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## QTL mapping of nitrogen deficiency tolerance by genome-wide association study approach in a nested association mapping (NAM) population of rice

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To develop green super rice varieties with high yield and improved nitrogen deficiency tolerance (NDT), a nested association mapping population was developed through a modified backcross breeding approach using a high yielding and widely adaptable Xian variety, Huanghuazhan (HHZ) as the recipient and 8 donor parents IR50, IR64, Teqing, PSBRC28, PSBRC66, CDR22, OM1723 and Phalguna. A total of 496 lines, plus the HHZ, were used for evaluation of heading date, plant height, grain yield, biomass yield, thousand grain weight under the low nitrogen (LN) and the normal nitrogen (NN) conditions in 2013 early season, 2013 last season and 2014 early season. Total of 48 QTLs were identified by R-package MAGICqtI based on 7388 bins derived from 400K high-quality SNPs under the LN, NN and LN/NN conditions. Among them, ten main-effect QTLs were simultaneously identified in the LN and NN conditions. Four genomic regions, including bin16 on chromosome 1, bin 2186 on chromosome 3, bin 3699 on chromosome 6, and bin 4859 on chromosome 8 were simultaneously identified for NDT-related traits. The *qTGW2-1* for thousand grain weight, which was simultaneously detected across three seasons under the LN condition, was delimited into a region of 50Kb by genotypic overlapping of recombinant lines inside the marker bin1459. The donor alleles at *qTGW2-1* contribute to NDT. Molecular designed pyramiding of favorable alleles at the consistently detected NDT-QTLs is under way to develop new breeding lines with high yield and NDT based on performance of NDT and QTL information of NAM lines in the elite background.

### Recent Publications

1. Yu J, Holland JB, McMullen MD, et al (2008). Genetic design and statistical power of nested association mapping in maize. *Genetics* 178: 539–551
2. Buckler ES, Holland JB, Bradbury PJ, et al. (2009). The genetic architecture of maize. *Science* 325: 714–718.
3. Hu B, Wang W, Ou SJ, et al (2015) Variation in NRT1.1B contributes to nitrate-use divergence between rice subspecies. *Nature Genetics*, 47(7): 834-838
4. Sun HY, Qian Q, Wu K, et al (2014) Heterotrimeric G proteins regulate nitrogen-use efficiency in rice. *nature genetics*, 46: 652-657.
5. Bo Feng, Kai Chen, Yanru Cui, et al (2018) Genetic dissection and simultaneous improvement of drought and low nitrogen tolerances by designed QTL pyramiding in rice. *Frontiers in Plant Science*, 2018.9:306

### Biography

Kai Chen got PhD degree on Crop Sciences in 2012 in Shenyang Agricultural University, China. After finishing postdoctoral career of molecular rice breeding for four years at CAAS, he joined the Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences, focusing on molecular breeding for hybrid rice and inbred rice for high yield, high grain quality, abiotic and biotic stress tolerances. So far, he has published 5 papers in international journals.

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