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# Genetic Analysis of Food Preference Character by Using Phenotypic Markers and Molecular Markers in the Silkworm, *Bombyx mori*

**Tetsuya Iizuka[1], Keisuke Mase[1], Toshio Yamamoto[1], and Wajirou Hara[2]**

*[1]Sericultural Science Laboratory, National Institute of Agrobiological Sciences (NIAS), Agata 1-10-1, Matsumoto, Nagano, Japan and [2]Insect Biotechnology and Sericology Department, NIAS, Oowashi 1-2, Tsukuba, Ibaraki, Japan*

Sawa-J strain has abnormal food preference controlled by a major recessive gene and several modifiers. This major gene, *pph*, was reported to be linked to the third chromosome (Kanda, 1992). In this study, we determined the *pph* locus by phenotypic markers, *Ze* and *lem* on the third chromosome, and carried out the linkage analysis using the Restriction Fragment Length Polymorphisms (RFLPs) detected by cDNA clones (cDNA clones' RFLP) on each 28 chromosomes.

We used an artificial diet without mulberry leaves, LP-1, and two silkworm strains, Sawa-J·*lem* and Daiankyo (*Ze/Ze*). Sawa-J·*lem* (*pph lem/pph lem*) is Sawa-J introduced *lem* gene by successive backcrossing over 20 generations. Although Sawa-J·*lem* well feeds on LP-1, Daiankyo never feeds on it. The BF1 progeny between Sawa-J·*lem* female and F1 male were screened by LP-1, and the survival larvae were phenotypically segregated on the ratios of $+^{Ze}$, *pph*, *lem*: $+^{Ze}$, *pph*, $+^{lem}$ : *Ze*, *pph*, *lem* : *Ze*, *pph*, $+^{lem}$ = 397:55:31:5. Penetrance value (2.94) was calculated from the segregation of BF1 between F1 female and Sawa-J·*lem* male ($+^{Ze}$, *pph*, *lem* : *Ze*, *pph*, $+^{lem}$ = 859:26). Therefore, the segregate ratios were converted to $+^{Ze}$, *pph*, *lem* : $+^{Ze}$, *pph*, $+^{lem}$ : *Ze*, *pph*, *lem* : *Ze*, *pph*, $+^{lem}$ = 397:54:29:0. From these results, the recombination values of *Ze-pph*, *pph-lem* and *Ze-lem* were 6.0, 11.3 and 17.3, respectively, and compensated to *lem*-16.1cM-*pph*-4.7cM-*Ze* by the authorized linkage maps.

Very effective linkage analysis and mapping methods of EST cDNA clones by using RFLP on BF1 segregants have been improved and the molecular map of cDNA clones' RFLP were constructed. These methods were applied to analyze this food preference character. To obtain the DNA marker of the food preference genes of Sawa-J, the genomic DNA of (Sawa-J·*lem* × Daiankyo) × Sawa-J·*lem* was prepared after screening by LP-1, and carried out the linkage analysis using cDNA clones' RFLP. As the results, the food preference of Sawa-J was completely linked with a cDNA clone belonging to RFLP linkage group 9 which dose not correspond to the third chromosome. This result suggests that food preference genes of Sawa-J is related with two linkage groups.