Colletotrichum spp.에 의해서 유발되는 고추 탄저병은 우리나라를 포함하여 아시아의 몬순지역에 있어서 고추 재배 및 생산에 가장 심각한 피해를 주고 있는 병이다. 병원균의 우점종은 나라와 지역에 따라서 달라질 수 있는데 *C. acutatum* 병원균은 우리나라, 대만, 중국, 인도네시아의 포장에서, *C. capsici*는 태국, 인도의 포장에서 실제 탄저병 발병에 관여하는 우점종인 것으로 확인되었다. 가장 효과적인 방제방법으로서 내병성 육종을 들 수 있으나 지금까지 여러 가지 이유에 의하여 단 하나의 저항성 품종도 재배되지 못 하는 실정이다. 따라서 본 연구에서는 병 저항성 품종 육성을 위한 기초 연구로서 탄저병 저항성 유전분석을 QTL mapping 방법을 통하여 수행하였고 각각의 QTLs에 연관된 분자표지를 개발하여 직접적으로 MAS에 이용함으로서 선발의 효율성을 높일 수 있는지에 관하여 논의 하였다. QTL 분석은 저항성 유전자원인 *Capsicum baccatum* 'PBC81'과 이병성 계통인 *C. annuum* 'Matikas'의 종간교잡으로부터 유래한 introgressed BC_1F_2 집단을 사용하였고 AFLP와 SSR 표지인자를 사용하여 mapping하였다. 분리집단의 표현형 분석은 *C. acutatum*과 *C. capsici*에 속하는 2개의 isolates를 사용하였으며 동정된 QTL 부근에 연관된 분자표지를 개발하기 위하여 target BSA 방법을 사용하였다. QTL 분석 결과 서로 다른 두개의 isolates에 대하여 각각 1개의 major QTL과 다수의 minor QTLs을 동정하였고 target BSA를 통하여 각각의 major QTL에 연관된 분자표지들을 개발하였다. MAS를 위한 선발 효율성 분석을 위하여 major QTL 단독과 다른 loci에 존재하는 monor QTLs의 조합으로 비교한 결과 서로 다른 loci에 존재하는 분자표지들을 같이 사용하는 것이 효율성을 높인다는 결론을 얻었으며 현재까지 개발된 분자표지를 사용할 경우 약 83%의 선발 효율성이 있음을 증명하였다.

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(O2-05)

Estimating Genetic diversity of Rice (*Oryza sativa* L.) Germplasm using microsatellite markers

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Genetic diversity of 1,870 accessions of rice, *Oryza sativa*, which consist of five groups, i.e., 228 landraces, 442 breeding lines, 515 weedy strains, 637 introduced lines and 48 IRRI core collection lines, was evaluated using 18 fluorescently labeled microsatellite markers. A total of 506 alleles were detected at the 18 microsatellite loci. The number of alleles per marker locus ranged from 13 to 56 with an average of 28. Gene diversity for the 18 microsatellite loci ranged from 0.479 to 0.940 with an average of 0.822, and the size difference of alleles varied from 28bp to 144bp. Gene diversity was highly significantly correlated with the highest allele frequency, the number of alleles and the number of rare alleles.

The number of alleles per marker locus, the number of group specific alleles and the average of gene diversity within a group were used to compare genetic diversity among groups. The number of alleles per marker locus ranged from 218 for the Korean breeding lines to 435 for the introduction lines. The number of group specific alleles ranged from 6 for the weedy strains to 86 for introduction lines. The average gene diversity varied from 0.659 for Korean landraces to 0.835 for introduction lines. Genetic diversity tend to be greater as the number of

accessions increased. These results indicated that the genetic diversity of the introduction lines was higher than those of the other groups.

This result indicated that microsatellite markers permit the fast and throughput fingerprinting of a large number of rice germplasm collections in order to assess genetic diversity. The assessment of genetic diversity of Korean rice collection by the present microsatellite analysis will be helpful in developing efficient strategy for the conservation of rice germplasm and the subsequent utilization of them for future rice breeding programs in Korea.

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Molecular Markers Linked To Downy Mildew ResistanceLocus in Chinese Cabbage

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Downy mildew, caused by *Peronospora parasitica*, is one of the most damaging diseases of vegetable *Brassica*crops in the world. To determine the mode of inheritance of the resistance to downy mildew, a segregating F_2 population was obtained by crossing resistant inbred line "Han" with susceptible inbred line "NRB". In a field assay under natural downy mildew infection, the F_2 plants were segregated in a ratio of 3 resistant : 1 susceptible, indicating the resistance of "Han" against *Peronospora parasitica* is under the control of a single dominant gene. In order to develop downy mildew resistant cultivars using marker assisted selection (MAS), we tried to identify resistance locus and DNA markers linkedto the locus. We identified three markers linked to the resistance locus using DNA fingerprinting technique combined with bulked segregant analysis. The markers showing low frequency of recombination with the locus in 254 F_2 plants were cloned and sequenced. A reliable conversion procedure allowed those RAPD markers to be successfully converted into more useful SCAR markers. These SCAR markers will be used efficiently for development of commercial downy mildew resistant cultivars in chinese cabbage (*Brassica rapa*).

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