NUS National University of Singapore | Department of Biological Sciences, Faculty of Science

SEMINAR

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Hosted by A/P Xu Jian

Plant genome contributions to microbiome establishment and services



Jeff Bennetzen received his Ph.D. in Biochemistry from the University of Washington for studies of yeast molecular genetics, did postdoctoral work for one year, worked in industry for two years, and then joined the Department of Biological Sciences at Purdue University as an Assistant Professor in 1983. He rose to the positions of Professor in 1991 and Umbarger Professor in 1999. Since 2003, he has been the Giles Professor in the Department of Genetics at the University of Georgia. He has had laboratories in China since 2012. Dr. Bennetzen was elected a member of the US National Academy of Sciences in 2004. He founded the Maize Genetics Executive Committee and the McClintock Prize. His laboratory is best known for its work investigating the very dynamic processes that determine the structure, function and evolution of plant genomes, and he has published more than 200 articles on this subject.

By **Jeff Bennetzen**

Professor, Department of Genetics, University of Georgia and State Key Laboratory of Tea Plant Biology and Utilization, Anhui Agricultural University

The microbial communities that surround and permeate all plant life are incredibly diverse. Little is known about how these communities are established, how they change or the services they provide. The Bennetzen lab has been using the microbiome as a phenotype to characterize the plant genes that contribute to microbial community establishment, and is using this information to determine the specific functions that these microbes provide, both to their communities and to their plant hosts. Microbes involved in the soil::root interaction are especially important for the contributions they make to the ability of the host to acquire essential nutrients, to tolerate abiotic stresses and to resist soil-borne diseases. All of the plant species that we've investigated differ in which microbes they attract and the communities they establish, and we have mapped plant genes that determine which communities and which services are provided. Examples will be provided for a wide range of plants, from highly desert-adapted organisms, to carnivorous plants in bogs, to temperate grain, forage and biofuel crops.

Artwork by Ann Nee, DBS, NUS