

구두발표

Complex structure of soybean genome around *Rxp* locus by comparative genomics

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A single recessive gene, *rxp*, controls bacterial leaf pustule (BLP) resistance in a soybean. The *Rxp* locus appears to be linked to the malate dehydrogenase (*Mdh*) locus and Satt372 on linkage group (LG) D2. Around the *Rxp* locus, four bacterial artificial chromosome (BAC) clones are anchored by Satt486, Satt498, BARC-022037-04263, and BARC-040963-07870. Using these BAC clone sequences, possible orthologous region of *Rxp* locus was identified: *Medicago truncatula* contig 962 at chromosome 3 and contig 283 and contig 1108 at chromosome 8. Sequence analysis of contig 962 had revealed microsynteny with three soybean BAC clones on LG A1, which are duplicated with other two soybean BAC clones anchored by Satt486 and Satt498. After BLAST search was performed with *M. truncatula* contig 962 against soybean ESTs, several soybean ESTs were identified. With developed single nucleotide polymorphism (SNP) markers and the RIL population from the cross of Pureunkong and Jinpumkong 2, SNP genotyping was able to locate two soybean ESTs: CO979743 at 1 cM away from Satt195 on LG C1 and BE021935 at 5 cM away from Satt363 on LG C2. Thus, our results indicate that structure of soybean genome around *Rxp* locus is very complicated.

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Difference in Aluminum-induced Plasma Membrane H⁺-ATPase in Al-Sensitive and Al-Tolerance Soybeans.

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Aluminum (Al) toxicity in plants is one of the major limitations to crop growth on acid soils. The Al-induced change of H⁺-ATPase expression has been regarded as an important mechanism for Al tolerance in soybean. To investigate whether translational regulation of plasma membrane H⁺-ATPase is involved in the response to Al stress, we conducted western - blot of this protein. The results show that western - blot of plasma membrane H⁺-ATPase in the "Sowon" (Al tolerance) significantly increased in translational expression level, while citric acid (50 μM) with Al (50 μM) treatment has not effected. In contrast, Al sensitive cultivar "Poongsannamool" inhibited expression level of plasma membrane H⁺-ATPase with Al treatment. Two - dimensional gel analysis were performed to determine the protein induction patterns of control and Al (50 μM, 24 h) treated soybean. There are many changes of plasma membrane proteins in both cultivars under Al stress. Especially "Sowon" was significantly enhanced the expression of the plasma membrane H⁺-ATPase in Al treatment. But protein expression of "Poongsannamool" was less than "Sowon". These results suggest that the regulatory role of plasma membrane H⁺-ATPase may involved the tolerance mechanism in soybean roots. At the present, transcriptional level of H⁺-ATPase is under investigation.

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