

Variation characteristics of the nitrate reductase gene of key inbred maize lines and derived lines in China

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ABSTRACT. Key inbred lines have played a fundamental role in maize genetics and breeding. Research on variation characteristics of key genes from key inbred lines and from derived lines is important for early identification and evaluation of inbred maize lines. The nitrate reductase (NR) gene, which plays a central role in nitrate acquisition, was the target gene for this research. Forty-one inbred maize lines were investigated, including four key inbred lines: Huangzaosi, Mo17, Dan340, and Ye478. Through multiple sequence alignment with the NR gene from B73, used as a control, we found that: 1) the NR gene of most inbred lines from Huangzaosi and from derived lines had two insertion fragments and two replacement fragments; 2) the NR gene of most inbred lines from Mo17 and derived lines had one insertion fragment and one replacement fragment; 3) there were two common variations and eight common SNPs in the NR gene of the four key lines.

Huangzaosi and Mo17 also had three common variations compared with the other key lines. Moreover, Mo17 had some unique variations; there were no unique variations in the other key lines, even for SNPs, and 4) phylogenetic tree analysis showed that the NR gene of the derived lines from the same key line had higher sequence homology. Based on the above NR gene variation characteristics and sequence homology of key inbred lines and derived lines, a candidate inbred line can be preliminarily selected and evaluated by marker development and/or sequence alignment of the NR gene.

Key words: Maize inbred lines; Derived lines; Variation characteristics; Nitrate reductase gene