D-D2-07

Molecular Markers Linked to Resistant Characteristics of Fusarium Race2 and Verticillium Wilt Disease in Tomato

Hee Young Hwang, Soo Kyoung Kim, Nam Hee Kim, Dong Chan Won, Byung Whan Lim, Nam Han Her, Jang Ha Lee and Chee Hark Harn*
Biotechnology Institute, Nongwoo Bio Co., Ltd., Yeoju, Gyeonggi, Korea

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. World volumeof tomato production has increased approximately 10% since 1985, reflecting a substantial increase in dietary use of the tomato.
One of the main constraints for tomato cultivation is the damage caused by pathogens, including viruses, bacteria, nematodes and fungi, causing severe losses in production. Among them, fungi such as *Fusarium* and *Verticillium* are ones notorious for tomato wilting.The first indication of Fusarium wilt (*Fusarium oxysporum f. lycopersici*) is yellowing and drooping of the lower leaves.As the disease progresses,wilting occurs and eventually the plant dies. Verticillium wilt (*Verticillium spp.*) affects the plant uniformly and the main symptom of this disease is the development of yellow blotches on the older leaves in the center of the plant.
For tomato, the genetic control for pathogens using DNA marker technique is a very useful practice.Recently, breeders at Nongwoo 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 characteristics of these wilt diseases in tomato have been developed.
*Chee Hark Harn; 031-883-7055; chharn@nongwoobio.co.kr

D-D2-08

Comparison of homologous soybean BACs around *Rxp* locus

Donghyun Kim[1], Kyujung Van[1], ChunMeiCai[2], Beom-SoonChoi[3], Moon Young Kim[1,4], Suk-Ha Lee[1,4,*]
[1]Department of Plant Science, Seoul National University, Seoul, 151-921, Korea
[2]National Institute of Crop Science, Suwon, 441-857, Korea
[3]National Instrumentation Center for Environmental Management, Seoul National University, Seoul, 151-921, Korea
[4]Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul, 151-921, Korea

Xanthomonas axonopodis pv. glycine (*Xag*) causes bacterial leaf pustule (BLP) in soybean that occurs in Korea and the southern United States, where hot and humid weather conditions are prevalent. In soybean, a single recessive gene, *rxp*, controls BLP resistance. The *Rxp* locus is known to be linked to Satt372 on LG D2. We selected two BACs (I029F06 and I024M16) by Satt486 and Satt498, and three BACs (I020O10, I089M01 and M077P21) were selected by their end sequences of two BACs. Two homologous contigs composed of five BACs were identified in the selection process of BAC clones around *Rxp* region. Alignment and annotation revealed that '2BAC' and '3BAC' contigs had 54 and 58 genes, respectively. Gene order was conserved among syntenic blocks and the same orientation between the predicted genes was observed. Especially, each of these aligned homoeologous regions showed homology with different kinds of protein kinases. With the RIL population from the cross of Pureunkong and Jinpumkong 2, SNP genotyping and SSR mapping showed location of '3BAC' contig on 1.9 cM away from Satt684 in LG A1. With comparison between the composite maps from the Soybase, LG A1 and LG D2 are shared the duplicated region. Therefore, these two contigs could be homoeologous regions.
*Corresponding author: Tel. 02-880-4545, e-mail: sukhalee@snu.ac.kr