

## **Geographical Divergence of the Wild Silkworm, *B. mandarina* in Korea and the Phylogenetic Relationships to the Domesticated Silkworm, *B. mori***

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The wild silkworm, *Bombyx mandarina*, is the same genus of *B. mori*. *B. mandarina* inhabits only Eastern Asia, which substances China, Korea and Japan. This was essentially discussed the study of the origin and evolutionary relationships of *B. mori*. Recently, the geographic dimorphism of *B. mandarina* inhabiting China and Japan was reported concerning the chromosomes and arylphorin gene. Geographically, Korea is located between China and Japan. This fact supports the study of the Korean population of *B. mandarina*. The Chinese population possess the same number of *B. mori* as  $2n=56(n=28)$ , whereas the Japanese population possess one pair less than that of China as  $2n=54(n=27)$ . The Korean population has the same number as the Japanese population. However, two kinds of chromosomes,  $2n=58$  and  $2n=54$ , were found in the southern Korean peninsula, including Jeju island.

The arylphorin gene dimorphism is the result of 66bp insertion in intron 3. According to their geographical origin, the Japanese population has this insertion but that of China does not. Interestingly, we observed 3 polymorphism in the Korean population. Two genotypes were the same as the Chinese and Japanese populations respectively. Another one is the hetero genotype of China and Japan. Chromosome and arylphorin gene polymorphism served as a good basis for the geographical character of *B. mandarina* inhabiting the Korean peninsula.

In addition, we sequenced the ITS-1 region to analyse the divergence of the population within the species. ITS region sequence comparison has become popular in the phylogenies of closely related species or among populations, because they appear to evolve at a relatively rapid rate.

The ITS-1 region of *B. mandarina* has 748~780 bp nucleotides. This region has highly conserved among the populations except 300~330bp and 336~350bp. The Korean population runs 5 GTs whereas that of China and Japan runs 7 GTs in 336~350bp. This GT differed by population. However,

there is relatively large variation in every individual in 300~330bp. Thus, we recognized that the ITS-1 region is unsuitable for analyses within the species, *B. mandarina*, because it evolves fastest.

Another notable finding is that several Korean native strains among the domesticated silkworm are markedly similar to *B. mandarina* in morphology. Thus, their phylogenetic relationships were analyzed inferring the isozyme genes. Korean native strains were different from other strains in some isozyme genes, and in many cases that genetic character is identical to *B. mandarina*. Therefore, we concluded that Korean native strains bear a closest relationships with *B. mandarina*. This study provides strong evidence that Korean native strains are useful as phylogeny resources for the speciation of *B. mori* and make clear the relationship of two species within a genus of *Bombyx*.