Centre of Excellence in Seribiotechnology

केन्द्रीय रेशम बोर्ड भारत
CENTRAL SILK BOARD, INDIA

SERIBIOTECH RESEARCH LABORATORY

Central Silk Board, Ministry of Textiles – Govt. of India
Carmelram Post, Kodathi
Bengaluru- 560 035

The Seri-Biotech Research Laboratory (SBRL) was set up during 1993 under the World Bank aided National Sericulture Project. Its aim is to carry out basic research in frontier areas of modern biology to improve silkworm breeds and their food plants.

MANAGEMENT

SBRL is under the overall administrative control of Central Silk Board headed by the Director. The progress of research activities is monitored by an in-house committee viz. the Research Council consisting of SBRL scientists followed by external committees' viz. the Research Advisory Committee and the apex Research Co-ordination Committee of CSB. Transgenic research is monitored by an Institutional Bio-Safety Committee.

VISION

To become a Centre of Excellence in Seribio-technology.

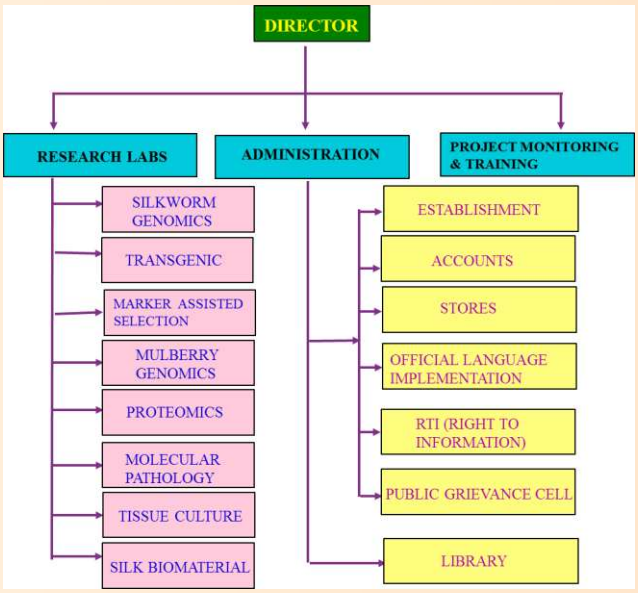
MISSION

To achieve excellence in research in frontier areas of modern biology to transform Indian sericulture industry into a competitive commercial production base.

MANDATE

- To conduct research in frontier areas of modern biology and to seek potential applications of these work towards improving silk productivity
- To interact with other institutions doing basic or applied research in areas related to sericulture and other allied areas
- To develop and disseminate technology to other R&D organizations

ORGANIZATIONAL STRUCTURE



MAJOR ACHIEVEMENTS

Marker Assisted Selection for breeding BmNPV resistant bivoltine silkworm lines

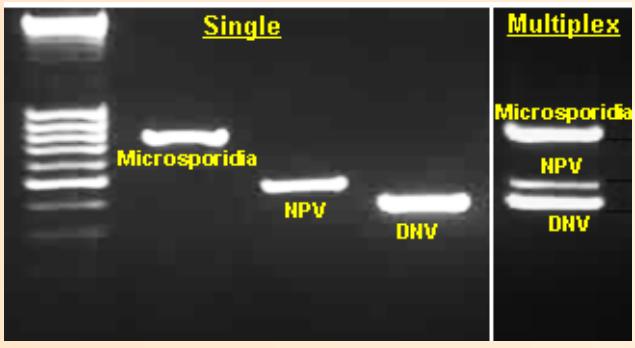
- Three bivoltine *Bombyx mori*silkworm lines (MASN4, MASN6 & MASN7) with better tolerance to *Bombyx mori* Nuclear Polyhedrosis Virus (BmNPV) causing “grasserie” disease have been developed through Marker Assisted Selection (MAS) by introgressing BmNPV resistance marker from Sarupat (multivoltine) to CSR2 (bivoltine).
- The lines showed upregulation of genes associated with NPV resistance in *B. mori*.
- The yield traits are normalized to CSR2 characters, whereas, NPV resistance is close to that of Sarupat, one of the resistant Indian silkworm breed.

DNA marker based development of Densonucleosis*virus* [DNV-2] resistant silkworm breeds

- In conventional breeding, races with resistance to pathogens are shortlisted only based on their survival rate after inoculation with pathogen which is influenced by environmental factors and takes more time to yield results.
- A DNA marker based simple and accurate PCR technology has been developed utilizing specific primers designed to amplify the gene for resistance to DNV-2 in *Bombyx mori*.
- This gene does not allow the virus to multiply in the silkworm.
- Using this technology parental breeds with gene for resistance to DNV-2 can be easily and accurately selected within a short time frame.
- Breeders can make use of these shortlisted accessions for developing new improved DNV-2 resistant breeds.

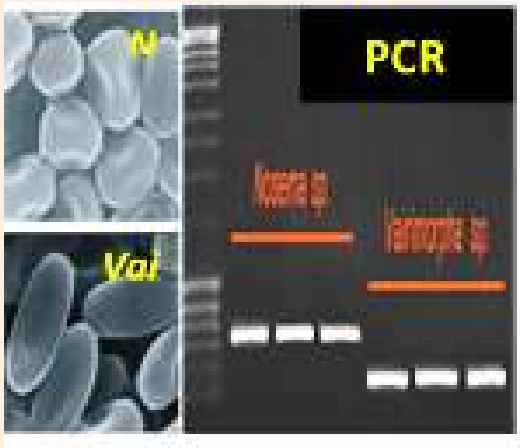
Multiplex Polymerase Chain Reaction (PCR) based simultaneous pathogen detection system

- A novel multiplex PCR assay has been developed under optimized PCR conditions for simultaneous detection of microsporidia, NPV and DNV using three primer pairs.
- The primer pair for microsporidia was designed from the conserved regions of 16S small subunit ribosomal microsporidian RNA gene, that for NPV from the NPV polyhedrin gene and for DNV from the internal sequences of *B.mori* DNV (BmDNV).
- The assay has high specificity and sensitivity for pathogenic DNA revealing discrete and pathogen specific PCR products.



PCR based early detection of pebrine causing microsporidia

- Pebrine is known for its destructive nature in mulberry silkworm *Bombyx mori*.
- PCR based molecular methods are widely utilized as they are rapid, known for superior sensitivity and ability to identify pathogens.
- Three novel sets of oligonucleotide primers were designed from a conserved region of the small-subunit (SSU) rRNA gene and a robust PCR-based diagnostic technique has been developed for early identification of microsporidia infecting mulberry and non-mulberry silkworms.
- One set of primers can detect all microsporidians like *Nosema* and *Vairimorpha spp*; second set to specifically identify *Nosema* sp. and a third for *Vairimorpha* sp.

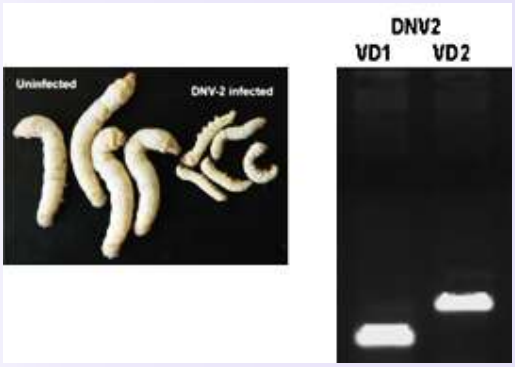


PCR based early detection of flacherie causing Densovirus (DNV-2)

- The highly virulent DNV-2 is widespread under field conditions in major South Indian sericulture practicing areas causing flacherie leading to substantial silkworm crop loss.
- Conventionally DNV-2 is identified/ detected through biochemical analysis/electron microscopy which are cumbersome.
- An easy, simple and accurate DNA based PCR

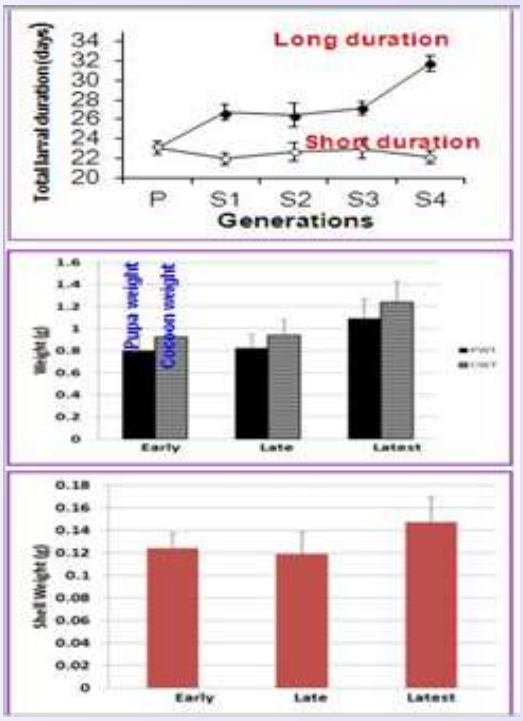
technology has been developed utilizing specific primers designed for detection of DNV-2.

- This technology can support the regular pest and disease survey and surveillance programme undertaken by CSB units.



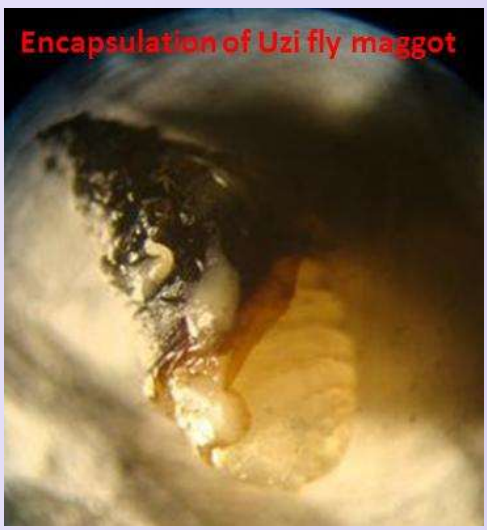
Long duration Nistari race with high cocoon traits

- *Bombyx mori* Nistari is characterized by shorter larval duration but high survival rate and disease tolerance.
- Short larval duration and accumulation of less stored nutrients contribute to low fecundity and low silk content in the cocoon.
- Through directional selection this institute evolved a Nistari strain through induction of significant increase in larval duration so as to provide significant extension of feeding time resulting in accumulation of more energy and its efficient allocation for silk and egg production.
- The evolved high yielding Nistari strain is a boon to farmers for its competent commercial utilization.



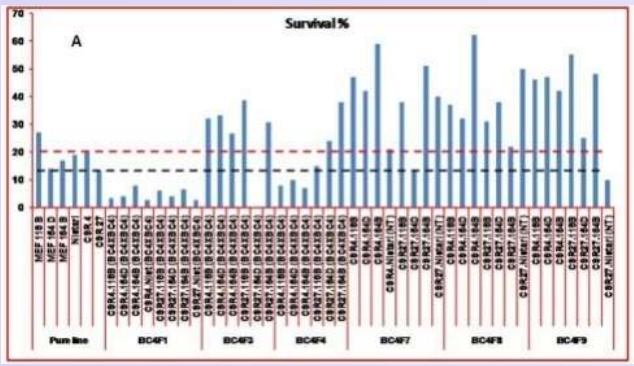
Host-responses of mulberry silkworm against uzi fly infestation

- Mulberry silkworm, *Bombyx mori* breeds are prey to the dipteran parasite, uzifly, *Exorista bombycis*.
- Though mechanical control measures and repellents have been developed to prevent its attack, the uzifly still remains a menace in many parts of the sericultural belt in the country.
- In addition to the organismal effect of infestation, uzifly activates host–responses including immune gene up-regulation, hemocyte-mediated detoxification responses and enhanced melanization leading to encapsulation of uzi fly maggot (**Figure**).
- However the maggot suppresses the immune reactions and survives successfully.
- Few traditionally known susceptible races of *B.mori* revealed enhanced immune gene expression in comparison to hardy races indicating the utility of functional host-response genes as markers to identify immune-competent strains of *B.mori*.



RNAi- based NPV resistance in B. mori

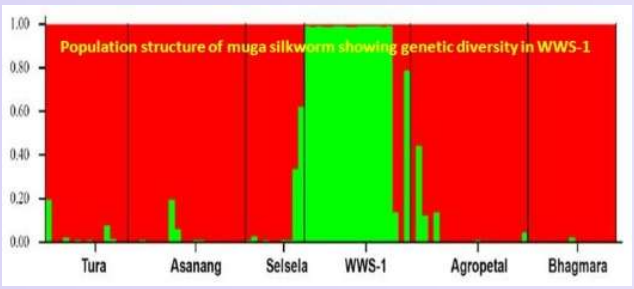
- Transgenic Nistari silkworm lines harboring transgene carrying four tandem sequences arising from four essential genes of the BmNPV to deliver dsRNA was developed at CDFD, Hyderabad.
- The dsRNA-encoding transgene conferred high level of baculovirus resistance in the transgenic silkworm.
- At SBRL the transgene construct was successfully transferred to high yielding but NPV susceptible breeds CSR4 and CSR27 through conventional breeding.
- The "transgenic CSR4 and CSR27 lines" revealed yield characters close to pure CSR4 and CSR27 but with better (up to 60%) NPV tolerance after inoculation (**Figure**).



Genetic diversity in wild silkworm populations

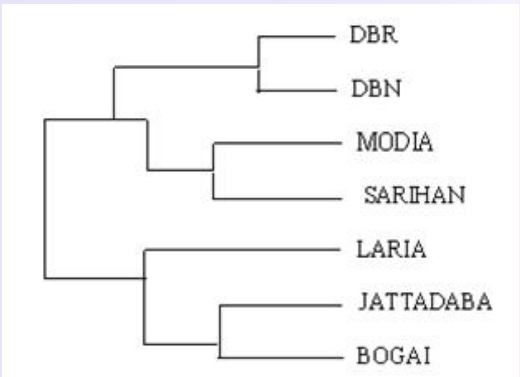
Muga silkworm

- Among six populations of the muga silkworm, *Antheraea assamensis* (WWS-1, Selsela, Asanang, Tura, Agropetal and Bhagmara), only WWS-1 derived from West Garo Hills of Meghalaya showed comparatively higher genetic diversity.
- All other populations were highly homozygous and showed marked reduction in the number of alleles at all the employed microsatellite loci.
- Structure analysis **(Figure)** showed the presence of two clusters, one formed by WWS-1 population and the other by the remaining five populations, inferring that there is WWS-1 population had significant genetic diversity which needs to be preserved. [PLoS ONE,7(8) 2012]



Tasar silkworm

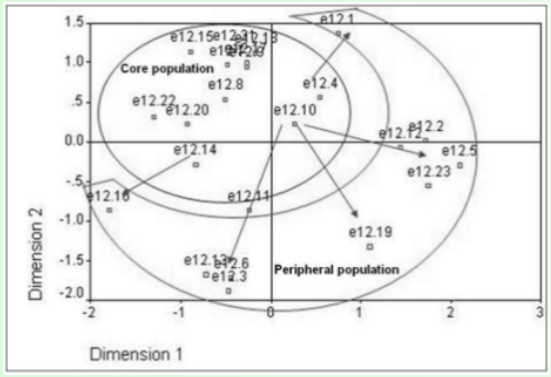
- Culture of tropical tasar silkworm, *Antheraea mylitta* has a long heritage in India and provides better scope for rural employment through its forest products.
- It is distributed randomly in forest patches of North and East India causing its biological richness and diversity.
- Analysis of seven tropical tasar silkworm ecotypes prevailing in Jharkhand using genetic markers revealed genetic closeness between Modia and Sarihan ecotypes.
- Laria, JattaDaba and Bogai ecotypes clustered to form a distant genetic group.
- Among these, the Jatta Daba ecotype collected from the forests of Chakulia, East Singhbhum was genetically distanced (average of 0.273) from other populations **(Figure)** indicating it as a naturally in breeding population with low genetic polymorphism.



Eri silkworm

- The Indian eri silkworm, *Samiacynthia ricini* contributes significantly to "Ahimsa" silk production in Northeast India.

- Deforestation has led to the fragmentation of eri habitats located at lowest to highest altitudes.
- Fifteen eri populations of Northeast India showed genetic distance which increased with altitude and geographic distance.
- Barpathar and Chuchuyimlang populations formed genetic intermediary that confirm to its geographic distribution.
- Intra-population polymorphism and genetic divergence were highest in the Lakhimpur population (58%), whereas, Dhemaji population revealed the lowest.
- Lakhimpur population showed separation of peripheral population from core population with genetic distance of 0.26, leading to differentiation of sub populations **(Figure)**



Number of Projects completed

- CSB funded:19
- DBT funded:10

Human resource development

Ph.Ds completed/ submitted: 8

Several Students from University of Mysore, Bangalore University, Periyar University have done their M.Sc and B. Tech dissertations.

Publications

- National journals: 09
- International journals: 72

Research facilities

- ELISA
- Table top centrifuges
- 2D Electrophoresis
- Spectrophotometer
- Nanodrop
- Biosafety cabinet
- Deep freezers
- Silkworm rearing house
- Mulberry garden

For further details please visit our web site www.sbrl.res.in or contact The Director, SBRL at sbrlban.csb@nic.in or sbrl@rediffmail.com.

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