

## Linkage Analysis of the Filament Size Using cDNA-RFLP Markers of *Bombyx mori*

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The filament size of cocoon is important character for silkworm breeding and is thought to be controlled by quantitative traits loci (QTL). Besides the male larva generally spins the thinner than the female, there is an interracial variation from 1.6 to 4.6 deniers in size. This fact suggests that filament size is not only affected by sex chromosome but also by the several genes located on the autosomes. In this study, we tried the linkage analysis of the genes controlling filament size using restriction fragment length polymorphism (RFLP) markers on each (28 RFLP) linkage groups (RFL1-28) of *Bombyx mori*.

Two silkworm strains, MK (1.6 denier) and J510 (4.6 denier) were crossed and the F1 (MKxJ510) female was backcrossed with MK male. The combinations of enzyme and cDNA clone were selected by checking RFLP patterns of each parental moth. The 42 pupal genomic DNA of BF1 [(MKxJ510) x MK] was prepared after reeling of the fresh cocoon individually in the 5% NaOH, and the RFLP patterns were detected by each cDNA probes.

The segregation of the filament size in BF1 individuals shown the continuous distribution from 1.51 to 2.78 denier, and that of RFLP pattern were from (MK/MK: MK/J510 = 10 : 32) in RFL4, 13, 17 and 19 (= 26 : 16) in RFL2 and 11. The significance of the homo: hetero segregation of the thinner 10 and 15 individuals was statistically analyzed against the all of 42 individuals by G-test. Only a cDNA clone in RFL19 was significantly correlated with the filament size at 10% level.