

1-6. Phylogenetic relationship of the wild silkworm, *Bombyx mandarina*, inferred from an internal transcribed spacer (ITS) of rDNA

Kyung-ah Kim, Si-kab Nho

College of Agriculture and Life Sciences, Kyungpook National University

The wild silkworm, *Bombyx mandarina*, was believed the only ancestor of *B. mori*, inhabits the limited area of Eastern Asia including China, Korea and Japan. However, the geographic dimorphism of *B. mandarina* was reported with chromosome number and arylphorin gene. In connection with those dimorphism, we studied the genetic differences of ITS-2 region in rDNA purposing the differentiation and geographic variation within the species of *B. mandarina*.

The ITS-2 region of *B. madarina* has about 850 bp nucleotides longer 60 bp than ITS-1 region. No differences were found every individual in the nine localities of the southern Korean peninsula, including Jeju island. In addition, the Chinese and Japanese population of *B. mandarina* and even *B. mori* has the little significance of nucleotide diversity with the Korean population in ITS-2 region. We could not found that genetical variation and differentiation of *B. mandarina* from the nucleotide of ITS region.

Furthermore, we concluded that the ITS region in the ribosomal DNA is unsuitable target to investigate the phylogenetic relationships among closely related species within the genus of *Bombyx*.