

## Profile of Dr. Yao-Guang Liu



Dr. Yao-Guang Liu was born in March 1954, in Guangdong China. He received his Bachelor's degree in agricultural science from South China Agricultural University (SCAU) in 1982. He received his Master's degree in agricultural science in 1988 from Kagawa University and Ph.D. in 1991 from Kyoto University in Japan. He worked in the Mitsui Plant Biotechnology Research Institute, Japan, from 1991 to 1996, and has been a professor at SCAU since 1997. He serves as vice director of the State Key Laboratory of Conservation and Utilization of Subtropical Agricultural Bior-resources.

Dr. Liu's research interests mainly focus on understanding of the molecular mechanisms for male fertility and sterility in rice, including cytoplasmic male sterility and restoration, environment-sensitive genic male sterility, and hybrid sterility. His significant contributions in these fields shed light on the regulation of fertility for hybrid rice breeding. He also has made outstanding contributions to biotechnology, such as the invention of Thermal Asymmetric InterLaced PCR (TAIL-PCR), Transformation-competent Artificial Chromosomes (TACs), multi-transgene stacking systems, as well

as a plant-oriented CRISPR/Cas9 genome editing tool-kit and related software platform. These technologies and methods have been widely used in scientific research.

Dr. Liu has published more than 140 papers in high-profile journals such as *Nature Genetics*, *Annual Review of Plant Biology*, *Cell Research*, *Nature Communications*, *Proceedings of the National Academy of Sciences of the United States of America*, *The Plant Cell*, and *Molecular Plant*; these papers have received more than 7,000 ISI citations. His findings on cytoplasmic male sterility/restoration and hybrid sterility have been written into textbooks of genetics and plant molecular biology, and his TAIL-PCR technique has been collected in many technical books including *Molecular Cloning*. In addition, Dr. Liu has won many honors and awards, including the National Science Foundation of China for Distinguished Young Scholars, the Changjiang Scholars Program of the Ministry of Education, Second Prize of National Natural Science Award, First Prize of Guangdong Provincial Science & Technology Award, First Prize of DBN (Da Bei Nong) Science & Technology Award. In recognition of his distinguished achievements and reputation in science, Dr. Liu was elected a member of the Chinese Academy of Sciences in 2017.

### Molecular basis of fertility regulation in hybrid rice breeding

The production of hybrid rice successfully harnesses hybrid vigor to improve crop yield and performance compared with inbred lines; however, without male-sterile lines, the generation of hybrid seed would be costly and laborious. Chinese scientists lead in the development of technology for hybrid rice production by the three-line and two-line breeding systems, using specific rice germplasm, i.e., cytoplasmic male sterility/fertility restorer (CMS/Rf) and environment-sensitive genic male sterility (EGMS) lines (Chen and Liu, 2014). Three types of CMS lines, namely, CMS-WA

(Wild-Abortive type), CMS-BT (Boro II type) and CMS-HL (Hong-Lian type) have been applied for hybrid rice seed production (Chen and Liu, 2014).

Over the past 22 years, Dr. Liu has led a number of projects to systematically decipher the molecular basis for CMS/Rf systems (CMS-BT/*Rf1* and CMS-WA/*Rf3Rf4*) and several chromosomal loci for hybrid sterility. His group found that CMS-BT is caused by the mitochondrial cytotoxic protein ORF79 encoded by a chimeric gene *orf79*, which is co-transcribed with *B-atp6* to form a dicistronic transcript *B-atp6-orf79*. The cognate restorer locus *Rf1* consists of two adjacent genes encoding the pentatricopeptide repeat (PPR) proteins RF1A and RF1B. RF1A mediates cleavage of the *B-Atp6-orf79* transcript, and RF1B promotes degradation of the whole dicistronic transcript, thus preventing translation of *orf79* in the mitochondria, and restoring the fertility of CMS-BT (Wang et al., 2006).

Moreover, Dr. Liu's group identified CMS-WA-associated mitochondrial transcripts and the causal gene *WA352* using a 'catch-all' strategy (Liu et al., 2007; Luo et al., 2013). His group revealed that the *WA352* protein interacts with nuclear-encoded Cytochrome C Oxidase Subunit 11 (COX11), leading to a burst of reactive oxygen species and cytochrome c release from the mitochondria into the cytosol. This causes premature programmed cell death of tapetal cells and pollen abortion in CMS-WA lines (Luo et al., 2013). This is the first finding that, like restoration of fertility in CMS, induction of CMS involves interactions between mitochondrial and nuclear genes. He cloned the CMS-WA restorer genes *Rf4* and *Rf3*. *Rf4* encodes a PPR protein that mediates the degradation of *WA352* transcripts (Tang et al., 2014), while *Rf3* may restore fertility on the protein level (Tang et al., unpublished data). By studying the evolution of *WA352*, Dr. Liu's group revealed for the first time how functional CMS genes originated from non-functional protogenes by multiple rearrangements of mitochondrial genomes and sequence variation (Tang et al., 2017). In addition, Dr. Liu collaborated with another research group to isolate a long non-coding RNA conferring photoperiod/thermo-sensitive genic male sterility at a genetic locus that is used for two-line hybrid rice (Zhou et al., 2012).

Hybrid sterility plays an important role in speciation and it is a reproductive barrier for utilization of hybrid vigor between distantly related species or subspecies. Dr. Liu studied the molecular basis for the action of the genetic loci *Sa* and *Sc* for hybrid male sterility between the Asian rice *indica* and *japonica* subspecies, and *S1* for hybrid male and female sterility between the African and Asian rice species. Genetic and molecular evidence revealed that *Sa* is a complex locus consisting of two adjacent genes, *SaF* and *SaM*, and that three proteins encoded by the diverged alleles of the two genes interact to determine the male sterility and compat-

ibility in the gametes of *indica-japonica* hybrids. Based on these findings, Dr. Liu proposed a two-gene/three-component interaction model for *Sa*-mediated hybrid male sterility (Long et al., 2008). The findings on the complex locus for hybrid sterility have prompted later studies in other laboratories to show that most of hybrid sterility loci in plants consist of multiple closely-linked genes that interact to control hybrid sterility.

Recently, Dr. Liu's group cloned another *indica-japonica* hybrid sterility gene, *Sc*, and revealed that the *indica* allele *Sc-i* has multiple tandem-duplicated copies of a novel DUF1618 gene essential for pollen development. The highly expressed product of *Sc-i* suppresses expression of the *japonica* allele *Sc-j*, leading to the abortion of male gametes carrying *Sc-j* (Shen et al., 2017). Liu's group isolated the gene at the *S1* locus encoding a peptidase protein, OgTPR1, which plays the key role in African-Asian interspecific rice hybrid sterility (Xie et al., 2017), and recently found that three adjacent genes at the *S1* locus interact to control the hybrid sterility (Xie et al., 2019). Based on these findings, Dr. Liu developed an effective technology using genome-editing technology to knock out or reduce the copy number of the key elements of these loci for hybrid sterility. This enables breeders to rapidly produce hybrid-compatible lines, which paves the way to overcoming the reproductive barrier for utilization of distant hybrid vigor in crop breeding.

## Innovations in plant biotechnology and genetic engineering

Dr. Liu has made significant contributions to plant biotechnology. He is the inventor of TAIL-PCR, which enables the isolation of unknown sequences flanking known sequences (Liu and Whittier, 1995; Liu et al., 1995). This technology has been widely used in molecular biology studies, and his TAIL-PCR papers have been cited more than 3,000 times. Dr. Liu also developed the TAC vectors and high-efficiency multi-transgene stacking systems (Lin et al., 2003; Liu et al., 1999), which have been used for synthetic biology in plants, such as successfully reconstructing the complex anthocyanin and astaxanthin biosynthesis pathways in rice endosperm (Zhu et al., 2017, 2018). Dr. Liu established a simple, high-efficiency plant-optimized CRISPR/Cas9 genome editing system for multiple targets (Ma et al., 2015), which has been applied for basic research and genetic improvement in more than 600 laboratories around the world. His group developed a web-based tool-kit, CRISPR-GE (<http://skl.scau.edu.cn/>) for genome editing (Xie et al., 2017). These new technologies significantly accelerated basic research in plant sciences and genetic modification in crops.

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