

Two-Day National Conference
on
Recent Advances in Biotechnology
April 26-27, 2017



**Department of Biotechnology & Genetic Engineering,
Kohat University of Science and Technology (KUST),
Kohat, Pakistan**

Table of Contents

Sr. No.	Content	Page No.
1	Welcome Note from the Chief Organizer	2
2	Conference Program	3
3	Technical Session 1:Plant Biotechnology	10
4	Technical Session 2: Industrial Biotechnology	14
5	Technical Session 3: Environmental Biotechnology	17
6	Technical Session 4: Molecular Biology	21
7	Technical Session 5: Medical/Nanobiotechnology	24
8	Technical Session 6: Agricultural Biotechnology/Bioinformatics	31
9	Poster Presentations	38

Welcome Note from the Chief Organizer

Dear Participants,

On behalf of the organizing committee, I welcome you all to the **Two Days National Conference on Recent Advances in Biotechnology** April 26-27, 2017, organized by **Department of Biotechnology and Genetic Engineering, Kohat University of Science and Technology (KUST), Kohat**. We are pleased to host biotechnologists belonging to different regions of Pakistan, ranging from Azad Jammu & Kashmir (AJK) to Sindh. We highly appreciate the participation of invited speakers and other renowned scientists in the conference. Thus, the conference provides a unique opportunity to bring together researchers/leaders in the field of biotechnology from across the country to share their ideas and showcase their research work to a wider audience consisting mostly of young researchers and students. Major problems faced at the national level pertaining to the field of biotechnology will be highlighted and the ways how to solve these problems will be discussed. Major themes of the conference are i) emerging trends in different fields of biotechnology, and ii) modern techniques and innovative methodologies used in different fields of biotechnology. The conference will be consisting of invited talks by eminent scientists, oral and poster presentations.

I hope that you will have a nice stay in Kohat during the conference and enjoy participating in all sessions of the conference.

With kind regards,

Dr. Muhammad Jamil

(Chief Organizer)

Tentative Schedule for Two-Day National Conference on “Recent Advances in Biotechnology” April 26-27, 2017

Time	Events
	Conference Day-I
8:30am-9:30am	Registration
9:30am -9:35pm	Recitation from Holy Quran
9:35am -9:45am	Welcome Address and Conference Objectives
9:45am -10:00am	Address by the Chief Guest
10:00am-10:25am	Recent Advances in Animal Genomics Research in Pakistan Prof. Dr. Masroor Ellahi Babar <i>Faculty of Science and Technology, Virtual University of Pakistan, Lahore</i>
10:25am- 11:00am	Refreshment Break
	Technical Session-1 (Plant Biotechnology) Chair: Prof. Dr. Masroor Ellahi Babar Co-Chair: Prof. Dr. Maqsood Ahmed Moderator: Dr. Muhammad Jamil/Dr. Zia Ur Rehman
11:00am-11:20am	A Biotechnological Pursuit to Improve Plants Performance in ever Changing Climate: Plants for Future Dr. Raza Ahmad <i>Biotechnology Program, Department of Environmental Sciences, COMSATS, IIT, Abbottabad</i>
11:20am-11:35am	Transgenic Approaches Towards Disease Resistant Tomato Plants Dr. Saad Imran Malik <i>Department of Plant Breeding & Genetics, PMAS-Arid Agriculture University, Rawalpindi</i>
11:35am-11:50am	Probing the Antidiabetic, Cytotoxic, Thrombolytic and Antibiofilm Activities of <i>Momordica charantia</i> Fruit Pulp Dr. Fatma Hussain <i>Department of Biochemistry, Faculty of Sciences, University of Agriculture, Faisalabad, Pakistan</i>

11:50am-12:05pm	<p>Evaluation of Antidiabetic and Wound Healing Activities of Aqueous Extract of Shilajit Collected from Gilgit-Baltistan Region of Pakistan</p> <p>Dr. Abdul Jabbar</p> <p><i>Department of Biotechnology, Mirpur University of Science & Technology (MUST), Mirpur-10250 (AJK), Pakistan</i></p>
	<p>Technical Session-2 (Industrial Biotechnology)</p> <p>Chair: Dr. Muhammad Mohsin Javed</p> <p>Co-Chair: Dr. Raza Ahmad</p> <p>Moderator: Dr. Muhammad Jamil/Dr. Zia Ur Rehman</p>
12:10pm-12:30pm	<p>Exploring New Thermophilic Cellulolytic Enzymes from Indigenous <i>Aspergillus fumigatus</i> Isolated from Soil</p> <p>Dr. Muhammad Javaid Asad</p> <p><i>Department of Biochemistry, PMAS-Arid Agriculture University Rawalpindi Pakistan</i></p>
12:30pm-12:45pm	<p>Role of <i>Lactobacillus delbruecki</i> ssp. <i>bulgaricus</i> in Induction of Probiotics and Antibacterial Properties to Dahi</p> <p>Dr. Talat Mahmood</p> <p><i>Department of Agricultural Sciences, University of Haripur, Haripur</i></p>
12:45pm-100:pm	<p>Two Silent Mutations in Mrna of Endoglucanase (Cel6A) From <i>Thermobifida fusca</i> Enhanced Its Expression in <i>E. coli</i></p> <p>Dr. Imran Ali</p> <p><i>Department of Biotechnology, Mirpur University of Science & Technology (MUST), Mirpur-10250 (AJK), Pakistan</i></p>
1:00pm-2:00pm	<p>Lunch/Prayer Break</p>
	<p>Technical Session 3 (Environmental Biotechnology)</p> <p>Chair: Dr. Qaisar Mahmood</p> <p>Co-Chair: Dr. Muhammad Jamil</p> <p>Moderator: Dr. Muhammad Jamil/Dr. Zia Ur Rehman</p>
2:00pm-2:20pm	<p>Isolation and Molecular Characterization of Heavy Metal Tolerant Bacteria for their Potential Usage in Bioremediation and in Agriculture</p>

	<p>Dr. Iftikhar Ahmed <i>Institute of Microbial Culture Collection of Pakistan (IMCCP), NARC, Park Road, Islamabad-45500, Pakistan</i></p>
2:20pm-2:35pm	<p>Hydrogen Sulfide Alleviates Chromium Stress on Cauliflower by Restricting Its Uptake and Enhancing the Antioxidative System Dr. Shafaqat Ali <i>Department of Environmental Sciences and Engineering, Government College University Allama Iqbal Road 38000 Faisalabad, Pakistan</i></p>
2:35pm-2:50pm	<p>Effect of Industrial Effluent from Pb Acid Battery Industry on Growth and Metal Accumulation in <i>Oryza sativa</i> Dr. Muhammad Dawood <i>Department of Environmental Sciences, Bahauddin Zakariya University Multan, Pakistan</i></p>
2:50pm-3:05pm	<p>Phytochemicals and Antioxidants Activities of the Medicinal Plant <i>Ammi majus</i> Dr. Iqbal Hussain <i>Department of chemistry, Islamia College University Peshawar KPK, Pakistan</i></p>
3:05pm-3:30pm	<p>Tea Break</p>
	<p>Technical Session 4 (Molecular Biology) Chair: Dr. Iftikhar Ahmed Co-chair: Dr. Mushtaq Ahmad Moderator: Dr. Muhammad Jamil/Dr. Zia Ur Rehman</p>
3:30pm-3:50pm	<p>Life from Death-Approach towards Sustainable Development Dr. Muhammad Mohsin Javed <i>Department of Industrial Biotechnology, GC University, Lahore</i></p>
3:50pm-4:05pm	<p>Identification of a Homozygous c.589G>A Mutation in <i>CDK6</i>, Causing Primary Microcephaly in a Saraiki Origin Pakistani Family Dr. Muzammil Ahmad Khan <i>Gomal Centre of Biochemistry and Biotechnology, Gomal University Dera Ismail Khan, Khyber-Pakhtoonkhwa, 29050, Pakistan</i></p>

4:05pm-4:20pm	<p>Cytogenetic Insights into DNA Damage and Repair of Lesions Induced by a Monomethylated Trivalent Arsenical</p> <p>Dr. Shaukat Iqbal Malik</p> <p><i>Capital University of Science & Technology (CUST), Islamabad, Pakistan</i></p>
4:20pm Onwards	<p>University Visit</p>
	<p>Conference Day-II</p>
	<p>Technical Session-5 (Medical/Nanobiotechnology)</p> <p>Chair: Prof. Dr. Fida Younous Khattak</p> <p>Co-Chair: Dr. Zaffar Mehmood</p> <p>Moderator: Dr. Muhammad Jamil/Dr. Aamir Shehzad</p>
9:00am-9:20am	<p>Nutraceutical Delivery through Nanotechnology</p> <p>Dr. Zaffar Mehmood</p> <p><i>Department of Biological Sciences, Forman Christian College University Lahore</i></p>
9:20am-9:35am	<p>Exploring the Cell Surface and Intracellular Trafficking of Nanocarriers for Gene Delivery</p> <p>Dr. Zia ur Rehman</p> <p><i>Department of Biotechnology and Genetic Engineering, Kohat University of Science and Technology, KUST, Kohat 26000, KP, Pakistan</i></p>
9:35am-9:50am	<p>Nano-Encapsulation of Drug(s) and Bio-active Reagents</p> <p>Dr. Abid Ali Khan</p> <p><i>Department of Biosciences, COMSATS Institute of Information Technology, Park Road, Tarlai Kalan, Islamabad</i></p>
9:50am-10:05am	<p>Expression Profiling of <i>Hspb1</i> and <i>Tp53</i> Genes through RT-qPCR in Different Cancer Types of <i>Canis familiaris</i></p> <p>Dr. Rashid Saif</p> <p><i>Department of Biotechnology, Virtual University of Pakistan, Lahore 54000, Pakistan</i></p>
10:05am-10:20am	<p>Color Segmentation Based Computer Aided Diagnosis of Early Tuberculosis Nodules in X-Ray Images</p>

	<p>Dr. Javed Ahmed Mahar <i>Department of Computer Science, Shah Abdul Latif University, Khairpur Mir's, Sindh, Pakistan</i></p>
10:20am-10:40am	<p>Phytoremediation-Ecotechnology for Developing Nations like Pakistan Dr. Qaisar Mahmood <i>COMSATS Institute of Information Technology, Abbottabad, Pakistan</i></p>
10:35am-10:55am	<p>Preparation and Characterization of Bio-based Composite Membrane for Water Treatment Dr. Muhammad Arshad <i>Institute of Environmental Sciences and Engineering, National University of Sciences and Technology, Islamabad</i></p>
10:55am-11:15am	<p>Tea Break</p>
	<p>Technical Session-6 (Agricultural Biotechnology/Bioinformatics) Chair: Dr. Raza Ahmed Co-Chair: Dr. Muhammad Jamil Moderator: Dr. Muhammad Jamil/Dr. Aamir Shehzad</p>
11:15am-11:35am	<p>Applications of Advanced Biotechnological Techniques in Agriculture Sector: A Case Study of China Prof. Dr. Maqsood Ahmed <i>Department of Biotechnology, Mirpur University of Science and Technology (MUST), Mirpur-10250 (AJK), Pakistan</i></p>
11:35am-11:50am	<p>A Comparative Analysis of Mesquite (<i>Prosopis juliflora</i>) and Sugarcane (<i>Saccharum officinarum</i>) Waste Biochar through Scanning Electron Microscopy Dr. H. Mumtaz Khan <i>Department of Soil & Environmental Sciences, Faculty of Agriculture, Gomal University, Dera Ismail Khan 29050, KP, Pakistan</i></p>
11:50am-12:10pm	<p>Plants Based Commercial Products Using Recent Biotechnology Techniques in Pakistan Dr. Mushtaq Ahmad <i>Biofuel and Biodiversity Lab, Department of Plant Sciences, Quaid-i-Azam</i></p>

	<i>University Islamabad – 45320 Pakistan</i>
12:10pm-12:25pm	<p>Determination of Capsaicinoids Content and Enzymes (Phenylalanine Ammonia-lyase, Cinnamic-4-hydroxylase, and Capsaicin Synthase) Activities in Capsicum Species</p> <p>Dr. Nargis Jamila</p> <p><i>Department of Chemistry, Women University Swabi, 23340 Swabi, Khyber Pakhtunkhwa, Pakistan</i></p>
12:25pm-12:40pm	<p>Inhibition of Photorespiratory Losses in C3 Plants for Improved Productivity: An <i>in-silico</i> Approach</p> <p>Ghazal Khurshid</p> <p><i>Biotechnology Program, Department of Environmental sciences, COMSATS, IIT Abbottabad</i></p>
12:40pm-12:55pm	<p>Identification and <i>in-silico</i> Analysis of GALNS Mutations Causing Morquio A Syndrome in Eight Consanguineous Families</p> <p>Dr. Irfanullah</p> <p><i>Department of Biochemistry, Quaid-i-Azam University, Islamabad</i></p>
12:55pm-1:10pm	<p>Construction and Analysis of a Comprehensive Protein Interaction Network of HCV with Its Host <i>Homo sapiens</i></p> <p>Quratul Ain Farooq</p> <p><i>Department of Computer Science and Bioinformatics, Khushal Khan Khattak University, Karak, Khyber-Pakhtunkhwa, Pakistan</i></p>
1:10pm-1:30pm	<p>Metabolomics as a Supplementary Tool for the Advance of Biotechnological Excursions</p> <p>Dr. Muhammad Jahangir</p> <p><i>Section of Food Science & Technology, Department of Agricultural Sciences, University of Haripur, Khyber-Pakhtunkhwa, Pakistan</i></p>
1:30pm-2:15pm	Lunch/Prayer Break
2:15pm-3:00pm	Concluding Ceremony

Recent Advances in Animal Genomics Research in Pakistan

Masroor Ellahi Babar*, Akhtar Ali, Tanveer Hussain, Rashid Saif and Fahad Rafiq

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Abstract

Animal genomic research has progressed rapidly from genome map to trait map in the recent years. Pakistan has rich treasury of Animal Genetic Resources. Molecular markers are reliable source for breed characterization of buffalo, cattle, sheep, goat, camel, yak, horse, dog and chicken. Nuclear and extra nuclear markers including microsatellites, mitochondrial D-loop, Cytochrome b, Cytochrome c, ATPase 6 and ATPase 8 genes, ZFX and SRY genes are examined. The molecular variations and phylogenetic analyses performed in selected animal breeds along with their comparison with international breeds. Apart from these, various genes having role in production traits including milk production, growth, energy metabolism, fertility, immunity and parasitic resistance were inspected in different species to have better insight. The outcomes of these studies have laid a path for future researchers to plan further genomic studies to better explore the genomic worth of local animals. With the advent of high throughput next generation sequencing technologies, we recently are studying the heat tolerance and immunity genes on a broader level with the goal to identify valued markers for better animal selection in future.

Technical Session 1 (Plant Biotechnology)

A Biotechnological Pursuit to Improve Plants Performance in ever Changing Climate:

Plants for Future

Raza Ahmad

Biotechnology Program, Department of Environmental Sciences, COMSATS, IIT, Abbottabad.

Abstract

The glycolate metabolism via the photorespiratory pathway in C3 plants consumes not only ATP and reducing equivalents but also results in 25% loss of already fixed carbon back into environment. This phenomenon makes C3 plants inefficient biomass accumulators. Hence, water use efficiency of C3 plants remains less than C4 plants. Transgenic potato (*Solanum tuberosum* L. cv. Desiree) plants expressing components of a novel cyanobacterial photorespiratory glycolate catabolism pathway were developed. Transgenic plant expressing *gld1* (glycolate dehydrogenase I) gene was referred to as synGDH and transgenic plants expressing *gcl* (glyoxylate carboligase) and *tsr* (tartronic semialdehyde reductase) genes simultaneously were designated as synGT. Both synGDH and synGT plants showed stable gene transformation, integration and expression. Enhanced glyoxylate contents in synGDH plants were detected as compared to synGT and non-transgenic (NT) plants. Phenotypic evaluation revealed that synGDH plants accumulated 11% higher dry weight, while, tuber yield was 38 and 16% higher than NT and synGT respectively. Upon challenging the plants in high temperature and high light conditions synGDH plants maintained higher *Fv/Fm* and showed less bleaching of chlorophyll as compared to synGT and NT plants. These results indicate that engineering the complete pathway in one plant holds promising outcomes in terms of biomass accumulation to meet future needs of food and energy.

Transgenic Approaches Towards Disease Resistant Tomato Plants

Saad Imran Malik*, Ghulam Rasool and Zahid Akram

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* Corresponding Author: Dr. Saad Imran Malik, E-mail: saad.malik@uair.edu.pk

Abstract

Diseases are a major tomato (*Solanum lycopersium* L.) production constraint globally as well as in the country. Being the 2nd most grown vegetable crop worldwide, there is a significant lack of tomato genetic resources for resistance (*R*) genes against a number of devastating tomato diseases, limiting the scope of conventional breeding approaches. Plant genetic transformation offers unlimited scope for the transfer of foreign genes into existing cultivars reducing yield losses and associated costs on chemicals. In pursuit of this technology, we have optimized for an efficient direct gene delivery system by employing *Agrobacterium*-mediated transformation and using *GUS* reporter gene. This was coupled with screening tomato genotypes amenable to transformation along with optimum media and hormone combinations. Besides, we have identified a few candidate genes in tomato previously published with important and established regulatory roles for disease resistance in the model plants. Initially, the transcriptional profiling of these genes was performed by capturing mRNA transcripts and employing RT-PCR. Further, these genes have been cloned and subsequently sub-cloned in the plant expression vectors for transformation. These data are making headway towards the development of transgenic tomato plants with improved and broad spectrum genetic resistance against pathogenic bacteria and fungi.

Probing the Antidiabetic, Cytotoxic, Thrombolytic and Antibiofilm Activities of *Momordicacharantia* Fruit Pulp

Fatma Hussain* and Abida Irshad

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Abstract

Momordica charantia is mostly known as bitter gourd or bitter melon and it belongs to the family Cucurbitaceae. *M. charantia* is significantly studied in the medicinal world due to its therapeutic properties and is used in treatment of many diseases. In the present research, *M. charantia* fruit pulp extracts were prepared in six different solvents (methanol, *n*-butanol, *n*-hexane, chloroform, ethanol and ethyl acetate). Antidiabetic (antiglycation activity, alpha

amylase and acetylcholinesterase inhibition) were performed along with cytotoxic (hemolysis), thrombolytic and antibiofilm activities. *n*-butanol fraction showed maximum (47%) glycation inhibition. Whereas ethyl acetate and ethanol fractions exhibited highest alpha amylase (45%) and acetylcholinesterase (78%) inhibitions respectively. Various fractions showed hemolysis in the range of 6-30% with *n*-butanol and ethyl acetate being the most potent hemolytic agents. Thrombolytic activity (23-40%) was observed for all tested samples and chloroform had the highest (40%) thrombolysis efficacy. *M. charantia* aqueous fraction showed 49.1% inhibition for *Pasteurella multocida* strain. The present research is an attempt to highlight the therapeutic efficacies of *M. charantia* fruit and calls for further clinical trials to elucidate its medicinal potency.

**Evaluation of Antidiabetic and Wound Healing Activities of Aqueous Extract of Shilajit
Collected from Gilgit-Baltistan Region of Pakistan**

Abdul Jabbar*, Shagufta Bashir, Muhammad Tariq, Raja Tahir Mahmood and Maqsood Ahmed
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Mirpur-10250 (AJK), Pakistan.*

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Abstract

Shilajit and various shilajit extracts have been successfully applied for variety of clinical indications but relatively little information is known about its medical importance. The objective of this study was to evaluate in vitro antioxidant activity of aqueous shilajit extract, antidiabetic activity of two preparations 300mg/kg/day and 600mg/kg/day in alloxan induced diabetic rabbits along with wound healing activities of shilajit 20% ointment. To find the antidiabetic activity blood glucose level and lipid profiling measurement were done. Aqueous extract of shilajit preparations reduced blood glucose level indicating that it had compounds with glucose and lipid profile reducing properties. There was no change in total cholesterol and triglycerides in treated diabetic rabbits as compared to the control ($p>0.05$). However, there was a decreased bilirubin, urea, creatinine and alanine aminotransferase (ALT) levels in treated rabbits when compared with control ($p<0.05$). It indicates that the shilajit along with lowering blood sugar, also protects against hemolytic anemia, jaundice, liver diseases, acute and chronic kidney disorders. When these two treatment groups were compared, group having treatment with 600mg/kg/day showed

better results than 300mg/kg/day. Wound contraction was enhanced significantly in normal and diabetic rabbit wound models, treated with 20% shilajit ointment topically. From the study, significant health benefits through the modulation of physiological functions including hypoglycemic and lipid profile lowering activities were noticed which can be used as prophylactic against several metabolic diseases. On the other hand, wound healing properties together with its antioxidant effects suggest that it has significant potential in the treatment of skin diseases.

Technical Session 2 (Industrial Biotechnology)

Exploring New Thermophilic Cellulolytic Enzymes from Indigenous *Aspergillus fumigatus* Isolated from Soil

Muhammad Javaid Asad^{1,*}, Raja Tahir Mahmood^{1,2} and Muhammad Asgher³

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Abstract

Current industrial era mainly depends upon enzymes isolated from microorganisms. Fungi can be a good biological agent for the economic production of new industrial enzymes like cellulases. Thermophilic cellulases can be used for biofuel production as well as to deal with environmental pollution problems. During current study, cellulolytic enzyme production potential of *Aspergillus fumigatus*, isolated from soil of high temperature regions was explored. The production was optimized by selecting suitable cultural and nutritional conditions. Maximum endoglucanase and exoglucanase production was observed after 72 hrs at 55°C, pH 5.5 and 70 % of moisture level. Addition of 0.3 % of fructose, peptone, and Tween-80 further enhanced the production of both cellulases. Maximum purification was achieved with 40 % ammonium sulfate and these were 2.63 fold (endoglucanase) and 3.30 fold (exoglucanase) purified by gel filtration chromatography. In the case of β -glucosidase, maximum activity was observed after 72 h at 55 °C, pH 5.5, and 70 % moisture level. The presence of 0.3 % of fructose, peptone, and Tween-80 in media has beneficial impact on β -glucosidase production. A 4.36-fold purification was achieved by 40 % ammonium sulfate precipitation and gel filtration chromatography. Optimum temperature for all three cellulases was 55 °C and optimum pH was 4.8. Study of kinetic parameters showed the values of K_m 3.97 mM (endoglucanase), 4.34 mM (exoglucanase) and 4.92 mM (β -glucosidase). The values of V_{max} were 8.53 μ M/mL/min (endoglucanase), 7.29 μ M/mL/min (exoglucanase) and 6.75 μ M/mL/min (β -glucosidase). It was also observed that

fructose is better carbon source than glucose, and peptone is better nitrogen than urea for the growth of *A. fumigatus*. The K_m and V_{max} values indicated that endoglucanase, exoglucanase, and β -glucosidase have good affinity for their substrates. These thermophilic enzymes can be very useful candidates for industrial uses at higher temperature.

Role of *Lactobacillus delbrueckii* ssp. *bulgaricus* in Induction of Probiotics and Antibacterial Properties to Dahi

Talat Mahmood^{1,*}, Tariq Masud² and Muhammad Imran³

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Abstract

In the current investigation different strains of *Lactobacillus delbrueckii* ssp. *bulgaricus* from dahi were analysed for certain probiotic and antibacterial properties. Fourteen isolates were obtained and five were found to have antibacterial activities against food born pathogens. These strains were confirmed by the amplification of 16S RNA regions with known primer of *Lactobacillus delbrueckii* ssp. *bulgaricus* and by determination of carbohydrates of API 50CHL system. The SDS-PAGE protein profiles of five identified strains of *L. bulgaricus* had shown nine prominent bands at 14, 18, 25, 38, 37, 48, 50, 62 and 69 kDa along some minor one. Similarly, it was observed that a single prominent plasmid of 10 kbp was present in all strains. On the basis of wide spectrum of killing pattern having ≥ 12 mm inhibition zone against pathogenic bacteria, a strain of *Lactobacillus delbrueckii* ssp. *bulgaricus* TLB06FT was further tolerated bile salt up to 2% concentration. TLB06FT was resistant to nalidixic acid, ciprofloxacin, gentamicin, vancomycin and sulphamethoxazole, whereas erythromycin showed intermediate behaviour.

Two Silent Mutations in Mrna of Endoglucanase (Cel6A) From *Thermobifida Fusca* Enhanced Its Expression in *E. coli*

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Abstract

The sequence and structure of mRNA plays an important role in solubility and expression of the translated protein. To divulge the role of mRNA secondary structure and its thermodynamics in the expression level of the recombinant endoglucanase in *Escherichia coli*, 5'-end of the mRNA was thermodynamically optimized. Molecular engineering was done by introducing two silent synonymous mutations at positions +5 (UCU with UCC) and +7 (UUC with UUU) of the 5'-end of mRNA to relieve hybridization with ribosomal binding site. Two variants of glycoside hydrolase (GH) family 6 endoglucanase, wild type (*cel6A.wt*) and mutant (*cel6A.mut*) from *Thermobifida fusca* were expressed and characterized in *E. coli* using T7 promoter-based expression vector; pET22b(+). Enhanced expression level of engineered construct (*Cel6A.mut*) with $\Delta G = -2.7 \text{ kcal.mol}^{-1}$ was observed. It showed up to 45% higher expression as compared to the wild type construct (*Cel6A.wt*) having $\Delta G = -7.8 \text{ kcal.mol}^{-1}$ and 25% expression to the total cell proteins. Heterologous protein was purified by heating the recombinant *Escherichia coli* BL21 (DE3) CodonPlus at 65°C. The optimum pH for enzyme activity was 6 and optimum temperature was 60°C. Enzyme kinetic parameters K_m and V_{max} were found to be 56 mg ml⁻¹ and 25 U min⁻¹ respectively. It is suggested from this study that mRNA secondary structure engineering can be a good tool for improved expression and enhanced production yield of proteins.

Technical Session 3

(Environmental Biotechnology)

Isolation and Molecular Characterization of Heavy Metal Tolerant Bacteria for their Potential Usage in Bioremediation and in Agriculture

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5. *School of Agriculture, University of Management and Technology, Lahore 54000, Pakistan*

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Abstract

Soil pollution with heavy metals have adverse effect on microbial community and soil health. The present study was conducted to isolate heavy metal tolerant bacterial strains and to elucidate their potential usage for soil bioremediation and in agriculture. More than 68 heavy-metals tolerant strains, isolated from industrial discharge, were screened for the maximum tolerance limit. The results showed that some strains tolerated concentration up to 3600 ppm for Cr, 3300 ppm for Cu, 3000 ppm for Cd, 1500 ppm for Pb and 1200 ppm for As. Phylogenetically different strains (23) were further analyzed for biosorption of heavy-metals. Maximum biosorption occurred for Pb followed by Cd and Cu, whereas biosorption of As and Cr was significantly lower by all the isolated strains. Identification based on comparative 16S rRNA gene sequence demonstrated that these heavy-metal tolerant strains belonged to 19 genera and majority of isolates were related to genera, *Bacillus*(21%), *Pseudomonas* (12%) and *Staphylococcus*(10%).

The results of molecular characterization for *nifH* and *acdS* gene(s) showed that at least 7 strains were found to contain both genes in their genome (15 isolates contained *nifH* gene, whereas at least 8 strains showed *acdS* gene). Five strains (NCCP-650^T, NCCP-644, NCCP-614, and NCCP-602) were further investigated for plant growth promotion activity in *Brassica napus* under axenic condition when irrigated with water containing 50 ppm of each metal separately. The results showed that all the strains tested in this study, played significant role in growth promotion of *Brassica* plants in comparison to control (no addition of strain or metal). Among the strains, NCCP-650 proved to be the best for increase in growth of *Brassica* plants due to presence of both *nifH* and *acdS* genes. These heavy-metals tolerant strains may have the potential for plant growth promotion and can be used as bioinoculants (biofertilizer) in agriculture. Our results also indicated that some of these isolates can be used for bioremediation of soil/water system contaminated with heavy-metals (Pb, Cd and Cu).

Hydrogen Sulfide Alleviates Chromium Stress on Cauliflower by Restricting Its Uptake and Enhancing the Antioxidative System

Rehan Ahmad¹, Shafaqat Ali^{1,*}, Muhammad Rizwan¹, Qasim Ali², Faisal Islam³, Fakhir Hannan¹, Mujahid Farid⁴, Muhammad Dawood⁵ and Zaid ul Hassan³

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Abstract

Soil contamination with chromium (Cr) is a major factor limiting crop growth and yield. The present study evaluated the physiological and biochemical mechanisms by which exogenous sodium hydrosulfide (H₂S donor) mitigates Cr stress in cauliflower (*Brassica oleracea botrytis*)

L.). Results showed that Cr exposure resulted in growth and biomass reduction, which is correlated with an increase in Cr concentration and reduction in chlorophyll contents, gas exchange parameters, and enzymatic antioxidants. Chromium stress also potentiated its toxicity by enhancing oxidative stress, as evidenced by increased production of electrolyte leakage (EL), hydrogen peroxide (H₂O₂) and malondialdehyde (MDA) contents. The Cr concentration increased in roots, stem, leaf, and flowers with increasing Cr concentrations in the growth medium. Exogenous H₂S improved physiological and biochemical attributes of Cr-stressed cauliflower. H₂S decreased Cr concentrations in different parts of Cr-stressed plants and increased the photosynthetic pigments and gas exchange attributes. H₂S reduced the Cr-induced oxidative stress, particularly by reducing the EL, H₂O₂, and MDA contents and enhancing the activities of antioxidant enzymes in Cr-stressed roots and leaves compared to the Cr treatments alone. Collectively, our results provide an insight into protective role of H₂S in Cr-stressed cauliflower and suggesting H₂S as a potential candidate in reducing Cr toxicity in cauliflower and other crops.

Effect of Industrial Effluent from Pb Acid Battery Industry on Growth and Metal Accumulation in *Oryza sativa*

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Abstract

Heavy metals are naturally found on Earth and are non-degradable. They tend to accumulate in soils, sediments and are entangled into our food chain. Lead (Pb) is one of major and dangerous heavy metal in our environment. Acid Battery industries deal with Pb in manufacturing of batteries and different electrochemical products. Pb is a major component of raw material of acid battery industry; effluent contains large amounts of Pb in it. Effluent is out flown to nearby canals and irrigation channels. Public relies on canal water and Pb toxicity is responsible for disturbance in CNS and damages kidney and liver. No lead exposure is safe. Pb damages plants too, on the other side, process of seed germination, photosynthesis and transpiration is affected due to elevated levels of Pb in water up taken by plants. Induction of leaf chlorosis, inhibition of

root and shoot growth, inhibition of cytoplasmic enzymes, damage to cell structure due to oxidative stress occurs. A similar study focusing on the role and distribution of Pb on rice seedling was conducted. Rice seedlings were grown by supplying with acid battery industry effluent, four treatments were employed during course of the experiment: T1 (0% effluent), T2 (25% effluent), T3 (50% effluent) T4 (100% effluent). After germination, the growth of plants was retarded gradually from control towards 100% effluent. After 15 days of observation, the trend gradually intensified. T1 was healthier and T4 got stunted severely, as the plant grew. There was a highly significant difference in heights and biomass of all treatments. The concentrated effluent was more detrimental for rice seedlings as compared to the diluted forms. On transmission electron microscope (TEM) analyses, it was observed that Pb is easily uptaken by rice plant and it is accumulated in the walls of organelles especially cell wall, mitochondria and golgi bodies. In conclusion, it is suggested that in order to avoid bioaccumulation of Pb in food chain. The industrial effluents should be treated before discharge to canals or to irrigation channels.

Phytochemicals and Antioxidants Activities of the Medicinal Plant *Ammi majus*

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Abstract

Ammi majus a species belonging to the family Umbelleifereae, containing bioactive phytochemicals such as alkaloid, flavonoid, saponins, tanins, polyphenols etc. The antioxidant activity of methanolic extract of *A. majus* (stem, seed) were determined by 2, 2-Diphenyle-1-pecryle-hydrazyl (DPPH) method. The antioxidant activities of different fractions of stem, seed, leaves and roots were evaluated. The stem of *A. majus* fractions in ethyl acetate, methanol, chloroform and n-hexane. The corresponding values of these frictions were 87%, 57%, 50%, and 38% respectively. While seed fractions in ethyl acetate, methanol, n-hexane, chloroform showed 74%, 57%, 53%, and 38% respectively. The crude extracts were evaluated for total reductive power by Fe^{3+} to Fe^{2+} transformation.

Technical Session 4 (Molecular Biology)

Life from Death-Approach towards Sustainable Development

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Abstract

In Pakistan, there is a MAFIA illegally dealing in business of “haram” (forbidden in Islam) by using dead animals for human food purposes that creates a lot of disturbance among the society and causes corruption elevation. Moreover, a lot of stray and wandering animals got accidentally killed on road side, which is a source of environmental pollution.

Meat and carcasses of all these animals are rich source of proteins and nutrients that can ultimately be utilized as culture media components for cultivation of microorganisms used for vaccines production. This scientific approach will not only eradicate environmental pollution but also discourage progression of negative culture in society.

Identification of a Homozygous c.589G>A Mutation in *CDK6*, Causing Primary Microcephaly in a Saraiki Origin Pakistani Family

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Abstract

Primary microcephaly (MCPH) is a rare neuro-developmental disorder that is characterized by small cranium size due to reduced brain volume. Genetic studies have reported seventeen MCPH genes that include *MCPH1*, *WDR62*, *CDK5RAP2*, *CASC5*, *ASPM*, *CENPJ*, *STIL*, *CEP135*, *CEP152*, *ZNF335*, *PHC1*, *CDK6*, *CENPE*, *SASS6*, *MFSD2A*, *ANKLE2* and *CIT*. The pathophysiologies of MCPH proteins have revealed their role in cell cycle and its regulation in neurogenesis. Here in this report, we present a consanguineous Pakistani family segregating primary microcephaly ascertained from the Saraki ethnic area of Khyber-Pukhtunkhwa province in Pakistan. Whole exome sequencing revealed a previously known missense mutation NM_001259.6: c.589G-A (p. Ala197Thr) in the *CDK6* gene. The previous study has shown that this mutation result in reduced cell proliferation and impairs the correct functioning of the centrosome in microtubule organization, which is the prime determinant during neurogenesis. The *CDK6* gene is previously mapped in a single consanguineous Pakistani family, and here we are reporting the second family. These results further extend the evidence of *CDK6* gene implication in MCPH and suggest its founder effect in the Pakistani population.

Cytogenetic Insights into DNA Damage and Repair of Lesions Induced by a Monomethylated Trivalent Arsenical

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Abstract

Arsenic is a human carcinogen, and only recently have animal models been developed that are useful in investigating its carcinogenic mode of action (MOA). However, how arsenic induces cancer is still an open question. In a previous paper, we proposed a model detailing how arsenic might induce DNA lesions leading to cytogenetic damage [Kligerman and Tennant, *Tox Appl Pharma* (2007)]. In this model we hypothesized that arsenic does not induce chromosome damage via DNA adduction but induces short-lasting lesions from the action of reactive oxygen

species (ROS). These lesions cause single-strand breaks (SSB) that induce chromosome breakage when treatment is in S-phase or late G₁ phase. However, if treatment is confined to the early G₁-or G₀-phase of the cell cycle, it is predicted that little or no cytogenetic damage will result at the subsequent metaphase. Here, we describe the results from testing this model using monomethyl arsonous acid and cytosine arabinoside, a DNA chain terminator, to extend the time that DNA lesions remain open during repair to allow the lesions to reach S-phase or interact to form DNA exchanges that would lead to exchange aberrations at metaphase. The results of our study only partially confirmed our hypothesis. Instead, the results indicated that the lesions induced by MMAIII are quickly repaired through base excision repair, that there is little chance for araC to extend the life of the lesions, and thus the DNA damage induced by arsenicals that leads to chromosome aberrations is very short lived.

The results partially confirmed the hypothesis. It indicated that the lesions induced by (MMAIII) are quickly repaired through base excision repair, that there is little chance for araC to extend the life of the lesions, and thus the DNA damage induced by arsenicals that leads to chromosome aberrations is very short lived.

Technical Session 5

(Medical/Nanobiotechnology)

Nutraceutical Delivery through Nanotechnology

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Abstract

Nutraceutical compounds have great surge in recent literature for their efficacy in human nutrition. It is however very important for these nutraceuticals to be actually bioavailable for human body to gain maximum nutritional benefits. Similarly, it is as important to have such delivery systems for nutraceuticals that are biocompatible. Whereas, the bioavailability is highly dependent on the solubility of such nutraceuticals compounds. The solubility of many nutraceuticals is limited in either oil or water based solvents making it difficult to formulate food grade solutions. The low solubility is caused by them having both hydrophilic and hydrophobic structures but the dual nature allows them to bind to an oil-water interface. Nanoemulsions have high capacity for interfacial absorption of these otherwise less soluble nutraceuticals. The research has examined the suitability of food grade sub-micron sized emulsions as a delivery medium to use nutraceuticals in a dip for the preservation of fresh fish. When the solubility of a nutraceutical in an emulsion was compared to the solubility in water the order of enhancement was ascorbylpalmitate (AP) > quercetin > rutin > vanillic acid > vanillin > caffeic acid > gallic acid with an enhancement factor of 40, 27, 15, 4, 3.2, 2.3 and 0.63 times increased solubility respectively. The solubility enhancement of the emulsion compared to oil was in the order rutin > AP > quercetin > vanillic acid > caffeic acid > curcumin > vanillin with an increase of 20, 15, 10, 7, 3.6, 3.5 and 2.3 fold respectively. Gallic acid was used as a model compound to test delivery into fresh fish muscles. There was a fourfold increase in the uptake of gallic acid by fish muscle after 30 minutes of dip in the nanoemulsion compared to uptake from a water control indicating that the emulsion was able to facilitate the binding of the nutraceutical to the fish surface.

Exploring the Cell Surface and Intracellular Trafficking of Nanocarriers for Gene Delivery

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Abstract

Gene therapy, which involves the transfer of nucleic acids, including genes or siRNA, into the cell for therapeutic purpose, holds a huge promise for the genetic problems and cancer treatments. The transfer methods that are currently used in the field can be broadly classified into viral vectors and nonviral vectors. Nonviral vectors, including lipoplexes (complexes of cationic lipids with DNA) and polyplexes (complexes of cationic polymers with DNA) gained considerable attention in recent years, mainly because of their lower toxicity, lesser immunogenicity and relatively easier production compared to their viral counterparts. However, their lower transfection ability put their therapeutic applications at question. Therefore, it is primarily important to decipher the intra- and extracellular processing of these nonviral vectors thereby finding new ways to increase their transfection efficiency. In this regards, while exploring the cell surface and intracellular trafficking of nonviral vectors, we have shown for the first time that before reaching to cell surface cationic nanocarriers are processed along actin rich cellular extensions (filopodia) to get access to the cell surface. After reaching to the cell surface, cationic nanocarriers are internalized into the cell using various endocytic pathways, which depends, among others, on size and type of nanocarriers and also type of the cells used. Moreover, we have found that the intracellular processing of nanocarriers can be modulated using specific kinases. Lysosome, that degrades foreign bodies after fusing with them, is one of the fundamental barriers in the overall transfection process of nanocarriers. We have shown that the movement of particular nanocarriers into lysosomes can be prevented using specific kinases, thereby increasing their transfection efficiency. In order to show its therapeutic effect, the nanocarrier must escape from endosomes. We have shown for the first time, with the help of various microscopic tools, how nanocarriers escape from endosome, and confirmed two basic theories that were there in the field for more than a decade without convincing evidences.

In order to show their effect, nanocarriers have to cross these various barriers and by determining the relative contribution of various barriers and underlying mechanisms, and, by finding new

ways to effectively cross these barriers, transfection efficiency of nanocarriers can be enhanced thereby providing an opportunity to use them as therapeutic alternatives.

Nano-Encapsulation of Drug(s) and Bio-active Reagents

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Abstract

Encapsulation of drugs, bio-active reagents, molecules and nanoparticles in nanoscale platforms is one of the most promising approaches in the development of nanomedicine that provides for efficient drug loading along with reducing systemic toxicity. Moreover, smart targeting of these nano-vehicular systems can greatly enhance the accumulation of the particular drug at its desired action site(s). Drugs encapsulated in nano-vehicular systems exhibit improved bioavailability, biodistribution and activity relative to non-encapsulated counterparts. A number of encapsulation strategies as well as nanoscale carriers have been exploited these days, e.g. polymers, dendrimers, liposomes, zeolites, peptides, viruses etc. In this work we report encapsulation of drug(s) and natural (refined) bioactive reagents for a number of different purposes. Tobacco Mosaic Virus (TMV) is a rod shaped plant virus that is 300 nm long and 18 nm in diameter with a 4 nm channel inside it. The plant virus had been encapsulated with Pt(II)-containing drugs followed by the effusion of it from the virus. Our group also encapsulated Virgin Coconut Oil (VCO) in Solid Lipid Nano-Particles (SLP). VCO loaded SLP showed improved skin penetration as well as better moisturization of the skin. Niosomes are the next generation of Nano-structured Lipid Carriers (NLC) that can be synthesized from non-ionic surfactants and cholesterol. Encapsulation of VCO along with emulsifying agents and nanoparticles showed great potential to inhibit growth of Multidrug Resistant (MDR) bacteria especially *Staphylococcus aureus*. The

drug encapsulated niosomes gave extended release of the drug, which could result in decreased dose, lesser days of treatment and more patient compliance.

Expression Profiling of *Hspb1* and *Tp53* Genes through RT-qPCR in Different Cancer Types of *Canis familiaris*

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Abstract

Diagnostic molecular marker studies are in vogue to have insight of most prevalent animal diseases including cancer, which is considered as disease of genome. So, an early and robust molecular diagnostic method was envisaged in this research. mRNA quantification of pro-apoptotic and anti-apoptotic genes was conducted in dog Lymphoma, CTVT, SCC, granuloma, perianal adenocarcinoma and mammary tumors using comparative Ct method to have an idea of involvement and differential expression of these markers. TaqMan gene expression assays of *Tp53* and *Hspb1* were used with reference control of *GAPDH*. Differential expression of target genes was determined through RT-qPCR using comparative Ct method. *Hspb1* showed ectopic expression in lymphoma, CTVT and mammary tumors; its down-regulation was observed in granuloma and oral SCC with the fold change (FC) difference of ± 35 . Similarly, *Tp53*, which belongs to tumor suppressor gene category and possesses pro-apoptotic properties, its altered expression was also observed in all tumor types, notably 80% of mammary tumors and 60% of CTVT portrayed its up-regulation with FD of 33.31 and 2.27 respectively. Altered transcriptomic response of *Hspb1* and *Tp53* was observed in all cancers types of *Canis familiaris*, this profiling might be helpful for diagnosis, prognosis, identification and classification of widespread neoplasms in this species alongwith other animals in general.

Color Segmentation Based Computer Aided Diagnosis of Early Tuberculosis Nodules in X-Ray Images

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Abstract

For the successful treatment of TB it is crucially essential to detect the disease at its early stage. In Pakistan, usually the fatal disease TB is diagnosed manually by the microbiologist based on the X-ray image, the detection becomes much complicated for the less vivid and little number of nodules. The perished condition of the image due to the finger spots and impacted stains does not show the nodules and their intensity, this makes it impossible for the microbiologist to identify the early stage of TB. Automatic image processing provides better tools and techniques for the improvement in manual screening of samples. The function of image processing particularly segmentation is used for auto-detection of TB nodules from X-ray image of lungs. Moreover, the color is a main feature utilized in the detection of TB nodules. Discontinuity and similarity are the two basic properties of grey-level values which are the bases of segmentation algorithms for X-ray images, both values relate with the requirement of the method. Therefore, for the accurate detection of TB in X-Ray image, color segmentation based Computer Aided Diagnosis system is design and developed. Image acquisition, image pre-processing, lung field segmentation, and feature extraction are the functions included in the developed system. For testing the developed system, 275 X-Ray images are collected from the various X-Ray diagnostic centers of Khairpur city. The window size of each image is set by (42x 42), and 70 Maximal Level + 30 Average Level is fixed for the grey-level threshold. The accuracy of 96.81% is calculated with the selection of these values. The bigger scanning windows can be used for detection of more advanced nodules but the fading nodules have been detected at acceptable level with a lower value of threshold. The developed system will provide better assistance to the medical technologist in the TB diagnosis process.

Phytoremediation-Ecotechnology for Developing Nations like Pakistan

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Abstract

With the advancement of science and technology a number of environmental issues rises and become the worldwide concerns. Flow of organic and inorganic pollutants directly or indirectly in to an ecosystem degraded not only the valuable resources of ecosystem but also causes threats for sustainable development of environment. Many conventional techniques remain less effective due to economic and social constrains but phytoremediation and its associated microbes are useful for the remediation of deteriorated soil, water and air. Phytoremediation is cost effective and innovative environmentally friendly approach which enhances the bioavailability, accumulation and detoxification of pollutants. Advancement in biotechnology also strengthens the bioremediation and phytoremediation techniques for the remediation contaminated sites. The existence of plants in contaminated areas is due to the presence of some specific pollutant resistant genes in such plants and related microbial community. In this respects environmental biotechnology promotes the study of specific genes expression which are responsible for the pollutant resistance and remain helpful in understanding the nature of pollutants their uptake, accumulation and detoxification pathways. So by using DNA and RNA recombinant technology such plants and microbes can be genetically modified and utilized for improved remediation of contaminated areas. Therefore, if such metal resistant, metal tolerant and metal accumulator or hyper accumulator plants and microbial species are isolated and further modified for decontamination of polluted sites it will improve the phytoremediation efficiency. Pakistan and other developing countries should get full advantage of low cost and environmental friendly ecotechnologies for environmental remediation.

Preparation and Characterization of Bio-based Composite Membrane for Water Treatment

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Abstract

Along with natural causes, anthropogenic activities have intensified the water scarcity issue. Apart from conservation techniques solution to water scarcity is recovery of clean water that could be done by desalination of inland brackish water or sea water by reverse osmosis membrane technology. When it comes to membrane technology polymer composite membranes are most efficient & inexpensive. The aim of the current study was to develop a composite membrane using carboxymethyl cellulose (CMC) as a basic component. For the purpose, carboxymethyl cellulose was prepared from already isolated cellulose by alkalization and etherification of cellulose. CMC along with polyvinylpyrrolidone (PVA) and polyvinyl alcohol (PVP) was then used to prepare composite membrane in order to treat (0.1, 0.3, 1, 3%) synthetic saline water. PEG was used as a pore forming agent. Furthermore characterization was done using Scanning Electron Microscopy, Fourier Transform Infrared Spectroscopy, Thermo-Gravimetric Analysis and Universal Testing Machine. SEM indicates that addition of PVP resulted in smoother surface as compared to the membrane fabricated without PVP and the membrane formed lies in microfiltration (0.1 - 10 micron) range. FT-IR spectroscopy images gave the bands that are attributed to the dispersion of PVA and PVP in substrate matrix. Weight loss started at 270°C which was 210°C in the absence of PVP, hence TGA results showed that PVP effectively enhanced the thermal stability of membrane. The trend of increase in salt rejection in selected salts i.e. NaCl < KCl < CaCl₂ was due to the increase in molecular mass respectively and overall efficiency ranges from 27 to 37%. The removal was highest for CaCl₂ followed by KCl and NaCl (i.e. 37 > 29 > 27%) respectively. It was concluded that PVP shows positive effect on thermal stability, surface morphology and mechanical properties of membrane. The fabricated membrane can be used for pre-treatment to Reverse Osmosis (RO) in order to improve efficiency and the life of RO membranes.

Technical Session 6

(Agricultural Biotechnology/Bioinformatics)

Applications of Advanced Biotechnological Techniques in Agriculture Sector: A Case Study of China

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Abstract

Biotechnology has brought revolution in the every field of human life including agriculture sector. Agriculture has direct impact on human life. Use of modern techniques in the agriculture sector can improve this sector to meet the need of current era. Agriculture sector in advanced countries is very well developed because of use of modern techniques. These techniques can be employed in developing and under developed countries. Pakistan being agriculture country has the potential of development of this sector like other developed countries. The agriculture sector in our neighbor country i.e. China is very well developed. Taking our agriculture sector in same pattern like China can increase the potential of this sector to almost double. This well bring more development in our society and makes people to live a better life.

A Comparative Analysis of Mesquite (*Prosopis juliflora*) and Sugarcane (*Saccharum officinarum*) Waste Biochar through Scanning Electron Microscopy

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Abstract

Slow pyrolysis of biomass produces carbon rich charred product: biochar. Different techniques have been used previously to characterize biochars made from different feedstock materials. In this study, a comparative analysis through scanning electron microscopy was done to characterize biochar made from mesquite (*Prosopis juliflora*) and sugarcane (*Saccharum officinarum*) waste at 500°C. Scanning electron micrographs revealed that feedstock materials and pyrolysis temperature greatly influenced the surface morphology of biochars. Mesquite biochar possessed integrated structure with large number of micro (<1µm) and macropores (>1µm) while sugarcane waste biochar had flake like structure having less porous appearance and large surface area due to trapped volatiles. Moreover, sugarcane waste biochar was characterized with white dots on its surface when the magnification was increased. Mesquite biochar, due its high porosity, is expected to increase soil porosity and enhanced microbial activity while sugarcane waste biochar, due to its larger surface area, is expected to enhance the supply of nutrients availability to plants. Current findings deserve field experimentation to evaluate the effects of mesquite and sugarcane waste biochars on soil properties and plant growth.

Plants Based Commercial Products Using Recent Biotechnology Techniques in Pakistan

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Abstract

In recent times, the world has been confronted with energy crises due to depletion of fossil fuel resources. At the same time increase in petroleum prices, environmental pollution and diminishing supply of fossil fuels are the key factors leading to search for alternative sources of energy. Currently the most often used type of biofuel is biodiesel which is renewable, biodegradable and non toxic fuel for diesel engines. It is derived from vegetable oils by transesterification with alcohols. This project is initiated in Pakistan with concept of mega tree plantation for green fuel for green Pakistan. The overall objective of this project is to reduce

carbon in atmosphere using renewable green fuel. To investigate the impact of mega tree plantation on degraded barren and eroded land to overcome the energy crises, environmental pollution and promote biodiversity and ecosystem conservations in Pakistan. This study described in detail an optimized protocol for biodiesel production from indigenous oil seeds. Based on qualitative and quantitative analysis of Biodiesel and their byproducts, the bioenergy from such resources can be feasible, cost effective, environment friendly, if mass plantation of such resources may initiated in suitable places at global perspective. The concept of green fuel from green plants has positive impact on climate stability and biodiversity promotion. The lesson learned from this study will be adopted throughout the country.

Determination of Capsaicinoids Content and Enzymes (Phenylalanine Ammonia-lyase, Cinnamic-4-hydroxylase, and Capsaicin Synthase) Activities in *Capsicum* Species

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Abstract

Peppers (*Capsicum*) in raw or dried form are important hot spice and condiment used worldwide for flavouring and colouring in cuisines. They are the good sources of vitamin C, vitamin A and β -carotene with significant anticancer, antimicrobial, and energy metabolism acceleration activities. Phenylalanine ammonia-lyase (PAL), cinnamic-4-hydroxylase (C4H), and capsaicin synthase (CS) are the enzymes involved in capsaicinoids biosynthesis pathway. These enzymes may be altered in cultivars with different pungency levels. This study was aimed to analyze the capsaicinoids content, and the activities of aforementioned enzymes by using high performance liquid chromatography (HPLC) and well established activity assays. The content of capsaicin

and dihydrocapsaicin were found to be 50.4–110.7 mg/kg and 14.7–58.3 mg/kg, respectively. Regarding the enzyme activities, PAL and CS showed an obvious trend associated with the capsaicinoids among hot pepper cultivars with different pungency levels. However, the C4H had an inconsistent relationship to capsaicinoids content. Therefore, it could be concluded that PAL and CS are the critical enzymes in capsaicinoids biosynthesis of different pungency levels of hot pepper cultivars.

Inhibition of Photorespiratory Losses in C₃ Plants for Improved Productivity: An *in-silico* Approach

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Abstract

The oxygenation reaction of Ribulose 1, 5, biphosphate carboxylase/oxygenase (Rubisco) enzyme in C₃ plants produces single molecule of phosphoglycerate (3PGA) and a toxic compound phosphoglycolate (2PG). 2PG is recycled to 3PGA via photorespiratory C₂ cycle which is a lengthy process and reduces the photosynthetic efficiency of plants. This problem is more evident in C₃ plants because they lack carbon concentrating mechanism. There is a need to utilize and introduce potential pathways in C₃ plants to by-pass photorespiratory losses. Cyanobacteria have such potential pathways which can be utilized to overcome photorespiratory losses. Engineering foreign genes may cause weird response in the plants and *in-silico* modeling is useful in simulating such responses. Therefore the present study aimed to develop an *in-silico* model of cyanobacterial photorespiratory by-pass in C₃ plant. The model was developed in matlab for basic photorespiratory cycle in plants as well as the proposed pathway. Simulations were performed to compare the models against different parameters. The simulations indicated positive results for the proposed photorespiratory by pass. The current study was helpful in determining and utilizing the potential pathways which can further be manipulated through genetic engineering.

Identification and *in-silico* Analysis of GALNS Mutations Causing Morquio A Syndrome in Eight Consanguineous Families

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Abstract

Genetic deficiency of lysosomal enzyme, N-acetylgalactosamine-6-sulfate sulfatase (GALNS, EC 3.1.6.4), due to mutations in the *GALNS* gene [OMIM: 612222] leads to intralysosomal accumulation of glycosaminoglycans (GAGs): chondroitin-6-sulfate (C6S) and keratan sulfate (KS), which ultimately cause mucopolysaccharidosis IV A [Morquio A disease (MIM: 253000)]. MPS IV A is a lysosomal storage disease characterized by systemic skeletal deformities including disproportionate short stature with a short neck, pigeon chest, lumbar kyphosis, genu valgum, broad mouth and prominent maxilla in association with joint laxity, corneal clouding, valvular heart defects, and pulmonary dysfunction. Comprehensive analysis of the disease-causing mutations reported in *GALNS* revealed that only 5% of mutations occur in the active-site residues, 65% in the buried residues of the core protein, and 27% in surface residues. That's why; bioinformatics analysis of these mutations is important to determine their effect on the structure and functions of the protein and to establish a correlation between genotype and phenotype. In the present study, eight Pakistani consanguineous families with Morquio A syndrome were clinically and genetically evaluated. Linkage analysis followed by sequence analysis of the gene detected four novel (p.Phe216Ser, p.Met38Arg, p.Ala291Ser, p.Glu121Argfs*37) and two reported (p.Pro420Arg, p.Arg386Cys) mutations in the eight families. *In silico* structural and functional analysis predicted that these mutations disrupt the function of *GALNS* protein through fluctuating its three-dimensional structure, stability, and binding affinity and produce severe phenotypes. This is the first comprehensive study on molecular analysis of patients with Morquio A syndrome from Pakistan that reports four novel mutations with their structural and functional consequences.

Construction and Analysis of a Comprehensive Protein Interaction Network of HCV with Its Host *Homo sapiens*

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Abstract

HCV is becoming a major health problem in Asia and across the globe as it is responsible for causing serious liver diseases including liver cirrhosis (Shanshan *et al.* 2012), chronic hepatitis (Dubuisson *et al.* 2004) and hepatocarcinoma (HCC) (de Chasse *et al.* 2008). Protein interaction networks have the potential to provide us valuable insights into the functional roles of different proteins and can also help us in finding potential candidates for targeting with drugs. Here we present a comprehensive protein interaction network of Hepatitis C Virus with its host, *Homo sapiens*, constructed from overlapping yet different datasets published in previous studies. The final network had 1325 interactions between 12 HCV proteins and 940 human genes, among which 21 were intra-viral and 1304 were HCV-Human. After analyzing the network, we ranked human proteins according to their number of interactions with HCV proteins. ANXA2 and NR4A1 were interacting with 6 HCV proteins while 11 human genes were interacting with 5 HCV proteins. Among the viral proteins, NS3 was interacting with most number of interactors followed by NS5A and so on. Furthermore, enrichment analysis of gene ontology and KEGG annotations of these proteins was carried out to find the pathways and the biological processes enriched in this set of proteins. The top 10 host proteins came up to be significant in Influenza A viral infections and not HCV infections, indicating that the set of proteins are not well studied in the HCV infection pathway despite their significant connectivity in the final network, and therefore, can be interesting candidates for further experimental studies. Additionally, the search result of different database and literature curated drug data targeting HCV revealed that the list of 17 human proteins highly interacting with the hepatitis c viral proteins are not targeted by the available drugs, thus indicating them to be potential candidates against HCV curing drugs.

Metabolomics as a Supplementary Tool for the Advance of Biotechnological Excursions

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Abstract

In recent decade a tremendous growth has been observed in Biotechnology research, demonstrating itself as a tool to improve plant yield (i.e. crops, ornamental and medicinal plants) in quantitative and qualitative aspect. The targets of biotechnology research are hard to achieve until the metabolomic pathways are not explored for their up/down regulatory behaviors in during any biotechnological adaptation. The exploration of such metabolomic flux of cells or tissues, a series of snapshots for the target biological material leads towards the metabolomics based system biology research. This strategy is of immense importance for identification of genes in metabolomic pathways of plants, altered through biotechnological excursions. Our groups demonstrate the application of these tools in the research of various plants, including tobacco and *Brassica*. In this view, multiple chromatographic and spectroscopic techniques i.e. GC/MS, NMR, HPLC etc. coupled with multivariate data analysis are being used as supplementary tools in biotechnology research.

Poster Presentations

P1: Biochemical and Therapeutic Effects of *Parthenium hysterophorus* Leaf

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Abstract

Parthenium hysterophorus is an herbaceous plant of *Asteraceae* (*Compositae*) family. It is poisonous weed and commonly known as carrot grass. Due to medicinal benefits it is employed for the treatment of many diseases like anemia, diabetes mellitus and heart troubles. In the present research, *P. hysterophorus* extracts were prepared in six different solvents (ethanol, ethyl acetate, *n*-butanol, *n*-hexane, methanol and chloroform). Antidiabetic (acetylcholinesterase alpha amylase inhibition and antiglycation activity) along with antibiofilm, thrombolytic and cytotoxic (hemolysis) activities were performed. Methanol fraction showed maximum (4%) glycation inhibition. Chloroform and ethyl acetate fractions exhibited highest acetylcholinesterase (76%) and alpha amylase (49%) inhibitory activity respectively. Different fractions showed hemolysis in the range of (0.4-5.61%) with ethyl acetate and aqueous being the most potent hemolytic agents. For all fractions thrombolytic activity (11-23%) was observed and highest (23%) thrombolysis efficacy was observed in chloroform. Ethyl acetate fractions was showed highest 94% inhibition against *Pasteurella multocida* strain. The aim of this research is mainly to explore the medicinal potentials of *parthenium hysterophorus*. The study reveals that the active fraction of *parthenium hysterophorus*. L. leaf extract is very promising for developing standardized phytomedicines.

P2: Bio-Efficacies of *Syzygium cumini* Fruit

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Abstract

Syzygium cumini an ever green tree, member of *Myrtaceae* family, commonly called jamun is important for its nutritional and medicinal value. Java plum juice and jam can be used to cure acute and chronic diarrhea, urine retention, sore throat and many other diseases. In the present research, *S. cumini* fruit extracts were prepared in six solvents such as methanol, ethanol, *n*-butanol, *n*-hexane, chloroform and ethyl acetate. Antidiabetic potentials (antiglycation activity, alpha amylase and acetylcholinesterase inhibition) were investigated along with cytotoxic (hemolysis), thrombolytic and antibiofilm activities. Chloroform extract showed maximum (48%) antiglycation activity. *n*-butanol and ethanolic extracts exhibited highest inhibition of alpha amylase and acetylcholinesterase (41% and 13%) respectively. Hemolytic activity in the range of 7-27% was shown by aqueous and ethyl acetate fractions. Thrombolytic activity (11-21%) was observed for all tested fractions and chloroform showed the highest (21%) thrombolytic efficacy. The chloroform fraction showed 82% inhibition against *Pasteurella multocida* strain. The findings of this study revealed that the different fruit extracts of *S. cumini* showed significant pharmacological actions and there is a need for further investigation on therapeutic potentials of plant.

P3: Pharmacological Potentials of *Z. officinale* Rhizome

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Abstract

Z. officinale is popular spice which is used in a variety of foods and beverages. Gingerol is the major bioactive element responsible for the anti-tumour, antioxidant and anti-inflammatory activities of *Z. officinale*. It is one of the vital medicinal plants which is naturally found around the globe. It has some useful effect to human body to treat a variety of diseases. In this present research work, *Z. officinale* extracts were prepared in six different solvents (*n*-hexane, chloroform, ethyl acetate, *n*-butanol and ethanol, methanol). Antidiabetic (antiglycation activity, alpha amylase inhibition) were performed along with cytotoxic (hemolysis) and thrombolytic activities. *n*-butanol and ethanol fractions exhibited highest alpha amylase (75.20, 92.01%) respectively. Whereas *n*-butanol fraction showed maximum (92%) glycation inhibition. Thrombolytic activity (2-30%) was observed for all tested samples and methanol had the highest (29%) thrombolysis efficacy. Various fractions showed hemolysis in the range of 2-29%

with ethyl acetate and *n*-hexane being the most potent hemolytic agents. *Z. officinale* ethanol fraction showed 15mm zone of inhibition for *Bacillus subtilis* strain. So, consumption of this plant material could be helpful against various diseases through oxidative stress elements. This research recommends the use of *Zingiber officinale* that could be helpful to cure life threatening disorders.

P4: Estimation of Water Quality from Various Areas of Tehsil Bhimber Azad Jammu and Kashmir

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Abstract

Inclusion of contaminants to environment makes it unclean or unsafe for life and is called “pollution”. Water pollution occurs when it is overloaded with over dose of micronutrients excreted by effluents of factories and sewerages lines. Present study deals with estimation of water quality through physiochemical analysis of thirteen water samples (hand pumps) collected from different areas of Tehsil Bhimber. Different parameters used are TDS, EC, Total Hardness, magnesium, arsenic, calcium and pH. The analysis of thirteen water samples showed different results. The electrical conductivity of water sample collected from Sathabawli showed highest value of TDS (1504 µs). The highest values of pH, EC, Turbidity, Arsenic, TDS, Total Hardness, Magnesium and Calcium were 6.24, 1504, 8.38, 0.005, 758, 204, 68 and 136, respectively. While the lowest values for these were 5.26, 529, 0.00, 0, 257, 96, 18 and 71 respectively. These values showed variations from site to site. These changes may be due to soil composition, texture, sanitation standards of urban area and other environmental factors. The data obtained was analyzed by using Two-Way Analysis of variance. There was a significant difference between mean values of collected samples. These findings depict that water of different areas of Bhimber is not safe and secure for hygiene and it needs to be treated and filtered as per WHO recommendations prior to be used for drinking and cooking purposes.

P5: Antibacterial and Anatomical Analysis of *Calotropis procera* (Aiton) Dryand from Different Areas of District Mirpur, Azad Jammu and Kashmir, Pakistan

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Abstract

This work presents antibacterial potential and anatomical investigation of *Calotropisprocera* (Aiton)Dryand. Populations from different areas of Mirpur (Azad Jammu & Kashmir), Pakistan. In the research, three different areas (viz: Jarikus, Khaliqabad and Jatlan) were selected for population sampling (leaf parts) having no symptom of disease. Leaf powder was macerated in two solvents and tested against four pathogenic bacterial strains (*Staphylococcus aureus*, *Bacillus subtilis*, *Escherichia coli* and *Pseudomonas aeruginosa*). The methanolic extract depicted highest zone of inhibition (ZI) values with 14.67±1 mm against *Pseudomonas aeruginosa* (PA) while aqueous extract showed good ZI (14±1 mm) against this bacterium. Extract from Jatlan sample showed highest ZI values for methanolic fraction against *Staphylococcus aureus* and least effect against *Bacillus subtilis* (13±1 mm). Against *E. coli* methanol showed 14.7±0.8 mm and aqueous showed 11±0.5 mm zone of inhibition. Against *Pseudomonas aeruginosa* methanol showed 12±0.76 mm and aqueous showed 12.7±0.5 mm zone of inhibition. Among all three sampled areas, methanolic leaf extracts of Jatlan area showed very good ZI activity with 19±1 mm against *Staphylococcus aureus* followed by extracts of Khaliqabad samples with 14.67±1 mm against *Escherichia coli*. Among aqueous extracts leaves of Khaliqabad area presented highest antibacterial potential (14±1 mm) against *Pseudomonas aeruginosa*. It was observed that maximum zone of inhibitions were showed by methanolic extracts as compare to aqueous extracts. The maximum zone of inhibition in methanolic extracts of Jatlan was 18.7 mm among all areas. An anatomical analysis was made to explore leaf phenetics and its impact on concentration of phytochemicals with subsequent variation analysis in antibacterial potential. It was found that plant leaf samples of Khaliqabad had highest stomatal index (SI) 538 and same was found best antibacterial activity against various strains of bacteria. SI of Jatlan 408.7 followed by samples of Jarikus with SI values of 242.8. It was confirmed that

there is direct and positive correlation between SI and ZI of leaves of plants collected from different localities. These findings depict that leaves of *Calotropis procera* (Aiton) Dryand have good antibacterial activity confirming the past ethnomedicinal folklore applications of the plant and this result findings can be used as source of novel drug development from such herbal therapeutic products.

P6: Performance of Wheat Genotypes against Cadmium Contamination of Soil

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Abstract

In order to evaluate different wheat genotypes against cadmium contamination of soil, an experiment was carried in the department of Plant Breeding and Genetics, PMAS-Arid Agriculture University Rawalpindi. The experiment was carried out under the control conditions. The experiment was laid out using the two factorial completely randomized design (CRD) with six treatments and four replications. The treatments included six cadmium concentrations of cadmium in soil i.e; (control treatment, 5ppm, 10ppm, 15ppm, 20ppm and 25ppm). Parameters studied were germination %age, plant height (cm), fresh shoot weight (g), dry shoot weight (g) and cadmium contents in shoot. The results showed the accumulation of cadmium in shoot of different wheat as compared to control treatment. Cadmium depicted the great variation as compared to control in the study of different parameters

P7: Protein Profiles in Wheat Seedlings under Nitrogen Stress

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Abstract

Increasing demands for wheat productivity together with environmental concerns about the use of nitrogen-based fertilizers dictate the importance of improving nitrogen use efficiency (NUE). Identifying biological processes responsible for efficient fertilizer use will provide tools for crop improvement under reduced nutrient inputs. Two wheat varieties Krichauff (tolerant) and Berkut (sensitive) were studied for protein profiles under recommended (N+, normal) and limiting (N0, stress) nitrogen conditions at Molecular Genetics Lab, The University of Sydney, Australia. Seedling characters viz. SPAD, shoot length, shoot weight and leaf nitrogen content were significantly decreased in both varieties under stress conditions. Compared with Krichauff, Berkut experienced more pronounced decrease in almost all seedling traits under stress condition. The SDS-PAGE analysis revealed that number and intensity of bands were greater under N+ than N0 in both wheat cultivars. The protein profile of nitrogen sensitive cv. Berkut showed decrease in intensity of almost all the bands as compared to Krichauff under N0 condition. The protein pattern analysis showed unique protein of 30 kDa occurred in wheat seedlings of cv. Krichauff under both N+ and N0, while in Berkut under N+ only. These findings highlight the significance of specific-protein (30 kDa) associated with nitrogen tolerance in wheat and verified the potential value of cv. Krichauff in improving nitrogen use efficiency of wheat.

P8: Waste water induced phytotoxicity using onion (*Allium cepa*) as a test plant

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Abstract

Environmental pollution due to hazardous substances has been increased unexpectedly in recent few years. Among these pollutants water pollution is one of the main issues worldwide. The main sources of water pollution are domestic and industrial effluents. Contaminated water is used for irrigation purpose in many countries that contain many hazardous compounds including heavy metals. Continuous use of such waste water to agriculture field may cause serious threats to plants and human health. The present research was conducted to evaluate the phytotoxicity induced by waste water using an onion (*Allium cepa*) as a test plant. Six different types of heavy metals were

investigated in waste water. The concentration of lead and chromium was recorded very high as compared to other heavy metals. Waste water declined onion root length and also decreased its fresh and dry weight. Increased levels of antioxidants (MDA, H₂O₂, SOD, POD, APX and CAT) were found in onion roots. In cytological study, a decrease in mitotic index was found in root of onion grown in waste water as compared to control. Abnormalities of chromosomes were also observed in roots. It was found that the aberrant chromosomes were increased in roots of *Allium cepa* which were grown in waste water of university road. A plasmid nicking assay was performed to check the genotoxic effect of waste water on plasmid. A plasmid was found open circular when it was treated with university road waste water. It can be concluded that waste water adversely affected onion growth and up-regulated antioxidant levels in its roots.

P9: Antibacterial Evaluation of Silver Nanoparticles Using *Fagonia cretica* Leaves

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Abstract

Nanoparticles have gained importance in recent years due to overuse of antibiotics. The small size of nanoparticles, their strong mechanism of action attribute to their significant antimicrobial activities and their use to treat various infections have gained attention. The aim of this study was to synthesize silver nanoparticles (AgNPs) by green method which is an environment-friendly and cost effective method of synthesizing nanoparticles. AgNPs were synthesized from Silver Nitrate using leaf extracts of *Fagonia cretica* as a reducing and capping agent. The synthesized AgNPs were capped with plant biomolecules. The particles were highly crystalline and pure. They were spherical in shape ranging in size from 30-50 nm as evidenced by UV-VIS spectroscopy, Scanning Electron Microscopy, X-Ray Diffraction and Fourier Transform Infra-Red spectroscopy. The AgNPs showed significant antibacterial activity in disc diffusion method against the tested human pathogens (*Staphylococcus aureus*, *Escherichia coli*, *Klebsiella pneumoniae*, and *Salmonella typhi*). The antibacterial activity of silver nanoparticles was compared with the positive control (Ciprofloxacin disc 10 µg), plant extract and silver nitrate solution. The resulted inhibition zones for AgNPs ranged from (29-33 mm), positive control (23-25 mm), plant extract (13-15 mm) and silver nitrate (4-5 mm). These results showed that AgNPs exhibited significantly high antibacterial activity as compared to the plant extract, silver nitrate and antibiotic discs (ciprofloxacin). Hence it was concluded that silver nanoparticles synthesized from *Fagonia cretica* are putative treatment of the infections caused by gram positive and gram negative human pathogenic bacteria.

P10: Application of Molecular Biological Tools in Environmental Bioremediation Studies

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Abstract

Identification of microbes involved in biodegradation of a pollutant is often hindered and become a challenge for classical microbiological analysis due to slow growth of microbes and their physiological dependency on other living organisms. Recent advances in biotechnology have provided opportunities for identification and characterization of pollutants degrading microbes through culture-independent and nucleic acid-based molecular biological tools such as high throughput next generation sequencing (NGS). In the present study, pyrosequencing analysis targeting bacterial 16S rRNA genes was used for microbial genetic profiling of explosives degrading microbes in microbial consortia enriched from explosive-contaminated soil. Results showed that *Rhizobium* and *Methylophilus* were dominant genera in RDX- and TNT-degrading microbial consortia, respectively. According to phylogenetic tree analyses, these bacteria may be novel explosive-degraders because their sequences were phylogenetically distant from those of known explosive-degrading bacteria. Furthermore, quantitative real-time PCR analyses revealed the presence of substantial amount of explosive-degradative xplA gene copy numbers in the explosive-degrading consortia. The findings imply that molecular biological methods such as q-PCR and NGS are suitable and important tools for exploring the novel microbial activities in environmental and/or engineered bioremediation systems.

P11: Alleviation of Salt (NaCl) Stress in Maize through Biofilm Producing Bacteria

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Abstract

Salinity is one of the important ecological problem that reduced crop yield and productivity around the globe including Pakistan. The present research was design to evaluate the mediated effects of biofilm producing bacteria *Bacillus licheniformis* NCCP-59 on physiological, biochemical and antioxidants profile of maize cultivar (Azam 2000) under saline conditions (0, 50, 100, 150 mM). Salinity drastically reduced the germination percentage while significant increase was noted in seeds primed with biofilm producing bacteria. Salt (NaCl) stress reduced the root and shoot lengths, fresh and dry weights, (Ca⁺⁺, K⁺) contents, and photosynthetic pigments. While significant increase was noted in sodium ion (Na⁺) content, proline (Pro), total soluble sugars (TSS) and antioxidants i.e. super oxide dismutase (SOD), peroxidase (POD), hydrogen peroxide (H₂O₂), malondialdehyde (MDA), ascorbate peroxidase (APX) and catalase (CAT). However the inoculation of maize seeds with biofilm producing bacteria NCCP-59 significantly increased the photosynthetic pigments chlorophyll a, chlorophyll b, carotenoid content while antioxidants and metabolites concentrations was decreased. SDS-PAGE protein profile of leaves showed different banding patterns under salt stress and bacterial inoculated plants. The study concluded that *Bacillus licheniformis* (NCCP-59) has a growth promotory effects on maize seedlings under various saline conditions and can reduce the deleterious effects of salt stress.

P12: Pb-Induced Changes in Roots of Two Rice (*Oryza sativa* L.) Cultivars Grown in Lead Contaminated Soil Mediated by Smoke

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Abstract

Nowadays, public concerns regarding deleterious effect of lead (Pb) is on rise due to its abundance and toxic effect on plants and other living organisms. In plants, it has no noticeable biological function but can cause various morphological, physiological and biochemical malfunctions. To evaluate the remediating potential of plant derived smoke (*Cymbopogon Jwarancusa*), a pot culture experiment was designed to investigate the physiological, biochemical, metabolic and antioxidant parameters of root in lead (0 (control), 500, 1000 and 1500ppm) contaminated soil. Under dark condition, seeds were primed in smoke solution with two dilutions (1:500 and 1:1000) for 24 hours. Surprisingly, with increasing concentration of Pb stress, fresh and dry weight, total nitrogen and protein contents decrease significantly while increase in smoke solution seed treatment. With increasing Pb stress level of metabolites (proline, total soluble sugar, total soluble protein, glycinebetain) and antioxidants (SOD, POD, CAT, APX, MDA and H₂O₂) of root increased, while with smoke solution seeds treatment reduced soluble solutes and antioxidant enzyme activity. These results suggest a positive role of smoke in alleviating Lead-induced changes in roots of two cultivated cultivars of rice grown in Pb contaminated soil.

P13: Distribution of Arsenic in Rice (*Oryza sativa* L.) Tissues and Its Alleviation through Microbes

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Abstract

Arsenic contamination in ecosystem is a widespread problem in many developing countries including Pakistan. Present study was aimed to elucidate the potential of microbe-assisted arsenic remediation in rice and their interactions under varied arsenic concentrations. In present study, microbial strains NCCP-82 (*Bacillus clausii*), NCCP-74 (*Bacillus safensis*) were used against 0, 50, 100 and 150ppm arsenic in the medium that are capable either to exclude or to sequester contamination. Seeds primed with microbes alleviates the drastic effect of arsenic, and showed significant positive results on physiological, biochemical, metabolic and antioxidant parameters of rice under arsenic stress. Results revealed that arsenic treatment caused significant reduction in plant growth, biomass, and chlorophyll content, whereas significantly higher germination and biomass production were observed under

microbe mediated priming. Significant reduction in protein and nitrogen content were occurred with increasing As stress, while microbial priming improved protein and nitrogen content. Metabolites (proline, total soluble sugar, total soluble protein, and glycine betain) and antioxidants (SOD, POD, CAT, APX, MDA and H₂O₂) contents were decreased with increasing As stress, which were recovered by microbial priming. The current findings support the beneficial uses of microbial priming in improving the remediation abilities of rice tissue in As contaminated soil.

P14: Characterization of Bacteria Isolated from Heavy Metals Contaminated Soil and Their Role in Bioremediation

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Abstract

Advancement in industrial processes results in the rapid production of industrial waste which release into the environment and may cause drastic effects on all living organisms. Due to its life threatening effects on mankind, this problem gain importance and need to be solved on immediate basis by applying some reliable techniques such as bioremediation to minimize the level of industrial waste. Twenty bacterial strains were isolated from soil contaminated with industrial waste of Hattar Industrial estate, Haripur, KPK, Pakistan. Bacterial strains were characterized on the basis of phenotypic and biochemical characterization. Bacterial strains were tested against 4 different heavy metals (Ni⁺², Cr⁺⁶, Pb⁺², Mn⁺²) to find out the level of maximum resistance. All the strains were resistant against heavy metals with Ni⁺²(350 ppm to 400 ppm), Cr⁺⁶ (50 ppm to 200 ppm), Pb⁺² (350 ppm to 800 ppm) and Mn⁺²(200ppm to 900 ppm). All the strains were tested against industrial waste to investigate their remediation ability and results indicated a considerable reduction in the level of heavy metals. Maximum reduction in lead (Pb⁺²) 75.56 % by isolate number 3, Chromium (Cr⁺⁶) 91.85 % by isolate number 8, Manganese (Mn⁺²) 37.10 % by isolate number 7 and Nickel (Ni⁺²) 62.82 % by isolate number 18. The present study showed that bacteria have a high potential to remediate heavy metals from contaminated soil with industrial waste and subsequently decrease environmental pollution.

P15: Treatment of Alloxan Induced Diabetic Rabbits with Hydroethanolic Extract of *Justicia adhatoda* Leaves

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Abstract

Diabetes mellitus (DM) has become a common disease of all countries in the World. More than 371 million people are diabetic in the World. Diabetes has many complications like cardiovascular diseases, peripheral vascular diseases, stroke, diabetic neuropathy, amputation, renal failure and blindness are common. So prevention and control program to stop the rising epidemic of DM and its complications. Treatment with insulin and oral hypoglycemic agents showed a remarkable breakthrough, however, difficulty in repeated administration and risk of hypoglycemia with other side effects seriously influence the quality of life. Plant materials which are cheap and within range of village folks are being used World over as a remedy for DM. In this study, hypoglycemic effect of leaves of *Justicia adhatoda* on alloxan induced rabbits is investigated. Pancreas of rabbits were infected by alloxan monohydrate and diabetes symptoms in them were confirmed on 5th day of alloxan injection. The diabetic rabbits were treated in three treatment groups i.e. with insulin, with 100 mg/kg and 200 mg/kg *Justicia adhatoda* plant extract. The treatment duration was two weeks and random blood glucose levels of treating rabbits were daily monitored and the values were compared with normal and diabetic control rabbits and treated rabbits. Rabbits treated with 100 mg/kg of plant extract showed P<0.05 value and that of treated with 200 mg/kg of extract showed P<0.001 value which is more significant. Hence, it is concluded that dose of 200 mg/kg of *Justicia adhatoda* plant extract once a day has more pronounced hypoglycemic effect as compared to 100 mg/kg of *Justicia adhatoda* plant extract. Similarly, oral glucose tolerance test (OGGT), serum insulin and histopathological studies revealed that *Justicia adhatoda* plant possess remarkable anti-diabetic effects in treated animals. So, further research on this medicinal plant can help to prepare commercial medicines for curing diabetes and its complications in humans.

P16: Comparison of Biodegradation Potential of Selected Disperse Textile Dyes by Two Indigenous Brown Rot Fungi and Study of Lignolytic Enzymes

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Abstract

Current study was designed to investigate the ability of *Daedalea dickinsii* IEBL-02 and *Piptoporus betulinus* IEBL-03 to decolorized disperse textile dyes. Biodegradation of disperse violet S3RL, disperse orange S2RFL and disperse red W4BS was monitored along with secretion of lignolytic enzymes. The decolorization process was observed for 10 consecutive days with the analysis of process on each day. The results showed that *Daedalea dickinsii* IEBL-02 (70-80 %) has the more potential of biodegradation of disperse dyes while *Piptoporus betulinus* IEBL-03 (47-59 %) has the least. The biodegradation process of dyes was optimized by Response Surface Methodology with *D. Dickinsii* IEBL-2 and more than 90 % biodegradation was achieved. The study of lignolytic enzymes i.e. lignin peroxidase, manganese peroxidase and laccase showed that *D. dickinsii* IEBL-02 produced most active enzymes. Higher enzymatic activities related with more degradation indicated that these are involved in decolorization process. Enzymes showed maximum activities at 30 °C and pH 6.5 with good affinity towards their substrates as indicated by kinetic parameters. This study will bring the attention of other scientist to use brown rot fungi for the treatment of wastewater.

P17: Study of Biodegradation of Vat Acta Yellow-Rk and Vat Acta Green-Ffb Dyes by Indigenous *Piptoporus betulinus*

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Abstract

Textile dyes are potential pollutants due to their toxicity and carcinogenicity. Industrial effluent after approaching water and food chain cause variety of diseases in human and animals. Brown rot fungi can be used for the biodegradation of dyestuffs due to their nonspecific enzyme system. In current study *Piptoporus betulinus*, a brown rot fungus was used for the decolorization of selected vat dyes Vat Acta Yellow RK (V-6) and Vat Acta green FFB (V-7). The process was optimized by Response Surface Methodology (RSM) by selecting temperature, pH, time interval, dye concentration and carbon and nitrogen sources. Up to 80 % biodegradation achieve at pH 5.5, Dye concentration 0.03%, Temperature 32.5°C for both dyes. Glucose and fructose were found better at low concentrations. Study of lignolytic enzymes showed that lignin peroxidase (LiP) (450 U/mL/min) is the most active enzyme involved in biodegradation followed by manganese peroxidase (MnP) (400 U/mL/min) and laccase (160 U/mL/min). This will help to reduced pollution caused by textile dyes in eco-friendly way and also to reduced health problems.

P18: Angiotensin Converting Enzyme Gene Polymorphism in Diabetic Patients

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Abstract

Diabetes Mellitus (DM) is possibly one of the oldest diseases known to man. The global occurrence of diabetes has continued to increase considerably. Globally an estimated 366 million people had DM, with type II making up about 90% of the cases. The number of people with type II DM is rising in every country with 80% of people with DM living in low and middle income countries. Because of the vital role of angiotensin converting enzyme in the rennin angiotensin system, numerous studies have addressed the role of the Insertion/Deletion polymorphism in microvascular disorders, particularly in diabetes. The study included 54 clinically diagnosed diabetic patients without any coupled disease condition and 5 apparently healthy controls. Genotyping was performed using a polymerase chain reaction (PCR) amplification of the intron 16 fragment harboring the 287 bp Alu repeat sequence. Three

possible genotypes, including two homozygous Deletion/Deletion, Insertion/Insertion and one heterozygous Insertion/Deletion, were analyzed. The PCR products were separated on 2% agarose gel. To confirm the polymorphism, confirmatory PCR was performed with an internal primer set. Statistical analysis was performed on SPSS 20 and there was no significance in frequency of any allele ($p=0.5405$). From this study we cannot conclude any result due to small sample size. To avoid false positive or false negative significance, if the sample size can be increased to study the polymorphism in a better way.

P19: Time to Explore Genomics of Indigenous Wild Species: Current Status and Future Prospects

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Abstract

Wildlife is considered as beauty of the earth. From decades the number of species is going to extinct from face of planet. There is a dire need to protect and preserve the wild animal species to maintain balance in ecosystem. Pakistan is blessed with precious wild animal species. Among these the wild ungulates are very important including urial (*Ovis vignei*), markhor (*Capra falconeri*) spotted deer (*Axis axis*), hog deer (*Axis porcinus*) and Nilgai (*Boselaphus tragocamelus*). Many wildlife species are endemic and endangered species in Pakistan according to International Union of Conservation of Nature and Natural Resources (IUCN) red list category. Unfortunately, these species has been grossly neglected by the scientific community for their effective conservation and genomic exploration. The exploration and better understanding of genomic architecture of these unique species can unveil their genetic positioning and potentials along with encouraging the efforts for their conservation. The taxonomy and phylogenetic positions of these wild animals will also be clarified using modern biotechnological and molecular biological techniques. As an example the urial is complex species that has undergone several classifications and revisions based on its morphology, geographic distribution and chromosome number. In addition to domestic animals our research group led the genomic investigations in wild animal species by targeting nuclear and extra nuclear genomic regions. The sequence analysis of mitochondrial DNA D-loop, Cytochrome b, Cytochrome oxidase1, ATP6 and ATP8, Prion protein (PrP), interleukin 2, interferon alpha-A genes as a member of Major Histocompatibility Complex Class I was carried out in selected species. Our findings have given useful information and unlocked the basic genomic architecture and provided foundation for further studies on these valued wild genetic resources of Pakistan. These findings may be used for designing comprehensive conservation plans to save the rich treasure of the country for the generations to come.

P20: Rational Drug Therapy for the Management of Myocardial Infarction

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Abstract

The project on myocardial infarction was completed in “Cardiology and CCU Ward” at DHQ Hospital Kohat. The data was collected on a standard history chart designed having a questions like patient name, age, sex, address, chief complaints, biochemical tests, Diagnosis, prescribed medication, past medication order, social and family history, past surgery and response to therapy etc. The main objective of my project is to evaluate that whether the therapy of the patient is effective or not and the patient medication order are either rational or irrational and what types of drug-drug interaction are present. I collected about 15 patients histories related to M.I. the age of majority of the patients was in between 45 to 60 years. After evaluation of these histories I came to the conclusion that most of the patient were suffering from myocardial infarction and these very patients belonged to low economical status. The major concurrent illnesses were hypertension and diabetes mellitus 33.33% both, then the CAD. Which account for 20%, and about 90% of patients are obese. The drug related problems include the ADR's, dose adjustment in the renal impairment and drug interactions which account for 14.7%, 67.64% and 17.64% respectively. The overall therapy

was good. The most common interactions were observed between Aspirin and spironolactone with the percentage of 26%. Similar is the case with beta-blocker and digoxin. Some of the drugs like digoxin and warfarin which are TDM. Drugs can leads to potential ADRs if their proper monitoring is not conducted. Moreover, the overall project was based on the clinical practice hence it is the responsibility of pharmacist to council and educates the patients about prescribed medication, drug dose regimen proper timing of administration etc, to minimize the complications in the drug therapy.

P21: Analysis of the Protein Interaction Network of *Mycobacterium Tuberculosis H37Rv*

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Abstract

Mycobacterium tuberculosis (Mtb) is causative agent of tuberculosis and the most studied strain is H37Rv. In this study, we built a comprehensive protein-protein interaction network of *Mycobacterium tuberculosis H37Rv* using Cytoscape. Experimental protein-protein interaction data was obtained from the STRING database. The final *Mycobacterium tuberculosis* network has 1638 nodes and the number of edges are 39776. For comparison, the Human-Human interaction network has 16080 nodes and the number of edges are 235243 (data from the BioGRID database). Analysis of the network identifies proteins having highest degree. The top three include Rv2524c (364), Rv0440 (334), Rv1843c (294) which can be considered for further characterization and analysis. We also analyzed genes in *Mycobacterium tuberculosis* in the context of Gene Ontology (GO) annotation which showed top 20 nodes which were involve in crucial biological processes, and represent the top highly connected nodes in *Mycobacterium tuberculosis* network. The top groups also included proteins involved in fatty acid biosynthetic process, growth, protein folding, cell redox homeostasis, and cellular response to oxidative stress. A considerable number of proteins were also involved in the regulation of signaling pathways linked to NF- κ B and phagocytosis. MCODE was used to find highly interconnected clusters in the network. Top 15 ranks were selected whose score was greater than six. Highly scored seed nodes include Rv0002, Rv0722, Rv2524c, Rv0035, Rv1218c, Rv1547, Rv0147, Rv0312, Rv0392c, Rv0819, Rv0565c, Rv0324, Rv0766c, Rv0263c, and Rv1164.

P22: Molecular Identification and Biotechnological Potential of a Thermophilic Bacterium Isolated From the Hot Spring of Azad Kashmir

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Abstract

Thermophilic facultative anaerobic, Gram positive, catalase and oxidase negative, motile, rod shaped bacteria that showed growth within the temperature range and pH range of 45-75°C with optimal growth observed at 70°C and pH 7.0 was isolated from Tatta Pani hot spring. Isolate TP-3 showed optimal growth at 1.5% and 1.0% NaCl concentration, respectively and produced acid from maltose, sucrose, glucose and mannose. Isolate TP-3 utilized glucose, maltose, fructose, lactose, sucrose, starch, CMC, wheat bran extract and filter paper for growth. 16S rRNA gene sequences showed that isolate TP-3 displayed 94% with *Geobacillus vulcani*. Isolate TP-3 gave extracellular activities for α -amylase, CMCase, FPase, lipase, protease and phytase enzymes. Intracellular CMCase and FPase activities were also recorded for isolate TP-3.

P23: Evaluation of Mosquito Fauna in Masti Khel District Karak Khyber Pakhtunkhwa, Pakistan

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Abstracts

The aim of the present research was to evaluate mosquito fauna in Amin Khel District Karak Khyber Pakhtunkhwa Pakistan. Duration of the study was 3 Years (March 2013-February 2016). Randomly sampling of male female mosquitoes was carried out from the selected zone of the study. The species collected and identified were *Culex mimeticus*, *C. theileri*, *Anopheles stephensi*, *C. annularis*, *Aedes albopictus* and *A. shortii*. All the identified species mosquitoes were properly arranged in a systematic way. From the present research, it can be concluded that this area of the District inhabits variety fauna of mosquito. Proper controlling steps should be taken to stop further growth of mosquito's population otherwise it may be very harmful in the disease spreading like Malaria and Dengue fever. All the three Genus *Culex*, *Anopheles* and *Aedes* comprise the same number of species i.e. two each.

P24: A Study of Mosquito Fauna of Amin Khel District Karak, Khyber Pakhtunkhwa, Pakistan

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Abstracts

A research plan was conducted to determine the mosquito fauna of District Amin Khel District Karak during 2013 to 2016. The mosquito species collected and identified belongs to one Class Insecta; one Order Diptera; one Family Culicidae; three genera Culex, Anopheles and Aedes; five species respectively. The five species were *Culex quinquefasciatus*, *C. theileri*, *Anopheles maculatus*, *A. annularis* and *Aedes albopictus* respectively.

The results revealed that Genus Culex and Anopheles comprising two species, each while the Genus Aedes consisting only one specie. The present results might be helpful in devising pest management techniques against the mosquito species of Amin Khel District Karak.

P25: Freshwater Fish Fauna of Khaisari (Ghundishahbaz Khan) Dam Izatt Khan Stream (Lak Kana) Located in District Karak K.P. Pakistan

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Abstract

The objective of the present research work was to find out the diversity of fish fauna of Khaisari (Ghundi Shahbaz Khan) dam and Izatt Khan Stream (Lak Kana) located in district Karak K.P. Pakistan. The fishes were caught with Hooks, container and different kind of nets. After that same specimen were preserved in 70% Alcohol and some in 10% Formalin solution in bottles. In the present study Four species were identified *Labeo rohita*, *Hypophthalmichthys molitrix*, *Cirrhinus cirrhosus*, *Cyprinus carpio* upto species level, all these four species belong family cyprinidae. So from the present study it may be concluded that Khaisari (Ghundishahbaz Khan) dam and Izatt Khan Stream (Lak Kana) is favorable for fish Cyprinidae family. Hence, the present study will provide useful information about the diversity of fish fauna of Khaisari (Ghundishahbaz Khan) dam and Izatt Khan Stream (Lak Kana) dam that could be later valuable in systematic, fisheries management and conservation.

P26: Detection of Carbapenem Resistance Genes in Gram Negative Bacteria Disseminated Through Wild Birds in Environment

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Abstract

The emergence and dissemination of antibiotic resistance is a global health problem sometimes resulting in therapeutic failure. Wild birds pick up *bacteria* of human origin, with antimicrobial resistance traits, and act as environmental reservoir and melting pot of bacterial resistance with a potential to re-infect human populations. The rapid spread of acquired carbapenemase producing clinical pathogens is a matter of great concern and with the addition of New Delhi metallo *beta* lactamase-1 (NDM-1), it poses major threat to public health. NDM-1 positive isolates show resistance to seven classes of antibiotics. The current study was carried out to determine the prevalence of acquired carbapenemase encoding genes in bacteria isolated from bird droppings collected from vicinity of a tertiary care hospital and recreational area. Bird dropping samples were collected from the vicinity of PIMS hospital. Gram-negative bacteria were isolated by gram staining and culturing on differential media and final identification was done standard biochemical testing. Susceptibility testing was performed using Disk diffusion method. Molecular identification of acquired carbapenemases, *bla*_{NMD-1}, *bla*_{BIC-1}, *bla*_{KPC}, and *bla*_{OXA-48} was done using a single multiplex PCR amplification. Out of 51 gram-negative strains were isolated. Among 51 isolates from hospital vicinity, 36 were *Pseudomonas aeruginosa*, 6 were *Escherichia coli*, 5 were *Klebsiella pneumoniae*, 3 were *Proteus mirabilis* while 1 strain was *Proteus vulgaris*. PCR amplification confirmed 16 isolates harboring MBL genes. Out of 16 isolates, 9 were *Pseudomonas aeruginosa*, 2 were *Klebsiella pneumoniae*, 2 were *Escherichia coli* and 1 was *Proteus mirabilis*. Three isolates were positive for *bla*_{NMD-1}, 11 isolates were positive for *bla*_{BIC-1} and 2 isolates were positive for *bla*_{OXA-48}. None of the isolates was positive for *bla*_{KPC-1}. This not only represents a high

prevalence of carbapenemases in the bird dropping but also signifies birds role as a vector in the spread of these MDR isolates.

P27: Mutation Analysis of *LPAR6* Gene in Two Consanguineous Families Segregating Autosomal Recessive Hypotrichosis

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Abstract

Hereditary hair loss in human is a heterogeneous group of disorders characterized by diffused or localized thinning or absence of hair affecting scalp, eyebrows and eyelashes, and other body parts. Hereditary hair growth abnormalities manifest as either hypertrichosis (excess hair) or hypotrichosis (lack/sparse hair). Hypotrichosis can grossly be characterized into two major groups depending upon the absence (isolated) or presence (syndromic) of non-dermatological features such as retinal degeneration, intellectual disability, and hearing impairment. At least seven autosomal dominant and eight autosomal recessive forms of isolated hair loss disorders have been mapped on different human chromosomes and among these three cases, the corresponding genes have been discovered. Genotyping in 2 families was carried out using polymorphic microsatellite markers linked to genes causing autosomal recessive hypotrichosis phenotype. For mutation analysis, gene specific primers were designed using Primer3 software. All of the exons and splice junction sites of known genes were amplified by PCR and sequenced using an automated DNA sequencer. Genotyping with polymorphic microsatellite markers showed linkage in both families to *LPAR6* gene. Sequence analysis revealed substitution of G with A at nucleotide 436 (c.436G>A, p.Gly146Arg) in all affected individuals in *LPAR6* gene. The sequence variant detected in affected members was present in heterozygous state in the obligate carriers. Analysis of the protein sequence by protein prediction tool Polyphen2 revealed that the substitution of glycine could have potentially a damaging effect on *LPAR6* structure. Comparison of the haplotype generated by genotyping *LPAR6* linked microsatellite markers in both families suggested common founder natures of this mutation. Mutations identified in the present study extend the body of the evidence implicating *LPAR6* gene in pathogenesis of human hereditary hair loss.

P28: Determination of Pesticides (Acaricides) Residues and Heavy Metal Detection in Honey

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Abstract

A number of mite infestation control product (Apistan, Amitraz and Formic acid) were used for 4 weeks period in September 2009. The objectives of the research work were to determine the infestation of varroa, distribution level of selected heavy metals like Copper (Cu), Zinc (Zn), Iron (Fe), lead (Pb) and Magnesium (Mg) and to investigate the residual levels of various pesticides. Treatments were given to different apiaries located in Kohat Karak and D I Khan regions. The residual concentrations determined in the honey, apistan residues were in the following range of 0.004-0.066 mg kg⁻¹, amitraz in 0.011-0.108 mg kg⁻¹ and formic acid was found high i.e (15-75 mg kg⁻¹) respectively. Heavy metal in honey is of interest not only for quality control but the determination of environmental contamination. The mean value for heavy metal Cu, Zn, Fe, Pb and Mn were 0.146, 0.191, 4.244, 0.056 and 0.030 mg L⁻¹ respectively. The result suggested that honey may be useful for assessing the presence of environmental contamination.

P29: Investigation of Genetic Polymorphism in Different Sheep Breeds in Malakand Division

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Abstract

Sheep is the most important livestock contributing in economic development of Pakistan. It has a major contribution to the food and wool industry in the country. The quality of wool is mainly depended on the genetic makeup of sheep breed. The wool fiber is mainly composed of proteins from the keratin family. These proteins are responsible for the major structural and mechanical properties of the wool fiber. Variation at these loci has the potential to be developed as genetic-markers associated with wool traits. We strive to characterize sheep wool samples collected from four different breeds with diverse genetic background. Genetic polymorphism can be used for association of wool quality with its breed. For this purpose, genetic polymorphism in the genes encoding key keratin-associated

proteins (*KAP*) was also investigated in sheep blood samples collected from Malakand Division. Polymerase chain reaction-single strand conformational polymorphism (PCR-SSCP) analysis and direct DNA sequencing approaches were used to identify variation in *KAP1-2* and *KAP1*. Our preliminary data shows genetic variation across different breeds lines.

P30: Protective Effect of Curcumin (*curcuma longa*) against the Liver Toxicity Caused by Cypermethrin in White Male Albino Rabbits

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Abstract

We investigated the protective effects of *curcuma longa* on cypermethrin -induced alterations in biochemical indices in blood and liver of white male albino rabbits .The study consisted of four treatment groups, with three animals each, designated as control, cypermethrin (20mg/kg) *curcuma longa* (50mg/kg), and *curcuma longa* (50mg/kg) + cypermethrin (20mg/kg). All the doses were dissolved in DMSO. Rabbits were administered their respective doses orally, every other day, for 45 days. Cypermethrin administration elicited significant increases in plasma aspartate aminotransferase and alkaline phosphatase activities, by 24% and 56%, respectively, compared to the control. Treatment with cypermethrin elevated bilirubin, creatinine, and total cholesterol levels in rabbits, but these were not significant relative to controls. Exposure to cypermethrin did not produce any significant changes in packed cell volume, neutrophils, and leukocyte counts. The supplementation of *curcuma longa* attenuated the adverse effects of cypermethrin intoxication by reducing the levels of serum enzymes and reduced glutathione. The present study showed that cypermethrin increased oxidative stress and altered some biochemical parameters in the rats but *curcuma longa* could afford some protection to attenuate cypermethrin-induced toxicity in the liver.

P31: Effect of Sulfur Nutrition on Growth, Nutrient Uptake and Amino Acid Profiling of Barley

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Abstract

Growth and yield responses of two hydroponically grown barley cultivars (Gairdner and ZD-9) to various sulfur (S) levels were studied via evaluating nutrient status of different plant tissues, grain composition including the amino acid profile, and yield components. S-deprivation resulted in reduced plant heights and biomass at maturity, and decreased chlorophyll content of flag leaves at anthesis. Gairdner was more sensitive to S deficiency than ZD-9 in terms of yield components. i.e. compared with normal S level, S0 (no sulfur) induced much more reduction in spikes per plant, grains per spike and thousand grain weight (TGW) in Gairdner than that in ZD-9. At anthesis, S-deficient plants had lower S concentration in flag leaves, shoots, spikes and roots of both cultivars over the normal S treatment. S-deprivation (S0, no sulfur) reduced P concentration in flag leaves and shoots of ZD-9 and accumulated more P in roots of both cultivars. S-free grown medium severely declined Ca and Zn concentration in mature grains of both the cultivars, and P, Mg and B concentrations of ZD-9 only. The highest grain N and protein concentrations were recorded in S0.5 applied solution in ZD-9 (being 15% and 10% higher than that in S0 and S2.0), while in S1.0 and S2.0 in Gairdner (being 21% and 30% higher than that in S0). The lowest N:S ratio was found in S1.0 and S2.0 treatments of both cultivars with ZD-9 lower than Gairdner. Similarly, N-rich amino acids like arginine, lysine, proline and glycine were increased in S-deficient grains, while S-containing Cys and Met were decreased. Rational S fertilization was found effective, especially in ZD-9 in maintaining growth, improving nutrient status of plant tissues and lowering undesirable higher-N:S (malting purpose) ratio in grains.

P32: Effect of Pre-treatment of Lignocellulose to Enhance Anaerobic Digestion for Biogas Production

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Abstract

Pakistan, being an agro-livestock based economy; has massive amount of biomass in the form of crop residues. Lignocellulosic waste as organic material can be widely used for sustainable production of energy such as biogas.

Anaerobic Digestion is one of the efficient technologies to produce biogas commercially. However, lignocellulosic biomass has a complicated structure that resists the microbial activity of degradation. Pre-treatment of lignocellulosic biomass helps to disintegrate the internal structure and enhance the anaerobic biodegradation. The main objective was to investigate the effect of alkali pre-treatment on corn cobs for biogas production. Corn cobs contain lignocellulose which is composed of cellulose, hemicellulose and lignin. Waste corn cobs were collected and crushed to fine particles (≤ 2 mm and >2 mm) and treat with NaOH using concentrations ranging from 1 - 45% based on dry matter of corn cobs, and exposed for different time periods ranging from 90 min to 7 days at 25 °C. Pre-treatment resulted in total biomass weight loss of 18.8 – 55.3 % of size ≤ 2 mm and 10.9 – 49.2% loss of total biomass weight of cobs of size >2 mm. Lignin content of cobs of particle size ≤ 2 mm was reduced by 3.8 – 49.9 % but reduction in lignin contents of particle size >2 mm was not significant. Optimum time of pre-treatment with NaOH 5% is 3 days, as it reduced the total biomass weight by 26.78% and lignin by 23.49 %, which can be use to treat cobs for biogas production through anaerobic co-digestion.

P33: Effect of Physicochemical Pretreatments on Delignification of Corrugated Paper Residues for Enhanced Biogas Production

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Abstract

Paper tubes and corrugated cardboard, is a significant fraction of municipal solid waste (MSW) Paper waste contributes up to 6 - 8% of total municipal solid waste generated in Pakistan. Chemical composition of paper waste is: cellulose 50 - 56 %, hemicelluloses 10 - 12 %, lignin 17 - 23 %, extractives 6 - 8 % and traces of other inorganic materials. Lignin is a very complex molecule and contributes in extending the enzymatic hydrolysis during biological fermentation by making it difficult for the bacteria to access the organic portion of the waste. Once lignin is converted into simple compounds, paper waste becomes a promising feedstock for biogas production via anaerobic digestion. In a study conducted at IESE, various pretreatments were applied for delignification including: hydrothermal (150 ° C – 200 °C) , alkaline pretreatment (2 % – 10 % NaOH) , ultrasonic (10 – 90 minutes) , combined hydrothermal + ultrasonic and combined alkaline + ultrasonic ; resulted in 7.9 % , 5.3 % , 13.7 % , 10.5 % , 8.5 % delignification , respectively, as compared to control: 19.7 % . Results proved alkaline treatment with NaOH as the most effective pretreatment for maximum delignification.

P34: Alleviation of Arsenic-Induced Toxicity in Maize by Application of Glutathione Reductase and Salicylic Acid

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Abstract

Arsenic can cause serious damage to plant germination, morphology, biochemistry and is responsible for producing ROS and excessive antioxidant enzymes. Salicylic acid is a plant hormone which serves to resist to environmental stress. Glutathione is an important antioxidant in plants, involved in cell protection from the toxic effect of excess oxidant stress. The general objective of our work was to determine the acute toxicity of arsenic at 200mg/L in maize seedlings and its alleviation by GSH and salicylic acid. All the experiments were done under laboratory conditions with three independents replicates in sand media. All physiological parameters (germination percentage, dry and fresh biomass, root shoot length) were gradually decreased with the increase in arsenic concentration and by alleviation with GSH and Salicylic acid all these parameters showed significant increase. Biochemical parameters showed almost similar pattern although some variation persists. Oxidative metabolites (MDA, H₂O₂) and antioxidant enzymes CAT, POD, SOD and APX increased significantly at 200mg/L level while decreased in GSH and salicylic acid pretreated seedling. Over all the results showed that As can cause severe damage to maize plant but the application of GSH and salicylic acid can significantly alleviate As toxic effects and make the plant enhance its effects.

P35: Cloning of Growth Hormone cDNA from Cholistani Cow

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Abstract

Pakistan is primarily an agricultural country and livestock plays a pivotal role in its economy. The cattle is an important domesticated animals in Pakistan. The total GDP of livestock comprises of cattle 34.3 million. Cholistan cow is famous for resisting harsh climatic conditions of Cholistan. Cholistan cow breed is a zebu (*Bos indicus*) or one humped breed of cattle being reared by the nomadic pastoralists of Cholistan desert, Pakistan. With an increasing human population and rising standards of living the demand for meat and milk is also increasing. To cope with such conditions in Cholistan recombinant technology is developed. Due to its importance in milk and meat production bGH has been cloned from a number of species like buffalo, sheep, goat, sheep, panda, horse etc. The study was carried out to clone bGH from Cholistan cow and camel. For this purpose total cellular RNA was extracted from pituitary gland of the animal, cDNAs was synthesized and amplified with the help of a set of primers designed on the basis of cow bGH. The PCR amplified products were cloned in T/A cloning vector followed by its transformation in *E.coli* strain DH5a. Positive clones were confirmed by restriction digestion. After confirmation the clones were stored at -70C° as glycerol stock.

P36: Impact on Worker’s Health upon Chronic Exposure to Chemical Industry in Punjab, Pakistan

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Abstract

Reports suggest that chemical and physical agents released from Chemical (Fertilizer and Pesticide) industry may impose a serious threat to human health. The male staff working there is in direct contact with these toxicants. Present work was conducted to study the impact of these chemicals on different haematological and hormonal parameters. For the said purpose three industries working under ‘Small and Medium Enterprises Development Authority’ were visited at different locations. A total of 45 blood samples were obtained (Fifteen from each station) for laboratory analyses. The sampling was done according to international standards and ethical approach. A decrease in Haemoglobin, Red blood cell, Neutrophils, Lymphocytes and Monocytes count was observed. Surprisingly few cases were observed with a high white blood cell count. Erythrocytes sedimentation rate was very high in all the cases while platelet count was also high in few cases. The lab analyses work is in progress and it is expected that levels of testosterone, SHBG, DHEAS, and androtenedion will also be affected as haematological parameters are not in normal range. It is assumed that continuous exposure to the toxicants of chemical industry may contribute to abnormalities in reproductive performance of the workers even at a very small level and this may affect the pre existing genetic or medical risk factors. Proper care and sensitive measures should be taken to avoid this life damaging threat.

P37: Systems Biology-Driven Approach to Study the Protein Interaction Network of *Plasmodium falciparum*

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Abstract

Malaria is an infectious disease caused by the protozoan parasite *Plasmodium falciparum* and is regarded a universal risk to human health and economy. To understand the mechanism of action of *Plasmodium falciparum*, we have to study it at its molecular level because there are proteins whose functions are not known and are termed as uncharacterized proteins. In this study a comprehensive and integrated protein-protein interaction network is constructed which is then visualized and analysed by Cytoscape 3.3. Network analysis is performed through network analyser and clusters analysis is performed using MCODE, a plugin of Cytoscape that identified and scores clusters of proteins within the network on the basis of its connectivity. Within the comprehensive network, we also identify highly connected nodes which are known as hubs. Functional analysis is performed through enrichment analysis of Gene Ontology annotations that are obtained from the uniprot database. These sets of analyses helps us to identify a set of proteins such as merozoite surface protein 1, Antigen 332, transcription factor with AP2 domain(S), ubiquitin specific protease, DNA repair protein RAD23 and Uncharacterized protein (MAL13P1.336) that are proposed for experimental characterisation on the basis of their appearance in high scored clusters, function and their connectivity.

P38: Simulation based Modeling of Photosynthetic System for Identification of Potential Targets for Improvement

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Abstract

Food security is one of the major challenges our society is facing. Increasing world population, global climate change and increasing energy costs, are endangering the global food security. To ensure that agricultural systems meet future production needs, it is required to overcome the physiological barriers to crop yield and improve the resilience of crops to adverse conditions such as climate change. Theoretical analysis suggest that increasing photosynthetic energy conversion efficiency is one of potential approach to significantly increase crop yield however being a complex process it is difficult to identify the potential targets to engineer photosynthesis. Two different photosynthetic pathways exist among plants: C₃ and C₄ photosynthesis. C₄ pathway owing to its beneficial attribute of carbon concentrating mechanism results in the production of more yield as compared to C₃ photosynthesis. One of the highly advocated strategies to improve photosynthesis is the engineering of C₄-traits into C₃ plants but besides the desired results, the engineered C₄-traits result in unexpected outcomes in the transgenic plants. Systems biology offers a solution to this problem. Computational modeling is a powerful technique for gaining sufficient quantitative understanding of complex metabolic pathways in order to alter the distribution of metabolic flux or to rationally redesign metabolic pathways for new products. This study is designed to enhance C₃ photosynthesis by transforming potato (C₃ plant) with two genes of the cyanobacterial carbon concentrating mechanism. The phosphoenolpyruvate carboxylase (PEPC) and phosphoenolpyruvate carboxykinase (PCK) genes are involved in sequestering CO₂ around RuBisCo ensuring efficient carbon fixation. Before carrying out the *in vitro* experimentation, a computational model was developed that predicted different outcomes of *in planta* transformation with desired genes. The concentrations of different metabolites predicted by the model were validated by comparing them to those quantified *in planta*. This study has not only helped to evaluate the robustness of to be engineered genes but also helped to identify the novel targets for the improvement of photosynthesis that can be successfully engineered in future for enhanced plant yield.

P39: Exploration of Bacillus Species for Enzymatic Potential and Antibacterial Activity of Its Exopolysaccharide

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Abstract

Microbes produce different kind of enzymes including protease and lipase which are frequently used in various industries such as textile, paper, food, pharmaceuticals and cosmetics industries. In addition to enzymes, many bacteria synthesize extracellular polysaccharides (EPSs) with commercially significant physiological and therapeutic activities. EPSs from bacteria are reported to possess anti-microbial, antitumor effects, and immunostimulatory activity. EPS also offer an alternative class of bio-thickeners, which are widely used in the food and dairy industries; and have strong emulsifying activity in food formulations. The objective of the present study was to explore *Bacillus* species (LS₂D₄2, BW₁D₁2, BN₁D₁1, and BH₂D₁) isolated from the soil samples of Bannu and Lakki Marwat for their enzymatic activities and anti-bacterial potential of EPS. *Bacilli* species were grown in culture and EPS were extracted followed by lypholization of EPS. Bacterial EPS were screened for antibacterial activity against four multiple drug resistant (MDR) bacteria including three Gram negative bacteria (*E.coli*, *Acinitobacter baumannii* and *Pseudomonasaeruginosa*) and one Gram positive bacterium (Methiciline Resistant *Staphylococcus aureus*) by agar well diffusion method. EPS shows good activity against *E. coli* and MRSA and average activity against *P. aeruginosa* and *A. baumannii*. These four *Bacillus* species were also checked for its proteolytic and lipolytic activity. In which LS₂D₄2, BW₁D₁2 and BW₁D₁2, BH₂D₁ were positive for lipase and protease activity respectively. These *Bacillus* species were also positive for emulsion activity after 48 hours of incubation. In conclusion, *Bacillus* isolates of the present study have the potential to produce different types of enzymes and their EPS exhibit anti bacterial activity. Furthermore, molecular characterization of EPS and enzymes are required.

P40: Clinical Characterization of Ocular Albinism in a Large Family of Pakistani Origin

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Abstract

Ocular Albinism is a genetic disease also known as Nettle ship-Falls syndrome. It is one of the two general forms of albinism, i.e, Oculocutaneous albinism (OCA) and Ocular albinism (OA). Albinism includes several heritable metabolic defects in the pigment cell (melanocytes) system of the eye and integument. Ocular albinism has four further types, with a prevalence rate of 1:50000, the Ocular albinism 1 (OCA1) is the most common type. Since it is an X-linked disorder, it occurs mostly in males, while females are carriers unless they are homozygous. About 60 missense and nonsense mutations, insertions and deletions have been identified in OAI. Ocular albino eyes become crossed, a condition called as ‘lazy eyes’ or strabismus. It appears green to bluish red and the most important part of the eye, the fovea which is responsible for acute vision, does not develop properly. These defects may be caused due to defect in OA1 receptor, or may be mutation in P gene or Human Tyrosinase (TYR) gene. Mostly TYR is reported in OA1 case. This study includes the individuals from a large consanguineous family of district Kohat, Khyber Pukhtunkhwa ,Pakistan, showing symptoms of ocular Albinism 1 (OA1). On basis of clinical analysis we screened the family and a family pedigree was drawn to get a clarifying genetic relationship of the family. We characterized the individuals based on phenotypic characteristics. Further more in order to find out the mutation in TYR gene an attempt was made to amplify TYR gene by using TYR primers. Blood sampling, DNA extraction, DNA purification and Polymerase chain reaction (PCR) was done according to the standard protocols, Currently we are optimizing the Polymerase chain reaction (PCR) condition for the study/characterization of this TYR gene. Later own other investigation related to this disease will be carried out.

P41: Callus Induction and Regeneration of *Solanum surattense* Burm. F

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Abstract

Solanum surattense Burm.f is a high value medicinal plant used to cure various ailments. Different parts of the *S. surattense* have significant antibacterial and antifungal activity against many cancer cells. The natural habitats of medicinal plant species are dwindling and many of them including *S. surattense* are facing extinction due to increasing anthropogenic activities and rapidly eroding natural ecosystems. There is a dire need of *ex situ* conservation efforts such as tissue culturing to ensure incessant and sufficient supply of such high value medicinal plants. Therefore, the current research aimed to study the callus induction and regeneration efficiency of different parts of *S. surattense*. Different callus inducing MS media supplemented with 2,4-D and BAP. Regeneration media with different concentration of auxin (2,4-D) and cytokinin (BAP) were prepared to regenerate plant from cotyledons and hypocotyls were evaluated. Days to callus induction and percent callus induction profiles showed similar trends in leaf and petiole explants on MS-media supplemented with 2, 4-D and varied response when supplemented with BAP. Highest dry weight of callus was obtained from leaf (2.7g) on all concentrations of the media. Highest % regeneration and shoots per explant was obtained from cotyledon on RM2 as compared to hypocotyl.

P42: Comparative Modeling and Docking Analysis of Envelope Protein from Yellow Fever Virus

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Abstract:

Yellow fever is an acute viral disease caused by Yellow fever virus. It has a high morbidity and mortality of global importance with an annual incidence rate of 200,000 infections and death toll of over 30,000. It is imperative to restrict the spread of this disease and to prevent huge human and economic losses. So far, no treatment or cure exists for yellow fever, there is great interest in developing strategies to control the disease. The viral genome encodes many proteins out of which, the E protein is involved in initiation of infection. We performed the comparative modeling and docking analysis of envelop gene (1YFE) from yellow fever virus. Homologous sequences were searched for the query 1YFE), Based on high sequence similarity and lowest E-value, the envelope protein of dengue fever virus (3G7T) was chosen as template. Homology modeling was performed using “EasyModeller 4.0”. The model was assessed by program “Procheck” and ProSA” web server resulting in 0.7% disallowed residues and Z score -6.18 respectively. ‘Moe’ was used for the superposition of the protein structure with the template and the

superposed model was then subjected to ligand interaction analysis using Ds viewer. The docking of drugs was performed using docking server. In short, this study can be a good initiative towards finding a good cure for the unchecked yellow fever infections with global applicability.

P43: Nonviral Vectors for Gene Therapy of Cystic Fibrosis and Related Monogenic Diseases: Limitations and Recent Advances

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Abstract

Gene therapy holds a huge promise in treating both acquired and genetic disorders by delivering desired nucleic acid fragment to the target site for therapeutic purpose. It tends to manipulate genetic information at targeted site by different ways including; replacement of non functional gene with functional one, inactivating mutated gene, or by introducing new gene into specific site to help fight a disease. Particularly, it is more useful in case on monogenic diseases, for example cystic fibrosis etc., where treatment of individual gene is required. Cystic fibrosis (CF) is a chronic autosomal recessive disorder, caused by mutations in the CF Transmembrane Conductance Regulator (CFTR) gene, a chloride channel expressed on the apical side of the airway epithelial cells. The lack of CFTR activity brings a dysregulated exchange of ions and water through the airway epithelium, one of the main aspects of CF lung disease. Due to poor diagnostic approaches, CF is usually treated symptomatically in Pakistan, although a curative approach would be to deliver a normal functioning CFTR gene into the target cells. Various physical and host immune barriers, however, in the lungs present challenges for successful gene transfer to the respiratory tract. Many efforts have been made to improve the safety and efficiency of gene-based therapies. In accordance various viral and nonviral vectors have been investigated for the efficient delivery of CFTR gene into the defective tissues. Viral vectors, although, are efficient in terms of efficiency, have some problems associated with them including but not limited to: possible mutagenesis, host immune response, higher toxicity and expensive vector preparation. Nonviral vectors, on the other hands have lesser toxicity, lesser immunogenic response and are easier to form. Particularly, lipoplexes (complexes of cationic lipids and nucleic acid fragments) and polyplexes (complexes of cationic lipids and nucleic acid fragments) have recently emerged as most promising alternatives to the viral vectors for the transferring genetic material to target site. However, these nanocarriers have to cross several barriers in order to show their therapeutic approaches. Various, approaches have been made to increase their systematic delivery and subsequently enhance their efficiency. These include but not limited to: surface coating with inert polymers, modification of surface charge with anionic polymers, enhanced endocytosis and reduce toxicity by modification with PEG. In the present poster, we try to pinpoint recent advances made to improve efficiency of lipids and polymers based vectors, highlight opportunities of their further development, address the therapeutic needs for which their use is a logical choice and discuss their future expansion into the clinical application.

P44: Identification of Disease Genes Involved in Autosomal Recessive Primary Microcephaly from South Waziristan and Kurram Agency

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Abstract

Autosomal recessive primary microcephaly (MCPH) is a rare disorder of brain development that is characterized by small volume of brain cerebral cortex and intellectual disability. The prominent clinical features of MCPH patients are reduced occipitofrontal head circumference (-2 SD) with sloping forehead. The incidence rate of MCPH is estimated to be 1 in 10,000 new born from northern area of Pakistan and the same ratio has been observed in Khyber-Pukhtunkhwa province due to traditional consanguineous marriages. To date, Mutation studies have reported sixteen MCPH genes. There are high rates of consanguineous marriages in Pakistani population resulting in a high prevalence of microcephaly. The most common cause of MCPH in Pakistan is mutation in ASPM gene at MCPH5 locus lying on chromosome 1. For the current study, three families from FATA with MCPH were enrolled. Two of these families were from South Waziristan having multiple affected members and one family was sampled from kurram agency having four affected individuals. The study was ethically approved by Kohat University (KUST) research ethical committee and the blood samples were collected in EDTA tube both from affected and

normal members of the families. Genomic DNA was extracted through phenol-chloroform followed by DNA quantification through photo spectrometer. For linkage analysis, already gene/loci involved in MCPH were amplified by polymerase chain reaction using highly polymorphic microsatellite markers. The PCR product were analyzed on 8% non-denaturing poly acrylamide gel. Successful linkage to the MCPH5 locus of ASPM gene was detected in two families (one from kurram agency and another from South Waziristan). The remaining one family was not linked to any known loci. The two families linked to MCPH5 locus were further subjected to sequencing using genetic analyzer in order to identify pathogenic sequence variant.

P45: Exploration of *Bacillus* Mk-12 from Soil of Pakistan as Potent Agent against Fungal and Multi Drug Resistant Bacterial Pathogens

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Abstract

Rapid emergence of multi drug resistant (MDR) bacteria is a global problem which leads to limited therapeutic options, so the need to find new antimicrobial agents is of paramount importance. The aim of the study was to explore the antimicrobial activity of soil *Bacillus* MK-12 against different fungal and MDR bacterial pathogens. MK-12 was isolated from soil sample collected from Karak, Pakistan. Colony morphology, biochemical tests and 16SrRNA sequencing were used to characterize MK-12. Agar well diffusion method was used to determine antibacterial activity of MK-12 against MDR bacteria including *E.coli*, *Acinetobacter*, *Pseudomonas* sp. and Methicillin Resistant *Staphylococcus aureus* (MRSA). While screening antifungal activity against *Fusarium* and *Alternaria*, dual culture technique was used. Enzymatic screening for lipase and amylase was also checked. Soil bacterium MK-12 was identified as *Bacillus* specie and its sequencing showed that MK-12 shows 99% similarity with *Bacillus pumilus* and *B. safensis*. *Bacillus* MK-12 has potent antibacterial activity against all the four MDR bacteria. During the optimization of culture conditions, *Bacillus* MK-12 showed best growth and antibacterial activity against all MDR bacterial isolates at 37°C after 48 hours of incubation at pH 7 and 9. It also exhibited approximately equal growth and antibacterial activity when subjected to static and shaking conditions. MK-12 also produced some antifungal compounds that inhibit the growth of *Alternaria* and *Fusarium* by 25% and 12.5% respectively. In case of enzymatic screening, it was positive for lipase and negative for amylase production. *Bacillus* MK-12 is a broad spectrum antimicrobial producing agent which can be further studied for exploration of antimicrobial compounds.

P46: Detection of CO and NO_x Levels in Vehicle Emissions Using New Composite Biobricks Devices

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Abstract

Air pollution is a major global problem, a significant amount of which is caused by vehicular emissions. This problem is particularly prevalent in developing nations, where regulations regarding vehicle emissions are either not present or not properly implemented. Peshawar, one of the major cities in Pakistan was on the top 10 list for cities with the most air pollution. This project, developed by the iGEM Peshawar 2016 team, aims to produce a portable, quick and easy to use Biosensor device for environmental law enforcement agencies and even consumers that can detect for levels of carbon monoxide and oxides of nitrogen in vehicle exhausts and express corresponding chromoproteins as a result. Carbon monoxide and oxides of nitrogen are two dangerous constituents of exhaust fumes. The system is based on two separate gas-sensing mechanisms that work together to give a range of results. The mechanism sensing for carbon monoxide uses the CooA transcription factor and two CooA dependent promoters: CooF and CooM. The NO_x sensing mechanism uses the NsrR repressed promoters, YeaR and NirK, as well as the NorV promoter. These are parts derived from *Escherichia coli* and *Rhodospirillum rubrum*.

P47: Utilization of Different Polymers for the Improvement of Catalytic Properties and Recycling Efficiency of Bacterial Maltase

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Abstract

The current study deals with the comparative study related to immobilization of maltase using synthetic (polyacrylamide) and non-synthetic (calcium alginate, agar-agar and agarose) polymers via entrapment technique. Polyacrylamide beads were formed by cross-linking of monomers, agar-agar and agarose through solidification while alginate beads were prepared by simple gelation. Results showed that the efficiency of enzyme significantly improved after immobilization and among all tested supports agar-agar was found to be the most promising and biocompatible for maltase in terms of immobilization yield (82.77%). The catalytic behavior of maltase was slightly shifted in terms of reaction time (free enzyme, agarose and polyacrylamide: 05 minutes; agar-agar and alginate: 10 minutes), pH (free enzyme, alginate and polyacrylamide: 6.5; agar-agar, agarose: 7.0) and temperature (free enzyme: 45°C; alginate: 50°C; polyacrylamide: 55°C; agarose: 60°C; agar-agar: 65°C). Furthermore, evaluation of kinetic study revealed that after entrapment the affinity (K_m) and maximum velocity (V_{max}) of maltase was affected. Stability profile of immobilized maltase also revealed that all the supports utilized have significantly enhanced the activity of maltase at higher temperatures than its free counterpart. However, recycling data showed that agar-agar entrapped maltase retained 20% of its initial activity even after 10 cycles followed by agarose (10%) while polyacrylamide and alginate showed no activity after 8 and 6 cycles respectively. Thus, it can be anticipated from current study that immobilization of maltase using various supports effectively improve the catalytic properties of enzyme for its efficient utilization in different bioprocesses.

P48: Characterization of Lytic Enzyme Producing Bacteria and Their Antagonistic Potential against Phytopathogenic Fungi of Tomato

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Abstract

Tomato is one of the most important and highly nutritious vegetable crop. Being a juicy plant, it is highly susceptible to variety of pathogens including fungal phytopathogens that cause significant loss to tomato crop. The only way to control these deleterious pathogen is by using fungicides and other chemicals which may cause serious environmental problems. Therefore, alternative control measures are needed. In the present study an antagonistic bacterial strain was isolated from the soil of tomato field from the Kohat region of Khyber Pakhtunkhwa and identified as *Bacillus subtilis* based on 16s rRNA gene sequencing. The strain showed high antifungal activity against *Fusarium* spp. and *Alternaria* spp. on dual culture plate. Biochemical and morphological characterization were also evaluated. *Bacillus* spp may be considered as a putative biocontrol agent against the soil borne fungi causing plant diseases which is the important perspective of the present study.

P49: Study of The Equilibrium, Kinetics and Thermodynamic of Pb(II) Adsorption from Aqueous Media by *Cucumis sativus* Peel

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Abstract

The potential of cucumber peel as a low-cost biosorbent for the removal of a Pb(II) ion from aqueous solution was investigated in this study. The influences of pH, contact time, initial metal concentration, temperature, and amount of adsorbent were studied in batch experiments. The cucumber peel used in this study were characterized by FTIR spectroscopy and it was found that O-H, -CH₂, C=C and C=O stretching were present. The adsorption was rapid at the first 30 minutes of contact, with uptake of more than 90%, and equilibrium was achieved in 60 minutes of agitation. Maximum adsorption was observed at pH 4 using 0.05 g of adsorbent for 100 ppm lead concentration in 60 min equilibration time at 293 K. It was found that Pb(II) adsorption onto cucumber peel for different initial Pb(II) concentrations, all followed pseudo-second order kinetics and were mainly controlled by the film diffusion mechanism. Langmuir and Freundlich, isotherm models were applied to describe the biosorption of Pb(II) ions onto cucumber peel. Langmuir model fitted the equilibrium data better, giving correlation coefficient of 0.9976 and a maximum adsorption capacity of 370.3 mg/g. This indicates monolayer coverage on adsorbent. The uptake of lead decreases with the rise in temperature (293–323 K). Thermodynamic parameters, i.e., ΔG , ΔS , and ΔH were computed through Vont's Hoff plot. The observed negative value of ΔG indicated the spontaneous and favorable

process at all temperatures. The negative value of ΔH and ΔS conformed the exothermic nature of process whereas the ΔS values suggested decrease in the randomness at solid - liquid interface during adsorption process. This study indicates that cucumber peel have the potential to be applied as an inexpensive and efficient biosorbent to remove and recover lead ions from aqueous media.

P50: Molecular Identification of *Salmonella Typhi* through Its Gene And It's Antibiotic Sensitivity Pattern

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Abstract

Salmonella genus has enteric pathogens such as *Salmonella typhi* and *Salmonella paratyphi* and they cause bacterial foodborne illness. *Salmonella typhi* only infect humans and cause typhoid. About 100,000 *Salmonella typhi* can cause infection in a healthy person. *Salmonella* is a gram negative and motile bacilli. *Salmonella* has developed resistance to many antibiotics such as ceftriaxon , ciprofloxacin and ceftiofur etc. Source of *Salmonella typhi* in human gastrointestinal tract is due to consumption of fecal contaminated. Present research includes isolation and molecular confirmation of *Salmonella typhi* through appearance of ITS bands on agarose gel and to check its antibiotic sensitivity pattern. DNA samples of 36 strains were run with primers of ITS gene at gradient PCR with the annealing temperature of 59°C for 2 hours and all the strains were molecularly positive for *Salmonella typhi* as there were bands of 284 bps ITS gene in agarose gel. Twelve antibiotics were assessed on Mueller Hinton agar to detect the sensitivity to the antibiotics. Out of 80 samples 36 samples were positive for *Salmonella typhi* presence and 100% strains were resistant to Streptomycin, Vancomycine, Meropenam, Ertapenam, Azetronam and Penecillin, Ceftriaxone and Ciprofloxacin while strains were 11% sensitive to Amikacin, 8% intermediate, 3% sensitive to Imepenam, 17% intermediate and 3% sensitive to Gentamycine and 22% intermediate. The studies lead to the conclusion that the imbalance use of antibiotics develops an antimicrobial resistance in microorganisms which leads to the ecological imbalance between resistant and susceptible flora, may create a super bug, a future threat.

P51: Bioinformatics Analysis of Gene Expression Involved in Human Prostate Cancer

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Abstract

Bioinformatics is an interdisciplinary field that develops methods and tools for understanding interpreting and extracting meaningful knowledge from large biological data. In the current research study Bioinformatics techniques are being employed to check the factors involved with gene expression and their involvement in various biological processes. The selected genes like FOXG1, GC, VAX1, SSSX2, TBX10, FOXB2, XAGE1E, and TFDP3 have been reported to over express in prostate cancer. To be able to unveil the factors involved with their high expression in prostate cancer the promoter region analysis of the selected genes was done. This identified several new transcription factors that can exclusively bind with the Promoter region sequence of 3000bp of the selected genes and have no binding site for the endogenous control GAPDH. This showed some possible new therapeutic targets for future studies that can help in combating prostate cancer. The role of the selected genes have been studied through a bioinformatics tool DAVID which showed their functional annotation and role in various biological pathways. To be able to study how they interact with each other the selected genes were processed with STRING which showed their mutual interaction and effect on each other. The study is expected to open up new avenues on transcription factors involved with prostate cancer.

P52: Performance of Microalgae in Leachate & Its Treatment

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Abstract

Increase in population, industrialization and resulting waste generation suggests now that sustainability is the future. Microalgae is a novel green technology that possess very high potential to remove pollutants from leachate. The resultant biomass can be utilized for biofuel and biodiesel production. Hence providing us two benefits at once i.e. leachate treatment & sustainable energy. In a study conducted at IESE, NUST, three locally isolated algal strains and three already identified strains were compared by inoculated in bold basal media (BBM) and then acclimatized in different concentration of leachate (10% to 100 %). The acclimatized strains were grown in leachate and their

performance was monitored with OD₆₈₀ and the removal of nitrates, phosphates and COD was also determined. Algae cultures were set up in 1.5 L PET bottles, illuminated with TLD 36W fluorescent lamps continuously and an air flow rate of 3.5 L/min was maintained. The COD of leachate was reduced up to 82%. The results showed that algae is capable of leachate treatment if the conditions are optimized and growth increases rapidly.

P53: The Effect of Chronic Kisspeptin Administration on Seminal Fructose Levels in Male Mice

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Abstract

The discovery that kisspeptin was critical for normal fertility in all mammalian species including humans, ushered in a new chapter in our understanding of the control of GnRH secretion. Kisspeptin, the product of the KISS1 gene, plays an essential role in the regulation of spermatogenesis acting primarily at the hypothalamic level of the gonadotropic axis. Among the many identified substances in human semen, fructose is becoming increasingly significant. Fructose is synthesized and secreted by the seminal vesicles. Its synthesis is regulated by androgens and it is correlated directly with the levels of testosterone. Dose dependent degeneration of seminal vesicle has been described following intraperitoneal kisspeptin treatment; however, effects of kisspeptin administration on the levels of seminal fructose remain elusive till date. The present study, therefore, addresses the effects of 12-day administration of kisspeptin on seminal fructose levels in male mice. Kisspeptin-10 was administered intraperitoneally at different dosage concentrations (1 lg, 1 ng, and 10 qg) to adult male mice, twice daily for 12 days. Seminal fructose levels were studied photometrically after 12 days of treatment. At the end of the treatment, seminal fructose levels decreased significantly after all tested doses. Chronic intermittent kisspeptin-10 administration negatively regulates seminal fructose levels in adult male mice.

P54: Two Dam Zebi and Changhoz Heavy Metals Comparison in Selected Plants and Their Impact on Surrounding Life Hold

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Abstract

Elaboration and application of modern methods for detection of heavy metals (Cd, Pb, Ni, Zn, Fe, Cu) for the purpose of investigating their distribution, accumulation, and translocation within plants four parts (Root, Stem Leaf, Flower or seed) of two dam namely Zabi and Changhoz Karak are discussed, great interest was given to the comparative analysis of heavy metals in these plants of two different Dams. Following plants of Changhoz and Zabi dam namely Typha, Fragonia, Cyprus (Cyprus cyclamen) and Cannabis, Euphorbia helioscopia respectively selected for this purpose, In plant samples of both dam Fe and then Pb were detected in higher concentration than other metals while Cd and Ni showed lowest accumulation. Individually Typha showed highest concentration of Fe and lowest for nickel, same case was observe for Fragonia and Cyprus plant. Euphorbia helioscopia and Cannabis Sativa showed higher concentration for Fe and Pd and lowest for Ni and CD. Overall more nearly permissible limit showed by plants of Zabi dam than Changhoz dam.