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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 MAGICqtl 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.

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