

Frame mapping using SSR markers for constructing genetic linkage map of apple trees (*Malus* spp.)

Do Young Na^{1*}, Sun Yong Lee¹, Hee Jae Lee¹, Daeil Kim², Jonghan Park², In Jung Kim³

¹Department of Horticultural Science, Seoul National University, Seoul 151-921, Korea;

²National Horticultural Research Institute, Rural Development Administration, Suwon

440-706, Korea; ³College of Applied Life Science, Cheju National University, Jeju

690-756, Korea (*fromundersky@hanmail.net)

Frame maps were constructed using SSR markers in a *Malus domestica* 'Red Fuji BC#2' × *M. Floribunda* 821 progeny of 98 individuals. Totally 56 SSR markers were detected from the screening analysis against 120 SSR markers with JoinMap 3.0. The 120 SSR markers were originated from apple and other Rosaceae. The maps for 'Red Fuji BC#2' and 'Floribunda 821' consisted of 49 and 51 loci, respectively. At least two SSR markers located each linkage group which showed segregating alleles in both parents. This SSR frame maps are needed to be saturated with dominant markers such as AFLP. 'Red Fuji BC#2' fruit with excellent fruit quality is susceptible to Marssonina blotch, while 'Floribunda 821' is resistant to the disease. Using this population, molecular markers related to Marssonina blotch resistance can be developed when frame maps are more saturated. The relationships between apple and the other species belonging to the Rosaceae are discussed based on the position of SSR markers.

† 주관과제명 (과제책임자): 분자표지를 이용한 사과 겹무늬썩음병 및 갈색무늬병 저항성 육종기반 확립
(농촌진흥청 원예연구소 김대일)

‡ 총연구기간 (년차): 2005년 - 2007년 (1년차)