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## Identification of rice landraces with promising yield and the associated genomic regions under low nitrogen

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With the priority of the low input sustainable rice cultivation for environment friendly agriculture, NUE of rice becomes the need of the hour. A set of 472 rice genotypes comprising landraces and breeding lines were evaluated for two seasons under field conditions with low and recommended nitrogen and > 100 landraces were identified with relative higher yield under low nitrogen. Donors were identified for higher N uptake, N translocation into grains and grain yield under low N. Grains on secondary branches, N content in grain and yield appears to be the selection criterion under low N. Through association mapping, using minimum marker set of 50 rice SSR markers, 12 genomic regions were identified for yield and yield associated traits under low nitrogen. Four associated genomic regions on chromosomes 5, 7 and 10 were fine mapped and QTL for yield under low N were identified from the marker delimited regions. Three candidate genes viz., 2-oxoglutarate /malate translocator (Os05g0208000), alanine aminotransferase (Os07g0617800) and pyridoxal phosphate-dependent transferase (Os10g0189600) from QTL regions showed enhanced expression in the genotypes with promising yield under low N. Marker assisted selection using SSR markers associated with three candidate genes identified two stable breeding lines confirmed through multi-location evaluation.