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QTL Identification for Somatic Embryogenesis from Immature Zygotic Embryo in Soybean

Jeong-Suk Bae^{1,2*}, Suk-Ha Lee²

¹Institute of Bioresources, Gyeongbuk Provincial Agricultural Technology Administration, Andong 760-891, Korea; ²School of Plant Science, Seoul National University, Seoul 151-742, Korea

Objectives

We investigated genotypic variation and chromosomal location of QTLs for somatic embryogenesis from immature zygotic embryo culture of recombinant inbred lines in soybean.

Materials and Methods

- Plant material : 141 _{8,9} soybean RILs (PI96188 x Jinju ho)
- Marker : SSRs(SOYBASE website)
- DNA isolation : CTAB method
- SSR analysis : Gel electrophoresis : ABI 377, Gel image analysis : GeneScan & Genotyper 3.0
- Statistical analysis : SAS v 8.0
- Map construction : Mapmaker 3.0, MAP MANAGER QTX v1.6

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 in a field from June 2003 to September 2003 at Seoul National University Experimental Farm. The mean value of the somatic embryo rate was 31.7±14.2%. The frequency distribution of the somatic embryo induction rate from in the field explants ranged from 0 to 90% with continuous variation. In multiple embryogenesis, SLG-Regr for the two markers of LG B1, B2, C1, and D2 retained Satt444, Satt020, Satt399, and Satt226. At the QTL detected by Satt444 and Satt226 the allele for multiple embryogenesis was contributed by Jinju1, while the allele for multiple embryogenesis at Satt020 and Satt399 was contributed by PI96188. MLG-Regr. analysis with the six independent markers were linked to markers Satt020. The multiple regression analysis accounted for 14.1% of the variation in multiple embryogenesis among the progeny