Research Paper

IDENTIFICATION OF SNP MARKERS LINKED TO GENES CONTROLLING POST-COCOON TRAITS IN THE MULBERRY SILKWORM, *BOMBYX MORI*

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ABSTRACT

For the identification of DNA markers closely linked to post-cocoon traits in the mulberry silkworm, bulked segregant analysis (BSA) was carried out using the low yielding polyvoltine race, Pure Mysore and the high yielding bivoltine race, CSR2 as parents which showed contrasting features for the selected traits. The data on filament length and denier were recorded in the parents, F1 as well as the high and low bulks of F2 progeny. Two hundred and forty SNP primers representing all the 28 linkage groups (LG) in silkworm were screened with genomic DNA of parents, PM, CSR2 and their F1 progeny. Forty-eight primers showed distinct polymorphism between the parents showing a clear size difference in the amplified products and the co-dominant expression of these polymorphic bands were observed in the F1 where two bands were detected. Screening of these 48 informative primers among the parents, F1 and bulks of F2 progeny revealed that SNP primer no. 09082 of LG 9 and SNP primer no. 12059 of LG 12 are closely linked to the QTL controlling the traits of filament length and denier, respectively. The results of the present study has shown the prospects of using SNP markers in silkworm breeding programme for improving cocoon traits in the low yielding polyvoltine breeds of India leading to the maximisation of silk yield and quantity.

Key words: *Bombyx mori,* bulked segregant analysis, denier, filament length, QTL, SNP.