

B-200

Identification of foxglove aphid resistance gene with high density SNP array in soybean [*Glycine max* (L.) Merr.]

*Suntaeg Kang**, Dankook University, Chungnam, Republic of Korea

Sunim Park, Dankook University, Chungnam, Republic of Korea

Kyung-Hye Kim, Dankook University, Chungnam, Republic of Korea

Hong-min Go, Dankook University, Chungnam, Republic of Korea

Foxglove aphid, *Aulacorthum solani* (Kaltenbach), is a Hemipteran insect that infected a wide variety of plants worldwide and caused serious yield losses in crops. The objective of this study was to identify the putative genes to foxglove aphid resistance in wild soybean, PI 366121 (*Glycine soja* Sieb. and Zucc.). One hundred and forty-one F4:8 recombinant inbred lines developed from a cross between susceptible variety, Williams 82 and foxglove aphid resistance wild soybean, PI 366121 were used. The two type of resistance response, antibiosis and antixenosis resistance were evaluated through choice and no-choice test, graded by the degree of total plant damage and primary infestation leaf damage; a genome-wide molecular linkage map was constructed with 29,898 single-nucleotide polymorphism markers utilizing a Axiom[®] 180K soyaSNP array. Using inclusive composite interval mapping analysis for foxglove aphid resistance, one major candidate QTL on chromosome 7 was identified. The major QTL on chromosome 7 showed both antixenosis and antibiosis resistance responses. The newly identified major QTL was consistent with previously reported QTL, Raso2, which showed around 5 times narrow down interval range with 8 candidate genes. Furthermore, total 1,115 soybean varieties including *Glycine soja* and *Glycine max* were exposed to germplasm screening, and 31 varieties, which showed significant antibiosis type foxglove aphid resistance were identified. This result could be useful in breeding for new foxglove aphid resistant soybean cultivars and developing novel insecticides.