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Profile of Dr. Qian Qian



Dr. Qian Qian graduated with a Bachelor of Science in Genetics from Nankai University in 1983, a Master of Science in Crop Genetics and Breeding from Hokkaido University in 1989, and a doctorate in Genetics and Breeding from the Chinese Academy of Agricultural Sciences in 1995. Dr. Qian served as a research intern (1983–1989), research assistant (1990–1996), research associate (1997–2001), and research fellow at the China National Rice Research Institute (since 2002). From 1996 to 1997, he served as a visiting scholar at the Japan International Research Center for Agricultural Sciences. From 1997 to 1998, he served as a senior visiting scholar at the Institute of Genetics and Developmental Biology of the Chinese Academy of Sciences. From 1998 to 2002, he served as a senior scientist at the China National Rice Research Institute. From 2002 to 2007, he served as a senior visiting scholar and visiting professor at Okayama University. Since 2006, Dr. Qian has been the director of the State Key Laboratory of Rice Biology in the China National Rice Research Institute.

Dr. Qian Qian has made contributions to crop germplasm genetic resources, from addressing the key issues in agricultural production to developing strategies for the utilization of genetic resources using modern biotechnology. He has also conducted systematic and in-depth research in the fields of exploration and innovation of rice genetic germplasm resources, analysis of important agronomic traits, and molecular breeding. Dr. Qian and colleagues have achieved a series of original research results, which have been translated into outstanding contributions in the relevant fields.

Along with being listed on the Elsevier list of "The Highly Cited Chinese Researchers" from 2019 to 2021, Dr. Qian has published more than 200 papers in high-profile journals, such as *Nature Genetics*, *Nature Plants*, *Nature Communications*, *Plant Cell*, *Molecular Plant*, and *Proceedings of the National Academy of Sciences of the United States of America*. He has also developed and commercialized ten rice varieties. Dr. Qian has won several national honors, including the National Natural Science First and Second Prizes and the Second Award of the National Scientific and Technological Progress. He has been a member of various scientific committees and an editor of numerous scientific journals. In 2019, Dr. Qian was elected as a member of the Chinese Academy of Sciences.

Developing important germplasm resources and genetic populations of rice

Dr. Qian Qian and colleagues excavated and produced nearly 50,000 accessions for functional genome research and genetic analysis. They also established a rice resource bank with more than 4,000 lines of high-yield, high-quality, and high-resistance. To conduct the genetic investigation of rice, he created the first collection of near-isogenic lines with an indica rice background (Zeng et al., 2003), which has been widely used as a tool for the genetic analysis of rice. The first japonica rice variety, new-Nipponbare, was developed by Dr. Qian. This species overcomes the problem of unstable fertility of Nipponbare in different ecological areas, and it is easy to be transformed with good stress resistance (Hu et al., 2014). To provide a unique model plant type for genetic

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analysis and functional genome research, he created a series of super dwarf rice germplasms called "Xiaowei", which have a short growth cycle, need small growth space, and can be grown indoors (Hu et al., 2018). The permanent genetic populations of japonica/indica rice developed have become valuable germplasm sources for the genetic research of rice (Zhang et al., 2014). He deciphered the genetic underpinnings and molecular mechanisms of the grain-shape genes *GL7*, *GS2*, *GL5*, *LG1*, and *WG1*, which coordinate the regulation of grain length and quality. This work provides a theoretical basis for developing high-yield and high-quality rice varieties (Hao et al., 2021; Hu et al., 2015; Lyu et al., 2020; Qiao et al., 2021; Wang et al., 2015; Yu et al., 2020). The nitrogen-efficient gene *OsNR2* was cloned using recombinant inbred lines derived from indica 9311 and japonica Nipponbare, and the introgression of indica *OsNR2* into japonica significantly boosted the NR activity, thereby providing new gene resources for sustainable rice production (Gao et al., 2019). Using the recombinant inbred lines derived from Huazhan and Reyan, the multi-tillering characteristics of Huazhan were analyzed. HTD1^{HZ}, a new allelic form of strigolactones synthesis gene *HTD1* in Huazhan, was effective in increasing the number of tillers without affecting the seed setting rate, and as the heterozygous state of HTD1^{HZ}, it can increase the number of tillers; the hybrid rice developed with Huazhan as the parent can achieve a stable yield (Wang et al., 2020).

Leading the concept development for molecular design and molecular breeding practices

Dr. Qian put forward a new viewpoint in 2003 that "rice genetic design breeding will become the breakthrough for the third revolution of rice breeding." He wrote the books "*Technical Guide to Rice Molecular Breeding*" and "*Rice Gene Design Breeding*," which elaborated on the implementation of rice molecular design breeding, analyzed the yield and starch synthesis pathway of super hybrid rice, determined the genes affecting yield and quality and their molecular mechanisms, and provided an important theoretical basis for molecular design breeding and genetic improvement of rice yield and quality. He developed recombinant inbred lines using a widely used hybrid rice "Liangyoupei 9" and analyzed the yield-related loci for this super hybrid rice; based on the fine structure of the genome of indica 9311, the regulation mechanism of the formation of yield traits was revealed (Gao et al., 2013). He put forward a molecular design model for developing future super hybrid rice by a combination of ideal plant architecture with indica-japonica heterosis and developed a molecular breeding strategy using the heterosis between indica and japonica subspecies, which provides a guideline for the third yield leap of rice production (Qian et al., 2016). Through molecular design breeding, 28 excellent alleles in japonica rice controlling rice quality were introgressed into indica variety "Teqing" with super high-yield but poor eating quality, and a variety with high quality and yield, Guangliangyou 7203, was developed and commercialized as a nationally approved variety. Additionally, technology and platform were established for efficient, precise, and directional rice molecular design breeding (Zeng et al., 2017).

Developing rice molecular breeding technology and coordinating integrated efforts of industry, universities, and institutions

In the 1990s, Dr. Qian took the lead in introducing DNA molecular marker technology into the fingerprint of hybrid rice, which was selected by the Ministry of Agriculture as the first molecular identification technology for hybrid rice quality standard in China and was widely used in numerous rice variety identification institutions all over the country, thereby laying a foundation for developing identification technology of crop varieties in China. To strengthen the exchange between rice geneticists and breeders and promote the transformation of theoretical research into breeding practice, Dr. Qian organized "National Rice Mutants, Functional Genomics, and Biotechnology Breeding Symposiums" four times and "China-Japan International Symposiums on Rice Morphogenesis" three times, which strengthened the academic exchanges between China and Japan in rice genetics and molecular breeding. He also organized the "International Symposium on Rice Science" between the National Natural Science Foundation of China and the International Rice Research Institute, which made a great contribution to rice science with a global impact.

References

Gao, Z., Wang, Y., Chen, G., Zhang, A., Yang, S., Shang, L., Wang, D., Ruan, B., Liu, C., Jiang, H., et al. (2019). The *indica* nitrate reductase gene *OsNR2* allele enhances rice yield potential and nitrogen use efficiency. Nat Commun 10, 5207.

Gao, Z.Y., Zhao, S.C., He, W.M., Guo, L.B., Peng, Y.L., Wang, J.J., Guo, X.S., Zhang, X.M., Rao, Y.C., Zhang, C., et al. (2013). Dissecting yield-associated loci in super hybrid rice by resequencing recombinant inbred lines and improving parental genome sequences. Proc Natl Acad Sci USA 110, 14492–14497.

Hao, J., Wang, D., Wu, Y., Huang, K., Duan, P., Li, N., Xu, R., Zeng, D., Dong, G., Zhang, B., et al. (2021). The GW2-WG1-OsbZIP47 pathway controls grain size and weight in rice. Mol Plant 14, 1266–1280.

Hu, J., Dong, G., Fang, Y., Rao, Y., Xu, J., Xue, D., Yu, H., Ge, C., Shi, Z., Pan, J., et al. (2014). A new-nipponbare rice germplasm with high seed-setting rate. J Genet Genomics 41, 549–552.

Hu, J., Wang, Y., Fang, Y., Zeng, L., Xu, J., Yu, H., Shi, Z., Pan, J., Zhang, D., Kang, S., et al. (2015). A rare allele of GS2 enhances grain size and grain yield in rice. Mol Plant 8, 1455–1465.

Hu, S., Hu, X., Hu, J., Shang, L., Dong, G., Zeng, D., Guo, L., and Qian, Q.

(2018). Xiaowei, a new rice germplasm for large-scale indoor research. Mol Plant 11, 1418–1420.
Lyu, J., Wang, D., Duan, P., Liu, Y., Huang, K., Zeng, D., Zhang, L., Dong, G., Li, Y., Xu, R., et al. (2020). Control of grain size and weight by the GSK2-LARGE1/OML4 pathway in rice. Plant Cell 32, 1905–1918.
Qian, Q., Guo, L., Smith, S.M., and Li, J. (2016). Breeding high-yield superior quality hybrid super rice by rational design. Natl Sci Rev 3, 283–294.
Qiao, J., Jiang, H., Lin, Y., Shang, L., Wang, M., Li, D., Fu, X., Geisler, M., Qi, Y., Gao, Z., et al. (2021). A novel miR167a-OsARF6-OsAUX3 module regulates grain length and weight in rice. Mol Plant 14, 1683–1698.
Wang, Y., Shang, L., Yu, H., Zeng, L., Hu, J., Ni, S., Rao, Y., Li, S., Chu, J., Meng, X., et al. (2020). A strigolactone biosynthesis gene contributed to the green revolution in rice. Mol Plant 13, 923–932.
Wang, Y., Xiong, G., Hu, J., Jiang, L., Yu, H., Xu, J., Fang, Y., Zeng, L., Xu, E., Xu, J., et al. (2015). Copy number variation at the GL7 locus contributes to grain size diversity in rice. Nat Genet 47, 944–948.
Yu, X., Xia, S., Xu, Q., Cui, Y., Gong, M., Zeng, D., Zhang, Q., Shen, L., Jiao, G., Gao, Z., et al. (2020). *ABNORMAL FLOWER AND GRAIN 1* encodes OsMADS6 and determines palea identity and affects rice grain yield and quality. Sci China Life Sci 63, 228–238.
Zeng, D., Qian, Q., Dong, G., Zhu X., Dong F., Teng S., Guo, L., Cao, Li., Cheng, S., and Xiong, Z. (2003). Development of isogenic lines of morphological markers in indica rice. Acta Botanica Sin 9, 1116–1120.
Zeng, D., Tian, Z., Rao, Y., Dong, G., Yang, Y., Huang, L., Leng, Y., Xu, J., Sun, C., Zhang, G., et al. (2017). Rational design of high-yield and superior-quality rice. Nat Plants 3, 17031.
Zhang, G.H., Li, S.Y., Wang, L., Ye, W.J., Zeng, D.L., Rao, Y.C., Peng, Y. L., Hu, J., Yang, Y.L., Xu, J., et al. (2014). *LSCHL4* from *japonica* cultivar, which is allelic to *NAL1*, increases yield of *indica* super rice 93-11. Mol Plant 7, 1350–1364.