OB-01

Selection of Potato Clones Resistant to Bacterial Wilt Disease and Evaluation of Their Genetic Diversity with RAPD

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Bacterial wilt (BW) is a soil borne disease caused by *Ralstonia solanacearum* and it is known to have five races in the field, but race 1 and 3 are main pathogens in potato (*Solanum tuberosum*) and tomato cultivation. Since BW was reported, it has been serious problem in spring and fall season cultivation in Southern area of Korean peninsula because of increasing temperature and double cropping of potatoes in a year. The most effective control method is breeding of potato clones resistant to BW, but there are no reports on resistant cultivars in Korea. This study was carried out to select potato clones resistant to BW and evaluate genetic diversity with RAPD. A total of 440 clones collected and maintained in Highland Agriculture Research Center were tested in the hydroponic culture system with *R. solanacearum* race 1 and 3. After 40 days in dipping in hydroponic culture system, the resistance was evaluated as a range from 0 (resistance) to 4 (susceptible). Seventy-two clones were selected in the first screening as a resistant to race 1 and 3 in 2007, and the selected lines were tested again as the same procedure above. After the second selection, a total of 20 lines were selected as resistance to BW in 2008. For the evaluation ofgenetic diversity of the selected 20 clones, RAPD analysis was carried out with potato URP primer sets. From the 11 URP primers, 5 to 7 polymorphic DNA bands were amplified in selected resistant clones with each primer. With RAPD analysis, the genetic similarity was shown from 0.56 to 0.82. The selected clones were separated into two distinct groups at the genetic similarity value point of 0.56. Four clones including AG14252 were integrated into first group, and the others, 16 clones, were grouped in second group. In the second group, the two sub-group were shown in genetic similarity value of 0.59. Seven clones including AG34326 and nine clones were separated into first and second sub-group, respectively.

OB-02

Expansion of the lipoxygenase gene family in Glycine max

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Soybean lipoxygenases (*Lxs*) play important roles in plant resistance and in conferring the distinct bean flavor. *Lxs* comprise a multi-gene family that includes *GmLx1*, *GmLx2* and *GmLx3*, and many of these genes have been characterized. We were interested in investigating the relationship between the soybean lipoxygenase isozymes from an evolutionary perspective, since soybean has under gone two rounds of polyploidy. Two *Lx* regions in *Medicago truncatula* showing synteny with soybean were analyzed. Differential evolutionary rates between soybean and Medicago were observed and the median Ks values of Mt-Mt, Gm-Mt, and Gm-Gm paralogs were determined to be 0.75, 0.62, and 0.46, respectively. Thus, the comparison of Gm-Mt paralogs (Ks=0.62) and Gm-Mt orthologs (Ks=0.45) supports the ancient duplication of *Lx* regions in the common ancestor prior to the Medicago-Glycine split. As a result, optimized rates of Ks per year should be applied for accurate estimation of coalescence times to each case of comparison. After speciation, no *Lx* regions generated by another polyploidy were identified in Medicago. Instead tandem duplication of *Lx* genes was observed. On the other hand, a lineage-specific duplication occurred in soybean resulting in two pairs of *Lx* regions. A total of 34 *Lx* genes (15 MtLxs and 19 GmLxs) were divided into two groups by phylogenetic analysis and the *Lx* gene family has been evolved from two distinct *Lx* genes in the most recent common ancestor. Expression patterns of *Lxs* were checked by RT-PCR from various tissues and times.