Agri-2014
OMICS Group Conferences
Accelerating Scientific Discovery
2nd International Conference on
Agricultural & Horticultural Sciences
February 03-05, 2014 Hyderabad, India

Exploration of novel stress tolerance genes from chaling wild rice

Zhilong Wang

Hunan Agricultural University, China

Abstract

Chaling wild rice grows in Chaling, Hunan Province, one of the two most northern distribution sites for wild rice in China. It displays cold tolerance and resistance to rice blast. To identify abiotic and biotic stress tolerance genes from Chaling wild rice, we sequenced the genome using Hiseq 2000. The sequence data contain 6,803 Mb and showed mapping rate 91.93% and coverage ratio 92.94% to the Japonica Nipponbare genome (IRGSP), and mapping rate 88.95% and coverage ratio 84.47% to the Indica 9311 genome. A total of 1,160,685 SNPs (Single Nucleotide Polymorphism) were identified between Chaling wild rice and Nipponbare, with a ratio of 71.25% transition and 28.3% heterozygosity. A total of 1,773,410 SNPs were identified between Chaling wild rice and 9311, with a ratio of 70.83% transition and 22.25% heterozygosity. In addition, 56,801 SVs (Structure Variation) were identified between Chaling wild rice and Nipponbare, with a ratio of 97.31% INSs (Insertion) and DELs (Deletion), and 72,987 SVs (Structure Variation) were identified between Chaling wild rice and 9311, with a ratio of 97.47% INSs and DELs. Further analysis of abiotic and biotic stress tolerance genes from Chaling wild rice is in progress. Our results suggest that Chaling wild rice is more closed to the Japonica Rice Nipponbare in evolution and provide a basis to utilize stress resistance genes for rice breeding.

Biography

Zhilong Wang has completed his PhD from National University of Singapore and postdoctoral studies from NIA/NIH and NCSU in USA. Now, he is a professor from Hunan Agricultural University, China. He has published more than 20 papers in reputed journals and serving as an editorial board member of ACST.