UKZN/JAAS Joint Postdoctoral Research Summary

1. ## Molecular mechanisms for the synthesis of amylose in rice

Amylose content is an important factor affecting the eating quality of rice. Rice with low expression of the amylose gene *Wx-mq* has excellent eating quality. However, the amylose content is still quite different among different varieties derived from the same combination and with the same *Wx-mq* gene. Therefore, it is important to understand the molecular mechanisms of amylose synthesis in rice endosperm to analyse the genetic mechanism affecting rice eating quality. We therefore propose:

- To characterize starch synthesis related genes that affect amylose synthesis in rice endosperm, excluding low amylose gene *Wx-mq*.

Required Skills: Agronomy/Food Science/Biology

2. ## Effects of genetic and environmental factors on the expression of aroma in rice

As one of the important cooking qualities of rice, aroma directly affects the eating quality of rice. The aroma of rice is determined by heredity, pre harvest (environment, planting methods), post-harvest (drying, storage, cooking methods) and other factors. Study of the effects of these factors on the aroma compounds in rice is important for rice processing and breeding of aroma concentrated and high quality rice varieties.

Objectives

- To determine the internal (genetic) and external (environmental) factors influencing the formation and stabilization of aroma in rice, so as to provide reference information to develop pre- and post- harvest cultivation, storage and processing strategies to ensure that rice has stable and excellent aroma and flavour.

Required Skills: Agronomy/Food Science/Biology

3. **Gene editing technology to create disease and insect resistant rice germplasm**

Rice is one of the most important food crops in China, but suffers from severe yield and quality losses due to pests and diseases, which include rice blast and the brown plant hopper, respectively. Presently, there is a dearth of broad-spectrum durable resistant germplasm, resulting in limited development of rice resistance breeding in Jiangsu province. The creation of rice germplasms with a broad-spectrum durable resistance to disease and insects has important theoretical and practical significance for ensuring rice production and productivity. CRISPR-Cas9 as an emerging safe genome editing techniques provides an efficient and feasible technical platform for creating broad-spectrum durable resistant new rice germplasms without selectable marker genes. The research aims are to:

- Create excellent rice germplasm resources resistant to disease and insect pests by using CRISPR-Cas9 gene editing technology.
- Based on identification of the genotype of resistance genes of rice varieties, to analyse distribution and the combination patterns of rice blast and BPH resistance genes, and
- Evaluate the application value of resistant rice breeding.

Required Skills: Genetics/Molecular Biology

4. **Mechanism of drought tolerance in rice**

Abiotic stress is the underlying cause of more than 50% of crop losses worldwide. Among the abiotic stressors, drought is the most complex and widespread, especially in Africa. We propose to investigate drought tolerance in rice through the introduction of the C_4 gene (C_4-phosphoenolpyruvate carboxylase, *C_4-pepc*) into C_3 rice plants.

The postdoc's primary responsibility will be to:

- Elucidate the mechanism of the photosynthesis in *C_4-gene* transgenic rice plants under drought stress with focus on sugar transportation and distribution by SnRKs in transgenic rice lines.
- To understand signal integration in *C_4-pepc* promoter response of both hexokinase signal and drought stress signal transduction from RNA-Seq data.
- To evaluate epigenetics of the molecular mechanisms of SnRK kinase participating in the specific regulatory regions of *C_4-pepc* and enzyme activations.
- Finally, sugar metabolism via CO_2 signal-SnRK-C4PEPC model will be identified, to infer the true picture of drought tolerance in rice plants.

Required Skills: Plant science/Crop Breeding

5. Effectiveness of genotype-by-environment interaction on crop breeding efficiency using meta data from multi-environment variety trials

A large number of multi-environment variety trials (MET) points to the ubiquitous existence of genotype-by-environment interactions (GEI), which make selection of superior cultivars and identification of ideal testing sites complicated. Exploration of the useful GEI to enhance the identification of discriminative and representative test sites, investigation of mega-environments and comprehensive evaluation of genotypes are of critical relevance to plant breeders and/or extension agronomists. We propose the following:

- To explore the effectiveness of the GGE biplot method in revealing GEI and put forward possible complementary measures to optimize GGE biplot methods in exploiting MET datasets.
- To use GGE biplot analysis for location evaluation in terms of discrimination ability, representativeness, and desirability, and
- To investigate the presence of multiple mega-environments in main cotton production regions in China, using the multi-year datasets of national cotton regional trials since 1990, as a case study.

Required Skills: Statistics/Crop Ecology/ Crop Breeding

6. Exploration and genomic analysis of favourable alleles from wild cotton species

Exotic *Gossypium* germplasm are rich sources of useful agronomic traits for improvement programs for cultivated cotton. The introduction of alien genetic variation into upland cotton from wild species is a valuable technique for broadening the genetic base of upland cotton.

The aims of the project are:

- Development of synthesized hexaploids derived from wild cotton species
- Development of chromosome segment introgression lines (CSSLs) by marker assisted selection.
- Identification of favorable alleles from wild cotton species by AB-QTL approach, and high-resolution mapping for the target QTL and introgression into commercial varieties in China.

Required Skills: Crop genetics/Breeding

7. **Molecular mechanisms of plant virus and vector interaction**

Plant viral disease significantly threatens the quality and production of crops. Our group's focus is on the important viral diseases that threaten crops and vegetables in China. Extensive research has been done to reveal the mechanisms behind the viral pathogenesis and vector-dependent transmission process. In this study, we propose to:

- Elucidate the molecular mechanisms behind vector-dependent transmission processes.
- Determine viral pathogenesis behind vector-dependent transmission processes.

Required Skills: Plant Virology/Interaction between virus and hosts

8. **Identification and functional analysis of genes associated with resistance to rice virus diseases**

Viral disease, especially rice black-streaked dwarf virus diseases cause great losses in rice yield. Development of resistant cultivars and research into resistance mechanisms will help to control this disease. We therefore propose the following:

- A genome-wide association study to map genes associated with resistance to virus in rice.
- Based on the mapping results, to raise transgenic plants expressing resistance genes.
- To test the expression level of virus and genes and to reveal the influence of virus movement by resistance-associated genes using the BiFc, Co-IP and Pull-down assay

Required Skills: Plant virology/ Crop genetics/Breeding

9. **Germplasm innovation of super hybrid Pennisetum for High Cd/Zn absorbability and nitrogen fixation**

For this project, we propose to:

- Optimize the endophyte-hybrid breeding of Pennisetum symbiont.
- Characterize Cd/Zn absorbability and nitrogen fixation in new germplasm.
- Determine molecular, physiological and biochemical mechanisms of synergism between endophytes and their hosts, resulting from high Cd/Zn absorbability and nitrogen fixation due to co-metabolism and interaction.

Required Skills: Microbiology/Plant Genetic/Breeding/Environmental Science

10. Genetic characterization of high fertility and heat tolerance in sheep and goats

The proposed objectives for this project are:

- To genetically characterize high fertility, growth and heat tolerance in sheep and goat.
- To identify the major genes responsible for ovulation rate, litter size, growth and heat tolerance and their effect on productivity and heat tolerance in sheep and goats.
- The ultimate goal is to develop markers to improve reproductive efficiency, growth and heat tolerance breeding in sheep and goats.

Required Skills: Animal Genetic Breeding and Reproduction/Genetics/ Biochemistry /Molecular Biology

11. Development and evaluation of recombinant vaccines against mycoplasmas in swine

Chronic respiratory infections represented by mycoplasmas have become the focus of disease control with the gradual control of malignant infectious diseases in pig farms. *Mycoplasma hyopneumoniae* and *Mycoplasma hyorhinis* adhere to and damage the tracheal epithelial cells, opening the portal for secondary infections by other pathogens, causing and aggravating the associated diseases. The global infection rate of *M. hyopneumoniae* and *M. hyorhinis* is greater than 70%, therefore, vaccines developed against swine mycoplasmas have important research value and good application prospects.

We wish to:

- Develop *Mycoplasma hyopneumoniae*, *Mycoplasma hyorhinis* and combined recombinant vaccines based on a genetic manipulation technology platform.
- Establish key protective antigen screening, adjuvant and delivery system development, and standardized research on challenge protection evaluation.

Required Skills: Veterinary Microbiology/ Immunology

12. Co-infection of swine respiratory pathogens and interaction with the host innate immune system

Severe respiratory diseases induced by pathogen co-infection are very common currently. These include: *Mycoplasma hyopneumoniae*, PRRSV, PCV2 and swine influenza virus. However, the mechanisms of co-infection among different pathogens and the interaction of pathogens with the host immune system are still not clear, especially regarding immunosuppression and immune escape pathways for the different pathogens. The absence of stable and accurate in vitro and in vivo infection models may be responsible for the slow progress.

- We propose an organoid in vitro model for identifying the mechanisms of persistent infection of some porcine respiratory pathogens, and
- To determine the interaction between infection pathogen and the host innate immune system, and the interaction among the different co-infection pathogens in the swine respiratory tract.

Required Skills: Immunology/Microbiology

13. Studies on the functions of the key surface proteins of swine mycoplasmas

The variable lipoprotein (Vlp) family is the only identified adhesion molecule critical for *Mycoplasma hyorhinis* to generate high-frequency surface antigenic variation in evading the host immune system. Size variation is an important form of Vlp variation, but the exact biological significance is not clear yet. In our previous study, the cytoadhesive abilities of all the Vlp members were found to reduce as the size of the molecules increased; an indication that Vlp size variation plays an important role in the cytoadhesion of *Mycoplasma hyorhinis*.

We propose the following:

- Detection and comparison of cytoadhesion mediated by Vlp alone, as well as cytoadhesion mediated by Vlp together with other adhesion molecules between strains.
- Determination of the underlying reason for the changes in cytoadhesion.
- Evaluation of the mechanism of cytoadhension at the atomic level.

Required Skills: Immunology/Microbiology/Biotechnology

14. **Construction of a recombinant subunit vaccine against *Mycoplasma ovipneumoniae***

M. ovipneumoniae is the causative agent of chronic non-progressive pneumonia in sheep, goats, bighorn and small wild ruminants. It is a global epidemic disease and has caused considerable loss to the sheep industry. Progressive wasting and spasmodic cough are some of the characteristic symptoms of the disease. It could also induce secondary infection, which sometimes results in fatal respiratory diseases. Multiple strains of *M. ovipneumoniae* have been isolated from infected flock in different countries. Gene polymorphism studies have shown obvious differences in immunogenicity and toxicity among the strains. Development of a recombinant subunit vaccine could be a possible option to address the limitations of traditional vaccines for disease prevention.

Aims and objectives
- Screening potential protective antigens of *M. ovipneumoniae*.
- Construction of a recombinant subunit vaccine against *M. ovipneumoinae*.
- *Required Skills: Veterinary Medicine*

15. **Effect and mechanism of nano-oxygen interface material on organic carbon mineralization and soil fertility improvement**

The long-term cultivation at a high intensity, blind fertilization and rough management technology of water and fertilizer causes severe degradation of soil property, which leads to challenges regarding food yield, quality and safety. This program will carry out the following investigations:

- The preparation and application the technology of nano-oxygen interface material, mainly the screening of this material for high nano-oxygen concentration and proper release pattern; application rate and method in different soils and seasons; determination of relevant soil parameters and crop characteristics.
- Study the effect of the nano-oxygen interface material on the content and form of organic carbon with physical, chemical and biological methods, such as Nuclear magnetic resonance, far infrared, GC-MS, target plant and microbe culture experiments.
- Study the effect of the nano-oxygen interface material on the microorganism community associated with target and nitrogen transformation and identify the specific isolates that can indicate the different organic carbon transformation stages. High throughput sequencing, target gene RT-PCR and some new data analysis methods will be used

Required Skills: Material Science/Soil science/Soil microorganism

16. **Effect of aggregate microstructure on the soil organic carbon sequestration under continuous straw return**

Soil aggregate is the basic unit of soil structure and function. Microstructure within aggregates determines the distribution of oxygen, water, microorganisms, etc., which to a great extent determines the turnover of soil organic carbon (SOC). Due to limitations of traditional techniques and methods, the microstructure within aggregates and the mechanisms of its effects on SOC turnover is still unclear. Development of new techniques makes it possible to explore the mechanisms of SOC sequestration after straw returning from the perspective of inner aggregate microstructure. Based on the long-term fertilization experiment on yellow brown soil of a rice-wheat cropping system. The aims of the project are:

- To study the comparative effects of straw return on the microstructure within aggregates in both flooded anaerobic and aerobic growing seasons;
- To trace the distribution and transformation process of straw-derived carbon within aggregates of different sizes, and reveal its persistence and the corresponding mechanisms in soil;
- To illustrate the correlations among characteristics of aggregate inner pores, microorganisms, and the concentration, fraction component, and existential state of SOC, and eventually reveal the key processes and main mechanisms of SOC sequestration. The results would be of scientific significance for revealing SOC sequestration mechanisms after straw return, and could provide a theoretical foundation for increase of soil carbon levels and the promotion of sustainable agricultural development.

Required Skills: Environmental Science/Soil Science

17. **Mechanisms for efficient removal of nitrogen from polluted water during low temperature seasons**

Water eutrophication, caused by the oversupply of nutrients such as nitrogen and phosphorous in aquatic systems has become a worldwide environmental problem in recent years. Removal mechanisms for nitrogen in polluted water is key to controlling water eutrophication. In order to purify and restore the water, ecological measures such as wetlands, ecological ditch, and ecological float beds are widely used. Improvement of nitrogen removal efficiency under low temperature is a great challenge. The main objectives of this research are to:

- Establish highly-efficient and environmentally-friendly N removal measures to purify the N–rich polluted water such as agricultural drainage, domestic sewage and eutrophicated river water through the combination of ecological, physical and chemical methods;

- Explore the mechanism of nitrogen removal;
- Evaluate its effects on water quality improvement and cost-benefits through a case study.

Required Skills: Environmental Science/Environmental Engineering/Ecology/Microbiology

18. **Development and application of environmentally-friendly material for the removal nitrogen, phosphorus and other harmful substances from polluted water**

Organic pollutants, excessive phosphorous (P) and nitrogen (N) releasing through runoff, frequently resulting in the eutrophication of water bodies, are harmful to human beings and ecological environments. It is urgent to establish environmentally benign and economically cost-effective measures to eliminate such pollution. The research activities of our team are focusing on different classes of materials; *e.g.* photocatalytic nanomaterials, iron nanomaterials, and biochar, to remove pollution from wastewater. The work encompasses nanomaterial synthesis, characterization by X-ray diffraction, electron microscopy and PL studies etc. Environmental aspects are an important part of the research activities. Thus, the development of new materials that have ultra-high uptake, selective adsorption of pollutants, and catalytic degradation is desired in the project. The effective removal of N, P and other harmful substances by using the new materials will also considered.

The project will address the following:

- Fabrication and characterization of new environmental materials such as nanomaterials, carbon materials and porous materials etc.
- Application of the materials in water treatment to remove nitrogen, phosphorous, organic pollutions and other harmful substances.

Required Skills: Material Science/Chemistry/Environmental Science/Environmental Engineering

19. Studies on the microbial mechanism for efficient anaerobic conversion of poor biomass to biogas

The production of renewable energy carriers is currently receiving increasing attention worldwide. Biogas is a promising candidate as the technology of its production may combine the treatment of various organic wastes with the generation of an energy carrier for the most versatile applications. Currently, biogas production by means of anaerobic degradation of renewable primary products and organic wastes significantly contributes to the contingent of renewable energy forms in China. The microbiology of biomass degradation and methane synthesis within biogas reactors is complex and requires the interaction of a specific microbial community. In consequence of the complexity of the microbial communities and metabolic pathways involved the biotechnology of the microbiological process leading to biogas production is poorly understood. In this study, both microbiological diversity and the regulatory role of the metabolism may be the driving forces optimizing biogas-producing microbial communities. A rational design of these communities to promote greater efficacy in large-scale practical systems is necessary. The composition of an optimal biogas-producing consortium can be determined through the use of this approach, and this systematic methodology allows the design of the optimal microbial community structure for any biogas plant.

Required Skills: Microbiology/Environmental Engineering/Molecular Biology/ Biochemistry and Molecular Biology

20. Gene discovery for nitrogen use efficiency in maize

Grain yields of maize are highly responsive to supplemental nitrogen, with significant amounts of nitrogen fertilizer required annually to maintain high yields. Although studies have identified numerous genes that constitute nitrogen responses, and thereafter nitrogen use efficiency, the changes in transcript interaction and their responding regulatory mechanisms are still not well determined in maize. We therefore propose:

- To analyse the coding and long non-coding transcriptome and protein/starch composition in developing seeds from more than 100 diverse inbreds following three nitrogen stress treatments.
- After identify the coding and long non-coding transcripts that are repressed or induced, we will build compression networks and infer the interactions among these transcripts.
- Study the network changes that are generalized and those that are nitrogen-specific, and compare how these transcripts interact with each other in response to different nitrogen treatments using support vector machine (SVM) linear regression and a series of *in vitro & in vivo* analyses.

- We expect that a set of key transcripts (hub linkers) will acquire different interaction partners to involve in nitrogen responses.
- These transcripts with changed co-expression sub-networks will be associated with grain composition alterations for pinpointing the responding causal networks and transcripts.

Required Skills: Crop genetics/Breeding

21. **Herbicide-resistant crop:: Identification of new loci for herbicide resistance and resistance mechanism analysis**

Cultivating herbicide resistant crops significantly promotes agricultural production, but the traditional transgenic approach by introducing foreign genes to the crops will raise health and environmental concerns. Chemical mutagenesis and base editing with CRISPR are generally considered safe as no foreign fragments are introduced. Our on-going projects have produced herbicide-resistant crops by chemical mutagenesis and base editing with CRISPR. In this project;

- We are interested in identifying new loci for herbicide resistance, and improving the efficiency of single base editing particularly with the CRISPR-Cas9 system.

Required Skills: Crop Genetic Breeding/Biochemistry and Molecular Biology/Plant Physiology/Cell Biology/Genetics/Plant Pathology

22. **Identification, distribution, and amplification mechanisms of transposable elements (TEs) in plant genomes**

Transposable elements (TEs) are major DNA components in plants. Their distribution, abundance, and functional roles in the host gene and genome evolution is still not clear. In this project, many sequenced model plants with different genome sizes and evolutionary positions will be investigated. This study includes:

- Identification, annotation, distribution, methylation and amplification mechanisms of TEs in different genomes, with an emphasis on their influence on and interaction with genes.
- This study also involve computational, evolutionary analysis and analysis of genomic dynamics of TEs in different species. We will use a combination of both computer assisted approach and experimental verification method.

Required Skills: Genetics/Bioinformatics/Genomics/Computational Biology/Plant Science

23. Exploring elite alleles and association mapping of QTL for Fusarium head blight resistance in wheat

Fusarium head blight (FHB) is one of the most important fungal diseases in wheat (*Triticum aestivum* L.) worldwide. It does not only lead to a significant reduction in grain yield, but also decreases grain quality. Fusarium head blight resistant wheat cultivars play an important role in FHB management and prevention of mycotoxin contamination. Fortunately, sources of genetic resistance are available in the wheat gene pool. During the last decades, many quantitative trait loci (QTL) mapping studies have been conducted for FHB resistance in wheat. In this context, genome-wide association analysis (GWAS) can be seen as a promising strategy for identifying QTL for traits of interest. A wheat panel of elite lines and wheat landraces is available for genome-wide marker-trait association studies, thus the aims of this study are to:

- Explore new alleles associated with FHB resistance, and
- Develop new SNPs through GWAS that are associated with FHB resistance for marker-assisted selection.

Required Skills: Crop Genetic Breeding/Genetics

24. Intervention mechanism of blueberry anthocyanin metabolites on diabetes

Blueberries have a wide range of health benefits because of their abundant anthocyanins. However, the structure-activity relationship and concentration-response relationship is not yet clear. This project proposes to comprehensively investigate the chemical structures and content of active anthocyanins from blueberry by fingerprint and metabolomics platform, which will help to clarify the pharmacological mechanism of blueberry anthocyanins. Diabetes is known to cause serious damage to human health. Blueberries can reduce the risk of type 2 diabetes. Clinically, the disorders of energy metabolism and cardiovascular system damage are the important characteristics of diabetic pathological changes. Thus we speculated that blueberry anthocyanins have the potential for diabetes prevention and treatment by improving glucolipid metabolism and antihypertensive effect. This study will determine the hypoglycemic, hypolipidemic, and hypotensive effects of blueberry anthocyanins at the cellular and molecular level in animals. This project can provide a theoretical basis for the development and application of blueberry anthocyanins as a functional food ingredient or nutraceutical. The aims of the project are:

- To investigate the influence of blueberry anthocyanins on blood glucose and blood lipids using animal models;

- To study the AMPK signal path in cells to explore the regulation metabolism of blueberry anthocyanins on glucolipid;
- To reveal the anti-inflammatory, antioxidant, and vasodilator effects and mechanism of blueberry anthocyanins based on I3K-Akt/PKB-eNOS-NO and NF-κB signaling pathway in HUVEC cells.

Required Skills: Food Science (Molecular nutrition, Metabolics)

25. Risk evaluation of multi-mycotoxins in wheat and their microbial/enzymatic degradation

Fusarium toxins comprise a range of different toxins including trichothecenes such as deoxyn ivalenol (DON), nivalenol (NIV), Diacetoxyscirpenol (DAS) and T- toxins, as well as zearale none (ZEN) and fumonisins are important hazardous agents in cereal crops. Different fusarium toxins are associated with certain types of cereal.

We focus on risk analysis and management of Fusarium toxins in wheat. The postdoctoral research will focus on the following:

- Occurrence investigation, migration and transformation of Fusarium toxin in wheat grain and its products.
- Understanding the co-toxicity of Fusarium toxins such as estrogenic activity with ER mediated reporter gene assay, immune activity with cytokine mRNA expression and so on.
- Toxigenic Fusarium evolution and distribution, epigenetic and environmental effects of toxigenic population.
- Microbial degradation of Fusarium toxins (DON, ZEN, FB) and their enzymatic characteristics, and
- Side effects of some field management such as fungicide application, no till and straw returning and their mechanisms.

Required Skills: Preventive Veterinary Medicine/Food Science/Molecular Biology/ Plant Pathology/Microbiology

26. Immunoassay-based identification of food fraud, drug and foodborne pathogenic microorganism

The issue of food fraud, illegal drug abuse in health care products, and foodborne pathogenic microorganisms cause serious problems for human health and has become a serious concern worldwide. This project consists of large-scale research field in food safety and interdisciplinary study.

- The postdoctoral candidates will be assigned to one of these research areas based on her/his background and mutual interest, aiming at a high-throughput method development, particularly for the antibody based immunoassay development.
- For food fraud, the protein biomarker would be the target for the immunoassay development, for Chinese herb related health care products and drugs.

Required Skills: Immunochemistry/Food Science/Pharmaceutics/Molecular Biology/Microbiology/Food Safety

27. Monitoring, regulation and diagnosis of growth indices in rice plant for improved rice yield

Rice is one of the most important food crops in the world, but increasing rice yield at reduced input costs is a challenge. Improved rice yields and reduced input costs rely mainly on the suitable regulation and management of fertilizer and water. Furthermore, to realize the suitable regulation and management of fertilizer and water in rice, nitrogen and water uptake, and growth indices in the rice plant need to be closely monitored, quantified, and diagnosed. We propose the following:

- System analysis of dynamic changes in indices for rice growth, nutrient, water, and spectrum.
- To evaluate the suitable indices dynamic models used in demands of multi-goals, and the practical methods for model parameter estimating.
- To set up the models for rice growth diagnosis, and for regulation and management of fertilizer and water.

Required Skills: Crop Modelling/Agricultural Informatics/Land Use and Information Technology/Water and Soil Engineering/Computer Simulation

28. **Study of the mechanisms of organic pollutants' absorption by plants**

With development, more and more toxic organic pollutants, such as pesticides and polycyclic aromatic hydrocarbons, are discharged into the environment causing serious harm to environmental safety and biological health. Organic pollutants such as pesticides are characteristically toxic, volatile and persistent. Organic pollutants in soils and water contaminate crops/plants, thus pose health risks to both humans and animals. Therefore, it is important to understand how organic pollutants enter crops/plants and further regulate the uptake process for agricultural product safety and enhancement in phytoremediation of organic pollutant-contaminated soil or water.

We will research uptake mechanisms, metabolism and phytotoxicity of organic pollutants in plant, and uptake models to develop this research area.

Required Skills: Plant Physiology/Biochemistry and Molecular Biology/Environmental Science/Chemistry

29. **Role of entophyte bacteria in the degradation of pesticides in host plants and farmland**

Pesticides have been in use for quite a long time. Less than 1% of all pesticides used reach the target, most of the pesticides end up in the environment. Pesticides are a cause of pollution affecting land, water wildlife and humans. The problem is huge and growing. Studies involving endophytes and their role in enhancing host resistance to biotic and abiotic stress are common. Endophyte-assisted pesticide degradation and phytoremediation offer much potential for food safety and remediation of soil contaminated with pesticides.

Our laboratory focuses on tackling environmental issues with a "green" solution. Our main research is;

- To use natural endophyte-plant partnerships to control and remediate pesticide pollution on farmland (we are interested in investigating the way they work together to benefit each other).

Required Skills: Food safety (farmland pollution control and remediation)

30. Development of nanostructured lipid carriers for the controlled release of curcumin in the intestinal tract

Curcumin is a natural hydrophobic polyphenol compound with preventive and therapeutic effects for chronic inflammation and tumor. It is usually encapsulated in delivery systems such as emulsions to improve its water-solubility and oral bioavailability. Nevertheless, emulsions suffer a rapid intestinal digestion leading to the burst release of curcumin, which restricts its bioactivity remarkably. Constructing highly-ordered nanostructured lipid carriers (NLC) through the introduction of solid lipid in the matrix is an effective way to control curcumin release. Nevertheless, the related mechanism and regulation approach remain unclear yet. The imperfect or multiple matrix structure formed by the disturbance of solid lipid crystals by liquid lipid and the interface structure formed by biomacromolecules assembly determine the release process of curcumin in intestinal tract.

- This project will focus on the critical characteristics of the matrix and interface structure of NLC, as well as their regulation approaches.
- The relationship of these critical characteristics with NLC digestion will be clarified and the regulation mechanism of matrix and interface structure on curcumin release will be elucidated.
- Furthermore, matrix/interface combinations will be selected and evaluated for their synergetic effect on the sustainable release of curcumin in intestinal tract.

***Required Skills**: Biochemistry/Food hydrocolloids/Functional foods/Food Science*