

Status on outcome and utilization of R&D Projects by CSB R & D institutes in the area of Host plant improvement executed during the last 10 years (2010-20)

#	Project Code and title	Project period	Objectives	Achievement / output	Utilization status of the output	Coverage / impact in the field	Remarks
1	PIP- 4678- Morpho-physio-anatomical characterization of <i>terminalia spp.</i>	2008 - 2012	1.To characterize the gene pool of <i>Terminalia</i> spp. 2.To isolate superior genotypes of <i>T. arjuna</i> and <i>T. tomentosa</i> from the gene pool for developing superior hybrids.	Isolated 09 superior accessions of <i>T. arjuna</i> .	01 accession of <i>T.arjuna</i> (102) is under multiplication trial and remaining 08 accessions have been included in a Project on “Development of superior hybrids of <i>T. arjuna</i> and <i>T.tomentosa</i> for high leaf yield and quality” .	02 saplings each of two improved accessions of <i>Terminalia arjuna</i> viz., 102 and 123 will be supplied to 5 RSRSs & 3 RECS for multiplication. These plants will be compared with the hybrid plants developed under the project PIB-4697 in the proposed project “Evaluation of selected hybrids of <i>Terminalia arjuna</i> and <i>T. tomentosa</i> and drought tolerant <i>T. arjuna</i> accessions, and popularization of superior <i>T. arjuna</i> accessions (acc. 102 & acc. 123) and <i>Lagerstroemia speciosa</i> in different tasar silkworm rearing regions”.	
2	PIB-4686- Studies on various provenances of <i>Terminalia arjuna</i> Bedd. and <i>T.tomentosa</i> W. & A.	2008-2011	1. To study the variability in seeds and growth performance of seedlings of different provenances to estimate the variability among plus trees of <i>T. arjuna</i> and <i>T. tomentosa</i> for	Twenty five plus trees of <i>T. arjuna</i> (11) and <i>T. tomentosa</i> (14) were selected from different locations in Jharkhand and M.P. and evaluated for seed morphology, germination parameters, seedling growth, variability and biomass production. Based on the date 03 plus trees were selected [01 of <i>T.arjuna</i> from Chakradaharpur; Jharkhand 02 of <i>T.tomentosa</i> Bahragoda (Jharkhand) and Mandla (M.P.)	03 plus trees were selected [01 of <i>T.arjuna</i> from Chakradaharpur; Jharkhand 02 of <i>T.tomentosa</i> Bahragoda (Jharkhand) and Mandla (M.P.)]	The information generated is being used to raise uniform population from plus trees.	

			identifying suitable ones for further multiplication.			
3	PIB-4697 - Development of superior hybrids of <i>Terminalia arjuna</i> and <i>T. tomentosa</i> for high leaf yield and quality.	2012 - 2018	<ol style="list-style-type: none"> 1) Identification of most suitable mother plant for raising a seedling orchard with uniform population. 2) Evolution of superior hybrids which can be multiplied vegetatively. 	<p>Superior hybrids identified under pot condition will be evaluated in field trial at different agro-climatic conditions.</p> <p>Based on their performance across the location stable hybrid (s) would be recommended for farmers cultivation.</p>	<p>Identified true hybrids with higher yield traits can be used for mass vegetative multiplication at farmers' level.</p> <p>Project on "Evaluation of selected hybrids of <i>Terminalia arjuna</i> and <i>T. tomentosa</i> and drought tolerant <i>T. arjuna</i> accessions, and popularization of superior <i>T. arjuna</i> accessions (acc. 102 & acc. 123) and <i>Lagerstroemia speciosa</i> in different tasar silkworm rearing regions" has been proposed.</p>	
4	PPA-4704- Development of package for cultivation of <i>Lagerstroemia speciosa</i> for rearing of Tasar silkworm, <i>Antheraea mylitta</i> D.	2014 - 2016	<ol style="list-style-type: none"> 1) Development of package for economic cultivation of <i>Lagerstroemia speciosa</i>. 2) Standardization of package for Tasar silkworm (<i>Antheraea mylitta</i> D.) rearing on <i>Lagerstroemia speciosa</i>. 	<p>Propagation through cuttings showed that days taken for rooting varies in different season and maximum days taken for rooting was 45 days in <i>L. speciosa</i> and 60 days in <i>T.arjuna</i> in the cuttings planted during December. Height of one year old saplings of <i>L. speciosa</i> was more (80.13 cm) in comparison to <i>T. arjuna</i> (59.10 cm). Overall growth performance along with total leaf yield/plant of two year old plants of <i>L. speciosa</i> was higher than <i>T. arjuna</i> under 10' x 5' spacing. First crop silkworm rearing results show that larval duration was slightly higher in <i>L.speciosa</i> (35 days) as compared to <i>T.arjuna</i> and <i>T.tomentosa</i> (32 days). Similar trend was observed in second crop of both the year (52 and 45 days in <i>L.speciosa</i> and <i>T.arjuna</i>, respectively). ERR (%) was almost at par in all the three plants in both the crops during 2014 and 2015. Silk ratio was in the range of 11.71 in <i>T.arjuna</i> 13.11 in <i>L.speciosa</i> in first crop during 2014 and 2015. However, silk ratio was higher in second crop during both years in all the three species studied. Filament</p>	<p>Findings revealed that plantation of <i>L.speciosa</i> can be taken up for tropical Tasar culture as additional tropical Tasar silkworm food plant species under block as well as forest plantation. It is very easy to propagate and fast growing as compared to <i>T.arjuna</i> and <i>T.tomentosa</i>. Furthermore, it has an added advantage over <i>T.arjuna</i> that two consecutive rearing can be taken up on same plants. The package of cultivation and silkworm rearing for <i>Lagerstroemia speciosa</i> is being utilized for field recommendation.</p>	

				length varied 630.40 m in <i>T.arjuna</i> to 695m in <i>L.speciosa</i> in first crop of year 2014. Filament length was higher in second crop of year 2015 (887 and 940m in <i>T.tomentosa</i> and <i>L.speciosa</i> , respectively). Denier of the filament was almost similar in all the three species. Grainage behavior in <i>L.speciosa</i> was at par with <i>T.arjuna</i> .			
5	PIC-4705- Development of in-situ soil health and nutrient management in tasar growing areas.	2014 - 2017	1) To make the farmers aware about the importance of soil fertility for the production of quality leaves and subsequently cocoons through soil health cards.	A farmer friendly package for in-situ soil health and nutrient management developed.	Package is utilized at farmers' field and the same will be adopted by more and more farmers in near future.	Field trials were conducted during 2019-20 at RSRS Dumka, REC CKP and REC Seoni-Champa.	
6	AIP 4711 - Screening of fast growing drought tolerant accessions of <i>T. arjuna</i> for raising block plantation.	2016 - , 2019	1) To select the fast growing accessions of <i>Terminalia arjuna</i> available in the gene bank of CTR&TI for drought tolerance at the early stage of its growth.	Accessions of <i>Terminalia arjuna</i> plant accession no. 525, 523, 123 and 135 could be used as the drought tolerant accessions under limited or severe water stress conditions.	These identified accessions under this project could be useful among the farmers to successful rearing of tasar silkworm and enhance their productivity in the drought prone regions. Project on "Evaluation of selected hybrids of <i>Terminalia arjuna</i> and <i>T. tomentosa</i> and drought tolerant <i>T. arjuna</i> accessions, and popularization of superior <i>T. arjuna</i> accessions (acc. 102 & acc. 123) and <i>Lagerstroemia speciosa</i> in different tasar silkworm rearing regions" has been proposed.		
7	PPS 4725 - Soil Health Cards for Sericulture Farmers.	2016 - , 2019	1) To make the farmers aware about the importance of soil fertility for the production of quality leaves and	A combination of secondary nutrients SM ₅ has been developed and found to increase leaf yield by 27.45% with simultaneous increase in cocoon characters.	Package for the application of the secondary nutrients combination SM ₅ for enhancing the leaf yield and cocoon characters		

			subsequently cocoons through soil health cards.		was prepared and distributed to all Regional Tasar Research Stations for multi location trial. Large scale field trial at farmer's level is also being taken in Hatgamharia, Jharkhand.		
8	PIT-4700 -Multiplication of elite accessions of <i>Terminalia arjuna</i> through tissue culture.	Jan, 2013- Dec, 2013	1)Standardization and optimization of in vitro technique for micro-propagation of the selected accession / plus trees. 2)In vitro screening of high responding accession / plus trees.	Standardized the protocol for micro propagation and hardening of elite strain (BLRD) of <i>T. arjuna</i> .	In totality this project has developed the integrated method of elite plant multiplication technique called" In-vitro cum in-vivo juvenile multiplication techniques for tasar host plant "which has a wide application		
9	ARP - 4714 - Identification of early sprouting and fast growing genotypes of <i>Quercus serrata</i> for raising block plantation in North – West India.	2016-2020	1. Identification of early sprouting and fast growing genotypes of <i>Q. serrata</i> in the existing population. 2. Multiplication of isolated early sprouting genotypes to raise block plantation for utilization in early spring crop (March – April).	i) Five plants were identified as early sprouters during four surveys conducted under the project. Out of total 5 identified plants, three were identified from Kumaon and two from Garhwal region. No rooting was observed in air layers tried on the plants. Twigs of selected genotypes were brought to RTRS Bhimtal and planted by appropriate methods. But even after repeated attempts and following different protocols, rooting was not observed. The PI also consulted the Horticulture Dept. G.B. Pant University, Pantnagar and Department of Plant breeding & Tree development, FRI, Dehradun. As suggested, treatment of 4000 ppm IBA with talcum powder & ethyl alcohol before sprouting was also tried but no positive result was found.	During the Institute review meeting on 04.09.2020, it was suggested to try the multiplication of identified early sprouters through seedlings under Programme of work and identify more such plants and try for their multiplication.		

Status on outcome and utilization of R&D Projects by CSB R & D institutes in the area of Silkworm improvement executed during the last 10 years (2010-20)

1. **CTR&TI, Ranchi**

#	Project Code and title	Project period	Objectives	Achievement / output	Utilization status of the output	Coverage / impact in the field	Remarks
1	AIG-4669- Selection aided molecular marker system for improvement in tropical tasar silkworm <i>Antheraea mylitta</i> Drury .	2006-2011	<ol style="list-style-type: none"> To find out association of molecular marker (s) with yield traits of tasar silkworm To assess DNA polymorphism and heterozygosity found at individual and population level. 	<ul style="list-style-type: none"> Cocoon and shell weight specific markers have been identified which are highly reproducible and can be used with grater fidelity for inheritance pattern analysis of yield traits. This is the first report of development of SCAR marker, diagnostic to specific yield parameters of <i>A. mylitta</i>. The SCAR marker SCOPW-16₈₂₆ could be effectively utilized to circumvent the problem of lab-to-lab reproducibility and dominant nature of inheritance in RAPD. The discrimination between HCSW and LCSW trait group achieved by these markers would make them as very useful diagnostic markers for silk yield improvement, breeding and marker assisted selection aiming at the development of <i>A. mylitta</i> for productivity. The differentially expressed mRNA patterns in tasar silkworm larvae are very interesting, because some of them are unique to this species 	The identified shell weight linked SCAR markers are being used in marker assisted selection for cocoon yield improvement in tasar silkworm.	Basic information generated	
2	ARP-4793- Studies on the biology and ecology of Laria ecorace of <i>Antheraea mylitta</i> D. on Sal flora	2012 – 2015	<ol style="list-style-type: none"> To study the life cycle, ecology, ethology and population dynamics of Laria ecorace in natural habitat. To standardize the rearing schedule of Laria ecorace for utilization of Sal flora 	<ul style="list-style-type: none"> The grainage technology for wild ecorace Laria have been standardized through which Laria dfls can be produced. A package of practice for the efficient utilization of vast Sal flora based on the studies of Laria ecorace biology and ecology <i>in situ</i> and <i>ex situ</i> is suggested. Through phase-wise brushing, it is observed that if brushing is conducted during Rainy season (July), there will be less success in productivity. During autumn season, the successful brushing period is third to fourth week of September. This can be recommended for the area where Laria is being conserved. Cocoons produced during first season help 	Outcome of the project is being utilized for Laria conservation.	Laria Conservation model developed and provided to DOS Jharkhand who implemented the same and got 30-35% success in conservation.	

				<p>in selective conscription of progenies in the next season with reasonably good survivability if they are left as such untouched and undisturbed by human beings.</p> <ul style="list-style-type: none"> ▪ During Rainy season, Laria should be allowed to proliferate in natural pockets. <i>Ex situ</i> rearing is not much successful. ▪ High phenols, tannin content in leaves may be among the causative factors for low gut enzyme activity leading to low protein accumulation. The exact enzyme inhibitor(s) need further studies. <p>Emphasis must be given for conservation of Laria in natural eco-pockets in forests of Jharkhand.</p>			
3	AIB-4694- Improvement of Daba ecorace of <i>Antheraea mylitta</i> Drury for higher fecundity	2012 – 2015	To improve the semi-domestic Daba race for higher fecundity in tropical tasar silkworm <i>Antheraea mylitta</i> Drury	<ul style="list-style-type: none"> • Three breeding lines with >230, > 250 and >270 were isolated/developed without detrimental effect to male shell weight and female pupal weight. Developed lines are having higher fecundity when compared with ruling Daba fecundity (200-220). • Multi-location trial of breeding line (> 250 eggs/dfls) named as CTR-14 were carried out in different agro-climatic conditions namely RTRS Baripada (Odisha), REC-Katghora (Chhattisgarh), REC-Purulia (West Bengal) and REC-Hatgamaria (Jharkhand) in both the crops. • It is recommended that developed lines may be multiplied at P4 station of CTR&TI, Ranchi and good performers are required to be introduced into seed channel through P4 for improving fecundity and in turn cocoon production at farmer's level. • A package of practice for rearing of high fecundity line CTR-14 was also worked out and recommended. 	Multiplication trials of improved tasar silkworm line, CTR-14 for higher fecundity are being conducted at RSRS, Dumka, Baripada, Jagdalpur, Warangal & Bhandara and REC, Kathgora (Siwani), Robertsganj Kapistha & Hatgamharia/ Chakradharpur.	As per the suggestions of Hybrid Authorization Committee (HAC), project for validation trial of CTR-14 has been submitted.	
4	AIP-4696- Management of abiotic factors to regulate emergence in diapausing seed cocoons.	2012- 2015	1) To find a mechanism to check erratic emergence and regulate moth emergence with the help of controlled regime of	<p>Temperature treatment at 20oC delayed the emergence.</p> <p>Treatment during month of April and May is comparatively found more sensitive to delay in emergence.</p>	Temperature treatment at 20°C for 15 days delays the moth emergence in tasar silkworm cocoons	The technology is under trial as On Farm Trial (OFT) during 2020-21.	

			temperature and humidity from the diapausing seed cocoons	Temperature treatment in month of June is less effective. Except delay in emergence period, no significant variation on emergence (%), fecundity and hatching (%) was observed between control and treated groups.			
5	AIT-4702 - Molecular cloning and heterologous expression of <i>Antheraea mylitta</i> cocoonase.	June, 2013 - May, 2015	1) Large scale Collection of cocoonase 2) To express the cocoonase gene in heterologous hosts for its future utilization in softening of tasar cocoons.	Large scale rearing of <i>A. mylitta</i> and 2150 ml of cocoonase collection from 3000 emerging tasar silkworm has been done successfully. Prior to present study cocoonase was the unutilized by-product of tasar industry. Molecular cloning has been done. The fragment released from PGMT-Clones by EcoRI digestion was gel eluted and sequenced. Expression of cocoonase was evaluated through SDS-PAGE. Native cocoonase secretion process, place of secretion, secretion volume, and sequential changes in cocoonase concentration, chronological secretion profile, quantification, purification, proper storage conditions, enzymatic action and enzyme activity has been worked out successfully. SDS-PAGE analysis of purified cocoonase showed molecular weight 26 kDa.	Standardize the cocoonase collection from emerged moth. Cloning of cocoonase enzymes.	Second phase of the project “Identification most-active cocoonase of sericigenous insects and its variant through molecular characterization”, funded by DBT is under progress. During the project, efforts will be made to develop commercial use of cocoonase enzyme. (Project code AIT 4728)	
6	ARP 4713 - Isolation of Thermo-tolerant line(s) of tasar Silkworm <i>Antheraea mylitta</i> Drury through molecular studies.	2016 - 2018	1) To isolate thermo-tolerant line(s) of tropical tasar silkworm, <i>Antheraea mylitta</i> . 2) To develop molecular marker for the identification of thermo-tolerant line(s). 3) To unravel the underlying molecular mechanism of thermal stress tolerance in tasar silkworm.	Developed SCAR Markers would be an useful tool for identifying thermo-tolerant lines. Understanding of molecular mechanism behind the thermal tolerance would give an insight for the basis of adaptation in tasar silkworm. The 2 nd phase project has been approved by CSB and given project code [AIT04002SI] (February, 2019- January 2022) and has also been initiated.	The isolated thermo-tolerant lines could be utilized successfully in hotter zones of India to overcome the loss of dfl production due to high temperature.	Second phase of the Project AIT04002SI is under progress	
7	AIB 4717 - Improvement of tropical tasar silkworm for high	Oct, 2016 - Sept, 2019	1) Improvement of tasar silkworm breeds for high silk yield	Analysis of variance in RBD revealed significant variation across crosses for male cocoon weight and pupa weight and not for	The finding of the project has been utilized in formulation of a new	A long duration breeding programme has	

	silk yield through recurrent selection.		through recurrent selection breeding.	remaining. This indicates the breeding material has attained genetically homogeneous. Therefore creation of genetic variation in breeding population is essential for further genetic improvement of population. To achieve this evaluated population needs to be crossed with Wild Daba or other cultivated Daba in next generation. However, mean performance of total crosses of second season was found to be better as compared to that of first crop crosses for all the traits.	project proposal entitled “Rejuvenation programme of ruling Daba using wild Daba in <i>Antheraea mylitta</i> its homeland in Singhbhum Jharkhand”.	to be taken for development of a high yielding breed which can be successful in the field.	
9	AIB 4687 Improvement of Andhra ecorace of <i>Antheraea mylitta</i> D through back cross method- RTRS, WARANGAL	2008 - 2012	1. To introgress the survival characters of Daba TV ecorace in Andhra ecorace having high superior commercial characters 2.To develop breeds best suited for on farm conditions	Evolved BC-IV line of Andhra Local which yielded 35 cocoons/dfi over the parents (Andhra Local – 12 cocoons and Daba TV – 20 cocoons/dfi).	Increase in cocoon production from 12 (Andhra Local) to 35 (improved line) has been achieved.		

Status on outcome and utilization of R&D Projects by CSB R & D institutes in the area of Biotechnology executed during the last 10 years (2010-20)

SL No.	Project code	Project Title	Project period	Outcome	Present status
1		Screening, Characterization and Identification of Disease Tolerant Variety in Tropical Tasar Silkworm of <i>A. mylitta D.</i>	2003 - 2006	<ul style="list-style-type: none"> Based on repeated observations and LC50, ecoraces grouped as, Tolerant: Modal, Sukinda, Daba BV; Moderate: Sarihan, Daba TV, Bhandara, Andhra local; Susceptible: Raily. The healthy stock (Tolerant) indicates specific bands at the RAPD fragment sizes of 500 bp for Daba, 750 bp for Sarihan, 1 kb for Sukinda and for Andhra ecorace which were not present in corresponding diseased (Susceptible) stock of the ecorace. Polymorphic bands showing specific variation in RAPD fragment sizes ranging between 3kb to 2.5 kb and 2 kb to 2.5 kb between tolerant and susceptible line. 	<ul style="list-style-type: none"> Ecorace specific RAPD markers had been recognized for the identification of eight <i>A. mylitta</i> ecoraces. AmCPV tolerance in the different ecoraces found that Modal>Sukinda>DabaBV>DabaTV>Sarihan>Raily and information would be utilized in the development of AmCPV tolerant breeds.
2		Phylogeography of <i>Antheraea mylitta</i> (Tropical tasar silkworm) and <i>Antheraea assamensis</i> (Muga silkworm)	2005 – 2008	<ul style="list-style-type: none"> Molecular studies indicated significant genetic variability among and within seven ecoraces. Seven ecotypes of the Indian tasar silkworm, <i>A. mylitta</i> analysed using ISSR and SSR primers showed inter- and intra population polymorphism. Daba reared at CTR&TI Ranchi and Daba natural collected from West Singhbhum showed close proximity indicating domestication did not cause significant genetic variability. This is supported by similar mating behaviour by the semi-domestic and wild populations. Among the wild populations, Modia and Sarihan showed genetic closeness 	<ul style="list-style-type: none"> Acquired information is helpful in conservation of wild ecoraces with a conservation genetic approach. Laria conservation programme is based on this information

				while Laria, JataDaba and Bogai clustered to form a distant genetic group.	
3	AIG 4669	Selection aided molecular marker system for improvement in Tropical tasar silkworm <i>A. mylitta Drury</i>	2007-2010	<ul style="list-style-type: none"> • Cocoon weight and shell weight specific markers have been identified which are highly reproducible and can be used with greater fidelity for inheritance pattern amongst yield traits. This SCAR marker, diagnostic to specific yield traits of <i>A.mylitta</i>.could be effectively utilized to circumvent the reproducibility and dominant nature of inheritance in RAPD. • Discrimination between high and low cocoon and shell weight group achieved by these markers make them useful diagnostic markers for silk yield improvement, Marker Assisted Selection aiming at the development of <i>A. mylitta</i> productivity • The differentially expressed m-RNA patterns in tasar silkworm larvae are very interesting because some of these are unique to this species. This has a relationship with adaptive significance and life cycle strategies of tasar silkworm. 	The SCAR marker associated with cocoon and shell weight could be utilized for Marker Assisted Selection programme.
4	AIP-4680	Ecogenetic analysis of diapause and reproduction in tropical tasar silkworm <i>A. mylitta Drury</i>	2007-2010	<ul style="list-style-type: none"> • The role of physical and environmental and genetic factors responsible for pupal diapause and mechanism was studied. • Role of bioactive molecules secreted by the male accessory gland responsible for enhancing fecundity was explored. • 23 EST sequences submitted to NCBI Database. • In order to identify the physical and environmental and genetic factors responsible 	Project was exploratory in nature.

				for pupal diapause and mechanism in <i>A. mylitta</i> , the larval growth and development pattern of the Dababivoltineecorace of <i>A. mylitta</i> was studied on the basis of instar specific green & dry weight, green & dry weight gain in non-diapause-destined (NDD) and diapause-destined (DD) generations along with available photoperiod/day length, relative humidity and temperature, it was found that the green and dry weight gain was higher during early instars and significantly higher growth was observed in the first half of each instar. There was no significant sex-specific variation of green and dry weight of larvae of the same generation.	
5	ARP 4681	Identification and characterization of disease causing pathogens (microsporidia and bacterial infections) of tropical tasar silkworm, <i>Antheraea mylitta D</i>	2007-2010	<ul style="list-style-type: none"> • Micosporidia and 19 bacteria isolated from tasar silkworm collected from different geographical tasar growing areas. The mirosporidia and bacteria characterized morphologically and biochemically have also shown variation with molecular characterization (RAPD and 16s rRNA gene). The amplicon obtained in 16s rRNA analysis were sequenced and obtained sequences deposited to NCBI database with different accession numbers. 	<ul style="list-style-type: none"> • The amplicon obtained in 16s rRNA analysis were sequenced and obtained sequences deposited to NCBI database with different accession numbers.
6	AIT-4702	Molecular cloning and heterologous expression of <i>A. mylitta</i> cocoonase.	2013 -2015	<ul style="list-style-type: none"> • Large scale rearing of <i>A. mylitta</i> and 2150 ml of cocoonase collection from 3000 emerging tasar silkworm has been done successfully. Prior to present study cocoonase was the unutilized by-product of tasarindustry. Identification of crucial stage for cocoonase collection was done based on temporal changes in colour of pupae 	<ul style="list-style-type: none"> • Phase-I completed successfully and second phase DBT funded project AIT 4727 (2018-2021) initiated as identification of most active cocoonase for its eventual commercial use. For prediction of protein structure from the sequence procured was constructed from the

				<p>integument. Native cocoonase secretion process, place of secretion secretion volume, sequential changes in cocoonase concentration, chronological secretion profile, and quantification, purification by sephadexG100 column, characterization, proper storage conditions, enzymatic action and enzyme activity has been worked out successfully. SDS-PAGE analysis of purified cocoonase showed molecular weight 26 kDa. Per insect cocoonase collection volume is 500 to 800µl volume with 221µg/ml concentration. Recognition of sericin as natural substrate of cocoonase and it is established that cocoonase directly acts on the sericin without affecting the fibroin protein. SEM study showed marked variation in silk fibre surface when cocoon softening was done using cocoonase. MaldiTof-Tof (MS and MSMS) data A& B of A. mylittacocoonase MS 1320.477 showed similarities with cocoonase/proteolytic enzyme of other sericigenous insects. Complete coding nucleotide sequences of cocoonase gene were retrieved from NCBI database and phylogenetic analysis conducted. Sequence annotation studied was conducted and sequence was submitted to NCBI (>gi 731516038 gb KM388539.1 UNVERIFIED: Antheraea mylitta genomic sequence). Molecular matching of Antheraea spp. cocoonase was also performed in order to identify the eventual analogues available in nature.</p>	<p>newly constructed sequence. The blast result obtained for particular sequence was subjected for contig construction using online tool DNA baser. In silico analysis of AmCoc gene was done. The structure of AmCOC protein was determined by Quark (ab initio protein folding and protein structure prediction) server determines 3D structure of protein. The TM- score for the best model was observed as (0.3461 ±0.0833).</p>
7	ARP 4713	Isolation of thermo-tolerant line(s)	2016-18	<ul style="list-style-type: none"> • S1 and S2 generation thermo-tolerant lines 	<ul style="list-style-type: none"> • Thermo-tolerant lines could be

		of tasar silkworm <i>Antheraea mylitta Drury</i> through molecular studies		<p>have been selected through high thermal stress.</p> <ul style="list-style-type: none"> • Three SCAR markers (TT-PB1, TT-PB2 and TT-PB3) have been developed. Among three, TT-PB1 showed more specificity towards thermo-tolerant lines. • Heat shock proteins and factors responsible for thermotolerance in thermo-tolerant line have been analysed. HSP70 and HSP21 have found to be upregulated in thermo-tolerant lines of Daba. • Expression pattern of α&β-esterase isozyme in fifth instar temperature treated and untreated male and female larval hemolymph of <i>A. mylitta</i> has been analysed. Esterase at Rf value 0.48 has found to be expressed only in temperature treated larvae. 	<p>utilized successfully in hotter zones of India to overcome the loss of dfI production due to high temperature.</p> <ul style="list-style-type: none"> • Developed SCAR Markers would be a useful tool for identifying thermo-tolerant lines. • Understanding of molecular mechanism behind the thermal tolerance would give an insight for the basis of adaptation in tasar silkworm.
8	AIT-4724	Isolation and characterization of sericin from tasar silk waste for Commercial utilization.	2016- 2018	<ul style="list-style-type: none"> • Boiling with 0.2% sodium carbonate removes the residual sericin. Residual sericin was 2.33-2.79%. Fibre waste sericin has anti-tyrosinase, anti-elaste and antioxidant properties. • Higher quantity of sericin has been isolated from Daba corace. Elemental compositions of different corace-specific sericin are 11.94-12.39% Nitrogen, 40.3-40.75% Carbon, 0.715-1.47% Sulphur and 6.33-6.55% Hydrogen. No significant variation of molecular weight distribution of protein was observed between different tasacoraces. Raily coraceserucin found to posses more • non-polar and aromatic amino acids. Railysericin posses higher inhibition percentage of tyrosinase, glutathione-transfease activity and hydrogen peroxide 	<ul style="list-style-type: none"> • For further utilisation of project findings Phase-II of project entitled "II phase project: Mass level extraction of sericin from tasar cocoon cooking waste water for its prospective utilization- sent to DBT New Delhi for funding.

				<p>scavenging potential.</p> <ul style="list-style-type: none"> • Higher phenolic and C: N ratio was observed in sericin separated from • cocoons of Sal food plant. No significant variation of molecular weight distribution of protein and thermal stability was observed in sericin separated from cocoons of different plants. More non-polar amino acids were • observed in case of Sal sericin. As compared with other food plants, sericin separated from cocoons of Sal fed larvae posses higher inhibition percentage of tyrosinase and DPPH scavenging potential. • The waste water sericin having higher amount of low molecular weight proteins (>35kDa) and lower amount of high molecular weight (<245kDa). Separated sericin was confirmed through CHNS analysis, amino acid analysis, FTIR spectra and • ELISA test. Higher anti-tyrosinase activity, DPPH scavenging potential and inhibition of lipid peroxidation potential was also detected in tasar waste sericin. 	
9	PIG-4682	Evaluation of gene pool of tropical Tasar silkworm host plants with reference to yield and quality of Tasar silk.	2007- 2010	<ul style="list-style-type: none"> • Morphological and biochemical characterization • Analysis of variance for different phenotypic and biochemical traits showed significant differences among accessions of both T. arjuna and T.tomentosa, indicating genetic variability among the accessions. • Cluster analysis indicated that geographical distribution and genetic divergence did not follow the same pattern in both the species. 	<ul style="list-style-type: none"> • High level of heterozygosity was found in both the species. Based upon overall characterization and evaluation, four promising accessions have been isolated for further multiplication and popularization.

			<p>The grouping of genotypes of different geographical locations into one cluster appears to be due to presence of some common genes controlling the most important characters through modifying effect of micro- and macro-environment, while the genotypes from same location were grouped in separate cluster indicating occurrence of wide diversity among genotypes from same location.</p> <ul style="list-style-type: none"> • Molecular characterization <p>RAPD profiling of 18 accessions of <i>T.arjuna</i> using 35 random RAPD primers generated a total of 641 RAPD bands. Among total bands, 589 bands were polymorphic (91.89%) and 52 bands were monomorphic. On an average 16.83 polymorphic bands were generated per primer ranging between 7-30 bands. Only 10 primers (OPM-03, OPM-04, OPM-05, OPM-07, OPM-11, OPM-16, OPW-08, OPW-12, OPW-18, and AM773315) generated 100% polymorphic products</p> <p>The RAPD profiling of 16 accessions of <i>T.tomentosa</i> using 37 random RAPD primers generated a total of 719 RAPD bands of which 693 bands were polymorphic (96.38%) and 26 bands were monomorphic. On an average 18.73 polymorphic bands were generated per primer ranging between 11-35 bands, maximum (35) generated by primer OPW 05. Among 37 primers only 20 primers (OPM-03, OPM-07, OPM-09, OPM-11, OPM-13, OPM-14, OPM-17, OPM-18, OPM-19, OPW-01, OPW-02, OPW-10, OPW-11, OPW-12, OPW-13, OPW-15, OPW-18, OPW-19, AM773371 and</p>	
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			<p>AM750045) generated 100% polymorphic products.</p> <ul style="list-style-type: none"> Genetic diversity analysis <p><i>T. arjuna</i> accessions were grouped in three major clusters. In cluster-I, accessions 209, 123 and 135 formed one sub-cluster. Out of them two are from Jharkhand and one from the neighboring State, Orissa. The other sub-cluster in the first cluster comprised of accessions 307, 211 and 302, where two of them were from Maharashtra and one from Jharkhand. In the Cluster-II accession 512 (from Jharkhand) was placed as an isolate. One sub-cluster comprised of accessions 332 and 333, one from Andhra Pradesh and other from Chhattisgarh. The other sub-cluster comprised of three accessions, two (508, 430) from Jharkhand and one (504) from Andhra Pradesh. The third cluster had two sub-clusters and the first one comprised of 533 (UP) and 622 (Uttaranchal). Accession 701, 702 and 703 (all from Maharastra) and 624 (from Uttarakhand) formed the second sub-cluster. The bootstrap values were significant except one i.e., 40 for accessions 123 and 135. In comparison to the cluster analysis done for phenotypic and quantitative traits, the number of clusters was less for RAPD data, indicating that the genotypes are more influenced by environmental factors.</p> <p>Three major cluster were observed for the sixteen accessions of <i>T. tomentosa</i> studied Cluster I comprised of seven accessions where accession 501 (Jharkhand) remained as isolate.</p>	
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				<p>Accessions 309, 128 (both from Jharkhand), 216 (Maharashtra) and 229 (Chhattisgarh) comprised of one sub cluster while other sub cluster had accessions 310 (Chhattisgarh) and 408 (Jharkhand). The second major cluster showed accessions 313 and 443 in sub-cluster and both are from Chhattisgarh. Accessions 409 (Maharashtra) and 438 (Jharkhand) formed other sub-cluster. Major cluster-III comprised of five accessions, 522, 535 and 610 (all from Jharkhand), 531 (Maharashtra) and 612 (Andhra Pradesh).</p>	
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