वार्षिक प्रतिवेदन

ANNUAL REPORT

2023-24

केरेबो-केन्द्रीय रेशम जनन्द्रव्य संसाधन केन्द्र

CSB-Central Sericultural Germplasm Resources Centre

केन्द्रीय रेशम बोर्ड, वस्त्र मंत्रालय, भारत सरकार, होसूर - 635 109

Central Silk Board, Ministry of Textiles, Govt. of India, Hosur- 635 109

45th RAC meeting of CSGRC on 12.10.2023

Workshop on Seri-biodiversity organised on 12.03.2024

Workshop on Prevention of Sexual Harassment at Workplace on 12.12.2023

Farmer's Awareness Programme organized on 21.12.2023

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प्रस्तावना

केन्द्रीय रेशम जननद्रव्य संसाधन केन्द्र, होसूर, की स्थापना 1991 में हुई थी, और केन्द्र ने अन्वेषण, संग्रह, लक्षण वर्णन, मूल्यांकन, संरक्षण तथा इसके उपयोग के अधिदेशानुसार व्यवस्थित रूप से शहतूत और रेशमकीट आनुवंशिक संसाधनों के संरक्षण को संबोधित किया है। इस केन्द्र को शहतूत जननद्रव्य के लिए राष्ट्रीय पादप आनुवंशिक संसाधन ब्यूरो (एनबीपीजीआर), आईसीएआर, नई दिल्ली द्वारा राष्ट्रीय सक्रिय जननद्रव्य साइट (रासजस) तथा रेशमकीट जननद्रव्य को राष्ट्रीय कृषि कीट संसाधन ब्यूरो (एनबीएआईआर), आईसीएआर, बेंगलुरु द्वारा मान्यता प्राप्त है। तदनुसार, शहतूत जननद्रव्य किस्मों/ रेशमकीट जननद्रव्य अभिगमों को विशिष्ट राष्ट्रीय अभिगम संख्याएं दी गई।

यह केंद्र 1317 शहतूत और 489 रेशमकीट आनुवंशिक संसाधनों के विशाल संग्रह का प्रबंधन तथा अधिकतम विविधता सुनिश्चित करता है और पारंपरिक तरीकों, जैव रासायनिक और आणविक मार्करों के साथ-साथ क्रायोप्रिजर्वेशन जैसी अन्य तकनीकों को नियोजित करके आनुवंशिक विविधता, आनुवंशिक अखंडता, जनसंख्या संरचना, प्रजातियों के संबंधों, विशेषता विशिष्ट होनहार अभिगमों की पहचान आदि के व्यवस्थित विश्लेषण पर जोर देता है। केरेजसंके, होसुर शहतूत और रेशमकीट जननद्रव्य संसाधन के फसल सुधार और फसल संरक्षण में सहायता करने हेतु शहतूत आनुवंशिक संसाधनों की साइटोलॉजिकल स्थिति, डुप्लिकेट की पहचान हेतु शहतूत आनुवंशिक संसाधनों के आणविक लक्षण वर्णन एवं उनके प्रभावी उपयोग, जैविक और अजैविक तनाव के लिए रेशमकीट जननद्रव्य संसाधनों की पहचान पर केंद्रित, रेशमकीट में आणविक लक्षण वर्णन और आनुवंशिक विविधता का आकलन आदि पर इन-हाउस और सहयोगी नेटवर्किंग अनुसंधान परियोजनाएं शुरू कर रहा है।

मैं इस अवसर पर सदस्य-सचिव, केंद्रीय रेशम बोर्ड और केंद्र की अनुसंधान सलाहकार समिति के साथ-साथ अन्य संस्थानों/संगठनों को अनिवार्य गतिविधियों के सफल निष्पादन में उनके समर्थन और प्रोत्साहन हेतु अपनी हार्दिक कृतज्ञता व्यक्त करना चाहती हूँ। मैं केंद्र के वैज्ञानिकों और कर्मचारियों को उनके बहुमूल्य योगदान और संघ-भावना के लिए ऋणी हूँ जो केंद्र की महत्वपूर्ण उपलब्धियों के लिए प्रेरक शक्ति रही है। यह वार्षिक प्रतिवेदन वर्ष 2023-24 के दौरान केंद्र की महत्वपूर्ण उपलब्धियों को दर्शाती है। वार्षिक प्रतिवेदन में सुधार के लिए किसी भी सुझाव का स्वागत है।

वी. निहिता नाइक

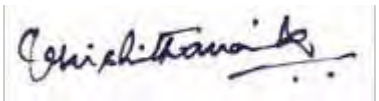
निदेशक

PREFACE

Central Sericultural Germplasm Resources Centre, Hosur was established in 1991, and the centre has systematically and strategically addressed conservation of mulberry and silkworm genetic resources against its mandate of exploration, collection, characterization, evaluation, conservation and utilization. The centre is recognized by the National Bureau of Plant Genetic Resources (NBPGR), ICAR, New Delhi as a National Active Germplasm Site (NAGS) for mulberry germplasm and by National Bureau of Agricultural Insect Resources (NBAIR), ICAR, Bengaluru for silkworm germplasm. Accordingly, the mulberry germplasm varieties/ silkworm germplasm accessions are assigned unique National Accession numbers.

The centre manages the vast collection of 1317 mulberry and 489 silkworm genetic resources ensuring maximum diversity and laying emphasis on systematic analysis of genetic diversity, genetic integrity, population structure, species relationships, identification of trait specific promising accessions etc. by employing conventional methods, biochemical and molecular markers as well as other techniques like cryopreservation. CSGRC Hosur is taking up in-house and collaborative networking research projects that focusses on cytological status of mulberry genetic resources, molecular characterization of mulberry genetic resources for the identification of duplicates and their effective utilization, identification of silkworm germplasm resources for biotic and abiotic stress, molecular characterization and assessment of genetic diversity in silkworm etc. to aid crop improvement and crop protection of both mulberry and silkworm germplasm resources.

I wish to take this opportunity to extend my deepest gratitude to the Member-Secretary, Central Silk Board, and the Research Advisory Committee of the Centre as well as other institutes/organizations for their support and encouragement in the successful execution of mandated activities. I am indebted to the scientists and staff of the centre for their valuable contributions and team spirit that has been the driving force for the significant achievements of the centre. This annual report depicts the significant achievements of the centre during the year 2023-24. Any suggestions for improvement of the annual report are welcome.



DIRECTOR

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1. अनुसंधान की रूपरेखा

वर्ष 2023-24 के दौरान, केरेजसंके, होसुर ने केंद्र में उपलब्ध विशाल मात्रा में सेरी-आनुवंशिक संसाधनों के व्यवस्थित प्रबंधन की दिशा में अपनी वैज्ञानिक खोज जारी रखी और इसके रोग मुक्त संरक्षण और उपयोग को सुनिश्चित किया। केंद्र ने 489 रेशमकीट जर्मप्लाज्म स्टॉक का संरक्षण और इनब्रीडिंग डिप्रेशन के लिए उनका मूल्यांकन किया। 1317 शहतूत आनुवंशिक संसाधनों का संरक्षण किया गया।रिपोर्टाधीन अवधि के दौरान शहतूत और रेशमकीट प्रभाग की उपलब्धियों का सार निम्नानुसार है:

शहतूत विभाग:

- **'अन्वेषण-संग्रह, लक्षण वर्णन, मूल्यांकन, पुन: स्थापना, संरक्षण और शहतूत आनुवंशिक संसाधनों (एमजीआर) की आपूर्ति-चरण-X' (पीआईई 06008 एसआई):** पिछली सर्वेक्षण रिपोर्टों के आधार पर अंतराल विश्लेषण किया गया और अज्ञात क्षेत्रों की पहचान की गई। कुल 170 विदेशी परिग्रहणों को दो भूखंडों में प्रत्यारोपित और स्थापित किया गया। एक्स-सिटू फील्ड जीन बैंक, शहतूत पत्ती आपूर्ति उद्यान और अन्य संरक्षण भूखंडों से कुल 32 मिट्टी के नमूने एकत्र किए गए और विश्लेषण के लिए सीएसआरटीआई, मैसूर को प्रस्तुत किए गए।

- विभिन्न उद्देश्यों के लिए विभिन्न सीएसबी/अन्य संस्थानों के 2 मांगकर्ताओं को कतरन एवं कलमों के पौधों के रूप में 8 स्वदेशी शहतूत परिग्रहण की आपूर्ति की गई।

- **'शहतूत आनुवंशिक संसाधनों की कोशिकीय स्थिति पर अध्ययन-चरण II' (पीआईजी 06010 एसआईसी):** अध्ययन के लिए डिप्लोइड (2x), ट्रिपलोइड (3x), टेट्राप्लोइड (4x), हेक्साप्लोइड (6x), और डेकोसैप्लोइड (22x) जैसे साइटोटाइप पर आधारित शहतूत परिग्रहण का चयन किया गया। प्ररूपी/ए संरचनात्मक चरित्र के आकलन के लिए प्रोटोकॉल और तरीकों का अनुकूलन प्रगति पर है।

रेशमकीट विभाग:

- **'बीएमएनपीवी और बीएमबीडीवी के प्रति सहिष्णु रेशमकीट आनुवंशिक संसाधनों की पहचान करने के लिए मार्कर सहायता प्राप्त स्क्रीनिंग' (एआईटी 06006 एमआई):** जैवपरख अध्ययनों से 2 मार्कर-पहचाने गए बीएमबीडीवी-सहिष्णु बहुप्रज अभिगम तथा 20 द्विप्रज अभिगमों की पहचान की गयी, जिनमें 10-87% कोशित उत्तरजीविता को दर्ज किया गया। बीएमएनपीवी के मामले में, 15 मार्कर- सहिष्णु अभिगम के रूप में पहचाने गए, जिनमें कोशित उत्तरजीविता का रेंज 10-54% के बीच था।

- **'रेशमकीट (बॉम्बिक्स मोरी एल) जननद्रव्य में आनुवंशिक विविधता का आणविक लक्षण वर्णन और मूल्यांकन' (एआईजी 06007 एमआई):** एनजीएस प्रौद्योगिकी के माध्यम से चार रेशमकीट जीनोम अर्थात पीएम, निस्तारी, सीएसआर-2 और एसके-6 का संपूर्ण जीनोम पुन: अनुक्रमण किया गया। प्रकार, कार्यात्मक वर्ग और एसएनपी वितरण द्वारा वेरिएंट कॉल और वेरिएंट एनोटेशन को चार जीनोम में दर्ज किया गया। एसएसआर खनन इलुमिना शॉर्ट रीड सीक्वेंस डेटा के साथ चार जीनोम में किया गया था और अत्यधिक बहुरूपी 20 हाइपरवेरिएबल एसएसआर का चयन किया गया। 350 रेशमकीट परिग्रहण का डीडीरैडसेक् पूरा किया गया।

- **'रेशमकीट आनुवंशिक संसाधनों का संग्रह, लक्षण वर्णन, मूल्यांकन, संरक्षण और उपयोग - X चरण' (एआईई 06009 एमआई):** मानक संचालन प्रक्रियाओं का पालन करके कुल 383 बाइवोल्टाइन, 84 मल्टीवोल्टाइन और 23 उत्परिवर्ती परिग्रहण संरक्षित किए गए। सूची विवरण के अनुसार परिग्रहणों की विशेषता बताई गई और उन्हें मूल वर्ण बनाए रखना पाया गया। फसल-वार मूल्यांकन डेटा एसजीआईएस डेटाबेस में अद्यतन किया गया। आउटसोर्सिंग के माध्यम से रेशमकीट डेटाबेस का डिजिटलीकरण प्रगति पर है।

- इस अवधि के दौरान, अनुसंधान और शैक्षणिक उद्देश्य के लिए 4 मांगकर्ताओं को 12 डीएफएलएस द्विप्रज और 17 बहुप्रज डीएफएलएस रेशमकीट अभिगमों की आपूर्ति की गई।

1. RESEARCH HIGHLIGHTS

During the year 2023-24, CSGRC, Hosur continued its scientific pursuit towards systematic management of the vast quantum of seri-genetic resources available at the centre and ensured its disease-free conservation and utilization. The centre carried out conservation and evaluation of its 489 silkworm germplasm stock for inbreeding depression. Conservation of 1317 mulberry genetic resources was carried out. The gist of achievements of mulberry and silkworm division during the period under report is as follows:

MULBERRY DIVISION:

- **'Exploration-collection, Characterization, Evaluation, Re-establishment, Conservation and Supply of Mulberry Genetic Resources (MGRs) Phase-X' (PIE 06008 SI)**: Gap analysis was carried out based on previous survey reports and identified the unexplored areas. A total of 170 exotic accessions were transplanted and established in two plots. A total of 32 soil samples was collected from ex-*situ* field gene bank, mulberry leaf supply garden and other conservation plots and submitted to CSRTI, Mysore for analysis.

- A total of 8 mulberry indigenous accessions were supplied in the form of cuttings and graftings to 2 indenters of different CSB/other institutes for different purposes.

- **'Studies on cytological status of mulberry genetic resources (Phase II)' (PIG 06010 SIC):** Mulberry accessions based on cytotypes including diploid (2x), triploid (3x), tetraploid (4x), hexaploid (6x), and decosaploid (22x) were selected for the study. The optimization of protocols and methods for the estimation of phenotypic/anatomical character is in progress.

SILKWORM DIVISION:

- '**Marker assisted screening to identify silkworm genetic resources tolerant to BmNPV and BmBDV' (AIT 06006 MI):** Bioassay studies revealed 2 marker-identified BmBDV-tolerant multivoltine accessions and 20 bivoltine accessions which recorded 10-88% pupal survival. In case of BmNPV, 15 marker-identified tolerant accessions were identified as BmNPV tolerant with pupal survival ranging from 10-54%.

- **'Molecular characterization and assessment of genetic diversity in silkworm (*Bombyx mori* L) germplasm' (AIG 06007 MI):** Whole genome re-sequencing of four silkworm genomes viz., PM, Nistari, CSR-2 & SK-6 was carried out through NGS technology. Variant call and variant annotation by type, functional class and SNP distribution was recorded across the four genomes. SSR mining was carried out in four genomes with Illumina short read sequence data and selected highly polymorphic 20 hypervariable SSRs. ddRADseq of 350 silkworm accessions was completed.

- '**Collection, Characterization, Evaluation, Conservation and Utilization of silkworm genetic resources - X Phase' (AIE 06009 MI):** A total of 383 bivoltine, 84 multivoltine and 23 mutant accessions were conserved by following standard operating procedures. The accessions were characterized and were maintained as per the catalogue data. Crop-wise evaluation data was updated in the SGIS database. Digitization of silkworm database through outsourcing is under progress.

- During the period, 12 dfls of bivoltine and 17 dfls of multivoltine silkworm accession were supplied to 4 indenters for research and academic purpose.

2. परिचय

केरेबो-केंद्रीय रेशम जननद्रव्य संसाधन केंद्र (केरेजसके), होसूर केंद्र रेशम बोर्ड द्वारा एक विशेष संस्थान है, जिसके अधिदेश में शहतूत रेशम आनुवांशिक संसाधनों को इकट्ठा करने, लक्षण वर्णन, मूल्यांकन और संरक्षण के साथ-साथ उक्त पहलूओं पर जागरूकता और कर्मियों को प्रशिक्षण देने शामिल है। प्रजनकों की अधिकारों के रक्षा के लिए संसाधन पंजीकरण समिति द्वारा विभिन्न संस्थानों में विकसित रेशम आनुवांशिक संसाधनों को पंजीकृत करने हेतु इस केंद्र को केरेबो द्वारा अधिकृत किया गया हैं। केंद्र को क्रमशः राष्ट्रीय पादप आनुवांशिक संसाधन ब्यूरो (रपअसब), भकृअप, नई दिल्ली और राष्ट्रीय कृषि कीट संसाधन ब्यूरो (रककसब), भकृअप, बेंगलुरु द्वारा शहतूत और रेशमकीट जननद्रव्य के लिए "नेशनल एक्टिव जर्मप्लाज्म साइट्स" के रूप में मान्यता प्राप्त है। इस केंद्र में संरक्षित संसाधनों को पूर्वोक्त संस्थानों द्वारा राष्ट्रीय अभिगम संख्याएं दी गई हैं। केरेजसके होसुर बेहतर प्रदर्शन करने वाले पैतृक स्टॉक की पहचान के उद्देश्य से विभिन्न स्वदेशी संसाधनों के मूल्यांकन के लिए कई आंतरिक और सहयोगी परियोजनायेँ लागू कर रहा है जो फसल सुधार में प्रजनकों की सहायता करेंगे।

अधिदेश

1. रेशमउत्पादन जननद्रव्य संसाधनों की खोज, संग्रह, लक्षण वर्णन, मूल्यांकन, संरक्षण और दस्तावेज़ीकरण।
2. रेशमउत्पादन जननद्रव्य संसाधनों का व्यावसायीकरण एवं सतत उपयोग को बढ़ावा देना।
3. रेशमउत्पादन जननद्रव्य संसाधनों के संरक्षण, प्रबंधन तथा उपयोग पर जागरूकता पैदा करना और हितधारकों को प्रशिक्षण देना।

गतिविधियाँ

1. शहतूत और रेशमकीट जननद्रव्य की खोज, संग्रह और परिचय।
2. आनुवांशिक संसाधनों के उपयोग को बढ़ावा देने के लिए लक्षण वर्णन, वर्गीकरण, प्रारंभिक मूल्यांकन, राष्ट्रीय अभिगमन और जननद्रव्य संग्रह की सूची बनाना।
3. रेशम उत्पादन विषयक आनुवांशिक संसाधनों के दीर्घकालिक राष्ट्रीय भंडार के रूप में सेवा करना।
4. जननद्रव्य संसाधनों के पंजीकरण और संदर्भ केंद्र के लिए नोडल एजेंसी के रूप में कार्य करना।
5. जननद्रव्य के परीक्षण / मूल्यांकन के लिए अंतर-संस्थागत सहयोग में प्रमुख भूमिका।
6. आनुवंशिक संसाधनों के आयात और निर्यात का समन्वय।
7. राष्ट्रीय डेटाबेस और हर्बेरियम/रेशम आनुवंशिक संसाधनों के प्रदर्शन के रूप में सेवा करें।
8. जरूरतमंद संगठनों को उनकी आपूर्ति के माध्यम से जननद्रव्य के उपयोग को बढ़ावा देना।
9. रेशम उत्पादन विषयक जननद्रव्य संसाधन प्रबंधन में प्रशिक्षण देना।

दृष्टिकोण

रेशम आनुवंशिक संसाधनों के पंजीकरण, मूल्यांकन, संरक्षण के लिए नोडल एजेंसी बनना।

मिशन

भारत में रेशम आनुवंशिक संसाधनों को पंजीकृत करना, फसल सुधार कार्यक्रम के लिए रेशम आनुवंशिक संसाधनों के उपयोग को सुविधाजनक बनाने के लिए अनुसंधान गतिविधियाँ, राष्ट्रीय भावी पीढ़ी को विलुप्त होने से बचाने के लिए रेशम आनुवंशिक संसाधनों का संरक्षण।

रोड मैप

लघु अवधि योजनाएं

1. विभिन्न राज्यों में अस्पष्टीकृत क्षेत्रों का सर्वेक्षण करें और आनुवंशिक स्टॉक को समृद्ध करने के लिए नए शहतूत आनुवंशिक संसाधनों के संग्रह के लिए अलग-अलग देशों से मार्ग का पता लगाएं।
2. विविधता और जीन समृद्धि के केंद्रों में शहतूत आनुवंशिक संसाधनों के सीटू संरक्षण में संवर्धन।
3. तनाव के प्रति सहिष्णु संसाधनों की पहचान के लिए हॉटस्पॉट क्षेत्रों में आनुवंशिक संसाधनों का मूल्यांकन।
4. शहतूत आनुवांशिक संसाधनों की सुरक्षा के लिए जलवायु लचीला रेशम उत्पादन को अपनाना।
5. आनुवंशिक वृद्धि के लिए पूर्व प्रजनन कार्यक्रमों का कार्यान्वयन।
6. अजैविक और जैविक तनाव के लिए रेशमकीट आनुवंशिक संसाधनों का मूल्यांकन।
7. मार्करों के माध्यम से सेरी-आनुवंशिक संसाधनों का आणविक लक्षण वर्णन।

दीर्घकालिक योजनाएं

1. एनबीपीजीआर, नई दिल्ली / आईएससी, सीएसबी कॉम्प्लेक्स, बैंगलोर के माध्यम से विदेशी शहतूत (मॉरस) प्रजातियों का परिचय।
2. इको फ्रेंडली और जैविक कृषि तकनीकों को अपनाना।
3. शहतूत प्रजनकों द्वारा नवीन जीनों / एलील्स के उपयोग और बेस चौड़ीकरण के साथ-साथ हेटेरोसिस के दोहन के लिए जंगली जीनों के अंतःक्षेपण के लिए प्रीब्रीडिंग कार्यक्रमों का कार्यान्वयन।
4. संरचित और टिकाऊ ऑन-फार्म का कार्यान्वयन और अपने मूल कृषि-पारिस्थितिक वातावरण में भूमि के संरक्षण का इन सीटू संरक्षण।
5. शहतूत और रेशमकीट जीन बैंकों के लिए एक्स सीटू संरक्षण रणनीतियों का उन्नयन, लागत प्रभावी संरक्षण के लिए उन्नत जैव प्रौद्योगिकी के साधनों को अपनाना।
6. आनुवंशिक वृद्धि के लिए पूर्व प्रजनन कार्यक्रम में उपयोग हेतु आणविक उपकरणों का उपयोग करके जंगली और भूमि जाति में होनहार जीन की पहचान।
7. केंद्र के एक आवश्यक अधिदेश के रूप में जीनोमिक्स को शामिल करके विभिन्न अजैविक तनावों / कार्यात्मक लक्षणों के प्रति सहिष्णुता के लिए आणविक साधनों की जांच हेतु आणविक उपकरणों का उपयोग।
8. कठिन श्रम कमी के लिए मेजबान संयंत्र की खेती और रेशम कीट पालन में मशीनीकरण।
9. जलवायु परिवर्तन के लिए लचीलापन हेतु विशिष्ट कार्यात्मक लक्षणों के साथ शहतूत जननद्रव्य की पहचान।
10. लक्षण और मूल्यांकन डेटा के साथ-साथ आणविक आईडी के साथ सेरी-आनुवंशिक संसाधनों के राष्ट्रीय डेटा बेस का विकास।

2. INTRODUCTION

Central Sericultural Germplasm Resources Centre (CSGRC), Hosur is an exclusive institute established by Central Silk Board (CSB) with a mandate to explore, collect, introduce, characterize, evaluate, conserve mulberry serigenetic resources as well as to create awareness and train personnel on the said aspects. The centre is authorized by CSB to register seri-genetic resources developed by various institutes through Germplasm Registration Committee to protect authorship rights of the breeders. The centre is recognized as "National Active Germplasm Sites (NAGS)" for mulberry and silkworm germplasm by National Bureau of Plant Genetic Resources (NBPGR), New Delhi and National Bureau of Agricultural Insect Resources (NBAIR), Bengaluru, respectively. The germplasm conserved at this centre are assigned national accession numbers by the aforesaid institutes. CSGRC Hosur has been implementing several in-house and collaborative projects for evaluating serigenetic resources aiming at identification of better performing parental stock that will aid breeders in crop improvement.

Mandate

1. *Exploration, collection, characterization, evaluation, conservation, and documentation of sericultural germplasm resources*
2. *Commercialization and promoting sustainable utilization of sericultural germplasm resources*
3. *Creating awareness and training stakeholders on conservation, management and utilization of sericultural germplasm resources.*

Activities

1. Exploration, collection and introduction of mulberry and silkworm germplasm.
2. Characterisation, classification, preliminary evaluation, national accessioning and cataloguing of germplasm collection for promoting utilization of genetic resources.
3. Serve as long-term national repository of sericultural genetic resources.
4. Act as nodal agency for registration and reference centre for germplasm resources.
5. Play lead role in inter-institutional collaboration for testing / evaluation of germplasm.
6. Co-ordinate import and export of genetic resources.
7. Serve as the national database and herbarium / display of sericultural genetic resources.
8. Promote utilization of germplasm through their supply to needy organizations.
9. Impart training in sericultural germplasm resource management.

Vision

To become the nodal agency for registration, evaluation and conservation of serigenetic resources.

Mission

To register the seri-genetic resources in India, research activity facilitating utilisation of serigenetic resources for crop improvement programme, conservation of serigenetic resources, national posterity and prevention of extinction.

Road map

Short term plans

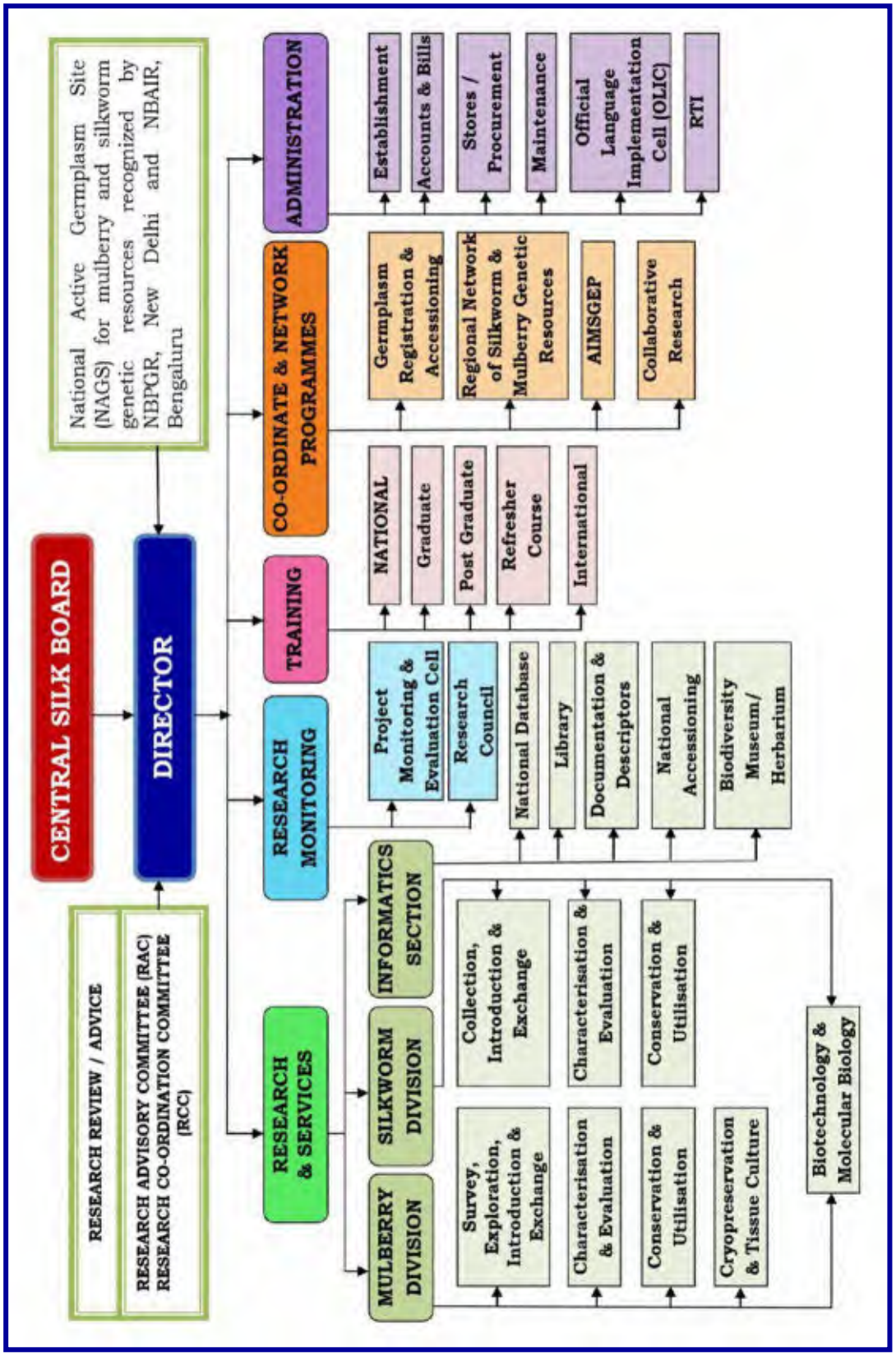
1. Survey of unexplored areas in different states and exploration of avenues from different countries for collection of new mulberry genetic resources to enrich the genetic stock.
2. Promotion of *in situ* conservation of mulberry genetic resources at the centers of diversity and gene richness.
3. Evaluation of seri-genetic resources in hotspot areas to identify resources tolerant to biotic and abiotic stress.
4. Adoption of climate resilient sericulture to protect seri-genetic resources.
5. Implementation of pre-breeding programmes for genetic enhancement.
6. Molecular characterization of seri-genetic resources through markers.

Long term plans

1. Introduction of exotic mulberry (*Morus*) species through NBPGR, New Delhi / ISC, CSB Complex, Bangalore.
2. Adoption of eco friendly and organic farming techniques.
3. Implementation of prebreeding programs for introgression of wild genes into the agronomic varieties to facilitate use of novel genes/alleles by mulberry breeders and for base broadening as well as exploitation of heterosis.
4. Implementation of structured and sustainable on-farm and *in situ* conservation of landraces in their native agro-ecological environments.
5. Upgradation of *ex situ* conservation strategies for mulberry and silkworm gene banks adopting advanced biotechnological tools with back up for cost effective conservation.
6. Identification of promising genes in wild and land races using molecular tools for utilization in pre-breeding programme for genetic enhancement.
7. Utilization of molecular tools for screening seri-genetic resources for tolerance to different abiotic stresses / functional traits by including genomics as an essential mandate of the centre.
8. Mechanization in host plant cultivation and silkworm rearing for drudgery reduction.
9. Identification of mulberry germplasm with specific functional traits for resilience to climate change.
10. Development of National Data Base of Seri-genetic Resources with molecular IDs along with characterization and evaluation data.

CSB-CSGRC, Hosur

3. ORGANISATIONAL CHART OF CSB-CSGRC, HOSUR



4. LIST OF RESEARCH PROJECTS

CODE	TITLE OF THE PROJECT	DURATION
Mulberry Division		
Single Institutional projects		
PIE-06008 SI	Exploration-collection, Characterization, Evaluation, Re-establishment, conservation and Supply of Mulberry Genetic Resources (MGRs)-Phase-X	Jan.23-Dec.25
PIG-06010SIC	Studies on the cytological status of mulberry genetic resources- Phase II	Feb,24-Jan,27
Silkworm Division		
Multi Institutional projects		
AIT-06006 MI	Marker assisted screening to identify silkworm genetic resources tolerant to BmNPV and BmBDV	Nov.20-Jan.24
AIG-06007 MI	Molecular characterization and assessment of genetic diversity in silkworm (*Bombyx mori* L)	Mar.21-Aug.24
AIE-06009 MI	Collection, Characterization, Evaluation, Conservation and Utilization of silkworm genetic resources - X Phase	Jan.23-Dec.25

5. OUTCOME OF CONCLUDED RESEARCH PROJECTS

AIT 06006 MI: Marker-assisted screening to identify silkworm genetic resources tolerant to BmNPV and BmBDV (November, 2020 to January, 2024)

CSGRC, Hosur: Ritwika Sur Chaudhuri (PI), G. Punithavathy (CI), G. Lokesh (CI), G. Ravikumar (CI) (upto 28.02.2023)
SSTL, Kodathi: R. Saravanakumar (CI)

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

Materials and Methods:

Rearing and collection of moth samples: A total of 452 (369 bivoltine and 83 multivoltine) silkworm accessions were reared as per CSGRC conservation crop rearing schedule. During grainage, the freshly emerged male and female moths were collected accession-wise in sterile tubes and stored in -80°C until further use.

Isolation of genomic DNA: Total genomic DNA was isolated from ~50 mg of moth tissue of each accession following PCI method. The isolated DNA was dissolved in TE buffer and stored at -20°C until further use.

PCR amplification using markers for BmBDV resistance: A total of 381 (369 bivoltine and 12 multivoltine) silkworm accessions were screened for detection of tolerance/susceptibility to BmBDV. The following two sets of primers were used for the detection of *nsd-2* resistant and/or susceptible allele:

Table 1: Details of the primers utilized for screening SWGRs for BmBDV resistance

Primer name	Gene (Chromosome)	Primer sequence (5'→3')
aa-trans 1 (resistant allele)	*nsd-2* (within exon 4,14) (Chr: 17)	F- TCTACGTGCTTTCATACTACGTATC R- TTCCTCACGTTTCTGAATTTCTCTTG
aa-trans 3 (susceptible allele)	*nsd-2* (at exon 13, 14) (Chr: 17)	F- GGTAAGAGGTCCAACGCTGTTAAGT R- TTCCTCACGTTTCTGAATTTCTCTTG

The PCR reaction mixture was prepared in 10 µL volume containing 2x EmeraldAmp GT Mastermix (Takara Bio), 10mM each forward and reverese primer, 2 µL DNA template and sterile water. PCR conditions included initial denaturation at 98°C for 1 min, followed by 30 cycles of denaturation at 98°C for 30 sec, annealing at 55°C for 30 sec, extension at 72°C for 1

min and final extension at 72°C for 7 min. The amplified PCR products were resolved on 1.5% agarose gel stained with ethidium bromide and the images were documented. The housekeeping *β- actin* gene was used as a reference gene.

PCR amplification using markers for BmNPV tolerance: A total of 452 (369 bivoltine and 83 multivoltine) silkworm accessions were screened for detection of tolerance/susceptibility to BmNPV. Initially 3 primers, viz., Nag 65, Nag84 and Nag88 (information obtained from SBRL, Kodathi) was proposed for screening of the silkworm accessions.
The RAC (Aug, 2021) suggested utilizing eight sets of SSR primers utilized by CSR&TI, Mysore (Concluded project AIB-3596) as per Miao *et al* (2005) for multi-viral tolerance instead for the detection of resistant alleles against BmNPV. A midterm correction was made in the project with eight SSR primers, having protein coding sequence, to be utilized for screening for BmNPV tolerance. The primer information was obtained from CSR&TI, Mysore and the details of the primers are given in Table 2.

Table 2: Details of the primers utilized for screening SWGRs for BmNPV tolerance/susceptibility

Primer	mRNA	Primer sequence (5'→3')	Resistant allele (bp)
LIP283 (Chr 3)	Pancreatic lipase-related protein 2	F- AACTTCTTTATTCACAGATTTTGCCA R- TTATGAAAATTGCACGGACGAA	283
IDH216 (Chr 8)	Isocitrate dehydrogenase	F- AAGTTCTTTACCAGTTCACAGACAGC R- CGCCATGCAACTGTCGTCAC	216
GDH306 (Chr 17)	Glucose dehydrogenase	F- GGTGGGTGGCGGCACTTAC R- CCCAGTCACATGGAAACAGCG	306
PTP284 (Chr 5)	Protein-tyrosine phosphatase	F- TTTGAAGAGCAGGTCAGCCG R- CGGGATCGATGGAAACAGCT	284
ATT (Chr 6)	Attacin	F- ATGAGATAATAATGTATGGAGGTTTT R- GATGAGGAATGATGTTGGGAA	700
ANK165 (Chr 21)	Ankyrin-2	F- CTCGGCACAAGCCTCGC R- TAGGGATTGATTTAGGCAGGGTA	165
PTP242 (Chr 21)	Protein-tyrosine sulfotransferase	F- CGGTAACCACTCACCATCAGG R- GAACAGGTGCCTAAATACCTTGTG	242
ATK285 (Chr 18)	ALK Tyrosine kinase	F- CGCTTACGGAGGTCCATGAGG R- CGCTTTTACCGATAAGACCGCT	285

The optimum annealing temperatures of the 8 SSR markers were confirmed by running a gradient PCR. The PCR reaction mixture was prepared in 10 µL volume containing 2x EmeraldAmp GT Mastermix (Takara Bio), 10mM each forward and reverse primer (desalted), 2 µL DNA template and sterile water. PCR conditions included initial denaturation at 94°C for 5 min, followed by 30 cycles of denaturation at 94°C for 1 min, annealing at varied temperatures (Table 3) for 30 sec, extension at 72°C for 1 min and final extension at 72°C for 10 min. The amplified PCR products were resolved on 2% High-resolution agarose gel stained with ethidium

bromide and the images were documented. The housekeeping *β- actin* gene was used as a reference gene.

Table 3: Annealing temperatures of 8 SSR markers utilized for detection of BmNPV tolerance/susceptibility

Primer name	LIP283	IDH216	GDH306	PTP284	ATT	ANK165	PTP242	ATK285
Ta (°C)	53.5	57	57.8	59	54.5	53	59	53.5

Bioassay studies for validation of BmBDV & BmNPV tolerance:

200 nos. of 3rd instar larvae from the marker-identified silkworm accessions were inoculated with pre-determined doses of BmNPV inocula ($1x10^6$ polyhedra/ml). 1 ml of inocula was per-orally inoculated to each larva and reared till spinning and observed till moth emergence. Three replications were maintained for each accession along with respective control to observe their survivability. In case of BmBDV, mulberry leaves smeared with a BDV suspension that consisted of a 50-100-fold diluted supernatant from a midgut homogenate of BDV-infected larvae. Unlike NPV, the BmBDV virus particles cannot be counted. Therefore, reference susceptible breed, CSR2 was included in all the experiments and results were considered when CSR2 shows 100% mortality when virus was infected. It is known from the literature that silkworm breeds are either completely resistant or completely susceptible irrespective of the BmBDV virus load. At the end of rearing, larval survival (no. of larvae spinning cocoons) and pupal survival (no. of live pupae after cocoon harvesting) were recorded in all three replications. The corrected pupal mortality for the bioassay studies conducted was calculated using Abbott's formula (Abbott, 1925) -

$$\text{Corrected mortality \%} = \frac{\%TM-\%CM \times 100}{100-\%CM}$$

Where,

TM= Mortality % in treatment group

CM= Mortality % in control group

Statistical analysis of mean of 3 replicates and standard deviation was calculated to assess the variation among the replicates.

Analysis of relative expression of genes for BmNPV tolerance:

Selection of silkworm accessions: From the accessions identified as BmNPV-tolerant through markers and validated through bioassay, 3 tolerant bivoltine silkworm accessions along with susceptible accession, were taken up for conducting real time quantitative PCR experiments.

Inoculation and tissue collection: Starved V instar Day 1 larvae from each accession were per orally inoculated with BmNPV inocula ($1x10^6$ OBs/ml) maintained at SSTL, Kodathi. The control group of the respective accessions was fed with normal mulberry leaves. Midgut was dissected in 1x PBS from each sample at 3 different timepoints, viz. 12hpi, 24 hpi and 48 hpi in

3 replicates. The tissues were collected in RNA stabilizing solution and stored at -80°C until further use.

Total RNA extraction: 30 mg of the midgut tissue was taken in pre-chilled sterile mortar and homogenized using liquid nitrogen. Total RNA extraction was carried out using Qiagen RNeasy Plus gDNA eraser kit™ according to manufacturer's instruction. Qualitative estimation of total RNA was carried out on 1% Agarose gel. The quality of the total RNA was estimated qualitatively and ratios of $A_{260}/_{280}$ and the concentrations for the RNA samples were determined as well as by using a NanoDrop 2000™ spectrophotometer (Thermo Fisher Scientific, USA).

cDNA synthesis: Total RNA samples were treated with RT reagent kit with gDNA Eraser (TaKaRa) to remove genomic DNA and synthesize the first strand cDNA according to the manufacturer's instructions. Briefly, 2.0 µL 5×g DNA Eraser buffer, 1.0 µL gDNA Eraser, and 1.0 µg total RNA were mixed in a 200 µL PCR tube and then RNase Free dH_2O was added up to 10 µL, and the solution was then incubated at room temperature for 5 minutes. 4.0 µL 5× PrimeScript buffer, 1.0 µL PrimeScript RT Enzyme Mix I, and 1.0 µL RT Primer Mix was then added to the previous tube, then RNase Free dH2O was added up to 20 µL, and the solution was then incubated at 37°C for 15 minutes followed by 85°C for 5 seconds and stored at −20°C for later use.

Selection of candidate genes: Through literature review, many candidate genes were identified that exhibited anti-BmNPV activity in silkworm *Bombyx mori.* The selection was narrowed down to genes that had higher expression levels in resistant strains during 12-48 hours post inoculation in the midgut. Accordingly, 5 candidate genes were shortlisted, and appropriate primers of HPLC grade for each gene were synthesized with amplicon sizes as given in Table 4. Two reference genes, viz. *Tif-4a* and *GAPDH*, which were reported to be relatively stable after BmNPV challenge (Guo *et al*, 2016), were selected for the present study.

Table 4: Primer details for RT-qPCR analysis

#	Gene	Primer sequence (5'-3')	Amplicon size(bp)
1	*Bmnitrooxidoreductase*	F-CGACGAGCGACTAACCCAAA R-CCGTCTTCGAAGGCGATAG	152
2	*Bmserineprotease*	F-CGTGCATATGGACACTGGAG R-TCTTGCTGGACTTGTGATCG	203
3	*Bmlipase1*	F-CTGGAACAGCAACGGAAACT R-TCCGTTGTTGATGAGCCAGA	189
4	*Bmcaspase1*	F-AACGGCAATGAAGACGAAGG R-GGTGCCCGTGCGAGATTTTA	185
5	*Bmargininekinase*	F-GTGGACACGCTCGGCAAC R-TGCTGCTGGGTCTCCTTCG	221
6	*TIF-4a (HK gene)*	F-GAATGGACCCTGGGACACTT R-CTGACTGGGCTTGAGCGATA	186
7	*GAPDH (HK gene)*	F-CCGCGTCCCTGTTGCTAAT R-CTGCCTCCTTGACCTTTTGC	97

Expression analysis of antiviral genes by real-time PCR: Real-time quantitative PCR was carried out in a 10 µL reaction mix containing 7 µL of SYBR Premix Ex Taq II RNAseH plus (TaKaRa), 2 µL of 1:10 diluted cDNA template, 0.5 µL of each of the primers (10 µM), and 2 µLddH_2O. The thermal cycling profile consisted of initial denaturation at 95°C for 30 sec and 40 cycles at 95°C for 5 sec, 60°C for 30 sec, and 72°C for 20 sec. Relative expression levels were calculated using the $2^{-\Delta\Delta Ct}$method (Livak and Schmittgen 2001). PCR reactions were performed in 96-well plates with InstaQ 96 Real Time PCR system (HiMedia, India) using SYBR Green to detect dsDNA synthesis. PCR amplification was carried out in triplicate wells. Each experiment was repeated thrice. The melt curves were checked to ensure the reaction specificity. SD and SE were calculated on the mean **Δ**Ct values. Student's t-test was applied to find out the p value to determine the significance of difference among the groups.

Result and Discussion

Out of 369 bivoltine and 12 multivoltine accessions screened [remaining 71 multivoltine accessions were screened by Ponnuvel *et al* (2011)], 69 accessions carried the resistant allele of *nsd-2*. Four silkworm accessions, viz. BMI-0076, BMI-0077, BBE-027 and BBE-0267 carried only the resistant allele in homozygous condition in all the individuals screened. Twenty one accessions were found to carry both the susceptible allele in homozygous condition and heterozygous resistant genotypes, one accession carried only the heterozygous resistant genotypes, five accessions revealed only the heterozygous and homozygous resistant condition. Thirty eight accessions had a mix of all the possible genotypes i.e. homozygous susceptible, heterozygous resistant as well as homozygous resistant. Remaining 312 accessions carried only the homozygous susceptible allele (Table 5).

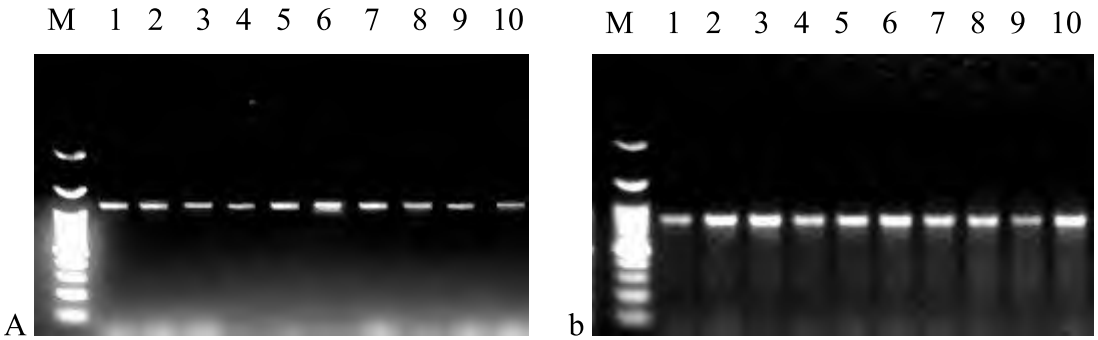


Fig.1: *nsd-2* gene as a functional marker for BmBDV resistance. (a) *nsd-2* resistant allele (~1200 bp) revealed by aa-trans1 primer; (b) *nsd-2*susceptible allele (~800 bp) as revealed by aa-trans3 primer. M denotes 100 bp ladder

Table 5: List of silkworm accessions carrying the resistant (*nsd-2*) and susceptible (+^{nsd2}) allele

SN	Acc.No	Frequency of different genotypes at *nsd-2* locus (%)			Exp. BmBDV resistant individuals (%)
		+*nsd-2*/+*nsd-2*	+*nsd-2*/ *nsd-2*	*nsd-2*/ *nsd-2*	
1	BMI-0076	0	0	100	100
2	BMI-0077	0	0	100	100
3	BBE-0027	0	0	100	100
4	BBE-0267	0	0	100	100
5	BBE-0216	0	10	90	90
6	BBI-0337	0	10	90	90
7	BBE-0266	0	20	80	80
8	BBI-0336	10	10	80	80
9	BBE-0014	10	10	80	80
10	BBE-0190	10	10	80	80
11	BBI-0382	10	10	80	80
12	BBE-0035	0	30	70	70
13	BBI-0369	10	20	70	70
14	BBE-0008	10	20	70	70
15	BBE-0177	0	40	60	60
16	BBE-0178	10	30	60	60
17	BBI-0371	30	10	60	60
18	BBE-0224	40	10	50	50
19	BBE-0227	20	40	40	40
20	BBI-0358	30	30	40	40
21	BBI-0338	50	10	40	40
22	BBE-0226	20	50	30	30
23	BBE-0225	20	50	30	30
24	BBI-0345	30	40	30	30
25	BBI-0128	50	20	30	30
26	BBE-0198	20	60	20	20
27	BBI-0126	40	40	20	20
28	BBI-0334	70	10	20	20
29	BBI-0365	70	10	20	20
30	BBI-0378	70	10	20	20
31	BBI-0325	70	10	20	20
32	BBE-0223	80	10	10	10
33	BBI-0124	80	10	10	10
34	BBE-0031	40	50	10	10
35	BBE-0206	80	10	10	10
36	BBI-0074	70	20	10	10
37	BBI-0064	70	20	10	10
38	BBE-0166	80	10	10	10
39	BBE-0011	10	80	10	10

40	BBE-0017	30	60	10	10
41	BBE-0026	30	60	10	10
42	BBI-0058	40	50	10	10
43	BBI-0121	70	20	10	10
44	BBI-0127	80	10	10	10
45	BBE-0197	80	10	10	10
46	BBI-0367	80	10	10	10
47	BBI-0368	80	10	10	10
48	BBI-0125	0	100	0	0
49	BBI-0370	20	80	0	0
50	BBE-0179	40	60	0	0
51	BBE-0188	50	50	0	0
52	BBI-0057	60	40	0	0
53	BBI-0122	60	40	0	0
54	BBE-0013	70	30	0	0
55	BBI-0364	70	30	0	0
56	BBI-0387	70	30	0	0
57	BBE-0041	80	20	0	0
58	BBE-0157	80	20	0	0
59	BBE-0250	80	20	0	0
60	BBE-0270	80	20	0	0
61	BBI-0376	80	20	0	0
62	BBE-0018	90	10	0	0
63	BBE-0020	90	10	0	0
64	BBE-0022	90	10	0	0
65	BBE-0036	90	10	0	0
66	BBE-0160	90	10	0	0
67	BBE-0162	90	10	0	0
68	BBE-0186	90	10	0	0
69	BBE-0252	90	10	0	0
	Remaining accessions	100	0	0	0

Eight sets of SSR primers were utilized to screen 452 (369 bivoltine and 83 multivoltine) silkworm accessions. The bivoltine silkworm accessions carrying resistant alleles of 4 out of 8 SSR markers and multivoltine accessions carrying resistant alleles of 6 out of 8 SSR markers were shortlisted as BmNPV tolerant. Results showed that among multivoltine accessions, BMI-0018 and BMI-0019 carried the resistant alleles of all the 8 markers in the range 30-100%, and three accessions, viz. BME-0012, BMI-0073 and BMI-0080 showed presence of resistant alleles of 6 markers. Among bivoltine accessions, BBI-0371 and BBI-0370 were found to carry the resistant alleles of 7 markers, twelve accessions showed presence of resistant alleles of 6 markers, twelve accessions with 5 markers and ten accessions with 4 markers (Table 6).

Table 6: Presence of resistant alleles (%) of SSR markers specific to BmNPV tolerance in silkworm accessions

Accession No.	ATT	GDH306	IDH216	LIP283	PTP284	ANK165	ATK285	PTP242	markers showing resistant alleles
Multivoltine accessions									
BME-0012	80	90	50	100	0	100	60	0	6
BMI-0018	100	100	100	80	100	30	100	30	8
BMI-0019	100	100	100	100	80	70	80	30	8
BMI-0073	30	60	0	100	100	80	0	60	6
BMI-0080	30	40	0	30	0	80	40	50	6
Bivoltine accessions									
BBE-0028	60	50	0	0	0	60	0	30	4
BBE-0029	30	40	40	0	30	60	30	0	6
BBE-0030	30	100	0	0	30	30	0	60	5
BBI-0052	30	30	50	30	70	0	0	20	6
BBI-0078	0	70	80	100	60	70	100	0	6
BBI-0096	0	60	20	0	0	70	30	50	5
BBI-0100	0	60	40	30	0	50	30	0	5
BBE-0170	0	100	0	30	60	60	80	0	5
BBE-0171	0	80	30	70	100	60	30	0	6
BBE-0177	0	30	0	30	30	30	0	0	4
BBE-0179	0	100	80	50	100	50	100	0	6
BBE-0182	100	0	50	100	60	0	50	0	5
BBE-0185	30	100	30	0	60	100	30	0	6
BBE-0186	60	100	40	100	0	100	0	0	5
BBE-0189	40	60	20	30	40	0	70	0	6
BBE-0191	0	30	0	50	30	0	30	0	4
BBE-0195	30	100	0	100	0	40	0	30	6
BBE-0196	0	30	20	30	30	30	0	0	5
BBE-0197	30	0	0	40	0	30	40	30	5
BBI-0204	60	0	0	70	0	60	0	40	4
BBE-0206	30	30	50	30	30	0	30	0	6
BBE-0209	30	0	0	50	0	30	0	40	4
BBE-0212	30	30	10	100	0	0	0	60	5
BBE-0217	50	30	0	30	0	0	30	0	4
BBE-0226	0	0	20	70	30	0	30	0	4
BBI-0237	0	100	30	100	0	100	0	100	6
BBE-0238	60	60	0	100	40	0	0	0	4
BBE-0245	60	40	0	0	30	30	0	50	5
BBI-0257	100	0	0	30	0	70	0	30	4
BBI-0258	0	100	40	100	100	0	50	0	5
BBI-0275	100	0	30	30	30	60	0	50	6
BBI-0276	60	0	50	60	0	70	50	0	5
BBI-0371	80	0	100	70	100	100	100	30	7
BBI-0370	70	30	100	70	100	60	100	0	7
BBI-0376	0	100	80	30	100	30	80	0	6

BBI-0380	0	30	0	0	30	50	30	0	4

Bioassay studies on BmBDV resistant accessions: Thirty one marker-identified silkworm accessions carrying atleast 20% resistant alleles were shortlisted for bioassay studies. Seven accessions with 10% resistant alleles were also taken up for bioassay in order to validate the markers. The data was recorded after calculating the corrected mortality percentage and the same is presented in Table 7.

Table 7: Bioassay studies showing larval and pupal survival % in marker-identified BmBDV resistant 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
23.	BBI-0128	22.00±5.22	7.47±2.29
24.	BBE-0031	7.50±2.29	7.30±2.60
25.	BBE-0224	41.50±7.55	7.08±1.76
26.	BBI-0126	18.17±4.86	6.29±2.29
27.	BBE-0198	12.50±4.77	2.90±2.52
28.	BBE-0226	30.00±5.50	2.17±1.80
29.	BBI-0345	21.33±2.36	1.75±1.80
30.	BBI-0124	8.83±1.26	1.05±1.04
31.	BBE-0227	34.50±6.87	0
32.	BBI-0334	16.83±4.07	0
33.	BBI-0365	12.47±3.36	0
34.	BBE-0223	8.17±3.88	0
35.	BBE-0206	7.00±3.28	0
36.	BBI-0074	6.83±3.22	0
37.	BBI-0064	5.67±1.53	0
38.	BBE-0166	5.17±1.26	0

From the results, ten accessions recorded >70% larval survival, five accessions >50-<70%, six accessions >30 - <50%, and seventeen accession recorded <30% larval survival after BmBDV challenge. In case of pupal survival, more than 70% survival was observed in five accessions, >50 to <70% in four accessions, >30 to <50% in four accessions, >10 to <30% in nine accessions and <10% pupal survival in eight accessions. The results of the bioassay study were aligned with the results of the marker-assisted screening using the *nsd-2* gene. Hence, phenotypic confirmation of the validity of marker data was obtained.

Bioassay studies on BmNPV tolerant accessions: Forty-one (5 multivoltine and 36 bivoltine) silkworm accessions were shortlisted for bioassay studies, based on the presence of resistant alleles of atleast 6 markers in multivoltine and 4 markers in bivoltine accessions. The data was recorded after calculating the corrected mortality percentage and the same is presented in Table 8.

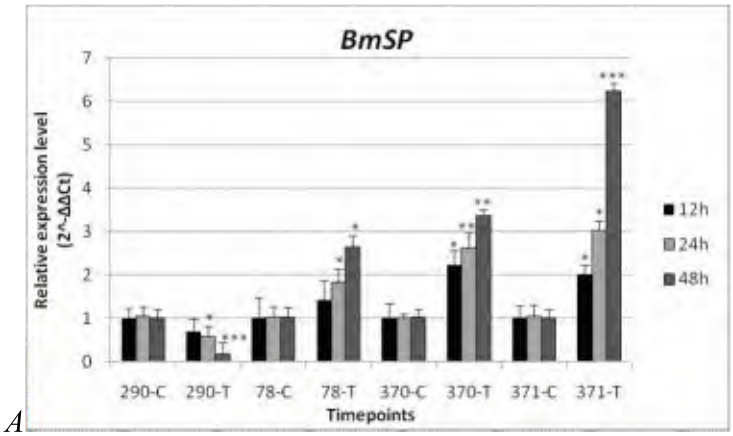
Table 8: Bioassay studies showing larval and pupal survival % in marker identified BmNPV tolerant silkworm accessions

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
16.	BBI-0052	31.67±8.51	9.78±3.50
17.	BBI-0275	25.17±9.07	9.32±1.89
18.	BBE-0171	47.67±4.48	9.26±2.08
19.	BBE-0189	35.67±1.53	9.14±1.80
20.	BBI-0100	61.17±9.22	8.52±4.44
21.	BBE-186	39.17±2.26	8.24±0.87
22.	BBE-0226	11.33±1.53	7.54±1.53
23.	BBE-0170	45.83 ± 2.255	4.68±1.26
24.	BBE-0030	16.00±7.76	4.21±1.16
25.	BMI-0080	7.00±0.87	4.04±1.26
26.	BBE-0245	20.67±1.44	3.22±2.26
27.	BBE-0195	46.5±1.80	3.08±1.16
28.	BBI-0257	4.83±4.25	2.88±2.36
29.	BBE-0212	31.00±5.27	2.49±0.76

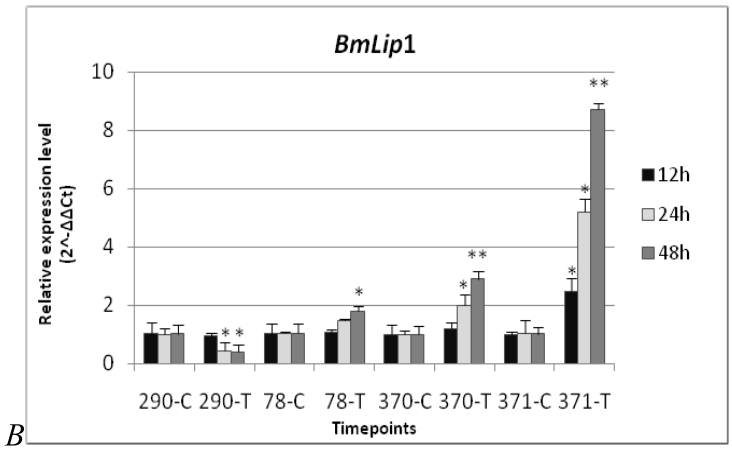
30.	BBE-196	44.17±4.51	2.04±1.89
31.	BBI-0204	4.83±0.76	1.65±0.50
32.	BMI-0073	6.17±1.26	1.46±1.04
33.	BBI-0096	39.00±6.5	1.31±2.02
34.	BBE-0177	3.67±1.76	1.3±2.02
35.	BBE-197	39.17±5.75	0.73±0.29
36.	BBE-191	7.17±1.53	0.57±0.50
37.	BBI-0380	5.00±2.00	0.36±0.58
38.	BBE-0028	6.00±1.73	0
39.	BBE-0209	0	0
40.	BBE-0217	0	0
41.	BBE-0238	0	0

Quantification of BmNPV tolerance in selected genotypes

From the bioassay studies, it was determined that BBI-0371 exhibited ~53% tolerance to BmNPV followed by BBI-0370 & BBI-0078 which recorded 39% and 31% tolerance to BmNPV respectively, whereas the popular breed CSR-2 was 100% susceptible to the virus. In order to determine the expression level differences of the anti-viral genes, analysis of the 5th instar larval midgut of the 3 tolerant and 1 susceptible silkworm accessions was carried out at different timepoints. The p values derived between infected and control groups at 3 timepoints are indicated in the graphs.



A



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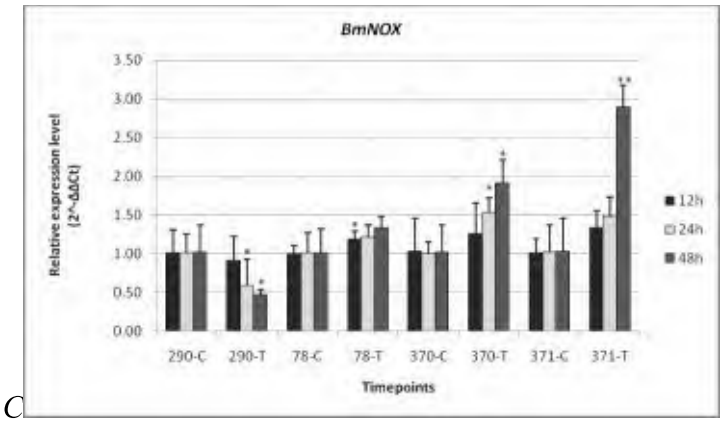

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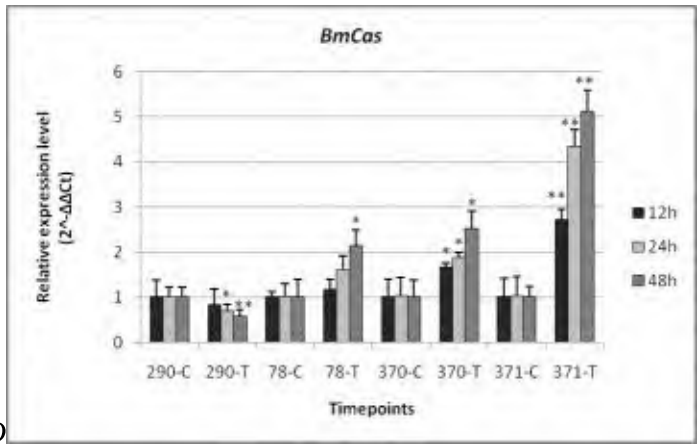

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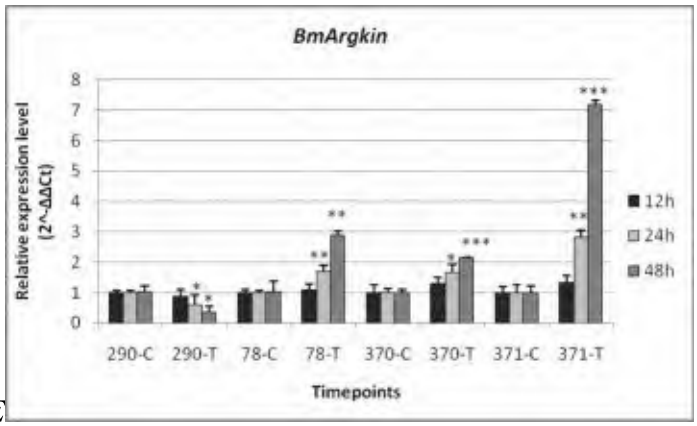


E

Fig.2: Fold changes in the expression level of candidate gene in the accessions- BBI-290, BBI-0078, BBI-0370 and BBI-0371 at 12, 24h and 48h post inoculation against their corresponding control (normalized to 1). A-*Bmsp*, B= *Bmlip1*; C=*BmNOX*; D=*BmCas1*; E=*BmAK*; Error bars denote the standard deviation of the mean ΔCt values.C=control group; T=treated group; *p<0.05; **p<0.01; ***p<0.001

The present study was taken up to characterize all the silkworm accessions available at CSGRC for their disease tolerance/susceptibility to BmBDV and BmNPV by using specific molecular markers, and further validating the marker data through bioassay studies. 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. The study confirmed the reliability of the *nsd-2* marker, which can be utilized for marker-aided breeding programmes. In case of BmNPV, the 8 SSR markers, especially IDH216 & ATK285 proved to be more efficient in identifying BmNPV tolerance in the silkworm accessions screened, and their utilization will be beneficial in disease breeding.

Resistance/tolerance to BmNPV is polygenic, governed by major dominant gene and many minor effector genes (Chen *et al*, 2003; Feng *et al*, 2012). Real time qPCR studies on four infected bivoltine silkworm accessions showing varying degrees of tolerance confirmed the differential expression levels of the previously reported five candidate genes conferring resistance against BmNPV. The expression levels of almost all the genes were significantly upregulated in the tolerant bivoltine accession-BBI-0371 at 12, 24 and 48 hpi timepoints indicating the early response of the genes to BmNPV invasion/infection. Further, the corresponding expression levels in the susceptible accession-BBI-290 significantly reduced at 24 & 48 hpi indicating the upregulation of these genes only in tolerant strains. The results from this study further strengthen the association of *BmSP, Bmlipase-1, BmNOX, BmCas and BmAK* genes in primary defense against BmNPV infection in Indian silkworm breeds. The regulatory mechanism underlying anti-viral immunity in indigenous silkworm breeds can be further explored utilizing these genes.

Future utilization

The information on germplasm characterization for viral tolerance will be added to the public database of silkworm germplasm at CSGRC, for the benefit of stakeholders. 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 molecular markers can be employed in quick and effective screening of new germplasm stocks.

Higher expression levels of the 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.

6. PROGRESS OF RESEARCH PROJECTS

MULBERRY DIVISION: [*Projects continued through 2023-24]*

1. PIE06008SI: Exploration-collection, Characterization, Evaluation, Re-establishment, conservation and Supply of Mulberry Genetic Resources (MGRs)-Phase-10 (Jan 2023-Dec 2025)

G.Thanavendan (PI), N. Sakthivel (CI-from April, 2023), M.C. Thriveni (CI), Raju Mondal (CI), G.R. Halagunde Gowda, (CI-CO, CSB)

CSGRC has a repository of 1317 mulberry genetic resources (1032 indigenous and 285 exotic) collected from donor institutes as well as through 82 survey and explorations in different geographical regions of India including arid and semi-arid regions of Rajasthan, Cold deserts of Leh - Ladakh, Himalayan region, Uttaranchal, Uttar Pradesh, saline regions of Andaman and Nicobar Islands, Central and South India. The details of indigenous mulberry germplasm collected from different part of India and exotic mulberry germplasm from different countries which are maintained in *ex situ* field gene bank are presented in Table 9 & 10 and Figues 3 & 4.

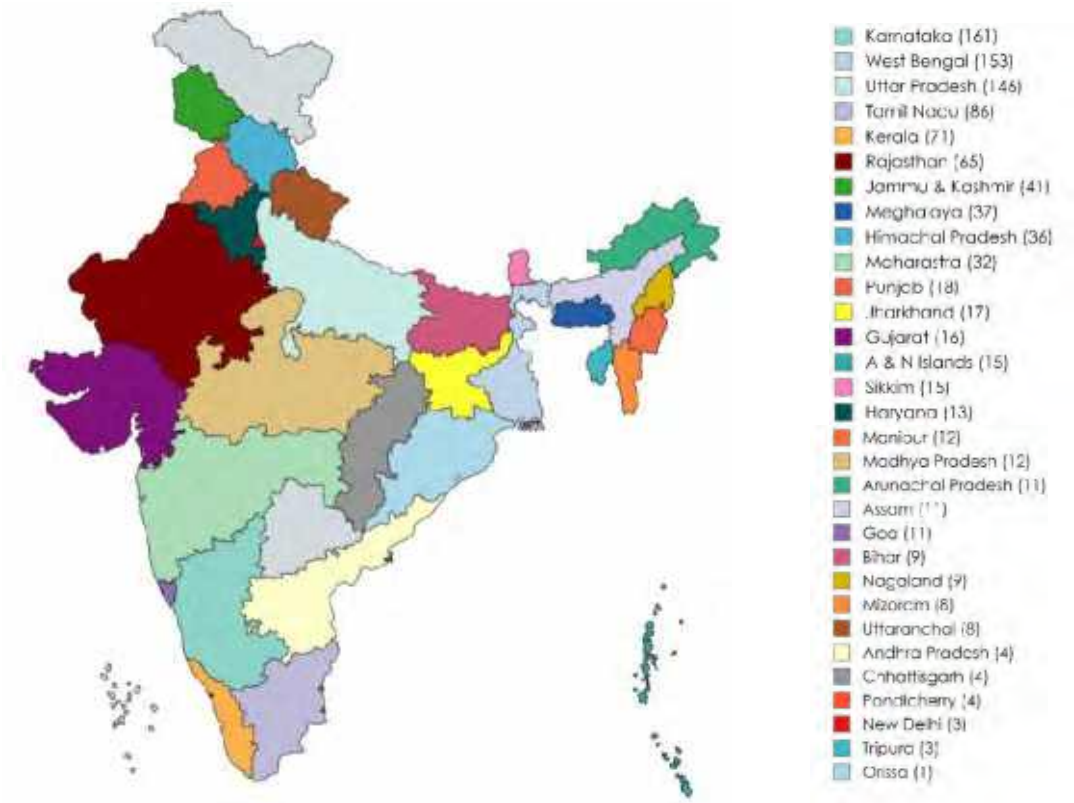


Fig.3: State-wise collection of mulberry genetic resources

Fig.4: Country-wise collection of mulberry genetic resources

Table 9: Details of state-wise surveys and collection of mulberry species from India

#	States /Union Territories	Exploration/ Survey (Nos.)	Category of *Morus* species collection(s)
1	Andhra Pradesh	1	*M. indica*
2	Arunachal Pradesh	3	*M. laevigata, M.indica*
3	Assam	3	*M. laevigata, M.indica*
4	Bihar	1	*M.indica, M. laevigata*
5	Chhattisgarh	2	*M. laevigata, M.indica*
6	Goa	2	*M.indica, M. latifolia*
7	Gujarat	1	*M. indica*
8	Haryana	1	*M.laevigata*
9	Himachal Pradesh	5	*M. indica, M.serrata,M.alba & M.laevigata*
10	Jammu and Kashmir	3	*M.indica, M.alba, M.serrata, M. laevigata*
11	Jharkhand	1	*M.indica, M. laevigata M. alba*
12	Karnataka	2	*M.indica,M. alba*
13	Kerala	4	*M.indica, M. laevigata*
14	Madhya Pradesh	5	*M. laevigata, M.indica, M. alba*
15	Maharashtra	4	*M.indica,M. laevigata, M. alba*
16	Manipur	1	*M. laevigata*
17	Meghalaya	7	*M. laevigata, M.indica, M.serrata*
18	Mizoram	1	*M. laevigata, M.indica*
19	Nagaland	1	*M.indica*
20	Odisha	1	*M.indica*
21	Punjab	3	*M.indica, M. alba, M. laevigata*
22	Rajasthan	4	*M.indica, M. laevigata, M. alba*

#	States /Union Territories	Exploration/ Survey (Nos.)	Category of *Morus* species collection(s)
23	Sikkim	3	*M. laevigata, M.indica*
24	Tamil Nadu	5	*M.indica, M.serrata,M.alba, M. laevigata*
25	Tripura	1	*M.indica*
26	Uttar Pradesh	14	*M.indica, M. laevigata, M. alba*
27	Uttarakhand	2	*M. serrata, M.indica,M.alba, M. laevigata*
28	West Bengal	4	*M. laevigata, M.indica, M. alba*
29	Andaman &Nicobar Island	3	*M. laevigata*
30	New Delhi	3	*M.indica, M. laevigata*
31	Pondicherry	1	*M.indica, M. laevigata*

Table 10: Details of country wise surveys and collection of mulberry germplasm

#	Country	No. of collections	#	Country	No. of collections
1	India	1032	17	Paraguay	4
2	Afghanistan	3	18	Philippines	1
3	Australia	2	19	Portugal	1
4	Bangladesh	5	20	Russia	1
5	China	55	21	South Korea	6
6	Cyprus	1	22	Spain	2
7	Egypt	3	23	Sri Lanka	2
8	France	32	24	Thailand	11
9	Hungary	1	25	Turkey	1
10	Indonesia	8	26	USA	4
11	Italy	8	27	Venezuela	1
12	Japan	72	28	Vietnam	5
13	Myanmar	7	29	Zimbabwe	11
14	Nepal	1	30	Unidentified	28
15	Pakistan	8		**Total collection(s)**	**1317**
16	Papua New Guinea	1			

Objective 1: Exploration and collection of new mulberry germplasm

Gap analysis was carried out based on previous survey reports and identified the unexplored areas. These areas were marked on geographical map and will be considered for upcoming explorations. Necessary correspondances were made to undertake survey for the collection of mulberry germplasm.

Objective 2: Re-establishment and Conservation of mulberry germplasm in *ex-situ* field gene bank

During the period, a total of 170 exotic accessions were transplanted and established in two plots (Plot 1 & 2). The viability of saplings was assessed and found that all the replanted saplings are well established. Monitoring and intercultural operations were carried out at regular interval. The removal of weeds, side branches pruning and pest monitoring were undertaken to maintain the health conditions of newly transplanted accessions. Chlorpyriphos 20% EC @ 3 ml per liter was sprayed for managing the infestation of termites and stem borers. The cuttings and grafted saplings of 913 indigenous accessions were raised in poly bags for re-establishment purpose. Due to poor precipitation during the year, life saving manual irrigation was provided to prevent loss of mulberry germplasm.

Fig.5: Land preparation and Tractor ploughing

Fig.6: Pit making, Transplatation and staking

Fig.7: Manual irrigation in FGB

A total of 1317 mulberry accessions (Indigenous - 1032; Exotic – 285) were conserved under *ex-situ* gene bank and intercultural operations (FYM and fertilizer application and plant protection strategies *etc*.) were carried out as per the SOP.

Total number of 32 soil samples was collected from ex-*situ* field gene bank, mulberry leaf supply garden and other conservation plots and sent to CSRTI, Mysore for analysis. The data revealed that the pH ranged from 6.01 to 7.61, EC from 0.2 to 0.5 ds/m, OC from 0.12 to 1.13%, Available NPK ranged from 94 to 780 kg/ha, 31 to 299 kg/ha and 90 to 806 kg/ha respectively.

Fig.8: Removal of buds below crown level, labelling, training and pruning of exotic germplasm


Fig.9: Drip irrigation operations, conservation of water and maintenance of healthy germplasm in *ex-situ* field gene bank

Objective 3: Characterize and Evaluation of Mulberry Genetic Resources (MGRs) in *ex-situ* field gene bank

Mulberry genetic resources were observed for the incidence of termites and stem borer and recorded the data for 100 accessions for two seasons (summer and winter). Yellow sticky traps were tagged to the plants to monitor the sucking pests in the FGB.






Fig. 10: Plant protection measures were taken *into ex-situ* field gene bank (FGB) for the management of economically important insect pests *viz*., tukra, termites and stem borers

Objective 4: Supply and collect feedback information on Mulberry Genetic Resources (MGRs)

During the period, a total of 8 mulberry indigenous accessions were supplied to 2 indenters (Table-11) for different purposes.

Table 11: Details of mulberry germplasm supplied from CSGRC, Hosur

#	Name of indenter	No. of Accessions			Purpose/ Utilization
		Indig.	Exotic	Total	
1	The Director CSB-CSR&TI, Central Silk Board, Srirampura, Mysuru.	3	0	3	Evaluation and used as check for AICEM Trial of AGB-8.
2	The Dean/Principal JSA College of Agriculture and technology, Podaiyur-Avatti, Cuddalore Dist.	5	0	5	PGResearch/Experimental and UG practical Class purpose
	Total	**8**	**0**	**8**	

Objective 5: Updating of Mulberry Germplasm Information System (MGIS)

The MGIS database descriptors in the data entry were updated with disease monitoring data. A query-based customised search provision was made in the database. Preparation of e-indenting system is under progress. The contents under catalogue data entry format was revised.

OTHER ACTIVITIES

Maintenance of mulberry leaf supply garden for silkworm conservation

During the period, a total of 6.0 acres of mulberry leaf supply garden was maintained and quality leaf was supplied to 5 multivoltine, 3 bivoltine and 2 mutant rearing crops of silkworm under maintenance and conservation of silkworm genetic resources as per the annual brushing schedule. The coreset mulberry plot comprising 150 mulberry accessions @ 8 plants / accession was also maintained for research purpose.


Fig.11: Pruning, tractor ploughing, FYM application and intercultural operations in mulberry leaf supply garden for conservation of silkworm germplasm.



Fig.12: (left to right) Application of fertilizer, foliar fertigation with Poshan and plant protection measures in mulberry leaf supply garden

Vermicomposting

Farm wastes including pruned twigs and green waste of the campus were collected and transferred to vermicomposting tanks. Cowdung slurry was sprinkled over the waste and left for decomposition. Earthworms were introduced to the semi-decomposed waste and covered with a thin layer of soil to maintain the moisture.






Collection of unused mulberry leaves, farm wastes Application of cowdung slurry & semi decomposing	Introduction of earthworms after semi decomposing	Cover with thin soil to maintain the moisture

Fig.13: Preparation of Vermicompost

Under the conservation activities, a museum plot comprising 14 numbers of *Morus* spp. and *10* morpho-types of mulberry genetic resources was re-established.

Fig. 14: *ex-situ* conservation of core-set germplasm and maintenance of Mulberry (*Morus* spp.) museum plot for 14 different *Morus* species and 10 different morphological types germplasm

2. PIG06010SIC: Studies on cytological status of mulberry genetic resources (Phase II) (Feb 2024-Jan 2027)

Raju Mondal (PI), M.C. Thriveni (CI)

Objective:

1. Identification of chromosome number and ploidy level of mulberry genetic resources.
2. Identification of ploidy-associated traits.

Progress:

To understand the impact of genome size on phenotype of mulberry, the present study focusses on identifying the ploidy-associated traits. The optimization of protocols and methods for the estimation of phenotypic/anatomical character is in progress. Mulberry accessions based on cytotypes including diploid (2x), triploid (3x), tetraploid (4x), hexaploid (6x), and decosaploid (22x) were selected for the study.

Silkworm Division: [*Projects continued through 2023-24*]

1. AIG-06007 MI Molecular characterization and assessment of genetic diversity in silkworm (*Bombyx mori* L)

CSGRC, Hosur: G. Lokesh (PI), Ritwika Sur Chaudhuri (CI), Raju Mondal (CI) (from 01.03.2023), Deepak K V (SRF),
SBRL, Kodathi: Himanshu Dubey (CI)

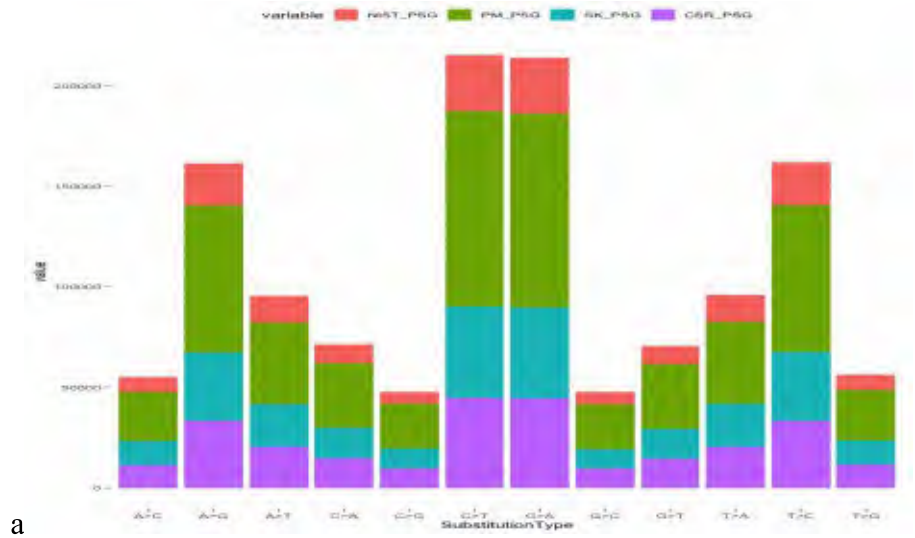
Objectives:

- To characterize silkworm genetic resources based on SNP marker analysis through ddRADseq approach for identification of duplicates.
- Whole genome sequencing (WGS) of indigenous silkworm races/ breeds, Pure Mysore (PM), Nistari, CSR-2 and SK-6 for reference genome and identification of hypervariable SSRs.
- Genetic diversity analysis of silkworm germplasm using SNP/ SSR markers.
- To update and enrich the silkworm genetic resource database based on molecular characterization.

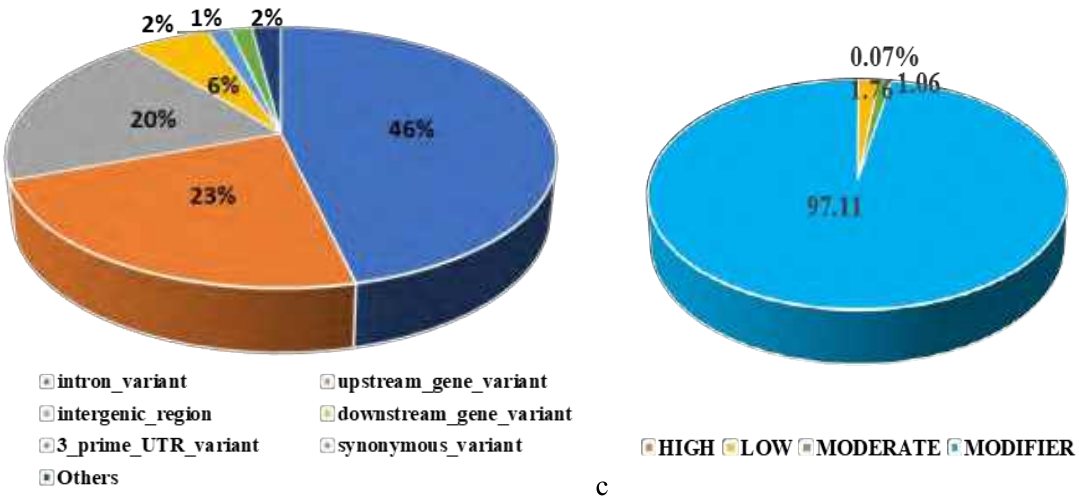
Progress

Whole genome re-sequencing of four silkworm genomes *viz.*, PM, Nistari, CSR-2 & SK-6 was carried out through NGS technology. Short read sequences were generated through Illumina and long read sequencing by Oxford Nanopore Technology (ONT). Quality assessment was done with FasQC/MultiQC and analyzed different quality parameters. 95% of raw data generated with high quality reads >=Q30. Phred score of reads observed >35 and base call accuracy recorded 99.99%. Alignment/Mapping of individual genome reads (filtered) was done with reference genome (p50 strain) and achieved >99% alignment. Using SnpEff variant analysis tool, Variant call and variant annotation by type, functional class and SNP distribution was recorded across the four genomes. Similarly, Long read sequence data was analysed for structural variation, region wise and type of variants, effects by functional class, Allele frquency & count (Homozygous & heterozygous) Codon changes & amino acid changes in the four genomes compared to p50 reference genome. SSR mining was carried out in four genomes with Illumina short read sequence data and selected highly polymorphic 20 hypervariable SSRs. Primer designing was done and synthesized for further genotyping. Validation of RNAsequence data: tissue specific gene were selected and corresponding protein related primers were mined from the SilkDB database and synthesized. ddRADseq of 350 silkworm accessions was completed Phenotypic database for ddRADseq (GBS) analysis was prepared and verified with SGIS database. Grouping of separate database for Bivoltine and multivoltine silkworm accessions to avoid overlap of data. Preliminary clusters were generated to confirm the correctness of the data. Formulated pipeline for SNP variation through *In silico* bioinformatic analysis. Raw data was filtered and high quality filtered reads were aligned on the reference genome (p50T silkworm

strain genome). More than 96% mapping was recorded. Based on the analysis, prepared SNP statistics, found 44732 unique SNPs across 350 silkworm accession and 135 common SNPs.



a



b c

Fig. 15 a,b,c: Variant Call & Base substitution in four genomes, position/region wise variants

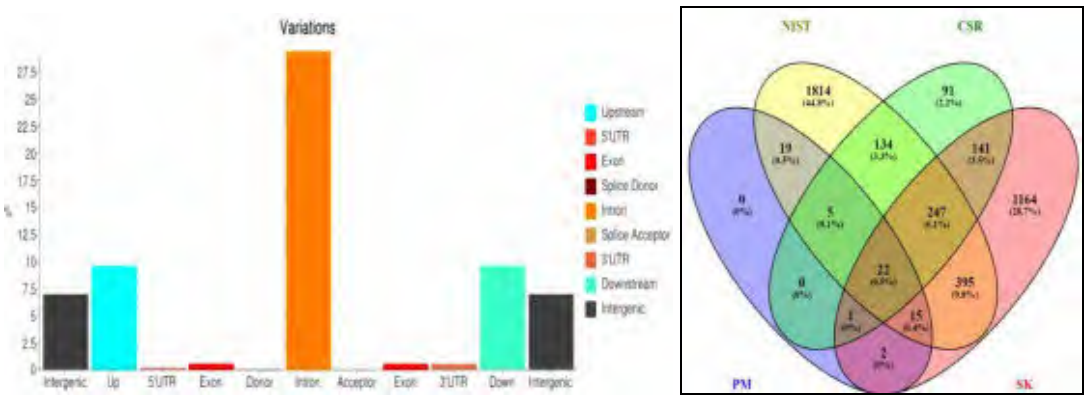


Fig.16: Region-wise structural variants in Long read sequences & Variant consistency across genomes

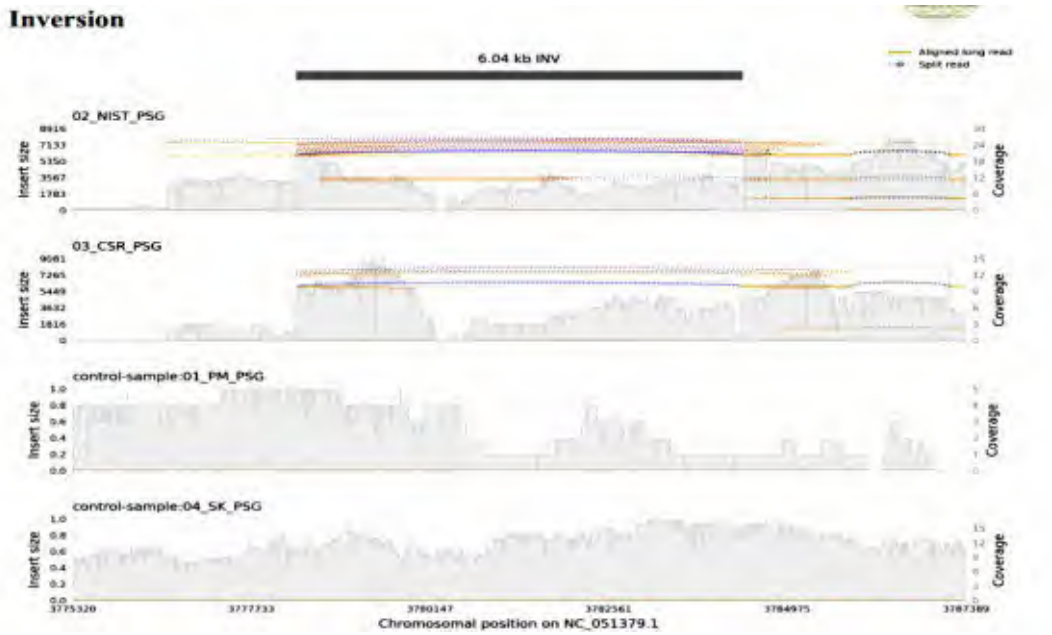


Fig.17: Visual analysis of structural variations (SVs)- IGV

Table 12: Tissue specific Genes selected for validation through qRT-PCR

Sl No			Genome ID NCBI	Genome ID SilkDB	Gene Name	Primer sequence 5'-3'
1.			NM_001126246.1	KWMTBOMO11748	egg-specific protein	TTACAACCAGGATGCGGATATAG
						CCGTACACTTTCATGTTGGTTTC
2.			XM_004924903.4	NA	chorion class A protein L11-like	GTTCTGTTATCTCAAGGTGACCA
						AGGTGGACATGTTGCAATGTA
3.			NM_001197251.1	KWMTBOMO12203	vitellogenin receptor	ATATTACAAAGAAGCCCGAAAGC
						TAGCAGAGTATCTCATTGGGTTC
4.			XR_002430293.2	KWMTBOMO01496	cyclin-dependent kinase-like 4, transcript variant X2	TACAGGGCTCCTGAATTATTG
						TCGTTATCATTCTTACCTACAGTC
5.			NM_001043788.1	KWMTBOMO08543	ribosomal protein S3	TGGTTGTGAAGTTGTTGTATCTG
						ACCTTGATTCCTAGTACTCCTTG
6.			NM_001043500.1	KWMTBOMO09320	beta-tubulin	ACAATTTACAGCCATGTTCAGAC
						TCCTCTACCTCTTCATCAAATTCC
7.			NM_001043556.1	KWMTBOMO08926	serine protease	AAACCAGTTCGACTCTATAAGCAC

					inhibitor 2	TCGTTACCTTCATACGCCATTTC
8.			XM_004925255.2	KWMTBOMO03191	arginine/serine-rich coiled-coil protein 2	GCTCAAGACTTATGTCGACTTTC
						TCAGAGGTATATACTAACGCATTCTC
9.			XM_004927633.2	KWMTBOMO10645	collagenase	TGTAAACTGGTAGTAGCCATGAAG
						ATACCGATCTTGTTGTGGTAGTC
10.			NM_001043501.1	KWMTBOMO02587	lipase-1	AACCTGCCTCTCTTTGTTATTG
						ATTGACGGCAGTGTTGTATAG
11.			XM_004929985.4	KWMTBOMO02955	trypsin, alkaline C	ACAGACCCATTAACCGTTCTATC
						ATATCTATGGCTTCAGCAGTATCG
12.			NM_001195462.2	KWMTBOMO02257	alpha amylase	ACCTGGTATAGCTGTAACTTATATGG
						ATTGAAATGGTGTGCGTTCAG
13			NM_001044023.1	KWMTBOMO08464	silk fibroin ligh chain	CAGCAGTGACTCTAGTTTCTTAAATG
						TCTGTGATTGATCCAGCTGATTG
14			NM_001113262.1	KWMTBOMO15365	silk fibroin heavy chain	TGACTTTGAAACTGGAAGCG
						GCAGATGACACAGAGGAAGC
15			NM_001145941.1	KWMTBOMO01001	silk protein P25	GGCTAACGACAGTGTTTGATAAG
						AGATGTGCTCTCTCTCGTAAATG
16			XM_012692169.3	KWMTBOMO06216	sericin 1-like	GGTGGATATTGATCTTGGCAATTTAG
						TTGAATCGGTGTTACTGGTACTG

2. AIE-06009-MI Collection, Characterization, Evaluation, Conservation and Utilization of Silkworm Genetic Resources- X phase

CSGRC, Hosur: Dr. M. Maheswari (PI), Smt. G. Punithavathy (CI), Dr. G. Lokesh (CI), Dr. Ritwika Sur Chaudhuri (CI), CST&RI, Bangalore: Mr.B.M.Mahadevaiah (CI)
RCS, C.O, Bangalore: Dr.G.R.Manjunatha (CI)

Progress

Objective 1: Collection, characterization evaluation and conservation of silkworm genetic resources.

The silkworm germplasm resources available at the centre include univoltine, bivoltine and multivoltine accessions. By the process of conservation of the genetic resources it is equally important to ensure that the original genetic characters are maintained and the rare and endemic strains are well protected from extinction. Precautionary measures are taken to protect the geographically isolated races, genetic stocks, and breeds collected from indigenous and exotic regions.

E-01: Collection of Silkworm Genetic Resources

During the period, two multivoltine silkworm genetic accessions viz. 8W and 12Y are evolved by CSR&TI, Berhampore were collected and quarantine rearing (first trial) was completed to ensure disease freeness. These breeds recorded 1.219 g and 1.358 g single cocoon weight and 15.43 and 17.77 SR% respectively. After successful quarantine rearing, these breeds will be evaluated and registered with NBAIR and added to the germplasm collection. The multivoltine breed KS-10 was collected from KSSR&DI, Thalaghattapura and quarantine rearing was completed. Evaluation of the breed for rearing and reeling parameters is under progress.

The gene bank currently holds a total of 490 indigenous and exotic silkworm genetic resources collected from 9 states of the country and 14 countries across the world. It includes 84 multivoltine (indigenous-74 & exotic-10), 383 bivoltine (indigenous-223 & exotic-160) and 23 mutant genetic stocks (exotic) representing 14 countries including India (**Table 13**)

Table 13: Details on the phase wise collection of SWGRs

Year	Phase	Bivoltine	Multivoltine	Mutant	Total
1993-1997	I	169	57	-	**226**
1997-2000	II	103	-	-	**103**
2000-2003	III	40	8	19	**67**
2003-2006	IV	25	7	1	**33**
2006-2009	V	2	1	-	**3**
2009-2012	VI	11	1	-	**12**
2012-2015	VII	15	7	-	**22**
2015-2018	VIII	4	2	3	**9**
2018-2022	IX	14			**14**
2023-2025	X		1		**1**
Grand Total		**383**	**84**	**23**	**490**

E-02: Conservation of silkworm genetic resources:

Conservation of Multivoltine Silkworm genetic resources: All the 84 multivoltine accessions were conserved by conducting rearing for four conservation crops (132 to 135 generations) and the eggs were preserved at a temperature of 5º C for 35 days with backups for 45 and 60 days in the cold storages (CSP) located at Hosur and Mysuru. The multivoltine accessions were maintained true to type on par with catalogue data without any loss ensuring disease freeness.

Conservation of Bivoltine Silkworm genetic resources: All the 383 bivoltine accessions were conserved by conducting rearing in three batches and the egg layings were preserved under 10 months hibernation schedule with one crop per year. As a backup, the egg layings of all the three batch accessions were also conserved under 12-month hibernation schedule in the cold storages (CSP) located at Hosur and Mysuru. The accessions were maintained true to type on par with the catalogue data without any loss and ensuring disease freeness. So far, first batch accessions have

completed 30 generations, second batch accessions 27 generations and third batch accessions 20 generations from the year 2004.

Conservation of Mutant SWGRs: All the 23 bivoltine mutant genetic stocks were conserved following 6 months hibernation schedule @ 2 crops per year. These 23 mutant accessions have completed 44-45 generations. As a back-up, the accessions were conserved under 8 months hibernation schedule in the cold storages located at Hosur and Mysuru. The accessions were maintained true to type on par with the catalogue data without any loss and ensuring disease freeness.

E-03: Characterization of SWGRs:

The collection, characterization, evaluation and conservation of silkworm germplasm are a continuous programme as it is the main mandate of CSGRC Hosur. The centre has so far collected 490 silkworm germplasm accessions comprises 84 multivoltine, 383 bivoltine and 23 mutants. These accessions collected in phase wise manner, characterized by using set of morphological descriptors and evaluated for important economic parameters for growth and reproductive traits in each crop and conserved following different conservation crop cycles (Table 13).

The variability in the morphological features of different stages of all the silkworm accessions (SWGRs) for each descriptor was found true to catalogue data. The data on the major important morphological parameters of 84 multivoltine, 383 bivoltine and 23 mutant silkworm accessions is presented in Table 14. The characterization on larval stage of multivoltine silkworm accessions revealed three types of larval patterns v*iz.,* plain, marked and mixed. The analysed data revealed that maximum accessions with plain larvae (47 accns, 55.95%) followed by marked (33 accns; 39.8%) and sex limited for larval marking (4 accns; 4.8%). In case of cocoon colour, maximum accessions revealed greenish yellow colour (35 accns; 42.2 %) followed by white (23 accns; 27.38 %), chrome yellow (20 accns; 24.1%), yellow cocoons (4 accns; 4.8%) and creamy white (2 accns; 2.4%). Similarly, the cocoon shape revealed maximum oval shaped cocoons (32 accns; 38.09%) followed by elongated with non constriction (24 accns; 28.9%), spindle shape (19 accns; 22.9%), spatulate (4 accns; 4.8%), dumbbell (3 accns; 3.6%) and elongated (2 accns; 2.4%).

In case of bivoltine, the morphological characterisation of the 383 bivoltine silkworm accessions recorded variability for important morphological descriptors which are presented in Table 2. Majority of the bivoltine accessions revealed plain (227 accns; 61.51%) followed by marked (136 accns; 36.85%), mixed (18 accns; 4.9%) and sex limited (2 accns; 0.5%). The cocoon colour revealed maximum accessions with white cocoons (349 accns; 91.12%) followed by creamish white (7 accns. 1.83%), Golden yellow (5 accns. 1.31%), Greenish yellow (4 accns 1.04%), Flesh yellow (4 accns 1.04%), Dull white (3 accns 0.78%), Flesh (2 accns 0.52%), Mixed (2 accns 0.52%), Off white (2 accns 0.52%), Chrome yellow (1 accn 0.26%). Similarly, the cocoon shape revealed that maximum accessions with oval (129 accns 34.96%), elongated faint constricted (61 accns 16.53%), elongated constricted cocoons (52 accns; 14.09%),

elongated (41 accns 11.11%), Dumbbell (31 accns 8.40%), oval faint constriction (29 accns 7.86%), Elongated oval (19 accns 5.15%), Elongated faint constriction (15 accns 4.07%), spindle (6 accns 1.63%). The accessions are conserved following Standard Operating Procedure (SOP) as per the voltinism and its utilization is promoted through collaborative programs and by supply to stake holders and users.

Mutant silkworm accessions revealed only two types of larval patterns i.e, plain larvae (9 accns; 39.1%) and marked larvae (14 accns; 60.9%). In case of cocoon colour, maximum accessions revealed white colour (14 accns; 60.9%) followed by chrome yellow (3 accns; 13.0%). The other colours being yellow, greenish yellow and flesh in 2 accessions each (8.7% each). Similarly, the cocoon shape revealed maximum dumb-bell shaped cocoons (16 accns; 69.6%) followed by elongated faint constriction (5 accns; 21.7%) and elongated non-constricted (2 accns; 8.7%).

Table 14: Morphological character variations in SWGRs

Parameters	Multivoltine		Bivoltine		Mutants	
	No.of accns.	(%)	No.of accns.	(%)	No.of accns.	(%)
Larval Pattern						
Plain (P)	47	55.95	228	59.33	9	39.13
Marked (M)	33	39.80	133	34.73	14	60.87
Mixed (both P & M)	-	-	6	1.57	-	-
Sex limited for Larval Marking (Plain-♂; Marked-♀)	4	4.80	16	4.18	-	-
Total	**84**	**-**	**383**	**-**	**23**	**-**
Cocoon colour						
White	23	27.38	357	93.21	14	60.87
Yellow	4	4.80	-	-	2	8.70
Greenish yellow	35	42.20	4	1.04	2	8.70
Chrome yellow	20	24.10	9	2.35	3	13.04
Creamish white	2	2.40	5	1.31	-	-
Flesh	-	-	6	1.57	2	8.70
Sex Limited for Cocoon colour (White -♂ Yellow-♀)	-	-	2	0.52	-	-
Total	**84**	**-**	**383**	**-**	**23**	**-**
Cocoon shape						
Oval	32	38.09	132	34.46	-	-
Dumb-bell	3	3.60	34	8.88	16	69.57
Spindle	19	22.90	6	1.57	-	-
Elongated non-constricted	24	28.90	37	9.66	2	8.70
Elongated constricted	-	-	164	42.82	-	-

Elongated faint constricted	-	-	9	2.35	5	21.74
Elliptical	-	-	1	0.26	-	-
Spatulate	4	4.80	-	-	-	-
Elongated	2	2.40	-	-	-	-
Total	**84**	**-**	**383**	**-**	**23**	**-**

E-04: Evaluation of SWGRs:

Evaluation of multivoltine SWGRs

During the period, 4 continuous conservation crops for the 84 multivoltine SWGRs taken up and evaluated the morphological characters as well as economic parameters. The analyzed data of the multivoltine genetic resources depict that the fecundity ranged from 377 (BMI-0033) to 496 (BMI-0003), the weight of 10 larvae ranged from 18.17 (BME-0028) to 36.49 (BMI-0013). With regard to Yield/10000 larvae by no., the minimum survival was recorded in BMI-0011 (93.31%) and maximum in BMI-0085 (96.81%) and whereas BMI-0047 recorded minimum yield/10000 larvae by wt. (8.39 kg) and maximum with BMI-0084 (11.44kg). In case of single cocoon wt., single shell wt. and shell ratio% the minimum was recorded with BMI-0028(0.831g), BMI-0047(0.094g) and BMI-0017 (10.92% respectively. Whereas BMI-0084 recorded maximum single cocoon weight (1.351g), single shell weight (0.235g) and cocoon shell percentage (17.38%). Average filament length of 480.23 m was recorded, with highest filament size of 2.79 d and lowest of 1.67 d. The details of individual trait-wise top performing ten accessions for all the 13 rearing and reeling parameters along with the range values are presented in Table 15.

Table 15: Overall performance of Multivoltine germplasm resources

Traits	Mean	Min	Max	SD	SE	CV%
Fecundity (No.)	426	377	496	21.84	2.39	5.11
Hatching percentage (%)	93.36	89.89	95.44	1.00	0.11	1.07
Wt. of 10 Larvae (g)	23.17	18.17	36.49	3.35	0.36	14.47
Total larval duration (h)	557.75	476	617	20.25	2.22	3.63
V age Larval duration (h)	130.702	104	178	15.57	1.71	11.91
Yield/10000 larvae by No.	9468	9331	9681	70.27	7.71	0.74
Yield/10000 larvae by wt (kg)	9.73	8.39	11.44	0.63	0.06	6.47
Pupation rate (%)	92.004	90.19	94.75	0.93	0.102	1.01
Single Cocoon wt (g)	1.057	0.831	1.351	0.11	0.01	10.55
Single Shell wt (g)	0.138	0.094	0.235	0.02	0.00	20.21
Cocoon shell percentage (%)	13.04	10.92	17.38	1.43	0.15	11.00
Average filament length (m)	480.23	300.00	723.00	93.62	11.61	19.49
Filament size (d)	2.079	1.670	2.790	0.237	0.029	11.377

Apart from the variability of silkworm resources, the traitwise top performing multivoltine accessions are presented in **Table 16**.

Table 16: Trait-wise top performing multivoltine SWGRs (Top 10)

Trait	Range	Accession No.
Fecundity (No.)	451-496	BMI-0003, BMI-0001, BMI-0004, BMI-0080, BMI-0084, BMI-0040, BMI-0083, BMI-0058, BMI-0039, BMI-0068
Hatching percentage (%)	94.45-95.44	BMI-0025, BMI-0034, BMI-0061, BMI-0007, BMI-0071, BMI-0077, BMI-0008, BMI-0055, BME-0005, BMI-0045
Wt. of 10 grown larvae (g)	26.69-36.49	BME-0013, BMI-0083, BMI-0084, BMI-0078, BMI-0085, BMI-0081, BMI-0066, BMI-0080, BMI-0044, BMI-0009
Total larval duration (h)	476-538	BMI-0018, BMI-0017, BMI-0019, BMI-0021, BME-0047, BMI-0045, BME-0050, BME-0049, BMI-0046, BMI-0056
V age larval duration (h)	104-112	BMI-0017, BMI-0018, BMI-0019, BMI-0021, BME-0047, BMI-0045, BME-0050, BME-0049, BMI-0029, BMI-0046
Yield/10,000 larvae by no.	9538-9681	BMI-0085, BMI-0001, BMI-0083, BMI-0084, BMI-0082, BMI-0080, BMI-0019, BMI-0040, BMI-0081, BMI-0010
Yield/10,000 larvae by wt. (kg)	10.54-11.44	BMI-0084, BMI-0078, BMI-0085, BMI-0083, BMI-0081, BMI-0067, BMI-0066, BMI-0077, BME-0048, BMI-0001
Pupation rate (%)	92.94-94.75	BMI-0085, BMI-0001, BMI-0082, BMI-0084, BMI-0019, BMI-0080, BMI-0083, BMI-0081, BMI-0040, BMI-0045
Single cocoon wt.(g)	1.196-1.350	BMI-0084, BMI-0083, BMI-0078, BMI-0085, BMI-0081, BMI-0067, BMI-0066, BMI-0001, BMI-0039, BME-0048
Single shell wt. (g)	0.169-0.240	BMI-0084, BMI-0085, BMI-0083, BMI-0081, BMI-0076, BMI-0078, BMI-0080, BMI-0073, BMI-0066, BMI-0001
Cocoon Shell percentage (%)	14.54-17.38	BMI-0084, BMI-0085, BMI-0076, BMI-0083, BMI-0081, BMI-0080, BMI-0079, BMI-0073, BMI-0074, BMI-0078
Avg Filament Length (m)	566-723	BMI-0076, BMI-0055, BMI-0078, BMI-0024, BMI-0066, BMI-0009, BMI-0073, BMI-0074, BMI-0084, BMI-0002
Filament size (d)	1.67-1.85	BME-0015, BMI-0028, BMI-0019, BMI-0059, BMI-0017, BMI-0029, BMI-0062, BMI-0055, BMI-0043, BMI-0008

The multiple trait evaluation for 13 rearing and reeling traits revealed that, accession BMI-0084 and BMI-0083 ranked first with best performance for 8 traits followed by BMI-0081 and BMI-0085 for 7 traits, BMI-0001 and BMI-0080 for 6 traits, and BMI-0078 for 5 traits (**Table 17**).

Table 17: Top ranking multivoltine SWGRs for multiple traits

Acc No.	No. of traits	Trait No. and Values
BMI-0084	10	1(468), 3(32.01), 6(9625), 7(11.44), 8(94.12), 9(1.351), 10(0.235), 11(17.38), 12(587), 13(2.75)
BMI-0083	9	1(456), 3(32.02), 6(9650), 7(10.91), 8(93.56), 9(1.311), 10(0.218), 11(16.59), 13(2.53)
BMI-0081	8	3(28.81),6(9556),7(10.89),8(93.19), 9(1.281),10(0.208), 11(16.4),13(2.4)
BMI-0001	7	1(495), 6(9662), 7(10.54),8(94.62),9(1.224),10(0.169), 13(2.4)
BMI-0080	6	1(473), 3(27.57), 6(9594), 8(93.75), 10(0.188), 11(15.94)
BMI-0078	6	3(30.4), 7(11.24), 9(1.302), 10(0.189), 11(14.54), 12(666)
BMI-0066	6	3(28.78), 7(10.7), 9(1.224), 10(0.171), 12(652), 13(2.48)
BMI-0045	4	2(94.45), 4(532), 5(106), 8(92.94)
BMI-0009	4	3(26.69), 9(1.195), 10(0.167), 12(651)
BMI-0019	4	4(530), 5(104), 6(9581), 8(93.81)

Figures in parantheses indicates the actual value of the traits-1.Fecundity (Nos.), 2.Hatching percentage (%), 3.Wt of 10 larvae (g), 4. Total Larval duration (hrs.) 5.V instar duration (hrs.) 6.Yield/10000 larvae by no. 7.Yield/10000 larvae by wt. (kg) 8.Pupation Rate (%) 9.Single cocoon weight (g) 10. Single shell weight (g) 11. Cocoon Shell percentage (%), 12. Average filament length (m), 13. Filament size (d)

Evaluation of bivoltine SWGRs

The 383 bivoltine silkworm genetic resources were evaluated in three conservation batches during the year. Variability statistics analysis of the data generated for 13 important quantitative traits is presented in **Table 18.** The data indicates that there is wide genetic diversity among the bivoltine accessions by exhibiting highest coefficient of variation (CV%) for most of the traits like ERR by wt. (kg) (19.36%), followed by fecundity (18.31%), average filament length (15.02%) and pupation rate (13.19%). The other characters such as hatching percentage (%), total larval duration, V instar larval duration, single cocoon wt and cocoon shell percentage did not show much variation in CV%.

Table 18: Overall performance of Bivoltine germplasm resources

Traits	Mean	Min	Max	SD	SE	CV%
Fecundity (No.)	375	210	540	84.87	4.35	18.31
Hatching percentage (%)	96.11	83.59	99.07	1.85	0.09	1.92
Wt. of 10 Larvae (g)	34.19	23.30	45.08	3.19	0.16	8.44
Total larval duration (h)	579	548	600	16.79	0.86	2.90
V age Larval duration (h)	154	140	168	11.65	0.60	7.53
Yield/10000 larvae by No.	8257	5900	9560	775.94	39.75	9.40
Yield/10000 larvae by wt (kg)	10.84	6.40	15.20	2.10	0.11	19.36
Pupation rate (%)	68.53	51.25	85.80	10.13	0.52	13.19
Single Cocoon wt (g)	1.424	1.054	1.794	0.11	0.01	7.21
Single Shell wt (g)	0.243	0.125	0.362	0.04	0.00	13.56
Cocoon shell percentage (%)	17.06	10.91	20.17	1.47	0.08	8.03
Average filament length (m)	805	195	1167	120.87	6.19	15.02

The better performing bivoltine accessions shortlisted based on performance as well as multiple trait analysis for individual and multiple important economic traits are presented along with the range values in **Tables 19** and **20**, respectively.

Table 19: Top performing bivoltine germplasm accessions for individual traits (Top 25)

Trait	Range	Accession No.
Fecundity (no.)	500-540	BBE-0150, BBE-0149, BBE-0157, BBI-0335, BBE-0153, BBE-0144, BBI-0123, BBI-0125, BBE-0010, BBI-0066, BBI-0300, BBE-0158, BBI-0380, BBI-0126, BBI-0095, BBI-0089, BBI-0340, BBI-0350, BBE-0160, BBI-0338
Hatching percentage (%)	98.34-99.07	BBE-0168, BBE-0161, BBI-0126, BBI-0380, BBI-0330, BBE-0167, BBE-0149, BBI-0105, BBE-0016, BBE-0181, BBI-0294, BBI-0089, BBI-0362, BBI-0125, BBE-0150, BBI-0087, BBE-0153, BBI-0293, BBI-0273, BBI-0394
Wt. of 10 grown larvae (g)	42.72-45.08	BBI-0086, BBE-0145, BBE-0154, BBI-0345, BBI-0342, BBE-0159, BBI-0349, BBE-0144, BBI-0337, BBE-0156, BBE-0149, BBI-0360, BBE-0162, BBI-0380, BBI-0132, BBE-0155, BBI-0378, BBI-0348,

		BBI-0121, BBI-0103
Total larval duration (h)	9300-9560	BBI-0111, BBE-0018, BBI-0284, BBI-0102, BBI-0138, BBI-0107, BBI-0115, BBE-0013, BBI-0079, BBI-0348, BBI-0278, BBE-0031, BBI-0354, BBE-0026, BBE-0005, BBI-0126, BBE-0030, BBE-0167, BBI-0281, BBI-0080
V age larval duration (h)	13.6-15.20	BBI-0347, BBI-0133, BBI-0116, BBI-0115, BBI-0290, BBI-0282, BBI-0102, BBI-0126, BBI-0285, BBI-0136, BBI-0079, BBI-0139, BBE-0003, BBI-0113, BBI-0284, BBE-0036, BBE-0149, BBI-0111, BBI-0107, BBI-0278
Yield/10,000 larvae by no.	80.80-85.80	BBI-0115, BBE-0018, BBI-0348, BBI-0102, BBI-0111, BBI-0107, BBI-0354, BBI-0095, BBI-0126, BBI-0133, BBE-0167, BBI-0109, BBI-0138, BBI-0093, BBE-0005, BBE-0030, BBI-0120, BBI-0116, BBE-0013, BBI-0278
Yield/10,000 larvae by wt. (kg)	1.675-1.795	BBI-0208, BBI-0136, BBI-0357, BBI-0382, BBI-0133, BBI-0375, BBE-0164, BBI-0348, BBI-0383, BBE-0149, BBI-0349, BBI-0363, BBI-0362, BBI-0370, BBI-0116, BBI-0347, BBI-0385, BBE-0162, BBI-0386, BBE-0165
Pupation rate (%)	0.338-0.360	BBI-0349, BBI-0363, BBI-0370, BBI-0364, BBI-0348, BBI-0136, BBI-0378, BBI-0362, BBE-0149, BBI-0376, BBI-0369, BBI-0357, BBI-0347, BBI-0374, BBI-0375, BBI-0343, BBE-0162, BBI-0377, BBI-0350, BBI-0382
Single cocoon wt.(g)	19.05-20.17	BBI-0349, BBI-0364, BBI-0369, BBI-0378, BBI-0363, BBI-0370, BBI-0324, BBI-0377, BBI-0360, BBI-0348, BBI-0376, BBI-0345, BBI-0374, BBI-0350, BBI-0359, BBI-0362, BBI-0343, BBE-0154, BBI-0361, BBI-0339
Single shell wt. (g)	994-1166.96	BBI-0326, BBI-0364, BBI-0389, BBI-0328, BBI-0279, BBI-0368, BBI-0350, BBI-0359, BBI-0358, BBI-0203, BBI-0290, BBE-0179, BBI-0378, BBE-0214, BBI-0375, BBI-0356, BBI-0291, BBE-0153, BBE-0169, BBI-0387
Cocoon Shell percentage (%)	937-1090	BBI-0350, BBI-0359, BBI-0203, BBE-0179, BBI-0378, BBE-0214, BBI-0328, BBI-0172, BBI-0380, BBE-0188, BBI-0364, BBE-0171, BBI-0358, BBI-0273, BBI-0347, BBE-0187, BBE-0216, BBE-0186, BBI-0290, BBI-0327
Avg Filament Length (m)	540-500	BBE-0150, BBE-0149, BBE-0157, BBI-0335, BBE-0153, BBE-0144, BBI-0123, BBI-0125, BBE-0010, BBI-0066, BBI-0300, BBE-0158, BBI-0380, BBI-0126, BBI-0095, BBI-0089, BBI-0340, BBI-0350, BBE-0160, BBI-0338

Filament size (d)	99.07-98.34	BBE-0168, BBE-0161, BBI-0126, BBI-0380, BBI-0330, BBE-0167, BBE-0149, BBI-0105, BBE-0016, BBE-0181, BBI-0294, BBI-0089, BBI-0362, BBI-0125, BBE-0150, BBI-0087, BBE-0153, BBI-0293, BBI-0273, BBI-0394

Data analysis indicated that, accession BBE-0149 and BBE-0348 performed better for six economic traits followed by BBI-0126, BBI-0378 and BBI-0350 which performed better for five traits. These accessions were followed by BBI-0349, BBI-0362, BBI-0347, BBI-0364 and BBI-0380 for 4 economic traits.

Table 20: Top ranking bivoltine germplasm accessions identified for multiple traits

Accession No.	No. of traits	Trait No. and Values
BBE-0149	6	1(683), 2(98.61), 3(43.19), 5(13.6), 7(1.727), 8(0.354)
BBI-0348	6	3(42.84), 4(9400), 6(92.6), 7(1.732), 8(0.366), 9(21.37)
BBI-0126	5	1(596), 2(98.89), 4(9360), 5(14), 6(91.8)
BBI-0378	5	3(42.86), 8(0.358), 9(21.82), 10(1025), 11(1025)
BBI-0350	5	1(594), 8(0.338), 9(21.11), 10(1090), 11(1090)
BBI-0349	4	3(43.64), 7(1.716), 8(0.382), 9(22.54)
BBI-0362	4	2(98.47), 7(1.712), 8(0.355), 9(20.92)
BBI-0347	4	5(15.2), 7(1.701), 8(0.349), 11(952)
BBI-0364	4	8(0.366), 9(22.01), 10(1153), 11(961)
BBI-0380	4	1(598), 2(98.75), 3(42.92), 11(974)

Figures in parantheses indicates the actual value of the traits
1.Fecundity (Nos.), 2.Hatching percentage (%), 3.Wt of 10 larvae (g), 4. Total Larval duration (hrs.) 5.V instar duration (hrs.) 6.Yield/10000 larvae by no. 7.Yield/10000 larvae by wt. (kg) 8.Pupation Rate (%) 9.Single cocoon weight (g) 10. Single shell weight (g) 11. Cocoon Shell percentage (%), 12. Average filament length (m), 13. Filament size (d)

Evaluation of mutant SWGRs

Two evaluation rearings were conducted for 23 mutant SWGRs and the variability statistics on the important growth and reproductive traits is presented in **Table 21**. Statistical analysis of data revealed higher co-efficient of variation for single shell wt. (22.18%), fecundity (18.24%), ERR by wt. (16.68%), single cocoon wt. (15.24%) and Wt. of 10 grown larvae (14.20%). The other characters such as yield per 10000 larvae by no., pupation rate, hatching (%) and total larval duration did not show much variation in CV% indicating the stabilized nature of genotypes to the rearing environment.

Table 21: Overall performance of Mutants germplasm resources

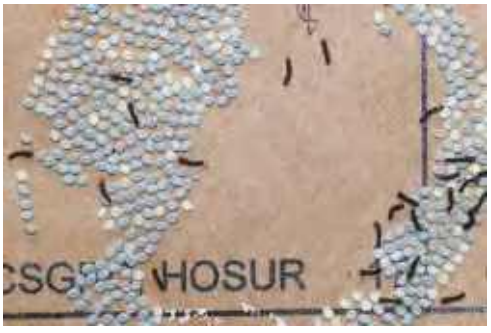
Traits	Mean	Min	Max	SD	SE	CV%
Fecundity (No.)	373	234	492	68.08	14.52	18.24
Hatching (%)	93.47	87.35	97.42	2.68	0.57	2.87
Wt. of 10 Larvae (g)	24.02	17.75	31.24	3.41	0.73	14.20
Total larval duration (h)	576	564	582	4.19	0.89	0.73
V age Larval duration (h)	132	120	138	4.19	0.89	3.18
ERR (No.) (10000 larvae)	7806	6610	9000	739.61	157.69	9.47
ERR (wt. in kg)	8.196	5.950	10.350	1.37	0.29	16.68
Pupation rate (%)	73.94	59.40	87.10	8.58	1.83	11.61
Single Cocoon Wt (g)	1.030	0.586	1.282	0.16	0.03	15.64
Single Shell Wt (g)	0.139	0.073	0.220	0.03	0.01	22.18
Cocoon shell percentage (%)	13.53	11.25	17.28	1.42	0.30	10.51

Objective 2: Maintenance and updation of SGIS database, cataloguing

During the period, morphological characterization for 489 silkworm germplasm resources using 27 descriptors on various growth stages viz., egg, larva, cocoon, pupa and moth, to confirm its maintenance true to catalogue data was carried out. The data generated were updated in the Silkworm Germplasm Information System [SGIS] database.

Objective 3: Digitization of distinct morphological traits of silkworm accessions and creation of database

Under digitization of silkworm genetic resources, it is proposed to establish a digital repository of silkworm genetic resources as a long-term national archive for sericulture germplasm. To create a virtual database, images of different developmental stages with variations in each accession is to be photographed and the database to be updated for all the important descriptors. During the period, captured the images of different stages of 50 MV silkworm accessions were captured and recorded the variability in each accession. The development of web application for a digital silkworm database is under progress. Representative photographs captured in high resolution from egg to moth stags are depicted in Figures 18a to g.

a 

b 

Fig.18: a. Egg stage b. Larval stage, c.Female pupa, d.Male pupa, e. Female and male cocoons, f.Female moth, g. Male moth

To promote utilization of sericultural germplasm for crop improvement programmes.

During the year, 12 dfls of bivoltine and 17 dfls of multivoltine silkworm accession were supplied for research and germplasm maintenance purpose (**Table 22**).

Table 22: Details on the dfls supply of silkworm germplasm resources during 2023-24

Sl. No	Name of the Indenter	Bivoltine accession		Multivoltine accession		Purpose
		Acc Name	No. of DFLs	Acc Name	No. of DFLs	
1	RSRS, Kalimpong	SH6	5	-	-	Maintenance of germplasm
2	CSRTI, Berhampore	-		M.Con.1	5	Replenishing of existing germplasm
3	RSRS, Kalimpong	BHR2	5	-	-	Maintenance of germplasm
4	Marathwada Agricultural University, Parbhani	GEN-3	2	BL-24	2	Research
				BL-26	2	
				MY-1	2	
				H-Mysore	2	
				P.Mysore	2	
				C.Nichi	2	
	Total	**BV**	**12**	**MV**	**17**	

7. SERVICES RENDERED

Trainings imparted:

Sl. No.	Date (Duration)	Type of training	No. of beneficiaries	Scientist involved
1	15.06.2023 – 30.06.2023 (15 days)	Internship programme on "Application of molecular biology tools in conservation of Seri-genetic resources"	6	All scientists
2	2023-24 (3 months each)	Dissertation training	7	Dr. G. Lokesh, Sci-D; Shri Raju Mondal, Sci-C
3	2023-24	Training classes on Sericulture technologies	899	Smt. G. Punithavathy, Sci-D; Dr. G. Thanavendan, Sci-C
4	2023-24	Training classes on Package of Practices for Mulberry Maintenance	514	Dr. N. Sakthivel, Sci-D
5	12.03.2024 (1 day)	one day Technical Workshop on Seribiodiversity: Conservation and Management for posterity'	35	All scientists

Exam duty

Dr. Ritwika Sur Chaudhuri, Scientist-C and Shri. Raju Mondal, Scientist-C served as Venue Officers for UDC recruitment examination during April, 2023.

Dead stock verification

Dr. Ritwika Sur Chaudhuri, Scientist-C carried out physical stock verification of SMOI, CSB, Bengaluru during September, 2023.

8. TRAINING PROGRAMMES

Trainings undergone:

1. Dr. G. Thanavendan, Scientist-C attended 21 Days International Training on "Agriculture in Future & Future in Agriculture" organized by RVSKVV, Gwalior, MP., JAU, Gujarat and ICRISAT, Hyderabad in collaboration with ICAR-IIMR, Hyderabad, ICAR-ATARI, Jabalpur and AGRI MEET Foundation Gwalior, MP from 20th November, 2023 to 11th December, 2023 (Virtual).

2. Dr. G. Lokesh, Scientist-D and Dr. G. Thanavendan, Scientist-C attended a training programme on “Vigilance awareness campaign organized by Central Silk Board at Capacity Building and Training Division, Central Office, Bengaluru on 18th and 20th October, 2023.

3. Dr. M. Nandan, Scientist-B attended the foundation training program for newly inducted Scientist-B, organised by CSB, Bangalore from 19th January to 23rd February, 2024.

9. PUBLICATIONS

Research papers

1) Maheswari, M., Naik, T., Chaudhuri, R. S., Lokesh, G., & Sreenivasa, B. T. (2023). Marker-assisted Selection of Bivoltine Silkworm Genetic Resources for Thermotolerance. Current Journal of Applied Science and Technology, 42(22), 17-33.
2) Gnanesh, B.N., Mondal, R., Arunakumar, G.S., Manojkumar, H.B., Singh, P.,Bhavya, M.R., Sowbhagya, P., Burji, S.M., Mogili, T. and Sivaprasad, V. (2023) Genome size, genetic diversity, and phenotypic variability imply the effect of genetic variation instead of ploidy on trait plasticity in the cross-pollinated tree species of mulberry. Plos One. 3.7.
3) M.C. Thriveni, Deepa, S., Thanavendan, G., Ravikumar, G. and Sreenivasa, B.T. 2023. Characterization and Evaluation of Mulberry Genetic Resources for the Identification of Promising Accessions. *Indian Journal of Plant Genetic Resources,* 36 (1): 85-95.

Popular articles

1) ग. थनवेंदन, ऋत्विका सुर चौधरी, एम.सी. त्रिवेणी, राजू मंडल, बी.टी.श्रीनिवास (2023) शहतूत के फल - एक नया दृष्टिकोण, रेशम भारती, के.रे.बो. पृष्ठ सं. 4-7.

Abstracts:

1) M.C. Thriveni, N. Sakthivel and V. Nishitha Naik (2023) Strategies for the Conservation of Mulberry Genetic Resources, 3rd International Scientific Conference on 'Environmental Research: issues, challenges and strategies for sustainable development and livelihood security', 1st & 2nd December 2023, Karwar, Karnataka, pp 21. (Oral presentation)
2) G. Lokesh, M. Maheswari, Ritwika Sur Chaudhuri, G. Punithavathy and V. Nishitha Naik (2024) Silworm seed management for efficient conservation, maintenance and utilization of silkworm genetic resources, Silkworm Seed Con-2024: Silkworm Seed Industry-Opportunities and Future Prospects, 30th & 31st Jan, 2024, NIFT Bengaluru, pp.78 (Poster presentation)
3) जी. लोकेश*, ऋत्विका सुर चौधरी, एम.महेश्वरी, जी. पुनीतावती और वी. निशिता नाइक (2024) सतत संरक्षण के लिए रेशमकीट आनुवंशिक संसाधनों के लक्षण वर्णन और मूल्यांकन मेंआणविक उपकरणों की भूमिका, राष्ट्रीय राजभाषा तकनीकी सेमिनार, रे जै प्रौ प्र, कोड़ती, केंद्रीय रेशम बोर्ड, 15.02.2024, पृ.सं.20. (Poster presentation)

4) ऋत्विका सुर चौधरी*, जी. लोकेश, एम.महेश्वरी, जी. पुनीतावती, वी. निशिता नाइक (2024) रेशमकीट आनुवंशिक संसाधनों के कुशल संरक्षण और उपयोग के लिए जनन्द्रव्य लक्षण-वर्णन, राष्ट्रीय राजभाषा तकनीकी सेमिनार, रे जै प्रौ प्र, कोड़ती, केंद्रीय रेशम बोर्ड, 15.02.2024, पृ.सं.27 (Poster presentation)

Book Chapter

1) Sakthivel, N. (2023) Organic Farming: Present Status and Future Scope in Mulberry Leaf Production. Recent Advances in Agricultural & Industrial Entomology & Environmental Sciences & their Impact on Food and Environmental Security. Eds. Dr B. Vasantharaj David & Fr Dr S. Maria Packiam, S.J. September 2023, Published by Entomology Research Institute, Loyola College, Chennai, Tamil Nadu. Pp.194-201.
2) Mondal, R., Rohela, G.K., Saha, P., Sangannavar, P.A. and Gnanesh, B.N., 2023. Mulberry Genome Analysis: Current Status, Challenges, and Future Perspective. In The Mulberry Genome (pp. 115-130). Cham: Springer International Publishing.
3) Gnanesh, B.N., Mondal, R. and Vijayan, K., 2023. Future Perspectives of Mulberry Genomic Research. In Book- The Mulberry Genome (pp. 293-298). Cham: Springer International Publishing.
4) Gnanesh, B.N., Mondal, R., Manojkumar, H.B., Bhavya, M.R., Singh, P., Arunakumar, G.S. and Mogili, T., 2023. Relationship Between Genome Size and Ploidy Level inMulberry. In The Mulberry Genome (pp. 131-147). Cham: Springer International Publishing.

Institute publications

1) CSGRC Annual Report, 2022-23
2) Bilingual CSGRC Newsletter, Oct, 2022-Mar, 2023
3) Bilingual CSGRC Newsletter, Apr-Sep, 2023
4) Mulberry Recipe Booklet, 2023 (Bilingual)

Invited Talk:

1) Sakthivel, N. delivered an invited talk on "Climate Change Resilience in Sericulture''in the International Conference on Recent Development in Frontiers of Biological Sciences (ICORD-FBS 2023) held on 22nd September, 2023 at Namakkal Kavignar Ramalingam Govt. Arts College for Women, Namakkal.

10. PARTICIPATION IN CONFERENCE / SEMINAR / WORKSHOP

1) Dr. G. Thanavendan, Scientist-C, attended an International seminar on World Earth Day: Agriculture, Food and Environment and the Global Earth Challenges and conducted by VIT School of Agricultural Innovations and Advanced Learning, Vellore Institute of Technology (VIT), Vellore (Virtual) on 03.05.2023.

2) Dr. G. Lokesh, Scientist-D, Dr. Ritwika, Scientist-C, Dr. G. Thanavendan, Scientist-C attended a Workshop on Development of diversified Seri-Byproducts: Recent achievements and future perspectives organized by CSRTI Mysore (Virtual) on 20.05.2023.

3) Dr. N. Sakthivel, Scientist-D, participated in an International Conference on "Recent Development in Frontiers of Biological Science" organized by PG & Research Department of Zoology, Namakkal Kavignar Ramalingam Government Arts College for Women, Namakkal, Tamil Nadu on 22.09.2023.

4) Dr. N. Sakthivel, Scientist-D, participated in a National conference on "Recent Advances in Agricultural and Industrial Entomology and Environmental Sciences and their Impact on Food and Environmental Security" organized by Entomology Research Institute, Loyola College, Chennai & Dr B. Vasantharaj David Foundation, Chennai, during 29-30.09.2023

5) Dr. M.C. Thriveni, Scientist-C participated in the 3rd International Scientific Conference on 'Environmental Research: issues, challenges and strategies for sustainable development and livelihood security' organized by Karwar, Karnataka during 01-02.12.2023.

6) Dr. V. Nishitha Naik, Director, Dr. G. Lokesh, Scientist-D, Shri. Raju Mondal, Scientist-C and Dr. M. Nandan participated in the two-day International Conference on 'Silkworm Seed Industry: Opportunities and Future Prospects' organized by CSB-NSSO at NIFT, Bengaluru on 30-31.01.2024.

7) Dr. V. Nishitha Naik, Director, Dr. G. Lokesh, Scientist-D and Dr. Ritwika Sur Chaudhuri, Scientist-C participated in the one-day Rashtriya Rajbhasha Technical Seminar organized by SBRL, Kodathi at Centre of Excellence, CSB, Bangalore on 15.02.2024.

8) Dr. V. Nishitha Naik, Director participated in Bharat Tex Expo-2024, New Delhi during 25.02.2024 to 01.03.2024.

9) Dr. M.C. Thriveni, Scientist-C attended National seminar on 'Flowing futures: committing to clean water and sanitation goals' organized by Central University of Kerala on 23.03.2024.

11. VISITORS

Sl. No.	Date of visit	Name/Institution	Purpose	No.
1	24.4.2023	Dr. Amrita Anantharaman, Asst.Professor, DKM college for Women, Vellore, T.N (with students)	To see the activities of the centre.	**47**
2	6.7.2023	Dr.P. Priyadarshini, Dept.of Sericulture, Forest College of Res.Institute, Mettupalayam, T.N.	To witness the activities of the centre.	**32**
3	26.7.2023	Dr. Ramakrishna Naika,& Dr.Pallavi, College of Sericulture, Chinthamani, Karnataka (with students)	To see the activities of the centre.	**38**
4	21.9.2023	Mrs. S. Anandhi, Dept.of Biotech, Vivekanada Arts & Science college for Women, Salem (with students)	To see the activities of the centre.	**36**
5	26.9.2023	Mrs.Sumathi, Teacher, Carmel International School, Hosur (with students)	To see the activities of the centre.	**56**
6	29.9.2023	Mrs.C. Vinaya, Jr. Inspector of Seric., Nallampalli Block, Dharmapuri District, T.N. (with trainees)	Field Exposure Visit	**53**
7	19.10.2023	Dr.M. Ramya, Asst.Professor, Agr.Entomology, JSACAT (with students)	To see the activities of the centre.	**131**
8	7.11.2023	Dr. JiluV.Sajan, Scientist (Entomo), CPCRI, Kayankulam, Alappuzha, Kerala (with staff)	Field Exposure Visit	**2**
9	22.11.2023	Sri.Anandkumar, Sericulturist, Ramnagar dist. (with 25 farmers & staff)	Field Exposure Visit	**28**
10	21.12.2023	Mrs.S. Jeyalakshmi, Asst.Inspector, TNSTI, Hosur (with farmers)	Field Exposure Visit	**46**
11	1.2.2024	Dr. Keiko Kadono-Okuda, Director General, Dr. Satomi Ikejima, Asst Professor, Insitute of Sericulture and Silk Science, Japan	To see the activities of the centre.	**3**
12	3.2.2024 & 13.3.2024	Mr.S.P. Muruganandam, Asst.Inspector (Retd.), TNSTI, Hosur (with farmers & staff)	Field Exposure Visit	**57**
13	18.03.2024	Dr. K.M. Vijaya Kumari, Director, CMER&TI, Lahdoigarh& Dr. N.B. Chowdary, Director, CTR&TI, Ranchi	To discuss collaboration opportunities with CSGRC.	**2**
14	28.03.2024	Sri. Sriganth, Farmer, Shoolagiri, KrishnagiriDist, Tamil Nadu	To see the activities of the centre.	**1**
			Total Visitors	**532**

12. COMPOSITION OF COMMITTEES

Research Advisory Committee

Dr. S. N. Sushil Director, ICAR-NBAIR, Hebbal, Bengaluru-560 008 (Karnataka)	**Chairperson**
Dr. M. Sankaran Division of Fruit Crops, ICAR-Indian Institute of Horticulture Research (IIHR), Hasaraghatta Lake Post, Bengaluru-560089 (Karnataka)	**Member**
Dr. Kamal Prasad Mohapatra Principal Scientist, Division of Germplasm Evaluation, ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110012 (Delhi)	**Member**
Dr. Manjunatha Gowda, Professor of Sericulture, University of Agricultural sciences, GKVK, Bengaluru- 560 065 (Karnataka)	**Member**
Dr. T. Venkatesan Principal Scientist & Head, Division of Genomic Resources, ICAR-National Bureau of Agricultural Insect Resources, P.B>No. 2491, HA Farm Post, Bellary Road, Bengaluru-560024 (Karnataka)	**Member**
Dr. Suresh Kumar Scientist-D (Retired), Flat No. 1B, Alish Tower, Olive Kalista, Near Kumbakonam Office, Edachira, Kakkamad, Kochi-682030 (Kerala)	**Member**
Dr. T. Mogili, Scientist-D (Retired), No.2 (Old No.1992), Srirampura 3rd Stage, Lingabudhi Lake Road, Behind Madhuvana Layout, Mysuru-570023 (Karnakata)	**Member**

13. राजभाषा कार्यान्वयन / Official language implementation:

राजभाषा कार्यान्वयन समिति की चार बैठकें 30 जून 2023, 30 सितंबर 2023, 23 दिसंबर 2023 एवं 28 मार्च 2024 को आयोजित की गई। उक्त रिपोर्टाधीन अवधि के दौरान प्रगति की समीक्षा की गई। सभी पदधारियों से अनुरोध किया कि वे अपने दैनिक सरकारी कामकाज में हिन्दी को बढावा दें, जो अधिदिष्टित है।

Four meetings of the Official Language Implementation Committee were organized on 30 June 2023, 30 September 2023, 23 December 2023 and 28 March 2024. The progress of work carried out during the period under report was reviewed. The staff was requested to put their best efforts in increasing the usage of Hindi in routine official work as mandated.

राजभाषा कार्यान्वयन के तहत केरेजसंके, एरीएसएसपीसी ,एससएपीसी एवं शीतागार भंडार ,होसूर के साथ चार कार्यशालाओं का आयोजन किया गया। चारों कार्यशालाएं बहुत ही उपयोगी एवं उदेश्यपूर्ण रही तथा केन्द्र के पदधारिगण टिप्पण ,आलेखन एव पत्राचार को तैयार करने हेतु प्रेरित हुए।

Four workshops were organized under Official language implementation, jointly with Eri SSPC, SSPC and Cold Storage Hosur. All the four workshops were very effective and staff of the Centre was inspired and motivated to use Hindi and various tools in the preparation of noting, drafting and letters.

क्रमसं. *Sl No*	दिनांक/ *Date*	विषय/ *Topic*	वक्ता/ *Speaker*
1.	30.06.2023	टंकण, गूगल वॉइस टाइपिंग, गूगल ट्रांस्लिट्रेशन व डिजिटल टूल्स Typing, Google voice Typing, Transliteration and Digital Tools	श्री. ललन कुमार चौबे, सहायक निदेशक (राजभाषा), बैंगलूर Shri. Lalan Kumar Chaubey Assistant Director (OL), Bengaluru
2.	12.09.2023	टिप्पण और मसौदा लेखन Noting and Drafting	श्री. कोमल सिंह, उप निदेशक (रा.भा.) (सेवानिवृत्त), हिं.क्षि.यो, गुवाहाटी Shri. Komal Singh, Deputy Director (OL) (Retired), Hindi Teaching Scheme, Guwahati
3.	15.12.2023	स्वयं अभ्यास: पत्र लेखन, सरल हिन्दी भाषा का उपयोग, टिप्पण और मसौदा लेखन Self Practice: Letter Writing, Use of Simple hindi Language, Noting and Drafting	श्रीमती. शीबा. वी. एस, व. अनुवादक (हिंदी), केरेजसंके, होसूर Smt. Sheeba, V.S., Senior Translator (Hindi), CSGRC, Hosur

4.	20.03.2024	राजभाषा अधिनियम एवं इसके विभिन्न पहलुएं Official Language Act and its various aspects	श्री. कमल किशोर बडोला, उप निदेशक (राजभाषा). केन्द्रीय रेशम बोर्ड, बैंगलूर Shri. Kamal Kishore Badola, Deputy Director (OL), Central Silk Board, Bangalore

के.रे.ज.सं.के द्वारा आयोजित हिंदी कार्यशालएं / Hindi Workshops organized by CSGRC

दिनांक 14.09.2023 को भारतीय भाषाओं के सौहार्द दिवस के रूप में हिंदी दिवस मनाया गया। केरेजसंके, ईएसएसपीसी व एसएसपीसी के वैज्ञानिकों / अधिकारियों / कर्मचारियों एवं कुशल श्रमिकों के सहयोग के साथ इस केन्द्र में 14 सितम्बर से 20 सितम्बर तक हिन्दी सप्ताह मनाया गया। हिन्दी सप्ताह के दौरान तीन प्रतियोगिताओं अर्थात शब्दावली, स्मृति परीक्षण, एवं गायन का आयोजन किया गया। हिन्दी सप्ताह के समापन दिवस पर सांस्कृतिक कार्यक्रम का आयोजन किया गया और निदेशक, सीएसजीआरसी द्वारा प्रतियोगिताओं के विजेताओं को पुरस्कार और प्रमाण पत्र वितरित किए गए।

Hindi Day was celebrated on 14.09.2023 as a cordial day of Indian languages. The Hindi Week was organized from 14th September to 20th September 2023 with the support of scientists, officials, employees and field workers of ESSPC and SSPC, Hosur. During the week, 3 competitions viz. Glossary, Memory test & Singing competitions were organized. On the concluding day of the week, cultural programme was organized and prizes and certificates were distributed to the winners of the competitions.

अन्य गतिविधियाँ

दिनांक 07.09.2023 को केरेबो द्वारा आयोजित अखिल भारतीय स्थर पर हिंदी निबंध प्रतियोगिता में केन्द्र, ईएसएसपीसी के डॉ. जी.लोकेश, डॉ. ऋत्विका सुर चौधरी, डॉ.जी. थनवेन्दन, डॉ. एम.सी. त्रिवेणी, श्री. राजू मंडल, श्री. ए. श्रीकुमार, ने भाग लिया। डॉ. ऋत्विका सुर चौधरी एवं डॉ. एम.सी. त्रिवेणी को सांत्वना पुरस्कार प्राप्त हुआ। दिनांक 21.09.2023 को केरेबो द्वारा आयोजित अखिल भारतीय स्तर पर हिंदी नारा लेखन प्रतियोगिता में केन्द्र, एसएसपीसी के डॉ.एम.सी.त्रिवेणी, श्री. बैरवा नरेन्द्र कुमार मोहरीलाल, तथा श्रीमती अंजू वारिकू ने भाग लिया। केन्द्र में दिनांक 05.03.2024 को के.रे.ज.सं.के. होसूर, के समस्त वैज्ञानिकों / अधिकारियों / कर्मचारियों को **"इडली अम्मा"** नामक हिंदी दस्तावेजी फिल्म दिखाया गया।

Dr. G. Lokesh, Dr. Ritwika Sur Chaudhuri, Dr. M.C. Thriveni, Shri. Raju Mondal, Shri. A. Sreekumar participated in All India level Essay Writing Competition organised by CSB on 07.09.2023. Dr. Ritwika Sur Chaudhuri and Dr. M.C. Thriveni obtained consolation prizes. Dr. M.C. Thriveni, Shri. B. Narendrakumar Mhorial and Smt. Anju Warikoo participated in All India Level Slogan Writing Competition organised by CSB on 21.09.2023. A Hindi documentary film- "Idli Amma' was shown to all scientists/ officers and staff of CSGRC, Hosur on 05.03.2024.

केरेजसंके में मनाया गया हिंदी सप्ताह / Hindi Week celebrated at CSGRC

14. OTHER ACTIVITIES

Research Council Meeting

The 71st, 72nd, 73rd and 74th meeting of the Research Council was convened on 20th July, 2023, 5th September, 2023, 19th December, 2023 and 24th March, 2024 respectively chaired by Dr. V. Nishitha Naik, Director, CSGRC, Hosur. The Committee and participants deliberated upon the research work undertaken at the Centre and provided suggestions for improvement.

Research Advisory Committee Meeting

The 45th meeting of the RAC of the Centre was organized on 12th October, 2023. The Committee and participants deliberated upon the research work undertaken at the Centre presented by the Scientists of the Centre and action to be taken for improvement were recommended.

Germplasm Review Committee Meeting

The 1st meeting of the Germplasm Review Committee was conducted on 18.05.2023 to review the silkworm germplasm status and future course of action for effective conservation.

Germplasm Registration Committee Meeting

The Germplasm Registration Committee Meeting was conducted at Central Office, Central Silk Board on 01.02.2024 by Director, CSGRC as Member Convener under the Chairmanship of Director (Technical) to assess the applications received for registration of silkworm and mulberry breeds.

Pebrine Monitoring

The Pebrine Monitoring Team consisting of nominated scientists from SSTL and RSRS, Kodathi and REC, Krishnagiri carried out the mandated microscopic testing during different stages of rearing for incidence of Pebrine. Approximately 13000 moth samples from Bivoltine and mutants (3 batches) and 15,000 samples of Multivoltine from four crops were screened.

Celebration of Official Events

1. WORLD ENVIRONMENT DAY

World Environment Day was celebrated on 5th June 2023 at CSGRC, Hosur. The Director In-charge addressed the gathering and emphasized on the rising levels of pollution which is causing a threat to the environment and climate change. She requested all the participants to plant more trees for a better future.

2. INTERNATIONAL YOGA DAY

As per instructions from Ministry of Textiles, Govt of India, International Yoga Day was celebrated at the centre on 21st June, 2023. Yoga instructor, Smt. Preethi, was invited to deliver lectures on the importance and benefits of yoga and to also demonstrate basic yoga techniques to the officers, officials and staff of CSGRC. She highlighted the health benefits of yoga and encouraged all to include yoga in their day to day life.

3. INDEPENDENCE DAY

On 15th August 2023, the Independence Day was celebrated at the Centre and the National flag was hoisted by the Director. The Scientists, Officers, Staff members, Skilled Farm Workers and their families participated in the celebration.


4. SILK DAY

Silk Day was celebrated in the centre on 20th September, 2023 to commemorate 75 years of establishment of Central Silk Board. A floral tribute was paid to Late Shyama Prasad Mookerjee, the first Minister of Commerce and Industry of free India, and also the ex-officio first Chairman of the Central Silk Board. A pledge on Silk Day was taken by all.

5. CONSTITUTION DAY OF INDIA

The Constitution Day of India, also known as Samvidhan Diwas, was observed at CSGRC on 26th November, 2023 to commemorate the adoption of the Constitution of India and to promote the Constitution values among citizens. The Preamble pledge was taken by all employees.

6. REPUBLIC DAY

Republic Day was celebrated on 26th January, 2024 by all the officers and staff at CSGRC, Campus. In his speech, Director, CSGRC explained the importance of the day for the citizens of India and the historical events that led up to the making of the country's constitution.

Superannuation, Promotion, Transfer



- Shri S. Somasekhar, SFW, superannuated from Board services on 08.05.2023
- Dr. B.T. Sreenivasa, Director, superannuated from Board services on 31.05.2023
- Shri. Gopalakrishnan, SFW, superannuated from Board services on 09.06.2023
- Shri. A. Sathyamurthy, STA, superannuated from Board Services on 31.01.2024



- Dr. V. Nishitha Naik, assumed charge as Director at CSGRC, Hosur on 02.06.2023
- Dr. M. Nandan joined as Scientist-B at CSGRC, Hosur on 07.11.2023
- Smt. B.N. Saraswathi, joined as Superintendent at CSGRC, Hosur on 11.03.2024

15. ADMINISTRATIVE AND FINANCIAL REPORT

a. Staff strength as on 31.03.2024

Category	No.
Director	1
Scientific	
Scientist-D	4
Scientist-C	4
Scientist-B	1
Sub-total	**10**
Technical	
Senior Technical Assistant [R & S]	1
Sub-total	**1**
Administrative	
Asst. Director (Computer)	1
Superintendent (Admin.)	1
Junior Engineer (Electrical)	1
Steno Grade-1	1
Library & Information Assistant	1
Senior Translator (Hindi)	1
Staff Car Driver	1
Assistant Technician	1
Field Assistant (Trainee)	1
Sub-total	**9**
Total	**20**
Supporting (Skilled Farm workers)	23

a. Research Fellows/Project Assistants

Senior Research Fellow (SRF)	1
Project Assistant	4
Sub-total	**5**

b. Superannuation/Voluntary Retirement from Service/Transfers

Sl. No.	Name & Designation	Remarks
1	Dr. B.T. Sreenivasa, Director	Superannuation on 31.05.2023
2	Shri A. Sathyamurthy, Sr. T.A.	Superannuation on 31.01.2024

c. Personnel posting position as on 31.03.2024

Division / Section	Name	Designation
	Dr. B.T. Sreenivasa (till 31.05.2023)	Director
	Dr. V. Nishitha Naik (from 02.06.2023)	Director
Mulberry	Dr. N. Sakthivel	Scientist-D
	Dr. G. Thanavendan	Scientist-C
	Dr. M.C. Thriveni	Scientist-C
	Shri Raju Mondal	Scientist-C
	Dr. M. Nandan (from 07.11.2023)	Scientist-B
	Smt. Thabhassum Banu	Field Asst. (Trainee)
Silkworm	Dr. M. Maheswari	Scientist-D
	Smt. G. Punithavathy	Scientist-D
	Dr. G. Lokesh	Scientist-D
	Dr. Ritwika Sur Chaudhuri	Scientist-C
Post Cocoon Technology	Shri R. Pugalendi	S.T.A. (R&S)
Administration & Computer Section	Shri. S. Sekar	Assistant Director (Comp.)
	Smt. B. N. Saraswathi (from 11.03.2024)	Superintendent (Admin)
	Smt. Poonam Ramashesha	Stenographer Grade-I
	Shri P. Nagadurai	Staff Car Driver (Grade-I)
	Shri A. Subramani	Assistant Technician
Hindi	Smt.V.S. Sheeba	Senior Translator (Hindi)
Library	Shri Bairwa Narendra Kumar M	Library & Information Assistant
Electrical Maintenance	Shri. M. Vijayakumar	Junior Engineer

e. Abstract of receipts and expenditure statement for the year 2023-24

Fund Head	Amount Received [in Rs.]	Expenditure [in Rs.]	Balance surrendered [in Rs.]
Contingent Amount	1317558.00	1317558.00	0.00

16. METEOROLOGICAL DATA OF CSGRC HOSUR FOR THE PERIOD FROM APRIL 2023 TO MARCH 2024

SUMMARY OF METEOROLOGICAL DATA FROM APRIL 2023 TO FEBRUARY 2024											
Month	**Temperature °C**			**Humidity (%)**			**Total Rain Fall (mm)**	**No. of rainy days**	**Avg. Wind Speed (m/sec)**	**Wind Direction**	**Sun Duration (mins)**
	Min.	**Max**	**Avg.**	**Min.**	**Max.**	**Avg.**					
April 2023	20.66	32.45	26.52	39.36	77.90	58.63	0	0	1.41	S	334
May 2023	20.91	28.91	24.91	47.83	86.38	67.10	0	0	1.63	SE	346
June 2023	20.43	28.43	24.43	62.96	93.10	78.03	80	11	2.19	WSW	327
July 2023	20.24	26.55	24.33	58.38	74.48	66.20	60	8	1.90	SW	321
Aug. 2023	21.56	31.41	26.48	67.77	80.87	74.32	0	0	1.99	SW	332
Sept. 2023	21.40	29.47	25.43	52.30	52.70	52.50	75	8	1.29	SW	327
Oct. 2023	19.06	28.88	23.97	64.74	80.10	72.42	37	4	1.38	S	312
Nov. 2023	19.98	27.97	23.38	56.76	65.53	61.14	12	2	1.41	SE	255
Dec. 2023	18.75	27.10	22.92	22.19	24.25	23.22	5	1	1.42	SE	289
Jan. 2024	17.24	27.95	22.59	27.87	37.83	32.85	0	0	1.60	SE	328
Feb. 2024	16.66	17.00	16.83	36.07	78.60	57.33	0	0	1.58	SE	342
Mar. 2024	17.65	33.66	25.65	24.41	91.80	58.10	0	0	1.63	158.4	304
						Total	**269**	**34**			

Minimum Temperature (February 2024)	**16.66 °C**
Maximum Temperature (March 2024)	**33.66°C**
Minimum Relative Humidity (December 2023)	**22.19%**
Maximum Relative Humidity (June 2023)	**93.10 %**


Visit of Hon. Member Secretary, Shri. P. Shivkumar to CSGRC on 28.10.23

Visit of Japanese delegates on 01.01.24


Field/Exposure visits of students and farmers to witness CSGRC activities during 2023-24


Celebrations at CSGRC during 2023-24

Activities under Swachhata Pakhwada at CSGRC during 2023-24

For further details, please contact:

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