(O2-07)

SSR markers scan of the soybean genome for seed protein QTL

<u>Tae-Hwan Jun</u>, Moon Young Kim, Kyujung Van, Suk-Ha Lee* Department of Plant Science, Seoul National University, Seoul 151-921, Korea

Association studies based on linkage disequilibrium (LD) can be used to test for association between molecular markers and quantitative trait loci (QTLs) in various crop species. We conducted SSRmarker scan of the soybean genome for seed protein QTL. An association map consisting of 159 markers was constructed on the basis of differences in allele frequency distributions between two subpopulations differing in protein content. In result of association studies, it was shown that tightly linked markers to QTLs for soybean seed protein content detected by linkage analysis revealed significant P values. Some markers exceptionally showed significant P-values, having some distance away from soybean seedprotein QTLs detected by linkage analysis. Thirty-five SSR markers on 16 linkage group (LGs) had P values <0.001, suggesting possible linkage to seed protein QTLs. Eleven putative QTLs were identified on the basis of highly significant markers. Two of the markers (Satt431 on LG J, and Satt551 on LG M) may be linked to unreported seed protein QTLs. Two additional population sets with different protein content were used for confirmation of the QTLs detected by our analysis. Satt405 and Satt571 showed significant P-values at P < 0.05. Like the association study with the original population set, Satt551 newly identified QTL was confirmed again as the QTL for soybean seed protein content. In conclusion, the results suggest that our association analysis approach, which was based on LD among SSR markers, could be a viable alternative to linkage mapping for the identification of new QTLs in soybean.

*corresponding author: Tel.02-880-4545, e-mail: sukhalee@snu.ac.kr

(02-08)

Molecular Markers Linked to Resistant and Susceptible Characteristics of Fusarium race2 and Verticillium Wilt Disease in Tomato

Hee Young Hwang, Nam Hee Kim, Hee Jung Choi, Dong Chan Won, Byung Whan Lim, and Chee Hark Harn*

Biotechnology Institute, Nong Woo Bio Co., Ltd., Yeoju, Gyeonggi, Korea

Tomato (Lycopersicon esculentumMill.) is considered as one of the most widely grown vegetable crops in the world because of the versatility of its uses both in fresh and processed food. One of main constraints from the tomato cultivation is damage caused by pathogens including viruses, bacteria and fungi as well as nematodes, which cause severe losses in productivity.

Our breeding program has been working with two wilt related diseases: firstly Fusarium wilt (Fusarium oxysporum f. lycopersici) that is a symptom showing yellowing and drooping of the lower leaves on one side of the stem due to wilt, and secondly Verticillium wilt (Verticillium spp.) that shows the development of yellow blotches and V-shaped lesions at leaf, and dark brown vascular discoloration. Both diseases kill the tomato plant eventually.