mands. (3) Improvement of disease resistance, stress tolerance and quality of horticultural plants by applying modern plant biotechnology: (i) Soma clonal variation and mutation selections succeeded in creating new quality rices with improved drought and chilling tolerance, neutral photo periodism response and reduced plant height, which are widely grown by farmers in ecological difficult areas; (ii) Multiple gene fragment approach as well as RNAi techniques are proved to be effective in creating papaya ring spot virus (PSRV) resistant papaya; Tristeza virus resistant citrus. (4) R/D in Plant-made oral vaccines: H5, N1 and M1 genes from highly pathogen avian influenza virus; gene from of hepatitis B; gene coding glycoprotein (G) of rabid virus … have been isolated, modified, constructed and introduced into tobacco, tomato, soy bean in order to express the antigen which will be used as vaccine. Numerous lines of transgenic plants are in laboratory testing stage. Opportunities and challenges related to the application of plant biotechnology in horticulture of Vietnam will be discussed.
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>> **Chairperson:** Byoung Cheorl Kang (Seoul National Unviersity)

S4-O-11 (12:30-12:45)
RAPD Markers Linked to Monoecious Gene in Muskmelon

Xian Zhang* and Rong Yu

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Muskmelon is growing popular in China and vast amount consumption of thisfruit is taken per year. Almost all commercial production uses F1 hybrid seeds for growing. Monoecius character is important for F1 hybrid seed production. For further research of utilizing monoecious character in muskmelon, the RAPD markers linked to monoecious gene of muskmelon were studied.The monoecious plant lines ATA-A, ATA-B which two were selected by Watermelon and Melon research group of Horticulture Department of Northwest A & F University and an andromonoecious line and their offsprings (F_1 and F_2 and BC_1, crossed with another two regular muskmeoln plant lines YJX-1 and MN-3) as materials, hereditying model and molecular marker of monoecious character were studied. 80 individuals of ATA-A F_2 plants were used for RAPD molecular mapping of the monoecious gene by bulk segregant analysis (BSA) method. The result showed that 840 random primers were chosen for polymerase chain reaction (PCR) amplification between monoecious pool and andromonoecious pool, two RAPD Sex phenotype of melon flower marker $S128_{1180}$ and $S493_{930}$ were obtained. Primer S128 was tightly linked to the monoecious character, and primer S493 was tightly linked to the andromonoecious character.
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S4-O-12 (12:45-13:00)
Construction of a Genetic Linkage Map and Mapping Quatitative Trait Loci for Bacterial wilt Resistance in Tomato Variety Hawaii 7996

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Bacterial wilt caused by race 1 strains of *Ralstonia solanacearum* is one of the most important and widely distributed plant diseases in the tropics and subtropics, particularly on tomato. Planting resistant material is the most suitable measure for the control of tomato bacterial wilt. To elucidate genetic control of resistance in Hawaii 7996, a stable resistance source, a population of 188 F_9 recombinant inbred lines (RILs) derived from a cross between *S. lycopersicum* Hawaii 7996 (resistance parent) and *S. pimpinellifolium* West Virginia 700 (susceptible parent) was used for this study. First, the genetic map was improved, and a total of 362 markers including 74 AFLP, 260 DArT, 5 RFLP, 1 SNP, and 22 SSR markers was used for map construction. Total of ten major and two minor linkage groups spanning 2131.7 cM were identified. A framework map of 106 loci (32 AFLP, 59 DArT, 6 RFLP, 11 SSR) distributed over 15 linkage groups covering 1089.1 cM was used for quantitative trait loci (QTL) mapping with the composite interval mapping method. The phenotypic data used for the QTL analysis included 9 datasets: 3 for disease evaluations and 6 for morphological traits. Disease reactions of the RIL population were evaluated against two phylotype 1, race 1 strains (Pss4 and Pss181) at seedling stage. A total of 13 QTLs were identified. Out of these 13 QTLs detected, 7 QTLs were identified for bacterial wilt resistance, one for sympodial index, two for citric acid, two for soluble solid content and one for fruit color (a/b). They explained between 5.0% and 20.1% of the phenotypic variation, depending on the traits. Resistance in Hawaii 7996 is related to the suppression of the pathogen colonization in the stem, as similar QTLs were found based on visual symptom data as well as colonization data caused by Pss4. Possible linkages between critic acid and bacterial wilt resistance was observed. QTLs located on chromosome 6 showed significant linkages with disease reactions against several pathogen strains should be targeted for fine mapping and developing closely linked markers for marker-assisted selection and gene cloning.
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Poster Session

December 11 (Thu)

Location: Event Hall, ICC JEJU

S4-P-001
Estimation of Insertion Date of a Retrotransposon, Gret1, into a Transcription Factor Gene, VvmybA1, Which Regulates Anthocyanin Biosynthesis in Grapes

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An Myb-related gene, VvmybA1, regulates anthocyanin biosynthesis in grapes. The strong association between the VvmybA1a allele, which contains a retrotransposon Gret1 upstream of the VvmybA1 coding sequences, and white-fruited phenotypes has been detected in many cultivars of the grapevine *Vitis vinifera*. Determination of the presence and distribution of the VvmybA1a allele in the wild grape *V. vinifera* subsp. *sylvestris* and other *Vitis* species would provide new information on the genomic relationship among these species and on the evolutionary differentiation of the genus *Vitis*. We detected the VvmybA1a allele in almost all of the cultivars of *V. vinifera* that we analyzed, including *sylvestris*. In contrast, the VvmybA1a allele was not detected in any of the North American or East Asian *Vitis* species. These findings suggest that Gret1 insertion to VvmybA1 may have occurred in *sylvestris* or an unknown ancestor of *sylvestris* after the North American and East Asian species had diverged from the common ancestor. The two LTRs of a retrotransposon are usually identical at the time of its insertion into the host genome. Therefore, the date of insertion can be estimated from the sequence divergence between the two LTRs. We analysed the two LTR sequences of Gret1 in the VvmybA1a alleles of the above cultivars. The sequences of the 5-LTR differed from those of the 3-LTR only five bases in each cultivar. However, no differences were observed within either sequence among cultivars, including *sylvestris*. From these sequence data, Gret1 insertion date was estimated roughly 0.2 million years ago.
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S4-P-002
Application of Cryopreservation to in Vitro Cultured Cells and Organs of Medicinal Plants: the Effect of Method and Pretreatment Conditions

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