TRƯỜNG ĐẠI HỌC CẦN THƠ
KHOA KHOA HỌC TỰ NHIÊN

CỘNG HÒA XÃ HỘI CHỦ NGHĨA VIỆT NAM
Độc lập – Tự do – Hạnh phúc

Cần Thơ ngày 04 tháng 01 năm 2019

THƠ MỜI
Tham dự báo cáo khoa học

Kính gởi: Quý Thầy Cô, nghiên cứu sinh, học viên và sinh viên

Nhân dịp GS. Patrick Van Dijck, Khoa Khoa học, Đại học Leuven, Bỉ đến thăm Bộ môn Sinh học, Khoa Khoa học Tự nhiên, Bộ môn sẽ tổ chức một buổi báo cáo khoa học để GS. Van Dijck và Thầy Cô thuộc các lĩnh vực nghiên cứu liên quan có thể trình bày, thảo luận các kết quả và định hướng nghiên cứu trong thời gian tới.

Thời gian: 7g45 thứ tư ngày 09/01/2019

Địa điểm: Phòng chuyên đề, Khoa Khoa học Tự nhiên

Chương trình làm việc:

Thời gian	Nội dung	Báo cáo viên
7:45 - 8:00	*Đón tiếp*	
8:00 - 8:30	Prospects for sustainable plant disease management in the Mekong Delta of Vietnam	TS. Nguyễn Đắc Khoa Viện NC&PTCNSH
8:30 - 9:00	Plant essential oils as a new source for antimicrobial research and beyond	GS. Patrick Van Dijck Khoa Khoa Học, ĐH Leuven
9:00 - 9:30	Screening for anti-diabetic medicinal plants in the Mekong Delta	PGS.TS. Đái Thị Xuân Trang Khoa Khoa học Tự nhiên
9:30 - 9:45	*Giải lao*	
9:45 - 10:15	Intra- and inter-field diversity of 2,4-dichlorophenoxyacetic acid degradative plasmids and their catabolic genes in rice fields of the Mekong delta in Vietnam	TS. Nguyễn Thị Phi Oanh Khoa học Tự nhiên
10:15 - 10:45	The development and use of animal model systems to study catheter-related microbial and fungal biofilm infections	Prof. Patrick Van Dijck Khoa Khoa Học, ĐH Leuven
10:45 - 11:15	The role of trehalose metabolism in abiotic stresses tolerance in *Arabidopsis thaliana*	Phan Lê Công Huyền Bảo Trân Khoa học Tự nhiên NCS Khoa Khoa Học, ĐH Leuven
11:15 - 11:30	*Bế mạc*	

Trân trọng kính mời quý Thầy Cô, nghiên cứu sinh, học viên và sinh viên quan tâm tham dự.

Trưởng Khoa

PGS.TS. Bùi Thị Bửu Huê

Tóm tắt nội dung báo cáo:

1. Prospects for sustainable plant disease management in the Mekong Delta of Vietnam

TS. Nguyễn Đắc Khoa, Viện NC&PTCNSH

The Mekong Delta of Vietnam is the main agricultural production area of this country. The overuse of chemicals by farmers to protect crops against different pests has currently reduced the quality of agricultural products and resulted in several adverse impacts on human health and the eco-system. Biological control is one of the alternative strategies for sustainable pest management, particularly important for the eco-friendly development of agriculture in Vietnam. This talk reviews some representative results of the Plant Pathology group at Can Tho University on biological control of plant diseases in the Mekong Delta, focusing on the use of antagonistic microorganisms and induced resistance. These strategies have been studied to control rice diseases, i.e., blast, sheath blight and bacterial leaf blight. Furthermore, results of the studies on shallot, sweet potato and rose are also presented. Although biological control is advantageous to the society and the environment, transferring this technology from researchers to subsistence farmers for large-scale application might be a challenge.

2. Plant essential oils as a new source for antimicrobial research and beyond

GS. Patrick *Van Dijck*[1,2]

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Essential oils (EOs) are plant secondary metabolites for which various functions have been described. One of them is that they may protect plants from microbial infections. One EO typically contains more than 100 EO components (EOCs) of which a few are present in larger quantities and the majority in minor quantities. Especially the latter group of compounds may be interesting as not much is known from them and because of their physicochemical characteristics, they are hydrophobic and volatile, they are typically not present in small compound libraries that pharmaceutical companies use to screen for new bioactive molecules. In our lab we are using about 250 different EOs that together comprise about 3000 different chemical molecules. We are using a number of assays to identify those molecules that show activity against human fungal pathogens, such as *Candida albicans* and *C. glabrata*.

In the search for antimicrobials, *in vitro* standardized bioassays are indispensable and commonly a first step in a long investigative process. To quantify their antimicrobial potential, the minimal inhibitory concentration is typically determined using a broth microdilution method. Because EOCs have a relatively high vapour pressure at room temperature they potentially could also exert their antimicrobial activity (AA) over a distance. We have developed a method to determine this vapour-phase mediated antimicrobial activity (VMAA) of a specific EO at a distance. To validate the assay, we determined the VMAA of a large collection of EOCs against two pathogenic human *Candida* species. We showed that there was no correlation between the VMAA and the minimal inhibitory concentration of the EOCs, indicating that these are complementary measures. Furthermore, we showed that *C. glabrata* was on average more susceptible to EOCs than *C. albicans* and identified the EOC citronellal as showing a differential VMAA with high VMAA against *C. glabrata* and only minimal against *C. albicans*. This is the first detailed characterization of a novel approach to qualitatively and quantitatively assess the VMAA of molecules using standard multi-well plates.

3. Screening for anti-diabetic medicinal plants in the Mekong Delta

PGS. TS. Đái Thị Xuân Trang, Nguyễn Thị Ái Lan, Khoa Khoa học Tự nhiên

Blood glucose levels are mainly regulated by the hormones of glucose absorption in instestine, hepatic glucose output and peripheral glucose uptake. Whole body glucose homeostasis is achieved through an intricate balance between glucose uptake and endogenous glucose production, mostly by the liver.

Carbohydrates are converted by alpha-glucosidase into simple sugars and then absorbed by the intestines. Nowadays targeting on inhibition of alpha-glucosidase is a common approach of anti-

diabetic drugs in order to control blood sugar levels. The present work deals with evaluating the anti-diabetic potential of plant extracts based on the α-glucosidase inhibitory activity *in vitro*. We found that 18 plant ethanol extracts inhibited α-glucosidase activity. The α-glucosidase inhibitory activity of fourteen of those (from IC_{50}=4.79 to IC_{50}= 98.29 μg/mL) was higher than the one of reference α-glucosidase inhibitor acarbose (IC_{50}=99.46 μg/mL).

Hepatic gluconeogenesis is essential to maintain the blood glucose levels, and its abnormal activation leads to hyperglycemia and type 2 diabetes. Hepatic glucose production occurs due to the breakdown of glycogen, and the de novo synthesis of glucose from precursors via gluconeogenesis. In this study, we screened medicinal plants exhibiting inhibitory effects on glucose-6-phosphatase (G6Pase) and glucose-6-phosphate dehydrogenase (G6PDase) which are key enzymes in regulating the rate of gluconeogenesis and the pentose phosphate pathway, respectively. The G6PDase has been suggested to play a key role in diabetes-associated complications. Several studies demonstrated that G6PDase activity enhances in adipose tissues of both obese mice and obese humans. This increase significantly correlates with the increase of oxidative stress, adipose tissue inflammation and insulin resistance. Some plant extracts in the Mekong Delta such as *Artocarpus altilis, Mangifera indica, Coccinia grandis, Vernonia cinerea, Morus alba, Pithecallobium dulce* hampered activities of G6Pase and G6PDase. Among those, *Mangifera indica* (ML) young leaves extract demonstrated the antihyperglycemic and antihyperlipidemic effects on diabetic mice models. The results showed that the ML at doses 150, 300, 450 mg/kg body weight significantly decreased the plasma glucose, G6Pase, G6Pdase activity, total cholesterol (TC), triglyceride (TG), low density lipoprotein cholesterol (LDL_C) levels and atherogenic index and greatly elevated the high density lipoprotein cholesterol (HDL_C) level in diabetic mice ($p<0.05$). Altogether, *Mangiferine indica* leaves extract could be considered as a promising therapy in preventing the complications of diabetes.

4. Intra- and inter-field diversity of 2,4-dichlorophenoxyacetic acid degradative plasmids and their catabolic genes in rice fields of the Mekong delta in Vietnam

TS. Nguyễn Thị Phi Oanh, Khoa Khoa học Tự nhiên

The Mekong delta is the largest agricultural area in Vietnam. To meet the food demand for a fast growing population and export, use of high yielding, short cultivation varieties has resulted in steady increase in application of diverse types of pesticides and herbicides. However, not much is known about the fate of pesticides in soil prior to reaching the water bodies. The herbicide 2,4-dichlorophenoxyacetic acid (2,4-D) has been used worldwide to control various broad-leaf weeds in agriculture and in pastures. In soils, bacterial degradation is the main route to remove 2,4-D from the environment. The catabolic pathway of 2,4-D degradation is one of the most extensively studied pathways for degradation of anthropogenic compounds at the genetic level. In addition, genes involved in 2,4-D degradation show a modular composition and are often located on MGEs, especially plasmids. The elucidation of the genetic context of 2,4-D biodegradation in different bacterial isolates from geographically distant areas provide us with information about the diversity and evolution of 2,4-D biodegradation genes and their vehicles worldwide, but is not informative about their dynamics at a 2,4-D-treated site. This study aimed at examining the composition of transferable 2,4-D degradation gene clusters & their genetic context in 2,4-D degrading strains isolated from 2 distantly located rice fields in the Mekong delta. Our data showed that all isolates were unique for each rice field and carried the catabolic genes on plasmids. Most plasmids were IncP-1β plasmids and carried *tfd* clusters highly similar to those of the IncP-1β plasmid pJP4. IncP-1β plasmids from the same field showed small deletions and/or insertions in accessory metabolic genes. One plasmid belonged to an unclassified plasmid group and carries a copy of both *tfdA* and *tfd-II* identical to those in the IncP-1β plasmids. Our results indicate intra-field evolution and inter-field exchange of 2,4-D-catabolic IncP-1β plasmids as well as the exchange of *tfd* genes between different plasmids within a confined local environment.

5. The development and use of animal model systems to study catheter-related microbial and fungal biofilm infections

Patrick Van Dijck[1,2]

[1] *Department of Molecular Microbiology, VIB, KULeuven, Belgium,* [2] *Laboratory of Molecular Cell Biology, Institute of Botany and Microbiology, KULeuven, Belgium*

In our lab, we are studying human fungal pathogens, such as *Candida albicans* and *Candida glabrata*. These species are commensal organisms in most people, but in immune-compromised patients, these pathogens can become deadly organisms.

Currently a major problem in hospitals with these species is that they easily form biofilms on different types of implants, such as catheters. Biofilms are three dimensional communities that protect themselves from the host immune system and from antifungal drugs by producing an extracellular matrix. Moreover, in many cases mixed species biofilms are identified consisting of bacterial and fungal cells which often seem to act synergistically regarding antimicrobial resistance. Over the last several years we have developed catheter-related biofilm model systems in rodents and optimized them for bioluminescence imaging. These in vivo model systems are ideal tools to study the importance of specific genes for biofilm formation under in vivo conditions but even more interesting is that we can test the efficacy of antimicrobial drugs on biofilms. We are also investigating the interaction at the molecular and cellular level that occurs between *Staphylococcus aureus* and *Candida albicans* when they are growing together in a biofilm. We study this both under in vitro as well as in vivo conditions, using mouse model systems for catheter-related infections as well as mucosal infections. We found that *S. aureus* and *C. albicans* communicate to each other via small molecules thereby stimulating each other resistance against antimicrobials. We also showed that the antifungal drug caspofungin is an interesting drug, for use in combination therapy, to fight bacterial biofilms as it is targeting an enzyme involved in extracellular matrix production.

6. The role of trehalose metabolism in abiotic stresses tolerance in *Arabidopsis thaliana*

Phan LCHB Tran[1,2,3]*, Rolland F*[4]*, Van Dijck P*[1,2]

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Trehalose is a non-reducing disaccharide consisting of two glucose molecules. Trehalose is well-known for its role in stress tolerance in a wide range of organisms such as bacteria, yeast, nematodes, vertebrates and some resurrection plant species. Plants encode many trehalose biosynthesis enzymes in their genome, but only very little trehalose is found. Despite of this, it seems that trehalose is important in drought stress tolerance as plants with lower trehalose levels by overexpressing of trehalase (AtTRE1), an enzyme which hydrolyzes trehalose into two glucose molecules, showed increased drought stress tolerance in *Arabidopsis thaliana (Van Houtte 2013)*. The precise mechanism of trehalase regulation in drought stress resistance in plants is not yet known. Moreover, AtTRE1 is known as a plasma membrane-bound protein and its catalytic domain orients toward the apoplast in plant cells (Frison 2007). It was indicated that infection of *Plasmodiophora brassicae* in *A. thaliana* resulted in trehalose accumulation and an induction of *AtTRE1* in infected organs (Brodmann 2002). This finding suggests that the plasma membrane-anchored trehalase might work as a defense against excessive accumulation of pathogen-derived trehalose. Yet, there is still a puzzling question: how do the plants get rid of endogenous trehalose? Trehalose-6-phosphate is predominantly located in the cytosol (Martins 2013) and the *A. thaliana* trehalose-6-phosphate phosphatases (TPPs) are predicted to be localized in the cytosol or plastids (Tanz 2013; Vandesteene 2012). These indicate that trehalose must be produced within the cell. The location of intracellular trehalose is clearly inaccessible to the apoplastic trehalase. Here, we present a novel finding of dual subcellular localization of trehalase and various locations might display different functions of AtTRE1. In addition, regulation mechanism of trehalase upon stress responses is also shown.