

The Use of Fibroin Light Chain Gene Sequence for the Genetic Marker of the Silkworm Origin, *Bombyx mori*

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Silkworms are classified into geographic races on the basis of their origin such as Japanese, Chinese, European and tropical. In Korea, most of the recommended variety was F1 hybrid between Japanese race and Chinese race. We have previously cloned and characterized the complete fibroin light chain gene from the silkworm Baekok-Jam, *Bombyx mori*. Two variable regions (I, intron 2-exon 3-intron 3; II, intron 6) from the fibroin light chain gene are surveyed to study genetic polymorphism of silkworm breeds. Japanese race (Jam 123, peanut shape cocoon), Chinese race (Jam 124, elliptical shape cocoon) and their F₁ hybrid Baekok-Jam (elliptical shape cocoon) were used in this study. DNA sequence divergence from the fibroin light chain gene was analyzed by PCR and sequencing. The PCR product size of I region (intron 2-exon 3-intron 3) was 787 bp to Jam 123, 771 bp to Jam 124 and 769 bp to Baekok-Jam, respectively. Furthermore, the PCR product size of II region (intron 6) was 470 bp to Jam 123, 455 bp to Jam 124 and 452 bp to Baekok-Jam, respectively. For the additional evidence, Japanese race (Jam 125, peanut shape cocoon), Chinese race (Jam 126, elliptical shape cocoon) and their F₁ hybrid Daeseong-Jam (elliptical shape cocoon) were also analyzed. The sizes of I- and II-regions in Jam 125, Jam 126 and Daeseong-Jam were similar to the results of Jam 123, Jam 124 and Baekok-Jam. DNA sequence divergence between the two geographic races of Jam 123 or Jam 125 and Jam 124 or Jam 126 was substantial. These results indicate that in the fibroin light chain gene and cocoon shape Baekok-Jam or Daeseong-Jam is more closely related to Jam 124 or Jam 126 than to the Jam 123 or Jam 125. Taken these data together, the primer sets designed from two variable regions in this study would be highly useful, at least in Japanese and Chinese races, for the genetic marker among silkworm races and/or breeds.