



Food and Agriculture
Organization of the
United Nations



The FAO Reference Centres for Antimicrobial Resistance and Aquaculture Biosecurity

Nitte University, Mangalore, India

in collaboration with

**Indian Council of Agricultural Research
New Delhi**

Organises

INTERNATIONAL HANDS-ON TRAINING COURSE

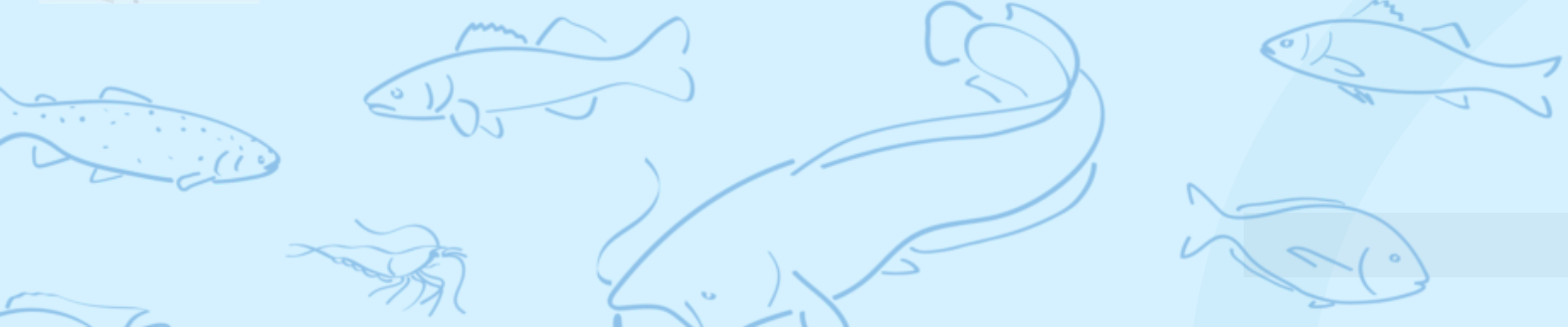
on

UTILISING MICROBIOME AND GENOMIC RESOURCES FOR UNDERSTANDING & MITIGATING ANTIMICROBIAL RESISTANCE IN THE ONE HEALTH CONTEXT

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**NITTE UNIVERSITY CENTRE FOR SCIENCE EDUCATION
AND RESEARCH**

Paneer Campus, Deralakatte, Mangalore, India



Context

Antimicrobial resistance (AMR) is the ability of microorganisms (bacteria, fungi, viruses and protozoan parasites) to persist or grow in the presence of drugs (called antimicrobials) designed to inhibit or kill them. When microorganisms become resistant to antimicrobials, standard treatments are often ineffective, and in some cases, no drugs provide effective therapy. Consequently, treatments fail. This increases illness and mortality in humans, animals and plants.

For agriculture (including aquaculture), this causes production losses, damages livelihoods and jeopardizes food security. Moreover, AMR can spread among different hosts and the environment, and antimicrobial resistant microorganisms can contaminate the food chain.

AMR is a major global threat of increasing concern to human and animal health. It also has implications for food safety, food security and the economic wellbeing of millions of farming households.

Microbes become resistant to antimicrobials because of random mutations and bacteria can also acquire the blueprints for resistance (DNA – genetic material) from other bacteria. Sharing of the genes that confer resistance to antimicrobials is common among bacteria.

When antimicrobials in humans or animals are used or are present in the environment, the microbes that lack the resistance are inhibited or are killed and the resistant microbes are able to outcompete the microbes and become the dominant members of the population.

The use of antimicrobials drives the selection for antimicrobial-resistant populations.

Genetic determinants of AMR are often associated with mobile genetic elements that can be easily transferred across bacterial genera and species and therefore can be horizontally transferred between human, animal pathogens, commensal bacteria as well as environmental bacteria. Recognising this, at international level, AMR issues are considered in a quadripartite manner involving FAO, WOAH, WHO and UNEP. It is now widely accepted that AMR issues need to be considered in One Health context recognizing that human, animal and environmental health are closely interlinked.

Until recently, most of our knowledge about AMR in clinical, foodborne, or environmental bacteria came from phenotypic studies of bacterial isolates from these sources. Antimicrobial susceptibility testing (AST) requires data on epidemiological cutoff (ECOFF) points to differentiate resistant and susceptible strains. Such cutoff points are used by standard setting bodies like Clinical Laboratory Standards Institute (CLSI) and EUCAST. But such breakpoints are not available for several aquatic bacteria and this poses great problem for applying AST for aquatic bacteria.

During recent times, a number of investigators have been applying metagenomics and whole genome sequencing for studying microbiomes in different aquaculture species and aquaculture systems. Whole genome sequences of large number of aquatic bacteria would be available in public databases like National Center for Biotechnology Information (NCBI) and this is an enormous resource for studying genes encoding AMR and a number of bioinformatic tools are available for mining AMR genes. But there are a number issues in using these tools to understand the direction of gene flow in resistant bacteria. Results from different tools may not be comparable and this is a constraint for using this very useful resource.

This is an emerging area and there is a need to build capacity to determine antimicrobial susceptibility in aquatic bacteria and generate data required to determine ECOFF using isolates from diverse geographical areas. In addition, there is a need to develop capacity to utilize genomic resources for AMR surveillance in the One Health context.

Objective

In view of the above, a five-day international hands-on training course is being organized.

The purpose is to utilize expertise from the FAO Reference Centres and partner institutions to deliver capacity building in the area of utilizing microbiome and genomic resources for understanding and mitigating AMR in the One Health context targeting participants from low and middle income member countries of FAO.

Resource persons

The resource persons will be drawn from FAO Reference Centres and other leading institutions working on AMU and AMR all over the world.

Participants

The targeted participants are aquatic organism health and aquaculture professionals working in the government, industry and academic sectors with current responsibility on aquatic health management and AMR in aquaculture.

Topics to be covered



- The Progressive Management Pathway for Aquaculture Biosecurity
- Responsible management of bacterial diseases in aquaculture
- Alternatives to antimicrobials
- AMR in One Health context
- Principles of antimicrobial susceptibility testing for aquatic bacteria – Epidemiological cutoff points, clinical breakpoints
- Standards for antimicrobial susceptibility testing from international organisations – CLSI and EUCAST
- Use of genomic tools for AMR detection
- Next Generation sequencing, metagenomics, aquatic microbiome Antimicrobial resistance genes, mobile genetic elements, gene cassettes, integrons
- Horizontal transfer of antimicrobial resistance genes
- Genomic tools to detect antimicrobial resistance and their performance AMR gene cassettes in environmental organisms, zoonotic pathogens Source attribution of AMR determinants from food, aquatic and human environments
- Use of genomic data in AMR surveillance



Call for Expression of Interest (EOI):

Interested professionals are invited to complete an Expression of Interest by filling up the google form available at <https://forms.gle/PeXzYGdLUL2kaj7L9>. No registration fee for attendance to the course; however, interested candidates are advised to secure travel support (self-funded or donor-supported) inclusive of travel cost and daily subsistence allowance (DSA, UN-rate for Mangalore is USD 164/day).

Forty candidates will be selected from applicants based on the following criteria:

- expression of interest in attending the course
- academic background and/or at least five years of relevant experience in any of the following fields: aquatic organism health management, aquaculture, microbiology; informatics
- post-training plan in utilizing the knowledge and skills acquired
- available self-funding or donor support

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