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SSR markers scan of the soybean genome for seed protein QTL

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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 SSR marker 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 seed protein 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.

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

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Tomato (*Lycopersicon esculentum* Mill.) 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.

Recently, breeders at Nong Woo Bio Co. have constructed new lines resistant to Fusarium and Verticillium wilt disease using resistant lines to generate elite varieties. In order to make all breeding process faster and to support marker-assisted breeding, DNA markers for identifying resistant and susceptible characteristics of these wilt diseases in Tomato have been developed.

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DEG screening에 의한 겹무늬 썩음병 감염에 의해 유도되는 유전자 분석

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사과는 과수중 재배면적이 2위(27천ha)인 작물로서, 생산액은 1위인 경제적으로 매우 중요한 작물이다. 현재 사과원에서 사용되는 살균제의 70%이상이 겹무늬썩음병과 갈색무늬병방제용이다. 주품종인 후지의 경우 겹무늬썩음병 감수성을 나타낸다. 사과 과실과 줄기에 발생하여 과실의 상품성을 떨어뜨려 농가소득에 큰 피해를 입히는 사과 겹무늬 썩음병의 저항성에 관련하는 유전자를 탐색하고, 분자 표지 소재 개발을 위한 연구가 수행되었다. 겹무늬 썩음병 병원균 (*Botryosphaeria dothidea*)을 감염시킨 과실과 상처를 낸 과실로부터 시료를 채취하여, 무처리 사과 과실과의 DEG screening을 수행하여 병원균의 감염에 의해 발현이 유도되는 18종의 유전자를 분리하였다. 생물정보분석을 통해 이들 유전자들은 flavonoid glucosyltransferase, PHI-1 protein, metallothionein-like protein, protease-inhibitor, senescence 관련 유전자, chalcone isomerase, chitinase, wounding-induced protein등과 상동성이 높음을 알수 있었다. 이러한 유전자들은 외부 스트레스에 반응하여 발현이 유도되는 유전자로서 질병저항성과도 밀접한 유전자들이다. 겹무늬썩음병에 의해 오히려 발현이 감소되는 16종의 유전자를 분리하여 염기서열을 분석중에 있다. 이들은 겹무늬썩음병저항성 사과 품종을 개발하기 위한 유전자 소재나 마커소재로의 이용가능성을 조사중에 있다

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