Executive Summary

1. Overall summary of the entire project in Phase IV

Ragi is being considered as one of the most important alternate cereals. This species is known to be the best source of important nutrients like Calcium, Iron and Zinc besides being an excellent source of dietary fibre. Ragi is also known to have low glycaemic index and hence is the most preferred food grain. Despite being a C₄ species with its known drought adaptive abilities, ragi productivity is severely affected by several abiotic stresses, especially drought. Since Ragi, is predominantly cultivated as a rainfed crop, most often on marginal lands by poor farmers, improving ragi productivity is expected to significantly contribute to the betterment of the Socio-Economic status of such farmers. Unlike the major cereal crops like rice and wheat, there has not been adequate research intervention to improve ragi. As a result, the yield potentials, stress resilience and the excellent nutraceutical values of ragi have not been harnessed completely.

In this background, the vision of our network project was that **Improved ragi varieties contribute to food and nutritional security and hence to the income of small and marginal farmers.** Thus, the proposal was developed to achieve this vision on a mission to develop nutritionally superior and climate resilient Ragi cultivars.

The proposal aimed at achieving the goal through FIVE well-defined outcomes

Significant progress has been made under each of these Outcomes which is summarized in this document.

### Outcome 1: Genetic resources for targeted Crop improvement in Ragi

<table>
<thead>
<tr>
<th>Traits</th>
<th>Min</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>Earhead emergence</td>
<td>45.00</td>
<td>79.0</td>
</tr>
<tr>
<td>Prod. Tiller (5pl)</td>
<td>8.00</td>
<td>42.00</td>
</tr>
<tr>
<td>SLW (g/m²)</td>
<td>5.30</td>
<td>100.0</td>
</tr>
<tr>
<td>LA (cm²/5 plants)</td>
<td>1341</td>
<td>16793</td>
</tr>
<tr>
<td>Seed Y (g/5pl)</td>
<td>9.90</td>
<td>172.8</td>
</tr>
<tr>
<td>TDM (g/5p)</td>
<td>57.55</td>
<td>801.0</td>
</tr>
<tr>
<td>HI</td>
<td>0.05</td>
<td>0.45</td>
</tr>
<tr>
<td>1000 seed wt.</td>
<td>1.03</td>
<td>3.56</td>
</tr>
</tbody>
</table>

- A core collection of 620 Ragi germplasm accessions comprising of genotypes, wild relatives and land races was phenotyped for yield potential traits under field conditions. The grains were used to assess the content of antinutritional factor like Phytic acid.
- Genomic DNA of the entire core collection was extracted and the molecular diversity at 35 SSR loci was determined.
- Based on the molecular and phenotypic diversity, a panel of 350 diverse germplasm accessions was assembled amenable for Association genetics for QTL discovery.
- The panel of germplasm was extensively phenotyped for various traits including drought adaptive traits, yield potential traits, nutrition content like Iron and Zinc, antinutrition factors etc.
- Significant genetic variability in root traits, leaf area, total biomass, yield under stress etc were noticed among the panel of germplasm
Low drought susceptibility index was noticed among genotypes with high leaf area and high root, illustrating the relevance of drought adaptive traits.

The phenotyping information will be subsequently used for QTL discovery Genome Wide Association Studies (GWAS).

**Outcome 2: Development of Genomic tools for molecular breeding**

- The whole genome of Ragi, variety: PR202, IC: 479099 was sequenced with a coverage depth of 160X using a variety of sequencing technologies and we assembled the genome with a novel assembly pipeline.
- The novel Hybrid de-novo assembly strategy resulted in covering more than 96% of the estimated 1.2 Gb of the tetraploid finger millet genome.
- The high accuracy of the assembly workflow with a N50 value more than 2.3 Mb led to the mapping of a predicted 62348 single copy genes on to the genome.
- The presence of exact two copies of some of the know genes like PEP carboxylase enhanced the confidence on the accuracy of the assembled genome.
- The genome of the diploid progenitor, E. indica has been sequenced with 60x coverage using Illumina NextSeq sequencer and assembled with platanus de novo assembler (ver. 1.2.4). The total assembled genome size was 521 Mb and N50 was 21 kb with 26,586 genes predicted. Based on this progenitor genome, we succeeded in phasing the homeologs of finger millet genome.

**Outcome 3: Evidence that Ragi can provide high Fe and Zn to vulnerable populations**

- Robust phenotyping technique for the quantification of Phytic acid and other anti-nutritional factors were developed and standardized.
- Significant genetic variability in phytic acid, tannins were noticed among the core germplasm as well as the Association mapping panel.
- Specific Ragi genotypes differing in Iron content with significant differences in phytic acid have been identified for further bioavailability studies.
- Kinetics of Phytic acid degradation during germination was determined. Genotypes significantly differed in the rate of phytic acid degradation during germination.

**Outcome 4: Assessment of Ragi production system, markets and policy**

- Low yield due to drought coupled with low price leads to reduced returns to farmers. Hence there is a need to develop drought adaptive cultivars with increased productivity to enhance the Socio Economic status of marginal farmers.
- TFP and yield gap analysis indicate that there is a need for intensifying extension support to enable farmers to achieve financially viable yields, with investment in machinery and irrigation projects.
• Procurement price must be fixed looking into the cost of production of rainfed Ragi and an enhancement of minimum support price is crucial in encouraging farmers to cultivate ragi.
• The potential for export of finger millet in the form of grain, flour and value added products needs to be explored. As domestic consumption of Ragi is on a decline, awareness programs need to be initiated to sustain the crop.

**Outcome 5: Strong inter-disciplinary linkage among the partners established**

• A robust common mailing system- B Fabric was established and is being effectively used for communications of technical information among all partners.
• Effecting human resource exchange was achieved through the visit of two Post Doctoral associates to Switzerland for Two months. One additional 2-month visit of one Post-Doctoral associate was undertaken to assist in whole genome re-sequencing of the panel of germplasm.
• One week interactive training was organised during August, 2017 which was attended by three faculty from India

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