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EVALUATION OF GENETIC DIVERSITY IN SILKWORM (*BOMBYX MORI* L.) STRAINS USING MICROSATELLITE MARKERS

CHANDRAKANTH N, MOORTHY SM*, ANUSHA P, DAYANANDA, ASHWATH SK, KUMAR V AND BINDROO BB

Central Sericultural Research and Training Institute, Mysore-570 008, Karnataka, India

*** Correspondence Author: E Mail: moorthysm68@gmail.com**

ABSTRACT

Genetic relationships among ten silkworm strains comprising of five each of bivoltine and polyvoltine were investigated by using 15 SSR markers. All the fifteen markers were polymorphic and generated 54 alleles with an average of 3.6 alleles per locus. The number of alleles scored at each locus varied from 2 (Fl0601, Fl0630, Fl0643, LFL0329 and LFL0944) to 6 (Sat1423 and FI0668). The silkworm strain CSR51 had 3 specific alleles, SK4C had 2 specific alleles and Pure Mysore, Cambodge, L14, CSR2, CSR50 and BHR3 each had one specific allele. The bands produced by FI0619 and LFL0944 markers were specific for voltinism character. The dendrogram generated by UPGMA based on 15 microsatellite loci differentiated silkworm strains into two major groups. Group I consisted of bivoltines and group II contained polyvoltines. Further the bivoltine group was subdivided based on cocoon shape and polyvoltine group was subdivided based on the cocoon colour spun by the silkworm strains. This study was also able to identify divergent parent which can be used in further breeding programme.

Keywords: Silkworm, SSR, Genetic Diversity, Bivoltine, Polyvoltine

INTRODUCTION

Silkworm (*Bombyx mori*) is the most domesticated Lepidopteran insect with economic value because of its silk secreting ability. In the long history of domestication, several thousands of silkworm strains have been developed through systematic breeding and maintained. Currently, more than 4000 strains of silkworm are available all around the world **[1, 2]**, which includes univoltine, bivoltine and polyvoltine and these silkworm strains exhibits wide variations in qualitative and quantitative traits, which