



Linkage and mapping analyses of the normal marking gene *+P* in the silkworm (*Bombyx mori*) using SSR markers

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ABSTRACT. In the silkworm, *Bombyx mori*, normal markings are mainly controlled by the *+P* gene, which is located on the second chromosome. Due to a lack of crossing over in females, reciprocal backcrossed F_1 (BC_1) progenies were used for linkage analysis and mapping of the *+P* gene based on an SSR linkage map using silkworm strains P50 and H9, which are normal marking and sex-limited marking, respectively. The *+P* gene was found to be linked to 3 SSR markers. Using a reciprocal BC_1M cross, we constructed a linkage map of 22.5 cM, with *+P* mapped at 11.3 cM and the nearest SSR marker S0206 at a distance of 3.0 cM. Based on a fine genome map of domesticated silkworms, Kaikoblast analysis showed that the physical distance between the nearest markers (containing the *+P* gene) is 995 kb. Further analysis showed that BGIBMGA009689, BGIBMGA009688, and BGIBMGA009687 are closer to *+P*, and that BGIBMGA009689 is closest to *+P*, with a physical distance of 19.1 kb.

Key words: Silkworm; SSR markers; Linkage analysis; Gene location; *+P*