

## Population Genetic Study to Trace Migration routes in *Metcalfa pruinosa* (Hemiptera: Flatidae)

Deok Ho Kwon<sup>1</sup>, Minyoung Kim<sup>2</sup>, Hyojoong Kim<sup>3</sup>, Yerim Lee<sup>2</sup>,  
Ki-Jeong Hong<sup>4</sup>, Si Hyeock Lee<sup>1,2</sup> and Seunghwan Lee<sup>1,2</sup>

<sup>1</sup>Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul 151-921, Republic of Korea

<sup>2</sup>Department of Agricultural Biotechnology, Seoul National University, Seoul 151-921, Republic of Korea

<sup>3</sup>Department of Biology, Kunsan National University, Daehangno 558, Gunsan, Jeonbuk 573-701, Republic of Korea

<sup>4</sup>Department of Plant Medical, College of Life Science and Natural Resources, Suncheon National University, 255 Joongang-ro, Suncheon 540-950, Republic of Korea

*Metcalfa pruinosa* has been spreading in Korea since 2005, which its first report at Gimhae in Gyeongnam province. It has been harmful to grape and major forest crops by direct sucking and indirect transmitting sooty mold disease causing economical loss. It is necessary to study its tracing route and movement conditions for the further efficient population management and prevention of its re-invasion. A total of 23 haplotype were observed in the analysis of nucleotide polymorphisms on mitochondrial cytochrome *c* oxidase I from total 124 voucher specimens among five countries. Only two haplotypes were exist in Korea and HAP1 was accorded with its of some European individuals. Moreover, the analysis of  $F_{ST}$  and AMOVA, the Korean population was relatively nearer with Spanish and Italian population than American populations, suggesting the Korean population might be originated from some European countries. Eight microsatellite loci were developed and characterized to facilitate more delegate population genetic analysis from 468 individual in five countries. The average character of each or overall population was revealed 18 average individual number, six alleles and 0.676 heterozygosity. The genetic distance ( $F_{ST}$ ) was a little bit high among each populations ranged as - 0.010~0.245. In the tracing route analysis, the originating country of Korean population was also shown as migrated from some European countries. The population genetic analysis using genetic markers will be useful to trace the origin of pest and prevent from re-invasion fro efficient pest management.

**Key words:** Population genetics, *Metcalfa pruinosa*, Migration, Microsatellite