

## **1. ARP – 3518: Expression profiling of genes associated with resistance to *Beauveria bassiana* in *Bombyx mori* strains (SBRL, Bengaluru project with CSGRC Hosur) Oct.2014 – Sept.2017**

### **Introduction**

Among the major diseases affecting *Bombyx mori*, muscardine caused by *Beauveria bassiana* is contagious inflicting 10-40% cocoon crop loss in India (Chandrasekharan and Nataraju 2008). Studies revealed identification of differential expressions of several genes in *B.mori* Daizo race in response to *B.bassiana* infection (Hou *et al.*, 2014). A pilot study carried out at SBRL, Kodathi revealed definite variations in the differential expression levels of few genes associated with resistance to *B.bassiana* post fungal inoculation among some of the promising silkworm races. In this backdrop, the differential expression of antifungal genes in response to *B.bassiana* infection among some of the *B.mori* strains was analyzed to correlate fungal proliferation with disease resistance and utility of the gene expressions as marker(s) for resistance / susceptibility to muscardine disease.

### **Objectives**

- To analyze differential expression profiles of antifungal genes among Indian silkworm strains in response to *B. bassiana* infection (Oct.14-Feb.17).
- To decipher the correlation of antifungal gene expression profile variations with fungal proliferation
- To study the suitability of antifungal genes as markers for resistance / susceptibility to muscardine disease in Indian *B.mori* strains

### **Methodology**

Twenty eight promising Indian *B.mori* silkworm strains [14 MV and 14 BV] were selected and maintained at CSGRC Hosur by rearing following standard method (Rajan&Himantaraj, 2005). The newly ecdysed final instar larvae were supplied to SBRL Kodathi for carrying out *B.bassiana* related molecular biology experiments.

### **Recommendations**

The study revealed that, the antifungal genes Amidase, Arylphorin and Glucose transporter gene expressions could function as potential markers for screening the germplasm to identify the races that are tolerant to muscardine disease and these races can be further utilized in the breeding program to develop disease resistant/tolerant races.