AIG-3431: MOLECULAR CHARACTERIZATION OF SILKWORM GENETIC RESOURCES THROUGH EXPRESSED SEQUENCE TAGGED SITES (EST) MARKERS FOR ASSOCIATING GENE SPECIFIC MARKERS WITH PRODUCTIVE TRAITS

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Introduction

The genes regulating growth rate, yield, silk fibre quality, virus resistance *etc*., can be identified with Expressed Sequence Tags (EST) markers. Development of expressed sequence tagged sites (EST) based molecular marker for yolk protein gene, clearly shows that there is a scope of utilizing such EST derived markers for characterization of top performing silkworm races with highly productive silkworm traits.

Objectives

- To characterize silkworm races with gene specific primer
- To identify band variations specific to productive traits
- To document productive races

Outcome

- The prothoracic gene of *Bombyx mori* is a polymorphic one. The gene for the prothoracicotropic hormone in *B. mori* has been already cloned and characterized Three alleles a, b, c were identified in the *ptth* locus which encodes PTTH in the silkworm, *B. mori*. These three alleles can be easily diagnosed by using the PCR technique.
- Three restriction banding pattern were observed among the screened silkworm genetic resources and their scoring revealed high, moderate and low fecundity and growth groups.
- Two major EST gene primers; PTTH and Yolk protein associated with productive traits were identified as markers that demarcated 75 BV and 30 MV silkworm accessions screened into three cluster groups as high, moderate and low productive ones consisting of 36, 22 and 17 accessions, respectively in case of BV and 17, 9 and 4 accessions, respectively in case of MV.

High productive Bivoltine accns. (36)	High productive multivoltine accns.(17)
BBE-0001, 0003, 0004, 0005, 0006, 0011, 0012, 0013, 0014, 0016, 0017, 0018, 0019, 0026, 0028, 0029, 0030, 0031, 0038, 0041, 0042, BBI-0044, 0047, 0048, 0051, 0052, 0054, 0058, 0061, 002, 0064, 0065, 0066, 0067, 0068, 0069, 0070	**BMI**-0001, 0007, **BME**-0015**, BMI-**0019, BMI-0041, BMI-0042, BMI-0043, BME-0044, BMI-0045, **BME-**0046, 0047, 0048, 0049, **BMI-**0061,0062, 0065, 0074.

Recommendations/ Utilization:

- Express Sequence Tag (EST) site technique was employed as an important molecular tool to identify productive breeds among promising silkworm genetic resources.
- Identified productive races based on growth and yield specific genes can be used as high productive/robust breeds by the breeders for marker assisted selection breeding to evolve robust breed for field utilization and augmentation of silk productivity in the field.

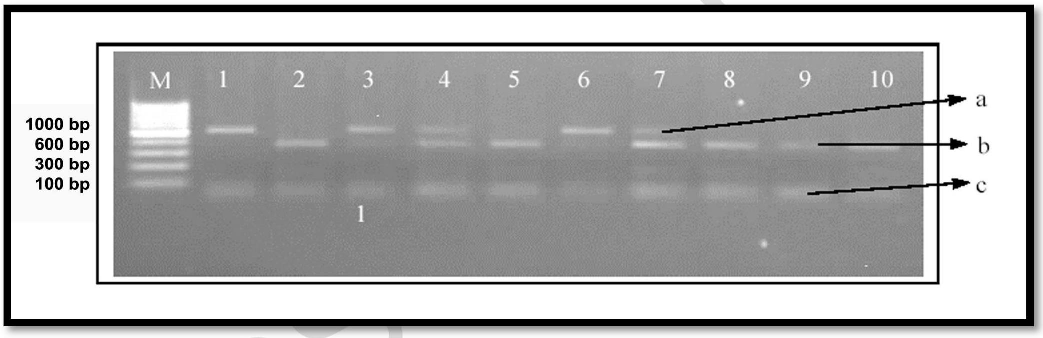

Fig. Restriction pattern profiles of Yolk protein gene among selected bivoltine silkworm races

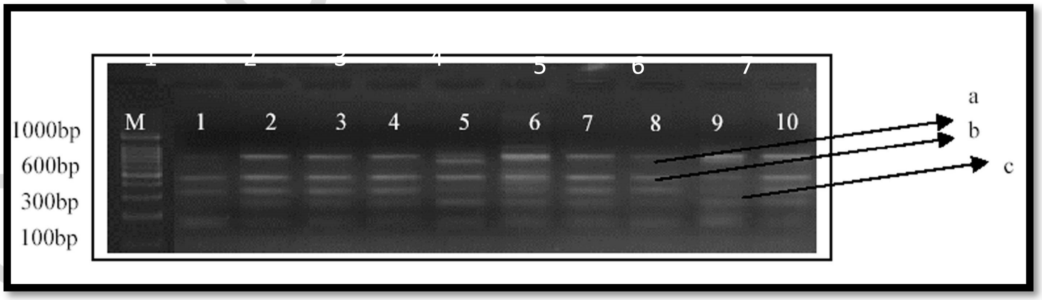

Fig.Restriction pattern profiles of PTTH gene among selected Bivoltine silkworm races