. RecA, SSB, RuvA, UDG, and LigA, these proteins are mycobacterium tuberculosis proteins. SSB & RecA proteins both are best in all proteins.

IN SILICO CHARACTERISATION OF PROTEIN CODED BY CYT-B GENE OF *Radopholus similis* FOR NEMATODE INFECTION IN *Musa paradisiaca*

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Abstract

Nematodes are most abundantly found animals on earth. There number is very much close to the number of insect species. There can be about to 50 million species of nematodes to 30 cm depth of a square feet moderately fertile soil. Out of the total nematode population 25% are free living soil inhabitant; in spite of modern technologies 5-10% crop production is lost due to nematode infection. Being the important source of diet Bananas are rich source of fiber, low in sodium, and are richest ready to eat source of vitamin B6 and potassium. Along with the movement of *Musa paradisiaca* species due to human interventions, the parasites and pathogens also moved. The most important pathogen among these is the *root burrowing* endoparasite nematode i.e. *Radopholus similis.* This mostly affects citrus crops, pepper and mainly *Musa paradisiaca*. The *Radopholus similis* molecular studies have greatly simplified to identify the effectors through transcriptome analysis. The complete mitochondrial (mt) genome sequence of *Radopholus similis* measures 16,791bp. This mt circular DNA contains 36 protein coding genes. The genome transcriptome reveals that 5,853 ESTs can be generated and only 1% is derived from mt – transcriptome. Among the 36 genes cytB gene was studied for its functional analysis. The translated sequence of 362 aa was analyzed from 1086 bps gene. The mt genome differs very much from the standard DNA, some peculiar features to it are, small transfer RNAs, truncated rRNAs and unidirectional transcription. Cytochrome B is a subunit of Cytochrome bcl, an 11 subunit mitochondrial respiratory enzyme. Any small mutation in mitochondrial Cytochrome b results in combined complex defect, hence showing the clinical significance. Further which the 3D molecular structure was developed using automated modeling tool. The sole idea of this analysis is to identify the translated protein structures which will comprehend the structural and functional studies.

In silico structure analysis and epitope prediction of MPT 32-45 kda glycoprotein of *Mycobacterium tuberculosis*, Erdman for vaccine design

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Abstract

Tuberculosis (TB) remains the second most common cause of death due to a single infectious agent. The cell envelope of *Mycobacterium tuberculosis* (*Mtb*), the causative agent of the disease in humans, is a source of unique glycoconjugates and the most distinctive feature of the biology of this organism. It is the basis of much of *Mtb* pathogenesis and one of the major causes of its intrinsic resistance to chemotherapeutic agents. At the same time, the unique structures of *Mtb* cell envelope glycoconjugates, their antigenicity and essentiality for mycobacterial growth provide opportunities for drug, vaccine, diagnostic and biomarker development, as clearly illustrated by recent advances in all of these translational aspects. We use numerous bio-informatics and immuno-informatics implements comprising sequence and construction tools for construction of 3D model and epitope prediction for MPT 32-45 kda glycoprotein of Mycobacterium tuberculosis, Erdman. The 3D structure of MPT 32-45 kda glycoprotein was generated and total of antigenic 8 B cell epitopes, 4 MHC class I and 6 MHC class II binding peptides were predicted. The study was carried out to predict antigenic determinants/epitopes of the MPT 32-45 kda glycoprotein of Mycobacterium tuberculosis, Erdman along with the 3D protein modeling. The study revealed potential T-cell and B-cell epitopes that can raise the desired immune response against MPT 32-45 kda glycoprotein and useful in developing effective vaccines against MPT 32-45 kda glycoprotein.

Evaluating expression of MHC class II molecules for association with resistance to mastitis in Indian buffaloes (*Bubalus bubalis*)

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Abstract

Genes encoded by Major Histocompatibility Complex (MHC) are highly polymorphic, contributing significantly to vertebrate immune response. The expression of MHC class II molecules is strictly specific to antigen presenting cells, binding and presenting the processed antigens to T helper cells. In this study, expression of MHC Class II genes was evaluated across PBMCs of mastitis affected and non-affected (healthy) Murrah buffaloes as well as in-*vitro* challenging of PBMCs of animals of both the groups with LPS. Primers were designed to monitor the transcript levels by SYBRGreen dye based real-time PCR assay using RNA purified and reverse transcribed from peripheral blood mononuclear cells (PBMCs). The basal expression analysis indicated more than two fold higher expression of DQA (2.3) and DRA (2.3) genes in non-mastitis buffaloes compared to mastitis. Real-time PCR based melt-curve analysis helped in identification of diverged alleles possibly arising through gene duplication by assessing shift of peak. There was significant difference in expression of DQA and DQB molecules in PBMCs of mastitis and non-mastitis groups examined after *in-vitro* LPS challenge. Further, we also established that duplicated DQ loci might have an effect on lower mastitis occurrence in buffaloes, as observed through association study in Nili Ravi buffaloes. PBMCs, thus, exhibited a unique ability to regulate surface expression of MHC class II molecules during mastitis in buffalo and will be helpful in better understanding the role of these molecules in mastitis occurrence and possible resistance in bovines. Further, real-time PCR assay could also help in identification of allelic diversity as well as duplication among MHC genes.

Millets Genomics: A Way Forward to Ensure Global Food Security

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Abstract

Small millets gained remarkable importance in agriculture due to their climatic resilience nature and high nutritional values. Recently Government of India has declared millets as “Nutri Cereals”including pearl millet, foxtail millet, finger millet, kodo millet, proso millet, barnyard millet and little millet. Among the millets, pearl millet occupies 95% of the production and foxtail millet is the second largest crop among the millets. Millets are nutritionally superior to rice and wheat, as their grains contain high amount of proteins, amino acids, minerals and vitamins.Next to cereals, millets are the primary sources of energy in the semi-arid tropics and drought-prone regions of Asia and Africa. Among millets, the sequencing of whole genomes of sorghum, pearl millet and foxtail millet has led to the rapid development of DNA markers which was effectively used for quantitative trait loci (QTL) mapping and association mapping.Nearly all of the minor cereals are drought tolerant and didn’t require fertilizer. The requirements for environmentally friendly, nutritious crops to feed growing population provide new opportunities to cultivate minor cereals in the drier and warmer environmental conditions to ensure global food security.Identification of modern molecular markers such as SNPs and InDels linked to nutritional traits will deliver the information on candidate genes controlling these traits. Identification of gene based markers linked to specific traits will speed up the process of marker assisted breeding in more precise way. Genomics, proteomics and metabolomics related studies should be done to get complete information for millet improvement.

Overview of the trends of bioinformatics in molecular breeding

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Abstract

Role of omics are very important for crop improvement and to understand complete biological process of breeding methods. Plant genomics is mainly concerned with the genetic and molecular basis of all biological processes in plants that are relevant to targeted trait. It is not possible to manage and correlate data without applying bioinformatics tools. Plant breeding mainly concerned with genetic gain and improvement of particular crop. Several molecular breeding approaches are being applied for that purpose including, marker assisted selection, QTL mapping, association mapping, gene tagging, gene pyramiding, sequencing and targeted resequencing. Traditional data bases are linear catalogues of DNA sequences, proteins, genes, genomes and sequence alignments. There are three primary sequence databases: GenBank (NCBI), the Nucleotide Sequence Database (EMBL) and the DNA Databank of Japan (DDBJ). These are repositories for raw sequence data, but each entry is extensively annotated with highlights of the important properties of each sequence. The three data bases exchange data on a daily basis. For storage of protein sequence databases, SWISS-PROT and TrEMBL are the major primary databases. There are also secondary databases of protein families such as PROSITE, PRINTS and BLOCKS. These are called secondary databases because the sequences they contain are not raw data, but they have been derived from the data in the primary databases.The next very important class of databases in near future could be considered as pathway databases. Advancement of unparalleled data in bioinformatics over the years is a major concern for storage, management and data interpretation. Such massive data can be handled efficiently using bioinformatics tools only to disseminate knowledge.

GIS Application in Study of Diversity of Root Knot Nematode, *Meloidogyne incognita* in Uttar Pradesh, India

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Abstract

A survey had been conducted to study the population dynamics of plant parasitic nematodes, belonging to the phylum Nematoda of animal kingdom. About 80 soil and root samples were collected from different localities of Rohilkhand Division of the province Uttar Pradesh. The samples were washed and the nematodes were extracted by Centrifugal Flotation Technique according to the modified method by De Grisse, 1969. They were fixed and transferred to glycerine, and then permanent slides were mounted. Morphological and morphometrical characters of collected species were carefully studied and the characters were compared with the original descriptions and differences were discussed and then Relative Percent Occurrence (RPO) and Relative Density (RD) were calculated.

Overall screening of total 80 soil and root samples of different vegetable crops from different localities revealed the presence of eleven (11) different genera of plant parasitic nematodes with varying density and frequency. Among all genera identified, root knot nematode, *Meloidogyne* had been found in 71 soil samples with highest frequency (88.75%) followed by Reniform nematode, *Rotylenchulus* (78.75%). Other nematodes observed were dagger nematode, *Xiphinema* (65.00%), lance nematode, *Haplolaimus* (45.00%), stylet nematode, *Tylenchohynchus* (26.25%), root lesion nematode, *Pratylenchus* and *Tylenchorhynchus* (20.00%), *Aphelenchus* (13,75%) and *Discolaimus* with 8.75%.; Whereas *Boleodorus* and citrus nematode, *Tylenchus* accounted only 5.00% and 3.75% frequency respectively. Relative Density of all the genera identified had also been calculated. Again the analysis of data depicted the severity of infection of root-knot nematode (46.85%) followed by Reniform nematode (15.48%), *Heterodera* (9.44%), *Pratylenchus* (5.07%), *Xiphinema* (4.98%), *Haplolaimus* (4.47%). *Tylenchus* (3.17%), *Aphelenchus* (2.10%) and *Discolaimus* (1.80%) had been found in middle range, followed by *Boleodorus* which showed only 1.29% relative density. Present investigation revealed that root knot nematode (*Meloidogyne*) was found in most of the vegetable crop fields in this region. Nakatiya , Nariaval, Khajuria, Bholapur and Mehattarpur were the more infested areas.

CHROMOTOXIC EFFECTS OF CABBAGE LEAF EXTRACT ON ROOT MERISTEM OF *ALLIUM SATIVUM* L.

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Abstract

Cabbages belong to the botanical family CRUCIFERAE. There are more than one hundred types of cabbages, some are: White cabbage, red cabbage, broccoli, collard, savoy cabbage, chinese cabbage etc. Cabbage is used for stomach pain, excess stomach acid, stomach and intestinal ulcers, and a stomach condition called Roemheld syndrome. Cabbage is also used to treat asthma and morning sickness. It is also used to prevent weak bones (osteoporosis), as well as cancer of the lung, stomach, colon, breast and other types of cancer Breast-feeding women sometimes apply cabbage leaves and cabbage leaf extracts to their breasts to relieve swelling and pain. But in the present study cytotoxic effects of cabbage leaves extract were investigated on meristematic cells of *Allium sativum* L. roots. Actively growing roots of *Allium* sativum L. were treated with five concentrations (100%, 75%, 50%, 25% and 10%) of the leaves extract for 2,4 and 6 hours respectively. The results showed that the leaves extract induced various types of nuclear and chromosomal abnormalities such as multinucleate cells, scattered metaphase, breakage of chromosomes, stickiness of chromosomes, bridge formation at metaphase and telophase and polarity abolition. It is recorded that cabbage leaves extract not only disturbs mitotic activity but also shows considerable impact on chromosomal behaviour.

Gene silencing: A revolutionary tool for improvement of animal kind

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Abstract

Gene silencing is an exciting field of functional genomics. It has been used as a research tool to discover or validate the functions of genes. RNA interference, transcriptional gene silencing, virus induced gene silencing, and micro RNAs comprise a series of mechanisms capable of suppressing gene expression in plants and animals. Short sequence of nucleic acid that can bind to RNA of the gene and interferes with the process of its expression as well as in applications. Recently, a new tool based on a bacterial CRISPR-associated protein-9 nuclease (Cas9) from Streptococcus pyogenes has generated for gene silencing. Cas9 is an RNA-guided DNA endonuclease enzyme that was originally associated with the adaptive immune system of *Streptococcus pyogenes* and is now being utilized as a genome editing tool to induce double strand breaks in DNA. CRISPR/Cas9 has advantages in terms of clinical applicability over other genome editing technologies such as zinc-finger nucleases and transcription activator-like effector nucleases because of easy in vivo delivery. The RNAi technology is a revolutionized and powerful mechanism for in built alternate cell defence of an organism. The foreign DNA intruders form double stranded RNA intermediate during their propagation, which further cleaved in small antisense RNA by the action of dicing enzyme Dicer and further coupled with the complementary RNA for nucleation. Now a days lot more transgene were developed that involved frequently different silencing tricks, in extreme cases threshold induced silencing, DNA elimination etc. Gene silencing techniques may be used to gene therapy, to improve animal health as well as in crop improvements.

Carcass characteristics, Chemical composition and sensory evaluation of meat of Shank Feathered Uttara Fowl

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Abstract

Genetic diversity of local poultry breeds is most important in the developing countries like India. These local breeds are well adapted to the husbandry systems or backyard poultry production, unlike the exotic breeds. These breeds are results of millennia of years of evolution and are therefore, well adapted to the local environment where it evolved (Ben Larbi et al, 2013). Present study was conducted for carcass traits, chemical composition and meat quality of shank feathered Uttara fowl of Uttarakhand state. For carcass traits 10 birds of each sex were slaughtered by standard protocol. Significant differences were observed between male and female local hill fowl for carcass traits. The mean values of dressed, eviscerated, giblet, skin, feet and shank, head, feather, wing and neck weight in shank feathered local hill fowl were 1512.5±67.30, 1150.0±46.50, 69.26±2.34, 167.50±7.33, 112.50±2.14, 103.75±1.68, 127.50±2.94, 148.75±2.94, 112.50±3.35 g in males and 1156.3±52.60, 826.3±16.30, 67.71±1.44, 120.63±4.93, 92.88±2.09, 83.75±2.55, 100.00±2.81, 113.75±3.64, 94.875±0.89 g in females, respectively. The mean values of dry matter, protein, fat and total ash in local hill fowl meat were 26.60±0.24, 85.40±0.814, 10.82±0.806, 3.59±0.065 %, respectively. The mean score for appearance, flavour, texture, juiciness and overall palatability/ acceptability in RIR male birds were found to be 6.50±0.224, 6.40±0.221, 6.1±0.233, 5.7±0.539 and 5.7±0.539%, respectively. The corresponding values were 7.0±0.211, 6.8±0.200, 6.6±0.163, 5.7±0.597 and 7.4±0.163% in shank feathered local hill fowl males, respectively.

In silico Molecular Subchronic Toxicity Studies of Blend of Food Colours in Swiss Albino Rat, Rattus Norvegicus

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Abstract

Colour is the vital constituent of the food which provides distinct appearance of food product. However artificial colouring becomes a technological necessity to enhance lost natural colour and flavour of food during processing and storage. So the present study was conducted to elucidate the oral ingestion of blend of tartrazine, metanil yellow and sunset yellow (1:1:1) at the dose level of 25, 50, and 75 mg/kg weight for the 30 consecutive days to swiss albino rat. The serological study showed an increase in serum total bilirubin SGOT, SGPPT, uric acid and alkaline phosphatease. It was observed that their was a significant increase in LPO level, superoxide dismutase (SOD) activity and CAT activity. In the insilico studies of the effects the molecular protein was identified which was observed the interaction with the food colour. The results revealed that oral administration of these blend did not affect the body weight gain. Result from this study showed that the prolonged consumption of the blend may cause adverse effect on liver.

Optic Lobe Neurosecretory cells In Orthopteran, Poekilocerus Pictus and Its Correlation with feeding Activity of Insect

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Abstract

Optic lobe neurosecretory cell found at the base of penduncle in small patch which later bifurcates in two arms-one extending towards dorsal side and other towards the ventral side of the optic penduncle under the perineurium. Their number and position are fixed for each species of insects and similar in both sexes. These cells may be unipolar or bipolar; bipolar with one arm running towards the eye and other towards the brain. It has been seen that a connection between the eyes and the brain through these cells may be responsible for the behaviour of the insect when stimulated physiologically the secretion of these cells which itself may be triggered by light and darkness.

In order to explore whether the optic lobe neurosecretory cells are in some way connected with the feeding activity of the insect, couples of experiment were performed on *Poekilocerus pictus*, an orthopteran. It was found that start of feeding coincides with the initiation of discharge of optic lobe nuerosecretory material. If the visual stimulus is cut off, it was found that optic lobe neurosecretory cells are completely devoid of neurosecretory material and the feeding is done at a very low rate. Exposure to light initiates the synthesis of neurosecretory material and the feeding activity also increases with enhanced secretory activity. The insect remain actively feeding till the discharge of the secretory material has not started.

Molecular modeling, docking and screening of benzimidazole nucleosides as MDMV inhibitor

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Abstract

A series of benzimidazole nucleosides with methyl group was designed and screened for their antiviral activity against maize dwarf mosaic virus. The benzimidazole derivatives possess some biological activities including antiviral, antifungal, anticancer, antimicrobial and antidiabetic. Through molecular modeling the representation of 3D structures of antiviral molecules is done with the help of computerized techniques based on theoretical methods and experimental data. MDMV is selected target for analysis as it infectivity on plants show low or stunned growth in plants and its leaves thereby making a heavy loss to commercial value of the plant. MDMV is a plant virus of potyviridae family and its strains are A, C, D, E and F which shows several implications on plant leaves, so leaves turn in to mosaic pattern. Computational drug designing has become one of the most effective ways to screen a ligand's ability as an antiviral. The viral protein was modeled by homology modeling by selecting templates from the PDB database through alignment searching. The activity sites were identified in the target protein structure as cavities within the tool for docking studies. The docking studies were performed with in the series of modeled molecules of benzimidazole nucleoside in which interaction between protein and ligand was analyzed. Among the series of benzimidazole nucleosides, there are two groups of condensed carbohydrate molecules were developed that is one is deoxyribose and other is ribose from which ribose molecules are showing lowest dock score. The molecule 2-(4,6-dimethyl-1H-1,3-benzodiazole-1-yl)-5-(hydroxymethyl)oxolane-3,4-diol with 4,6-dimethyl group **3-o** on the aromatic ring showed good antiviral activity with good dock score however lower than the 2-(6-methyl -1H-1,3-benzodiazole-1-yl)-5-(hydroxymethyl)oxolane-3,4-diol with 6-methyl group **3-l.**

In Sillico Analysis of Cardio Troponin T (TNNT2) Gene For its SNP Identification and Molecular protein

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Abstract

Cardiomyopathy is a group of diseases which effect the heart muscle. Early on there may be few or no symptoms. Some people may have shortness of breath, feel tired or have swelling of the legs due to heart failure. An irregular heart beat my occur as well as fainting. Those affected are at an increased risk of sudden cardiac death.Cardiomyopathy are a clinically heterogeneous group heart muscle disorders. That are defined by the presence of abnormal myocardial structure and function in absence loading condition. The current classification of the cardiomyopathy continue to be based on phenotype defined by clinical evaluation of affected individual , incorporating genotype when possible. Type of cardiomyopath– Hypertrophic caridomyopathy, Dilated caridomyopathy, Restrictive caridomyopthy, Arrhythmogenic right ventricular dysplasia and broken heart syndrome in hypertrophic cardiomyopathy the heart muscle enlarges and thickness. dilated cardiomyopathy the ventricles enlarges and weeken. The current body of knowledge on genetics of cardiomyopthy suggests a basis for understanding the pathophysiology of disease provides potential target for therapeutic intervention, contributes diagnosis allows for cascade screening and occasionally informs prognosis. Used appropriately genetic testing can provide important additional information for patients and their families .The gene (TNNT2 troponin T2 ,cardic type) was identified from the gene database of NCBI. We resume the graphical identification of gene.

RELATIONSHIP BETWEEN BRCA1 GENE WITH SOME SELECTED SPECIES – AN *IN SILICO* APPROACH

Shreshtha Gaur

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Abstract

BRCA1 widely known as breast cancer type 1 plays a key role in DNA double-strand break repair, homologous recombination, chromatin remodeling, cell cycle regulation and transcription regulation. By seeing the importance of this protein, the present study was done to analyze BRCA1 gene of different mammalian species. The identity and similarity, phylogenetic relationship, physicochemical properties, predict the motifs, secondary and the tertiary structures were analysed. Seventeen nucleotide and protein sequences of BRCA1 gene of different mammalian species were retrieved. Multiple sequence alignment was done using CLUSTAL W software, while physicochemical properties of BRCA1 protein of the five mammalian species were determined using the Expert Protein Analysis System (Expasy). Results obtained at the end of the experiment showed that the least theoretical pl was for human BRCA1 protein (5.21) while the highest was for pig BRCA1 protein (5.60). The highest time of divergence which resulted out to be 95MYA of the BRCA1 gene was observed between the BRCA1 gene of killer whale and human, while the least time of divergence resulting 4.6MYA was observed between the BRCA1 gene of cattle and American buffalo. In the case of prediction of motifs the following 9 motifs were present at various positions in the BRCA1 gene of the five mammalian species; zinc finger RING, BRCT domain, N-myristoylation site, N-glycosylation, cAMP and cGMP dependent protein kinase phosphorylation site, tyrosine kinase phosphorylation, casein kinase 2 phosphorylation site, protein kinase C phosphorylation site and cell attachment sequence but leucine zipper pattern and microbodies c-terminal motifs were found in only human BRCA1 gene. The secondary structures of BRCA1 protein was predicted using GORIV software for the 5 selected mammalian species which showed that their BRCA1 protein contained alpha helix, extended strand as well as random coil. Based on all the above results, we can say that BRCA1 gene has identical homologue, functional similarity with these mammalian species.

Designing of the guide RNA sequence for the genome-scale CRISPR-Cas9 knockout in cells

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Abstract

Forward genetic screens are the powerful tools for the unbiased discovery and functional characterization of specific genetic elements associated with a phenotype of interest. Recently, the RNA-guided endonuclease Cas9 from the microbial CRISPR (clustered regularly interspaced short palindromic repeats) immune system has been adapted for genome-scale screening by combining Cas9 with pooled guide RNA libraries. Particularly, the RNA-guided endonuclease Cas9 from the microbial CRISPR immune system has proven powerful for precise DNA modifications. In the present study the guide RNA (gRNA) will be designed for the genome knockout study. For the guide RNA designing the coding sequence (CDS) taken from the NCBI and design the gRNA sequences. The gRNAs were designed by four different softwares Genscript (http://www.genscript.com/gRNA-design-tool.html) CHOPCHOP (http://chopchop.cbu.uib.no), MIT (http://crispr.mit.edu), CRISPRko (http:// portals.broadinstitute. org/gpp/public/analysis-tools/sgrna-design). Thehuman genome was kept as a reference for the calculation of the off-target sites. The gRNA that were found to be common in all the four softwares based on high selectivity score and low off-target potential were selected for further study.

Long non-coding RNAs identification and annotation using RNA-Seq approach

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Abstract

Long noncoding RNAs (lncRNAs) (length > 200 nt) play a role in regulating occurrence and progression of many diseases and are identified as effective biomarkers for diagnosis and prognosis of several diseases. They are also known to modulate innate and adaptive immune responses during virus infection. lncRNAs are species and tissue specific, their function in most of the species such as goats and sheep is not known. LncRNAs identification pipeline is divided in to 4 steps. In the first step, raw RNA-seq reads of specific condition must be aligned and mapped to desired species genome using a Bowtie2 aligner. In step2, transcripts must be generated and merged using Cufflinks and Cuffmerge software and these merged transcripts must be filtered on the basis of length and orf size (length>=200 and orf<=300). In step 3, filtered transcripts can be classified into five different classes i.e intronic ("i"), novel isoform ("j"), exonic overlap ("o"), intergenic ("u") and antisense ("x"). In the last step i.e step4, filtered and classified transcripts must be checked for coding potentiality using Pfam and CPC software and produce novel and known lncRNAs. The expression of lncRNAs can further be predicted using Cuffdiff or edgeR or DESeq2. Using a Bedtools window software lncrnas co-expressed genes or target genes can be identified. The genes identified can be annotated using The Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) software. The pipeline designed above for novel and known lncRNAs identification can also be applied to other newly assembled genomes for understanding the function of lncRNA transcripts.

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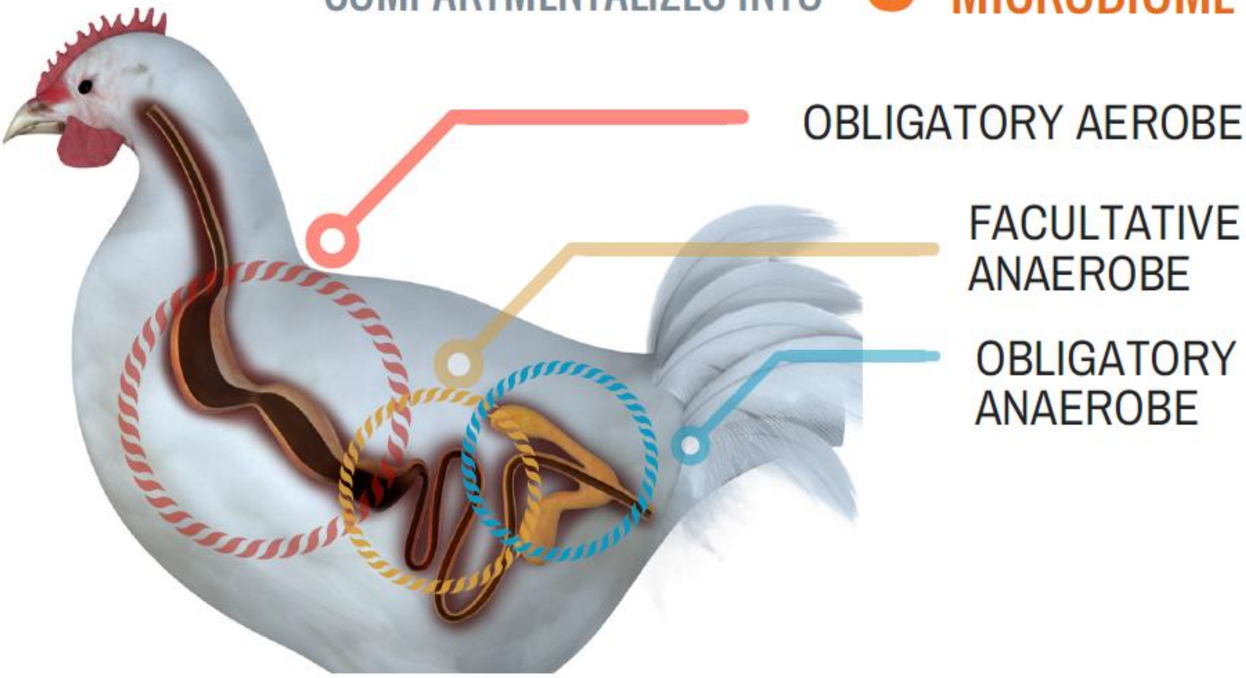
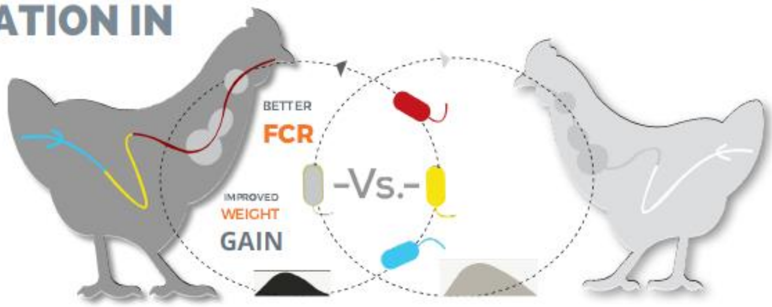


STRATEGIC COMBINATION OF AEROBES & ANAEROBES ENSURES PROLIFERATION IN

NICHE ENVIRONMENT

AND

TOTAL GUT



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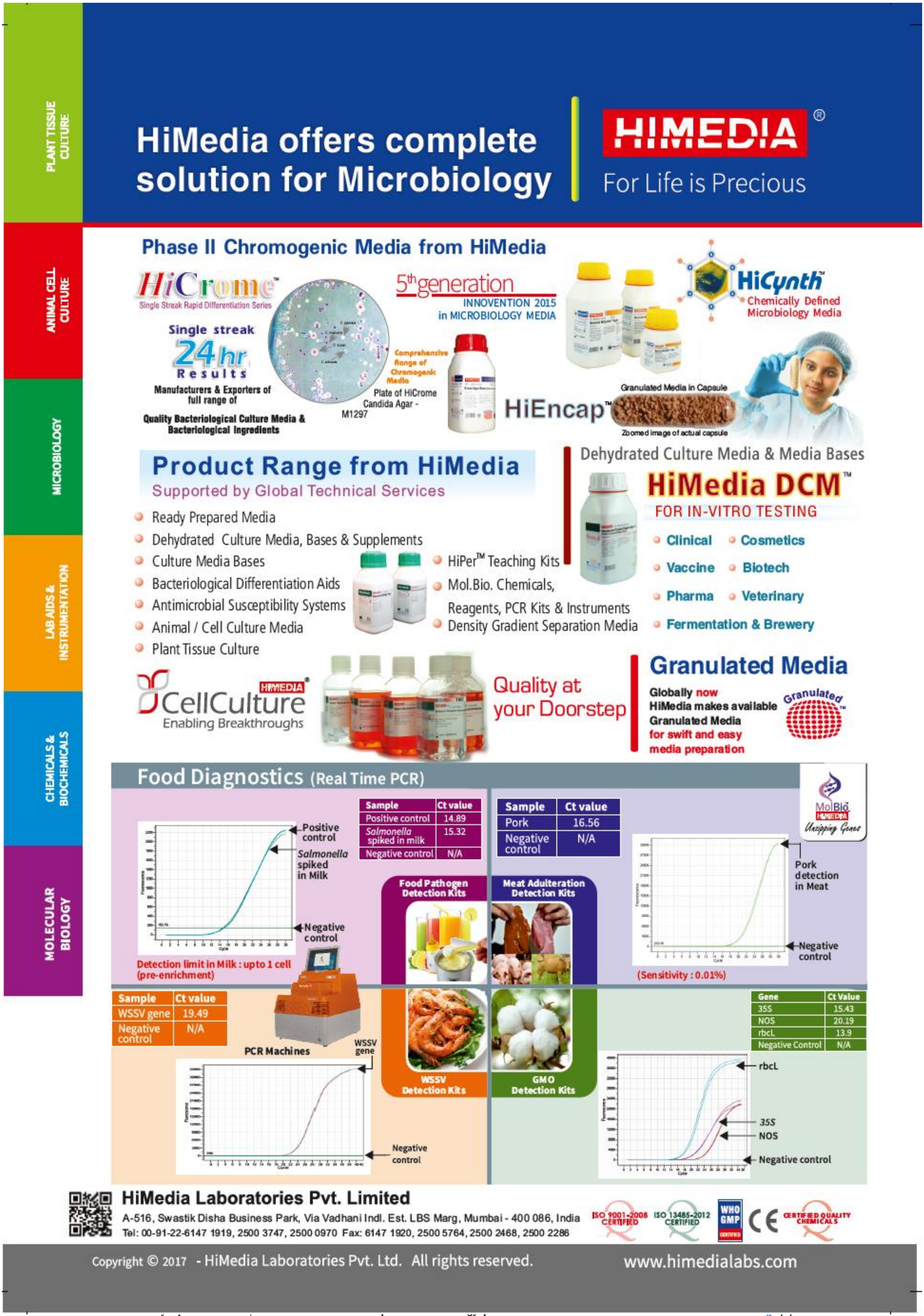

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Sample	Ct value
Positive control	14.89
Salmonella spiked in milk	15.32
Negative control	N/A

Positive control
Salmonella spiked in Milk
Negative control
Detection limit in Milk : upto 1 cell (pre-enrichment)

Food Pathogen Detection Kits

Meat Adulteration Detection Kits

Sample	Ct value
Pork	16.56
Negative control	N/A

Pork detection in Meat
Negative control
(Sensitivity : 0.01%)

Sample	Ct value
WSSV gene	19.49
Negative control	N/A

PCR Machines
WSSV gene
Negative control

WSSV Detection Kits

GMO Detection Kits

Gene	Ct Value
35S	15.43
NOS	20.19
rbcL	13.9
Negative Control	N/A

rbcL
35S
NOS
Negative control

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