中村友輝

中央研究院植物暨微生物學研究所助研究員

代表作名稱：

★ Y. Nakamura*, F. Andrés, K. Kanehara, Y.-C. Liu, P. Dörmann, and G. Coupland. "Arabidopsis Florigen FT Binds to Diurnally Oscillating Phospholipids that Accelerate Flowering." *Nature Communications* 5 (2014): 3553.

★ Y. Nakamura*, N.Z.W. Teo, G. Shui, C.H.L. Chua, W.-F. Cheong, S. Parameswaran, R. Koizumi, H. Ohta, M.R. Wenk, and T. Ito*. "Transcriptomic and Lipidomic Profiles of Glycerolipids during Arabidopsis Flower Development." *New Phytologist* 203 (2014): 310-322.

得獎簡評：

中村友輝博士目前是在中央研究院植物暨微生物學研究所擔任助研究員，其在「脂肪分子可作為開花的分子訊號」上的新穎發現是獲選中央研究院年輕學者研究著作獎的主要原因。這個發現不僅在調控植物發育之基礎分子機制上有重要的影響，並且在控制觀賞植物花朵發育的花期以及同步開花調控的未來應用上也有相當的重要性。

中村博士最近的研究重點是在「FT 蛋白質」。此一蛋白質複合體的作用是透過轉錄調控來活化莖尖的開花基因。中村博士的重要發現在於磷脂的脂肪分子可以與 FT 蛋白質結合，以啟動植物之間光週期影響開花時機的訊息傳遞。這個新發現闡明控制花朵發育的調節機制，並為植物生長發育創造出可能調控的新契機。

得獎人簡歷：

Yuki Nakamura (1978-) received his PhD degree in 2007 from Tokyo Institute of Technology for his research on plant glycerolipid metabolism under normal and phosphate-starved conditions. After 6 months of extensive work at the same lab as a postdoc, he received 2-year postdoc fellowship from Japanese Society for the Promotion of Science (JSPS) to join Temasek Life Sciences Laboratory (Singapore), where he started to work on lipid function in flower development. In 2009, he moved to National University of Singapore

to study lipidomics technology. In the following year, he was awarded Alexander von Humboldt Research Fellowship to carry out his research in Max-Planck-Institute for Plant Breeding Research (Cologne, Germany) and University of Bonn (Germany) for a year. Since September 2011, he has been an assistant research fellow at IPMB, Academia Sinica. He has been awarded the 2nd Paul K. Stumpf Award (2009), 7th Shang-Fa Yang Award (2014) and EMBO Young Investigator 2014. His current research interest is "Lipid diversity in plant growth and development".

代表作簡介：

Lipids are fundamental biological molecules, which have multiple functions in the biological processes such as the component of biological membranes and epidermal surface, a form of energy storage and signaling molecules. Most of lipid molecules have hydrophobic acyl groups. For example, glycerolipids are composed of hydrophilic head group and two hydrophobic acyl groups on the basis of glycerol backbone. Thus, combinations of different polar head groups and acyl species with positional specificity could result in hundreds of different molecular species. Such complex lipid molecular species are unevenly distributed across different organelles, and to a greater extent at different tissues or organs. Moreover, these lipid compositions are continuously changing in the process of growth and development, characterizing different membrane systems and the surrounding cellular environment.

Our biological interest is thus "Lipid Diversity", which is defined here as the spatiotemporal profiles of lipid molecular species. The fundamental questions to address are;

Q1: How is lipid diversity established and maintained throughout plants' life cycle?

Q2: How does lipid diversity interact with core modules of developmental regulator through lipid-protein interaction?

We have been addressing these questions by taking flower development of *Arabidopsis thaliana* as a model. Although ample evidence suggests important roles for glycerolipids in flower development, stage-specific lipid profiling in tiny Arabidopsis flowers is challenging. By utilizing a unique transgenic plant that synchronizes flower development in Arabidopsis, our concurrent lipidomic and transcriptomic profiling of glycerolipid metabolism revealed distinct set of pathways stimulated at different stages of flower development in Arabidopsis. A functional link of these profiles with flower development is lipid-protein interaction; we revealed the binding of phosphatidylcholine (PC) to FLOWERING LOCUS T (FT), which is a component of florigen, a long-range flowering signal transmitted from leaf companion cells to the shoot apex where it initiates flowering. Previous analysis of the crystal structure of FT identified a putative ligand binding pocket predicted to be filled by a phosphate derivative. Here, we showed that *in vitro* FT specifically binds PC. A transgenic approach to increase PC levels *in vivo* in the shoot apical meristem accelerated flowering whereas reduced PC levels

delayed flowering, demonstrating that PC levels are correlated with flowering time. The early flowering was related to FT activity, because expression of two FT-effector genes, *SUPPRESSOR OF OVEREXPRESSION OF CONSTANS1* (*SOC1*) and *APETALA1* (*AP1*), was increased in these plants. Simultaneous increase of FT and PC in the shoot apical meristem further stimulated flowering, whereas a loss of FT function led to an attenuation of the effect of increased PC. Specific molecular species of PC oscillated diurnally, and night-dominant species were not the preferred ligands of FT. Elevated night-dominant species of PC during the day delayed flowering. We suggest that FT binds to diurnally changing molecular species of PC to promote flowering.

得獎感言：

It is my great honor to receive this prestigious award. This would be my important milestone to drive further motivation of my scientific career. I would like to thank Academia Sinica for being in support of my successful set-up of independent research program. Special thanks to all present and past colleagues at IPMB, as well as my external collaborators and mentors for their support and encouragement. I would like to share this honor with our members in the lab.