List of Completed Projects: Genetics & Tree Improvement Division

S. No.	Title of the Project	Name of the Principal Investigator	Duration of the Project	Funding Agency	Project Status	Project Objectives	Research Findings
1.	Development of *in vitro* cloning protocol for micropropagation of thornless variety of *Prosopis cineraria* (Khejri)	Dr. Pooja Sharma	2023-2025	ICFRE	Concluded	*1.* To explore in vitro propagation response of thornless genotype of *P. cineraria* 2. To study factors affecting in vitro rooting response in shoot cultures of wild type *P. cineraria* in developing complete plantlets *3.* To analyse genetic fidelity of tissue culture raised saplings of *P. cineraria* 4. To establish demo-field trial of *in vitro* raised hardened plants	*In vitro* studies showed that shoot proliferation in thornless khejri improved significantly when cultures were treated with a combination of cytokinin (BAP 10 mg/l), auxin (NAA 0.5 mg/l), and neem oil (0.5 ml/l), resulting in increased leaf number, shoot number, and biomass compared to control. However, root induction attempts using different auxin concentrations (IBA 2–3 mg/l) combined with ABA, neem oil, or activated charcoal were unsuccessful. Similarly, in thorned *P. cineraria*, shoot cultures survived up to one month at higher BAP concentrations (10 mg/l) but later declined due to browning and leaf fall, and root induction using IBA pulse treatments (50–200 mg/l) did not occur, indicating challenges in achieving complete plantlet development under *in vitro* conditions.
2.	Cloning and characterization of a Na^+ and Ca^{2+} homeostasis gene – *spcbl-10* (calcineurin b-like protein 10) from	Dr. Tarun Kant	2022-2025	DBT	Concluded	1. Isolation and Cloning of *Spcbl-10* gene from Salvadora persica and construction of over-expression binary	*CBL10* gene from halophytic tree species of the arid regions *Salvadora persica* (*SpCBL10*) was isolated, cloned and functionally characterized. The

	facultative halophytic tree – *Salvadora persica* L.					vector 2. *Agrobacterium*-mediated transfer of Spcbl-10 gene to Tobacco 3. Functional validation of cloned gene through molecular, morphological and physiological analysis of transgenic plants	cloned gene was successfully validated through sequence, phylogenetic, and structural analyses, revealing conserved EF-hand calcium-binding domains and strong homology with known CBL10 proteins. Protein modelling and post-translational modification predictions indicated its role in membrane association and calcium-mediated signaling. Functional validation using transgenic tobacco lines confirmed enhanced tolerance to salinity, with improved chlorophyll retention, biomass, and root growth under NaCl stress compared to wild type plants.
3.	Development of seed production areas of economically important tree species of Rajasthan	Dr. Desha Meena	2021-2025	RFD	Concluded	1. Identification of seed production areas of *Tecomella undulata, Prosopis cineraria, Ziziphus nummularia, Ziziphus mauritiana, Salvadora persica* and *Salvadora oleoides*, in Rajasthan	A total of 53 seed stands representing the 6 economically important species were identified and systematically evaluated using quadrate methods and standardized scoring criteria. The assessment included growth parameters such as tree height, girth at breast height, bole height, crown characteristics, and overall performance scores to compare and rank the stands effectively. Species-wise evaluation covered 9 stands of *Tecomella undulata*, 7 of *Prosopis cineraria*, 6 of

							Salvadora persica, 8 of *Salvadora oleoides*, 16 of *Ziziphus nummularia*, and 7 of *Ziziphus mauritiana*. The study successfully identified superior and inferior seed stands, demonstrating that the scoring approach is a practical and reliable tool for selection and management of quality seed sources. The findings will support operational plantation programmes, enhance productivity, and strengthen future breeding and conservation efforts in Rajasthan.
4.	**CAMPA- National Programme for Conservation and Development of Forest Genetic Resources - FGR Component 3 - Characterization cell**	Dr. Tarun Kant, Regional Coordinator	2020-2025	CAMPA	Concluded	**A. FGR Documentation** 1. To Organize Regional conservation assessment & management prioritization (CAMP) workshops for assessment of threat status of FGRs and preparation of Action Plans for conservation of species assessed as Re-listed under guidance of FGR-CoE. 2. To Prioritize FGR species and conduct field surveys to document FGR diversity & their population status with GPS referencing	**FGR Documentation Cell:** The FGR Documentation Cell conducted extensive field inventories and documented the population status and threat factors of 119 prioritized dryland species out of the targeted 150 species. Studies on regeneration status revealed that 65 species exhibited healthy natural regeneration, whereas several others showed poor or absent regeneration due to climatic stress and excessive grazing pressure. The cell also carried out eco-distribution mapping and habitat suitability modeling for 25 important arid tree species, including *Tecomella undulata* and *Prosopis*

						[Target-150 Species] 3. To Extract FGR distribution records from accredited national herbaria (including international herbaria viz. Kew) and from Forest Working Plans [Target 150 species] 4. To Prepare eco-distribution maps of priority FGR species, including orientation and training of project staff. [Target 25 species] 5. To Collect seeds of FGRs for long-term storage. Seed of each species to be collected from an average of five provenances/ seed zones. [Target 50 species] **B. FGR Seed & Germplasm Storage** 1. Seed extraction, cleaning, grading, data recording, packing, labeling with passport data, etc. and putting the seeds under medium-and long-term storage, (may seek collaboration with NBPGR). [Target 50	*cineraria*, using GPS-based surveys, LANDSAT-8 remote sensing data, and MaxEnt bioclimatic modeling techniques. **FGR Seed Cell:** The FGR Seed Cell focused on conservation and management of seed germplasm by collecting and processing provenance seed lots of 37 economically important arid-zone species to preserve genetic variability. Detailed studies on seed physiology standardized parameters such as moisture content, germination value, and seed half-life, enabling classification of species into orthodox and recalcitrant categories. In addition, slow-growth storage and micropropagation protocols were developed for eight highly threatened species, including *Commiphora wightii*, *Boswellia serrata*, and *Salvadora oleoides*, facilitating medium-term in vitro conservation under sterile conditions. **FGR Characterization Cell:** The FGR Characterization Cell undertook biochemical and molecular profiling of prioritized species to assess their commercial and medicinal value. Quantification of

						species] 2. Minimum moisture content and periodic seed viability and vigor trials on stored seed along with working out half-life of the seeds in storage. [Target 50 species] 3. Collection, development protocols for in vitro medium-term storage of germplasm of FGR species of very high conservation concern and those having recalcitrant seeds. [Target 8 species] **C. FGR Charactarization** 1. Characterization of FGRs for biochemical traits. [Target 4 species] 2. Genetic diversity studies of FGRs of conservation concern and high commercial value with germplasm collected from across the range of distribution of the species. [Target 2 species] **D. FGR Conservation** 1. Development and	important bioactive compounds such as β-sitosterol, phenols, benzyl isothiocyanate, guggulsterones, and boswellic acids was completed for species like *Capparis decidua*, *Salvadora persica*, *Commiphora wightii*, and *Boswellia serrata*. Molecular diversity studies using SSR markers were also conducted for *Tecomella undulata* and *Prosopis cineraria* across multiple wild populations, enabling identification of genetic diversity hotspots and landscape-level admixture patterns. **FGR Conservation Cell:** The FGR Conservation Cell standardized nursery techniques, potting media, and dormancy-breaking treatments for six highly degraded arid species to improve propagation success. Field Gene Banks (FGBs) were established at AFRI Ecology Field and Jasol Malajaal Field as living ex-situ conservation repositories for long-term monitoring of survival, adaptability, and stress tolerance. Furthermore, the AFRI Jodhpur Arboretum was significantly enriched through the introduction of 63 new Forest Genetic Resource

						standardization of nursery techniques of FGR species of very high conservation concern. [Target 6 species] 2. Establishment of Field Gene Banks of priority FGR species. Includes collection of germplasm of selected species from across the country, multiplying and maintaining it in the nursery, site preparation, planting, site protection, and maintenance. [Target 6 species]	(FGR) species, strengthening regional conservation and research efforts.
5.	All India Coordinated Research Project on Genetic improvement of *Azadirachta indica* A. Juss. (Neem) (AICRP 26)	Dr. Tarun Kant [National Project Coordinator (NPC)]	2019-2025	CAMPA	Concluded	1. Identification of superior genotypes and seed sources from different agro-climatic zones of India for high Azadirachtin and oil content. 2. Chemical evaluation of seed samples collected by different Institutes from different agro-climatic zones of India. 3. Genetic Characterization of high azadirachtin and oil yielders identified after three years. 4. Phenology and Reproductive biology	Nationwide survey across 9 agroclimatic zones led to selection of 1000 Candidate Plus Trees (CPTs). Seeds collected from these CPTs were processed and analyzed for azadirachtin and oil content using HPLC, revealing that southern agro-climatic zones, particularly ACZ 10A, 10B, and 11, possessed the highest azadirachtin content, while ACZ 10B, 8, and 9 showed superior oil yield. Based on three years of evaluation, 100 elite performers were selected for genetic characterization using Start Codon Targeted (SCoT) markers. Studies on flowering

						studies 5. Development of genetic transformation methods for frost/cold tolerance 6. Production of Azadirachtin through cell suspension culture	behaviour, seed traits, pollinator interactions, breeding systems, pollen viability, and in vitro germination provided important reproductive biology insights. A genetic transformation protocol for Neem was successfully developed using the pCAMBIA 1304 vector, and integration of the *glyIII* gene into Neem was confirmed through PCR and sequencing. Additionally, cell suspension culture systems from flower and leaf callus were established for azadirachtin production, with flower callus showing the highest accumulation, further enhanced through elicitor treatments.
6.	All India coordinated research project on bamboo (AICRP 02)	Dr. Pooja Sharma	2019-2025	CAMPA	Concluded	*In-vitro* propagation for mass multiplication/ conservation of elite bamboo genotypes	Under this project, efforts were undertaken at AFRI for the multiplication of elite germplasm of *Bambusa bambos* and *Dendrocalamus strictus* through vegetative explants. In addition, medium-term conservation protocols for both species were standardized using different physical and chemical factors. The conservation studies were successfully carried out, achieving maintenance of propagules for periods ranging from 3 months to 12 months.

7.	All India coordinated research project on Conservation, Improvement, Management and Promotion of Sandalwood (Santalum album Linn.) cultivation in India (AICRP 03)	Dr. Aditi Tailor [NPC: Dr. Modhumita Dasgupta, IFGTB]	2019-2025	CAMPA	Concluded	1. Establishment and evaluation of base population in sandalwood for breeding and conservation programs. 2. Development of sandalwood based agroforestry system and its promotion in selected agroclimatic zones of India. 3. Evaluation of heartwood formation, yield and chemical profiling of oil in sandalwood populations.	A pan-India survey across six states identified 70 potential sandalwood populations and 1076 candidate plus trees (CPTs), leading to the establishment of five base population trials and the documentation of superior seed sources. Significant advances were made in sandalwood genomics, including methylome mapping, ceRNA network construction, and identification of RNA-edited sites, along with the development of the online portal SandalGDB. Genetic diversity studies revealed unique and rare gene pools in Karnataka and Kerala populations, while agroforestry trials across six states highlighted the superior performance of local seed sources and suitable host species. Surveys also identified optimal soil, irrigation, and intercropping practices, with wheat and groundnut proving economically viable intercrops in some regions. Eco-friendly pest management methods and non-invasive ERT technology for heartwood estimation were developed, while studies on oil content and isotopic signatures showed significant variability linked to

							geography and extraction methods.
8.	Cloning and Characterization of salt tolerance conferring vacuolar Na^+/H^+ antiporter (NHX1) genes from *Prosopis juliflora* (SW.) DC. & *Salvadora persica* L.	Dr. Tarun Kant	2019-2025	ICFRE	Concluded	**Short Term** *1.* To carry out isolation and full length cloning of Na^+/H^+ antiporter (PjNHX1) from *Prosopis juliflora* and *Salvadora persica* 2. To construct over-expressing *PjNHX1* and *SpNHX1* 3. To carry out *Agrobacterium*-mediated genetic transformation. 4. To do molecular confirmation *PjNHX1* and *SpNHX1* gene in transgenic tobacco and analysis of for salt tolerance characters **Long Term** Isolation and characterization of a genes from salt tolerant tree species for use in genetic improvement of crop plants for salinity tolerance	Using molecular biology fundamentals and gene cloning approaches, the project successfully achieved the isolation and full-length cloning of *NHX1* genes from both target species. Detailed characterization revealed conserved structural features typical of vacuolar Na^+/H^+ antiporters, along with species-specific variations that are likely linked to their high stress tolerance. The cloned genes were further subjected to functional validation through transgenic approaches, reinforcing their role in conferring salt tolerance. The outcomes of the project provided experimental evidence that *NHX1* genes from arid forest trees are functional and biologically relevant, supporting the original hypothesis that native tree genomes represent valuable reservoirs of stress-resilience genes.
9.	Assessment of variability, improvement and refinement of cloning techniques of Tecomella undulata (Sm.) Seem	Dr. Desha Meena	2012-2017	RFD	Concluded	**Short term** 1. To carry out the survey and selection of the candidate plus trees of Tecomella undulata in Rajasthan. 2. To establish progeny	Surveys conducted across 6 districts of Rajasthan identified 41 CPTs based on growth and morphological traits such as height, DBH, crown diameter, health, and flower colour. Progeny trials established at

						trials/germplasm bank of the selected candidate plus trees. *3.* Maintenance and evaluation of existing progeny trials of *Tecomella undulata.* 4. To carry out the assessment of genetic variability in the natural populations using suitable DNA markers **Long Term** Genetic improvement of *Tecomella undulata*	Jodhpur and Jhunjhunu revealed superior performance of progenies from Pali, Churu, Jodhpur, and Barmer districts in terms of height and collar diameter growth. Genetic diversity analysis of 120 individuals from 12 populations using 26 ISSR primers showed clear genetic differentiation among populations. The findings provide valuable information for selecting superior and genetically diverse populations for future tree improvement and breeding programmes.
10.	Non-destructive *in vitro* Production of Pharmacologically-active natural extract containing Guggulsterones – a Potent Cardio-protective and Anti-cancer Drug from *Commiphora wightii* (Guggul) using Bioreactor	Dr. Tarun Kant	2017-2021	NMPB	Concluded	1. To optimize guggul cell suspension cultures in a bioreactor format 2. To optimize production of guggulsterone-rich guggul cell lines in bioreactor 3. To extract and purify guggulsterone containing fraction from bulked-up cell lines using Ethyl acetate extraction 4. To carry out qualitative and quantitative analysis of guggulsterones and other active metabolites in the extract	The project focused on developing a non-destructive *in vitro* system for the production of pharmacologically important guggulsterones from *Commiphora wightii* (Guggul) using bioreactor technology. Callus initiation was successfully achieved from multiple explants, with apical buds showing the highest response (88.88%), followed by leaf explants, while tissue culture-derived immature embryos exhibited superior callusing and faster somatic embryogenesis compared to seed-derived sources. Biomass production studies revealed that maximum biomass accumulation occurred on the

							27th day of inoculation, with tissue culture-raised materials outperforming seed-derived cultures. HPLC analysis showed that natural twig samples contained the highest concentrations of Guggulsterone-Z and E, whereas in vitro cultures also demonstrated appreciable guggulsterone production. GC-MS profiling of embryogenic callus identified several important bioactive compounds, including palmitic acid derivatives and siloxane compounds. A novel fed-batch solid-state bioreactor was successfully designed and optimized for large-scale biomass production, effectively eliminating contamination and operational issues commonly associated with conventional liquid bioreactors, leading to a patent filing for the technology.
11.	Studies on phenology, molecular analysis and wood properties of *Tecomella undulata* with respect to three flower colour morphotypes	Dr. Desha Meena	2017-2021	ICFRE	Concluded	**Short term** 1. To study the distribution pattern and phenology of *Tecomella undulata* with respect to different flower colour morphotypes. 2. To study the physical and mechanical wood properties of different flower colour morphotypes of	Extensive surveys across 8 districts of Rajasthan identified 14 sites for studying morphological, phenological, and population density variations among orange, red, and yellow flower morphotypes. The orange morphotype showed higher population density and superior pod length, seed length, and leaf size, while

						Tecomella undulata 3. Identification of suitable DNA markers for differentiating the three-flower colour morphotypes of *Tecomella undulata* **Long Term** Genetic improvement of *Tecomella undulata*	yellow morphotypes had wider pods and red morphotypes exhibited greater seed weight. Flowering behaviour varied among morphotypes, with orange and red variants flowering earlier than yellow, though peak flowering occurred in February for all types. Analysis of wood properties revealed that red flower morphotypes possessed significantly different mechanical strength, likely due to differences in specific gravity. Molecular analysis using SCoT markers showed limited differentiation among morphotypes, although clustering analysis grouped yellow morphotypes separately from red and orange types. The findings suggest that the orange flower morphotype may have evolved through natural outcrossing in this cross-pollinated species, providing valuable insights for conservation and breeding programmes.
12.	*In Silico* Identification of Abiotic Stress-Tolerance Candidate Genes Using Co-Expression Network Analysis and Comparative Genomics	Dr. Tarun Kant	2016-2018	ICFRE	Concluded	**Short Term** 1. To identify new orthologous genes in a tree species involved in salinity response mechanisms. 2. To identify genes that may have role in	A comprehensive study on salinity stress tolerance identified 74 key genes associated with plant responses to salinity stress and developed a database containing 395 Arabidopsis genes along with their protein sequences and

						management of other abiotic stresses but are tightly associated with salinity response genes **Long Term** Identification of new gene(s) directly responsible for abiotic stress tolerance and their use in genetic improvement endeavors though transgenic approach.	functional annotations. Co-expression network analysis using the EAGLE algorithm identified 11 significant gene clusters, leading to the discovery of 140 interconnected genes involved in salinity tolerance. Through comparative genomic analysis, 140 orthologous genes were identified in *Populus trichocarpa*, including several previously uncharacterized genes with potential functional significance. The study also identified multiple Domains of Unknown Function (DUFs) and transcription factors (TFs) in both Arabidopsis and Poplar species. Gene Ontology enrichment analysis revealed that these genes are involved in critical biological processes such as responses to salt, osmotic stress, cold, and water deprivation, validating their importance in abiotic stress tolerance. The findings provide a strong foundation for future genetic improvement programmes aimed at enhancing salinity tolerance through genetic engineering and related approaches.
13.	A Coordinated Project on Integrated Management of Khejri Mortality for Socio-Economic Upliftment in	Dr. Tarun Kant	2010 - 2017	ICFRE	Concluded	**Short Term** 1. Studies on biotic and abiotic factors affecting for large-	The project addressed pathology, biotechnology, biochemistry, and socio-economic aspects associated

	Rajasthan					scale Khejri mortality 2. Bio-ecological studies on the causative species involved in mortality of Khejri 3. Isolation and identification of pathogens, their pathogenicity test and Induction of systemic acquired resistance (SAR). 4. Assessment of socio-economic impact of Khejri mortality 5. Selection and evaluation of CPT, establishment of germplasm bank and development of clonal propagation techniques. 6. Screening of selected material for the disease and insect pest tolerance / resistance. 7. Molecular marker-based characterization of CPTs and disease escape / tolerant / resistant phenotypes. 8. Development of integrated pest and disease management and its dissemination to stakeholders. **Long Term**	with dieback disease in *Prosopis cineraria* (Khejri) caused by *Ganoderma lucidum*. High pathogen diversity with 94.4% polymorphism and variable virulence among isolates was observed, with isolates GL15 and GL6 identified as highly virulent. Eco-friendly disease management strategies involving VAM, *Prosopis juliflora* leaf extract, and *Trichoderma harzianum* proved effective alternatives to chemical fungicides. Tissue culture studies highlighted severe rooting challenges in Khejri, although a six-fold multiplication breakthrough was achieved using coppice shoots from partially pollarded trees. Genetic analyses revealed high within-population variability and identified superior breeding populations such as Jaisalmer for seed collection and Sikar (Pinjarpole) for cloning. Biochemical investigations identified reliable infection biomarkers, including changes in sugar, proline, phenols, and mineral ash content, while Mid-IR spectroscopy showed promise for early non-invasive disease detection. The study also documented significant

						To develop and provide technology to control Khejri mortality, provide genetically superior quality planting material and uplift socio-economy of the farmers.	economic losses due to Khejri mortality and emphasized the need for integrated pest management, restricted lopping practices, and conservation-oriented regeneration strategies for sustaining arid-zone livelihoods.