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## Identification of nitrogen use efficiency genes in Barley: Searching for QTLs controlling complex physiological traits

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Over the past half century, the use of nitrogen (N) fertilizers has markedly increased crop yields, but with considerable negative effects on the environment and human health. Consequently, there has been a strong push to reduce the amount of N fertilizer used by maximizing the nitrogen use efficiency (NUE) of crops. One approach would be to use classical genetics to improve the NUE of a crop plant. This involves both conventional breeding and quantitative trait loci (QTL) mapping in combination with marker-assisted selection (MAS) to track key regions of the chromosome that segregate for NUE. To achieve this goal, one of initial steps is to characterize the NUE-associated genes, then use the profiles of specific genes to combine plant physiology and genetics to improve plant performance. In this study, on the basis of genetic homology and expression analysis, barley candidate genes from a variety of families that exhibited potential roles in enhancing NUE were identified and mapped. We then performed an analysis of QTLs associated with NUE in field trials and further analyzed their map-location data to narrow the search for these candidate genes. These results provide a novel insight on the identification of NUE genes and for the future prospects, will lead to a more thorough understanding of physiological significances of the diverse gene families that may be associated with NUE in barley.

### Biography

Mei Han is an associate professor at the College of Biology and Environment, Nanjing Forestry University. In 2013, she obtained Ph.D. degree from Heidelberg University, Germany. She did his postdoctoral research at University of Alberta, Canada. She has published more than 15 research articles in Plant Molecular Biology and Genetics field. She has been serving as a guest reviewer of Plant Science and BMC Plant Biology.