ICAR Sponsored Centre of Advanced Faculty Training in
Current Prospectives In Molecular Microbial Diversity
(3rd - 23rd Feb, 2011)

Department of Agricultural Microbiology
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भाकृ अनुप.
ICAR

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CURRENT PROSPECTIVES IN MOLECULAR MICROBIAL DIVERSITY

Introduction

Microorganisms that are associated with plant, soil and other biological systems are diverse in nature, both functionally as well as metabolically. The classical microbiological techniques applied to study the diversity of microbes on an ecosystem revealed that the there are several potential genes, proteins and other metabolites, which could be explored from these organisms. Further, molecular analyses confirmed that the culture-dependent approach could able to resolve only 0.5% of the microbial diversity, while remaining is unexplored.

A number of methods with higher resolving power have been developed for characterization of microbial communities that include both culturable and unculturable microorganisms. Most of them are based on analyses of ribosomal RNA genes (rDNA). The composition of the microbial communities is accessed using stable universal markers such as 16S rRNA. They have uncovered part of microbial diversity in soil and complex ecological niches, yielding sequences from many novel phylogenetic lineages. Measures of microbial patterns (fingerprinting) and taxonomic variability have been coupled with analysis of functional genes and activity measurements. Such investigations aim to reveal and understand the relationship structural and functional diversity in soil microbial ecosystem. Similarly DNA fingerprinting of PCR-amplified rDNA using methods such as DGGE and TGGE provide information about the community composition. DGGE profile from reverse transcriptase PCR might give fingerprints of active microbial populations. Direct amplification and sequencing of 16S rRNA from heterogeneous soil DNA will also be used to reveal the real microbial diversity of soil including unculturables. Apart from these common fingerprinting techniques, SSCP, T-RFLP, FISH are also used to identify genetic diversity of microorganisms present in soil, which in turn correlated with soil fertility. Construction of a genomic library with the total metagenome would provide a valuable source for various genes and their products and materials for microbial ecological studies.

Expected benefits of studying microbial diversity analyses include

- The untapped diversity of microorganisms is a resource for new genes and organisms of value to biotechnology
- Diversity patterns of microorganisms can be used for monitoring and predicting environmental change
- Microorganisms play a role in conservation and restoration biology of higher organisms
- Microbial communities are excellent models for understanding biological interactions and evolutionary history.
- Data bases are becoming more widely available as a source of molecular and macromolecular information on microorganisms

In this context, this training programme is designed to ensure that the participants have a basic understanding of the molecular methods and principles involved in microbiological diversity analyses and to provide hands on experience of DNA isolation and manipulation techniques and molecular microbial detection assays.

Trainees

Teachers and researchers working in this area in SAUs, ICAR and other institutes are eligible. The number of participants will be limited to twenty.

Course Outline :

Microbial diversity – importance and challenges –Molecular tools for culturable microbial diversity: RAPD, SCAR marker, ERIC and REP PCRs; Ribosomal based molecular diversity analysis: ARDRA, RISA. Mycorrhizal diversity by Nested PCR; PCR application for functional genes; Identification and phylogeny of bacterial strains by 16S rRNA sequencing.

Extraction of HMW DNA (metagenomic DNA) from different environmental samples – Culture independent molecular methods: DGGE, SSCP, t-RFLP, ALH-PCR, 16S rRNA cloning and sequencing; Application of quantitative Real-time PCR in microbial diversity analysis – Use of microbial proteins and lipids for microbial diversity – Microscopy applications: FISH, Microarray.

Duration

Twenty one days (3rd to 23rd Feb, 2011)

Venue

Department of Agrl. Microbiology, Tamil Nadu Agricultural University,
Coimbatore – 641 003, Tamil Nadu

Travel

Travelling allowance will be met by the organizers. Depending on the availability of funds, reimbursement will be restricted to III tier AC / Sleeper class fares. No DA will be paid for the journey period.

Food & Accommodation

DA for the stay at Coimbatore during the training period will be paid as per the recently revised rates of ICAR. Food and accommodation will be arranged at the University campus only for the participants on payment basis.

Last Date

Completed application form in the prescribed format through proper channel should reach the **Course Director** on or before **31.12.2010.**

Course Director

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Current Prospective in molecular microbial diversity
(3rd to 23rd Feb, 2011)

APPLICATION FORMAT

Affix Recent Passport size Photo

1. Name :
2. Designation :
3. Age and Sex :
4. Institute employed :

5. Total Service :
6. Experience :
7. a) Teaching
   i) Undergraduate :
   ii) Postgraduate :
   b) Research :
8. Academic record :

9. Field of specialization :

10. Address for communication (Include mobile no., e-mail id & Fax nos.) :

11. Accommodation : Required / Not required
12. Address of the sponsoring institute :

Signature of the candidate

Recommendation of the sponsoring authority

Signature and designation of the sponsoring authority