

Newsletter: 2015, No. 1



Asia Oceania Agricultural Proteomics Organization <http://www.aoapo.org/Default.aspx>

## The 7th International Symposium on Frontiers in Agriculture Proteome Research

The 7<sup>th</sup> International Symposium on Frontiers in Agricultural Proteome Research will be held on September 23-24, 2015 at Dongjincheon in Goesan-eup, Goesan-gun (International Organic Expo Farm) Chungcheongbuk-do, Goesan-gun, ISOFAR, Korea.

The goal of this symposium is to promote the development of proteome research in the areas agriculture and plant biology and to enhance communication and cooperation among members of the international agricultural proteomics community. The conference will invite leading scientists in the field of plant and agriculture proteomics to share their knowledge on using cutting edge and advanced proteomics technologies to solve important agricultural and plant biology problems.

Scientists from Asia and all over the world who worked on the related areas are welcome to attend this important conference in the beautiful place at Dongjincheon in Goesan-eup, Goesan-gun (International Organic Expo Farm).

The conference is primarily organized by AOAPO and the Korean Society for Crop Science and hosted by the ISOFAR and Chungbuk National University.

### **I. Conference time and Important dates**

Arrival on September 22, 2015. Conference starts from September 23-24, 2015

Abstract Submission Deadline: August 20, 2015

Registration Deadline: August 20, 2015

Opening of the Conference: September 23, 2015

Closing of the Conference: September 24, 2015

## **II. Conference location**

Dongjincheon in Goesan-eup, Goesan-gun (International Organic Expo Farm)  
Chungcheongbuk-do, Goesan-gun, ISOFAR, Korea.

## **III. Website open date**

**Website address:** <http://aoapo.or.kr> (It will be accessible at the end of March, 2015)

Provided by Prof. Sun-Hee Woo

## **Introduction to AOAPO Joint Project Initiative**

Knowledge of plant proteomics is required to accelerate the processes of plant improvement, provide great assurance of food security, expand uses of plant products and the utility and value of crop plants beyond traditional uses. Understanding the proteomic composition of plants and the function of the gene products will greatly accelerate traditional approaches to plant improvement and crop breeding. Recently, efforts have been made to curate some plant proteome databases. None of these databases represent comprehensive and complete collections of the translated product of their genomes. The next challenge in the field of crop plant proteomics is, therefore, to characterize the entire complement of the proteome for a given species. In comparison to yeast, animal, and human proteomics, crop plant proteomics still has a long way to go, which underscores the need for greater funding and integrated approaches in order to obtain a deeper understanding of food crop biology.

Of all the food crops, rice and cereals share the major part of crop production worldwide and are thus of primary importance. Most importantly, availability of genome sequences, large collections of publicly available transcriptome datasets including micro-array and RNA-seq makes this food crop the immediate choice for in-depth proteome analysis. Against the back drop of the recent 1st AOAPO Conference, the 6th International Symposium on Frontiers in Agricultural Proteome Research & 5th Plant Proteomics Conference in China held during June 23-27, 2014 there was a discussion in the AOAPO council for launching an AOAPO joint project. Council members decided to conduct a joint project related to agricultural proteomics.

The proposed project is aimed at developing the PeptideAtlas and Chromosome centric proteome project in rice as a representative cereal that would ensure a resource base for fully annotated proteome representing at least one representative protein encoded by the predicted number of genes from the genome projects, besides discovering potential organ-specific, organelle-specific, and stress-responsive bio-markers in the first phase. This would not only be useful in developing bio-markers, but also would aid in identifying potential candidates for yield enhancement in agricultural production and to optimize food quality as a long term goal.

AOAPO propose to identify the National teams across countries to collaborate and develop complementary protocols, techniques, and niche areas, and to generate resources needed to launch this multinational programme.

Provided by Prof. Subhra Chakraborty

## Introduction of AOAPO Research Group: Dr Chin Chiew Foan (Malaysia)

Dr Chin Chiew Foan is an Associate Professor working at the University of Nottingham Malaysia Campus. It is a branch of University of Nottingham (UK) located on the outskirts of Kuala Lumpur.



Photos of campus and facilities

Dr Chin Chiew Foan's research mainly involves using biomarkers to investigate plant cell growth and development. As a plant grows and multiplies, especially in the

artificial environment, it will sometimes differentiate into different biological forms. Some of these forms are undesirable and can affect the economic value of the products. These biomarkers could then be used to identify the cells that make up these forms and detect the causal agents for these deviations. Different types of biomarkers were developed in my lab including DNA, RNA and protein biomarkers. There are two PhD students in Dr Chin Chiew Foan's group. They are Ms. Tan Hooi Sin and Chai Li Chin. Hooi Sin is working on identifying protein markers associated with high proliferation rate of callus culture in oil palm tissue culture samples. She has performed protein profiling for the oil palm leaf. Differential protein expressions from high and low proliferated oil palm were also investigated. The isolated protein markers are currently being verified using real-time PCR and Western Blotting. Li Chin is working on using RNA transcriptomic sequencing to investigate the occurrence of somaclonal variations in vanilla orchid tissue culture. Tissue culture of vanilla orchid serves as a promising alternative source of planting materials due to the high demand for setting up vanilla plantations. However, the potential occurrence of off-type culture samples will deter production of high quality tissue culture plantlets. Through genome-wide study on gene expression of the culture samples, it will help to unravel the underlying causes for the genetic changes.



Provided by Dr. Chin Chiew Foan

**Newsletter Editor:**

**Pingfang Yang (China),** Tel/fax : +86-27-87510956; Email: yangpf@wbcas.cn