

QTLs Analysis for Yield Component Characters of Grain in the M/G RILs by Different Years

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Objective

The goal of this study was conducted to analysis for QTL regarding characters related to the yield component, straw weight, harvest index and productivity score for the inbred lines from Milyang 23 and Gihobyeo

Materials and Methods

- Materials : 164 Inbred Lines from Milyang 23 and Gihobyeo
- Characters for Investigation :
Grain Yield Components, Straw Weight, Harvest Index, Productivity Score During Two Years 2002 ~ 2003
- Mapping and QTL Analysis :
MAP MAKER 2.0 Program
QGENE 3.0 Program

Results and Discussion

- The yield component, straw weight, harvest index and productivity score were measured at 2002 and 2003 years. Nine significant QTLs ($LOD \geq 2.0$) were detected at the same location by different years. One QTL for number of panicles was detected on chromosomes 12, each accounting for 10.0% and 14.7% of the phenotypic variation. One QTL for number of spikelets was detected on chromosomes 1, each explaining from 20.3% and 13.7% of the phenotypic variation. Five QTLs for 1000 grain weight were detected on chromosomes 2, 5, 6, 8 and 12, each accounting for 9.6% to 29.2% of the phenotypic variation.

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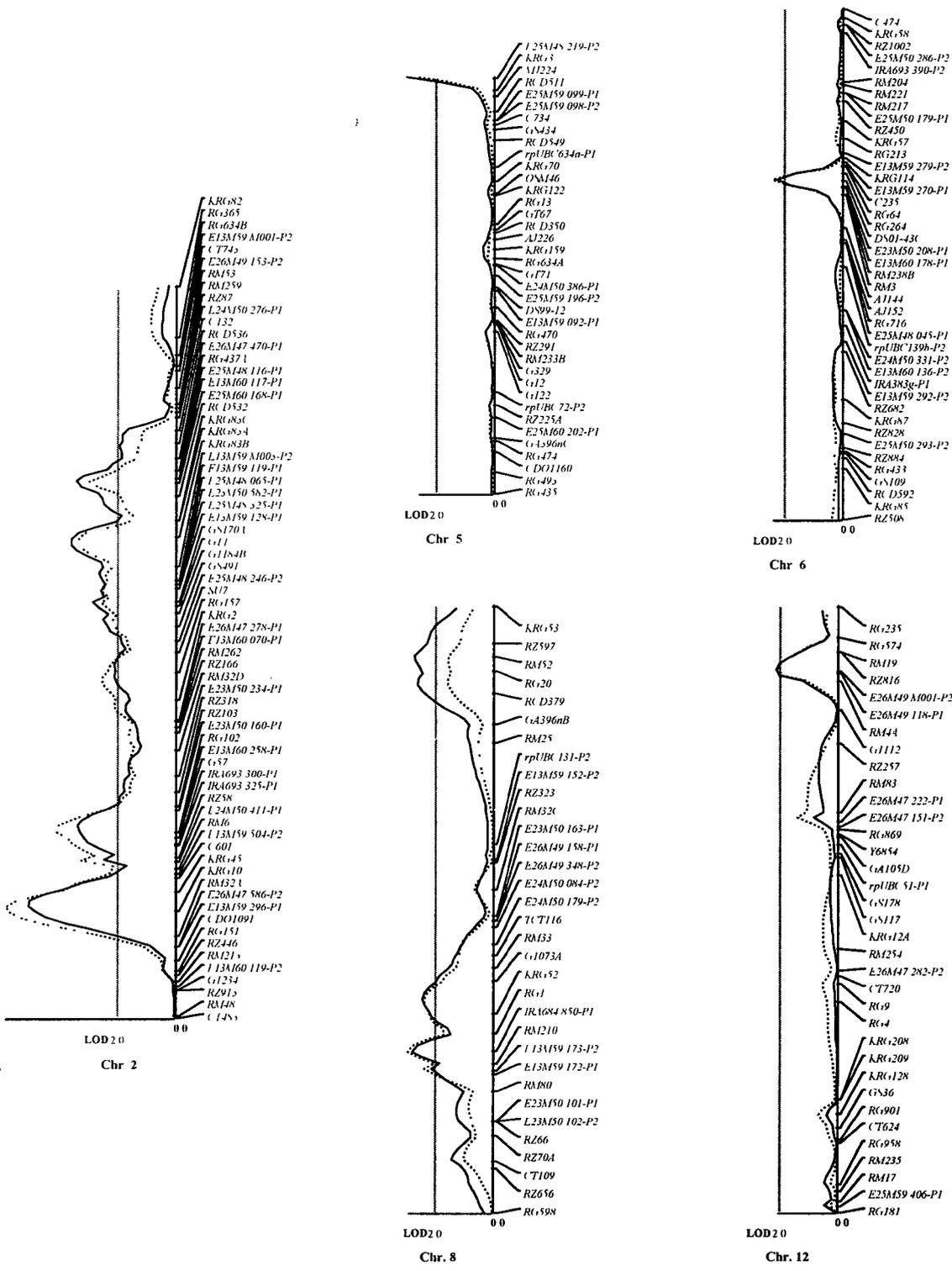


Fig. Genetic linkage map showing locations of QTLs associated with 1000 weight of grain in the M/G RILs by different years

2002 - - - - - 2003 - - - - -