

QTL Identification for Immature Pod Formation Appeared at Green House in Winter

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Objectives

To develop QTL marker associated with the immature pod formation appeared at green house during winter in soybean

Materials and Methods

- Plant material : 141 F_{8,9} soybean RILs (PI96188 x Jinju 1ho)
- Marker : SSR (SOYBASE website)
- DNA isolation : CTAB method (Weising et al. 1995)
- SSR analysis
 - Gel electrophoresis : ABI 377
 - Gel image analysis : GeneScan & Genotyper 3.0
- Map construction : Mapmaker 3.0 (LOD >3.0, max Dis. 37.2)
MAP MANAGER QTX V b 1.6
- Statistical analysis : SAS v 8.0

Results and Discussion

The population consisted of 141 recombinant inbred lines (RILs) developed by single seed descent, in an F₈ soybean population derived from a cross of PI 96188 x Jinju1, and was used to construct a genetic linkage map. This population was planted at a green house from October 2002 to March 2003 in Seoul National University Experimental Farm.

Immature pod formation was shown at green house during winter. This was characterized with multiple pods which didn't developed well after pollination. Distribution of soybean sterility in RILs (PI96188 x Jinju 1ho) was expected to be a ratio for the developed and underdeveloped pod formation. SLG-Regr analysis revealed that three markers at LG C1, C2 and G (Satt399, Satt460, and Satt50, respectively) were associated with pod formation. At the QTL detected by Satt505, the allele for sterility at green house was contributed by PI96188. MLG-Regr. analysis with the independent markers were linked to markers Satt156. The interval mapping accounted for 32% of the variation in pod formation among the progeny.

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Fig 1. Pod formation at green house in winter; A:immature, B:normal.

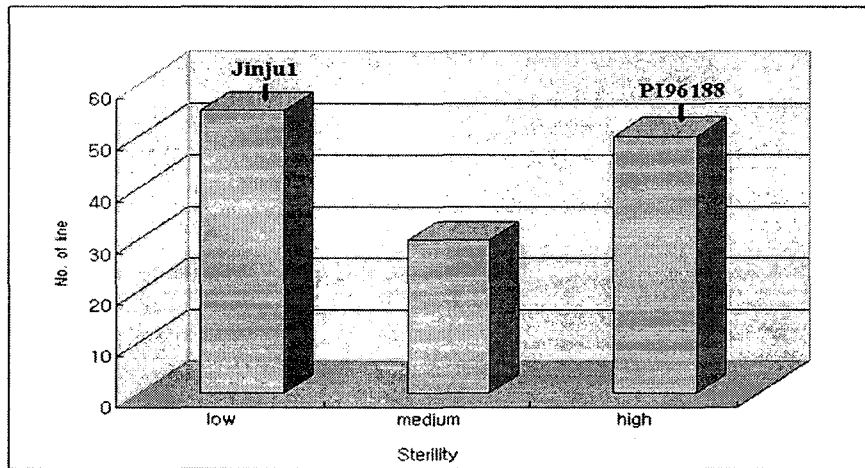


Fig 2. Distribution of soybean pod formation in RILs (PI96188 x Jinju 1ho)

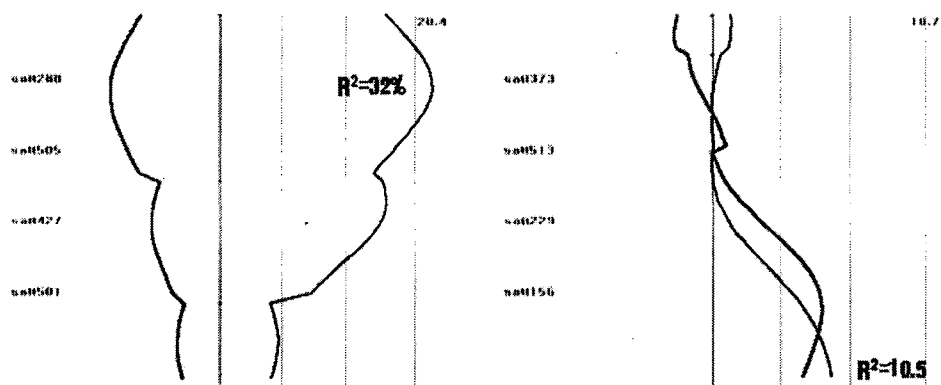


Fig 3. Interval mapping of soybean pod formation in LG-G and LG-L.