

PROJECT INFORMATION

ICAR-Network Project on Functional Genomics and Genetic Modification in Crops (ICAR-NPFGGM)

PROJECT OVERVIEW

Funding Agency	ICAR through ICAR-NIPB
Total Outlay	6.6 lakh per year
Duration	2026-31
Single / Multi-Institutional	Multi-Institutional
Lead Centre if Multi-Institutional	ICAR-National Institute Plant Biotechnology, New Delhi
Principal Investigator	Dr Manohara KK
Co-Investigators	None

RATIONALE

Coastal rice growing areas of Goa, Karnataka, and Kerala are frequently affected by salinity during germination, early seedling and at reproductive stage due to tidal ingress, seawater intrusion, and poor drainage in low-lying fields. While most high-yielding varieties show drastic yield loss under these conditions, several traditional landraces (e.g., Korgut, Kagga, Pokkali, etc) display high level of tolerance to salinity and water-logged conditions. Previous studies have focused mainly on seedling-stage salinity tolerance (e.g., Saltol QTL), leaving the reproductive-stage tolerance which is very critical for grain yield stability. The landraces collected from these regions hold untapped alleles for tolerance, which can be identified and deployed through QTL mapping and marker-assisted breeding. Further, ruling popular rice varieties though high yielding but yield very low under low lying coastal saline conditions. Hence, introgression of genes / QTLs for salinity and submergence will enhance tolerance of these ruling varieties. The proposed project will focus on following objectives.

RESEARCH GAPS

Identification of novel donor for salinity tolerance at seedling and reproductive stage. Mapping of genes for salinity tolerance at reproductive stage.

OBJECTIVES

- To phenotype germplasm collections for reproductive stage salinity tolerance under controlled and field conditions.
- Development of mapping populations using selected tolerant × susceptible parents.
- Genotyping and QTL mapping using high-density molecular markers.
- Validation of identified QTLs in diverse genetic backgrounds.
- Introgression of salinity and submergence QTLs into the background of ruling varieties of the region.

ACTIVITIES

- Screening of germplasm collections for reproductive stage salinity tolerance under controlled (microplot) and field conditions. (EC ~ 8 dS/M)
- Crossing tolerant x susceptible parents to develop mapping populations (RILs) through Single Seed Descent method.
- Phenotyping and genotyping of RIL populations under controlled and field conditions
- QTL mapping using SNP genotyping array.
- Marker-assisted introgression of QTLs for salinity (seedling, reproductive) and submergence into elite high-yielding but sensitive varieties.

EXPERIMENTAL DETAILS

Treatment:	Mapping populations, Backcross derived lines
Fertilizer Doses	100-50-50
Variety	NA
Replications:	Two
Observations:	Growth and physiological parameters
GPS Coordinates:	15°29'52.92"N 73°54'59.49"E

EXPECTED OUTPUT

- Identification of novel QTLs for reproductive stage salinity tolerance.
- Broadening the genetic base of breeding populations through use of novel donors for salt tolerance.
- Introgressed elite breeding lines with dual tolerance to salinity and submergence tolerance.

EXPECTED OUTCOME

Increased performance of stress tolerant rice varieties under coastal salinity condition. Increase in farmers income.

FIELD INFORMATION

When the field was developed:	2014 (microplots)
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What are crops being cultivated season-wise:	Kharif - Paddy; Rabi - paddy and pulses
Soil type:	Clay loam
Soil pH, EC, OC:	pH - 7 (Normal Soils); 6-7 (Coastal saline soils); EC-0.5 in normal soil; 4-9 dS/M in coastal saline soils
Soil depth:	NA
Soil NPK and Micronutrient status:	NA
Common pests and diseases:	Pests - Leaf folder, stem borer, BPH, Gundhy bug; Diseases- Bacterial Leaf blast, Blast, Sheath blight