

# **Summary Report**

## **Training Course for Microbiome Data Sharing**

WFCC-MIRCEN World Data Center for  
Microorganisms (WDCM)  
Beijing, China

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By

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## **Personal introduction**

I received my B.Sc. (Microbiology) in 1996 and M.Sc. (Industrial Microbiology) in 2000, both from Chulalongkorn University, Thailand. Then, I received D.Eng. (Material and Life Science) from Osaka University in 2004. After four years Postdoctoral experience in Hokkaido University and Oregon State University, I returned back to National Center for Genetic Engineering and Biotechnology (BIOTEC), Thailand as a Researcher. In 2014, I have been assigned as a Senior Researcher in Microbial Cell Factory Laboratory. My current research interests are focusing on development and application of microbial cell factories for heterologous protein production and functional genomics. Currently, I am in the curator team responsible for molecular materials in Thailand Bioresource Research Center (TBRC).

**Culture collection** : BIOTEC Culture Collection (BCC) and Thailand Bioresource Research Center (TBRC).

## **ABSTRACT**

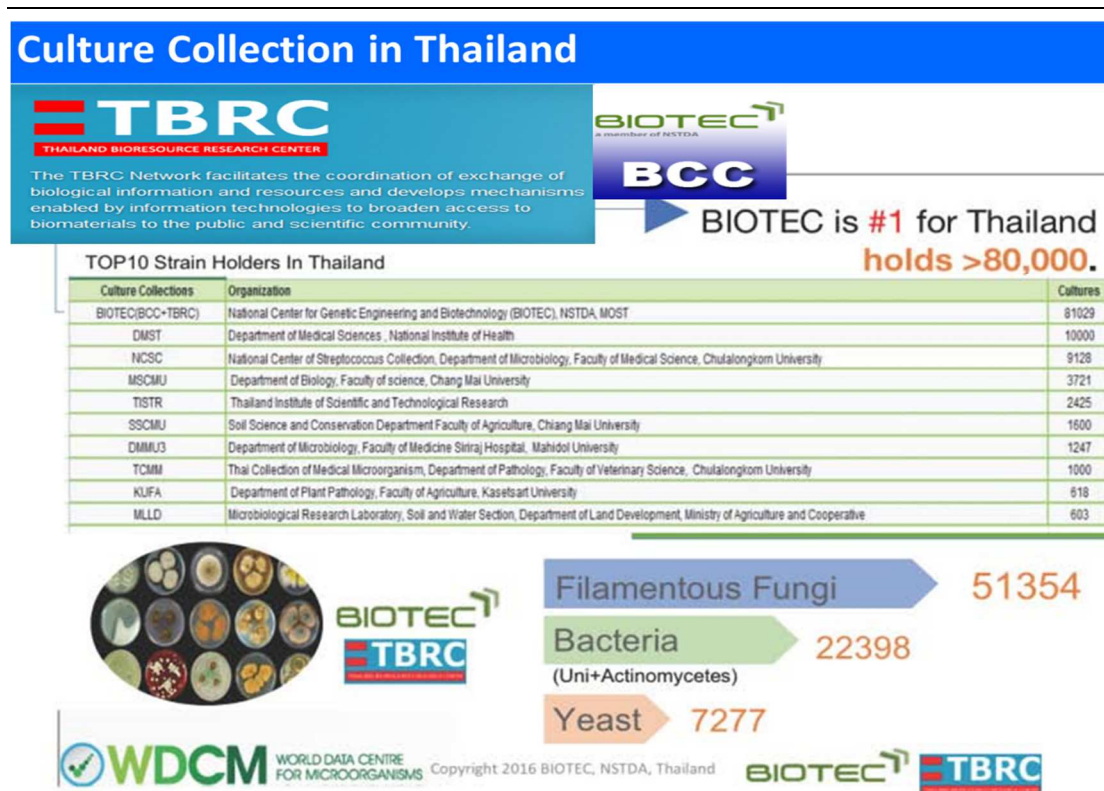
In order to promote the sharing and utilization of bioresources and microbiome data around the world, WDCM has arranged the training course on microbiome data sharing during 15-30 October, 2017 in Beijing, China. The training course program contains informative lectures

from basic information to advanced technology. The main training program are focusing on data management of microbial resources. In addition, advanced technology in microbial genome, metagenomics and microbiome is also described. The participants consisted of 15 persons from 14 countries namely Bulgaria, Belarus, Chile, Cuba, Estonia, Fiji, India, Indonesia, Malaysia, Morocco, Pakistan, South Africa, Thailand and Vietnam.

**Key words:** Microbial taxonomy, genomics, genome mining, metagenomics, microbiome, TBRC Thailand, WDCM

### **1. Brief introduction of BCC and TBRC.**

Thailand has a rich source of biodiversity, especially microorganisms including bacteria, yeasts, and filamentous fungi. Currently, BIOTEC host two culture collections namely BIOTEC Culture Collection (BCC) and Thailand Bioresource Research Center (TBRC) that hold a large collection of these microorganisms more than 80,000 strains. There are >7000 strains of yeasts, >20,000 strains of bacteria, and >50,000 of filamentous fungi (Figure 1).



**Figure 1.** Culture collection in Thailand.

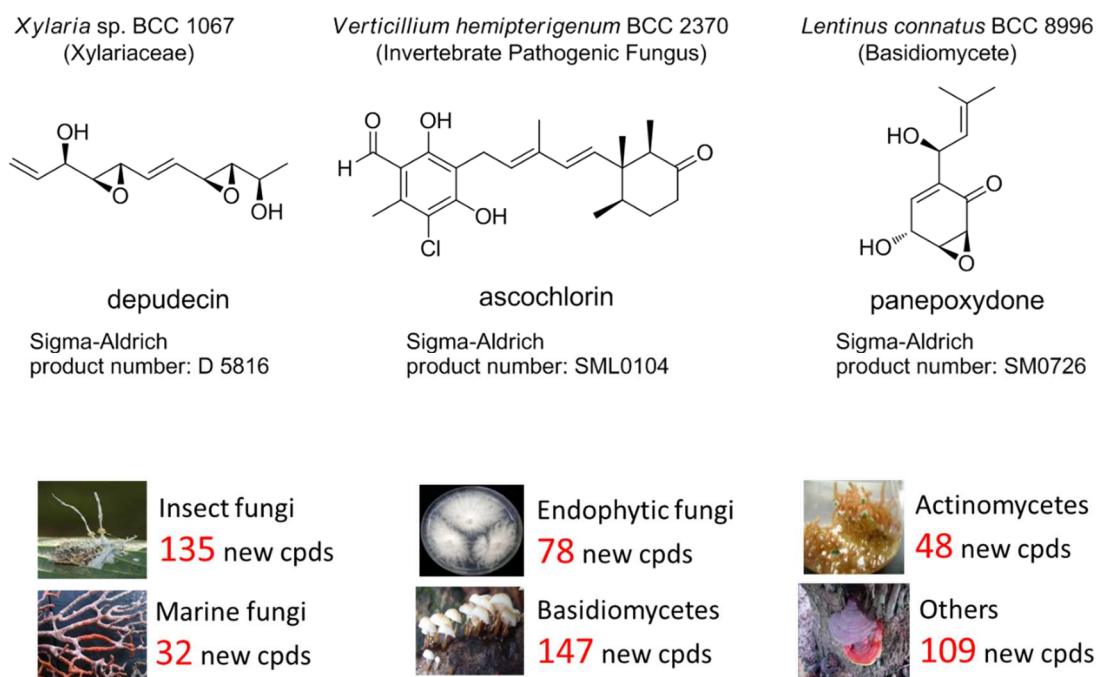
BCC and TBRC are the largest culture collection in Thailand.

BCC established in 1996. The primary objective of BCC is to collect and maintain microorganisms and their relevant data for BIOTEC's in-house research. Approximately 75 percent of the BCC microorganisms holds are filamentous fungi, which are taxonomically and ecologically diverse (Figure 2). The largest group is those isolated from insects (insect pathogenic fungi). The rest were isolated from soil, seeds, decayed wood, plants, lichens, dung, fresh water and sea water, etc. BCC also holds a high diversity of ascomycetous and basidiomycetous yeasts. For bacteria, acetic acid bacteria, lactic acid bacteria, and actinomycetes are the major groups. Microorganisms in BCC are routinely tested by BIOTEC

researchers to find valuable products such as secondary metabolites, enzymes, and bioactive short peptides (Figure 3). Almost all strains in the collection are cryopreserved at  $-80^{\circ}\text{C}$  as working cultures. Freeze drying, liquid-drying and storage in the vapour phase of nitrogen are used for long-term preservation for strains with special characteristics such as newly described species from Thailand, biologically active compound producers, and safe deposit strains.



**Figure 2** Fungi biodiversity in BCC and TBRC.



**Figure 3** Natural products produced by BCC microorganisms.

TBRC established in 2015 and serves as a non-profit center to preserve, provide and facilitate the coordination of exchange of biological information and resources. Currently, more than 11,000 strains of microorganisms are on services (<http://tbrcnetwork.org>) (Figure 4). TBRC also develop mechanisms to broaden access to biomaterials to the public and scientific community and provide quality technical services and supports that meet international standard practices. TBRC also offers top quality cell culture for industrial applications (Figure 5). TBRC has established strong network with more than 60 departments from leading universities and companies in Thailand and with more than 10 research institutes in ASEAN as well as with leading national and international networks (Figure 6).



# WDCM-Training Course for Microbiome Data Sharing

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**TBRC**  
THAILAND BIORESOURCE RESEARCH CENTER

Home > Products > Microorganisms

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Microorganisms(11,909) | Molecular Materials(38) | Antibodies(15) | Viruses(1)

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Collection

- TBRC
- BCC
- TISTR
- MSCU
- SDBR
- FerVAAP

Showing 1 – 10 of 11,909 item(s)

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*Abundisporus fuscopurpureus* (BCC 16679)

Source: Branch  
Category: Plant

Overseas: 2,500 Baht  
Thailand: 1,500 Baht

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*Acetobacter aceti* (TBRC 474)

Type strain: ✓  
Source: Alcohol turned to vinegar


Overseas: 3,000 Baht  
Thailand: 2,000 Baht

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**Figure 4** Microorganisms and biomaterials service in TBRC.

## Industrial Applications


### Health and Medicine



TBRC offers top-quality cell cultures and microbial strains that produce authentic bioactive compounds for pharmaceutical, food supplement and cosmetic research applications.

- Bioactive compound
- Food supplement
- Probiotics and prebiotics
- Cosmetic


### Agriculture



TBRC offers a selection of microorganisms for agriculture research or industry e.g. Bio-control strains to control insect pests and plant pathogens or bio-fertilizer strains to digest agriculture waste.

- Bio-fertilizer
- Bio-control
- Plant growth promoter


### Food and Feed



TBRC is holding a wide variety of microbes that support manufacturing food and feed such as extremophiles, or lactic acid bacteria for fermented food, or pentosanase and heat-tolerant phytase producing *Aspergillus* sp. for feed processing, or bacteria strains for the production of DHAs, long/short chain fatty acid, or biopolymer.

- Food
- Feed
- Probiotics and prebiotics


### Environment



TBRC encourages "go green" movement by committing to environment protection and sustainability. Whether you are involved in textile, pulp and paper, waste management or bioremediation process, TBRC offers fully characterized microbial strains to support your research and further expand knowledge on environmental responsibility.

- Waste treatment
- Bioremediation


### Energy



The TBRC collection offers organisms enable to utilize cheaper substrates such as lignocellulosic biomass to make bio-ethanol for green technology and environment sustainability.

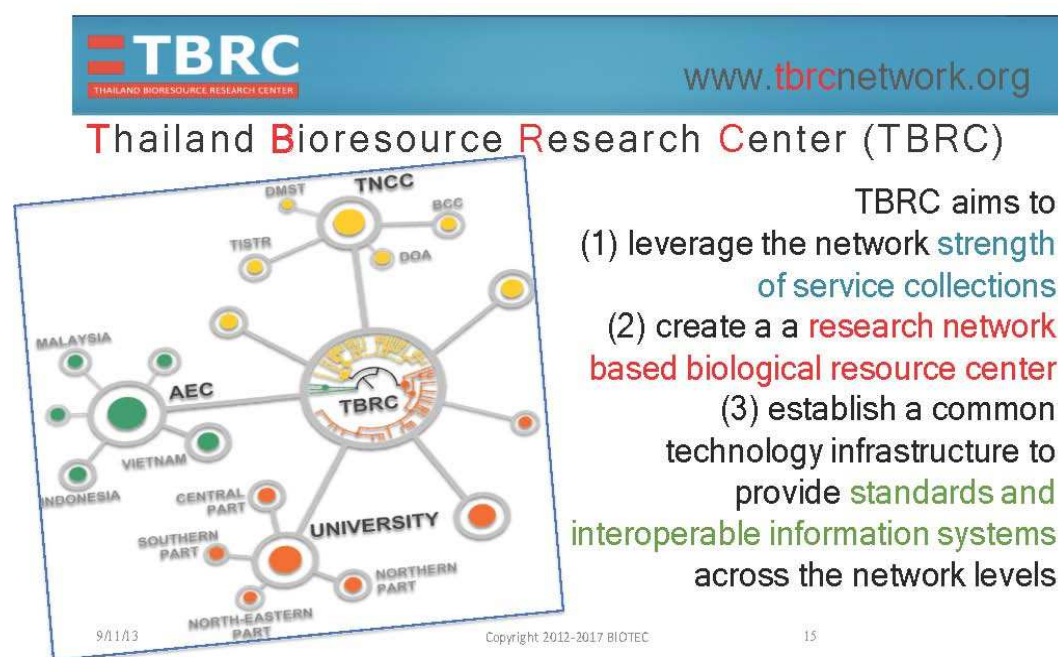
- Biofuel

### Other Industries



- Textile
- Pulp and paper

**Figure 5** Industrial applications of TBRC microorganisms.



**Figure 6** TBRC network.

## 2. Benefit from the training courses.

The training course for microbiome data sharing provided information on following four major topics:

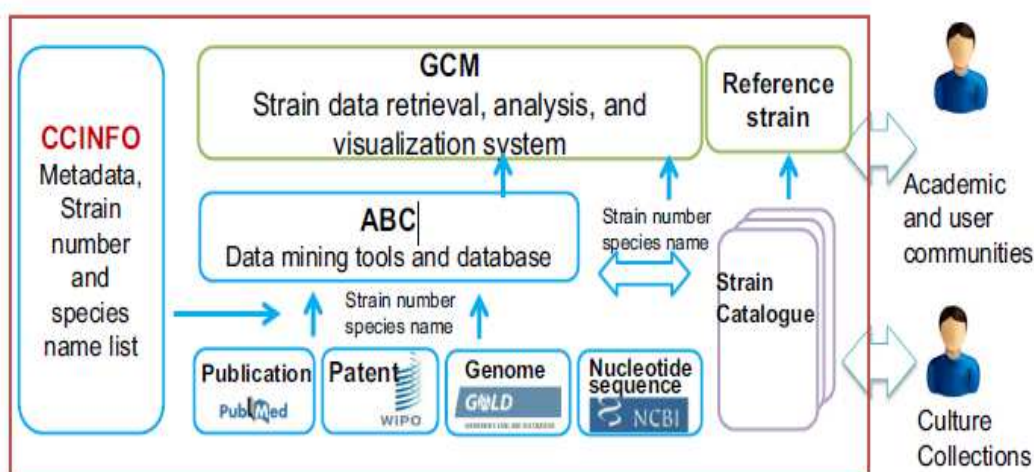
- 1) World Data Centre for Microorganisms (WDCM) and its management
- 2) Microbial taxonomy
- 3) Microbial genomics, metagenomics and microbiome
- 4) Microbial genome mining and engineering

### 2.1 World Data Centre for Microorganisms (WDCM) and its management

WDCM was established 50 years ago as the data center of the World Federation for Culture Collections (WFCC)-Microbial Resource Center



(MIRCEN). WDCM aims to provide integrated information services using big data technology for microbial resource centers and microbiologists all over the world (Figure 7). WDCM including all of its integrated services. Culture Collections Information Worldwide (CCINFO) provides metadata information on 708 culture collections from 72 countries and regions. Global Catalogue of Microorganism (GCM) gathers strain catalogue information and provides a data retrieval, analysis, and visualization system of microbial resources. Currently, GCM includes more than 368,000 strains from 103 culture collections in 43 countries and regions. Analyzer of Bioresource Citation (ABC) is a data mining tool extracting strain related publications, patents, nucleotide sequences and genome information from public data sources to form a knowledge base. Reference Strain Catalogue (RSC) maintains a database of strains listed in International Standards Organization (ISO) and other international or regional standards. RSC allocates a unique identifier to strains recommended for use in diagnosis and quality control, and hence serves as a valuable cross-platform reference. WDCM provides free access to all these services at [www.wdcm.org](http://www.wdcm.org) (Wu et al., 2017).



**Figure 7** A system-level overview of the WDCM databases (Wu et al., 2017).

## 2.2 Microbial taxonomy

Microbial taxonomy means which microorganisms can be grouped together. Microorganisms that show similarities with respect to the criteria used are in the same group, and are separated from the other groups of microorganisms that have different characteristics. There are a number of taxonomic criteria that can be used. For example, numerical taxonomy differentiates microorganisms, typically bacteria, on their phenotypic characteristics. Phenotypes are the appearance of the microbes or the manifestation of the genetic character of the microbes. Examples of phenotypic characteristics include the Gram stain reaction, shape of the bacterium, size of the bacterium, where or not the bacterium can propel itself along, the capability of the microbes to grow in the

presence or absence of oxygen, types of nutrients used, chemistry of the surface of the bacterium, and the reaction of the immune system to the bacterium. A well-known example of taxonomic characterization is the kingdom, division, class, family, genus, species and strain divisions. Such a "classical" bacterial organization, which is typified by the Bergey's Manual of Determinative Bacteriology, is based on metabolic, immunological, and structural characteristics.

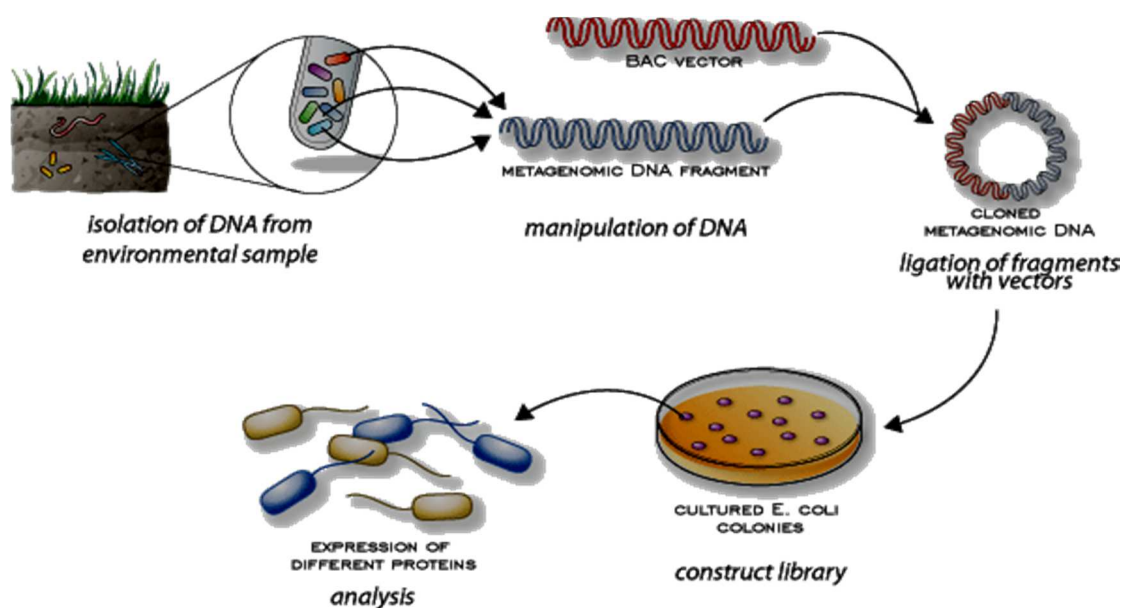
For a meaningful genetic categorization, the target of the comparative sequencing must be carefully chosen. Molecular microbial taxonomy of bacteria relies on the sequence of ribonucleic acid (RNA), dubbed 16S RNA, that is present in a subunit of prokaryotic ribosomes. Ribosomes are complexes that are involved in the manufacture of proteins using messenger RNA as the blueprint. Given the vital function of the 16S RNA, any mutation tends to have a meaningful, often deleterious, effect on the functioning of the RNA. Hence, the evolution (or change) in the 16S RNA has been very slow, making it a good molecule with which to compare microorganisms that are billions of years old.

### **2.3 Microbial genomics, metagenomics and microbiome**

**Microbial genomics** is a field of science that analyzes and compares the complete set of genetic material of a microorganisms or a large number of genes in a simultaneous fashion. Microbial genomics involves the sequencing and analysis of genomes and also concerned with the

structure, function, comparison, and evolution of genomes. Study of genomics uses high throughput DNA sequencing and bioinformatics to assemble, and analyze the function and structure of entire genomes. Advances in genomics have triggered a revolution in microbial biotechnology which facilitates the understanding of complex biological systems in microbes.

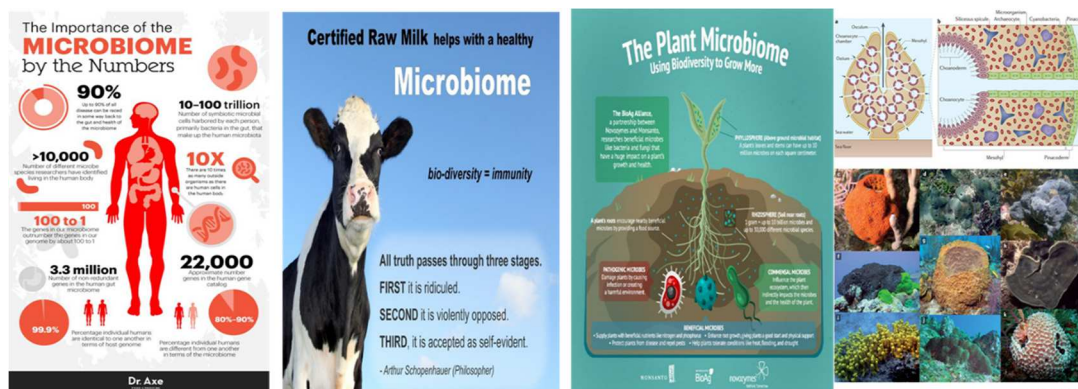
**Metagenomics** is the study of genetic material recovered directly from environmental samples (metagenomes) (Figure 8). While traditional microbiology and microbial genome sequencing rely upon cultivated clonal cultures, early environmental gene sequencing cloned specific genes (often the 16S rRNA gene) to produce a profile of diversity in a natural sample. Such work revealed that the vast majority of microbial biodiversity had been missed by cultivation-based methods. Recent studies use high throughput DNA sequencing to get largely unbiased samples of all genes from all the members of the sampled communities. Metagenomics is a powerful strategy for viewing the microbial world that has the potential to understanding the entire microbial communities.



**Figure 8** Strategy for metagenomics analysis.

For metagenomics analysis, the sample from several environment was collected and DNA was isolated. Genomic DNA library was constructed and screen for target protein of interested. In addition, 16 sRNA gene was analyzed and sequenced for bacterial biodiversity.

**Microbiome** is the total microbial cells and their genetic materials presents in living hosts such as human, animal, plant, as well as in soil and oceans (Figure 9). It dynamic interaction effects the physiology of the hosts and provides novel solution for improve human and animal health and also agriculture and environment. With recent advances in genome sequencing and ‘meta-omics’ tools, analyses of microbiomes have been made possible, thus accelerating the progress of microbiome research. As it becomes clearer how microbiome composition can influence ecosystems, there is a growing interest in engineering microbiomes for shaping microbiota to alter ecosystems of interest.



**Figure 9.** Microbiome diversity

Microbiome can exist persistently in or on living hosts, such as humans, animals, and plants, as well as in soil, oceans and air.

## 2.4 Microbial genome mining and engineering

Genome mining refers to deriving various information about the organism based on genome analysis. For microorganisms, microbial genome mining is a rapidly developing approach to discover new and novel secondary metabolites for drug discovery. It is an alternative approach to more traditional methods for the discovery of novel secondary metabolites, which continue to serve as scaffolds for further embellishment by medicinal chemistry and combinatorial biosynthesis. The concept of genome mining has been maturing as a discipline since the discovery by David Hopwood and coworkers by whole-genome sequencing that *Streptomyces coelicolor* encodes many more secondary metabolites than had been anticipated from decades of study.



### **3. Suggestion on WDCM work.**

WDCM should support research funding for collaborative project between China and other country. The budget should be remitted to international country for research working.

### **4. Comments or suggestion on the training courses.**

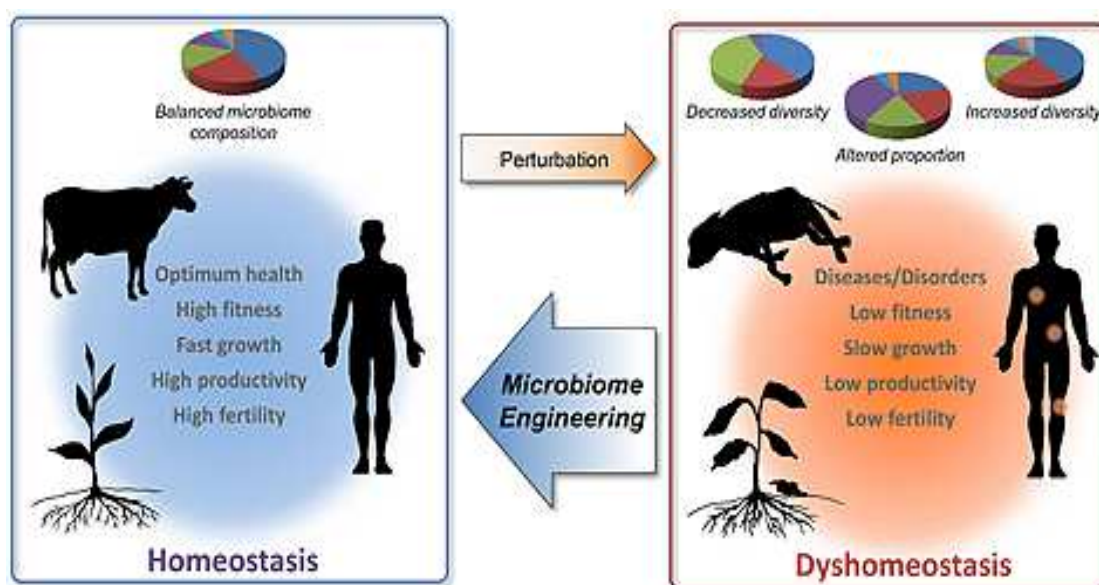
The training course should focus on “**Microbiome Data Sharing**” as officially scheduled. It would be excellent if the training course should have more practices in the laboratory for microbiome analysis. For example, the participants have to do experimental work on DNA extraction from environmental samples and practice on DNA sequencing. Then, the sequencing data can be used as model for bioinformatics analysis of microbiome in this training course.

### **5. Suggestion on further cooperation between WDCM and your collections.**

Possible collaborative project: “Engineering microbiomes to improve soil fertility and plant productivity”.

Microbiome of ecosystems in Thailand remains largely unexplored especially in agricultural field such as soil and plant. Soil microbiome refers to microbial communities in the bulk soil. In Thailand about 46% of land was used for agriculture and 75% of agriculture land has been

degraded by several factors. Imbalance in agricultural development results in environmental problems such as soil deterioration. This would result in perturbation to balanced microbiomes of ecosystems which brings about deleterious effects such as increased rates of plant diseases and reduced crop productivity. Rebalancing of the microbial communities by microbiome engineering should relieve these negative influences and lead to enhance host phenotypes (Figure 11).



**Figure 11** The application and progress of microbiome engineering (Foo et al., 2017).

Engineering or synthetic microbiomes can be used to engineer microbiomes in soil. Microbial strains with verified function can be combined into simple synthetic microbiomes containing few to several

dozen species and use to improve soil fertility. By engineering soil microbiome, more balanced soil microbial communities are established for improve soil quality and further influence the productivity of crops.

Our research goal in microbiome is to elucidate microbiome functions that alter host performance. Microbial strains with specific functions in soil will be identified. Then, they can be combined and manipulated experimentally to test their contributions to host fitness by inoculating hosts with specific microbial strains. This research should provide valuable information about microbial community in soil which would be applied to improve soil fertility and plant productivity in many countries.