AIT-06006-MI: Marker assisted screening to identify silkworm genetic resources tolerant to BmNPV and BmBDV

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Introduction:

In India, viral diseases, viz., grasserie, flacherie, etc. in silkworms contribute to significant crop loss. The productive silkworm breeds/hybrids that are commercially exploited for production of mulberry silk are susceptible to diseases. The most important character that determines the commercial success of any silkworm breed is its resistance to diseases under adverse conditions. Utilization of the disease-tolerant/resistant nature of silkworm breeds is one of the cost-effective and reliable methods of preventing crop loss due to viral diseases in silkworm. Before initiation of any breeding programme for disease resistance/tolerance, the tolerance level of the available breeding resource materials should be explored. CSGRC, Hosur, maintains a vast collection of bivoltine and multivoltine silkworm genetic resources. However, comprehensive study to identify trait-specific parental stocks, with reference to disease resistance/susceptibility, has not been carried out so far.

Objectives:

- To identify silkworm resources tolerant to BmNPV and BmBDV using molecular markers
- To validate disease tolerance of the accessions through bioassay studies.
- To quantify the level of resistance/tolerance among selected tolerant genotypes.

Outcome:

A total of 22 silkworm accessions were identified to be tolerant in the range of 10-88% to BmBDV and 15 silkworm accessions with 10-57% tolerance to BmNPV. Accession BBI-0371 (SK6) showed tolerance to both BmNPV and BmBDV with pupal survival rate of 53% and 35% respectively Further, qPCR analysis using tolerant and susceptible silkworm genotypes confirmed the role of 5 candidate genes in providing immunity against BmNPV through higher relative gene expression levels in BmNPV tolerant accessions.

Larval and pupal survival % in marker-identified BmBDV tolerant silkworm accessions

Sl No.	Accession No.	Larval survival % (Mean±SD)	Pupal survival % (Mean±SD)
1.	BBE-0027	97.67±0.76	87.68±5.51
2.	BBE-0267	97.00±1.00	87.14±6.01
3.	BMI-0077	76.33±3.06	74.12±3.22
4.	BMI-0076	79.67±6.11	73.68±3.50
5.	BBE-0216	79.67±5.49	70.35±9.29
6.	BBI-0382	78.50±0.87	68.32±9.24
7.	BBI-0337	84.83±4.65	60.51±5.84

8.	BBE-0014	70.50±6.50	60.33±6.95
9.	BBE-0266	79.83±1.26	54.44±5.39
10.	BBE-0190	53.67±6.81	43.75±4.00
11.	BBI-0336	75.33±6.03	38.24±4.54
12.	BBI-0371	44.00±4.50	34.73±2.78
13.	BBE-0035	63.83±10.37	32.61±6.53
14.	BBE-0177	48.00±6.06	26.00±5.64
15.	BBI-0369	65.00±7.09	24.24±3.78
16.	BBE-0008	60.83±7.37	22.84±2.75
17.	BBI-0358	22.00±2.78	21.35±2.64
18.	BBI-0338	30.33±8.28	20.45±2.93
19.	BBE-0178	53.33±3.88	16.26±1.53
20.	BBI-0378	17.50±3.04	16.11±3.97
21.	BBE-0225	26.00±4.58	12.68±2.47
22.	BBI-0325	11.50±1.32	10.80±2.50

Larval and pupal survival % in marker identified BmNPV tolerant silkworm accessions

Sl No.	Accession No.	Larval survival % (Mean±SD)	Pupal survival % (Mean±SD)
1.	BMI-0018	62.67±5.51	57.27±6.25
2.	BMI-0019	59.83±3.79	53.33±2.26
3.	BBI-0371	67.67±5.84	52.90±4.04
4.	BBI-0370	60.33±4.48	39.01±5.11
5.	BBI-0078	46.67±8.74	31.21±6.33
6.	BBE-0179	57.50±10.54	25.72±3.01
7.	BBI-0376	64.00±5.00	20.79±5.13
8.	BBE-0182	20.50±4.09	18.00±4.25
9.	BBI-0276	28.00±3.12	14.44±2.50
10.	BME-0012	19.50±2.78	13.79±3.01
11.	BBI-0237	16.00±3.28	13.26±3.82
12.	BBE-0206	41.83±3.88	12.68±4.51
13.	BBI-0258	56.17±6.60	11.96±3.97
14.	BBE-0185	53.67±5.20	11.72±0.76
15.	BBE-0029	28.00±4.82	10.93±4.19

Recommendations/Utilization:

The identified tolerant silkworm accessions can be utilized as parental stocks in disease breeding programmes to evolve robust and disease resistant silkworm breeds to mitigate crop losses due to viral disease and for improved productivity. The information on germplasm characterization will be added to the public database of silkworm germplasm at CSGRC, for the benefit of stakeholders. The molecular markers can be employed in quick and effective screening of new germplasm stocks. Further, the five candidate genes in indigenous tolerant bivoltine accessions elucidate their role in providing resistance against BmNPV. These accessions can be further utilized to explore the gene regulatory mechanism in response to BmNPV infection. Over-expression of these genes in the tolerant accessions through transgenic technology could be explored towards development of BmNPV resistant breeds in India.