Genetic loci mapping associated with maize kernel number per ear based on a recombinant inbred line population grown under different nitrogen regimes

X.H. Liu¹, S.L. He³, Z.P. Zheng², Z.B. Tan¹, Z. Li² and C. He²

¹Key Laboratory of Southwest China Wildlife Resources Conservation, Ministry of Education, College of Life Sciences, China West Normal University, Nanchong, P.R. China
²Nanchong Institute of Agricultural Sciences, Nanchong, P.R. China
³Beijing IPE Bio-Technology Co., Ltd., Beijing, P.R. China

Corresponding author: Z.P. Zheng
E-mail: lxhxhsfdx@yahoo.com.cn

Received March 15, 2011
Accepted September 28, 2011
Published December 22, 2011
DOI http://dx.doi.org/10.4238/2011.December.22.5

ABSTRACT. Kernel number per ear (KNE) is one of the most important yield-related agronomic traits in maize (Zea mays). To clarify its genetic basis, we made a quantitative trait locus (QTL) analysis of KNE in a recombinant inbred line population derived from lines Mo17 and Huangzao4, under two nitrogen (N) regimes. Seven QTLs, on chromosomes 4, 6 and 9, were mapped under the high N regime, which explained phenotypic variation ranging from 5.03 to 15.49%. Under the low N regime, three QTLs were located on chromosomes 6 and 9, which accounted for phenotypic variation ranging from 8.54 to 12.21%. These QTLs had different mapping intervals to their nearest markers, ranging from 0 to 16.5 cM. According to the chromosome positions and genetic effects of these QTLs, only seven QTLs for KNE were identified in our experiment, out of which three were found under both N regimes, on chromosomes 6 (one) and 9 (two); the other four
were mapped only under the high N regime, on chromosomes 4 (three) and 6 (one). This information could be useful for developing marker-assisted selection in maize-breeding projects.

**Key words:** Maize (*Zea mays*); Kernel number per ear; Nitrogen; Quantitative trait locus