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Address for Correspondence:

Dr. R. Balagurunathan The
Editor-JCPAM Department
of Microbiology Periyar
University
Salem - 636 011, Tamil Nadu, India
Phone: +91-427-2345779 Ext: 217
Email : rbalaperiya@gmail.com

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PREFACE

Many miracle things are done by micron sized living bodies, i.e. microorganisms day-by-day in this world. They are 3.5 billion years old in nature and do beneficial and harmful to the other living things. The microorganisms such as bacteria, fungi, virus and protozoa are playing a main role in causing diseases to the human beings. Normally, more than 1500 pathogenic species cause more than 20,000 diseases in worldwide. Various traditional methods are used to control these kinds of infectious diseases. But, the microorganisms are very claver; they change their genetic nature generation to generation and results with antibiotic resistant strains.

Now we are in 21st century, it"s fulfilled with advanced techniques and technologies. Our scientists do many researches with the help of these technologies. Among that, treatment of diseases using molecular analysis is the major concern. The research based on the identification of gene, which are responsible for pathogenesis and their metabolic product is in emerging condition. Both of genomic and proteomic interaction between a pathogen and their host, leads to generate a new type of field is called "Infectomics".

Infectomics is the study of infectomes, which are encoded by both host and microbial genomes, and mirror the interplay between pathogens and their hosts.

Very few scientists are working on Infectomics in our country and countable number of papers is published in the related journals. This clearly indicates that the necessity of sharing information regarding infectomics among the scientific community especially among the molecular microbiologists.

The first time in India, National level seminar on "Current Trends in Infectomics" (NCTI - 2013) is organized by the Department of Microbiology, Periyar University with exclusive objective of bringing together scientists from various places to exchange ideas, views, thoughts and dreams on a wide range of topics related to Infectomics.

I hope this seminar will address recent advances in the field of Infectomics and the role of genomic and proteomic analysis of pathogenic microbes, provide a juncture for Indian scientists to find new solution and make aware the student community in the field of Infectomics.

I wish the delegates an enjoyable and memorable stay at Periyar University, Salem.

R. Balagurunathan
Organizing Secretary, NCTI 2014
Editor, JCPAM

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PLENARY LECTURES

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PL1: MICROBIAL COMMUNITY IN HUMAN BODY- METAGENOMIC APPROACH AND BIOMEMS

M. Ananthasubramanian
Department of Biotechnology, PSG College of Technology, Coimbatore - 641 004, Tamil Nadu.

The human body offers, several ecological niches to the thriving of prokaryote systems through the surfaces in contact with the external environment. The diversity of human microbiome is extensive. Each part of the human body like skin, mouth, intestine, etc has its own metagenome. Metagenomics is a discipline that enables the genomic study of uncultured microorganisms. Faster, cheaper sequencing technologies and the ability to sequence uncultured microbes sampled directly from their habitats are expanding and transforming our view of the microbial world. Genomic analysis of microorganisms is done by direct extraction and cloning of DNA from an assemblage of microorganisms.

Studies have suggested that healthy individuals to have up to 15,000 species-level phylotypes in their gastrointestinal tracts as determined by 16S rRNA sequencing. The average genome size of sequenced organisms from these groups is 3.4 Mb, and the percentage of these genomes that codes for protein-coding genes is approximately 92%.My lecture will cover the types and methods followed in metagenomics and their relevance in human body

BioMEMS, the abbreviation for Biomedical or Biological Micro-Electro-Mechanical-Systems, is now a heavily researched area with a wide variety of important biomedical applications. In general, BioMEMS, and its synonym BioChip, can be defined as "Devices or systems, constructed using techniques inspired from micro/ nanoscale fabrication, that are used for processing, delivery, manipulation, analysis, or construction of biological and chemical entities". I"ll be presenting our work on sorting biological cells through the principle of dielectrophoresis. My talk will cover on the role of electrochemical characteristics of bacteria and the parameters supporting the separation.

PL2: Leptospiral Research in to its new Transformation: Conventional to Molecular Approaches

K. Natarajaseenivasan, S. Shanmughapriya, K.V.L. Aishwarya, M. Kanagavel
Department of Microbiology, Bharathidasan University, Tiruchirappalli - 620024
Email: natarajaseenivasan@rediffmail.com

Leptospirosis is a common public health problem in developing countries. Since the significant limitation of available microscopic and serological methods for diagnosis of leptospirosis, the new diagnostic methods those are accurate, simple and economical are urgently needed. Epitopes finding is a new approach for identifying peptide based diagnostic methods. Identification of B-cell and T-cell epitopes is very essential in vaccine, diagnostics kit development and antibody production. We have delineated immunodominant B and T-cell epitopes of candidate antigen LigA by *in silico* analysis. Predicted epitopes were characterised by *in silico* analysis for their potential candidature in diagnostics test development. Among all peptides the LigA-C pep-3 showed a significant sensitivity for the diagnosis of human leptospirosis. The predicted synthesized peptides also showed a tremendous immune response

among poneys. The predicted epitopes were exposed in surface of the protein than others. These finding indicate that immuno-dominant peptides of leptospiral proteins may serve as a vaccine and diagnostics candidate for human leptospirosis during the early stages of disease.

PL3: Marine Drugs and nanoparticles for the treatment of infectious diseases

K. Kathiresan

CAS in Marine Biology, Faculty of Marine Sciences, Annamalai University,

Parangipettai - 608502, Email: kathirsum@rediffmail.com

The demand for safer, cheaper and potent antibacterial therapeutics has become greater with the increased incidence of bacterial infections. Many natural products from marine sources are endowed with promising antibacterial activities, thus representing invaluable leads in antibiotic drug discovery and are playing pivotal role in medicine and, in particular, marine metabolites have increasingly become major players in recent drug discovery. It cannot be denied that with 3.5 billion years of existence on earth and experience in biosynthesis, the marine organisms remain nature"s best source of chemicals. The marine organisms produce novel chemicals to withstand extreme variations in pressure, salinity, temperature, and so forth, prevailing in their environment, and the chemicals produced are unique in diversity, structural, and functional features. Marine floras, such as bacteria, actinobacteria, cyanobacteria, fungi, microalgae, seaweeds, mangroves, and other halophytes are extremely important oceanic resources, constituting over 90% of the oceanic biomass. They are taxonomically diverse, largely productive, biologically active, and chemically unique offering a great scope for discovery of new anticancer drugs. The marine floras are rich in medicinally potent chemicals predominantly belonging to polyphenols and sulphated polysaccharides. The chemicals have displayed an array of pharmacological properties especially antioxidant, immunostimulatory, and antitumour activities. The phytochemicals possibly activate macrophages, induce apoptosis, and prevent oxidative damage of DNA, thereby controlling carcinogenesis. The biologically diverse marine environment has a great promise for nanoscience and nanotechnology. Marine organisms produce remarkable nanoparticles of 1–100 nm size which have a greater surface area per weight than larger particles, and this property makes them to be more reactive to certain other molecules and they are used or being evaluated for use in many fields. Biosynthesis of nanoparticles is advantageous over chemical and physical methods as it is a cost-effective and environment friendly method, where it is not necessary to use high pressure, energy, temperature and toxic chemicals. Microbes and plants are currently used for nanoparticle synthesis. The use of plants for the fabrication of nanoparticles is a rapid, low cost, eco-friendly and a single step method for biosynthesis process. The usage of plants can also be suitably scaled up for large-scale synthesis of nanoparticles in a controlled manner according to their size, shape and dispersity. Moreover, the use of plants in process of nanoparticle synthesis is more beneficial than other processes since the nanoparticles are produced extracellularly.

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PL4: HOST AND PATHOGEN BASED MOLECULAR ELEMENTS FOR FUTURE MEDICINE

K. Balakrishnan

Department of Immunology, School of Biological Sciences, Madurai Kamaraj University, Madurai- 625021.

Introduction:

Recent approaches of functional genomics have the potential for reunifying studies of bacteriology, virology and parasitology under an umbrella of how human and other mammalian host and microbes interact. In this instance it is informative to examine the effect of microbial products on immune and non-immune system cell types. Again, this serves to illustrate the functional complexity of transcriptional responses to a common signal. For example, when HeLa cells (epithelial cells) and peripheral blood dendritic cells are exposed to bacterial lipopolysaccharide (LPS), cell-type specific transcriptional profiles are clearly seen documented. Following LPS exposure dendritic cells massively up-regulate a set of genes that are transcriptionally unresponsive in these cells. In case of dendritic cells exposed to a virus, a bacterium or yeast, such transcriptional plasticity could be rationalized into core and pathogen-specific transcriptional responses (Haung et al 2001). There is likely to be even greater differential gene regulation *in vivo*, taking into account cell interactions, tissue location and the shifting cytokine environment. Perhaps the greatest challenge of such systems biology and immunoinformatics is to define and model such complex biology within the appropriate contextual environment of the host.

Microbes effectively co-evolve with other organisms present in their environment. As host immune complexity evolves, pathogens also co-evolve, and vice versa, in a Darwinian process. Immunoinformatics should therefore encompass pathogen bioinformatics. Post genomic research therefore allows us to understand how a finite human genome facilitates and maintains essential biological functions and homeostasis whilst guarding against and responding approximately to acute, persistent or commensal infections (Kellam 2001). Perhaps more importantly, as viruses are obligate intracellular parasites and utilize many normal cellular pathways and components during their replication cycle, bioinformatics strategies can be used to identify virus proteins that interfere with the host system.

Host and Pathogens:

This analysis can lead to functional insights into host and pathogen processes. For example, the Kaposi"s sarcoma-associated herpesvirus (KSHV; human herpesviruses 8, HHV8) encodes two proteins K3 and K5 that were shown to promote the down-regulation of cell surface protein. In particular K3 promotes the endocytic down-regulation of major histocompatibility complex (MHC) class I (HLA-A, -B, -C and -E) cell surface expression by increasing the rate of endocytosis and targeting the internalized proteins for degradation. Six unannotated human proteins were identified using the BKS PSSM, all containing the highly conserved BKS finger motif. In the herpesvirus proteins the motif is always found in the N-terminus but in one human protein it appeared in the central part of the peptide whilst in another, the counterpart of murine axotrophin, at the C-terminus (Holzerlandt et al 2002, Jenner & Boshoff 2002). Interestingly, the K5 protein of KSHV, in addition to removing HLA-A and –

B from cell surface also reduces the level of cell surface, expression of intercellular adhesion molecule 1 (ICAM1) and the co-stimulatory molecule B7-2 (Coscoy & Ganem 2001, Ishido et al 2000). This suggests the possibility that the entire family of host and viral BKS motif proteins can selectively remove specific cell surface proteins. The herpesviruses can interfere with MHC class I cell surface presentation, but many other diverse virus types also use this strategy. Representing this information within a DAG not only makes analysis computationally tractable but leads to a continuously updateable cross-species, information resource.

As viruses are obligate intracellular parasites, a range of regulated host-cell factors and pathways are used by viruses to enable viral gene expression and replication. Integrated viral data resources can provide information-rich but static data. This needs to be interpreted in the context of the dynamic process occurring in the host cells and tissues during infection and immune response. Determining which mRNAs are expressed in a cell gives an idea of which proteins are present. Large scale gene expression mapping using gene arrays is motivated by the premise that the functional state of the organism is largely determined by its expressed genes. Thus it is possible to define an organism‟s or cell‟s phenotypic state in terms of the range of genes that are expressed. This field of functional genomics has been called "transcriptomics".

The effects of viral infection on the transcriptome of cells *in vitro* and *in vivo* has been determined for viruses as diverse as retroviruses, herpesviruses, orthomyxoviruses, enteroviruses, adenoviruses, hepatitis B and C viruses and papiloma viruses. These initial studies show that viruses cause both common and unique changes in cellular gene expression profiles during their replication cycle (Fruh et al 2001, Kellam 2000, 2001). However, the degree of host transcriptional modulation is likely to be more complicated than to be observed for a virus causing the infection.

The immune system is interwined with all other body systems. Bioinformatics applications are relatively well developed for some immunological areas such as, databases (Brusic et al 2000), genomic applications (Glyne and Watson 2001), study of T cell epitopes (Brusic and Zeleznikow 1999), or modeling immune responses (Bernaschi and Castiglione 2002). In other fields of immunology , bioinformatics applications are still in their infancy, such as analysis of allergenicity of proteins (Gendel 2002) or proteomics (Klade 2002). Because of the combinatorial nature of immunological data, the importance of efficient, accurate and comprehensive use of immunoinformatic tools will continue to grow in importance for support of immunology research.

The identification of T cell epitopes relies heavily on bioinformatics for initial screening followed by experimental validation. MHC (Major histocompatibility complex) molecules bind short peptides produced mainly by intracellular (MHC class I) and extracellular (MHC class II) degradation of proteins and display them on the cell surface for recognition by the T cells (using TCRs) of the immune system. Binding of peptides to the MHC molecules is a prerequisite for immune recognition and elicitation, but the number of peptides that can bind to a specific MHC molecule is limited. Peptides that can bind specific MHC molecules are involved in initiation and regulation of immune responses. Determining peptides that bind specific MHC molecules is important for understanding immunity and has application to vaccine discovery and

immunotherapies. The combinatorial nature of this problem makes computational approaches necessary for systematic mapping of T cell epitopes.

Bioinformatics to Vaccines:

As the process of epitope mapping accelerated and confidence in the new algorithms grew, researches began to conceptualize vaccines built entirely out of epitopes linked together like a string of beads (Whitton et al 1993). This approach to vaccines can be explained using the following analogy: an epitope is to a pathogen as a word to a language. Thus, a single epitope may signal the presence of an infection to the immune system and stimulate the protective response, just as a single word (Bonjour, for example) remains the hearer of a language (French) (Olsen et al 2000). By extending the analogy, researchers have hypothesized that protective immune response to an entire pathogen might be generated by recognition of repertoire of epitope words" derived from the proteins of the pathogen. This method of designing vaccine on regions (sequences) of pathogens that are presented by MHC molecules was recently termed reverse immunogenetics" by Hill and Davenport (1996).

PL5: ROLE OF HERBAL PRODUCTS IN CURING INFECTIOUS DISEASES

R. Rajendran

CEO & Founder, Green Chem, Bangalore

Email: rajendran@greenchem.biz

Mother Nature has gifted us a wide spectrum of herbs for our well being. It is amazing to know herbal remedy is there for every ailment. Herbs can cure diseases, can prevent diseases and can maintain the lifestyle. It can do wonders without side effects. This is the major plus point of herbal products over synthetic allopathic products.

No doubt herbs are good and user-friendly. But herbs should be used as per Ayurveda guidelines and established as per Pharma guidelines. This approach only will ensure successful maintenance of health. Herbal products can cure many infections in humans, animals and in plants too. There are many established herbal products. Extensive work has been made in making excellent multiple herbal ingredients for various infections. Apart from this, efficient herbal drug delivery system also has been established like sub lingual route, patches, deep throat spray, permeable gels, chewing gums, cookies, biscuits, beverages etc.,

Few examples are given below:

Throat Infections:

Vitex negundo, Mentha species, Tulasi, Ginger , Sage, Echinacea are good for throat infections. Vitex negundo is known as Nirgundi, this is plenty available in Salem and other parts of Tamil nadu. This has many Iridoid glycosides and alkaloids which are good for throat infections. Nirgundi is widely used in traditional medicine. There are many cough syrups with this and in combination with Mint, Tulasi, Ginger. This is also available in chewable formats for faster recovery through sub-lingual entry.

Garlic is widely used in alternative medicine for its antibiotic properties. When crushed, garlic presence smells due to presence of Alliin and Allicin, natural potent antibiotic, but for the

odour!. Sage is common in folk medicine for sore throats and relieves symptoms of cold and flu. Sage contains antimicrobial and anti-inflammatory properties due to presence of Sclareolides which help reduce inflammation. Sage tea with honey is often used in traditional medicine. Chamomile tea is known for its anti-inflammatory properties in alternative medicine. It soothens irritated membranes. Aromatic herbs like Thyme, Caraway and eucalyptus have powerful infection-fighting and cough suppressive qualities.

Eucalyptus is commonly used for cold, flu symptoms in losanges. Eucalyptus contains tannins, flavonoids and volatile oils with anti-inflammatory and antioxidant properties. Gargling warm Eucalyptus tea relieves the pain and inflammation from sore throats, bronchitis and sinusitis. There are many herbs having Anti tussive and Cough Suppressing properties. Vitex negundo, Fennel, Lemon, Ginger are good examples.

Dental infections:

Acacia catechu, Spilanthes acmella, Hawthorn berry are commonly used for tooth infections. Amla, Clove, Garlic, Tea tree oil, Camellia sinensis, Holy Basil, Rosmarinus officinalis Leaf, Turmeric, Echinacea Purpurea, Olive Leaf are good for dental complaints. Tea tree oil is extracted from Melaleuca leaves. It is powerful antiseptic and antibiotic. This fights infections such as an abscess tooth. Applying a few drops of tea tree oil on a tooth brush and brushing several times a day can help with infection. Peppermint extract and Fennel extract have same activity. Garlic is most effective nature's antibiotic because as it is a powerful anti bacterial herb. Echinacea can cure infection like tooth abscess and the Inflammation that follows!. Echinacea tea with Acacia bark is excellent for tooth infection.

Urinary Tract Infections:

Cranberry is an essential remedy for preventing and treating UTIs. Equisetum arvensis (Horsetail) is a diuretic that can help urine flow and stop bleeding from the urinary tract. Uva ursi, helps to kill bacteria. It has a compound Arbutin, which the body converts into a bacteria-killing substance. Arbutin works better if the pH of urine is slightly alkaline. If the UTI patient takes acidic Cranberry or Orange juices, the urine may be acidic and Arbutin may not work well. Hence bicarbonate soda can make the pH of urine alkaline so that Arbutin works well. This type of administration is essential when the patient uses multiple herbs like Uva ursi and Cranberry.

Combination of Alfalfa Leaf (Medicago sativa) and Sesbaania grandiflora (Agathi) treat urinary tract infection and neutralises bloating and water retention. Carotenoids are the precursors of Vitamin A. Herbs like Paprica, Bixa orellana, Carrots can help to increase the cell health and integrity, thereby making their defence stronger to avoid infections. Vitamin C is present in Amla, Acai, Acerola, Guava fruits. This helps the cells to improve immunity by making more infection-fighters! This can create some acidity in the urine; there are some bacteria which can not survive in acidic medium! But too much acidity is not preferable.

The seeds, leaves and flowers of Nasturtium (water cress) contain natural antibiotics that may be helpful in preventing UTIs. Horseradish root also contains an antibiotic substance along with a good dose of vitamin C, both of which may be helpful in treating this condition. Marshmallow and Parsley's seeds are good combination for treating UTI. Goldenseal and Oregon grape contain Berberine and other alkaloids that kill bacteria and stimulate the immune

system. These herbs inhibit infection-causing bacteria from adhering to the wall of the urinary bladder, so they are flushed off in urine.

Skin infections:

There are many types of skin infections – Bacterial infections, Fungal / Yeast infections, Viral infections etc., Bacterial infections are Impetigo, Folliculitis, Furunculosis, Carbunculosis, Ecthyma, Erysipelas ,Cellulitis etc., Fungal infections are Dermatophytosis, Candidiasis, Pityriasis Viral infections are Herpes Simplex, Herpes Zoster, Warts, Molluscum Contagiosum**.**

There are many herbs for tackling these infections. Aloe vera gel is an universal product to treat and manage skin infections. Aloe vera gel is a good vehicle to permeate the phyto compounds across the skin. A good example is a formula containing aloe vera gel, Wrightia tinctoria, Salvia officinalis, Neem etc to manage and treat Psoriasis even! Garcinia mangostina, Amla alongwith Aloe vera is good for treating acne. Lavender, Chamomile, St John wort, Tridax procumbens, Tulasi, Alfalfa leaf, Dandelion leaf and root, Milk Thistle seed, Ginkgo leaf, Hawthorn berry, Oats, Garlic and Sesbania.are widely used for Skin infections.

There are enough information available on herbs for infections. Now the challenge is how to develop a safe and working product from herbs? Quality and safety need to be incorporated during development stage itself. To develop competent products, innovation and pharmaceutical approach are needed.

There are no stringent quality standards available for Herbal products unlike pharmacopeial monographs. Ayurveda recommends use of crude herbs powders, tinctures, Churnas, crude extracts etc., These are all not standardized for actives. Quality of herbs can vary a lot due to many factors. This means the health benefits are not assured. Therefore a standardization is needed to get consistent quality.

In addition to quality consistency, innovation is also needed to overcome competition. Innovation can be done in new product identification, Herb selection, extraction methods, testing methods, packaging, Formulations, marketing concepts etc.,

Each herb and each extract should be studied in depth to specify quality standards, covering impurities relating to physical, chemical, biological in addition to purity parameters, similar to Pharmacopeial products. This should cover the dosage, expiry dating, compatibility parameters in multiple ingredients formula as well. Concept of delivering herbal ingredients with Pharmaceutical Quality by adapting innovative technology is the key for consumer safety. This assures quality consistency in herbal ingredients where pharmacopeial standards are not available. In India AYUSH has taken a serious step to develop herbal monographs. GREEN CHEM is part of this program.

Now, the testing of products includes herb identification (botany, chemistry), physiochemical parameters, organoleptic properties, assay of active phyto-compounds, heavy metals, residual solvents, residual pesticides, organic volatiles, microbial tests, stability monitoring, impurity profiling, compatibility with other combinations, expiration dating etc.

The bioactivity and safety of the product are confirmed by pre clinical studies. Suitability for human consumption is ensured by double blind, randomised, placebo controlled

study as per requirement. Mechanism of action of the product is established to know more about the product. Herbal Products are ensured non toxic by conducting various toxicity studies. Toxicity study should be carried out elaborately covering acute oral toxicity, mutagenicity and sub-chronic toxicity and teratogenicity. Efficacy confirmation and dosage levels should be established. Complimentary medicines are the new innovative approach, being attempted to get the benefits of Natural and synthetic products in supplements industry.

Herbal extracts can work better at a different platform as compared to drugs. Synthetic Drugs can help in controlling the disease and thereafter herbal extracts can take over to maintain the effect. The inter phase has to be gradual to avoid imbalance due to sudden abrupt change over. By this way long use of synthetic drugs can be minimized with lesser side effects. When Black Pepper extract is taken alongwith synthetic antibiotics the bio efficacy is enhanced. Due to this benefit, the dose of antibiotic can be reduced. Few countries like Philippines allow combined formulation of synthetic pharma products with standardized herbal products. Regulatory bodies should consider careful handling of this issue.

Innovation and patent protection are essential for safeguarding business stability. Innovation means newness and that should be properly validated for human safety. The scope for developing innovative herbal ingredients using pharma approach is very big. It is important to establish the safety and efficacy first and then market it.

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SPECIAL SESSION ON "TUBERCULOSIS – PAST, PRESENT AND FUTURE"

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SL1: ANTI TB MICROBIAL PRODUCTS: CURRENT STATUS AND FUTURE PROSPECTS

R. Balagurunathan[1] and M. Radhakrishnan[2]

[1]Department of Microbiology, Periyar University, Salem – 636 011. Tamil Nadu

[2]Centre for Drug Discovery and Development, Sathyabama University, Chennai – 600 119.

Tuberculosis (TB) caused by *Mycobacterium tuberculosis* is a highly prevalent infectious disease with almost one third of global population believed to be infected. According to statistics, India is 17th among the 22 high burden countries in terms of TB incidence rates. Emergence of drug resistance among *M. tuberculosis* isolates and long term therapy using combination of drugs for its treatment are the major problem in TB control. Hence, there is an urgent need for new antitubercular drugs to fight against drug resistant *M. tuberculosis* strains. The new anti-TB drugs are expected to have less side effects, improved pharmacokinetic properties with extensive and potent activity against drug resistant strains and/or should be able to reduce the total duration of treatment.

Microorganisms of both terrestrial and marine origins are proven to be excellent sources of novel natural products. Secondary metabolites from microbial sources have a long history in the treatment of TB. Among the microorganisms, bacteria including actinomycetes and fungi are the major producers of antibiotics including anti-TB metabolites. Actinomycetes are common soil inhabitants with an unprecedented ability to produce clinically useful secondary metabolites including antibiotics. They are ubiquitous in nature, taxonomically diverse and metabolically talented. Of the total microbial bioactive metabolites, around 50% are reported from the members of actinomycetes. From the discovery of streptomycin, first antibiotic used for anti-TB therapy from *Streptomyces griseus*, numerous anti-TB antibiotics such as kanamycin and rifampicin have been reported from actinomycetes of terrestrial origin. Most of the commercially available anti TB antibiotics in market and those which are in the pipeline are mainly from actinomycetes. In recent years, exploration of actinomycetes from routine ecosystems frequently results in re-isolation of known actinomycetes and antibiotics. Instead, bioprospecting of rare ecosystems like marine, desert, forests, caves and hills have been proved as useful method for tapping innumerable number of bioactive compounds from novel bioactive actinomycetes including anti TB metabolites. In addition, fungi especially the marine-derives, entomopathogenic and endophytes are emerging as novel source for anti TB antibiotics. However, research on actinomycetes and fungi from rare ecosystems of our country with special reference to anti TB antibiotics is still in the stage of infancy. Gainful utilization of these nature"s treasures will add on to the armamentarium to tackle the rare and drug resistant forms of tuberculosis.

SL2: TUBERCULOSIS CONTROL IN INDIA: PRESENT AND FUTURE CHALLENGES

S. Balaji

Department of Bacteriology, National Institute for Research in Tuberculosis (NIRT), Chetpet, Chennai - 600 031. Tamil Nadu

Tuberculosis (TB) caused by *Mycobacterium tuberculosis* remains the major killer among infectious diseases in developing countries. The World Health Organization (WHO) report on the global burden of disease ranked TB as the seventh most morbidity-causing disease

in the world, and expected it to continue in the same position up to 2020. In 1993, WHO declared TB is a global health emergency and it is the first infectious disease declared as global emergency by WHO. In 2012, an estimated 8.6 million people developed TB and 1.3 million died from the disease. A recent WHO survey on the estimation of number of new TB cases revealed that India is ranking first among 22 countries with high burden of TB.

The spread of TB in the community is linked to the poor socio-economic and unhygienic conditions of human dwellings. The situation is further worsened by HIV infection and malnutrition especially in Asia and in Africa. The emergence of drug resistance in TB is another major hurdle for most of the TB control program. Multi drug resistant (MDR) TB (organism resistant to isoniazid and rifampicin) and extensively drug resistant (XDR) TB (MDR-TB resistant to any one of the flouroquinolones and one of the three injectable drugs namely Kanamycin, Amikacin and Capreomycin) is a major threat for the community especially in developing countries like India. Considering the seriousness of the disease, microbiologists have major challenges to face especially to develop a rapid diagnostic tool for the detection of drug resistant TB, to search for a novel antibiotic to shorten TB treatment and to mediate good preventive measure to control TB in the community.

TB Control in India:

Internationally recommended Directly Observed Treatment Short course, "DOTS", was established in India for the treatment of TB. Since 1993, the Revised National Tuberculosis Control Programme (RNTCP) is utilizing the DOTS strategy that got implemented in India. As of now, the entire country is fully covered under RNTCP. Since RNTCP relies only on sputum smear microscopy for diagnosis, categorization of patients and assessment of treatment progress, the credibility, success and sustainability of the programme depends on the strength of the laboratory network. As a result, poor quality microscopy services have serious implications for the programme, including the failure to detect persons with infectious TB who continues to spread the disease in the community, or lead to unnecessary treatment for "non-cases." Errors in the reading of follow up smears may result in either the patients being placed on prolonged treatment or in treatment being discontinued prematurely. Programmatic management of drug resistant TB (PMDT) services is being implemented in India under RNTCP for the accurate diagnosis and effective treatment of MDR-TB and XDR-TB in the community. Since its perception in 2007, state wise implementation was initiated and at present the entire nation is fully covered by PMDT services. The progress made by each state is actively monitored by RNTCP on a regular basis.

Challenges:

Poor quality of TB and MDR TB laboratory diagnosis in the private sector: TB is often diagnosed with serology, which frequently results in mis-diagnosis. . The use of serological testing for diagnosis of TB has been banned by WHO, RNTCP, and expert groups from India, but such tests are widely available from foreign and domestic manufacturers leading to their wide use by the private sector. Similarly, very few private laboratories has been certified for quality in performing drug susceptibility testing.

Lack of information about patients diagnosed with TB and MDR TB in the private sector: Patients properly diagnosed with TB and MDR TB in private laboratories are not notified to

public health authorities, who would be able to take actions to confirm diagnoses, offer supportive services, and offer free treatment to patients from public sources or at least supervise the quality of care in the private sector.

Anti-TB drugs available without prescription and subsequent widespread irrational and irresponsible use: As with all schedule drugs, provision of TB drugs without prescription is widespread and common, and pharmacists are not expected to maintain records of such provision that could be used to identify patients with possible TB or MDR TB. Furthermore, second-line anti-TB drugs are widely available in the private sector and used inappropriately, even to treat drug sensitive TB leading to wastage of precious drugs on one hand and resulting in unwarranted adverse reactions in patients on the other..

Capacity for rapid diagnosis of MDR/XDR TB: The establishment of a network of quality assured Culture and Drug Susceptibility testing Laboratories across the country for diagnosis and follow up of MDR/XDR TB patients is a major challenge for RNTCP in India. As of now, diagnosis of XDR TB can only be confirmed at 3 laboratories in India, which are quality assured for second-line anti-TB drug susceptibility testing of flouroquinolones and injectables.

MDR TB treatment and XDR-TB Prevention: The report on emergence of extensively drug resistant tuberculosis emphasizes the importance of aggressively supporting the Government of India's efforts to control TB and MDR TB, including basic MDR TB prevention through effective TB diagnosis and treatment the first time around, as well as the crucial need for the country to improve the standard of care in the private sector. While it is best to prevent MDR TB, when it occurs, prompt diagnosis and effective MDR TB treatment can still save the patient and prevent the development of further drug resistance and XDR TB.

SL3: DRUG RESISTANCE IN TUBERCULOSIS: STATUS AND DETECTION METHODS

Gomathi Sekar

Department of Bacteriology, National Institute for Research in Tuberculosis (NIRT), Chetpet, Chennai – 600 031. Tamil Nadu

TB organisms, that are resistant to the antibiotics used for treatment, are widespread and occur in all countries surveyed. Drug resistance emerges as a result of inadequate treatment and once the organisms acquire resistance they can spread from person to person in the same way as that of drug-sensitive TB. Multidrug resistant TB (MDR-TB) is defined as TB caused by organisms that are resistant to the most effective anti-TB drugs viz. isoniazid and rifampicin. MDR-TB results from either infection with organisms which are already drug-resistant bacilli or that may develop during the course of a patient's treatment.

Extensively drug resistant TB (XDR-TB) is a form of TB caused by organisms that are resistant to isoniazid and rifampicin (i.e. MDR-TB) as well as any one fluoroquinolone and any of the second–line anti-TB injectable drugs (amikacin, kanamycin or capreomycin). MDR and XDRforms of TB must be detected as soon as possible to curtail transmission. They do not respond to the standard six-month treatment with first-line anti-TB drugs and can take two years or more to get treated with drugs that are less potent, more toxic and much more expensive.

About 3.7% of new tuberculosis patients and 20% of previously treated patients in the world have multidrug-resistant strains (MDR-TB). The scenario differs in each region and WHO (2011) estimates that about 220,000 to 400,000 MDR-TB cases occur among TB cases in the world. About 60% are in Brazil, China, India, the Russian Federation and South Africa alone. Approximately 9% of MDR-TB cases also have resistance to extensively drug-resistant TB (XDR-TB). As on October 2012, 84 countries had reported at least one XDR-TB case each. Children below15 years of age constitute up to 20% of the TB caseload in high-burden settings and the number of children with drug-resistant TB is likely to be substantial, as paediatric TB diagnosis remains a challenge. In the Western Cape, repeat surveys among children, done in1997–1998, 2001–2002, and again in 2005–2006, showed that resistance to isoniazid (INH) or rifampicin (RIF) increased from 6.9 % to 12.9 % and to 15.1 % and MDR ranged from 2.3 % to 5.6 % and to 6.7 % respectively. Drug resistance among children has been documented in both pulmonary and extra pulmonary diseases. In settings with a high burden of TB and HIV, up to 40 % of children with MDR-TB are also infected with HIV.

Drug resistance is detected by performing indirect drug susceptibility testingon primary cultures isolated on Lowenstein-Jensen media. Conventional methods require skill and need a BSL facility, longer time to grow, necessary equipments and power supply. Rapid assays yield early identification of TB patients, initiation of treatment, sputum conversion and prevention of spread in the community. WHO insist molecular detection of MDR and XDR-TB from the unprocessed sputum. These rapid and molecular methods have their own advantages and disadvantages. LPA is now made available widely in developing countries. This method yield an overall 95.8% of interpretable results in smear-positive specimens..GenoType MDR-TB assays demonstrates excellent accuracy for rifampicin resistance, even when used on clinical specimens. While specificity is excellent for isoniazid, sensitivity estimates were modest and variable. The pooled sensitivity (98.1%; 95% CI 95.9, 99.1) and specificity (98.7%; 95% CI 97.3, 99.4) estimates for rifampicin resistance were very high and consistent, across all subgroups, assay versions and specimen types. The accuracy for isoniazid was variable, with sensitivity lower (84.3%; 95% CI 76.6, 89.8) and more inconsistent than specificity (99.5%; 95% CI 97.5, 99.9). Xpert® MTB/RIF identifies all the clinically relevant rifampicin resistance inducing mutations in the RNA polymerase beta (rpoB) gene in the *M. tuberculosis* genome in a real time format using fluorescent probes called molecular beacons. Results are obtained from unprocessed sputum samples in 90 minutes, with minimal biohazard and very little technical training to operate the instrument. The sensitivity is 72% in smear negative and in smear positive, the sensitivity and the specificity are 98% and 99% respectively.

SL4: MECHANISM OF DRUG RESISTANCE IN TUBERCULOSIS

R. Lakshmi

Department of Bacteriology, National Institute for Research in Tuberculosis (NIRT), Chetpet, Chennai – 600 031.Tamil Nadu.

The increasing emergence of multidrug-resistant (MDR) and extensively drug-resistant (XDR) tuberculosis (TB) in the era of human immunodeficiency virus (HIV) infection presents a major threat to effective control of TB. Despite effective chemotherapy for tuberculosis was

introduced 40 years before, the molecular mechanisms of these compounds on *Mycobacterium tuberculosis* have been revealed during the past 15 years. The rapid development of resistance to single agent therapy led to the principle of multi drug chemotherapy that remains the cornerstone of treatment.

Drug resistance in *M. tuberculosis* mostly occurs as a result of man-made selection during disease treatment. Resistance in *M. tuberculosis* develops through a limited number of mechanisms at low frequency. Mutations in the enzymes that either activate antimycobacterial drugs or are targets of drug action most commonly associated with drug resistance.Drug inactivation mechanisms that result in resistance has been of limited clinical interest because such compounds are not used in the treatment of tuberculosis. Limited number of drug efflux mechanisms has yet been described that can account for drug resistance in *M. tuberculosis,* although diffusion and transport into mycobacterial cells is an extremely important variable in drug activity. Role of these efflux pumps in clinical scenario in different patient population is not yet completely defined or explained. Episomal or transposon-mediated transfer of resistance genes into *M. tuberculosis* has not been demonstrated till date, though this is a common mechanism for the acquisition of drug resistance in other bacteria. The biochemical transformations occurring in mycobacteria during the acquisition of drug resistance are generally inferred, rather than demonstrated, and can be identified as thrust area for research in future.

Use of high throughput DNA sequencing for whole genome sequencing of unique drug-resistant strains will facilitate the identification of new and unknown mechanisms of drug resistance and ultimately lead to more efficient detection of drug resistance. Adequate monitoring of drug resistance and its transmission, molecular characterization of the drug-resistant strains and genetic susceptibility will aid in addressing the problem of fitness, virulence and transmissibility of drug-resistant *M. tuberculosis* strains in the community.The molecular mechanisms involved in the development of mycobacterial drug resistance will be reviewed and the possible implications for therapy will be discussed.

SL5: LUCIFERASE REPORTER PHAGE ASSAY – A JOURNEY AT NIRT

V. N. Azger Dusthackeer

Department of Bacteriology, National Institute for Research in Tuberculosis (NIRT), Chetpet, Chennai – 600 031. Tamil Nadu

Development of improved tools for the diagnosis of tuberculosis, including smear negative TB has been considered as a top priority. Even with the advent of various rapid automated liquid based methods, diagnosing and performing drug susceptibility testing for tuberculosis remains a bottleneck in the management of tuberculosis cases. Luciferase reporter phage assay (LRP assay) and FAST Plaque TB (PhaB) test are the two techniques utilizing mycobacteriophages for identifying *M. tuberculosis* and testing susceptibility to drugs.LRP assay uses genetically engineered mycobacteriophages with firefly luciferase (*fflux)* gene in their genome, which can infect, replicate, and express *fflux* gene only within viable mycobacterial cells. Mycobacterial viability could be assayed in the cultures containing antimycobacterial drugs using LRP constructs and thus drug susceptibility testing of *M. tuberculosis* is possiblemore rapidly.

LRP assay is ideal for screening new drugs to test their antiTB activity as results can be obtained rapidly using very little quantity of the drug/extract to be screened.

Initiatives aiming to develop phage constructs with increased and sustained luciferase activity in *M. tuberculosis* had been taken up using different strategies. Beginning with the first generation LRP phAE40 developed from TM4 mycobacteriophage and phAE129 of D29, all LRP constructs fell short in their sensitivity to be qualified to be used as a diagnostic test. The poor sensitivity was attributed to the lytic nature of the phage constructs proceeding to the lysis of host bacteria prematurely leading to rapid disintegration of ATP before it takes part in the biochemical reaction to release photons.

At NIRT, attempts to develop reporter phages using Che12, the only temperate mycobacteriophage that infects and lysogenizes *M.tuberculosis* and a ts mutant of TM4 using different promoters resulted in four reporter phages. The constructs phAETRC16 and phAETRC21 have *fflux* driven by hsp60 and *icl*promoter respectively while TM4 based constructs phAETRC201 and phAETRC202 had *hsp60* and *acr* promoters, respectively. These constructs are capable of measuring actively growing cells as well as those adapted to hypothetical dormant models *in vitro*. Diagnostic luciferase reporter phage assay detected 30 additional positives which failed to grow on standard Lowenstein Jensen medium. Presence of viable bacilli in these samples was confirmed by a real time reverse transcriptase-PCR for *Mtb* 16S rRNA gene, indicating that either the improved sensitivity of the assay was by improved detection of actively growing bacilli or due to its ability to detect non-replicating persistor bacilli, ultimately increasing the diagnostic potential of culture-based assays leading to the first growth based highly sensitive phenotypic assay indigenously developed.Detecting drug susceptibility using LRP assay had brought down the time to detection of drug resistance from 2-4 weeks to 3 days which is now being evaluated in a multi-centric trial and will shortly hit the market.

SL6: MTBSD - A COMPREHENSIVE STRUCTURAL DATABASE FOR *Mycobacterium tuberculosis*

Sameer Hassan

National Institute for Research in Tuberculosis (NIRT), Chennai – 31. Tamil Nadu

Mycobacterium tuberculosis, the etiological agent for tuberculosis, causes approximately 8-10 million new infections and 3 million deaths worldwide every year. In 1993, World Health Organisation (WHO) declared tuberculosis a global emergency. TB is one of the leading causes of mortality in India, killing 2 persons every 3 min, nearly 1000 every day.

The complete genome of *M. tuberculosis* comprising of 4,411,529 bp and around 4000 genes was sequenced in 1998. Availability of the mycobacterial genome sequence and advancement in structural genomics has set up a platform to answer questions such as the functioning of the organism as an integrated system and its activity in conjunction with the host. Three dimensional structures of proteins are important for understandingtheir biological function as well as their interaction with ligands. Structure determination for hypothetical proteins could help in the identification of the biological function of a particular protein based on clues obtained from proteins with even distant structural homology and no apparent sequence identity.

Protein Data Bank (PDB) is a valuable resource of structural data for proteins of all eukaryotes and prokaryotes. TBSGC, also hosts similar information but is specific for *M. tuberculosis*. Currently, both databases contain 853 protein structures for 328 gene products of *M. tuberculosis*, resulting from multiple solved structures for many of these proteins, viz. mutant forms, structures for individual or multiple domains, and complexes with different ligands. Since proteins are flexible molecules capable of changing their structure based on external stimuli, binding of ligands may induce certain changes in the structure. These changes may be important for protein function. Exploring the changes that have occurred in the protein structure due to ligand binding will further help inunderstanding the functions of the proteins, since some of these structural changes may be important for protein function.

When ligand-bound protein conformations are not available, structure-based drug design becomes highly challenging. Several studies have shown that virtual screening with an apo structure usually results in a poor enrichment factor compared to screening with holo structure even when the structural difference between the two is small. X-ray or NMR structures of a protein/enzyme are not always in complex with its natural substrate or product. Binding of ligands other than cognate ligands could also bring about a range of structural deviations in the proteins. These changes can result in poor enrichment factor. Identification of the appropriate protein-ligand complex based on structural similarity between the bound and cognate ligands is very essential for proper modelling, docking, as well for drug designing studies.

Further, in order to understand the catalytic activity of a target protein, availability of its crystal structure in combination with its appropriate ligand is very essential. At present, information on catalytic activity and similarity between cognate and bound ligands are available in SwissProt and PROCOGNATE databases respectively. Though Swissprot and other databases such as TBSGC, Tuberculist and TBDB contain information on M. tuberculosis protein structures, none of these databases provide systematic grouping of structures for each protein, or highlight the differences between structures in the context of domain coverage, bound ligands etc.

In this scenario, users have to visit multiple databases and employ many tools to acquire complete information on a given protein for protein modelling, docking and structure-based drug designing studies. Keeping in mind the need for a complete structural database for *M. tuberculosis* proteins, that would incorporate all the above mentioned features, we developed a database called MtbSD (http://bmi.icmr.org.in/mtbsd/MtbSD.php).

SL7: PHAGE THERAPY

A.S. Shainaba

Department of Bacteriology, National Institute for Research in Tuberculosis (NIRT), Chetpet, Chennai – 600 031. Tamil Nadu

Bacteriophages are viruses that infect bacteria. They are considered to be the most abundant organisms in the world. Phages are potentially a very valuable tool for dealing with infections caused by antibiotic resistant bacteria. Over the years bacteriophages have developed unique proteins that arrest critical cellular processes to commit bacterial host metabolism to phage reproduction system leading to host cell lysis. Using bacteriophages to kill the infection

causing bacteria specifically is called phage therapy. There are two kinds of phages namely lytic and temperate phages. Lytic phages can multiply within bacteria and kill the cell by lysis to release the progeny virions. Temperate phages can either multiply via the lytic cycle or can enter a quiescent stage by integrating into the host bacterial genome. Generally lytic phages are preferred over temperate phages for phage therapy.

The advantages of phage therapy are: 1. Phages are the natural enemy of bacteria and can be used as self replicating and self limiting antibiotics. 2. Phages can be targeted more specifically towards a particular bacteria. 3. The problem of resistance development will be ruled out and the side effects will be minimal. 4. Phages can even cross the biofilm barrier to attack the bacteria. Some of the hurdles which are to be faced while using phage therapy are: 1. Inactivation of the phages in *in vivo* conditions (eg. gastric pH inactivates phages). 2. Activation of host immune system against phages making it ineffective in killing the bacteria. 3. Chances of phages taking toxic genes from pathogenic bacteria through horizontal gene transfer. 4. Selection of phages in case of mixed infections.

Because of the unproven safety and rapidly evolving characteristics of phages, FDA has not recognised phage therapy. Phage therapy is an approved treatment only in Russia and Georgia. Despite all these difficulties, phage therapy can be attempted in case of incurable situations with conventional antibiotics in diseases like tuberculosis (TB). TB remains one among the major cause of infectiousdiseases, despite the worldwide use of Bacillus Calmette Guerin (BCG) as a live attenuated vaccine and the availability of severalantibiotics. The difficulty of treating tuberculosis and the emergence of drug resistance has culminated in the need to look for alternatives and to explore whether phages could provide a complementary means of therapy.

Mycobacteriophages specifically infect mycobacteria. They are known to infect mycobacteria over evolutionary time and till now no resistance have been developed naturally in them towards mycobacteriophage infection. Phage proteins interact very specifically with unique critical targets in a way that the mycobacteria cannot introduce mutations to develop resistance to phages.. Thus, we need to explore the possibilities of mycobacteriophage therapy, taking full advantage of the power of modern biological tools to cut short the hurdles and enhance its effectiveness.

SL8: METHODS IN TUBERCULOSIS DIAGNOSIS

S. Anbarasu

Centre for Drug Discovery and Development, Sathyabama University, Chennai – 600 119.

Tuberculosis (TB) is a disease caused by *Mycobacterium tuberculosis.* The bacteria usually form a primary focus in the lungs and infect any part of the body such as the kidney, spine, and brain. The increase in the number of HIV-related TB, pediatric TB, latent TB, Multi Drug Resistant (MDR) and Extensively Drug Resistant (XDR) TB pose serious problem around the world. There are obstacles in the diagnosis of TB due to lack of accurate, cost effective rapid diagnostic tools. The delay in diagnostic process is an unresolved bottleneck that slows down thetreatment initiation. Currently available diagnostic tools for TB except some of the liquid culture methods and molecular tests take long time. TB culture and drug susceptibility test

(DST) need specialized laboratory setup, which is very expensive. The New Diagnostics Working Group (NDWG) on TB is supporting development of new tools and also provides information to World Health Organization (WHO) for endorsement. TB diagnostic tools such as Mycobacterial Growth Indicator Tube (MGIT), rapid tests for species confirmation called Capilia test, Line-Probe assay (LPA), Light-emitting diode (LED) microscopy, microscopic observation of drug susceptibility (MODS), nitrate reductase assays (NRA) and colorimetric redox indicator assays (CRI) had been recommended by WHO in reference laboratories under strict laboratory protocols. Recently WHO endorsed a rapid, fully automated nucleic acid amplification test- Xpert MTB/RIF assay for detection of *M .tuberculosis* and detection of rifampicin resistance.

There are other assays being developed and expected to be approved by WHO. They are loop-mediated isothermal amplification process (LAMP), QuantiFERON-TB Gold Test, T-SPOT.TB, ClearviewLipoarabinomannin antigen enzyme-linked immunoabsorbent assay (LAM-ELISA) and Thin layer Agar (TLA) test.

Research continues on finding innovative tools for TB that are now inthe early phases of development. They include phage-based tests, breathalyser screening test, sodium hypochlorite (bleach) microscopy, sputum filtration, TB patch test and vital fluorescent staining of sputum smears.

New diagnostics working group has to quickly identify and respond to the full spectrum of issues that form the critical path to improving the prevention and control of TB. Researchers working on discovery of antimycobacterials have to identify active compound /compound classes to prevent drug resistant TB. Sufficient funding is also required for health care systems, and better-funded systems are an incentive to the development of even better diagnostic tools and better drugs for tuberculosis.

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MEDICAL MICROBIOLOGY

OP1: INFECTIOUS DISEASES, INFECTOMICS AND DRUG DISCOVERY: AN OVERVIEW

M. Radhakrishnan[1], R. Balagurunathan[2] and Vanaja Kumar[1]

[1]Centre for Drug Discovery and Development, Sathyabama University, Chennai - 600 119.

[2]Department of Microbiology, Periyar University, Salem - 636 011

Infectious diseases are one of the leading causes of death in the world. The major medical concern is due to the continued emergence of new infectious diseases and re-emergence of old pathogens together with an increasing number of pathogens resistant to antimicrobial drugs. Emerging infectious diseases (EID) are diseases of infectious origin whose incidence in humans has increased in the recent past or threaten to increase in the near future. These include new, previously undescribed diseases as well as old diseases with new features which may include the introduction of a disease to a new location or a new population with new clinical features including resistant to antibiotics. Re-emerging of infectious disease is the reappearance of disease which was once endemic but had since been eradicated or controlled.

A literature survey identified 1407 species of human pathogens with 177 (13%) species regarded as emerging or re-emerging. Over 30 new infectious agents have been detected worldwide in the last three decades; 60% of these are of zoonotic origin and more than two-thirds have originated in the wildlife. SARS and H1N1 influenza are the two most important infectious diseases reported in the 21st century. The EID accounts for 26% of annual deaths worldwide. Nearly 30% of 1.49 billion disability adjusted life years (DALYs) are lost every year to diseases of infectious origin. The burden of morbidity and mortality associated with infectious diseases falls most heavily on people in developing countries and particularly on infants and children.In the recent past India has witnessed many large outbreaks of emerging infections. A review of the list shows that they were caused by eight aetiological agents (5 viruses and the rest bacteria) of which 6 are of zoonotic origin.

The microbial attributes that confer the potential for virulence – called as virulence factors - fall primarily within several categories, including the ability to enter a host, the ability to evade host defences, the ability to grow in a host environment, the ability to counteract host immune responses, the ability to acquire iron and nutrients from the environment and the ability to sense environmental changes. However, attempting to fit virulence factors within neat categories of function is probably anunsuccessful exercise since some categories overlap and some attributes can be assigned to more than one group. For example, in enzymes that digest host tissue damage the host generate nutrients and can promote entry, and mechanisms that permit a microbe to evade phagocytosis enable survival in a host. When the outcome of these adaptations causes host damage, the microbe is a pathogen and its virulence is a relative measure of the damage it can induce. When assessing the contribution of virulence factors to virulence, it is important to consider the following themes: (1) very few virulence factors function as all-or-none determinants of virulence; (2) host damage can result from both direct microbial damage, the interaction of microbial components with the host or the immune

response to microbial components and (3) immune responses, and in particular specific antibody responses, can neutralize many virulence factors.Discovering virulence factors is important in understanding bacterial pathogenesis and their interactions with the host, which may also serve as novel targets in drug and vaccine development.

The term Infectomics had been recently coined and defined as an integrative omics approach to globally study microbial infections. The most important omics approaches include genomics, proteomics and more recently the glycomics and each branch of omics embraces two essential aspects such as structural and functional studies. Infectomics is the study of infectomes – phenotypic and genotypic changes in microbes and their hosts, which are encoded by both host and microbial genomes, and mirror the interplay between pathogens and their hosts. There are three major types of infectomics approaches for dissecting of microbial infections: ecological infectomics, immunoinfectomics and chemical infectomics. The most challenging issue in infectomics is how to dissect the dynamic duality relationship between symbiosis and pathogenesis in microbial infections, and to predict and to mitigate infectious diseases. Infectomics is emerging as the combination of integrative omics sciences, computational biology and conventional discipline of microbial infection.

Recently chemical omics strategies such as, genomics, proteomics andglycomicshave been used as high throughput approaches for the discovery and development of drugs. Chemical Infectomics refers to the use of chemical omics for the discovery and development of new antimicrobial drugs. This will greatly increase research productivity in the development of new anti-infective agents.

OP2: PREVALENCE OF HUMAN PAPILLOMA VIRUS INFECTION AMONG COLLEGE GOING GIRLS USING SELF COLLECTED URINE SAMPLE FROM ERODE DISTRICT, TAMIL NADU

M. Jasmine and B.T. Sureshkumar

Vivekanandha College of Arts and Sciences for Women, Tiruchengode - 637 205

Human papilloma virus infection remain the most common sexually transmitted infection of females particularly afflicting adolescents & women in their early 20s.In the present study a total of 200 urine samples were collected from college going girls with healthy cervix to investigate the prevalence of HPV infection. Two different DNA extraction protocol was evaluated to find suitable method for HPV DNA extraction from urine sample. Out of 200 urine samples 5 were positive L1 consenus primer & 2 for HPV 16. The overall prevalence of HPV positive & HPV 16 were found to be 5 & 2 .In age wise distribution 3 positive subjects were found in 18-20 age group & 2 subjects were found to be 21-23 age group. HPV prevalence in variables among married women were also compared & statistically analysed to calculate Odds Ratio & 95% Confidence Interval. Though there was no statistical significant association , HPV prevalence was higher in subjects from rural area , age group 18-20,annual income above 25,000.Risk factors of positive & negative cases were assessed statistically & irregular menstruation was positively associated with both HPV positive & HPV prevalence.

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OP3: ANTIPLASMODIAL ACTIVITY OF CHEMO SYNTHESIZED NANOPARTICLES AGAINST CHLOROQUINE SENSITIVE *Plasmodium faliciparum*

S. Prasannakumar and S. Ravikumar

School of Marine Sciences, Department of Oceanography and Coastal Area Studies,

Alagappa University, Thondi Campus, Thondi - 623 409

Malaria is one of the most prevalent human infectious diseases with upto 500 million infections occurring each year. Plasmodium falciparum is the most virulent of the four human malarial parasites causes 1-3 million deaths each year. The development of Plasmodium falciparum malarial resistance to the current armory of antiplasmodial drugs requires the development of new antiplasmodial agents. Nanotechnology is the source of exciting progresses in the drug delivery field, offering suitable means of small molecular weight drugs, proteins, peptides, oligosaccharides, vaccines and nucleic acids. Many advantages of nanoparticle based drug delivery have been recognized, including improving serum solubility of the drugs, prolonging the systemic circulation lifetime, releasing drugs at a sustained and controlled manner, preferentially delivering drugs to the tissues and cells of interest, and concurrently delivering multiple therapeutic agents to the same cells for combination therapy. The biosynthesized and chemically synthesized nanoparticles showed various biological activities. In this regard the present study made an attempt to find out the new antiplasmodial activity of chemo synthesized nanoparticles against P. falciparum. The various concentrations of chemo synthesized nanoparticles (100, 50, 25, 12.5, 6.25, and 3.125 $\mu g.ml^{-1}$) were tested against P. falciparum. The selected nanoparticles showed the excellent antiplasmodial activity of IC50 = <2 µg.ml-1 and IC50 = 3 $\mu g.ml^{-1}$ after 48 h incubation. Statistical analysis reveals that the significant antiplasmodial activity ($P< 0.05$) was observed between the concentrations and time exposure. The result of the present study suggests that, the chemo synthesized nanoparticles can be used as a putative antiplasmodial drug in future.

OP4: BIOSYNTHESIS AND CHARACTERIZATION OF CdS AND ZnO NANOPARTICLES BY USING ACTINOBACTERIA AND ITS ANTIMICROBIAL PROPERTY

G.Ushabharani and R. Balagurunathan

Department of Microbiology, Periyar University, Salem - 636011

Biosynthesis of nanoparticles is an important area in the field of nanotechnology which has economic and eco-friendly benefits over chemical and physical methods of synthesis. The study deals with biosynthesis of zinc oxide and cadmium sulfide nanoparticles by using the actinobacterial isolates. The functional group of CdS and ZnO nanoparticles was determined by FTIR. Absorption peaks was observed in UV-spectrophotometer. XRD confirmed the crystalline nature of the nanoparticles. By Using SEM, surface morphology of nanoparticles was determined and size of the particles was determined by using TEM. EDX was used to confirmed the elemental composition of the metal ions and scattering pattern of our selected nanoparticles was identified by SAED. The synthesized nanoparticles were found to be effective against many pathogenic bacterial strains. These nanoparticles also applicable in light emitting, photo catalyst, photo luminescence, solar cell, cosmetics and also in biomedical fields such as drug carrier and therapeutics.

OP5: CYTOTOXICITY OF SILVER NANOPARTICLES SYNTHESIZED BY *Streptomyces* SP. (MA30) AGAINST HELA CELL LINE

T. Shanmugasundaram and R. Balagurunathan

Department of Microbiology, Periyar University, Salem - 636011

There is a growing interest in the use of biologically synthesized nanoparticles to reduce the use of chemically synthesized nanoparticles in order to avoid environmental side effects. The cancer is one of the dangerous diseases in the worldwide. Among that, the cervical cancer is in major concern. So, the present study reports the cytotoxicity of silver nanoparticles synthesized by *Streptomyces* sp. (MA30) against HeLa Cell line. The biosynthesized silver nanoparticles were found to be the most effective cytotoxicity against HeLa cell line, with LC50 value of 30.05 µg and the control silver nitrate showed the value of 50.24 µg. The silver nanoparticles were characterized by UV - Vis Spectroscopy, X-ray diffraction (XRD) and scanning and transmission electron microscopy (SEM & TEM). The efficacy in killing cancer cells may make this biosynthesized silver nanoparticles promising for the development of new anti-cancer drug in future.

OP6: COMPARATIVE STUDIES ON THE ANTIMICROBIAL ACTIVITY OF VARIOUS TYPES OF MUSHROOM

E. Poongothai and N. Hemalatha

Department of Microbiology, Periyar University, Salem - 636011.

About 10,000 of mushroom which about 3,000 species are edible and over 1,800 species are considered to have medicinal properties (antimicrobial, antioxidant, antitumor, antihypertensive and antiaging potentials). For cultivation of mushroom, various substrates viz., sorghum straw, paddy straw, sugarcane bagasse, and banana leaves were attempted by using standard procedures.To study the antimicrobial activity of mushroom extracts against human pathogens, such as *Escherichia coli*, *Klebsiella pneumonia*, and *Staphylococcus aureus* were identified from the clinical samples. *Pleurotus florida* (oyster) and Calocybe indica (milky) was cultivated on various agro wastes. All the substrates gave good yield. The extracts from *Pleurotus florida* and *Calocybe indica* was showed good activity against human pathogens. The protein and carbohydrate in the mushroom was estimated by Lowry"s method and Anthrone method. In future, these *P. florida* and *C. indica* will be a sources for novel compounds against pathogens.

OP7: BIOLOGICAL ACTIVITY OF PHENOLIC COMPOUNDS PURIFIED FROM METHANOLIC EXTRACTS OF *Pleurotus florida* MUSHROOM

D. Menaga and P.M. Ayyasamy

Department of Microbiology, Periyar University, Salem - 636011

For thousands of years therapy have been closely linked through the use of traditional medicines. Mushrooms have been known for their nutritional and culinary values and used as medicines for several diseases. In modern terms, they can be considered as functional foods which can provide health benefits beyond the traditional nutrients. There are monographs that

cover the medicinal and healing properties of some individual traditional mushrooms. There has been a recent increase of interest in mushrooms not only as a health food which is rich in protein but also as a source of biologically active compounds of medicinal value which include complementary medicine/dietary supplements for anticancer, antiviral, hepatoprotective, immunopotentiating and hypocholesterolemic agents. In this present investigation, Pleurotus florida mushroom was cultivated using horse gram as nutrient supplement and extracted with methanol, and tested for phytochemicals present in the extract. Bioactive compounds were purified using chromatographic techniques and determined the antioxidant activity using 1, 1-diphenyl-2-picrylhydrazyl (DPPH) and reducing power assay. The purified fractions of phenolic compounds possess significant antioxidant activity comparing to the synthetic antioxidant ascorbic acid. Hence, the purified phenolic compound fractions of Pleurotus florida mushroom could be used as a potential antioxidant agent to overcome the usage of synthetic antioxidants and further investigation may lead to the development of drug formulation.

OP8: SCREENING OF ACTINOBACTERIA FROM MANGROVE AND ESTUARY SEDIMENTS FOR ITS ANTIMICROBIAL PROPERTY

V. Gopikrishnan and R. Balagurunathan

Department of Microbiology, Periyar University, Salem - 636 011

The emerging multidrug resistance pathogenic microorganisms are the major challenging problem faced by currently used antibiotics. Similarly, infectious diseases of human beings are leading health problems with high morbidity and mortality in the developing countries like India. In this scenario, microorganisms have been intensively screened from soil, marine and various plants as a source of therapeutically important molecules. Now a day"s research on structurally new compounds is apparently decreasing. Availability of natural antibiotic producing microorganisms in soil had been exhausted and need of the hour is to search unutilized microorganisms from unexplored sources. In the present study, 50 actinobacterial strains isolated from Pitchavaram and Parangipettai mangrove and estuary sediments, southeast coast of Tamil Nadu, India screened against *Staphylococcus* sp, *Bacillus* sp, *E.coli*, *Pseudomonas* sp and *Klebsiella* sp clinical pathogens by agar plug method. Compare with Pitchavaram ecosystem, actinobacteria from Parangipettai mangrove and estuarine ecosystems were showed promising activity against the clinical isolates. Present study reveals that marine sediments like mangrove and estuary are the potential source for newer antibiotics.

OP9: BIOACTIVE POTENTIAL COMPOUND FROM *Streptomyces* sp. (TK3) AGAINST RESISTANT ENTERIC PATHOGENS

R. Pazhani Murugan and R. Balagurunathan

Department of Microbiology, Periyar University, Salem - 636 011

Enteric diseases are a major public health problem in worldwide. It is endemic in many regions of Asia especially in India and it is the leading cause of high degree of morbidity and mortality among paediatrics. Multi drug resistance among enteropathogens in various geographic regions presents a major threat in the control of diarrhoea. Due to the resistance

emerging in organisms against antimicrobial drugs, it is an immediate need to develop alternate way such as search out novel and new antimicrobial drugs which are more active against enteric pathogens. Actinobacteria are the group of filamentous bacteria which are considered as the power house of secondary metabolites. At present there is no effective drug for control of enteric pathogens and actinobacteria also unexplored for drugs against enteric diseases. For the search of enteric drug, the actinobacterial strain TK3 was obtained from actinobacterial research laboratory, Department of Microbiology, Periyar University, Salem, Tamil Nadu. In preliminary screening TK3 strain showed promising antagonistic activity against resistant enteric pathogens (*Salmonella typhi , Shigella dysenteriae, Shigella dysenteriae, Staphylococcus aureus,* Entero toxigenic *E.coli* (ETEC), *Vibrio cholerae, Klebsiella pneumoniae, Pseudomonas aeruginosa*) by adopting cross streak method and agar plug method. In solid state fermentation and ethyl acetate extraction of TK3 showed good activity against *S. aureus* and *E. coli*. The present study emphasized the solid state fermentation system and culture conditions effectively influencing the growth and bioactivity of actinobacteria strain TK3 with special reference to enteric diseases. In future the potential strain TK3 will be a novel source for controlling the enteric pathogens.

OP10: MYCOSYNTHESIS OF SILVER NANOPARTICLES USING *Ganoderma lucidum* AND ITS ANTIBACTERIAL ACTIVITY

S. Santhosh, P. Balashanmugam and P.T. Kalaichelvan

Centre for Advanced Studies in Botany, University of Madras, Chennai - 600 025

Ganoderma lucidum, has been used over the ages as highly medicinal fungi in the orient. Many useful properties of this fungus are still being studied; we report here a new facet for this "elixir of life" as a mycosource for synthesis of metal nanoparticles. After 24hrs of incubation with ($AgNO_3$), the solution changes to yellow-brown colour indicating the formation extracellular synthesis of Ag NPs. The synthesized Ag NPs were characterized with UV-visible spectroscopy, X-ray diffraction (XRD), Scanning Electron Microscopy (SEM), and energy dispersive X-ray (EDX) spectroscopy. The synthesized Ag NPs were recorded by UV-visible spectrum at 426nm and XRD patterns showed the nanoparticles as crystal in nature. SEM image of Ag NPs showed spherical in shape, the average size of synthesized Ag NPs was 40-80 nm. The spot EDAX analysis showed the complete chemical composition of the synthesized Ag NPs. The Ag NPs where evaluated for their antibacterial activity against pathogenic bacteria. In addition, it showed significant antibacterial activity to Gram-negative bacteria *Pseudomonas aeruginosa, Klebsiella pneumonia, Enterobacter aerogens* and *Escherichia coli*.

OP11: BIO SYNTHESIS OF SILVER NANOPARTICLES FROM *Polypodium aureum* L. AQUEOUS EXTRACT AND EVALUATION OF ITS ANTIBACTERIAL

M. Arul Kumar, P. Balashanmugam and P.T. Kalaichelvan

Centre for Advanced Studies in Botany, University of Madras, Chennai - 600 025

Different biological methods are gaining recognition for the production of silver nanoparticles (Ag-NPs) due to their multiple applications. One of the most important applications of Ag-NPs is their use as an anti-bacterial agent. The use of plants in the synthesis

of nanoparticles emerges as a cost effective and eco-friendly approach. In this study the biosynthesis of silver nanoparticles using Polypodium aureum L. extract and its antimicrobial properties has been reported. The resulting silver nanoparticles are characterized using Scanning electron microscopy (SEM), X-ray diffraction (XRD) and UV-visible (UV-Vis) spectroscopic techniques. The SEM study showed the formation of silver nanoparticles in the 10-30 nm range and average 15 nm in size. The XRD study showed that the particles are crystalline in nature, with a face centered cubic structure. The silver nanoparticles showed the antibacterial activity against Gram positive and Gram negative bacteria. Polypodium aureum L. was found to display strong potential for the synthesis of silver nanoparticles as antimicrobial agent by rapid reduction of silver ions (Ag+ to Ag0).

OP12: COMPARASION OF L.J MEDIA USING HEN EGG'S VS DUCK EGG'S FOR THE ISOLATION OF *Mycobacterium tuberculosis*

G. Nagarajan[1], P. Madhumathi[2], P.M. Ayyasamy[1] and D. Arvind prasanth[1]

[1]Department of Microbiology Periyar University Salem - 636 011

[2]IRL, Chetpet, Chennai.

The efficacy of Lowenstein-Jensen (LJ) media containing Duck eggs vs. Hen eggs for culture isolation of *Mycobacterium tuberculosis* (M. tb) was evaluated from sputum specimens obtained from the suspected pulmonary tuberculosis patients referred to the Intermediated Reference Laboratory, (IRL) at the Chetpet, Chennai for a period of 3 months from January 2012 to March 2012. The clinical specimens were screened for the presence or absence of acid fast bacilli. A total of 200 patients, of which One fifty (75%) smear negative and 50 (25%) smear positive sputum specimen were taken for this study. The sputum specimen was processed by the L.J Duck egg contain media and Hen egg contain media. An aliquot of the sediment was inoculated onto each Duck egg and Hen egg media culture tubes. These culture tubes were incubated at 37oC and observed for growth until eight weeks. In smear negative specimen, growth of *Mycobacterium tuberculosis* was present in 49% in Duck, 38% hen egg media. While in smear positive specimens, contamination rate was 0% in Duck and 1% in Hen egg. The findings of the study suggest that the Hen medium can replace Duck egg in culture isolation of *Mycobacterium tuberculosis*. Egg contain solid media (L.J) is a best GOLD STANDARD for MTB culture in our study. Further it can be said L.J media with duck egg carried more advantage of being more nutrients, more voluminous, quick recovery of bacilli from sputum, and very least contaminations than L.J media with hens" egg.

OP13: ISOLATION OF BACTERIOPHAGES SPECIFIC TO *Vibrio* SPP. AND ENTEROBACTERIACEAE GROUPS DERIVED FROM MANGROVE BIOTOPE

S. Anandhan[1], T. Thilagam[2] and K. Kathiresan[3]

[1, 3] CAS in Marine Biology, Annamalai University, Parangipettai - 608 502

[2]Sri Ganesh College of Arts and Science, Salem

Mangrove forests are the only tall tree forests, situated between land and sea in tropical and subtropical latitudes. The mangrove forests are biologically diverse, ecologically vigorous

and exceedingly valuable systems. Bacteriophages are realized to be numerous and important components of oceanic food webs principally because of their lytic capabilities. Viral lysis may also be a mechanism controlling bacterial community composition. These viruses are important components of the marine food web infecting specific bacteria, archaea and eukaryotic organisms, with consequences for nutrient and energy cycling, control of species diversity and exchange of genetic material among organisms in marine environments. The estimated overall abundance in the world"s oceans is in the order of 1030, this abundant occurrence of viruses helps in three principal processes viz., (i) recycling of nutrients and energy, (ii) controlling of species diversity and (iii) exchanging of genetic material among marine organisms. However, their role in mangrove environment is largely unknown. Therefore the present work was undertaken to study the occurrence and distribution of bacteriophages specific to host bacteria such as Vibrio species and enterobacteriaceae groups which are abundant in mangrove biotopes to delineate their role in functioning of mangrove ecosystem.

OP14: A STUDY ON ISOLATION OF BIOACTIVE METABOLITES FROM SEAWEEDS *Gracilaria edulis* AGAINST HIV URINE SAMPLE ASSOCIATED PATHOGENS

T. Vinodhkumar

Department of Microbiology, AVS College of arts and Science, Salem - 636 106

Seaweeds Are Macroscopic Algae Found Attached to the Bottom in Relatively Shallow Coastal Waters. *Gracilaria corticata* is a red alga which can be collected from many sea coasts around the world such as China, India, Persian Gulf, etc. The Persian Gulf is a unique marine habitat infested with diverse seaweeds. Seaweeds are rich and varied source of bioactive natural products and have been studied as potential biocidal and pharmaceutical agents. In recent years, there are numerous reports of macro algae derived compounds that have a broad range of biological activities such as antibacterial, antifungal, antiviral, antineoplastic, antifouling, anti inflammatory, antitumoric, cytotoxic and antimitotic activities. These compounds probably have diverse simultaneous functions for the seaweeds and can act as allelopathic, antimicrobial, antifouling, and herbivore deterrents, or as ultraviolet-screening agents. They are also used by the pharmaceutical industry in drug development to treat diseases like cancer, acquired immune-deficiency syndrome (AIDS), inflammation, pain, arthritis, infection for virus, bacteria and fungus Currently, algae represent about 9% of biomedical compounds obtained from the sea. Compounds with cytostatic, antiviral, antihelmintic, antifungal and antibacterial activities have been detected in green, brown and red algae. Recently marine micro organisms have become important in the study of new microbial products exhibiting antimicrobial, antiviral, anti-tumor, anticoagulant and cardio active properties. Indiscriminate use of these chemicals may cause mortalities & cause resistance among bacterial pathogens. To overcome these problems, cost effective, safe & ecofriendly therapeutic agent is the need of the hour and to find out the potential antimicrobial agents from the marine bacteria for the control of bacterial borne disease in human. With increased occurrence of multi-resistant pathogens, the search for new antibiotics has gained urgency. Marine bacteria being heterotrophy with simple cell multiplication process, which can be cultivated in large

amount in expensively. This has prompted the present study, to asses the possible utilization of associated bacteria as resources, to meet the sufficient supply of desired metabolites.

OP15: NEW FACE IN THE ROW OF HUMAN THERAPEUTICS: BACTERIOCINS

S. Revathi[1], N. Rameshkumar[2], M. Krishnan[2] and N.Kayalvizhi[1]

[1]Department of Zoology, Periyar University, Salem - 636 011

[2]Dept. of Environmental Biotechnology, Bharathidasan University, Thiruchirapalli- 620024

Staphylococcus aureus remains one of the most intensively investigated bacterial species. As a human and animal pathogen, it can cause a variety of nosocomial and community-acquired infections ranging from minor skin abscesses to serious, potentially life-threatening diseases, such as bone and soft tissue intra-surgical infections, sepsis and invasive endocarditis. *S. aureus* can be carried asymptomatically on the nasal epithelium in healthy carriers, however, epidemiological studies link the carriage of S. aureus with a significantly higher risk for the development of staphylococcal diseases. Thus, the need to introduce effective bactericidal substances for therapy of MRSA infections is pressing. Bacteriocins are large and functionally diverse family of antimicrobials found in all major lineages of bacteria and that these proteinaceous toxins play a significant role in mediating competitive dynamics between bacterial strains and closely related species. The aim of the present study was to assess in vitro the potential of bacteriocin for inhibit of methicillin resistant *Staphylococcus aureus*.

OP16: SCREENING OF MARINE ALGAE FROM INDIA FOR THEIR ANTITUMOR ACTIVITIES

V. Devi, M. Priyanka, S. Anupriya and K.C.P. Rajamanikandan

Email: bts.raj1987@gmail.com

Nine species of marine algae collected from the coast of India were screened for their antitumor activities, and eight species *Leathesia difformes, Polysiphonia urcedata, Scytosiphon lomentarius, Gloiopeltis furcata, Punctaria latifolia, Symphyocladia latiuscula, Rhodomela confervoides* and *Ulva pertusa* showed potent cytotoxic activities. Three, *Rhodomela confervoides, Scytosiphon lomentarius* and *Gloiopeliis furcata*, were used for further investigation. More than 30 compounds were isolated and purified, and 14 bromophenols, 1 steroid and 1 carotene were identified by advanced spectroscopic methods including IR, MS, and NMR techniques. Amongst the 16 identified compounds, 7 showed vigorously selective activities against KB, Bel7402 and A549 cancer cells, and 6 bromophenols were new compounds.

OP17: IN-VITRO ANTIBACTERIAL EFFICACY OF ESSENTIAL OIL OF *Thymus vulgaris* L. AGAINST MULTI-DRUG RESISTANT CLINICAL ISOLATES OF *E.coli*

A. Anuswedha and M. Raiza

Department of Applied Microbiology, JBAS College for women, Teynampet, Chennai.

Escherichia coli, a member of the Enterobacteriaceae family of bacteria, is a frequent cause of life-threatening bloodstream infections and other common infections, such as urinary

tract infections, cholecystitis, bacteremia, cholangitis traveler's diarrhea, and other clinical infections such as neonatal meningitis and pneumonia. The emergence of multidrug resistance in *E. coli* is also becoming a global concern. Thus, it is urgent need to find out new antimicrobial agents. Various essential oils have been used medicinally at different periods in history. Essential oils exhibit antibacterial activity against Gram positive as well as Gram negative bacteria. The aim of the study was to analyse the antibacterial efficacy of *Thymus vulgaris* L. essential oil against multidrug resistant clinical isolates of *E.coli*. The oils were screened using two methods viz., Agar disc diffusion and agar well diffusion and the inhibition zones were identified. The concentration of the oil which showed maximum zone of inhibition were analysed for determination of MIC. The essential oil of thyme showed efficacy against most of the *E.coli* strains. Therefore, the study proves that *Thymus vulgaris* L. essential oil can be used as a potential candidate for treatment of infectious diseases caused by *E.coli*.

OP18: ISOLATION, CHARACTERIZATION AND ANTIMICROBIAL SENSITIVITY TESTING OF ISOLATES FROM DENTAL CARRIES

W. Parveen and G. Shameem fathima

PG Dept of Applied Microbiology, JBAS College for Women Teynamepet

Dental carries, often called cavities are erosion of the surface of the tooth caused by the combined effects of bacteria, acid, and plaque. Dental carries are common in both children and adults, they occur most often as a result of poor hygiene. Dental carries are usually painless first, but they may become painful if they spread to the nerve or root of a tooth. Left untreated dental carries can progress to a tooth abscess, which is a more painful and potentially serious condition. In our study the bacteria with the highest percentage isolated was *Bacillus subtilis* followed by *Escherichia coli, Streptococcus mutants* and *Pseudomonas aeruginosa*. The antibiotic sensitivity test was done for all these isolates according to Kirby Bauer Disc Diffusion Method. MIC Studies for chloramphenicol was done by agar dilution method. Most of the isolates showed MIC value of <16µg/ml, 4 isolates had the MIC of 16µg/ml. In our study it has been noted that the organism isolated from the patients suffering from dental carries were resistant towards various antibiotics.

OP19: ANTI BACTERIAL ACTIVITY OF *Termanalia chebula* AGAINST URINARYTRACT INFECTION

U.K. Priya

Vivekanandha College of Arts and Sciences For Women, Trichengode - 637 205

Urinary tract is a common community- acquired bacterial diseases. Urinary tract infection are also important complication of pregnancy and associated with structural or neurological lesions of the UT at any age. It is a common cause of fever. Varieties of antibiotics are available for UTI includes Amoxicillin, Cephalosporin, Tetracycline are most common used for catheter induced infection. Termanalia chebula is called king of medicine in Tibet for centuries indigenous foods. Herbal have been used in herbal medicine for curing various diseases. Isolation and identification of UPEC from urine sample. To determine antibacterial

activity by Kirby bauer disc diffusion method. To check the efficacy of medicinal plant extracts of *Termanalia chebula* against UPEC. Isolation and identification of organisms by following these methods Gram staining, Biochemical tests and Carbohydrate fermentation tests. For the susceptibility of organisms was tested by Antibiotic sensitivity. Morphology and biochemical characteristic of the uropathogenic isolates were identified. In antibiotic Ceftazidime 50µg) show 96% high concentration and Tetracycline 30µg) show 80% low concentration. In antibacterial activity of the dried fruit extract from Termanalia chebula was studied against UTI using disc method. In cold water and acetone extract having good antibacterial activity and other extract having low anti bacterial activity.

OP20: MULTIPLE DRUG RESISTANT OF *Escherichia coli* ISOLATED FROM URINE SAMPLE

V. Saipriyanga

Vivekananda College of Arts and Sciences for Women, Tiruchengode - 637 205

E.coli is one of the most important pathogen that cause nosocomial infections and shows high level of antibiotic resistance the emergence of multidrug resistance and extended spectrum of β-lactamase producing *E.coli* faces of serious illness in clinical setting and antibiotic resistant system. A total of 80 urine samples were collected from various clinical laboratories. Among 80 samples, *E.coli* was fomed to be (19) which was identified by the microbiologically experimental test under the guidelines of bergey's manual of determinative bacteriology. The isolates were highly resitant to various antibiotics such as ampicillin, amoxicillin, tetracycline, tobramycin. The sensitivity patterns of isolated and analysed. MDR *E.coli* isolates were identified as38% with a different pattern of resistant. This is clearly demonstated that ESBL of producing *E.coli* had excellence reduced susceptibility to beta lactam antibiotics as a result of multidrug resistance we are in very critical stage to treat the nosocomial infection by using with β- lactam antibiotic.

OP21: STUDIES ON ANTIBACTERIAL, ANTIOXIDANT AND PHYTOCHEMICAL ANALYSIS OF LEAVES OF *Cleome viscosa* L.

C. Swaminathan[1], P. Kavitha[1], V. Hemalatha[1], **K. Vaishnavi[1]** and R. Balagurunathan[2]

[1]Department of Microbiology, Vysya College, Salem - 636 103.

[2]Department of Microbiology, Periyar University, Salem - 636 011.

Cleome viscosa is a weed distributed throughout the tropics of the world and plains of India and is known as dog mustard, used in Ayurvedha for therapeutic purposes. To validate this use, leaves of the plant was subjected to phytochemical analysis, antioxidant activity determination by DPPH free radical scavenging assay and in-vitro antibacterial activity against *Staphylococcus aureus, Escherichia coli, Klebsiella pneumoniae, Proteus mirabilis, Pseudomonas aeruginosa* and *Vibrio parahaemolyticus*. Preliminary phytochemical analysis revealed the presence of carbohydrates, flavonoids, alkaloids, fixed oil and phytosterols. Methanol extract of leaves showed highest antibacterial activity followed by ethanol extract and acetone extract. Ethanol, methanol and acetone extracts of leaves of the plant showed significant

antioxidant activity compared to standard antioxidant ascorbic acid. The DPPH radical scavenging activity of the extract was increased with increasing concentration. The present study suggests that appropriate bioactive compounds may be developed from the leaves of *Cleome viscosa* L. for the treatment of various ailments.

OP22: ANTIBACTERIAL ACTIVITY OF MEDICINAL PLANT AGAINST WOUND INFECTED PATHOGENS

N. Divya

Vivekananda College of Arts and Sciences for Women, Tiruchengode - 637205

Herbal medicines have been basis of treatment for various diseases and physiological conditions in traditional methods practiced such as Ayurveda, Unani, and Siddha. The effects of plant extracts on bacteria have been studied by a very large number of researchers in different part of the world. Plant derived drug have been a part of the evolution of human. Healthcare for thousands of years. In this study antimicrobial activity of *Acalypha indica* were investicated against two strains of Human pathogenic bacteria. A total of 15 pus samples were collected from namakkal private hospital, among that 2 strains were isolated as *Staphylococcus aureus*, *Pseudomonas aeruginosa*. The above isolated organisms were tested for their sensitivity towards different type of medicinal plant leaves extract by Agar well and disc diffusion methods. Isolation and identification of bacterial isolates by using standared biochemical methods. In this study the highest antibacterial activity were observed in water extract of *Acalypha indica* than compared with acetone extract. Inhibitory effect of medicinal plant against *Staphylococcus aureus* in well diffusion is (17mm), and *Pseudomonas aeruginosa* is (20mm) in water extract. In acetone extract 7mm, 9mm inhibitory zone showed by *Staphylococcus aureus* and *Pseudomonas aeruginosa*.

OP23: ANTIBIOTIC SUSCEPTIBILITY OF BACTERIAL PATHOGENS FROM DIABETIC FOOT ULCER PATIENTS

G. Kalaivani and N. Hemalatha

Department of Microbiology, Periyar University, Salem - 636011.

Diabetic foot ulcer is an important complication among diabetes mellitus. Improper use of topical antibiotics use can cause non healing of ulcers. Microbiological culture and antibiotic susceptibility testing are the proper methods to address this issue but it may not be possible in all health care facilities especially in rural areas. Knowledge about the bacteriological profile of diabetic foot ulcer in our community will guide health professionals to manage foot ulcers. A case study was made on the bacteriological profile of diabetic foot ulcers and attempted to find out the antimicrobial susceptibility of those organisms. A record based study was conducted among 104 diabetic foot ulcer patients admitted in the Medical college hospital and antibiotic susceptibility of organisms (pus samples from foot ulcers) from these 104 patients were collected from Department of Microbiology GH Salem. *Pseudomonas* organism was isolated in 23% of the samples, *Staphylococcus aureus* (21%), *Klebsiella* (17%), *Proteus mirabilis* (15%), *E. coli* (12%) were also found. 22% of the amputees showed infection with *Pseudomonas*

aeruginosa and *Proteus mirabilis*. Most of the Gram positive cocci were found to be highly resistant to penicillin, gentamicin, and erythromycin. Most gram negative bacilli were highly resistant to antibiotics such as ampicillin, gentamicin, cephalosporins, ciprofloxacin and aztreonam. Appropriate antibiotic therapy is an essential part of diabetic foot ulcer management. This study suggests that empirical antimicrobial therapy should comprise of antibiotics sensitive for gram negative and gram positive microorganisms.

OP24: ANTIMICROBIAL ACTIVITY ON SELECTED MEDICINAL PLANTS AGAINST DENTAL PLAQUE BACTERIA

M. Sankareswaran[1], S. Anbalagan[1], R. Rajendran[2], and A.Manikandan[2]

[1]PG & Research Department of Microbiology, Muthayammal College of Arts and Science, Rasipuram - 637408

[2]PG& Research Department of Microbiology, PSG College of Arts and Science, Coimbatore,

The present study antimicrobial activity from methanol extract of *Adhatoda vasica* ,*Cynodon dactylon*, and *Laportea crenulata* a was investigated against Dental Plaque pathogenic microorganisms (*S. aureus, K.pneumoniae, B.cereus, Lactobacillus sp*).The tested extracts showed very strong antimicrobial activity against all organisms. The antimicrobial activity was evaluated by measuring the zone of inhibition using disc diffusion method. The results of Adhatoda vasica root of methanol extract against the dental pathogens shows the best results when compared to the other two plants extracts of *Cynodon dactylon* and *Laportea crenulata*. The maximum zone of inhibition was observed in the extract of Adhatoda vasica against *S.aureus, Lactobacillus sp* (16mm, 12mm zone of incubation) at 100 mg/ml of leaf extract followed by *K. pneumoniae* which showed 10 mm inhibition zone at 100 mg/ml leaf extract. This study also investigated the role of environmental factors on the antimicrobial activity of this plant.

OP25: ISOLATION OF SECONDARY METABOLITES FROM MARINE ALGAL BACTERIAL POPULATION AGAINST FOOT ULCER ASSOCIATED PATHOGENS

S.S.Maithili

Department of Microbiology, AVS College of Arts and Science, Salem

Marine algae have been reponed to possess a wide range of bio active properties. The seaweed *Gracilaria* is a group of marine algae belonging to the class Florideophyceae has come to attention for more pharmacological products and have received comparatively less bioassay attention.From this present the study endophytic bacteria were isolated from seaweeds along the East Coast of India, Palk Strait to find out the potential of antibacterial activity of Total Heterotrophic bacterial(THB). Based on the morphological characters, 36 different strains were isolated.The effect of bioactive compound from chosen Heterotrophic bacteria strains were assayed for antibacterial effect through Minimum inhibitory concentration and Minimum Bactericidal concentration and tested for the antimicrobial sensitivity against *Staphylococcus aureus, Escherichia coli, Klebsiella pneumonia* and *Pseudomonas aeruginosa* Sp by cross streak assay. Of them, 12 strains were showed sensitivity against pathogenic bacteria. The

isolated endosymbiotic strains which shown sensitivity against four pathogenic bacteria were subjected for the Minimum Inhibitory Concentration (MIC) assay by following standard methodology. It shows that the strain no ENG6 shown the MIC value of 250µg against *Staphylococcus aureus* and *Escherichia coli* the ENG30 showed MIC value of 1000µg against *Klebsiella pneumonia*, the ENG36 showed MIC value of 250µg against *Pseudomonas aeruginosa* and *Staphylococcus aureus*.The ENG6 showed MBC value of 250µg to two of the pathogenic bacteria against *Staphylococcus aureus* and *Escherichia coli*, ENG30 showed MBC value of 1000µg against *Klebsiella pneumonia*. The ENG36 showed MBC value of 250µg against *Pseudomonas aeruginosa*.

OP26: INFLUENCE OF COMMERCIALLY AVAILABLE LOTIONS ON FUNGI OF HUMANS HAIR AND SCALP

V. Usha

Vivekananda College of Arts and Sciences for Women, Tiruchengode - 637205

Microorganisms can infect the human body. They are mainly 4 types: viruses, bacteria, fungi and parasites. All of them offer unique challenges to treatment and fungal pathogens can be particularly problematic. The present investigation was carried out with the collection and screening of humans scalp fungi and their influence with different commercially applied lotions. The investigation showed common hair fungi such as *Aspergillus flavus, A.niger, Penicillium* sp, and dermatophytic hair fungi of humans such as *Microsporum, Trychophyton rubrum, T.mentagrophytes* and *Trychophton* sp. Many type of commercially applied lotions had been used to check their effectiveness on the isoltated human hair and scalp fungi. Standard anti-fungal agents to check the effectiveness of the commercially applied lotions namely Amphotericin B, Itraconozole, Ketoconozole and Fluconozole were used.

OP27: PREVALENCE OF *Candida* SPECIES IN MEDICAL DEVICES AND THEIR VIRULENCE FACTORS ROLE IN PATHOGENICITY

P. Rajeswari and P.Vijayalakshmi

Vivekananda College of Arts and Sciences for Women, Tiruchengode - 637205

The yeast especially Candida is an opportunistic pathogen, which colonizes at several anatomically distinction site including skin, oral, gastrointestinal tract and vagina. *Candida* species now rank as the fourth most common cause of nosocomial blood stream infections. The increase in the proportion of blood stream infections due to opportunistic fungal pathogens is likely associated with increasing number of critically ill patients. The rise in the prevalence of fungal infections has exacerbated the need for the new effective antifungal agents. Because *Candida* species possess number of virulence factors. Totally 50 samples were collected from government hospital. By preliminary identification and sugar tests 20 isolates was confirmed as *Candida* spp. Further subjected to antibiotic disc diffusion method, azole and amine derivatives are used to identify the susceptibility of isolates. Virulence factors like Biofilm (tube method), proteinase (skim agar medium) phopholipase (egg yolk agar medium), hemolysin (blood agar),

and cell surface hydrophobicity of the isolates also determined. These virulence factors are mainly responsible for drug resistance.

OP28: INVITRO ANTIBACTERIAL ACTIVITY OF THE ESSENTIAL OIL AGAINST BIOFILM FORMING UROPATHOGENIC *Escherichia coli* AND RAPD ANALYSIS

S. Nithiya and M. Thaila

Urinary tract infection is a serious health problem with respect to antibiotic resistance and high recurrence rates. *Escherichia coli* is the predominant organism causing urinary tract infections. Uropathogenic *E.coli* forms intracellular bacterial communities with many biofilms within the bladder epithelium.A Biofilm is a multicelluar layer is made up of extracellular polysaccharide.They can cause significant problems in many areas, in medical persistant and recurrent infections. The aim of this study is to evaluate the antibacterial activity of the essential oil and antibiotics against biofilm forming uropathoenic *E.coli*.The essential oil are volatile compounds from plant produced during secondary metabolism having antibacterial activity. The urine samples are collected from Salem private hospital. The 30 urine samples 13 samples were showed positive *E.coli* growth. The biofilm assays were performed with grew *E.coli* by using TCP, tube and plate methods. This study also analysis the biofilm producing *E.coli* by the RAPD technique.

OP29: STUDIES ON ANTI-MICROBIAL ACTIVITY OF *Ganoderma lucidum* ISOLATED IN THE FOREST AREAS AROUND PUTTAPARTHY, ANANTAPUR DISTRICT, A.P.

B.S.Vijayakumar

Sri Sathya Sai Institute of Higher Learning Prasanthinilayam

During the Preliminary studies a mushroom growing on the bark of the trees was isolated from Prasanthinilayam, Anantapur district, A.P. and identified as *Ganoderma lucidum*. The identification was confirmed by the experts of Himachal Pradesh University.This wood rooting fungi was grown in Potato sucrose broth first in conical flask and then in 1 litre Baby Fermenter in the Department of Biosciences, SSSIHL, A.P. The crude metabolite was isolated from the fermenter after the fungus was grown for two weeks. The crude metabolite was tested for the Anti-microbial activity. The results of the paper disc method and spectrophotometric method revealed that the extract of the metabolite of *Ganoderma lucidum* found to have very significant antibacterial activity.

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OP30: ISOLATION AND CHARACTERISATION OF *Clostridium histolyticum* AND IT'S TOXIN

B. Rohini and S. Jayalakshmi
Centre of Advanced Study in Marine Biology, Annamalai University, Parangipettai

A gram positive, motile, strictly anaerobic bacterium was isolated from the sediment samples of Vellar estuary, India and was identified as *Clostridium* sp. by gene sequencing and as *Clostridium histolyticum* by biochemical methods. Phylogenetic analysis based on 16S rRNA sequence showed high similarity to *Clostridium histolyticum*. The organism was found to be resistant only to Erythromycin among the various antibiotics tested. The culture supernatant was checked for its protein concentration by lowry method and optimum conditions for maximum toxin production was found out as 42hrs incubation, pH 8, temperature of 35°C and 1.5% salinity. Extraction of the toxin was carried out under optimum conditions and was partially purified by ammonium sulphate precipitation and dialysis against acetate buffer. From 500 ml culture broth used for mass scale production, it was possible to get 1.6 g of toxin from 3g of biomass. When the antibacterial activity of the toxin was tested it was found to be high against *Proteus vulgaris* and *Klebsiella pneumoniae* with a maximum inhibition zone of 48mm and 27mm respectively. Antifungal activity was absent. The toxin extract was found to be highly β-hemolytic. Molecular weight of the toxin was found by SDS PAGE and it was found to contain 3 bands with the molecular weight of 56KDa, 47 KDa, 39KDa. Brine shrimp acute toxicity assay confirmed that the LC50 value of the toxin was 1.5 mg/ml. The toxin was also characterized for its functional groups by the FT-IR analysis and some novel findings were obtained. Further studies on collegenase production by the organism is to be characterized.

OP31: EXPLORATION OF BIOACTIVE SUBSTANCES FROM MANGROVE ACTINOBACTERIA

M. Sanjivkumar and G. Immanuel
Marine Biotechnology Division, Centre for Marine Science and Technology, Manonmaniam Sundaranar University, Rajakkamangalam – 629 502

This present work was aimed to assess the production and characterization of bioactive compounds such as enzymes and antibiotics from extremophilic actinobacteria namely Streptomyces sp (MSA2), isolated from the mangrove sediment soil of Manekkudi, Tamilnadu, India. The strain was characterized and identified by using Nonomura keys and actino database and it was tested for its enzyme and antibiotic production capacity at optimized submerged culture conditions. The organism produced the enzymes such as xylanase, and chitinase at pH 8, temperature 37°C and 1 % each of the substrates like xylan and chitin. But the maximum activity of all the two enzymes was observed at pH 8 ± 0.5 (4 to 11), temperature 40°C (20 to 80°C) and 500 µg of substrate concentrations (100 to 800 µg). The presence of metal ions EDTA, Mg2+and Zn2+ were inhibited the enzyme activity, whereas Cu2+, Co2+ and Fe2+ were induced the enzyme activity. The production of antibiotic compound was carried out by agar plate solvent extraction method and it was partially purified using thin layer chromatography & bioautography, tested against clinically resistant pathogens. Probably the

enzymes were partially purified by using (80%) ammonium sulphate precipitation, dialysis and DEAE-cellulose chromatography. The partially purified enzymes showed the activity of 1214.02 (xylanase) and 975.20 (chitinase) IU/mL. The protein content of the partially purified enzymes was found to be 600 and 700 µg/ml in xylanase and chitinase respectively. The molecular weight of the protein was determined to be 98 (xylanase) and 32 (chitinase) kDa. Furthermore the bioactive compounds (enzyme and antibiotic) were characterized by FT-IR and XRD method and the enzymes could be used in pulp fibrillation, water retention, and selective removal of xylan from dissolving pulps.

OP32: ISOLATION AND PRODUCTION OF XANTHAN GUM FROM MARINE ISOLATE *Xanthomonas campestris*

S. Jayalakshmi

CAS in Marine Biology, Annamalai University, Parangipettai - 608 502.

Xanthan gum helps suspend solid particles, such as spices and also used in frozen food and beverages. The present study is on xanthan gum production by *Xanthomonas campestris* strain isolated from Vellar estuary. The bacterial density from water and sediment samples was found to be respectively, $4.9x10^6$ CFU/ml and 8.2x106 CFU/g. Strains were screened for extracellular polysaccharide production in particular xanthan production medium supplemented with mineral sources. Morphologically different forms of colony showing mucous formation were isolated. Growth optimization study revealed that maximum polysaccharide recovery was obtained in 3days old culture, so an inoculation period of 72hrs was selected for biomass determination and xanthan extraction and quantification. Optimum growth of the potential strain was strongly influenced at pH8, salinity1.5%, and carbon source-glucose and nitrogen sources-ammonium nitrate. Xanthan gum production seemed to be growth dependent. When the culture was centrifuged (30,000xg, 30min.), the supernatant from *X.campestris* was viscous and formed stringly precipitate with solvents, ethanol, acetone and isopropyl alcohol were used in which respectively 12 g/L, 8.2 g/L and 25 g/L were obtained. Their dry weight was respectively 8 g/L, 4.2 g/L and 20 g/L. Among solvents used (i.e.) isopropyl alcohol, acetone and ethanol maximum xanthan production was obtained in isopropyl alcohol. The FT-IR spectrum of the product suggested the strong presence of CH of methyl group, C=O and COO- bonds of organic compounds, confirmed the nature of obtained polymer as xanthan, the biopolymer. Hence the present study, the xanthan gum yield from marine *Xanthomonas campestris* was found to be higher. The optimal conditions also found to be suitable for industrial scale production.

OP33: PRODUCTION OF INDOLE ACETIC ACID FROM AZOTOBACTER

I. Muthuselvan[1,2] and R. Balagurunathan[3]

[1]Department of Microbiology, VELS University, Old Pallavaram, Chennai - 117
[2]Research Scholar, Bharathiar University, Coimbatore - 641 046
[3]Department of Microbiology, Periyar University, Salem - 636 011

Indole acetic acid is a member of the group of phytohormones called auxin. Plants are producing indole acetic acid less amount. Microorganisms are capable of producing indole acetic acid. Azotobacter is a good nitrogen fixer .Besides nitrogen fixation it also produces

thiamin, riboflavin, indole acetic acid and gibberellins. In certain condition they also exhibit anti-fungal activities and thereby fungal diseases may be controlled indirectly. Azotobacter using as a biofertilizer for the cereals and cash crops viz. Wheat, Paddy, Bajra, Jowar, Maize, Mustard ,Cotton, cumin, banana, sugarcane, tobacco, castor vegetable etc..Based on the above mentioned characters of Azotobacter, in present study Azotobacter species will be isolated from soil and tested for the production of indole acetic acid. 17 isolates were isolated from soil of various districts in Tamilnadu by using Ashby"s Mannitol medium. Out of 17 isolate, eight isolates were found to be *A. chrocooccum*, seven were found to be *A. nigricans* and two isolates were found to be *A. armeniacus*. The production of IAA was high at the temperature of 25°C - 30°C and the pH range 6-7 during the optimization studies. Out of seventeen isolates T1 (*Azotobacter nigricans*) and Ka5 (*Azotobacter chroococcum*) were found to produce higher amount of IAA 21.6 µg/ml and 16.8µg/ml respectively. The IAA production was confirmed by Thin Layer Chromatography and colorimetric assay. The Rf value of standard IAA was 0.940 and test samples Rf values were 0.970 and 0.985.From the present study, isolates T1(*Azotobacter nigricans*) and Ka5(*Azotobacter chroococcum*) can be used for production of IAA and as a biofertilizer after strain improvement.

OP34: SCREENING OF LIGNOCELLULOSE HYDROLYZING ENZYME PRODUCING FRESH WATER MICROORGANISMS FROM COIMBATORE LAKES

Sudarshan Singh Rathore, A. Manivannan and R.T. Narendhirakannan

Department of Biotechnology, Karunya University, Karunya Nagar, Coimbatore.

Most of the aquatic systems are infested with *Eichhornia crassipes* (water hyacinth). These plants are difficult to control and disturb whole aquatic system in mean of nutrient, water, oxygen and all. In this present study, the attempt was made to isolate microorganisms from plants (water hyacinth), water and soil collected from two fresh water lakes from Coimbatore city, Tamil Nadu, India. A total of 36 microorganisms were isolated; of these, 8 were fungi, 8 were bacteria, 14 were yeasts and 6 were actinomycetes. The enzyme producing organisms were qualitatively confirmed by Congo red method. Out of these, 4 best cellulase and xylanase enzyme producing filamentous fungal strains were identified. Different substrates viz., Carboxy-methyl-cellulose (CMC), filter paper, cellulose powder, xylan and water hyacinth plant powder were used for enzyme production. The optimal pH, temperature and incubation time for enzyme production was found to be 5.0-5.5, 25-30° C and 6-7 days respectively by fungal strain. Enzyme activity was quantitatively confirmed by DNS (Di-nitro-salicylic-acid) method. The optimal substrate, pH, temperature and incubation time for enzyme activity was found to be cellulose, xylan, filter paper, 5.2, 50° C and 1-2 hours respectively and maximum 2.3 mg/ml of glucose and 2.1 mg/ml of xylose measured by DNS method after enzyme activity. Lowry method was used for the estimation of enzyme concentration and ammonium sulfate precipitation and dialysis used for partial purification of enzyme. In SDS-PAGE, 3-4 bands observed in partially purified enzyme produced from water hyacinth plant substrate.

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OP35: OPTIMIZATION OF MEDIUM FOR THE PRODUCTION OF CELLULASE FROM *Trichoderma viride* BY USING VARIOUS AGRO WASTE FOR POULTRY FEED SUPPLEMENT

Amutha, R., S. Karunakaran, S. Dhanasekaran, N. Gayathri, P. Nivetha and K. Sangavi
Vivekanandha College of Engineering for Women, Thiruchengode - 637 205

Poultry production has undergone an enormous expansion and development during the past half century throughout the world. In India, Tamilnadu ranks second in poultry meat and egg production .The cost of the digestive feed is very expensive when compared to indigestible feed.so the Indigestive feed is mixed with cellulase enzyme for the easy digestion process. The cellulose was produced from *Trichoderma viride* which can degrade cellulose .Then it was given as feed supplementary for the poultry animals. Agro-industrial residues are generally considered the best substrates for the production of enzymes in liquid state fermentation. So the present study deals with the identification of medium which produces high amount of *Trichoderma viride* by using various agro waste. The *Trichoderma viride* was isolated from soil by serial dilution method ,for fungal identification the culture was grown in Potato Dextrose Agar medium (PDA) .Lacto phenol cotton blue staining was carried out for the confirmation of *Trichoderma viride*. For the bulk production of *Trichoderma viride* produced from the various agro waste like rice brawn, wheat bran, molasses, saw dust and vegetable waste by using Liquid state fermentation process .Based on the dry weight basis we got the following concentration in rice brawn-8.59g/lit, wheat bran-9.34g/lit,molasses-8.21g/lit, saw dust-10.54g/lit, vegetable waste -14.32g/lit. Finally the maximum yield of *Trichoderma viride* was identified in the vegetable waste medium when compared to other substrates. In order to increase the on-farm efficacy of enzyme technology, research has to be carried out so as to decrease the cost of enzyme production and make enzyme supplementation more practically feasible. With these facts in the background, the present study has been designed to explore the technology to synthesize cocktail fibro lytic enzymes at farm gate level and make the farmers as successful entrepreneurs.

OP36: BIOSYNTHESIS OF SILVER & GOLD NANOPARTICLE FROM MICROBE

S.Tamilarasi and S.Velumani
Dept. of Biotechnology, Prof.Dhanapalan College, Kelambakkam

The use of microorganism in the synthesis of nanoparticles emerges as an eco-friendly and exciting approach. In this study, the gold nanoparticles was synthesised from the organism *Klebsiella pneumoniea, Staphylococcus aureus, Proteus*. The produced gold nanoparticles are of different shapes and size ranging from 31-100nm. The important parameter which controls the size and shape of the gold nanoparticles was pH value. In the same way the Silver nanoparticles were synthesised from *Klebsiella pneumoniea, Staphylococcus aureus, Proteus*. Silver nanoparticles produced are of different shapes and size. The important parameter which controls the size and shape of the silver nanoparticles was pH value. The spherical silver nano particles in the range of 125-200nm were observed at pH value of 7 in *Klebsiella* and *Staphylococcus aureus* Antibacterial activity of the synthesized nanoparticles from the *Klebsiella* and *Staph* were checked against the Pathogenic organisms like *Escherichia coli, Pseudomonas, Proteus,*

Staph, Salmonella .Klebsiella showed inhibition against all the organisms and *Staph* showed inhibitory activity against *Salmonella typhimurium* and *Pseudomonas*.

OP37: STUDIES ON ANTIMICROBIAL ACTIVITY, PHYTOCHEMICAL ANALYSIS OF *Indigofera linnaei*

T. Punitha[1], K. Moorthy[2], R. Vinodhini[1] and A.S. Saranya[1]

[1]Vivekanandha College of Arts and Sciences for Women (Autonomous), Tiruchengode - 05

[2]B062-Department of Biology, Wolaita Sodo University, Wolaita Sodo Zone, Post Box No.: 138, Ethiopia, Eastern Africa.

The present study has been under taken with an objective to determine the phytochemical constituents and antimicrobial activity of methanolic plant extract of *Indigofera linnaei*. The selected medicinal plant was collected from nearby region of Salem, Yercaud. Antimicrobial activity was carried against bacteria (both G+ve and G-ve) and fungi and the compounds present in the plant extract were identified by standard methods. The methanolic plant extract of extract of *Indigofera linnaei* screened for phytochemical analysis was found to contain the bioactive compounds like carbohydrates, glycosides, alkaloids, proteins and amino acids, fixed oils and fats, saponins, phenolic compounds, tannins and flavonoids. The methanolic plant extract shown the ability to inhibit the growth of bacteria namely *Enterobacter aerogenes, Bacillus subtilis, Shigella boydii* and *Salmonella paratyphi* B, and with zone of inhibition of 27-29 mm, respectively but not shown growth of inhibition on fungi *Candida albicans* and *Cryptococcus neoformans*. This study suggests that methanolic plant extract of *Indigofera linnaei* have profound antimicrobial activity against the tested pathogenic microorganisms and could be a source for new anti-infectious agent.

OP38: EXTENDED SPECTRUM BETA LACTAMASES PRODUCING GRAM NEGATIVE BACILLI FROM VARIOUS CLINICAL SAMPLES

A.S. Saranya[1], K. Moorthy[2], T. Punitha[1] and R.Vinodhini[1]

[1]Vivekanandha College of Arts and Sciences for Women, Tiruchengode - 05

[2]B062-Department of Biology, Wolaita Sodo University, Wolaita Sodo Zone, Post Box No.: 138, Ethiopia, Eastern Africa.

The frequency of Extended Spectrum Beta Lactamases producing strains among clinical isolates has been steadily increasing over the past few years resulting in limitation of the therapeutic options. The present study has been undertaken to detect the presence of ESBLs producing species in various clinical samples. A total of 80 samples were received from VIVA laboratory there were 20 urine samples, 20 pus, 20 stools and 20 throat samples were collected. The study consists of 76 various clinical isolates from various clinical samples such as *Staphylococcus aureus* 24(31.58%), *Escherichia coli* 15(19.74%), *Klebsiella spp.* 23(30.26%), *Pseudomonas aeruginosa* 7(9.21%), *Salmonella spp.* 4(5.26%) and *Shigella* spp. 3(3.95%). The majority of isolates were obtained from pus, stool and throat samples followed by urine. Antimicrobial susceptibility test be performed using Kirby-Bauer disc-diffusion method. There were 6 various antibiotics such as Ampicillin, Amoxicillin, Gentamycin, Amikacin,

Chloramphenical and Tetracycline were used against clinical isolates. Among the antibiotics tested, all the antibiotics showed the maximum inhibitory activity against particular organisms. Then these 76 clinical isolates were tested for ESBL production by using screening test and double disc synergy test. From the primary screening *Staphylococcus aureus* (1), *Escherichia coli* (9), *Klebsiella spp*. (21), *Pseudomonas aeruginosa* (6), *Salmonella spp.* (3) and *Shigella spp.* (1) showed the positive result for the ESBL production. Among that *Escherichia coli* 6(40.0%), *Klebsiella spp.* 19(82.60%), *Pseudomonas aeruginosa* 2(28.57%), and *Salmonella spp.* 2(50.0%) were confirmed as ESBL producers by double disc synergy test.

OP39: IN VITRO SCREENING OF ANTIMICROBIAL ACTIVITY AND PHYTOCHEMICAL ANALYSIS OF *Indigofera cassioides*

R. Vinodhini[1], K. Moorthy[2], T. Punitha[1] and A.S. Saranya[1]

[1]Vivekanandha College of Arts and Sciences for Women (Autonomous), Tiruchengode - 05

[2]B062-Department of Biology, Wolaita Sodo University, Wolaita Sodo Zone, Post Box No.: 138, Ethiopia, Eastern Africa.

The study was undertaken to identify the antimicrobial activity, phytochemical and analysis of methanolic extract of *Indigofera cassioides* against 26 microorganisms (24 bacteria and 2 fungal strains). Antimicrobial activity of plant extract was assayed by disc diffusion method and standard procedure was used to identify the phytochemical constituents. Methanolic extract shown maximum inhibitory activity against *Enterobacter aerogenes* (29.6 mm), *Bacillus subtilis* (29.2 mm), *Haemophilus parahaemolyticus* (26.8 mm), *Salmonella paratyphi* B (26.4 mm), *Shigella boydii* (25.2 mm), *Streptococcus thermophilus* (22.4 mm), *Staphylococcus epidermidis* (22.0 mm), *Salmonella enterica* (21.4 mm), *Salmonella brunei* (20.6 mm) and *Klebsiella pneumoniae* (20.4 mm) respectively. The methanolic extract was ineffective against fungi. Then organisms were further tested for MIC by broth dilution method. The result of broth dilution method showed better inhibitory activity against most of the organisms. The result revealed that the antimicrobial properties of I. cassioides might be associated with the presence of phytochemical constituents like carbohydrates, glycosides, alkaloids, proteins and amino acids, fixed oils and fats, phenolic compounds, tannins, flavonoids, phytosterol and triterpenoids.

OP40: NOVEL SCHIFF BASE TRANSITION METAL(II) COMPLEXES AS POTENTIALLY BIOACTIVE IN VITRO ANTIBACTERIAL AND IN VITRO ANTIOXIDANT AGENTS

E. Akila, M. Usharani, R. Ashokan, and R. Rajavel

Department of Chemistry, Periyar University, Salem - 636011.

Metal complexes of Cu(II) with a tetradentate NNOS donor Schiff base ligand (H2L), synthesized by condensation of 3, 3′-dihydroxybenzidine, 2, 3- pentanedione and 4-choloro aminothiophenol were prepared and characterized by elemental analyses, IR, electronic, ESR, NMR studies, as well as conductance measurements. Square-planar geometry for the Cu(II) complex have been assigned to the prepared complexes. The antibacterial activities of the synthesized compounds were tested in vitro against the sensitive organisms *Staphylococcus*

aureus, Bacillus subtilis as Gram positive bacteria, *Escherichia coli* and *Klebsilla pneumonia* as Gram negative bacteria, and the results are discussed. We found that the antioxidant activity of the complexes on DPPH, ABTS and reducing power activity is concentration dependent and higher than that of the free ligand.

OP41: SYNTHESIS, CHARACTERIZATION AND BIOLOGICAL STUDIES OF MIXED LIGAND SCHIFF BASE WITH METAL(II) COMPLEXES DERIVED FROM O-PHENYLENEDIAMINE

R. Ashokan, E. Akila, G. Anbarasu and R. Rajavel
Department of Chemistry, Periyar University, Salem 636011

In the present study a novel Schiff base mixed ligand chelates of Mn(II) complexes with two newly synthesized Schiff base mixed ligands derived from 2,4- dihydroxybenzaldehyde and o-phenylenediamine (H2L1), anisaldehyde and o-phenylenediamine (H2L2). The ligands and their transition metal complexes were characterized on the basis of various physico-chemical methods including elemental analysis, molar conductance, infrared, electronic spectra and magnetic. The mixed ligand complexes are formed in the 1:1:1 (L1:L2:M) ratio as found from the elemental analyses and found to have the formulae [ML1L2] where M= Mn(II). The molar conductance data reveal that the chelates are non-electrolytes. The IR spectral data suggest the involvement of azomethine nitrogen in co-ordination to the central metal ion. The electronic spectral results indicate that all the complexes have octahedral geometry. The ligands and their metal chelates have been screened for their antibacterial activities and the findings have been reported, explained and compared with known antibiotics.

OP42: ISOLATION AND CHARACTERIZATION OF ENDOPHYTIC FUNGUS FROM AN INDIAN MEDICINAL PLANT, *Cyperus scariosus*

J. Ragupathy[1], S.P. Balasubramani[2] and P. Venkatasubramanian[2]
[1]Biotechnology, Kumaraguru College of Technology, Coimbatore.
[2]Institute of Ayurveda & Integrative Medicine (IAIM), 74/2, Jarakabande Kaval, Attur PO, Yelahanka Via, Bangalore - 560106.

Endophytic fungi have been creating a considerable interest globally, owing to their recognition as an inexhaustible source of structurally and biologically active novel compounds. They have been considered as an alternative source of metabolites similar to the secondary metabolites of plants. *Cyperus scariosus* is a small grass-like herb with angular soft stem and underground rhizomatous tubers. This plant has been described with medicinal properties in Ayurveda. Endophytic fungi were isolated from roots of *C. scariosus*. The isolates from the different accessions were found to be similar in their colony characters and microscopic examination. The molecular identification of the fungus was performed using the PCR amplified Internal Transcribed Spacer (ITS) sequence. It gave <300 bps amplicon, which was both forward and reverse sequenced. Phytochemical screening was performed with both the fungal culture filtrate and *C. scariosus*. It showed the presence of flavonoids, phenolics, tannins, protein and amino acids, sterols, carbohydrates, saponins in common. Comparative HPTLC

profile of the fungal culture filtrate and the C. scariosus aqueous extract indicated presence of common bands at 254nm and 366nm (Rf-0.37, 0.48, 0.54, 0.65). The secondary metabolites of *C. scariosus* have already been reported to possess anti-inflammatory, antimicrobial, hepatoprotective, antidiabetic, anti-diarrheal and antiviral activity. We intend to do bioactivity studies for ascertaining the role of the endophytic fungus in active metabolite production in *C. scariosus*.

OP43: INHIBITORY EFFECT OF CAFFEINE ON GROWTH OF *Brevibacterium* SP. AND OTHER BACTERIA

J. Sumitha[1,2] and T. Sivakumar[3]

[1]Research and Development Centre, Bharathiar University, Coimbatore - 641 046

[2]Department of Microbiology, JBAS College for Women, Teynampet, Chennai- 600 018

[3]Department of Microbiology, Kanchi Shri Krishna College of Arts and Science, Kilambi, Kanchipuram-631551

The study was undertaken to investigate the effect of caffeine (1, 3, 7-trimethylxanthine) on growth, morphology and viability of caffeine degrading *Brevibacterium sp*. and other non caffeine degrading bacterial strains. Growth, morphology and cell viability of the bacterial strains were studied in caffeine medium, minimal medium without caffeine and in minimal medium with caffeine. The caffeine degrading *Brevibacterium sp*. achieved a maximum cell dry weight of 1.2 g L-1 after caffeine addition without any change in morphology. The growth and viability of *E. coli* DH5α and other bacterial strains was greatly reduced upon addition of caffeine. *E. coli* DH5α strain formed long filamentous cells on caffeine exposure and changes in morphology occurred for other Gram negative bacterial species and *Bacillus subtilis*. *E. coli* DH5α transformed with plasmid from caffeine degrading *Pseudomonas* sp. was found to be tolerant to caffeine.

OP44: DETERMINATION OF PUTRESCINE AND CADAVERINE CONTENT AND HUMAN PATHOGENIC BACTERIA FROM THREE COMMERCIALLY IMPORTANT FISHES OF THONDI COAST

A. Arulkumar and S. Paramasivam

Department of Oceanography and Coastal Area Studies, School of Marine Science, Alagappa University, Thondi campus-623 409, Ramanathapuram District, Tamilnadu

Biogenic amines (BAs) are chemically defined as low molecular weight (aliphatic, aromatic and heterocyclic) organic bases. BAs are the most important health hazard formed during decarboxylation of certain free amino acids. Putrescine and cadaverine are among the important BAs in the HACCP point of view, next to histamine in the seafood industries. The purpose of this present study was to determine the putrescine and cadaverine content and identify the putrescine and cadaverine forming human pathogenic bacteria from commercially important marine fishes such as *Chirocentrus dorab*, *Gerres filamentosus*, and *Siganus oramin* from Thondi fish market. Among the fishes tested the highest load of cadaverine forming bacteria 5.3x10^{4}cfu/g and putrescine forming bacteria 4.2x104cfu/g were recorded from *Siganus oramin* and *Chirocentrus dorab* respectively. The highest putrescine content was observed from

S. oramin muscle (0.64 mg/100g) and the cadaverine content from *C.dorab* muscles (0.62mg/100g). The predominant putrescine, cadaverine forming and human pathogenic bacteria such as *Shigella* sp., *Serratia* sp, *Salmonella paratyphi*, *Proteus sp*, *Enterobacter aerogenes*, and cadaverine forming bacteria *Enterobacter aerogenes*, *Escherichia coli, Klebsiella sp., Salmonella typhi* and *Serratia sp*. were isolated from the gill, gut and muscle of fishes. Though the fishes are containing the cadaverine and putrescine producing bacteria, the concentration of cadaverine and putrescine were found to be below the safety level 5 mg/100g.

OP45: PREVALANCE OF METHICILLIN RESISTANT *Staphylococcus aureus* IN GOVERNMENT HOSPTAL KARUR

S. Gajapriya

Vivekanandha College of Arts and Sciences for Women, Tiruchengode - 05

To determine the prevalance methicillin resistant Staphylococcus aureus (MRSA) in pus sample from wound infections Government general hospital and also to define the antimicrobial susceptibility pattern of the strains isolated. Pus swabs from patients who had undergone common infection of the wounds were collected and inoculated on blood agar, macconkey agar plates. After incubation for 24-48 hours plates were examined for the growth of Staphylococcus aureus antimicrobial susceptibility tests was performed by using MIC method to detect methicillin resistants an inhibition zone are >10mm was taken as indicative of (MRSA). A total of 36 pus swabs yielded growth of bacterial pathogens out of which 100 were found to be Staphylococcus aureus analysis of the antimicrobial susceptibility pattern of the isolates revealed that 32(88%) were strains of methicillin resistant Staphylococcus aureus(MRSA) compare with other antibiotic vancomycin showed 100% sensitive to all isolates the prevalence of (MRSA) was found to be significantly higher is pus sample from wound infections all the isolates were found to be susceptible to vancomycin. It is concluded that (MRSA) is a series nosocomial pathogens wound infection and requires strict intervention for the prevention and control.

OP46: DISTRIBUTION OF VIRULENCE FACTORS IN *Aeromonas* SPP. ISOLATED FROM FISH SAMPLES

S. Thenmozhi

Vivekanandha College of Arts and Sciences for Women, Tiruchengode - 05

Aeromonas spp. is a gram-negative opportunistic pathogen of animals and humans. It is associated with a wide varity of human infective syndromes both as a primary pathogen as well as an opportunistic agent in immune-compromised host. In this study fish samples were collected from local market, Tiruchengode, Tamilnadu, India. The totally 50 fish samples were collected, among these only 28 samples were found to be positive for *Aeromonas hydrophila* and *Aeromonas salmonicida*.The starch ampicillin agar were used as a selective presumptive isolation medium. The in vitro susceptibility of the *A.hydrophila* and *A.salmonicida* isolates to a variety of antibiotics revealed that higher number of isolates was sensitive to gentamycin (100%), while it was resistant to penicillin and ampicillin.The pathogenesis of *Aeromonas spp*. is multifactorial and the virulence factors plays a key role in the pathogenesis of Aeromonas

spp. Infection in fish.Although most of the active research on *Aeromonas* spp. concerns the identification of virulence factors (or) mechanisms potentially operative in human or animal infection. All the isolates are screened for the presence of virulence factors such as hemolysin, protease, lipase and Beta-lactamase were detected by using in vitro methods. These finding may help to better known about virulence characters of *Aeromonas* spp.The public health significance and the economic losses arising from infection of the fishs.

OP47: INTERACTION OF CYSTEINE PROTEASES IN *Leishmania* SPECIES

Sindhuprava Rana[2], Md. Yousuf Ansari[2], Rani Mansuri[2], **S. Jinendiran**[1], Ganesh Chandra Sahoo2, Manas Ranjan Dikhit[1], Rishikesh Kumar[2], V. Ali[2] and Pradeep Das[2]

[1]Department of Marine Biotechnology, Bharathidasan University, Tiruchirappalli – 620 024,
[2]BioMedical Informatics Center, Rajendra Memorial Research Institute of Medical Sciences (RMRIMS), Agam Kuan, Patna – 800 007, Bihar

Cysteine proteases play an important role in the infection, replication, development and metabolisms of protozoan parasites. The three-dimensional structure was predicted by using modeling and docking was performed with the available cathepsin L-like cysteine protease compounds using available programs. The best template (PDB ID: 1aimA) were used as a template, the total model energy of the model was -7271.275 kJ/mol. Validation of different models of papain family (c1) cysteine protease (LdCPb) was carried out and ramachandran plot was computed, which showed 98.9% residues in allowed regions. Cysteine protease protein docking inhibitor compounds group showed the highest binding affinity. Compounds 11 and 3 are more active on Leishmania donovani Cp with IC50 of 25 and 35µM, respectively. The hope of identifying novel drug targets and vaccine candidates against parasitic protozoan is laying on their peptides, currently. The homology or comparative modeling due to its simplicity to predict the structure of the target proteins or peptides with the help of available protein structure as temples has come as a rescue. Thus, it could be concluded that our generated experimental compounds could have potential as pharmacological tools against the visceral leishmaniasis. Considering that cysteine protease is essential for survival of Leishmania, including for virulence to the mammalian host, it may be viewed as an attractive drug target.

OP48: PRODUCTION OF NARINGINASE ENZYME FROM BACTERIA

Subasini.M and R.Dhandapani

Department of Microbiology, Periyar University, Salem - 636011.

Naringinase enzyme is one of the dibittering enzyme. This enzyme is widely used in grape fruit juices and other citrus fruit juices for making debitterness. This enzyme is also used in brewing industries. Based on the above applications the naringinase enzyme was identified as one of the important industrially product. So far the enzyme was produced in fungi, yeast and plants. The main drawback of producing this enzyme is its high cost and time consuming. In the present study naringinase enzyme producing bacteria were isolated and identified as an alternate source for fungi, yeast, and plants. Further the amount of enzyme produced by these bacteria was optimised. Naringinase enzyme producing microorganisms were isolated from humus of

waste fruit and vegetables. The enzyme producing organisms were identified by the utilisation of naringin in the culture medium. A production media will be optimised for the production of naringinase enzyme. Further the amount of enzyme produced by the bacteria was analysed quantitatively and qualitatively using UV-Spectrophotometer. The enzyme produced by these organisms were further purified using column chromatography.

OP49: ISOLATION AND CHARACTERIZATION OF AMYLASE PRODUCING *Bacillus* SPP., FROM SHRIMP CULTIVATED POND

R.Dhanasekar and R. Dhandapani

Department of Microbiology, Periyar University, Salem - 636011.

The present study was to isolate amylase and protease producing bacteria from the pond and soil samples collected from shrimp pond environment of marakkanam and Chidambaram, India. The isolation was performed by serial dilution and plating method. Total 25 bacteria were isolated from the collected pond samples. All the isolates were screened for amylolytic activity by starch agar plate and Proteolytic activity by Skim milk agar plate. 25 bacterial isolates were screened and only 4 isolates showed the amylolytic and Proteolytic activity. Among the four one isolate was selected for further study. The isolated strain was identified as *Bacillus* spp., by microscopic observation and biochemical characterization. The optimum condition of the activity of the enzyme was observed at pH 7.0, temperature 40°C and 5.5% NaCl concentration. The carbon source and nitrogen source for effective growth of the isolate was found to be starch and yeast extract respectively.

OP50: OPTIMIZATION OF MACRO-ELEMENTS FOR LIPID, TOTAL CHLOROPHYLL, BIOMASS AND BIODIESEL PRODUCTION BY MICROALGAE *Scenedesmus quadricauda* USING RESPONSE SURFACE METHODOLOGY

T. Silambarasan and R. Dhandapani

Department of Microbiology, Periyar University, Salem - 636011.

The present study deals with the production of biodiesel from the microalgae *Scenedesmus quadricauda*. The response surface method and experimental design were applied as an alternate to conventional methods for the optimization of microalgal growth medium (BBM) and different concentration of macro-elements. A box-Behnken design, with 3 axial points, 6 factorial points and 9 replicates at the center point were used to 3 factorial models for predicting and optimizing the microalgal growth, lipid, total chlorophyll, biomass and biodiesel production process. Mathematical model equations were derived by computer simulation programming with a box-Behnken model using the design. The maximum predicted value of lipid, total chlorophyll, biomass and biodiesel obtained were 218.98 mg/L, 322.80 mg/L, 14.51 g/L and 4.5 ml/L. It has been concluded that RSM approach eventually helps in bulk production of Biodiesel from *Scenedesmus quadricauda* for industrial applications.

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OP51: OCCURANCE OF METHICILLIN RESISTANT *Staphylococcus aureus* FROM UNTREATED HOSPITAL WASTE WATER

G.Vanitha

Vivekanandha College of Arts and Sciences for Women, Tiruchengode - 05

Staphylococcus aureus is an important opportunistic pathogen carried asymptomatically on the human body. Methicillin resistant *Staphylococcus aureus* is major cause of health care and community associated infections in world wide. The present study was carried out by investigate the presence of Methicillin resistant *Staphylococcus aureus* in untreated government hospital waste water. In our study about 18 different isolates were identified in untreated government hospital waste water. Among these i select *Staphylococcus aureus* only. After isolation know the antibiotic sensitivity pattern of *Staphylococcus aureus* with special reference of Methicillin resistant *Staphylococcus aureus*. Resistant colony was selected for detection of plasmid mediated drug resistance by plasmid curing and conjugates the resistant strain and sensitive strain.

OP52: ISOLATION AND CHARACTERIZATION OF EXTRACELLULAR A-AMYLASE PRODUCING MICROORGANISM FROM SHRIMP CULTURE POND

M. Vikramthithan and R. Dhandapani

Department of Microbiology, Periyar University, Salem - 636011.

The aim of the current study was to isolate extracellular amylase producing bacteria from the water samples collected from various marine shrimp culture pond in Nagapattinam district, Tamil Nadu, India. Totally 126 isolates were obtained from the samples. Only 25 isolates show amylolytic activity by starch agar plate method, among them only 4 isolates show high amount of amylolytic activity, for this study only one isolates was selected. The selected strain was undergone with these parameters such as effect of incubation period, pH, Temperature, metals and chemicals was optimized. The isolate was identified as a Bacillus sp. by microscopy and biochemical characterization.

OP53: PRODUCTION OF ARABINASE ENZYME FROM BACTERIA

N.Malathi and R.Dhandapani

Department of Microbiology, Periyar University, Salem - 636011.

Arabinase enzyme is widely used in brewing industries. In fruit juice manufacturing it is used to remove pectin in the clarification process and also maintains concentration. The enzyme is also used in core washing and pulp washing in citrus fruit industries. Based on the above applications the arabinase enzyme was identified as a industrially important product. So far the arabinase enzyme was produced from fungi and plants. The main drawback of producing this enzyme is its high cost and minimal secretion of the enzyme by the fungi. In the present study arabinase enzyme producing bacteria were identified as an alternate source for fungi and plants. Further the amount of enzyme produced by these bacteria was optimised. Arabinase enzyme producing microorganisms were isolated from humus of waste fruit and vegetables. The enzyme

producing organisms were identified by the utilisation of arabinogalactan in the culture medium. A production media will be optimised for the production of arabinase enzyme. Further the amount of enzyme produced by the bacteria was analysed quantitatively and qualitatively using UV-Spectrophotometer. The produced enzyme was purified using column chromatography.

OP54: ISOLATION OF BETA – GLUCOSIDASE (SALICILINASE) ENZYME FROM BACTERIA

S. Ramya and R. Dhandapani

Department of Microbiology, Periyar University, Salem - 636011.

Cellulose is one of the most abundant polymer found in nature. It occurs in almost pure form in cotton fiber and in combination with other materials, such as lignin and hemicelluloses, in wood, plant leaves stalks, etc... β-Glucosidase is an important component of the cellulose complex. It hydrolyzes cellobiose and short-chain cellooligosaccharides to glucose. This enzyme is mostly used in animal feed for growth supplement and digestion process. In the present study β-glucosidase enzyme producing bacteria were isolated from agricultural waste soil. From the agricultural waste soil some of the bacteria were found to possess β-glucosidase activity. These positive strains were characterized biochemically and checked for their ability to produce β-glucosidase. A production media will be optimized for the production of β-glucosidase enzyme. Further the amount of enzyme produced by the bacteria was analyzed quantitatively and qualitatively using UV-spectrophometer.the produced enzyme was purified using column chromatography.

OP55: INTENSIFIED SYNTHESIS OF SELENIUM NANOPARTICLES FROM *Streptomyces minutiscleroticus* (M10A62) AND ITS POTENTIAL TO INHIBIT THE BIO FILM FORMATION BY *Acinetobacter* SP.

S.Ramya and R.Balagurunathan

Department of Microbiology, Periyar University, Salem - 636011.

Nanobiotechnology as the name itself suggests the amalgamation of two different sectors nanotechnology and biotechnology to provoke a new escalating technology. Nanoparticle synthesis from microbes predominantly thrive under extreme condition attains much attention than conventional method due to their downside in synthesis. Actinobacteria act as a treasure reserve for secondary metabolites. Recently actinobacteria isolated from the rare extreme environment were documented as impending producer of gold and silver nanoparticles. Selenium possess unique photoelectric, semiconducting and X-ray sensing properties along with distinctive mechanical, optical, electrical, biological and chemical properties as compared with bulk materials. Totally 99 actinobacterial isolates were isolated from Magnesite site, Salem and selected for biosynthesis of selenium nanoparticle. Based on the results of visual inspection five potential isolates have ability to synthesis selenium nanoparticle extracellularly. Secondary screening of the five strain results with one strain M10A62 synthesis selenium nanoparticle with a quantity of 0.82 g/50 ml. The UV - spectral analysis of selenium nanoparticle indicated that the samples have maximum absorption at 410 nm. FT-IR spectral analysis confirms the

presence of capping protein, peptide, amine and amide groups bound to the nanoparticle. All the diffraction peaks in the XRD pattern of the Selenium nanoparticle was similar to previous literature. TEM and AFM validate the size of selenium nanoparticle ranges from 100-250 nm and spherical in shape. The energy dispersive X-ray analysis study shows strong selenium signals, which confirms the presence of selenium nanoparticle. Bio film formation by six resistant Acinetobacter strains was inhibited by selenium nanoparticle in a dose dependent manner. The production of bio film was observed early at 37oC at 24 h after inoculation on contrary at 20oC even extended time of 48 h did not exhibit inhibition as in 37oC. The anti-bio film activity of the nanoparticle increased proportionally with the raise in concentration, and the test strains reduced to 75% at a concentration of 32µg. Phonotypical characterization and SEM images confirm the potential strain showed 99% similarity with Streptomyces minutisclerotic us.

OP56: ISOLATION AND SCREENING OF Β-GLUCANASE ENZYME FROM BACTERIA

A.Velesan and R.Dhandapani

Department of Microbiology, Periyar University, Salem - 636011.

Beta glucanase is aenzyme which has high activity of beta glucanase (gumase), and moderate activity of cellulase and xylanase. Beta glucanasearewidely used in animal feed industries and agricultural products processing industries. Beta glucans create up to 60% of the cell wall of many forms. Beta-glucans are health-promoting in that they act as intestinal fiber. The presence of beta glucanase enzyme in the feed can increase the digestion of heavy cereal grains such as wheat, barley and rye. This enzyme is mostly used for growth supplement and digestion process. In the present study β-glucanase enzyme producing bacteria were isolated from agricultural waste soil. From the agricultural waste soil some of the bacteria were found to possess β-glucanase activity. These positive strains were characterized biochemically and checked for their ability to produce β-glucanase. A production media will be optimized for the production of β- glucanaseenzyme. Further the amount of enzyme produced by the bacteria was analyzed quantitatively and qualitatively using UV-spectrophometer. The produced enzyme was purified using column chromatography.

OP57: STUDIES ON ISOLATION CHARACTERISATION PURIFICATION OF BACTERIOCIN PRODUCED BY LACTIC ACID BACTERIA

Chinchu sunny and P.Palanivel

Vivekanandha College of Arts and Sciences for Women, Tiruchengode - 05

Todays consumers are increasingly aware of the importance of the maintaince of their environment ,health and nutrition .In recent years ,lactic acid bacteria recently used in Dairy products and other fermented foods has become well known as probiotics. Lactic Acid Bacteria associated by their common metabolic and physiological characteristics.which produce lactic acid as the major end product of the fermentation of carbohydrates. The bacteriocin produced by LAB are relatively heterogeneous group of ribosomally synthesized small proteins. They normally act against “closely related “bacteria but not against the producing organism.

Bacteriocins are antimicrobial proteineous compounds that are inhibitory towards sensitive strains and are produced by both Gram +ve and Gram –ve bacteria. In present study 25 samples were taken and 35 different colonies were isolated,in this 10 were producing Bacteriocin.

ENVIRONMENTAL MICROBIOLOGY

OP58: IDENTIFICATION OF SOURCE OF FAECAL POLLUTION OF TIRUMANIMUTTAR RIVER, TAMILNADU, INDIA USING MICROBIAL SOURCE TRACKING

Prabhakaran. P and P. M. Ayyasamy

Department of Microbiology, Periyar University, Salem-636011, Tamilnadu, India.

Efficient management of deteriorating water bodies can be achieved by determining the sources of faecal pollution. Resourceful techniques for discrimination of the sources of Escherichia coli in surface water have recently been developed, including the use of river water to facilitate faecal indicator surveillance, identification of sources of faecal contamination and employing relevant management practices to maintain water quality. This study was conducted to employ microbial source racking (MST) techniques for the determination of the sources of faecal pollution based on a water quality investigation of the physico-chemical characteristics and coliform count point of the Tirumanimuttar River. To accomplish this, an MST library based antibiotic resistance analysis, serotyping and the genomic tool rep-PCR techniques were applied, and the obtained results were analysed statistically. Among 135 isolates, 70 E. coli isolates present in the library and water samples collected from the river and nearby well water sources, respectively, most showed intrinsic, high or moderate resistance to antibiotics. Isolates from human and pig faecal sources were 92% homologous with the samples from the river, whereas isolates from sewage and dairy cattle showed 89% and 80% homology, respectively. These findings indicated that the Tirumanimuttar River is subjected to stress from anthropogenic activities and run–off contaminated with agricultural and human faecal contamination. The sources of faecal pollution identified in this study may facilitate the monitoring and management of the Tirumanimuttar River.

OP59: IRON OXIDE TOXICITY AND ITS BIOREMEDIATION IN AQUEOUS MEDIUM AMENDED WITH ORGANIC SUBSTRATE AND BACTERIAL ISOLATE

Baby, V. and P.M. Ayyasamy

Department of Microbiology, Periyar University, Salem - 636 011, India

Iron is one the most abundant naturally occurring element making up the earth; most of this iron is found in various forms of iron oxides. It is an essential metal and its compounds have many applications deliberately for industrial purposes like iron oxide pigments are used in coatings and as colorants in ceramics, glass, plastics, rubber also its magnetic properties frequently used to make magnets. Although generally considered nontoxic however, iron oxide compounds have been investigated for possible harmful effects to humans also cause serious environmental issues. In mining areas, iron oxide into ponds, rivers and lakes; this can

poisonous to aquatic life also cause the staining of plumbing fixtures or laundry, it give water an unpleasant appearance and taste. In atmosphere, iron oxide dust can cause breathing problems and serious potentially life-threatening allergic reactions like exacerbate asthma, allergies and sinus infections. The magnetic property of iron oxide have been linked to a variety of health problems in intestinal walls, creating a blockage that can have serious or even deadly medical repercussions. Inhalation of iron oxide fumes, can give rise to roentgenologic changes like siderosis, iron pneumoconiosis, hematite pneumoconiosis, iron pigmentation of the lung due to deposition of inhaled iron particles. So, it reflects the fact that it has been approved as an occupational hazardous material. In physical and chemical dissolution of iron oxides leads to environmental pollution, so biologically mediated mobilization process carried out to overcome these environmental problem. Hence, in the present study, attempt was made to isolate iron resistant and reducing bacteria from the areas around industries in Salem district. The reduction study was performed by using the given (JS43) bacterial isolates under the optimized condition; subsequently iron oxide reduction was carried out in the medium enriched with humic acid and AQS. Since, it is a microbial approach this method could be novel, applicable and ecofriendly to detoxify the iron contamination in soil also enhances the benefits for the human welfare.

OP60: MICROBIOLOGY OF TANNERY EFFLUENTS FROM CENTRAL TREATMENT PLANTS

M. Sakthivel and N. Hemalatha
Department of Microbiology, Periyar University, Salem - 636 011

Chromium is a heavy metal. It is called an "essential trace element" since very small amounts of chromium are necessary for human health. In contrast, hexavalent Cr (Cr (VI)) is highly toxic carcinogen and may cause death to animals and humans if ingested in large doses. Recently, concern about Cr as an environmental pollutant has been escalating due to its build up to toxic levels in the environment as a result of various industrial and agricultural activities. Most treatment plants are adopting inefficient treatment technologies involving physico-chemical and biological methods not effective to treat the contaminants to acceptable level. The use of biological remediation technologies such as microbial bioremediation and phytoremediation for the cleanup of Cr-contaminated areas has received increasing interest from researchers worldwide. At many places the tannery effluents were pooled from various tanneries to form the raw influent for a common central treatment plant. Hence for the present study the isolation of indigenous bacterial and fungal strains from pooled untreated tannery effluents from Dindugul area having high chromium tolerance is attempted which is an important step to use them for further bioremediation studies. The effluent samples were subjected to serial dilution and inoculated on to chromium screening media. The screened organisms are grown on various differential and selective media and subjected to biochemical tests for microbial identification. The bacterial colonies outnumbered fungal colonies in total count. Aerobic heterotrophic bacteria were present at a concentration of about 1.1 x 10^5 cells per ml of untreated tannery effluent which was found to be much lower when compared to the bacterial load in other polluted water like sewages suggesting the microbial toxicity of chromium in tannery effluents.

The bacterial strains mostly belonged to Bacillus and *Pseudomonas*. The fungal colonies showed high chromium tolerance when compared to bacterial colonies.

OP61: PREVALENCE OF MDR STRAINS IN THE DUMPING REGION NEAR VELLAR ESTUARY

Pingal Kumari[1], A. Divya[2], Arun Kumar. S[1] and Thirugnanasambandan Somasundaram[1]

[1]Centre of Advanced Study in Marine Biology, Faculty of Marine Sciences, Annamalai University, Parangipettai - 608502.

[2]School of Chemical and Biotechnology, Shanmugha Arts, Science, Technology and Research Academy, SASTRA University, Thajavur - 613402.

Antibiotics and their metabolites are discharged in various amounts into the environment as a result of indiscriminate use of those organic compounds in medical, veterinary, agriculture, animal husbandry and aquaculture practices. The present study revealed that the microbial community of the municipal waste has wide incidence of antibiotic resistance strains. High incidences of resistance to bacitracin, penicillin and tetracycline whereas most sensitivity to chloramphenicol were noticed from the isolated bacterial strains in this study. Most virulence factors are either found on the bacterial cell surface or secreted into their immediate environment. Secreted/Extracellular proteins are of particular importance for vaccine development because they are often immunogenic and have the potential to be recognized early in infection. In this study, different strains showed varied concentrations of extracellular protein levels with increasing concentrations of ampicillin such as50,100,200, and 300µg/100ml. In all the cases, the resistant strains yielded higher percentage of protein whereas the control strains (without ampicillin) found to produce lesser concentration of protein. It can be concluded that the concentration of secreted proteins is directly proportional to the increasing concentration of antibiotic. The higher protein content of PDS2 provides possible indication of increased production of protein like metabolites. There is thus a need to know the kind of proteins expressed by resistant strains so as to provide a basis for developing an interference/ intervention. Further work is being done to characterize the proteins and to investigate their potential for use as vaccine target through antigenicity tests.

OP62: ISOLATION AND IDENTIFICATION OF TOXIN SHOCK SYNDROME TOXIN PRODUCING *Staphylococcus aureus* FROM POTABLE WATER

S. Gajapriya

Vivekanandha College of Arts and Sciences for Women, Tiruchengode - 05

The present study were designed to identify toxic shock syndrome toxin (TSST) producing *Staphylococcus aureus* from potable water. Water is a good that must serve for the development of the whole person and every living thing ,infectious diseases caused by pathogenic bacteria ,viruses and protozoan parasites are among the most common and wide spread health risk of drinking water .people are introduced to these microorganisms through contaminated drinking water,water drops aerosols and washing or bathing .a total of 33 samples river water ,potable water ,well water,municipality water were collected from namakkal area.

Out of 33 samples 18 isolates were identified as staphylococcus aureus by using mannitol salt agar (MSA) and confirmed by biochemical test the 18 isolates of *Staphylococcus aureus* above were subsequently tested for Kirby bauer disc diffusion method .virulance character of *Staphylococcus aureus* were determined out of 18 isolates 55% of isolates were showed coagulase negative in hemolysis were performed on human blood agar out of 18,33%of isolates were produced the hemolysis activity .Amplification of TSST gene from *Staphylococcus aureus* were performed by using PCR assay. In our study concluded that among the 4 types of sample highest percentage were occur in river and municipality water.

OP63: DEVELOPMENT OF ANTIBACTERIAL WATER FILTER BY COATING ZINC OXIDE NANOPARTICLES ON FLEXIBLE POLYURETHANE FOAMS

A. Manikandan[1], R. Rajendran[1], S. Anbalagan[2], M. Sankareswaran[2], K. Hemalatha[1], M. Mary Sweety[1], P. Prabhavathi[1], M. Abirami[1] and B. Kanimozhi[1]

[1]PG& Research Department of Microbiology, PSG College of Arts and Science, Coimbatore
[2]PG & Research Department of Microbiology, Muthayammal College of Arts and Science, Rasipuram - 637408,

Nanotechnology research has gained momentum in the recent years by providing innovative solutions in the field of biomedical, materials science, optics and electronics. Nanoparticles are essentially a varied form of basic elements derived by altering their atomic and molecular properties of elements. In The present work were fabricated Zinc oxide Nanoparticles coated polyurethane foams and used it as a bacterial filter for contaminated drinking water. Flexible PU foams were soaked in Zinc oxide colloidal solutions for 10hrs, then washed and air-dried at room temperature. The Zinc oxide Nanoparticles -coated PU materials were characterized by several techniques including TEM, FE-SEM, EDS, UV-Vis, and FTIR. The TEM images showed that the size of Zinc oxide nanoparticles in colloidal solutions varies from 6 to 12nm. The FTIR, FE-SEM and ED"s data illustrated that Zinc oxide nanoparticles were stable on the PU foam and were not washed away by water. Furthermore, the microbiological tests (tube tests and flow test) were carried out on Zinc oxide -coated PU materials with the Coliforms, E. coli, and Pseudomonas aeruginosa. The obtained results showed that the bacteria were killed completely with antibacterial efficiency of 100% being observed. Our research suggests that Zinc oxide Nanoparticles polyurethane foams can be used as excellent good antibacterial water filters and would have several applications in other sectors.

OP64: ISOLATION OF BIOELECTRICITY PRODUCING BACTERIA FROM VARIOUS RESOURCES

R. Ratha, S. Saranya and V. Lavanya

Vivekanandha College of Arts and Sciences for Women, Tiruchengode - 05

Microbial fuel cell (MFC) use bacteria as biocatalyst to convert biodegradable substrates into electricity. The natural cow dung was found more sustainable as it generated open circuit voltage in the H- shaped MFC. “Exoelectrogens” that is capable of transferring electrons outside their cell. In order to produce current the cells must use the anode as electron

acceptors and not other electron acceptors such as oxygen. Microorganisms that grow in a MFC are therefore bacteria typically grow under completely anoxic condition. In our study about 27 isolates belonging to the genera *Pseudomonas ,Bacillus, Escherichia, Salmonella, Serratia, Micrococcus* were isolated from marine sediment, paper industry effluent, hydro carbonated soil. Among the 6, only *Pseudomonas, Bacillus, Escherichia, Micrococcus, Serratia, Salmonella* grew on the Iron sulphite agar medium. So they were choosen for the electricity production because only those that reduce iron can release more number of electrons which helps for the current generation. Electricity in need of the hours and various microorganisms can be used to produce more amount of current. The world today is undoubtedly facing a serious energy crisis energy demand continues to increase at an unsustainable pace. This method of electricity generation from cowdung without a net CO_2 emissions are much desired requirement for the near future.MFC have drawn increasing world- wide attention in generating electricity directly from the organic matter.

OP65: EFFECT OF HEAVY METAL ON DIAZOTROPHS

S. Jothi and P. Palanivel

Vivekanandha College of Arts and Sciences for Women, Tiruchengode - 05

Diazotrophs are bacteria that fix atmospheric nitrogen gas into a more usable form such as ammonia. Eg: *Rhizobium, Pseudomonas, Klebsiella, Bacillus*. Soil contamination with Heavy Metal is a major constraint for plant growth and for microbial density, diversity and processes includingbiological nitrogen fixation. Heavy Metals at elevated concentration are known to effect of soil microbial population and the associated activities which may directly influence the soil fertility. The concentration of toxic metals that affect the growth and survival of different microorganisms varied greatly. In the present study salts of heavy metals like Cu,Cd,Hg,Co,Zn were added in organism under laboratory conditions with different concentration (2,5,10,20,50,100,150,200µg ml1).Toxicity of heavy metal was concentration as well as time dependent. Loss of microbial diversity is evident as we move towards higher concentration of heavy metal in soil. Further experimentation is needed to understand the genetic diversity of the sensitive and metal tolerant microbial population and metal microbe interaction under natural condition in soil.

OP66: REMOVAL OF FLUORIDE IN AQUEOUS SOLUTION AND GROUND WATER USING FUNGAL BIOSORBENTS

A.Sakthi Thesai and P.M. Ayyasamy

Department of Microbiology, Periyar University, Salem - 636 011

This research is focused on the search of a biomass for the remediation of fluoride from drinking water. Adsorption of fluoride from water was carried out by batch shaking vessels and column experiments in fungal biosorption (*Aspergillus niger*) process. Influence of varying the experimental methods for removal of fluoride, such as fluoride concentration, dosages of live and dead biomass, various pretreated biomass, immobilized fungal biomass. Sorption interaction of fluoride on to fungal species obeyed the pseudo first order rate equation. Experimental data

showed good fit with the kinetics of fluoride adsorption isotherm model. The biomass was found to reduce fluoride to permissible limit 1.5 mg/L as prescribed by WHO. Increase the dosages of fungal biomass directly proportional to found fluoride removal. In batch mode experiments, the Maximum biosorption capacities for live and dead biomass at 40, 50, 60 minutes of treatment and maximum biosorption capacities for pretreated biomass at 10 to 60 minutes of treatment. In column experiments, the maximum biosorption was observed at 5 to 65 minutes of treatment. Column biosorption (live and dead biomass) experiments were applied to environmental fluoride contaminated water, the maximum fluoride adsorption was observed at 5 to 75 minutes of treatment. The fluoride concentrations were analyzed by UV-Vis Spectrophotometer.

OP67: STUDY OF AIRBORNE FUNGI AT A VEGETABLE MARKET IN SALEM-A PRELIMINARY STUDY

V.Thangamuthu, P.Sugandhi, S.Umamaheswari and D.Arvind Prasanth

Department of Microbiology, Periyar University, Salem - 636011.

The air contains various micro flora namely bacteria, fungi, pollen grains and insects. Many of these matter float in the atmosphere either as particulate or particles of biological origin. Molds are frequent contaminants of fresh vegetables. Air borne fungi are also considered as a key factor and as indicator of the level of pollution. Many investigators have studied the association of the mold and the type of allergic diseases associated and the type of spoilage caused by these fungi. The study of fungal aerospora of the market gives us the health status of the people working in such environments as well as the causative agents of vegetable and fruit spoilage. Hence this present study is attempted to study the distribution of airborne fungi in a local vegetable market environment near the railway junction of Salem district, Tamilnadu. The plates of Sabouraud dextrose agar (SDA) were prepared and sampling was done by open plate method. The sampling was done weakly twice during morning and in the evening when the market activities were high. The plates were kept open for 5-10 minutes at a few meters above the ground level (05 -1.0 meter). After the exposure time, the plates were sealed and brought back to the laboratory and incubated at 28- 30ºC for 2-4 days. After the growth of the fungal colonies, the colonies were counted and identified based on the macroscopic and microscopic features. Deutromycetes (85%) contributed highest percentage to the total air borne fungi isolated in this study. Among the various spore types, *Aspergillus niger* was the most prevalent fungal genera followed by *Aspergillus flavus*, *Aspergillus fumigatus*, *Penicillium spp*., *Cladosporium spp*., *Alternaria spp.,* and *Bipolaris spp*. High occurrences of the fungal spores were found during the evening time. Pollen grains, algal fragments, trichomes, insect parts, scales, and protozoan cyst are not concerned in this study. Further studies are needed to correlate seasonal fluctuation of fungal communities and the potential risk of contamination and health implications of the personals working in the market environment.

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OP68: BIODIVERSITY OF ENDOPHYTIC FUNGI FROM MEDICINAL PLANT

S. Rajeswari, J. Jayamathi Sofia and D. Arvind Prasanth
Department of Microbiology, Periyar University, Salem - 636 011.

During the last 20 years it has been observed that much of the wealth of microbial biodiversity with novel biochemistry and secondary metabolite production resides in the plant tissues. Endophytes are metabolically more active than their free counterparts due to their specific functions in nature and activation of various metabolic pathways to survive in the host tissues. The medicinal plant *Moringa oleifera* was traditionally known and reported to have various biological activities like anti-cancer, anti-oxidant, anti-pyretic hypocholesterolemic agent, regulation of thyroid hormone status, anti-diabetic agent, gastric ulcers and hypotensive agent. In this study an attempt has been made to determine the diversity of endophytic mycoflora in *Moringa oleifera* collected from the plains of Salem district. The leaves stem and flower materials of *Moringa oleifera* was collected and screened for endophytic fungi. The segments were surface sterilized and placed on sterile Sabouraud dextrose agar (SDA) plates. A total of 15 endophytic fungi from 72 segments were isolated and identified. The most predominant endophytic fungal species isolated was *Aspergillus spp.* (53.3%) followed by *Mycelia sterilia* (40%) and *Bipolaris spp.* (6.6%). The Colonization Frequency (CF %) and Endophytic Infection Rate (EIR%) was found to be 83.31% and 20.83% respectively. The stem segments showed a maximum repository for endophytic fungi than the leaf and flower segments. The results of this study suggest that endophytic populations of these medicinal plants must be studied in detail with an ecological perspective which may help to understand the community structure of their endophytes and warrant isolation of diverse endophytic fungi with useful bioactivities.

OP69: SCREENING FOR ARSENITE OXIDIZING BACTERIA FROM INDUSTRIAL AREAS IN RANIPET

U. Priyadharshini[1], S. Rajakumar[2] and P.M. Ayyasamy[1]
[1]Department of Microbiology, Periyar University, Salem - 636011
[2]Department of Marine Biotechnology, Bharathidasan University, Tiruchirappalli - 620024

Arsenic, toxic metalloid, is ubiquitously distributed in the environment with a crustal abundance of 0.0001%. The sources of environmental arsenic are varied and reported to be detrimental biologically as long term exposure to elevated levels of arsenic through ingestion of contaminated water or food causes many types of cancer, skin lesions, respiratory illness, cardiovascular disease, birth defects, and also death has been attributed due to its contamination. Though there are reports on arsenic contamination worldwide, West Bengal, India is also been reported as one of the severely arsenic contaminated regions. Numerous remediation techniques for removing arsenic have been applied and studied wherein these methods require large amount of chemical reagents which further add as secondary environmental pollution. Due to these apparent demerits, research focus has been diverted for developing new techniques that are cost effective and reduce the contaminant toxicity. In the present study, samples were collected from different industrial sites in Ranipet for isolating the arsenic resistant and oxidizing bacteria.

Cumulatively, 151 bacterial pure culture isolates were obtained from random soil sampling at four industrial sites in Ranipet. Out of these, on primary screening around 73 isolates showed MIC at >1000 ppm, 6 isolates at 1000 ppm and 2 isolates at 800 ppm. These were further screened for the arsenite-oxidizing bacteria using standard silver nitrate method. Among 81 isolates screened, 57 were identified to be arsenite-oxidizers and 24 isolates are arsenate-reducers. These 81 isolates were further identified up to their genus level following the traditional morphological and biochemical criteria reported in Bergey"s Manual of Systematic Bacteriology. To best of the knowledge, in contrary, this is the first report on isolating arsenic resistant bacteria from these cities which were not to be reported in the risks due to arsenic contamination. Thus, this study would through lime light for future venturing and exploring these indigenous bacteria for the application in arsenic bioremediation.

OP70: BIOGAS AND BIOMETABOLITE PRODUCTION FROM DAIRY MILL EFFLUENT: A GENERAL VIEW

R. Gowthami[1]. and P.M. Ayyasamy[2]

[1]Department of Microbiology (External), Bharathiar University, Coimbatore - 46

[2]Department of Microbiology, Periyar University, Salem - 636 011

Ddairy industry produces huge volumes of wastes such as solids and liquids. This waste poses escalating disposal and pollution problems and represents a loss of valuable biomass and nutrients. However, despite their pollution and hazard aspects, in many cases, dairy processing wastes have a good potential of converting into useful products of higher value as by-product, or even as raw material for other industries. Organic acids are examples of such valuable by-product of the fermentation of high carbohydrate containing industrial substrates. They therefore could be utilized cheaply as substrate for microorganisms producing intermediate volume high value organic acids like lactic acid, lactase enzyme, gibberellic acid, biomethane and etc. Biogas is a clean and efficient fuel. Biogas is produced when organic materials, such as cattle dung, are digested in the absence of air, in 'Biogas Plant'. Hence, this study is aimed to provide clean gaseous fuel mainly for cooking purposes and also for other applications for reducing use of LPG and other conventional fuels, using dairy mill waste. Lactic acid from dairy product, is used as a humectant, or moisturizer, in some cosmetics, in making pickles and sauerkraut, and as a mordant, a chemical that helps fabrics accept dyes, in textiles. Lactase enzyme is commercially used as capsules, which acts as a supplement for people who have trouble digesting milk and other dairy products (lactose intolerance). It is estimated that 70% of the world population and 30-50% of Indians are lactose intolerant. Gibberellic acid is a growth regulator found in plants. It is used in commercial agriculture to improve plant development, stimulate flowering and increase fruiting. Hence by using dairy mill effluent as a raw material and basal medium along with microbial consortium, the essential biometabolites, lactic acid, lactase enzyme, gibberellic acid and bioenergy can be produced at low cost.

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POSTER PRESENTATION

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PP1: HOST VIRAL GENETICS OF CERVICAL CARCINOMA

Thirumalairaj. J[1] and K. NatarajaSeenivasan[2]

[1]Department of Microbiology, Periyar University, Salem- 636 011

[2]Department of Microbiology, Bharathidasan University, Trichy-620 024

Although cervical cancer is one of the leading causes of cancer deaths among women worldwide, it is not associated with hereditary cancer. More than 98% of them were associated with Human papillomavirus (HPV) infection undoubtedly the major etiologic factor in HPV. However infection with HPV is not sufficient for the development cervical cancer other genetic factors also plays an important role. In this paper we present the molecular association of Human papillomavirus infection, somatic genetic alterations concerning the genes p53, pRb, Notch1, hTer, PDZ and Tuberin proteins. In addition to these factors susceptibility associated with HLA haplotypes and role of fragile sites were also discussed. Other than HPV infection other factors, either environmental or genetic factors contribute to the progression of cervical cancer.

PP2: ZINC AS AN ANTIMICROBIAL AGENT AGAINST BACTERIA

Neethu Asokan, K.M. Jiji, A. Revathi, M. Bharathi, S. Divya, S.M. Saranya,
R. Thamaraiselvi, and S. Mithenabee

Department of Microbiology, Periyar University, Salem – 636 011.

Microbial growth and antimicrobial killing of the bacteria were both found to have diminished in abscesses caused by bacteria. *Streptococcus pneumonia* is found to be responsible for more than one million deaths, mostly killing children, and then the elderly and vulnerable people by causing pneumonia, meningitis, and other serious, fatal infectious diseases. It was postulated that zinc depletion in abbesses can be responsible for these effects. In abscesses fluid supernatants, the growth of bacteria without antibiotic and its killing were enhanced by the addition of zinc. Through the zinc binding effects inhibited microbial growth within an abscess. Researchers have found that zinc can starve one of the world"s most deadly infectious microbe "*Streptococcus pneumoniae"* by preventing the uptake of essential metal, manganese which is required in its essential pathway. This has led to the scope and idea of designing an antibacterial agent to fight against *Streptococcus pneumoniae.*

PP3: WHIPPLE'S DISEASE Sarranya

dhevi. D. and R. Balagurunathan

Department of Microbiology, Periyar University, Salem - 636 011.

Whipple's disease is a chronic multi systemic disease. The infection is very rare and the causative bacterium like *Tropheryma whipplei* is ubiquitously present in the environment. The disease is common in farmers and those exposed to soil and animals. It enters through respiratory track and the symptoms are arthropathy, weight loss, abdominal pain, diarrhoea, joint pains but also systemic and neurological manifestations may occur. The small intestinal mucosa is always affected with lesions that are specific to this disease. The diagnosis of Whipple"s disease is not easy and depends on a combination of clinical features like the

characteristic histopathological findings, presence of pathogenomonic PAS positive macrophages and the 16S ribosomal RNA of *Tropheryma whipplei*. New tools such as monoclonal antibodies and serology could also be developed to improve the diagnosis. Whipple's disease can usually be cured with long-term antibiotic therapy. If the disease untreated, it leads to fatal condition. Whipple's disease should be treated with doxycycline with hydroxychloro quine for 12 to 18 months and penicillin, ampicilin, co-trimaxazole for one to two years. Sulfonamides (sulfadiazine or sulfamethoxazole) may be added for treatment of neurological symptoms. Currently, there is no known way to prevent Whipple's disease.

PP4: ANTIMALARIAL & LEISHMANIASIS ACTIVITY OF SELECTED ACTINOBACTERIAL BIOACTIVE COMPOUNDS

Sivarajan and R. Balagurunathan

Department of Microbiology, Periyar University, Salem - 636 011.

Malaria (*Plasmodium spp)* and Leishmaniasis (*Leishmania spp*) are vector born diseases caused by Protozoan parasite. Plasmodium having four different species such as *P.falciparum, P.vivax, P. ovale, P.malaria and Leishmania having three different species* such as *L.donovani, L.major, L.tropica*. There are estimated 500 million new cases of malaria particularly more than 1 million cases leads to death and 12 million cases suffered Leishmaniasis and 50,000 cases leads to death each year. Actinobacteria are aerobic gram positive bacteria with high G+C (guanine+cytosine) content.Actinobacteria produced bioactive metabolites, 60% of new antibiotic were isolated from Actinobacteria. Approximately 33500 number of bioactive microbial compounds were reported .The secondary metabolites of actinobacteria poses different kinds of activity such as antibiotic,anticancer and antiparasitic activity etc.In the present study Antimalarial and Antileishmanial compounds from selected Actinobacteria were discussed.

PP5: LOOK YOUR FOOT IF U HAS DIABETICS…..

Sugandhi. P and D. Arvind Prasanth

Department of Microbiology, Periyar University, Salem - 636011

Type 2 Diabetes is one of the various lifestyle diseases which have gripped the youth of today, tightly and fiercely, in their long, jagged tentacles. Patient with Type 2 diabetes mellitus (T2DM) had known to have an increased risk of micro vascular coronary heart disease, nephropathy, cardiovascular disease and diabetic foot ulcerations. According to the World Health Organization about 15% of diabetic patients developing the foot ulcer are in need of medical care. Diabetic foot (DF) infections are one of the major causes of social and economic problem and the long term complications which can result in gangrene and lower extremity amputation. Diabetic foot (DF) infections are serious complication in the western world and even in India. In 84% of cases, amputation is the final step in the treatment of a non-healing foot ulcer. The review presented here deals with the clinical complications associated with diabetic foot infections. The microbiology of diabetic foot wound is complex. The infection often starts locally with an ulcer affecting immediate surrounding skin with a purulent discharge and erythema. Common microbes such as *Staphylococcus sp., Citrobacter sp., Escherichia coli, Pseudomonas sp., Acinetobacter* and *Serratia sp* were often cultured from such diabetic wound.

Gram negative anaerobes such as *Bacteroides fragilis, Prevotella spp., Fusobacterium spp,* and *Veillonella spp*. *Eubacterium, Propionibacterium spp.* and *Actinomyces spp.* were very occasionally isolated from clinical specimens of Diabetic foot infections. Till now, the incidence of Multi drug resistant (MDR) organism"s namely Methicillin Resistant *Staphylococcus aureus* (MRSA) and Extended Spectrum Beta Lactamase (ESBL) producing gram negative bacteria have posed a major challenge for the clinician dealing with this type of infections. In order to reduce the amputation rate, it is very essential to prevent the foot ulcer formation and devise certain methods to effectively tackle the resistance organisms in the treatment of these infections.

PP6: EPIDEMIOLOGY AND CLINICAL FEATURES OF HUMAN CORONAVIRUS

V. Harish, M. Arul, R. Gopi and A. Murugan

Department of Microbiology, Periyar University, Salem - 636 011

Human coronaviruses (HCoV) were initially identified as major causes of acute respiratory tract disease in the 1960's. The epidemiology of two HCoV, OC43 and 229E, was established using only serological methods, due to difficulty culturing the viruses. Three new HCoV have been described in the last three years severe acute respiratory syndrome coronavirus (SARS-CoV), human coronavirus Netherlands (HCoV-NL) and human coronavirus Hong Kong (CoV-HKU1). Each of these new viruses has been described in association with lower respiratory tract illness (LRI). The discovery of these viruses has renewed interest into the previously known HCoV OC43 and 229E which were known to cause upper respiratory tract illness (URI). HCoV OC43 and 229E have also been associated with LRI like the newly discovered coronaviruses. However, there are no published large-scale epidemiologic studies of OC43 and 229E using highly sensitive molecular diagnostic methods. The objectives of this study are to define the prevalence and clinical illnesses associated with the new human coronavirus HCoV-NL and the prototypic HCoV, OC43 and 229E, over a 20-year period in a cohort of over 2,000 previously healthy outpatient children. We also will determine the genetic variability of these viruses by amplifying and sequencing the HCoV spike protein gene. The Vanderbilt Vaccine Clinic (WC) clinical database and sample archive provide us with the tools to accomplish these goals. The WC provided comprehensive medical care to a large cohort of outpatient children who routinely had surveillance cultures of respiratory secretions and serum samples obtained, thus thousands of nasal wash and serum specimens are available for study, along with robust, prospectively collected clinical data. This provides a unique opportunity to investigate the importance of emerging human pathogens. Our preliminary data using samples from the WC indicate that coronaviruses are a significant cause of respiratory tract infection in children with a spectrum of illness and morbidity.

PP7: THE ROLE OF BIOINFORMATICS IN GENOMIC MEDICINE

H. Irsath, and S. Prabu

Department of Microbiology, Periyar University, Salem - 636 011

For more than a century vast progress has been made in genetics and molecular biology. During the last decade new high-throughput experimental techniques have rapidly emerged. The automation of DNA sequencing has set the stage for the Human Genome Project in 1990, which has led to genomics (the branch of genetics that studies organisms in terms of their full DNA

sequences) and a range of related disciplines such as transcriptomics (the study of the complete gene expression state), proteomics (the study of the full set of proteins encoded by a genome), and metabolomics (the study of comprehensive metabolite profiles). Genomics has greatly accelerated fundamental research in molecular biology as it enables the measurement of molecular processes globally and from different points of view. This led to a range of applications in the biomedical sector and increasingly affects patient.

PP8: FRUIT AND VEGETABLE PEELS – NEWER SOURCE OF ANTIBIOTICS

A. Jeevitha, K. Vinothini and A. Murugan

Department of Microbiology, Periyar University, Salem – 636 011.

Infectious diseases are leading cause of death worldwide due to multidrug resistant strains of bacteria. Natural products provide unlimited opportunities for new drug leads because of the unmatched availability of chemical diversity. Because of increasing threat of infectious diseases, the need of the hour is to find natural agents with novel mechanism of action. Fruit and vegetable peels are thrown into the environment as agro waste which can be utilized as a source of antimicrobes. The present approach will be economic, eco friendly and reduce pollution. This research over-view will definitely open, scope for future utilization of the waste products for various other therapeutic purposes.

PP9: ADVANCES IN THE RAPID DIAGNOSIS OF TYPHOID M.

Santhakumar , A. Manikandan, S.Thiyagarajan and C.Selvanathan

Department of Microbiology, Periyar University, Salem - 636 011

Typhoid is a common worldwide illness, caused by the ingestion of food or water contaminated with bacterium *Salmonella enterica serovar typhi*. The bacteria cross the intestinal wall and phagocytized by macrophages. Then the bacterium is degraded in the vacuole of macrophage and releases the endotoxin that induces the macrophage to produce Interluenkin-1 (IL-1). This IL-1 travel to hypothalamus through blood stream and produce prostaglandin in turn it reset the body temperature. This syndrome associated with enteric fevers are produced only by a few of the *Salmonella typhi* most important *Salmonella paratyphi* A, B,C . The term "enteric fever" is a collective term that refers to typhoid and paratyphoid. Widal test is an old serologic assay for detecting IgM and IgG antibodies to the O and H antigens of *Salmonella*. The test is unreliable, but is widely used in developing countries because of its low cost. Recent Advances in rapid diagnostic test (Tubex TF, IDL Biotech, Bromma, Sweden) Typhidot PCR amplification for the detection of pathogens in biological material is generally considered a rapid and informative diagnostic technique.

PP10: ESCHERICHIA COLI O157:H7 INFECTION IN HUMANS

M. Sangeetha, M. Nanthinii and D. Arvind Prasanth

Department of Microbiology, Periyar University, Salem - 636 011

To review the clinical relevance of *Escherichia coli* O157:H7 infection, including the epidemiology of the infection and its clinical presentations, pathogenesis, microbiology,

diagnosis, treatment, and prevention. The data were abstracted without judgments about study design. Data quality and validity were assessed by independent author reviews. DATA SYNTHESIS: Infection with *E. coli* O157:H7 presents with a wide spectrum of clinical manifestations, including asymptomatic carriage, nonbloody diarrhea, hemorrhagic colitis, the hemolytic-uremic syndrome, and thrombotic thrombocytopenic purpura. Not only is *E. coli* O157:H7 an important agent for hemorrhagic colitis, it is also one of the leading causes of bacterial diarrhea. Patients at extremes of age have an increased risk for infection and associated complications. Transmission of *E. coli* O157:H7 is primarily food-borne. Undercooked meat is the most common culprit, and secondary person-to-person spread is also important. The organism produces at least two Shiga-like toxins that differ antigenically, physicochemically, immunologically, and in their biological effects. These toxins are thought to have direct pathogenic significance in *E. coli* O157:H7 infection. This infection is usually diagnosed from a positive stool culture, from the presence of Shiga-like toxins, or both. Timely collection (within 7 days of illness onset) of a stool sample for culture is imperative for a high recovery rate. Treatment is primarily supportive and includes the management of complications as necessary. Antibiotic therapy has not been proved beneficial. Important public health measures include educating the public on the danger of eating undercooked meat, increasing physician awareness of *E. coli* O157:H7 infection, and mandating case reporting.

PP11: STRUCTURE BASED-LIGAND DESIGN: MOST IMPORTANT PROMISING COMPUTER BASED METHOD FOR ANTIPROTOZOAN DRUG DISCOVERY

Pankaj kumar sahu, Iniyan shan, Hitanshu Das and Vaisakh. M.D.

Department of Biotechnology, Aarupadai Veedu Institute of Technology, Vinayaka Missions University, Rajiv Gandhi Salai Paiyanoor – 603104, Kanchipuram

There are several health problems exist now-a-days, which are mostly caused by protozoan parasites. But recent trends in genomic science, molecular and structural biology and computational biology provide an useful impact against most of the protozoan infection. Current status of structure based approaches exhibits a promising impact on discovery of ant protozoan drug. "Pharmacophore" is the term coined by Paul Ehrlich to explain about the molecular structure and chemical interaction properties of a compound which are responsible for pharmological response. For identification and characterization of those compounds requires the manufacturing of a specific dye which has a remarkable chemical impact on the compound. Sometimes these type of investigation with dyes extends to arsenical compound which produces Salvarsan, the first chemotherapeutic agent for the treatment of bacterial infection.The same mechanism can be implemented on the discovery of antiprotozoan drug development. Most of the parasite such as Plasmodium, Leishmania and T.cruzi shows remarkable variability and antigenic variation in their membrane bound surface protein which prolongs, parasite circulation in blood and helps in degradation of immune system. For major protozoan diseases like malaria, only few acceptable drugs are available. The current treatment for these type diseases due to high toxicity high cost and poor efficiency. Moreover, increasing of drug resistance of the inactivity of the drug. All these factors initiates the need of new drugs. In this regard, investment on antiprotozoan vaccine development will gain scant reward.

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PP12: PRIMARY AMOEBIC MENINGOENCEPHALITIS CAUSED BY BRAIN EATING AMOEBA (*Naegleria fowleri*)

M. Rajeswari and P.M. Ayyasamy
Department of Microbiology, Periyar University, Salem - 636011

Amoebas are single-celled organisms especially *Naegleria fowleri* is a Brain-eating amoeba which discovered in 1965. It is an only species that infects human beings. It commonly found in warm freshwater (for example, lakes, rivers, and hot springs), soil and it grows best at higher temperatures up to 115°F (46°C) and it can survive only short periods for this condition. This typically occurs when people go swimming or diving in warm freshwater places, like lakes and rivers. It causes the disease named as primary amoebic meningoencephalitis (PAM). In this disease the amoeba enters through the nasal route and affects cribriform plate, olfactory nerve and finally where it destroys the brain tissue and it causes the death within 1 to 12 days after the starting of symptoms. The initial symptoms include changes in taste and smell, headache, fever, nausea, vomiting, and stiff neck. Secondary symptoms include confusion, hallucinations, lack of attention, ataxia, and seizures. The risk of Naegleria fowleri infection is very low. Presence of *Naegleria* can be confirmed by flagellation test. There is no vaccine to protect against *Naegleria fowleri* infection and efforts are being made in vaccine research.

PP13: APPLICATION OF NANOMEDICINE TO CURE HUMAN INFECTIOUS DISEASES: AN OVERVIEW

Tamthingla Shatsang, R.Gaithuilung and P. Thangavel
Department of Environmental Science, Periyar University, Salem - 636 011

Nanotechnology has gained importance in medicine and is referred to as nanomedicine. Various tools of nanomaterials have been investigated for their application in imaging, diagnosis, therapy and treatment. Nanoparticles can be used in medicine for cancer treatment, infectious diseases, immunization purposes and diagnostic procedures with new imaging sensors and agents. Nanotube drug delivery is providing for cancer therapy with high treatment efficacy and minimum side effects. There is an increasing use of nanoparticles as carrier system for chemotherapeutic drugs as their ability of specifically target cancer cells and reduces systemic toxicity. Further, nanoparticles can be used to create antimicrobial agents, vaccine adjuvants to target different microbes such as HIV, Salmonella, tuberculosis etc. Nanotechnology applied to the dermatology (nanodermatology) is one of the most advanced fields in medicine. Administration through the oral route effects gastrointestinal system and intra-dermal injection can lead to dermatological problems since the skin being the first point of contact for whole host of nanomaterials. Gold nanoparticles are used to interact with the human dermal fibroblasts where they penetrate the plasma membrane and accumulate in large vacuoles. They are used in non-invasive nanoimaging of high resolution dermoscopy, microscopy, spectroscopy and therapeutic modalities. Other application includes the use of emollients (moisturizing cream), sunscreens, cosmetics, vaccination etc. Silver nanoparticles have potential antimicrobial activities towards many pathogenic microbes. Chronic exposure to silver cause adverse effects such as permanent bluish-grey discoloration of skin (argyria) and eyes

(argyrosis). The application of different nanomaterials used for therapeutic purposes to cure various human infectious diseases also discussed.

PP14: INDIA: ENDURING TASK OF INFECTIOUS DISEASES

Languluri Reddenna, Donthu Venu Gopal, Sheik Ayub Basha

Pharm-D, Department of Pharmacy Practice, Rajiv Gandhi Institute of Medical Sciences, Kadapa, Andhra Pradesh - 516003

In India, the array and problem of infectious diseases are massive.Even though the burden of infectious diseases has reduced as a result of increasing use of vaccines and antimicrobials in the past 60 years, they still subsidize about 30% of the disease problem in India.Tuberculosis, malaria, filariasis, visceral leishmaniasis, leprosy, HIV infection, and childhood cluster of vaccine preventable diseases are given importance for control through centrally managed vertical programmes.Scarce containment of the vector has resulted in recurrent outbreaks of dengue fever and re-emergence of Chikungunya virus disease. Additional infectious diseases caused by faecally transmitted pathogens (enteric fevers, cholera, hepatitis A and E viruses) and zoonoses (rabies, leptospirosis, anthrax) are not in the manner of being systematically controlled.India needs to reconsideration and review its health policy to widen the plan of disease control. A complete review and reform of the health system is desirable urgently to safeguard equity and quality in health care.For an official cadre of public health personnel at district, state, and national levels, reformation of the system and acceptable training programmes will be essential to control infectious diseases.

PP15: CURRENT STATUS OF ALLERGIC FUNGAL SINUSITIS

K. Muniyaraja, S. Vairamuthu, M. Sivakumar and C. Nirmal

Department of Microbiology, Periyar Unviersity, Salem - 636011.

The fungal are evolutionary intermediates bridging plants and microorganisms. They live as saprophytes or parasites or symbionts. The world health organization"s reported fungi, 15 lakhs were estimated, 8000 were described and 15000 were deposited. Fungal causes about 30000 diseases in agricultural plants. They cause the enormous number of human diseases. Allergic fungal sinusitis (afs) is a common type of fungal infection in the sinus. There are four types of sinus infection, subacute sinus infection, chronic, infectious and non-infectious sinusitis. The patients with afs may have allergies nasal polyps,asthma,thick funal debris,sticky mucus etc,. We have attempted to study the different types of diagnosis, treatment and complication of sinus infection.

PP16: NANOTECHNOLOGY IN MEDICINE

M. Dhivya, B. Yuvasri, C. Rajalakshmi, P. Narmadha, P. Agalya, P. Namdhini, and J. Pazhaniammal

Department of Microbiology, Periyar University, Salem - 636 011.

Nanotechnology, the technology of manufacturing, helps economically to build a broad range of complex molecular machines. Nanotech has helped to evolve and create many new

materials and devices with dimensions with at least one dimension sized from 1-100 nanometres, with vast range of useful applications in the field of medicine and others like electronics, biomaterials and energy production. The major culprit for disease and ill health is the damages caused at the molecular and cellular level. Many new possibilities have come into account in relation to use of nanotechnology in medicines. It deal with applications of nanoparticles and also involves nano-robots to make repairs at the cellular levels. On the other hand, nanotechnology raises many of the same issues as any new technology, including concerns about the toxicity and environmental impact of nanomaterials.

PP17: SECRETOMICS: A NEW INSIGHT INTO DERMATOPHYTE PATHOGENESIS

S. Umamaheswari and D. Arvind Prasanth

Department of Microbiology, Periyar University, Salem - 636 011

Globally, there is an urgent need for approaches that can efficiently, precisely and integrative study structural and functional genomics and proteomics of microbial infections (infectomics). Two major global approaches, genomics and proteomics, have been used to study microbial pathogenesis. Dermatophytosis, an infectious disease caused by a group of keratinophilic fungi, was selected to serve as a model organism for elucidation of general pathogenicity mechanisms. Dermatophytes secrete a large number of proteolytic enzymes from different protease families, numerous proteins of carbohydrate and lipid metabolism as well as functionally uncharacterized proteins. There are three different approaches for secretome analysis viz., Genome sequence analysis, Proteomics approaches and Bioinformatics approach. Genome sequence analysis is based on transcript profiling and computational analysis whereas gel-based proteomic analysis uses one, two-dimensional gel electrophoresis (1, 2-DE), SDS-PAGE, contour-clamped homogeneous electric field (CHEF) gel electrophoresis and Pulse-field gel electrophoresis (PFGE). Gel-free proteomic analysis uses several steps of capillary chromatography, and finally analyze by tandem MS (MS/MS) or matrix-assisted laser desorption ionization (MALDI). With the generation of large-scale expressed sequence tag (EST) and genomic data, secretome analysis can be advantageously carried out using bioinformatics analysis systems. Although secretome analysis is a promising area of research providing insights into dermatophyte pathogenesis, work remains to be done in generating secretome data for several species of these infectious fungi, which will provide us with a working knowledge of host-pathogen interactions and the immune evasion strategies adopted by dermatophytes and in turn guide in the development of therapeutics or vaccines.

PP18: INFECTOMICS IN THE DISCOVERY AND DEVELOPMENT OF NEW ANTIMICROBIAL AGENTS

C. Sudhakar and C. Prabhakaran

Department of Microbiology, Periyar University, Salem - 636 011

Infectious diseases are one of the leading causes of death in the world. This major medical concern is due to the continual emergence of new infectious diseases and reemergence of old pathogens, together with an increasing number of pathogens resistant to antimicrobial drugs. The generation of new anti-infective agents for resolving these medical problems has

emerged as an urgent issue in modern medicine. The availability of genome sequences, and the development of various high-throughput techniques and computational tools offer holistic and integrative strategies for dissecting the interplay between microbial pathogens and their hosts (infectomics). Both microbial and host signatures of infectomes, which mirror the interplay between pathogens and their hosts, provide invaluable fountains in the search for novel antimicrobial therapies. There are several major issues in the discovery and development of new drugs, from target discovery and validation to animal models and clinical trials. However, infectomic approaches integrating genomics, proteomics and glycomics will become increasingly important. Essential Therapeutics Inc. has successfully used functional genomics methods to identify several hundred antimicrobial targets in representative bacterial, fungal and viral pathogens. Recent advances in chemical genomics and proteomics have revolutionized drug discovery research by allowing the parallel processing of multiple genomic targets against large numbers of diverse compounds. The identification of small-molecule modulators of biological functions that are usually executed by large molecules (DNAs, RNAs, proteins and polysaccharides), and the process of transforming these into high-content lead series, are key activities in modern drug discovery.

PP19: INFECTOMICS: GENOMICS AND PROTEOMICS OF MICROBIAL INFECTIONS

G. Subramani and R. Gopi

Department of Microbiology, Periyar University, Salem - 636 011

The completion of genomic sequences is the greatest triumph of molecular reductionism since the discovery of the DNA double helix in 1953. However, the utility of reductionism is becoming limited and holistic approaches, including theories and techniques, are desperately needed in the postgenomic era. In the field of infectious diseases there is an urgent need for global approaches that can efficiently, precisely and integratively study structural and functional genomics and proteomics of microbial infections (infectomics). The combination of new (e.g. DNA and protein microarrays) and traditional approaches (e.g. cloning, PCR, gene knockout and knock in, and antisense) will help overcome the challenges we are facing today. We assume that the global phenotypic changes (infectomes) in microbes and their host during infections are encoded by the genomes of microbial pathogens and their hosts, expressed in certain environmental conditions devoted to specific microbe-host interactions. Global drug responses (pharmacomes) in microbes and their host can be detected by genomic and proteomic approaches. Genome-wide approaches to genotyping and phenotyping or expression profiling will eventually lead to global dissection of microbial pathogenesis, efficient and rapid diagnosis of infectious diseases, and the development of novel strategies to control infections. The key fundamental issue of infectious diseases is how to globally and integratively understand the interactions between microbial pathogens and their hosts by using infectomics. In this review, we focus on the events that are considered important in infectomics.

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PP20: PATHOGENOMICS OF BACTERIA CAUSING INFECTIOUS DISEASES IN FISH

S. Kamatchi and R. Gopipriya
Department of Microbiology, Periyar University, Salem - 636011

Fish living in the wild as well as reared in the aquaculture facilities are susceptible to infectious diseases caused by a phylogenetically diverse collection of bacterial pathogens. The common fish pathogenic bacteria species belong to the genera *Vibrio, Aeromonas, Flavobacterium, Yersinia, Edwardsiella, Streptococcus, Lactococcus, Renibacterium,* and *Mycobacterium*. Fish are always bathed in a continuous medium of water, and fish disease treatment is essentially a population medicine. Control and treatment options using vaccines and drugs are inadequate, inefficient, or impracticable. The classical approach in studying fish bacterial pathogens has been looking at individual or few virulence factors. Recently, genome sequencing of a number of bacterial fish pathogens has tremendously increased the understanding of the biology, host adaptation, and virulence factors of these important pathogens. The genome sequencing has uncovered several complex adaptive evolutionary strategies mediated by horizontal gene transfer, insertion sequence elements, mutations and prophage sequences operating in fish pathogens and also the genomes evolved from generalist environmental strains to highly virulent obligatory pathogens. In addition, the comparative genomics has allowed the identification of unique pathogen-specific gene clusters. The current advances in functional genomics, structural genomics and bioinformatics have contributed to extract the useful biological information from the vast genomic data and new gene sequences discovered in the genomes will be the major task of genome biologists in the coming years.

PP21: CONVERSION OF FISH WASTES INTO LIQUID FERTILIZER BY USING MICROBES FOR SUSTAINABLE -ORGANIC AGRICULTURE

E. Nandhini, S. Raja, K. Logankumar, M. Lekshmanaswamy and P. Abirami
Kongunadu arts and science college, Coimbatore.

Organic farming system which primarily aimed at cultivating the land and raising crops in such a way, as to keep the soil alive and in good health by use of and other biological materials like fish wastes along with beneficial microbes (biofertilizers) to release nutrients to crops for increased sustainable production in an eco friendly pollution free environment. Fermenting microbes breakdown organic matter, thereby releasing complex compounds such as amino acids for utilization by plants. A mixture of beneficial microorganisms is used to enhance productivity of conventional organic farming. These microbes are known as Effective Microorganisms (EM). Effective microbes – *Brevibacillus agri, Bacillus cereus*, *Bacillus licheniformis*, *Brevibacillus parabrevis*- Potential fish waste degrading bacteria. Microbial function in this bio-fertilizer degrades the wastes and converts into manure suitable for farming as they cause mineralization by their metabolic activity and so plants can uptake minerals effortlessly. A significant additional benefit of fish as a fertilizer is the dramatic stimulation to the soils beneficial microorganisms such as bacteria and fungi which consume, digest and release the abundant nutrients in the fish when it is applied to the soil. This fertilizer helps to getting back to basics and getting away from the havoc chemicals can wreak on our health and our environment. To stabilize agricultural production but also to increase it further in

sustainable manner. This fish wastes is a complete fertilizer as it contains all the essential minerals needed for plant growth. Compost can also be used and is excellent for disease prevention and general plant health.

PP22: PLANT GENOMICS AND PROTEOMICS

T. Abinaya, D. Haritha, M. Indhumathi and N. Swaminathan
Department of Biotechnology, Aarupadai Veedu Institute of Technology, Vinayaka Missions University, Rajiv Gandhi Salai, Paiyanoor, Kanchipuram - 603604

Genomics studies focuses on the genomic information and function of an organism. The genomics approaches to plant biology will result in an enhanced knowledge of gene structure, function and variability in plants. *Arabidopsis thaliana* (a dicot plant) was the first plant chosen for genome sequencing as it had one of the smallest C values known for angiosperms. Rice was the second genome sequenced and was the first monocot chosen as it had the smallest C value among the world"s major cereal crops. A detailed characterization of a more and more plant genomes will be important in developing an understanding of the functional and evolutionary constraints on genome size in plants. The application of plant genomics and proteomics will also lead to new methods of improving crop production and pathogen resistance which are necessary to meet the challenge of sustaining food supply in the future.

PP23: NECROTIZING FASCIITIS

T. Sarupriya and P.M. Ayyasamy
Department of Microbiology, Periyar University, Salem - 636011

Necrotizing fasciitis is a rare but very severe type of bacterial infection that primarily involves the fascia and subcutaneous tissue. It can affect all part of body and destroy the muscle, skin and underlying tissue. The most common causative organism is Streptococcus pyogenes, which is sometimes called flesh eating bacteria. Necrotizing soft tissue infection develops when the bacteria enters the body, usually through a minor cut or scrape. The bacterium begins to grow and release harmful substance (toxins) that kill tissue and affect blood clot to the area. As the tissue dies, the bacterium enters the blood and rapidly spread throughout the body. It also called as β-hemolytic streptococcal gangrene, meleney ulcer, acute dermal gangrene, hospital gangrene and necrotizing cellulitis. Some cofactors like diabetes mellitus, hypertension, chronic renal insufficiency, alcoholism, immune-suppression, heart, lungs or liver disease and obesity may increase the risk. In early stage patients usually present with the pain, swelling, fever, tenderness and erythema are common signs. In advanced stage the person having excessive swelling, loosened skin, subcutaneous tissue and yellow-green necrotic fluid appearance. It diagnosed by using CT scan, Blood test, skin tissue biopsy and early treatment with adequate antibiotics with or without surgical intervention are vital because of high mortality. Recent investigation have suggested that patients taking painkillers of the type known as 'Non-steroidal Anti-inflammatory Drugs'(NSAIDs) may be slightly more risk.

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PP24: GENE THERAPY FOR INFECTIOUS DISEASES

G. Kaviyarasan and P.M. Ayyasamy
Department of Microbiology, Periyar University, Salem - 636011

Infection is one of the leading causes of human mortality and morbidity. Infectious diseases are caused by pathogenic microorganisms, such as bacteria, viruses, parasites or fungi; the diseases can be spread, directly or indirectly, from one person to another. Many infectious diseases, such as measles and chickenpox, can be prevented by vaccines. Many diseases are not prevented by vaccines or medicines but Gene therapy can be considered a method of drug delivery for these diseases. Gene therapy for infectious diseases requires the introduction of genes designed to specifically block or inhibit the gene expression or function of gene products, such that the replication of the infectious agent is blocked or limited. Gene therapy is a new approach to treating medical conditions that uses genes instead of drugs. The most common form of gene therapy involves inserting a working gene into the cells of a patient in order to treat or to try to prevent the cells from dying. Gene therapy holds considerable potential for the treatment of both hereditary genetic disorders and infectious diseases. Gene therapy is being investigated as an alternative treatment for a wide range of infectious diseases that are not amenable to standard clinical management.

PP25: APPLICATION OF BIOPOLYMERS IN MEDICINAL PURPOSES: A REVIEW

G. Devmanjuri Devi, R. Santhiya, K. Sivaraj and P. Thangavel
Department of Environmental Science, Periyar University, Salem - 636 011

Polyhydroxyalkanoates (PHAs) are intracellular microbial thermoplastics which are widely produced by bacteria existed in the terrestrial environment. The easily biodegradable PHAs can be produced commercially by fermentation of microorganisms in the presence of an inexpensive carbon sources. Due to biocompatibility in nature, they cannot cause severe immune reactions when introduced to soft tissues or blood of a host organism during medical applications. Typically, PHA polymers are degraded by the action of non-specific lipases and esterases in nature. The sutures of polyhydroxybutyrate (PHB) and its compounds were shown to be able to facilitate healing of muscle-facial wounds. Bioactive compound delivery by PHA matrixes will continue to generate interest, as PHA drug delivery systems offer unique methods by which to control release. The various applications of PHA in the medical industry are discussed.

PP26: ISOLATION OF *Salmonella* SPP FROM LIZARD FAECES

V. Vijayashree, R. Sindhumathia and V. Lavanya
Vivekanandha College of Arts and Sciences for Women, Tiruchengode - 05

The word "zoonosis" was introduced by Rudolf Virchow in 1980 that collectively define the diseases shared in nature by animals and man. In 1959, WHO defined zoonosis as, "those diseases and infections which are naturally transmitted between vertebrate animals and man". Today man is exposed directly or indirectly to the dreadful risk of more than 200 zoonosis diseases. Many infectious diseases in human can be acquired through contact with pet

animals, zoo animals and house hold animals like flies and lizard"s, reptiles themselves are susceptible to a variety of gram positive and gram negative organisms present. The transmission of zoonosis in reptile is from two major routes: the faecal oral route or the tactile oral route. Salmonella is naturally occurring bacteria found in reptiles and it is one of the greatest health problems of concern. Salmonella in reptiles was first isolated in snakes in 1994 and from turtles and lizards in 1946. Salmonella has been reported with in dried reptile faeces from cages 6 months after removal of the reptile. Salmonella sop are a leading cause of human infectious diseases world-wide and pose a serious health concern. While we have an improving understanding of pathogenesis and the host pathogen interactions underlying the infection process comparatively little is known about the survival of pathogenic salmonella outside their hosts. Invitro evidence that salmonella spp can survive for long periods of time under harsh conditions; observation and conclusions about salmonella persistence obtained from human outbreaks.

PP27: QUORUM SENSING IN THE RHIZOSPHERE OF FIELD GROWN AND PLANT TISSUE CULTURED BAMBOO

P. Chinnathambi and A. Murugan

Department of Microbiology, Periyar University, Salem - 636011

Bacterial cell-to-cell signaling systems were initially described as mechanisms through which bacteria regulate gene expression via cell density and, therefore, they have been collectively termed quorum sensing. Quorum sensing bacteria produce and release chemical signal molecules called autoinducers that increase in concentration as a function of cell density. The detection of a minimal threshold stimulatory concentration of an auto inducer leads to an alteration in gene expression. Gram-positive and Gram-negative bacteria use quorum sensing communication circuits to regulate adiverse array of physiological activities. In general, Gram-negative bacteria use acylated homoserine lactones as auto inducers, Gram-positive bacteria use processed oligo-peptides to communicate. Recent advances in the field indicate that cell-cell communication via auto inducers occurs both within and between bacterial species. Further more, there is mounting data suggesting that bacterial autoinducers elicit specific responses from host organisms.Although the nature of the chemical signals, the signal relay mechanisms, and the target genes controlled by bacterial quorum sensing systems differ, in every case the ability to communicate with one another allows bacteria to coordinate the gene expression, and there fore the behavior, of the entire community. Presumably, this process bes ows upon bacteria some of the qualities of higher organisms. The evolution of quorum sensing systems in bacteria could, therefore, have been one of the early steps in the development of multicellularity.

PP28: WHITE SPOT SYNDROME DISEASE IN SHRIMP AQUA CULTURE

Suganya. V. and R. Balagurunathan

Department of Microbiology, Periyar University, Salem - 636 011.

Shrimp was one of the most important aquaculture species in the world. Different viruses are affected to shrimp (*Penaeus monodon*, *Litopenaeus vannamei* and *L. stylirostris*, among others) especially White Spot Syndrome Virus (WSSV) is a major penaeid shrimp

pathogen with a high mortality rate and causes disease outbreakes. These viral disease are caused major constriction causing an enormous loss in the production in shrimp farms and create a economic problems in shrimp aqua culture worldwide. The virus is a highly lethal, stress- dependent, which belongs to the family Nimaviridae, genus *Whispovirus*. Clinical signs of WSSV include a sudden reduction in food consumption, lethargy, loose cuticle and often reddish discolouration and white spots inside surface of the carapace, appendages and cuticle over the abdominal segments. Several methods are available for the detection like PCR, dot blot hybridization, ELISA, western blot analysis. To prevent the outbreaks with the help of disinfectants, antibiotics and dried feeds should suggest providing in shrimps. But the antibiotics and disinfectants are contaminated the aquatic environment and it also affected to the food chain. There are no treatments are available at present. Only the preventive measures are practised and in future this major problem in the aquatic biotechnology will be solved by developing the resistance against viral pathogens by providing probiotics as a feed for shrimps.

PP29: NEW IMPENDING OMICS TECHNOLOGIES IN ENVIRONMENTAL MICROBIOLOGY: A REVIEW

R. Palanivelan and P.M. Ayyasamy

Department of Microbiology, Periyar University, Salem - 636011.

Microbes play an essential role in driving earth„s biogeochemical cycles. The study of the microbial reservoirs is limited by our inability to cultivate a majority of the microbes, known as the “great plate count anomaly” and “cultivation independent approaches”. Metagenomics is the forefront of environmental microbiology research in recent years. This leads to the rapid development of metagenomic and other tools, witnessed a rapid advancement of environmental microbiology. These new omics technologies are revolutionizing the field of environmental microbiology in revealing the genetic potentials and functional activities of microbial communities. The new emerging metagenomics techniques in the field of environmental microbiology are metagenomics-sequencing, metagenomics-microarray, metatranscriptomics, metaproteomics, community metabolomics and bioinformatics. To date, sequencing-based metagenomics approaches have been applied to assess microbial community and ecosystem functioning. Metatranscriptomics randomly sequences mRNA fragments and requires computational assembly, thus serves as readily accessible entry point for studying microbial community. Metaproteomics analyzes protein profiles of microbial communities and address the function more directly than metagenomics and metatranscriptomics. Community metabolomics is the large-scale metabolite profiling in a given environmental sample by utilizing analytic chemistry tools. Bioinformatics is the application of informatics tools to biological data, including high-throughput sequence, quality scoring, alignment, assembly, relative abundance, data access and comparison across various platforms. The use of omics for microbial communities is still in the infancy only. Omics breakthroughs have greatly facilitated the interactions within microbial communities and environment. These methods hold great promise in revealing the overall picture of microbial diversity and activity, as well as rare spheres of previously unknown and uncharacterized microbes but possibly with functions that are important for the community.

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PP30: CROBIAL BIOSURFACTANTS AND ITS INDUSTRIAL APPLICATION

S. Jayalakshmi

CAS in Marine Biology, Annamalai University, Parangipettai - 608502.

Biosurfactants are a structurally diverse group of surface active molecules synthesized by microorganisms. Formerly, biosurfactants attracted attention as hydrocarbons dissolution agents, but the interest in these molecules have been increasing considerably in the past years as alternative to chemical surfactants especially in food, pharmaceutical, cosmetics and oil industry. They are mainly classified into two classes as low-molecular weight (lipopeptide, glycolipids) and high molecular weight (bioemulsifiers). Biosurfactants are biochemically hydroxylated and cross linked fatty acids (mycolic acids), glycolipids, lipopolysaccharides, lipoproteins and phospholipids. Marine microorganisms such as *Acinetobacter, Arthrobacter, Pseudomonas, Halomonas, Myroides, Corynebacteria, Bacillus, Alteromonas* etc had been studied for production of biosurfactants. The main reason for the spreading growing interest in biosurfactants is their environmental friendly nature, as they are non-toxic and biodegradable. Their unique structure provides new properties that traditional chemical surfactants may lack. Microbial biosurfactants exhibit a variety of useful properties for the food industry especially as emulsifiers, foaming, wetting and solubilizing agents. They exhibit strong antibacterial, antifungal and antiviral activity. Other medically relevant uses of biosurfactants include their role as antiadhesive agents to pathogens, making them useful as a protective coating for surgical instruments. Chances for developing new therapeutic and probiotic agents from biosurfactants are also bright.

PP31: HUMAN HEALTH IMPACTS DUE TO ORGANIC PESTICIDE POLLUTION

R. Janarthanan and R. Balagurunathan

Department of Microbiology, Periyar University, Salem - 636011.

Nowaday¨s farmer mostly used chemical pesticide for all plants of agriculture field. A pesticide poisoning occurs when chemicals intended to control a pest but it will affect non-target organisms such as humans, wildlife and bees. There are three types of pesticide poisoning. The first of the three is a single and short-term and very high level of exposure which can be experienced by individuals who commit suicide, as well as pesticide formulators. The second type of poisoning is long-term high-level exposure, which can occur in pesticide formulators and manufacturers. The third type of poisoning is a long-term low-level exposure, which individuals are exposed from sources such as pesticide residues in food as well as contact with pesticide residues in the air, water, soil, sediment, food materials, plants and animals. It has been introduced in the 1950¨s and in India has become a leading chemical used against pests in agriculture. It is used as an insecticide and also to kill fishes in lakes and rivers. It is not recommended for household use as it is known as a potent poison that can cause harm upon contact, eating food contaminated by it, swallowing, and even inhaling the odor. The chemical came into spotlight in India when at Kasargad in Kerala, it was sprayed aerially and the local population of many villages was exposed to it. What followed was very shocking. It led to physical and mental defects in poor farmers and their families. Studies have shown endosulfan to accumulate in a mother's breast milk and it has been linked to appalling birth deformities, the

like of which are still being observed at Kasargad, "Kerala"s Bhopal". Such events have occurred across the Globe and 62 countries all over the world have either banned it or restricted its use. Unfortunately India has done nothing to stem the use of this endocrine disruptor which can cause changes at the genetic level. Only in the state of Kerala where the endosulfan tragedy occurred that activists, scientists and doctors have been able to enforce a banned.

PP32: MICROBIAL SOURCE TRACKING: AN IMPROVED HEALTH RISK ASSESSMENT

A. Gayathri, V. Mamtha, S. Navamani, M. Rajeswari, P. Prabakaran and P.M. Ayyasamy
Department of Microbiology, Periyar University, Salem - 636 011

Outbreaks of waterborne disease pose threats to human health. Municipal health inspectors and other watershed managers need new science-based tools to help them target cleanup strategies more effectively to deal with faecal pollution and damage to ecosystems. Faecal waste may contain disease-causing microorganisms. Human faecal waste contains, in addition to cross-species pathogens. Thus, human faecal pollution in water is more hazardous to humans than faecal pollution from animals. In addition, there have been many documented human disease outbreaks in recent years due to pathogens from domestic animals but far fewer recorded outbreaks due to pathogens from indigenous (wild) animals. In India, we are using surface waters, especially water flowing through rivers as an important source of drinking water. These rivers are subjected to contamination by all the above sources. Microbial source tracking (MST) is an emerging field that aims to identify specific sources of faecal pollution. In general, the MST approach is based on comparing the similarity of microorganisms collected from aquatic ecosystems to microorganisms collected from nearby faecal pollution sources, then making inferences about the likely source of faecal contamination. There are four categories of methods currently being developed and used in MST: biochemical (phenotype), molecular (genotype), chemical, and immunological. Though all four categories have the same goal of identifying sources of faecal pollution, they each accomplish this goal with various degrees of labour and expense.

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