



Leveraging Genetic Resources for Accelerated Genetic Improvement of Linseed using Comprehensive Genomics and Phenotyping Approaches

Under Mission Programme on
"Minor Oilseeds of Indian Origin"
Department of Biotechnology, Govt. of India



Project Coordinator: Dr. Ashok Kumar, Co-coordinator: Dr. Vikender Kaur

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LINSEED RESEARCH NETWORK PROJECT

Linseed or flax (*Linum usitatissimum* L.) is an important oilseed crop having centre of origin and diversity in Indian subcontinent. It is cultivated worldwide for its stem fiber as well as its seed oil with many health promoting products such as its omega-3 fatty acid (alpha linolenic acid), dietary fiber and lignans. However, lack of systematic efforts towards utilization of available genetic resources and targeted breeding are the main concerns for its impeded commercialization. To address varied constraints for increased productivity and facilitate fast genetic improvement, a network project has been formulated under the 'Mission Programme on Minor Oilseeds of Indian Origin' Department of Biotechnology, Government of India. This project aims at multi-location evaluation of entire linseed accessions available at National Genebank for agro-morphological traits, biochemical profiling, major abiotic and biotic stresses. Further, in order to generate genomic resources, genome sequencing of one dominant variety of linseed and resequencing of core set will be done. All the genebank accessions will be genotyped by SNP based genotyping approaches. The Genome Wide Association Studies (GWAS) will be performed to identify genomic regions associated with key agro-morphological (yield contributing), nutritional traits as well as biotic and abiotic stress tolerance.

Coordinating Centre: ICAR-National Bureau of Plant Genetic Resources, New Delhi

Collaborating Institutes: 12 (ICAR: 4, CSIR: 1, SAUs: 6, Private university: 1)

Duration of project: 5 years (2020-21 to 2024-25)

Date of Sanction: 29th February 2020

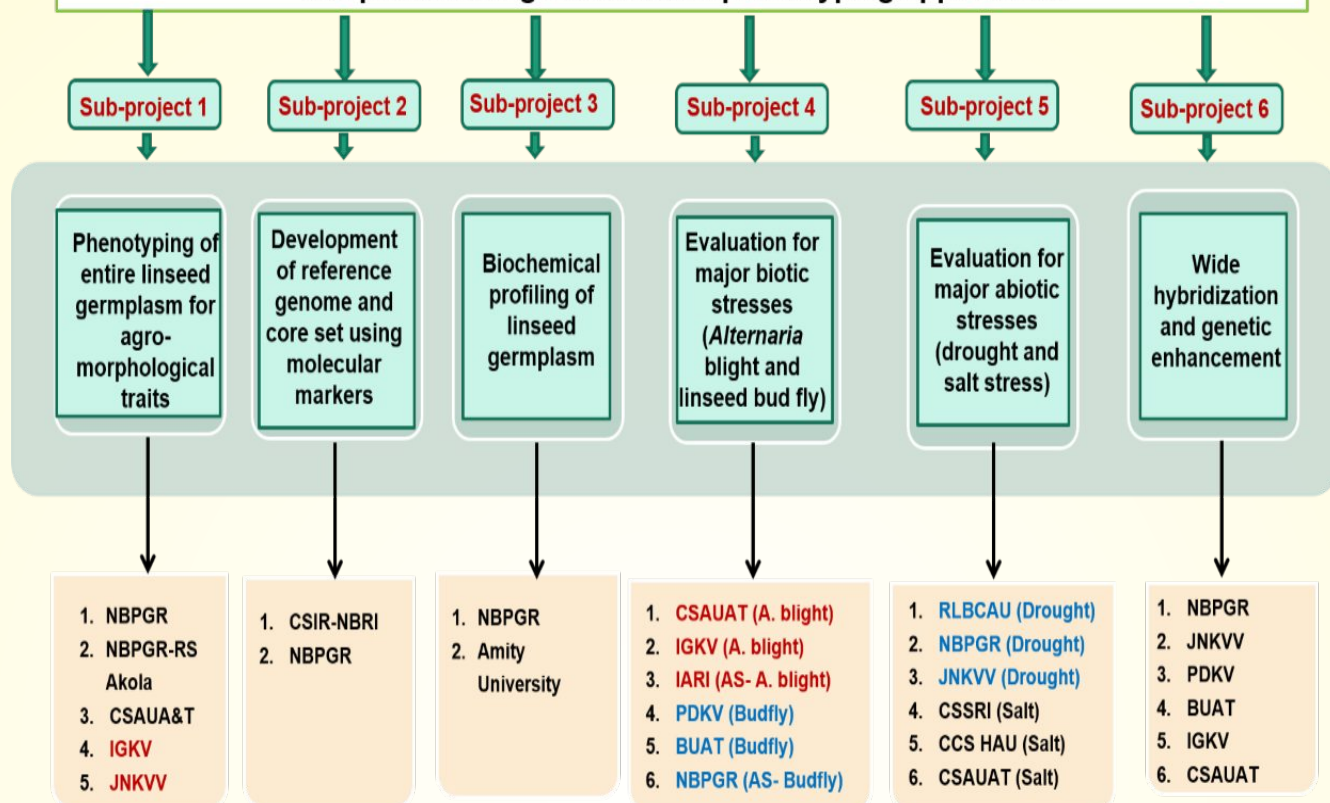
Total budget: Rs. 2255.8142 Lakhs

MAJOR OBJECTIVES

- ❖ Multi-location characterization of the entire linseed germplasm conserved at National Genebank (NGB) for agro-morphological traits and SNP genotyping for development of composite core set.
- ❖ Screening of whole collection at natural hot spot locations for *Alternaria* blight and linseed bud fly followed by validation under artificial epiphytotic conditions to develop reference set for association studies and functional genomics.
- ❖ Evaluation for drought and salt stress tolerance and development of reference set to delineate functionally relevant molecular markers/genomic regions
- ❖ Whole genome sequencing and re-sequencing of core set and trait specific accessions for marker/alleles discovery.
- ❖ Genome wide and candidate gene association mapping for important agro-morphological traits and resistance/tolerance to key biotic and abiotic stresses.
- ❖ Development and utilization of Near Infra-Red (NIR) prediction model for high throughput non-destructive estimation of major biochemical constituents of nutritional and nutraceutical value in linseed germplasm
- ❖ Development of pre-breeding resources to widen the genetic base and to incorporate long lasting resistance against major biotic/abiotic stresses and yield related traits in cultivated background.

Linseed Network Project: An Overview

Leveraging genetic resources for accelerated genetic improvement of linseed using comprehensive genomics and phenotyping approaches

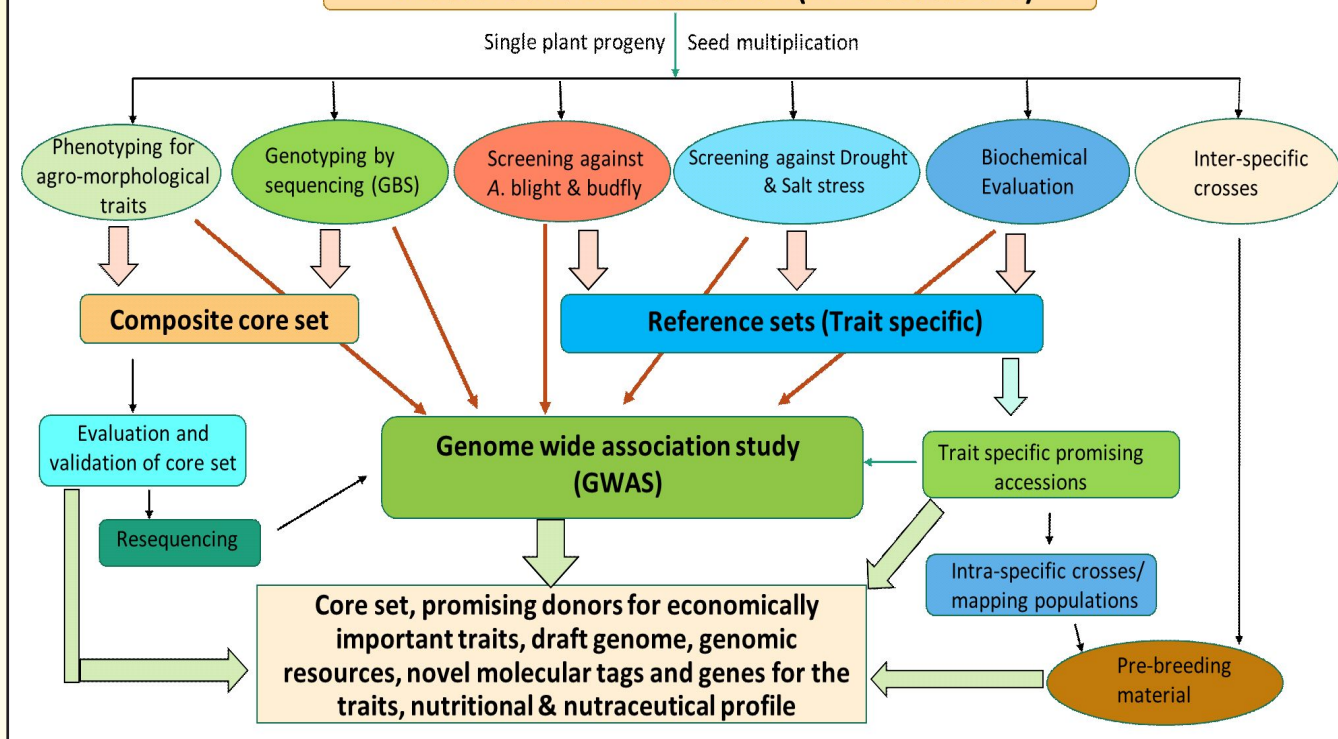


EXPECTED OUTCOMES

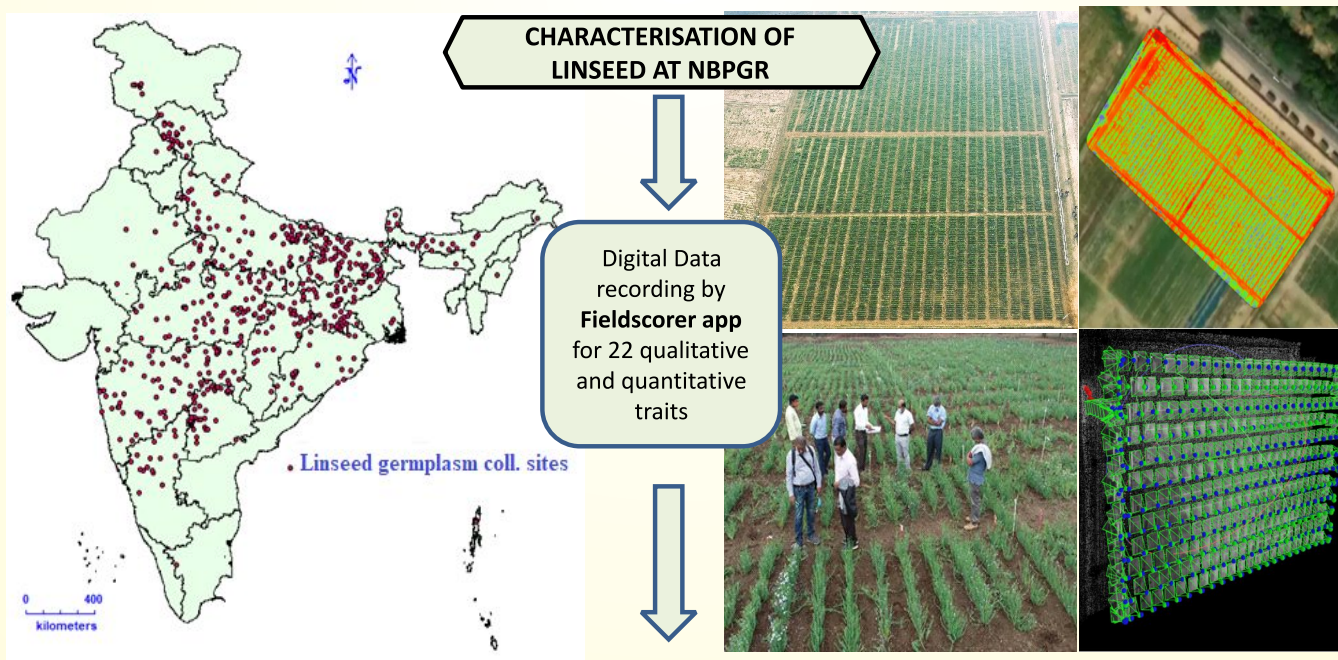
- ❑ Phenotypic and genotypic characterization of complete genebank accessions of linseed and composite core set representing morphological and molecular diversity
- ❑ Whole genome sequence of dominant linseed variety (T-397) and genomic resources in the form of SNPs, markers, genes, alleles identified from resequencing of composite core set and GBS of complete gene bank accessions. Genomic regions associated with important traits.
- ❑ Trait specific germplasm accessions/genetic stocks for key agronomic (earliness, no. of capsules/plant, seed weight, oil content, yield) and nutritional traits (omega-3 FA, lignan, protein), as well as for biotic and abiotic stress resistance
- ❑ References sets for major biotic and abiotic stress
- ❑ Superior recombinants/ pre-breeding lines for marker-assisted introgression of potential traits to incorporate long lasting resistance against major biotic/abiotic stresses and yield related traits.
- ❑ Interactive database on linseed based on phenotypic and genotypic resource information for efficient utilization and commercialisation.

WORKPLAN FOR THE EXECUTION OF PROJECT

Linseed Gene Bank collection (2748 accessions)



PROJECT ACTIVITIES

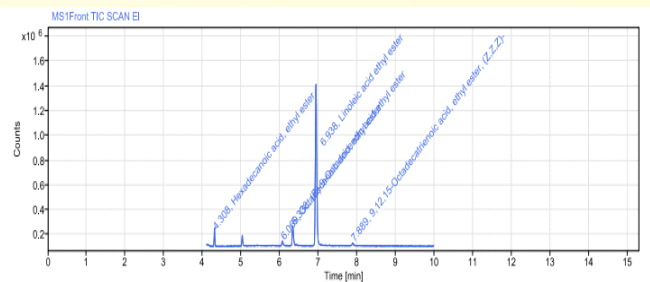
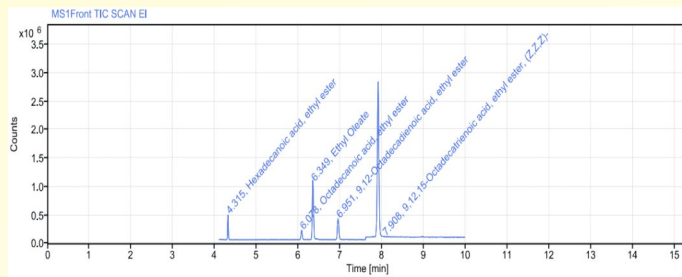


Oil type: 2416 acc. with bushy or semi-erect growth habit, more branching and less plant height (40-70 cm).

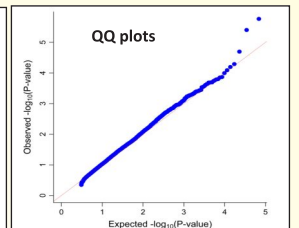
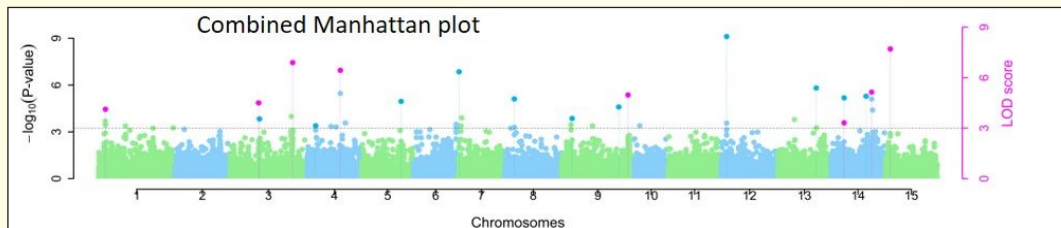
Fibre type/dual purpose: 218 acc. with erect growth habit, less no. of primary branches and plant height >70 cm)



TRAIT SPECIFIC GERMPLASM AND GENOME WIDE ASSOCIATION STUDIES



GC-MS FAME chromatogram of linseed accessions with highest (65.88%) and lowest (1.70%) α -linolenic acid (ALA)

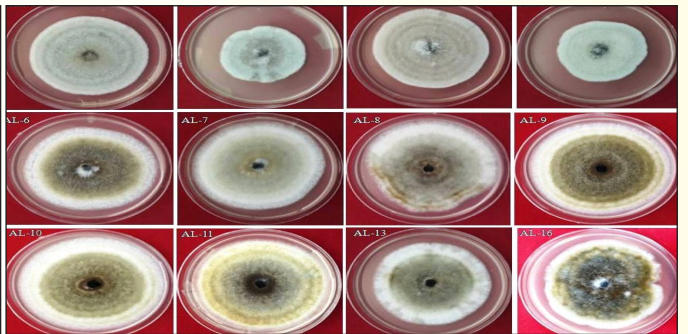


GWAS for Thousand Seed Weight trait using multi-locus methods

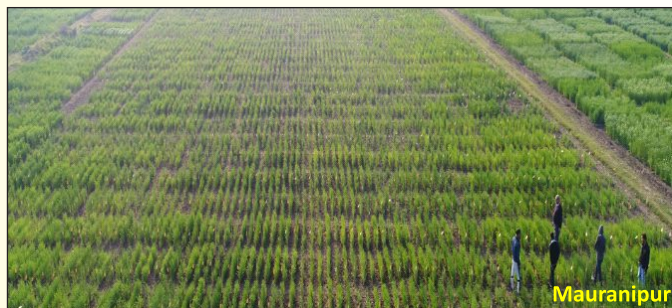
EVALUATION OF LINSEED GERMPLASM FOR MAJOR BIOTIC STRESSES (*Alternaria* blight and budfly)



Screening for *Alternaria* blight at hot spot locations



Cultural and morphological variability of different *A. lini* isolates



Screening against linseed budfly (*Dasyneura lini*) and artificial rearing



EVALUATION FOR MAJOR ABIOTIC STRESSES (DROUGHT AND SALT STRESS)



Screening of linseed germplasm under optimum and alkaline conditions at CSSRI, Karnal



Aerial view of linseed field under irrigated and rainfed conditions at JNKVV RARS

PRE BREEDING AND WIDE HYBRIDISATION



Augmentation of 113 wild accessions

Exploration of indigenous wild *L. mysorens*

In vitro regeneration of rescued embryos

GERMPLASM FIELD DAY AND FIELD VISITS



Linseed Field Day on 6th Feb. 2021



Visit of ICAR Dignitaries on 4th March 2021



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