COMPENDIUM OF CONCLUDED RESEARCH PROJECTS
(2009-2019)

Central Sericultural Germplasm Resources Centre
Central Silk Board, Hosur-635109

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FSL-3417: DEVELOPMENT OF DATABASE MANAGEMENT SYSTEM FOR MULBERRY GENETIC RESOURCES

Period: April, 2008 – March, 2010

Investigators: *S. Sekar, A. Tikader, M. M. Borpuzari, S. Nanjunda Sastry and Kamble C.K.*

Introduction:

The project was initiated to develop mulberry germplasm database with photo documentation of habit, leaf, flower and fruit of each accessions and was successfully completed during the year under report. In order to handle huge data, CSGRC has developed a database namely, Window version of Mulberry Germplasm Information System (Win-MGIS) incorporating various facilities for data storage along with retrieval facilities including photo documentation.

Objectives:

- To develop window version of Mulberry Germplasm Database System including pictorial presentation this will help the mulberry breeders/scientists to select the germplasm resources suitable for development of improved genotypes.
- Easy identification of similar accessions based on morphological features
- Preparation of Mulberry Germplasm Database CD

Features of Win-MGIS

The project was successfully completed as per the objectives. The database system is now installed in mulberry division and data has been updated as on date. The facilities of the system are as follows:

A. Data Entry: This module has the facility of entering passport, characterization, evaluation data etc. In order to enter the data entry, easy and error free descriptors states were provided in combo boxes.

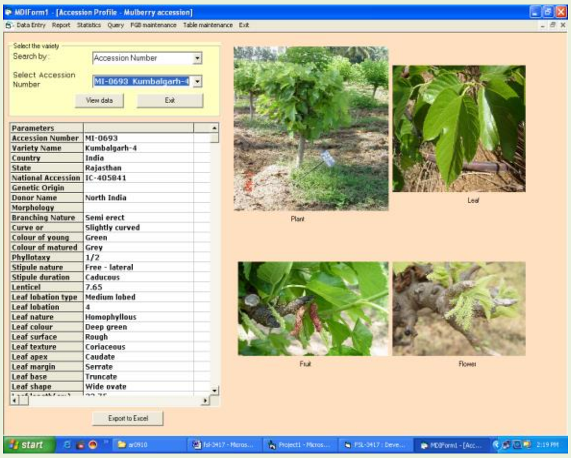
B.Reports:

a. Frequency of collection: This option gives the frequency of mulberry collection based on country, state, species, donor etc or on multiple combinations.

b. Listing of collection: This option lists out mulberry collection based on country, state, species, donor etc or on multiple combinations.

c. Data listing: This option lists out the data on selected parameters / selected accessions. The list can be stored in Excel file also.

d. Accession profile: Accession Profile of mulberry germplasm gives complete information about an accession, which includes passport data, morphological data, anatomical data, reproductive data, growth and yield attributes and biochemical data. In addition to this, it gives the photo images of plant view, leaf, flower and fruit, which help the scientists to select the germplasm for their further research work. The sample page print is given below:



Search by: Accession Number

Select Accession Number: MI-0693 Kumbalgarh-4

Parameters	
Accession Number	MI-0693
Variety Name	Kumbalgarh-4
Country	India
State	Rajasthan
National Accession	IC-405841
Genetic Origin	
Donor Name	North India
Morphology	
Branching Nature	Semi erect
Curve or	Slightly curved
Colour of young	Green
Colour of matured	Grey
Phyllotaxy	1/2
Stipule nature	Free - lateral
Stipule duration	Caducous
Lenticel	7.65
Leaf lobation type	Medium lobed
Leaf lobation	4
Leaf nature	Homophyllous
Leaf colour	Deep green
Leaf surface	Rough
Leaf texture	Coriaceous
Leaf apex	Caudate
Leaf margin	Serrate
Leaf base	Truncate
Leaf shape	Wide ovate

e. Similar accessions: This option list out the accessions those are morphologically similar to the accession, which is entered in the text box.

f. Compare Accessions: This option displays all descriptor values in two columns so that it is easy to compare the values for further selection.

g. High and low performing accessions: This option list out the accessions, which are performing better for the particular parameter. Also it will display the low performing accessions.

h. Qualitative frequency table: This option displays the frequency table for morphological and reproductive parameters

i. Query: This option displays the accessions, which are satisfying the input selected criteria. This option is very useful for selection of mulberry accessions for further research based on multiple parameters.

CD on Mulberry Germplasm

CD on mulberry germplasm database is also prepared for the use of Scientists, Breeders and Researchers which contains facilities like View Accession Profile, listing of similar accessions, comparing mulberry accessions, general statistics, frequency table, better performing accessions and query etc. Further, digital images of habit, leaf, flower and fruit of mulberry accessions were recorded from Mulberry Field Gene Bank of CSGRC and stored along with the database. The users can view the data of individual accessions along with the photo images of mulberry accessions.

Data of 700 accessions, which has been published in the form of printed catalogue in Volume 1, 2, 3 and 4, have been stored in the CD along with digital images of the accessions.

* * *

PIT-3254: CRYOPRESERVATION OF PROMISING MULBERRY GENETIC RESOURCES COLLECTED FROM DIFFERENT GEOGRAPHICAL REGIONS OF INDIA.

(Collaborative project with NBPGR, New Delhi)

Period : October,2008 – September, 2011

Investigators: A. Ananda Rao, R.Radhakrishnan, K. Jhansilakshmi, Anuradha H Jingade and C. K. Kamble,-**CSGRC, Hosur :**S K Malik, Ravish Choudhary-**NBPGR**

Introduction:

The recent advancement of cryo-biological research and its role in long-term preservation of biological materials more particularly for the plants propagated through vegetative means have recognized the cryopreservation technique as practical and efficient biotechnological tools for long-term conservation. In this study, mulberry accessions collected through survey and exploration in North western, Northern, North-Eastern states and semi arid regions (Rajasthan and Madhya Pradesh) and also exotics and poor rooters selected targeted for cryopreservation.

Objectives:

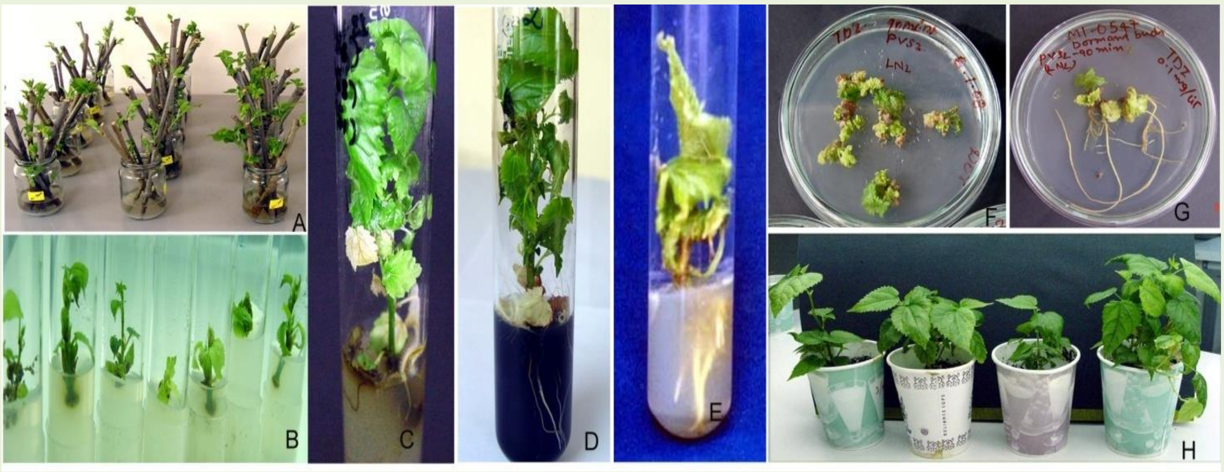
- Cryopreservation of winter dormant buds of different mulberry accessions using dehydration and slow freezing protocol.
- Application of plant vitrification protocol for cryopreservation of apical shoot tips and winter dormant buds of different mulberry accessions

Outcome:

Sl. No.	*Morus* species	No. of Exotic accessions	No. Indigenous accessions	Total No. of accessions	Survival range (%)	Average survival (%)
1	*Morus alba*	02	11	13	0-80	49.84
2	*Morusbombycis*	01	--	1	66.67	66.67
3	*Morusindica*	-	43	43	0-70	30.67
4	*Morus laevigata*	--	02	2	10-20	15.00
5	*Moruslatifolia*	05	02	7	30-60	36.11
6	*Morus macroura*	01	--	1	33.33	33.33
7	*Morusmulticaulis*	01	--	1	20	20.00
8	*Morusspp.*	26	03	29	0-40	20.17

- The survival (%) of winter dormant buds of different mulberry accessions ranged from 0 % in 16 accessions, 20 % in 25 accessions, 21-40 % in 37 accessions, 41-60% in 14 accessions and 61-80 % in 8 accessions.
- Species-specific variations were observed for the survival of the cryopreserved dormant buds.

- ❖ Higher survival was recorded in the accessions belonging to *Morusbombycis* (66.66%), *Morus alba* (49.84%) followed by *M. indica*(30.67%).



Recommendations/ Utilization:

- ✓ The cryopreservation technology developed is safe and efficient for long term conservation of mulberry genetic resources.
- ✓ Vitrification technique can be used for cryopreservation of mulberry, more particularly for the accessions, which are difficult to cryo-preserve through dehydration and slow freezing protocol.

* * *

PIG-3432 : PHYSIOLOGICAL CHARACTERIZATION OF SELECTED MULBERRY GENETIC RESOURCES WITH REFERENCE TO WATER AND NITROGEN USE EFFICIENCY.

Period: January, 2010- June, 2013

Investigators: K. Jhansi Lakshmi and A. Ananda Rao

Introduction:

The major challenge for sustainable sericulture will be to increase crop production with limited water and other inputs particularly Nitrogen. For developing mulberry varieties with high input use efficiency, it is highly pertinent to identify mulberry genotypes with high water and nitrogen use efficiency and specific traits associated with these processes are prerequisite.

Objectives:

- To identify mulberry accessions with high water and nitrogen use efficiency
- To identify characters associated with NUE and WUE and to estimate the genetic variability for associated characters

Outcome

- High variability was observed for leaf senescence, proline content, early vigour, leaf yield/plant, growth during stress period, reducing sugars, drought resistance index under water-limited conditions.
- Under low Nitrogen conditions high CV was recorded for total N uptake, leaf yield/plant (Nitrogen use efficiency), chlorophyll content and plant height whereas medium variability was observed for *GST* activity.
- 17 accessions found to be superior based on multiple traits under water limited conditions.

Promising accessions based on nitrogen use efficiency (NUE)		
Efficient and non responders (low N input)	**Inefficient Responders (high N input conditions)**	**Efficient and Responders (low and high N input)**
MI-0685 and MI-0683	**MI-0139, MI-0178, MI-0573, MI-0416, MI-0193, MI-0533**	**MI-0256, MI-0332, MI-0768, MI-0762, MI-0477, MI-0622, MI-0226, MI-0657, MI-0763, MI-0346, MI-0025, MI-0699, MI-0314, MI-0214, MI-0670, MI-0827, MI-0161**

- Leaf yield under water stress and drought resistance index had significant positive association with early vigour, growth during stress, chlorophyll content, specific leaf area, reducing sugars, proline and root characters.
- Leaf yield under low N is positively associated with N uptake, plant height, %N in leaf, glutamine synthetase activity and total chlorophyll whereas negatively correlated with harvest index. The accessions with high harvest index could not tolerate low N stress under repeated pruning.

Association of different morph-physiological parameters with leaf yield and drought resistance index

Parameter	leaf yield under water stress	drought resistance index
Days to sprouting	-0.664**	-0.535**
Early vigour	0.789**	0.512**
Relative water content	0.144	0.163
Growth during stress	0.642**	0.510**
Chlorophyll content	0.307**	0.316**
Specific leaf area	0.184*	0.216*
Single leaf weight	0.287**	0.097
Membrane stability	0.038	0.094
Leaf senescence	-0.139	-0.280**
Leaf moisture	0.122	0.081
Reducing sugars	0.364**	0.187*
Proline content	0.292**	0.060
No.of roots/sapling	0.471**	0.327**
Root weight/sapling	0.431**	0.318**
Root length	0.427**	0.386**
Drought resistance I	0.748**	

Association of morpho-physiological parameters with leaf yield and tolerance limit to Nitrogen stress

Parameter	leaf yield under low N	Tolerance limit to N
Plant height	0.764**	0.481**
%N in leaf	0.230*	0.183*
Total chlorophyll	0.181*	0.125
GA activity	0.200*	0.252**
Harvest index	-0.319**	-0.265**
N uptake	0.937**	0.511**

S.No	Cross	S.No	Cross
1	MI-0437 × ME-0125	8	MI-0827 × MI-0012
2	MI-0437 × MI-0256	9	MI-0685 × MI-0308
3	MI-0214 × MI-0670	10	MI-0685 × MI-0314
4	MI-0762 × ME-0016	11	ME-0065 × MI-0670
5	MI-0762 × ME-0065	12	MI-0835 × MI-0670
6	ME-0244× MI-0768	13	MI-0828 × MI-0161
7	MI-0763 × MI-0012	14	ME-0244× ME-0065

Recommendations/ Utilization:

- ✓ Exotic mulberry accns. and accessions with very high harvest index cannot tolerate low N condition in repeated pruning.
- ✓ Mulberry accessions with high shoot elongation and leaf area expansion showed high response to N input.
- ✓ Selected accessions from the identified germplasm were utilized under the project on development of drought tolerant genotypes for rain fed sericulture under CSR&TI Berhampore and six genotypes combined with high yield have been identified.
- ✓ The crosses are expected to give better progeny with drought tolerance characters and can effectively utilize water and nitrogen.

PIE-3443: SCREENING OF MULBERRY GERMPLASM ACCESSIONS FOR TOLERANCE TO ABIOTIC STRESS (ALKALINITY AND SALINITY) CONDITIONS

Period: October, 2010 – December, 2013

Investigators: M.M. Borpuzari, K. Jhansi Lakshmi, S.R. Ramesh

Introduction:

Saline and alkaline soils are of widespread occurrence in arid and semi-arid regions. High concentration of salts in the root zone soil reduces the productivity of nearly 6.73 Mha of otherwise productive lands in India. Similarly, 25% of the ground water resources in the country are saline and brackish. Continuous use of such water for irrigation to agricultural crops is bound to increase the problem of salinity and sodicity in India. The projections indicate that the country will have 11.7 m ha area affected by salinity and sodicity by 2025. The present study was an attempt to investigate the whole plant responses by imposing salinity stress and to identify tolerant accessions, as first step to future breeding efforts.

Objectives:

- Screening of short-listed mulberry accessions along with the promising cultivated checks by imposition of salinity and alkalinity stress to identify tolerant accessions.
- Identification of suitable screening technique and physio-biochemical traits for stress tolerance

Outcome:

- 102 mulberry accessions were screened for salinity tolerance and identified 20 mulberry accessions showed better performance at EC 8ads/m than check S-776.
- A total of 100 mulberry accessions were screened for alkalinity in micro plots. 18 accessions were identified as alkaline tolerant at pH 9.0. These accessions showed better performance than check AR-12.

Salinity tolerant mulberry accessions	Alkalinity tolerant mulberry accessions
MI-0437, MI-0376, MI-0327, MI-0670, MI-0657, MI-0012, MI-0476, MI-0242, MI-0129, MI-0245, MI-0161, MI-0763, MI-0716, MI-0310, MI-0145, MI-0497, MI-0499, MI-0027, MI-0139 & MI-0764	**MI-0226, MI-0670, MI-0836, MI-0652, MI-0762, MI-0449, MI-0764, MI-0437, MI-0716, MI-0822, MI-0310, MI-0248, MI-0702, MI-0190, MI-0643, MI-0499, MI-0788 & MI-0466**

Recommendations/ Utilization:

- ✓ The identified tolerant mulberry accessions to salinity and alkalinity can be used as parents for developing salt tolerant mulberry varieties.
- ✓ Micro plot technique was most suitable for evaluation of salt stress tolerance.

✓ Genotypic score (Response index x Tolerance index) along with leaf necrosis, low leaf Na and Na+/K+ ratio can be used as parameters for salinity tolerance whereas Genotypic score and leaf chlorophyll stability can be used for screening for alkalinity tolerance.

✓ Molecular analysis of these tolerant accessions gives more information about differences among these accessions for their tolerance (osmotic stress tolerance, ion exclusion, tolerance to accumulation of ions etc.) and also for development of markers.

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PIE-3451: DNA MARKER AIDED ANALYSIS OF MULBERRY GENE BANK TOWARDS A CORE ASSEMBLY FOR SUSTAINABLECONSERVATION AND ENHANCED UTILIZATION IN CROP IMPROVEMENT (DBT sponsored collaborative project with CSRTI, Mysore)

Period: September, 2010 – December, 2013

Investigators: S. R. Ramesh, K. Jhansi Lakshmi –**CSGRC, Hosur**,
Dr. V. Girish Naik and M. K. P. Urs **–CSR&TI, Mysore**

Introduction:

The vast collection and maintenance of 1269 mulberry genotypes at CSGRC, Hosur and many breeders' collections maintained at other Institutes of CSB such as CSR&TI, Mysore. Large collection and redundant genotypes are of matter of concern of its effective utilization and conservation. Identification of core-subset / panel of germplasm are important requirement for effective utilization of mulberry genetic resources in breeding /crop improvement programmes. Accordingly, an attempt was made to develop a core set of mulberry germplasm using phenotypic and SSRs & AFLPs molecular markers so as to get maximum diversity representation.

Objectives

- Identification of a panel of diverse mulberry germplasm amenable to association mapping by marker (by genomic and EST SSRs) aided analysis
- Evaluation of panel of diverse mulberry germplasm for important traits *viz.*, sprouting, senescence, rooting, leaf quality, yield contributing traits and key morphological characters
- Construction of a core sub-set of mulberry germplasm by molecular marker (SSRs and AFLPs) and phenotypic analysis

Outcome:

- Highest coefficient of variability (59.27%) was observed for stem yield followed by leaf yield/plant (51.12%) and weight of 100 leaves (50.29%).
- Number of branches ranged from 1 to 25 with mean of 10 branches. Higher number of branches in the range of 7-13.
- Leaf yield ranged from 930 – 1938 g/plant with mean yield of 1492.8g. Most of the accessions were in the range of 205-805 g/plant.
- Though harvest index ranged from 28.34 – 89.92%, most of the accessions were in the range of 50-60%.
- Days to sprouting in exotic accessions ranged from 9 to 32 days with mean 23 days and coefficient of variation 22% while in indigenous accessions, days to sprouting varied from 7-35 with mean of 19 days and coefficient of variation 19.86%.

Recommendations/ Utilization:

- ✓ A panel of diverse germplasm (300 entries) and core sub set (150 entries) with maximum genetic and phenotypic diversity were sampled for use in linkage disequilibrium (LD) mapping and mulberry crop improvement programme.
- ✓ A total of 36 mandatory accessions were included in the core collection, which have been the integral part of Indian mulberry breeding programme over last four to five decades.
- ✓ By assessment of total diversity available in mulberry germplasm and construction of a core subset helps for effective utilization of natural gene pool in crop improvement.

PIE-3566: EVALUATION OF CORESET OF MULBERRY GERMPLASM FOR PHYSIOLOGICAL EFFICIENCY AND LEAF QUALITY

Period : March, 2016 – March, 2019

Investigators : K. Jhansilakshmi, G.Thanavendan, & N. Boopathi, SRF

Introduction :
Though mulberry leaf yield increased gradually through crop improvement, most of the variations observed were for yield associated traits. Hence, further increase in yield potential is possible only through utilizing other unexploited variations available in mulberry germplasm. One such possibility is improving photosynthetic efficiency for improved yield at high CO_2, reducing yield loss under high temperature which is anticipated in lieu of climate change while maintaining/ improving leaf quality. The project was thus taken up to evaluate the mulberry accessions for different physio-biochemcial and leaf quality/nutritional parameters to identify promising mulberry accessions through high physiological efficiency traits with leaf yield.

Objectives:

- To identify important physiological parameters associated with high leaf yield
- To estimate variability for different leaf nutritional components which reflect leaf quality
- To identify MGRs with high physiological efficiency and leaf quality to enhance mulberry leaf yield and leaf quality.

Outcome:

- Highest variability observed in physiological parameters in early vigour (LAI) (CV - 60.83%) followed by Sprouting percentage (34.45%), Leaf fall per cent (45.45%), Total chlorophyll (19.60%), Glutamine synthetase (42.28%), Stomatal conductance (40.36%), Intrinsic WUE (51.37%) and Transpiration rate (34.89%).
- With regard to Leaf nutritional components, highest variability were in Leaf yield (CV – 61.88%) followed by Nitrogen (56.98%), Water use efficiency (38.36 %), Leaf area (35.28%), Ascorbic acid (35.13%), Potassium (23.87%), Phosphorus (22.05%), Leaf Temperature (17.72%), Protein (12.81%), Water soluble carbohydrates (12.99%) and Moisture (6.50 %).
- Identified 15 top performing mulberry accessions for different physio-biochemical and leaf quality parameters and physiological efficiency with leaf yield cum nutritional components based on multiple traits in all the seasons at par with the respective checks.

Acc. No.	No. of Traits	Parameter (value)
MI-0099	12	1(100), 2(1.077), 3(0.58), 4(14.513), 6(5.003), 7(2.901), 8(38.667), 13(0.854), 14(2.148), 15(2.622), 16(68.67), 18(1315.667)
MI-0011	12	1(87.5), 2(1.405), 3(0.564), 4(16.73), 5(0.565), 6(5.036), 7(3.322), 8(32), 9(3.29), 13(0.878), 14(2.166), 17(952)
ME-0033	12	1(87.5), 5(4.972), 6(2.675), 7(23.667), 8(70.66), 9(2.59), 10(0.936), 12(0.24), 13(1.76), 15(13), 17(511.444), 18(1136)
MI-0108	11	1(87.5), 2(1.395), 3(0.478), 6(3.683), 7(3.211), 9(2.45), 10(0.29), 11(2.03), 13(0.923), 15(2.503), 18(801)
MI-0214	11	1(87.5), 2(1.738), 4(15.59), 6(5.437), 7(2.867), 10(0.23), 11(1.93), 12(0.496), 13(0.96), 16(73.48), 18(696),
MI-0286	11	1(70), 4(14.471), 6(4.75), 7(3.047), 9(2.73), 10(0.24), 13(0.892), 14(2.574), 15(3.124), 16(71.78), 18(1089.667)
MI-0665	11	1(87.5),3(0.602),5(0.415),8(36.54),9(3.08),12(0.492),13(0.841), 14(2.159), 15(2.78), 16(76.92), 18(646.333)
MI-0376	11	1(75), 4(22.498), 7(2.968), 8(30.333), 9(2.8), 10(0.23), 13(0.837), 14(2.699), 15(2.53), 16(71.29), 18(717.667)
Victory -1	11	1(87.5), 2(15.496), 5(4.038), 7(20.628), 8(72.09), 10(0.851), 13(2.132), 14(17.478), 15(12), 17(685), 18(1068.25)
MI-0341	10	4(17.114), 6(3.714), 7(4.608), 8(35.167), 9(2.45), 10(0.24), 12(0.426), 14(2.235), 16(70.62), 18(1121.667)
ME-0220	10	4(20.892), 5(0.474), 8(25.333), 10(0.3), 11(1.78), 13(0.909), 14(2.158), 15(3.243), 16(70.29), 18(792.333)
MI-0173	10	1(87.5), 2(2.278), 4(15.606), 6(4.764), 7(3.276), 10(0.31), 11(2.06), 13(0.902), 14(2.519), 16(72.33)
MI-0197	10	1(75), 2(1.368), 4(18.506), 6(5.404), 7(3.425), 9(3.71), 10(0.26), 11(1.8), 13(0.874), 15(2.67)
MI-0290	10	1(75), 2(1.094), 4(14.106), 6(2.659), 7(5.305), 8(17), 12(0.493), 13(0.877), 14(2.646), 16(68.33)
MI-0068	10	1(87.5), 2(15.835), 3(0.476), 6(2.955), 7(16.333), 10(0.882), 12(0.31), 13(2.13), 14(13.136), 16(4.46)
MI-0231	10	1(87.5), 2(2.019), 6(3.131), 7(2.968), 10(0.862), 12(0.598), 14(2.427), 15(3.096), 16(71.82), 17(1136)
Vishala	10	1(87.5), 2(1.372), 3(0.458), 4(14.77), 5(0.42), 8(18.7), 12(0.431), 13(0.848), 14(2.214), 16(69.014),
S-13	9	2(0.987), 5(1.316), 8(19.3), 9(2.555), 10(0.242), 12(0.499), 15(3.098), 16(70.13), 18(1086.667)

Recommendations/ Utilization:

- ✓ The top15 performers, viz., MI-0099, MI-0011 ME-0033, MI-0108, MI-0214, MI-0286, MI-0665, MI-0376, MI-0341, ME-0220, MI-0173, MI-0197, MI-0290 MI-0068 and MI-0231 in all the seasons at par with the respective checks.
- ✓ These identified mulberry genetic resources could be utilized by other institutes as potential parents for crop improvement programmes.

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COLLECTION, CHARACTERIZATION, EVALUATION, CONSERVATION AND SUPPLY OF MULBERRY GENETIC RESOURCES- Continuous project- Phase VI, VII and VIII

Introduction:

Mulberry genotypes are available in different geographical regions of India both under natural and managed habitats that are potential sources of different adaptive traits, resistance / tolerance to different stresses etc. These are valuable assets and basic raw material for developing high yielding varieties tolerant to different abiotic and biotic stresses alongwith high nutritional value for different agro-climatic regions. CSGRC, Hosur is a nodal centre conserving a large number of diversified mulberry genetic resources in *ex situ* field gene bank which are collected through exploratory surveys. To make use of these resources, systematic characterization and evaluations are being carried out since 1994 in a phased manner to identify promising accessions for different traits.

Objectives:

- Survey, exploration and collection of new mulberry genetic resources
- Characterization of mulberry genetic resources
- Evaluation of mulberry genetic resources
- Conservation and supply of mulberry genetic resources
- To update national Mulberry Germplasm Information System (MGIS)

Outcome: Phase-VI (2009-12)

- 15 mulberry germplasm were collected from union territories i.e. Goa & Pondicherry from 2 explorative surveys. 23 mulberry genotypes were collected from KSSRDI, Thalagattapura.
- The evaluation results of 25 mulberry accessions indicate that branching nature are erected in nature. The young shoot colour varies from green and purple green. The Phyllotaxy grouped the accessions into 1/2 (9), 1/2, 1/3 (3) 1/3 (3), 1/3, 2/5 (2) and 2/5 (1 Accs.). The colour of the leaf was dark green.
- Key morphological characters were identified and important physiological parameters were documented. Survival percentage with above 90 % was recorded in 4 accessions viz. MI-0865 MI-0877, MI-0884 and MI-0939
- Sixteen accessions performed better than V-1 for leaf yield/plant, Six mulberry accessions found promising with multiple desired traits on leaf anatomical characters.
- Mean leaf yield/plant/crop among the check varieties was 684 g in V-1, among the test accessions, the leaf yield was in the range of 523 to 836g

Figure-1: Exploration and Collection site map

Recommendations /Utilization:

✓ Six mulberry germplasm accessions: MI-0872, MI-0879, MI-0867, MI-0870, MI-0868 and MI-0884 found better for anatomical characters and other multiple traits are recommended for development of drought tolerant mulberry varieties.

Outcome :Phase-VII (2012-15)

✓ One explorative survey was conducted in GOA, 10 mulberry genetic resources belonging to 3Morus species viz., *M.indica* (8), *M. alba* (1) and *M. laevigata* (1) were collected.

✓ Out of 44 indigenous accessions were evaluated for survivability, 3 accessions MI-0865, MI-0877 and MI-0884 showed >90% survivability.

✓ 31 new mulberry genetic resources comprising both indigenous and exotic were registered and assigned national accession numbers.

✓ 125 mulberry accessions were tested for amenability for cryopreservation. Eight accessions showed more than 70% survival after cryopreservation of the dormant buds.

✓ A total of 918 accessions viz. 696 indigenous and 222 exotic, were supplied to 16 indenters.

Recommendations /Utilization:

➢ Five accessions MI-0872, MI-0879, MI-0883, MI-0890, MI-0871 performed better for growth and yield traits and four accessions ME-165, ME-0024, ME-0108, ME-0139 showed better leaf yield than V-1 can be recommend for crop improvement programme.

➢ Accessions MI-0778, MI-0788, MI-0789, MI-0792, MI-0796, MI-0797, MI-0798 and MI-0828 can be utilized for long term preservation through cryopreservation.

Outcome: Phase-VIII (2015-18)

- ✓ Total of 55 mulberry genotypes were collected from three explorative surveys Ziro valley of Arunachal Pradesh (2), Alsigarh, Pai and Marli villages of Rajasthan (5), Bidar, Karnataka (3) and from donor Institutes KSSRDI, Thalagattapura (42), CSRTI, Pampore (1) and CSRTI, Mysore (2).
- ✓ 69 accessions were characterized and evaluated based on descriptors and identified top 14 promising accessions for multiple traits.
- ✓ Higher leaf yield/ plant from 532- 836 g/plant was recorded in 16 accessions and in two accessions viz., MI-0622 and MI-0633 the leaf yield was comparatively high over V-1 variety among 147 accessions evaluated during the period.
- ✓ Safety backup of 50 temperate mulberry accessions were raised at Manasbal located in Ganderbal District of Jammu and Kashmir under CSRTI, Pampore and 319 mulberry accessions (coreset) were planted at CSRTI, Mysore

MI-0657, MI-0458, MI-0665, MI-0670, MI-0827, MI-0246, MI-0568, , MI-0643, MI-0486, MI-0470, MI-0677, MI-0675, MI-0226, MI-0499, MI-0310, MI-0286, MI-0491, MI-0812, MI-0828, MI-0828, MI-0437, MI-0548, MI-0834, MI-0640, MI-0288, MI-0376, MI-0829, MI-0324, MI-0376, MI-0326, MI-0439

Recommendations /Utilization:

- ➢ Thirty one promising accessions were identified based on morphological, anatomical, growth, yield, biochemical and propagation parameters are recommended for utilization in crop improvement in tropical regions.




* * *

AIP-3430:BIOCHEMICAL CHARACTERIZATION AND EVALUATION OF PROMISING SILKWORM GERMPLASM THROUGH ENZYME KINETICS TO SCREEN GENETIC HARDINESS AMONG SILKWORM GENETIC RESOURCES

Period: April, 2009 – March, 2012

Investigators: P. Somasundram, K. Ashok Kumar and N. Balachandran

Introduction:

The silkworm genetic resources with heat stable esterase and protease isozyme markers against chemical inhibitor and their association was studied through enzyme kinetic properties to identify thermo-tolerant/hardy breeds in the silkworm germplasm stocks. It was also attempted to catalogue the database to document these identified hardy genotype/s.

Objectives:

- To study the kinetic properties of enzymes in promising silkworm germplasm.
- To identify the hardy genotypes based on kinetic value.
- To catalogue the database on kinetic values against each breed and document hardy genotypes

Outcome:

- Among the MV and BV silkworm accessions were screened for inhibition studies on esterase and protease enzymes showed that a minimum inhibition was observed in multivoltine race viz., Pure Mysore (3.33 % in esterase and 3.85 in protease enzyme), whereas it was high in LMP (9.41 % in esterase and 9.15% in protease enzyme). Similar studies in bivoltine indicated a minimum inhibition in Meigitsu (2.62% in esterase and 4.49% in protease enzyme), while it was found higher in Sanish E1 (P) (8.88% in esterase and 9.33 % in protease enzyme).
- The multivoltine silkworm accessions exhibited higher resistance (55.55%) to chemical inhibitors by minimum inhibition activity of the esterase and protease enzymes compared to bivoltine accessions (27.4%).

% Inhibition	Accessions/Races	No. of accessions
0 to 5% level (Higher resistance)	BMI-0001 (Pure Mysore 2), BMI-0017 (Nistari), BMI-0018 (Nistari (M)), BMI-0043 (MW-13), BME-0049 (NK-4)	5
	BBE-0005 (Meigitsu), BBE-0009 (B-40), BBE-0010 (J-112), BBE-0012 (Yakwei), BBI-0286 (SPC-1), BBI-0324 (CSR-3 (SL)), BBI-0359 (CSR-27), BBI-0048 (JD-6)	8

Recommendations/ Utilization:

- ✓ Biochemical characterization and evaluation of silkworm genetic resources through enzyme inhibition activities is an important biochemical tool for screening of silkworm races/breeds with genetic hardiness.
- ✓ Enzyme inhibition technique using chemical inhibitor PMSF specific to esterase and protease enzymes associated with hardiness was developed and used to identify the resistance silkworm genetic resources for its use by researchers and breeders to choose hardy parental race/breeds for silkworm improvement.
- ✓ The higher resistance group of Multivoltine silkworm accessions, Pure Mysore, Nistari, Nistari (M), MW-13 and NK-4 and Bivoltine, Meigitsu, B-40, J-112, Yakwei, SPC-1, CSR-3 (SL), JD-6 and CSR-27 silkworm accessions have been identified as hardy races can be use by breeders for future crop improvement programme.

◆

AIP-3430: BIOCHEMICAL CHARACTERIZATION AND EVALUATION OF PROMISING SILKWORM GERMPLASM THROUGH ENZYME KINETICS TO SCREEN GENETIC HARDINESS AMONG SILKWORM GENETIC RESOURCES

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Objectives:

- To study the kinetic properties of enzymes in promising silkworm germplasm.
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	BBE-0005 (Meigitsu), BBE-0009 (B-40), BBE-0010 (J-112), BBE-0012 (Yakwei), BBI-0286 (SPC-1), BBI-0324 (CSR-3 (SL)), BBI-0359 (CSR-27), BBI-0048 (JD-6)	**8**

Recommendations/ Utilization:

- Biochemical characterization and evaluation of silkworm genetic resources through enzyme inhibition activities is an important biochemical tool for screening of silkworm races/breeds with genetic hardiness.
- Enzyme inhibition technique using chemical inhibitor PMSF specific to esterase and protease enzymes associated with hardiness was developed and used to identify the resistance silkworm genetic resources for its use by researchers and breeders to choose hardy parental race/breeds for silkworm improvement.
- The higher resistance group of Multivoltine silkworm accessions, Pure Mysore, Nistari, Nistari (M), MW-13 and NK-4 and Bivoltine, Meigitsu, B-40, J-112, Yakwei, SPC-1, CSR-3 (SL), JD-6 and CSR-27 silkworm accessions have been identified as hardy races can be use by breeders for future crop improvement programme.

◆

AIE-3434: COLLECTION, CHARACTERISATION, PRELIMINARY EVALUATION, CONSERVATION AND SUPPLY OF SILKWORM GENETIC RESOURCES

Period : April, 2009 – March, 2012

Investigators: N. Balachandran, H. V. Vijayakumar, G. K. Srinivasa Babu,
M. Muthulakshmi and A. Manjula

Introduction:

One of the important mandates of Central Sericultural Germplasm Resource Centre is the collection and conservation of silkworm (*Bombyx mori L)* genetic resources with unique characteristics and new breeds developed by CSRTIs and State sericulture research Institutes of the traditional sericulture states and also the breeds authorized by Central Silk Board. Utilization of the seri-genetic resources depends on the wide genetic variability available in the silkworm genetic resources.

Objectives:

- To collect silkworm genetic resources
- To characterize silkworm genetic resources
- To evaluate silkworm genetic resources for utilization
- To supply silkworm genetic resources for better utilization.
- To conserve silkworm genetic resources for posterity

Outcome:

- ✓ 72 multivoltine, 349 BV and 20 mutants silkworm germplasm accessions were characterized for different descriptors, evaluated for 12 important economic traits.
- ✓ Potential silkworm germplasm accessions identified based on the evaluation data and the same was documented in the SGIS database for usage by the breeders.
- ✓ In order to promote utilization of silkworm genetic resources, CSGRC supplied 159 MV accessions (includes repeat supply) to six indenters in 11 spells and 43 BV accessions (includes repeat supply) to nine indenters in 12 spells for their research purposes
- ✓ Top performing multivoltine and bivoltine accessions were identified for multiple traits and also for individual traits.

Accession Number	No. of traits	Trait No. and Values
BMI-0065	7	1(456.9), 3(25.783), 7(11.55), 9(1.355), 10(0.216), 11(16.089), 12(46.206),
BMI-0073	7	3(26.127), 4(689.2), 7(11.22), 9(1.339), 10(0.221), 11(16.683), 12(44.924),
BMI-0066	6	1(468.7), 3(28.123), 7(12.51), 9(1.462), 10(0.222), 12(49.998),
BMI-0062	6	2(96.37), 3(26.478), 7(11.58), 9(1.334), 10(0.195), 12(46.353),
BMI-0043	6	3(26.104), 7(11.87), 9(1.333), 10(0.208), 11(15.664), 12(47.482),
BBE-0010	8	1(630), 2(98.0), 7(21.5), 8(95.5),(1.71), 10(0.32), 11(19.3), 12(86.0)
BBI-0291	6	1(613), 7(18.4), 9(1.6), 10(0.31), 11(19.5), 12(73.8),
BBE-0035	6	1(638), 3(46.5), 7(20), 9(1.88), 10(0.31), 12(79.8),
BBI-0137	6	2(97.4), 7(18.2), 9(1.64), 10(0.32), 11(19.7), 12(72.9),
BBE-0197	6	3(44.7), 7(17.6), 9(1.63), 10(0.35), 11(22.01), 12(70.6)

Recommendations/ Utilization:

- The promising accessions will be evaluated under AISGEP and hotspot evaluation programmes.
- The top performing accessions identified is recommended for utilization by the breeders in breeding programmes for specific conditions.

◆

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

Period: November, 2009 – November, 2012

Investigators: K. Ashok Kumar, P. Somasundaram, R. Radhakrishnan and Anuradha H. Jingade

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.

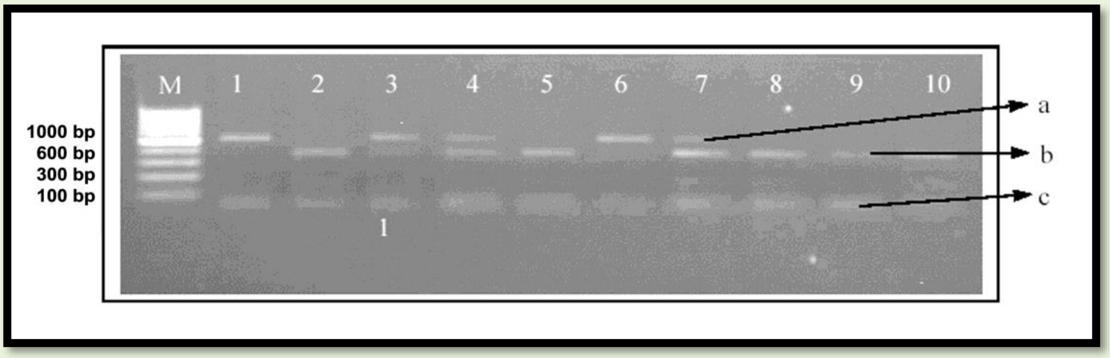


Fig. Restriction pattern profiles of Yolk protein gene among selected bivoltine silkworm races

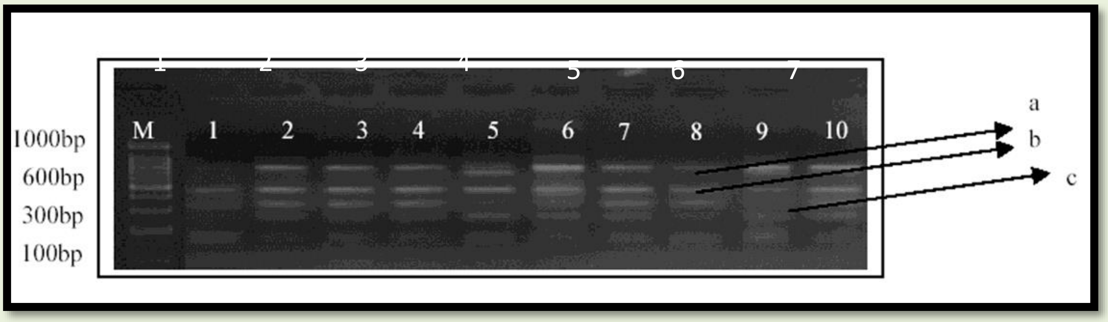


Fig.Restriction pattern profiles of PTTH gene among selected Bivoltine silkworm races

FSL-3447: DEVELOPMENT OF DATABASE MANAGEMENT SYSTEM FOR SILKWORM GENETIC RESOURCES

Period : July, 2010- June, 2012

Investigators:S. Sekar, N. Balachandran, M. Muthulakshmi, G.K.SrinivasaBabu, R. Radhakrishnan, Kiran B. Malali, P.B.V. Shankar, H.V. Vijayakumar

Introduction :

The development of silkworm genetic resource database was initiated during 2008 for photo documentation of morphological structures & long-term systematic data storage, customized data retrieval, statistical reports, selection of accessions for further research and easy identification of similar accessions based on phenotypic parameters. In order to handle huge data, CSGRC has developed a database namely, Window version of Silkworm Germplasm Information System (SGIS) incorporating various facilities for data storage along with retrieval facilities including photo documentation.

Objectives:

- To develop a silkworm database with photo documentation for long-term systematic data storage customized data retrieval, statistical reports, selection of accessions for further research and easy identification of similar accessions based on phenotypic parameters.
- Preparation of silkworm germplasm database CD

Outcome:

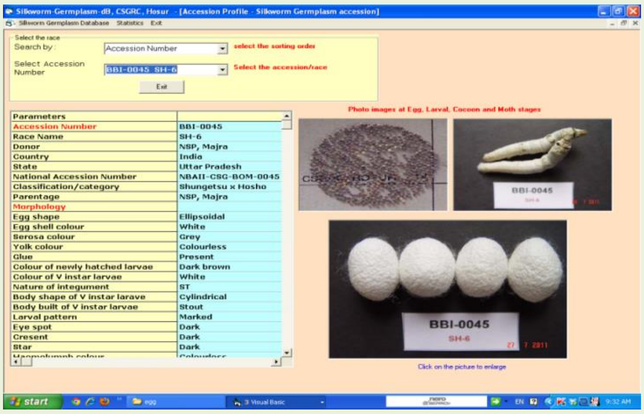
Features of Window-SGIS

A. Data Entry: This module has the facility of entering passport data, characterization & evaluation data etc. In order to enter the data entry, easy and error free descriptors states were provided in combo boxes.

- ✓ Modified the DOS based Silkworm Germplasm Information System [SGIS] as Window Version of SGIS was developed.
- ✓ Designed user friendly data entry screens and shifted, stored all back data in the new system for future use.
- ✓ The Win-SGIS developed in this line by CSGRC involves storing data and retrieval of information in terms of qualitative and quantitative data along with photograph of morphological structures/life stages of each accession.

Crop-wise rearing and reeling data management module

In order to enter crop-wise data and its report generation and data analysis a separate module is developed (Win-Rear) and installed in silkworm division and all data from the year 1995 has been imported to this new system and stored crop-wise for further analysis and pooling data.



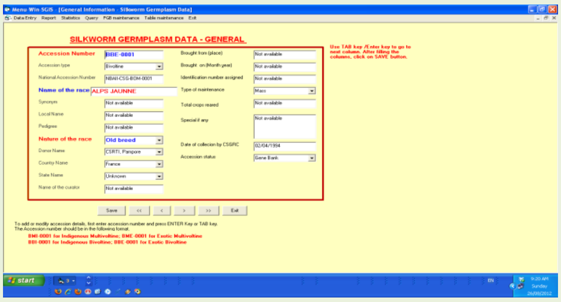
Silkworm-Germplasm-dB, CSGRC, Hosur - [Accession Profile - Silkworm Germplasm accession]

Select the race
Search by: Accession Number — select the sorting order
Select Accession Number: BBI-0045 SH-6 — Select the accession/race

Parameters	
Accession Number	BBI-0045
Race Name	SH-6
Donor	NSP, Majra
Country	India
State	Uttar Pradesh
National Accession Number	NBAII-CSG-BOM-0045
Classification/category	Shungetsu x Hosho
Parentage	NSP, Majra
Morphology	
Egg shape	Ellipsoidal
Egg shell colour	White
Serosa colour	Grey
Yolk colour	Colourless
Glue	Present
Colour of newly hatched larvae	Dark brown
Colour of V instar larvae	White
Nature of integument	ST
Body shape of V instar larave	Cylindrical
Body built of V instar larvae	Stout
Larval pattern	Marked
Eye spot	Dark
Cresent	Dark
Star	Dark

Photo images at Egg, Larval, Cocoon and Moth stages

- *Accession data, Morphological data, Crop-wise rearing data ,Crop-wise reeling data*



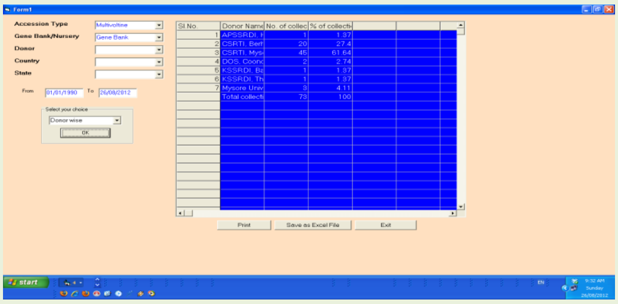
Menu-Win-SGIS - [General Information - Silkworm Germplasm Data]

SILKWORM GERMPLASM DATA - GENERAL

Accession Number: BBE-0001
Accession type: Bivoltine
National Accession Number: NBAII-CSG-BOM-0001
Name of the race: ALPS JAUNNE
Synonym: Not available
Local Name: Not available
Pedigree: Not available
Nature of the race: Old breed
Donor Name: CSRTI, Pampore
Country Name: France
State Name: Unknown
Name of the curator: Not available
Brought from (place): Not available
Brought on (Month year): Not available
Identification number assigned: Not available
Type of maintenance: Mass
Total crops reared: Not available
Special if any: Not available
Date of collecion by CSGRC: 02/04/1994
Accession status: Gene Bank

Use TAB key /Enter key to go to next column. After filling the columns, click on SAVE button.

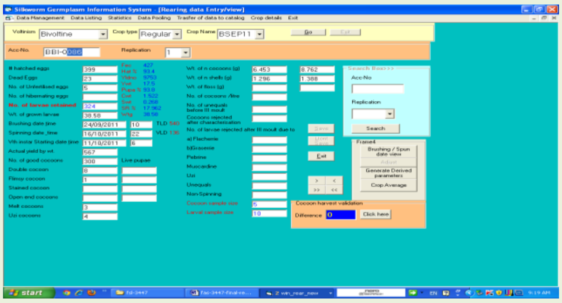
To add or modify accession details, first enter accession number and press ENTER Key or TAB key.
The Accession number should be in the following format.
BMI-0001 for Indigenous Multivoltine; BME-0001 for Exotic Multivoltine
BBI-0001 for Indigenous Bivoltine; BBE-0001 for Exotic Bivoltine



Form1

Accession Type: Multivoltine
Gene Bank/Nursery: Gene Bank
Donor:
Country:
State:
From 01/01/1990 To 26/08/2012
Select your choice: Donor wise

Sl.No.	Donor Name	No. of collec	% of collecti
1	APSSRDI, I	1	1.37
2	CSRTI, Berl	20	27.4
3	CSRTI, Mys	45	61.64
4	DOS, Coonc	2	2.74
5	KSSRDI, Ba	1	1.37
6	KSSRDI, Th	1	1.37
7	Mysore Univ	3	4.11
	Total collecti	73	100



Silkworm Germplasm Information System - [Rearing data Entry/view]

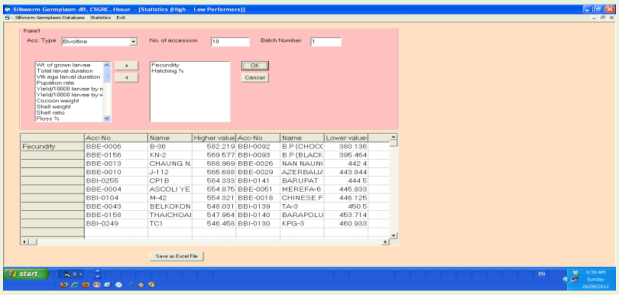
Voltinism: Bivoltine   Crop type: Regular   Crop Name: BSEP11
Acc-No.: BBI-0086   Replication: 1

hatched eggs: 399
Dead Eggs: 23
No. of Unfertilised eggs: 5
No. of hibernating eggs:
No. of larvae retained: 324
Wt. of grown larvae: 38.58
Brushing date time: 24/09/2011 10
Spinning date _time: 16/10/2011 22
Vth instar Starting date time: 11/10/2011 6
Actual yield by wt.: 567
No. of good cocoons: 300
Double cocoon: 8
Flimsy cocoon: 1
Stained cocoon:
Open end cocoons:
Melt cocoons: 3
Uzi cocoons: 4

Fec 427
Hat % 93.4
Yldno 9753
Ywt 17.5
Pupa % 93.8
Cwt 1.522
Swt 0.268
SR % 17.962
Wlg 38.58
TLD 540
VLD 136
Live pupae

Wt. of n cocoons (g): 6.453 8.762
Wt. of n shells (g): 1.296 1.388
Wt. of floss (g):
No. of cocoons /litre:
No. of unequals before III moult:
Cocoons rejected after characterisation:
No. of larvae rejected after III moult due to
a) Flacherie
b)Grasserie
Pebrine
Muscardine
Uzi
Unequals
Non-Spinning
Cocoon sample size: 5
Larval sample size: 10

Cocoon harvest validation
Difference: 0



Silkworm-Germplasm-dB, CSGRC, Hosur - [Statistics (High - Low Performers)]

Acc. Type: Bivoltine   No. of accession: 10   Batch Number: 1

Wt. of grown larvae
Total larval duration
Vth age larval duration
Pupation rate
Yield/10000 larvae by n
Yield/10000 larvae by w
Cocoon weight
Shell weight
Shell ratio
Floss %

Fecundity
Hatching %

	Acc-No.	Name	Higher value	Acc-No.	Name	Lower value
Fecundity	BBE-0006	B-36	582.219	BBI-0092	B.P(CHOC	380.136
	BBE-0156	KN-2	569.577	BBI-0093	B.P(BLACK	395.464
	BBE-0013	CHAUNG N.	568.969	BBE-0026	NAN NAUN	442.4
	BBE-0010	J-112	565.688	BBE-0029	AZERBAIJA	443.844
	BBI-0255	CP1B	564.333	BBI-0141	BARUPAT	444.5
	BBE-0004	ASCOLI YE	554.875	BBE-0051	MEREFA-6	445.833
	BBI-0104	M-42	554.321	BBE-0018	CHINESE F	446.125
	BBE-0043	BELKOKON	548.031	BBI-0139	TA-3	450.5
	BBE-0158	THAICHOAI	547.964	BBI-0140	BARAPOLU	453.714
	BBI-0249	TC1	546.458	BBI-0130	KPG-3	460.933

Recommendation/Utilization

- ✓ The SMGIS is installed in the computers and is being used by the scientists for systematic data storage and retrieval of data on query basis for further research work.
- ✓ The silkworm database of silkworm germplasm with limited characters is also made available in the CSGRC website www.silkgermplasm.com under the web page “Research”.
- ✓ A national silkworm germplasm databank has been developed at CSGRC, Hosur for the use of all Sericultural scientists throughout the country and the database will be made available under CSGRC website.

◆

AIT-3450: LONG-TERM CONSERVATION OF EGGS/ EMBRYOS OF SILKWORM GENETIC RESOURCES (*BOMBYX MORI* L) THROUGH CRYOPRESERVATION (DBT, New Delhi funded projects)

Period: November, 2010 – October, 2013

Investigators: Anuradha H. Jingade, A. Ananda Rao, Sreenivasa Babu

Introduction:

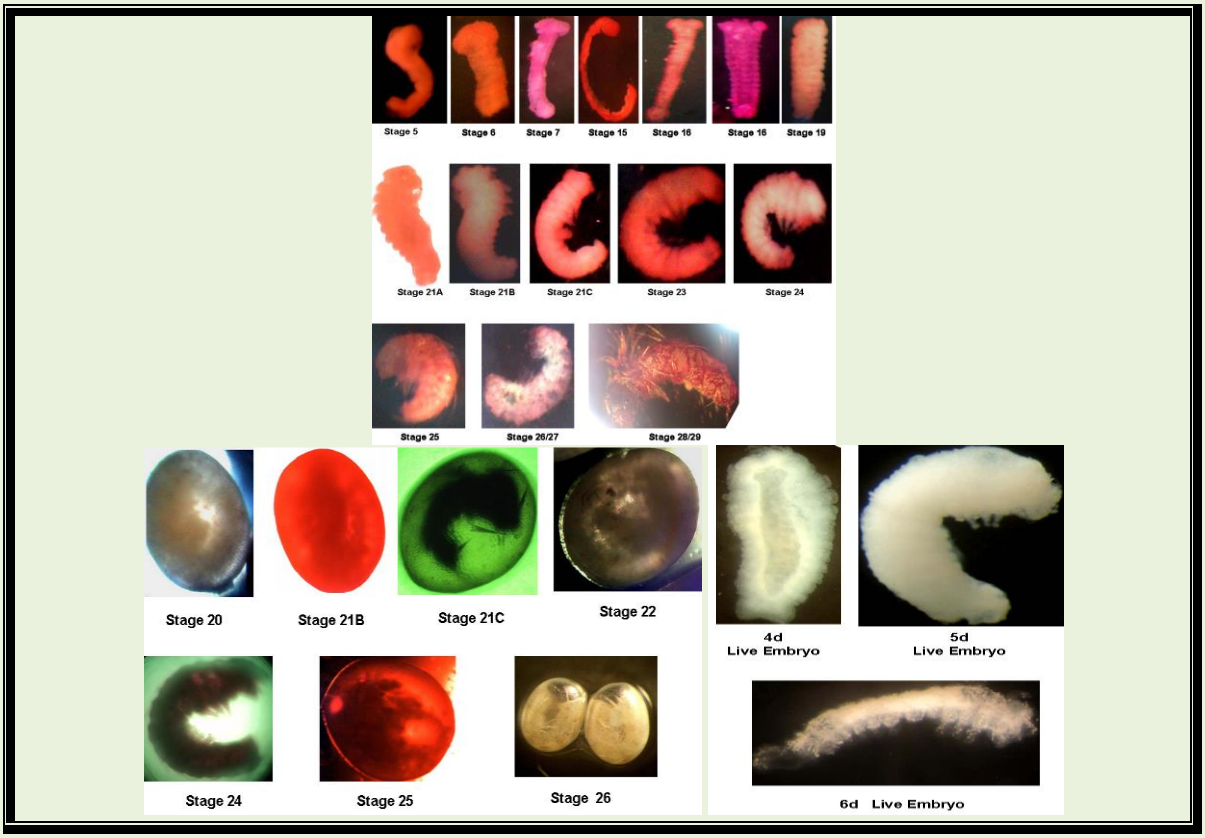
Conservation of the invaluable Silkworm genetic resources is of prime importance with respect to their utilization and improvement for wider exploitation. The newer techniques such as cryopreservation are available from which the genetic resources can be conserved *ex situ* for a longer period. This project was undertaken with an objective to develop suitable protocol for dechorionation of silkworm eggs, extraction of embryos, *in vitro* culture of silkworm embryo and cryopreservation of egg/embryos to establish cryo gene bank of embryos of silkworm genetic resources for commercial/future exploitation.

Objectives:

- To develop suitable protocol for dechorionation of silkworm eggs, extraction of embryos, in vitro culture of silkworm embryo and assessment of survival rates.
- To develop suitable protocols for cryopreservation of egg/embryos of silkworm genetic resources.
- To establish cryo gene bank of embryos of silkworm genetic resources for commercial exploitation.

Outcome:

- Technique for dechorionating silkworm eggs was developed. Treating silkworm eggs with 2% NaOH for two minutes followed by 5 % NaOCl for 10 minutes showed complete dechorionation of eggs.
- The eggs upon treatment with different chemicals at known concentrations have shown varied responses. It was found that silkworm of embryonic age upto 36 h were cold tolerant and embryo of 48 h was cold sensitive.
- *In vitro* culture of Silkworm embryos of early stages (20 to 36 h), incubated with yolk in insect media (TNM-FH) for development. The embryos survived for one day and further development of the embryo was not observed.
- Equilibration time for the CPA tolerance of different cryoprotectants on silkworm eggs after dechorionation, for 10 multivoltine races, was determined for use in cryopreservation of egg/embryos at room temperature. However, CPA tolerance is required to be standardized with respect to cryo-temperature of Liquid Nitrogen (LN) at -196° C.



Recommendations/Utilization

- ✓ Cryopreservation of embryos involves a series of complex and dynamic physio-chemical processes of temperature and water transport between embryo and the surrounding medium. At this stage there is no conspicuous evidence to explain the exact chill tolerant embryonic age.
- ✓ Silkworm eggs can tolerate cryoprotectants with 60% survival and embryos of 36hrs age are chill-tolerant and 48hrs embryos are chill-sensitive.
- ✓ Survival of eggs at cryo temperature could not be established as *in vitro* culture of silkworm embryos was not successful and requires further investigations taking leads from the observations obtained in the present study.
- ✓ Based on this outcome, one research project “Cryopreservation of tropical tasar silkworm *Antheraea mylitta* D semen and its artificial insemination” was proposed.

◆

CYR - 3484: EVALUATION OF SILKWORM GENETIC RESOURCES FOR POST COCOON TRAITS

Period : April, 2012 – March, 2015

Investigators: S. Nivedita, N. Balachandran and M. Muthulakshmi

Introduction:

Raw silk or post cocoon characteristics are important from the point of view of reelers. Therefore, breeders and research institutes engaged in developing silkworm breeds that yield better quality cocoons for commercial exploitation, need basic information about the accessions for selection of parents. Of late, sericin and fibroin, the two proteins in natural silk are gaining extensive research attention due to the fact that these two proteins have unconventional technical and biomedical applications because of their bio compatibility and bio-degradablity. In view of the fact that the protein content in silkworm accessions is variable, the evaluation of sericin and fibroin content in the silkworm accessions becomes very important.

Objectives:

- ➢ To evaluate conserved silkworm genetic resources for post cocoon traits
- ➢ To identify donor parents for specific post cocoon traits

Outcome:

- ❖ BBI-363 has longest filament length (975.5m), maximum raw silk percentage (16.25%) and renditta is the least at 6.15. Reelability varies from 84.6% to 93.8 %.
- ❖ BMI-0079 has the maximum neatness (86%) and minimum evenness variation (60 stripes). Boil-off loss varies from 21.5% to 25.3%.
- ❖ Sericin content was found high in bivoltine and to vary from from 18.6 to 35.0 % and 20.1 to 32.0 % in multivoltines races evaluated.
- ❖ Mutant races showed higher average fibroin content whereas, bivoltine races showed variation from 64.00% to 81.34%.

#	Silkworm Type	Multivoltine	Mutants	Bivoltine
	No. of accessions	73	19	178
SERICIN CONTENT (%)				
1	Average	26.43	26.00	27.38
2	Minimum value	20.14	21.04	18.63
3	Maximum value	31.96	32.34	35.01
FIBROIN CONTENT (%)				
1	Average	73.55	74.00	72.62
2	Minimum value	68.04	67.66	64.99
3	Maximum value	79.86	78.96	81.37

Recommendations/Utilization

- ✓ The list of the top performing accessions on post-cocoon parameters have been catalogued which can be selected as parents for breeding experiments, depending on the characters preferred.
- ✓ Longer filament length and NBFL, higher reelability and raw silk recovery and a lower renditta would improve the productivity and economics of reeling, finer denier would produce better quality with respect to evenness of raw silk.
- ✓ A higher value for neatness, Cleanness, Tenacity, Elongation and cohesion and a lower number for evenness are preferred for superior grades of raw silk. Also, a higher boil-off loss would decrease the value of raw silk. While selecting parents for breeding experiments these parameters should be kept in mind for better reeling performance, better economics as well as better quality of raw silk.

◆

AIE-3454: EVALUATION OF ELITE BIVOLTINE SILKWORM GERMPLASM UNDER DIFFERENT AGRO CLIMATIC CONDITIONS: ALL INDIA SILKWORM GERMPLASM EVALUATION PROGRAMME (AISGEP)"

(Networking collaborative Research programme with CSB Research Institutions)

Period : August, 2012 – February, 2015

Investigators: N. Balachandran, M. Muthulakshmi and S. Nivedita

Introduction:

The 350 bivoltine silkworm germplasm accessions conserved and maintained are preliminarily evaluated for economic parameters of 12 rearing and 16 post cocoon traits. The evaluation data collected over the years were updated in the Silkworm Germplasm Information System (SGIS) for the benefit of silkworm breeders to use information and genetic resources for silk improvement programmes.

Objectives:

- To identify the suitability of bivoltine silkworm germplasm for specific agro climatic area.
- To identify the bivoltine silkworm germplasm which have a wider adaptability to varied climatic conditions.
- To identify the potential germplasm as parent for silkworm hybridization programme suitable for different agro-climatic condition.

List of bivoltine germplasm accessions selected for the study

Sl. No	Accession No.	Name of the Accession	Sl. No	Accession No.	Name of the Accession
1	BBE-164	ShongetsuHoshu	7	BBI-338	DD-1
2	BBE-329	MIR-4	8	BBE-263	101-D
3	BBE-268	J 1 M	9	BBE-216	HO (SL)
4	BBE-202	C124 (SL)	10	BBI-348	NP-2
5	BBE-266	J 2 P	11	Local Control	Popular local Breed
6	BBE-225	JZH (PO)	12	National Control	CSR-2

Outcome:

- Out of selected ten elite BV accessions evaluated in 8 network centres under different agro-climatic regions, the accession BBI-0348 performed better in 7 centres followed by BBE-0329, BBI-0290 in 5 centres and BBE-0266, BBE-0216 in 4 centres in spring season.
- The accession BBE-0266 performed better in 6 centres followed by BBI-0348 BBE-0266, BBI-0338 and BBE-0268 in 5 centres in autumn season.
- The accessions BBI-0348, BBE-0329 BBE-0266, BBE-216 and BBI-0348 are identified as better performers having wider adaptability under different agro-climatic conditions and seasons.

Overall ranking of accessions based on the Spring crop								
Rank	CSRTI Berhampore	CSRTI Pampore	CSRTI Mysore	RSRS, Jammu	RSRS, Jorhat	RSRS, Sahaspur	RSRS, Kalimpong	CSGRC, Hosur
I	BBI-0348	BBI-0338	BBI-0290	BBE-202	BBE-0216	BBI-0225	SK6	BBE-0329
II	BBE-0216	BBI-0290	BBI-0348	BBE-263	BBI-0348	BBE-0263	BBI-0290	BBI-0348
III	BBI-0290	BBI-0045	BBE-0216	BBE-348	BBE-0268	BBE-0329	BBI-0348	BBE-0266
IV	BBE-0329	BBE-0329	BBE-0164	BBE-338	BBE-0263	BBE-0268	BBE-0268	BBE-0263
V	BBE-0266	BBE-0263 BBE-0216	BBE-0268	BBE-268 BBE-225	BBE-0202 BBE-0164	BBE-0164	BBE-0329 BBE-0202 BBE-0164	BBI-0338

Recommendations/ Utilization:

- ✓ The identified better performers having wider adaptability in different ago climatic conditions and seasons can be included in future breeding programmes as parental resource materials for crop improvement.

Overall ranking of accessions based on the Autumn crop								
Rank	CSRTI Berhampore	CSRTI Pampore	CSRTI Mysore	RSRS, Jammu	RSRS, Jorhat	RSRS, Sahaspur	RSRS, Kalimpong	CSGRC, Hosur
I	BBE-0268	BBI-0290	BBE-0266	BBE-268	BBE-0266	BBI-0290	BBE-0268	BBE-0329
II	BBE-0216	BBI-0348	BBE-0263	BBI-0338	BBI-0290	BBE-0263	BBE-0202	BBI-0338
III	BBI-0338	BBE-0329	BBI-0348	BBI-0348	BBE-0225	BBE-0329	BBE-0266	BBE-0268
IV	BBE-0263	BBE-0268	BBE-0202	BBE-0329	BBE-0216	BBE-0268	BBI-0348	BBE-0266
V	BBE-0266	BBE-0263	BBE-0216	BBE-0263	BBE-0268	BBE-0164	BBI-371	BBI-0263

- ✓ The accessions BBE-0329, BBE-0266, BBE-0268 were utilized in an in-house project for evaluation of exotic bivoltine breeds to identify promising parental genetic resources.

AIG-3483:COLLECTION, CHARACTERIZATION, PRELIMINARY EVALUATION, CONSERVATION AND SUPPLY OF SILKWORM GENETIC RESOURCES

Period : April, 2012 – March, 2015

Investigators: P.Somasundaram, N.Balachandran, Veeranna Gowda, M.Muthulakshmi, R.RadhaKrishnan

Introduction:

The important mandate of Central Sericultural Germplasm Resource Centre is the collection of silkworm (*Bombyx mori*) genetic resources with unique characteristics and new breeds developed by CSRTIs and State sericulture research Institutes and the breeds authorized by Central Silk Board. During the Phase-VII, all the conserved silkworm germplasms (443) were considered for the evaluation and generation of data to update in the SGIS database. Besides new collection silkworm races were also made and characterized, assigned accession numbers and enriched the silkworm germplasm.

Objectives:

- To collect silkworm genetic resources
- To characterize silkworm genetic resources
- To evaluate silkworm genetic resources for utilization
- To supply silkworm genetic resources for better utilization.
- To conserve silkworm genetic resources for posterity

Outcome:

- 23 new silkworm genetic resources [SWGRs] (8 MV and 15 BV) collected from 5 Institutes CSRTI, Berhampore (6), CSRTI, Pampore (4), APSSRDI, Hindupur (8), CSRTI, Mysore (4) and SSTL, Kodathi (1) and were accessioned by NBAIR, Bengaluru and added to the gene bank.
- 81 multivoltine, 365 BV and 20 mutants silkworm germplasm accessions were characterized for different descriptors, evaluated for 12 important economic traits and data updated in SGIS which confirmed their conservation as per passport data.
- 600 BV accessions were supplied to 15 indenters in 68 spells and 128 MV accessions to 10 indenters in 29 spells for PG research, evaluation and as breeding resource materials.
- Top performing multivoltine and bivoltine accessions were identified for multiple traits and also for individual traits.

List of accessions collected from different institutes

Sl. No.	Name of the race	Voltinism	Donor Institute	Institute Accn. No.	National Accn. No.
1	SK-6	Bivoltine	CSRTI, Berhampore	BBI-0371	NBAII-BBI-0371
2	SK-7	Bivoltine	CSRTI, Berhampore	BBI-0372	NBAII-BBI-0372
3	DUN-6	Bivoltine	CSRTI, Pampore	BBI-0373	NBAII-BBI-0373
4	DUN-22	Bivoltine	CSRTI, Pampore	BBI-0374	NBAII-BBI-0374
5	PAM-114	Bivoltine	CSRTI, Pampore	BBI-0375	NBAII-BBI-0375
6	PAM-117	Bivoltine	CSRTI, Pampore	BBI-0376	NBAII-BBI-0376
7	APS-12	Bivoltine	APSSRDI, Hindupur	BBI-0377	NBAII-BBI-0377
8	APS-45	Bivoltine	APSSRDI, Hindupur	BBI-0378	NBAII-BBI-0378
9	APDR-105	Bivoltine	APSSRDI, Hindupur	BBI-0379	NBAII-BBI-0379
10	APDR-115	Bivoltine	APSSRDI, Hindupur	BBI-0380	NBAII-BBI-0380
11	APDR-126	Bivoltine	APSSRDI, Hindupur	BBI-0381	NBAII-BBI-0381
12	PM (M)	Multivoltine	SSTL, Kodathi	BMI-0075	NBAII-BMI-0075
13	APM-2	Multivoltine	APSSRDI, Hindupur	BMI-0076	NBAII-BMI-0076
14	APM-3	Multivoltine	APSSRDI, Hindupur	BMI-0077	NBAII-BMI-0077
15	APDR-15	Multivoltine	APSSRDI, Hindupur	BMI-0078	NBAII-BMI-0078
16	Mcon-1	Multivoltine	CSRTI, Berhampore	BMI-0079	NBAII-BBI-0079
17	Mcon-4	Multivoltine	CSRTI, Berhampore	BMI-0080	NBAII-BBI-0080
18	Bcon-1	Bivoltine	CSRTI, Berhampore	BBI-0382	NBAII-BBI-0382
19	Bcon-4	Bivoltine	CSRTI, Berhampore	BBI-0383	NBAII-BBI-0383
20	Gen-2	Bivoltine	CSRTI, Mysore	BBI-0384	NBAII-BBI-0384
21	Gen-3	Bivoltine	CSRTI, Mysore	BBI-0385	NBAII-BBI-0385
22	L14	Multivoltine	CSRTI, Mysore	BMI-0081	NBAII-BMI-0081
23	L15	Multivoltine	CSRTI, Mysore	BMI-0082	NBAII-BMI-0082

Recommendations/ Utilization:

- ✓ Enrichment of gene bank through addition of 23 new silkworm breeds (8 MV and 15 BV) providing wider genetic base for the stakeholders in selection of potential parental stock for crop improvement programs.
- ✓The identified top performing multivoltine and bivoltine accessions for multiple and individual traits can be utilized for crop improvement programs.
- ✓ The supply of 600 BV and 128 MV accessions for PG research, evaluation and as breeding resource materials promoted utilization of the conserved germplasm.

AIE 3542: COLLECTION, CHARACTERIZATION, EVALUATION, CONSERVATION AND SUPPLY OF SILKWORM GENETIC RESOURCES (PHASE VIII)

Period : April, 2015 – March, 2018

Investigators : N. Balachandran, M. Muthulakshmi, G. Lokesh, M. Maheswari, Veeranna Gowda, and S. Nivedita

Introduction:

The collection, characterization, evaluation and conservation of silkworm germplasm is a continuous programme which is the main mandate of the centre and silkworm *Bombyx mori* accessions have been characterized using set descriptors, evaluated for important economic parameters and conserved following different conservation crop cycles every year. All the 475 silkworm germplasm accessions data on the characterization and evaluation have been updated in the SGIS database. The accessions are conserved following different conservation protocols as per the voltinism for promoting utilization for crop improvement and supply of the materials to the users.

Objectives:

- To collect silkworm genetic resources
- To characterize silkworm genetic resources for utilization
- To document silkworm genetic resources
- To supply silkworm genetic resources for better utilization

Outcome:

- Nine new collections included four bivoltine breeds, two new multivoltine breeds as well as three mutant breeds. Exhibit great variability in terms of origin, nature of breed as well as qualitative and quantitative traits with unique characteristics
- 475 silkworm germplasm accessions were evaluated and maintained true-to-type as per catalogue data.
- Systematic documentation of evaluation data for the 12 rearing and 16 post cocoon traits in the Silkworm Germplasm Information System (SGIS).
- Collected the wild species of mulberry silkworm *viz*. *Bombyx huttoni* from the Ziro valley of Arunachal Pradesh through explorative survey.
- The multivoltine accession BMI-0082 has been identified as best performer for 8 rearing traits followed by BMI-0074, BMI-0081, BMI-0080, BMI-0078 and BMI-0076 for 7 traits and BMI-0077, BMI-0067 for 6 traits and BMI-0079 for 5 traits.
- The bivoltine accession BBI-0377 has been identified as best performer for 4 rearing traits followed by BBI-0070, BBI-0345, BBE-0035, BBI-0068, BBI-0059 and BBI-0344 for 3 traits and BBE-0034, BBE-0036 and BBI-0303 for 2 traits.

Plate No-1: Life cycle of *Bombyx huttoni* Westwood

Recommendations/Utilization

- ✓ 451 silkworm genetic resources supplied, majority were utilized by various CSB R&D institutes (86%).
- ✓ Collection of the wild species of mulberry silkworm *viz. Bombyx huttoni* from the Ziro valley of Arunachal Pradesh provides a basis for taking up studies on their conservation.
- ✓ The identified top performing multivoltine and bivoltine accessions for various parameters can be utilized for crop improvement programs.

AIB- 3577: EVALUATION OF MULTIVOLTINE GERMPLASM TO IDENTIFY POTENTIAL PARENTS FOR DEVELOPING CROSS BREEDS FOR SOUTHERN AND EASTERN INDIA

(Collaborative project with CSR&TIs Mysore and Berhampore)

Period :June, 2016 – May, 2019

Investigators: G. Punithavathy, N. Balachandran, D. S. Somaprakash, Jameela Khatoon, K. B.Chandrasekar, P.V.Soudaminy, G. C. Das and N. Chandrakanth

Introduction:

Though silkworm germplasm constitute the potential raw material and having wide variation in their genotypic expressions, there is always under utilization of silkworm germplasm resources for breeding programmes. Therefore, the silkworm breeding strategy oriented towards involving multivoltine silkworm genetic resources at CSGRC, Hosur in preparation of Improved cross breeds with specific qualitative and quantitative traits. Multivoltine silkworm genetic resources available at CSGRC, Hosur was not explored by the breeders so far and also studies related to pre-breeding involving multivoltine silkworm genetic resources from CSGRC gene bank is not yet attempted. Therefore, one project was taken up to conduct pre-breeding involving promising multivoltine silkworm genotypes.

Objectives:

- To evaluate multivoltine germplasm accessions for the identification of crossbreeds suitable for Southern and Eastern Zones.

Outcome:

- Identified region and season specific superior multivoltine accessions with improved rearing & reeling traits and better combiners with CSR2.
- Among the top performing multivoltine accessions as parental breeds, the accessions viz. BMI-0025, BMI-0079 and BMI-0048 recorded their superiority in all seasons under all the test centers proving their utility as potential parents for region specific crop improvement.

CSR&TI, Berhampore	CSR&TI, Mysore	CSGRC, Hosur
BMI-0080, BMI-0025, BMI-0079, BMI-0048 & BME-0068	BME-0048 , BMI-0054, BMI-0001, BMI-0025 and BMI-0079	BMI-0025, BMI-0076, BMI-0074, BMI-0079 and BME-0048

Recommendations/Utilization:

- ✓ The top performing hybrid combinations of each region can be recommended for large-scale multi-location trials (MLT). After MLT, the best combination with improved traits can be utilized for commercial exploitation.

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AIB-3578: EVALUATION OF EXOTIC BIVOLTINE BREEDS TO IDENTIFY PROMISING PARENTAL GENETIC RESOURCES

Period : June 2016 – September 2019

Investigators: M. Maheswari, M. Muthulakshmi, G. Lokesh, Veeranna Gowda, S.Nivedita and Jameela Khatoon

Introduction :

Selection of parents as resource material is a prerequisite contributing to the success of breeding to produce potential breeds / hybrids. Thorough and proper evaluation of the genetic resources and utilization of the native breeds of potential nature will help the breeder to select most effective genotypes before choosing the materials for breeding. The study has been taken up to utilize the promising exotic bivoltine breeds shortlisted from bivoltine germplasm resources for preparing hybrids by crossing with CSR2/CSR4 to evaluate their performance. The identified potential exotic bivoltine parental breeds can be utilized in breeding and hybrid seed production for commercial exploitation.

Objective:

- To identify bivoltine silkworm germplasm for specific qualitative and quantitative traits.

Outcome:

- Region specific better performing parental combination of exotic bivoltine silkworm accessions were identified through field trials conducted at CSR&TI-Mysuru, Berhampore, Pampore& CSGRC-Hosur.

CSGRC, Hosur	CSRTI, Mysore	CSRTI, Berhampore	CSRTI, Pampore
BBE-0266 x CSR2 BBE-0329 x CSR2 BBE-0197 x CSR4	BBE-0201 x CSR2 BBE-0169 x CSR4 BBE-0197 x CSR4	BBE-0163 x CSR2 BBE-0169 x CSR4 BBE-0197 x CSR4	BBE-0197 x CSR4 BBE-0267 x CSR4


BBE-0163 X 290


BBE-0197 X 291


BBE-0154 X 290


BBE-0201 X 290


BBE-0267 X 291


BBE-0169 X 291

Recommendations/Utilization:

- ✓ Identification of top performing region specific breeds for respective Institutes which can be recommended for large scale trial so as to exploit commercially for enhanced cocoon production in these regions.