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Fine-mapping of a novel major soybean maturity locus QNE1 physically near E1 gene  
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Soybean maturity and flowering time are key agronomic traits influencing distribution of soybean cultivars. Since E1 to E10 have been mapped, however, additional genes controlling maturity and flowering time were reported. Using a population of Suinong 14 (Chinese cultivar) and Iwaheme (Japanese cultivar), we mapped a new major QTL (quantitative trait loci) near E1, referred as to QNE1 (major QTL near E1) for flowering time. Both parental cultivars have been confirmed to carry the dominant E1 locus. Using recombinants identified F2:3 and F2:4populations, QNE1 was delimited to Chr06:18883704—19395996, in which 2 candidate genes whose coding region are polymorphic between parents. In addition, a major QTL was mapped to the region on Chromosome 20, which was preliminarily considered to be an allelic variation of E4/e4-kam at the E4 locus. Analysis of a mapping population of Zhonghuang13 ´ Heinong 51 identified a single major QTL for flowering time in the region of QNE1. We already have convincing evidence that two populations shared the same QNE1. This new gene QNE1 can explain that why cultivars having E1 genotypes can adapt to the Northern latitudinal region. Currently, fine-mapping and functional confirmation are being conducted.