Workshop on Mycotoxigenic Fungi & Food/
Feed-Borne Hazards — From Isolation to Microbiome & Genomics
21 November 2025, Thailand Science Park, Pathum Thani, Thailand

Organized by:
National Center for Genetic Engineering and Biotechnology (BIOTEC),
National Science and Technology Development Agency (NSTDA),
Ministry of Higher Education, Science, Research, and Innovation (MHESI), Thailand

In collaboration with:
- Mahidol University
- Thammasat University

Rationale:
Mycotoxigenic fungi (e.g., *Aspergillus, Penicillium, Fusarium*) pose persistent risks across food and feed value chains, undermining public health, trade, and farmer livelihoods. Rapid, reliable detection and identification—from culture-based isolation to DNA barcoding, long-read microbiome profiling, and genome-enabled mycotoxin biosynthetic gene cluster (BGC) analysis—are now essential capabilities for laboratories in Thailand and the ASEAN region. This workshop convenes experts from BIOTEC-NSTDA and partner universities to 1) harmonize practical, field-to-lab workflows; 2) strengthen technical capacity for polyphasic fungal identification; and 3) connect classical mycology with amplicon/metagenome pipelines and genomics tools for risk assessment and mitigation. By integrating morphology, molecular methods, microbiome approaches, and genomics, participants will gain end-to-end competencies applicable to surveillance, quality control, and research programs supporting safer food/feed systems

Objectives:
1) **Field-to-lab foundations:** Build core skills in field sampling, sterile isolation, and diagnostic morphology for common mycotoxigenic genera, including the recognition of look-alikes and common pitfalls.
2) **DNA-based identification proficiency:** Execute and interpret barcoding workflows (ITS, TEF1; plus benA/CaM where relevant), choose appropriate sequencing platforms (Sanger vs. NGS), use BLAST confidently, and apply basic phylogenetic reasoning.
3) **Microbiome & genomics toolkit:** Introduce streamlined amplicon/metabarcoding workflows (e.g., ONT library prep and analysis) and provide a practical overview of whole-genome strategies (assembly/annotation; antiSMASH/FUNannotate/MycoCosm) to assess mycotoxin BGCs.
4) **Operational decision-making & collaboration:** Compare cost–speed–accuracy trade-offs across methods (culture, MALDI-TOF MS, barcoding, amplicon, WGS), develop simple decision trees for routine lab use, and foster post-event collaboration (shared protocols, datasets, ring trials).

Language: The workshop will be conducted in English without translation.
Target group: Lecturers and researchers in the fields of Microbiology, Food Biotechnology, Agricultural Biotechnology and related areas.
Participants number: 60 people
Registration fee: Free of charge
Registration: Online registration through the provided URL link or QR code below:
- **URL:** https://event.nstda.or.th/event-nstda/#/register/add-register/85
- **QR:**

Draft program:

Opening & Framing the Day

09.00 – 09.30 **Welcome Remarks**

By Dr. Nitsara Karoonuthaisiri
National Center for Genetic Engineering and Biotechnology

Why Mycotoxigenic Fungi Matter in Food/Feed Safety (regulatory + public-health context)

By Assoc. Prof. Dr. Awanwee Petchkongkaew
Faculty of Science and Technology, Thammasat University

Session 1: Isolation (Polyphasic) & Morphology

09:30 – 10:45 **A Practical Guide from Sampling to Morphological Identification of Mycotoxigenic Fungi**

By Dr. Sayanh Somrithipol
National Center for Genetic Engineering and Biotechnology

10:45 – 11:00 Coffee break

Session 2: Molecular & Alternative Identification

11:00 – 12:00 **Integrating Sequencing and Phylogenetic Analysis in Fungal Taxonomy**

By Mr. Sarunyou Wongkanoun
National Center for Genetic Engineering and Biotechnology

- MALDI-TOF MS for rapid ID (library limitations, spectra QC)
- Cost, speed, reliability comparison; decision tree for choosing methods

By Dr. Piyanun Harnpicharnchai
National Center for Genetic Engineering and Biotechnology

12:00 – 13:00 Lunch

Session 3: Microbiome/Metagenome

13:00 – 14:00 **Amplicon sequencing (ITS/16S) for food/feed matrices using Oxford Nanopore Technologies: streamline workflow, library preparation, sequencing, data analysis using EPI2ME, and case studies of contaminated/processed samples**

By Dr. Worarat Kruasuwan
Siriraj Long-read Lab (Si-LoL), Faculty of Medicine Siriraj Hospital, Mahidol University

14:00 – 14:30 Coffee break

Session 4: Lab visit (tentative)

14:30 – 16:00 - Plant Microbe Interaction Research Team
- Advanced Diagnostics and Biomarker Discovery Research Team/IJC-FOODSEC
- Thailand Bioresoucre Research Center
- National Omics Center

For more information: Please contact
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