International Conference on Innovations to Transform Drylands

21–23 February 2023

ICRISAT, Hyderabad, India

Abstract Book

Organised by

ICRISAT
INTERNATIONAL CROPS RESEARCH INSTITUTE FOR THE SEMI-ARID TROPICS

ICRISAT 50

INTERNATIONAL YEAR OF MILLETS 2023

Co-organisers

कृषि एवं किसान कल्याण मंत्रालय
MINISTRY OF AGRICULTURE AND FARMERS WELFARE
सत्यमेव जयते

भाकृअनुप ICAR

AGRA
Sustainably Growing Africa's Food Systems

T6PP021:

Towards trait mapping and comprehensive transcriptome profiling to uncover blast disease resistance mechanism in finger millet.

Naik JV[1,2], Joshi P[1], Barmukh R[1], Ojulong H[3], Sharma R[1], Vetriventhan M[1], Sagurthi SR[2], Gupta SK[1] and Kudapa H[1]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India

[2]Osmania University, Hyderabad, India

[3]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Nairobi, Kenya

*Correspondence: himabindu.kudapa@icrisat.org

Finger millet [*Eleusine coracana* (L.) Gaertn.] is a key C4 grain crop cultivated in southern Asia and eastern Africa. Its grain possesses exceptional nutritional value with climate-resilience properties. Finger millet blast disease, caused by *Pyricularia oryzae*, is a serious constrain of crop production and is threatening global food security especially in the arid and semi-arid regions. This disease causes leaf, neck and finger blast which results upto 80% yield losses. However, the genetic mechanism underlying blast disease resistance in finger millet remains largely unknown. In the present study, QTL mapping and RNA-seq approaches are employed to identify genomic regions and molecular mechanisms associated with blast resistance in finger millet. Two mapping populations using contrasting parental genotypes for blast disease resistance, VR 708 (susceptible) IE 4497 (resistant) and IE 5306 (susceptible) IE 4497 (resistant) have been made using novel hot water emasculation crossing method. F_1 seed was harvested and hybridity confirmation of F_1s is underway using the Quality Control 48 SNP panel developed at ICRISAT. QTL analysis will be performed using $F_{2:3}$ lines to detect genomic loci controlling blast resistance. Also, transcriptomics of blast resistant and susceptible genotypes to identify differentially expressed genes (DEGs) is being performed using RNA-seq approach. Functional analysis of DEGs by gene ontology (GO) and KEGG pathway analysis will be performed to gain insights into the biological processes and molecular mechanisms associated with blast disease resistance. SNPs and indels associated with potential candidate genes identified through combined QTL mapping and transcriptome analysis will be targeted for marker development. Findings from this study will serve as a valuable resource for developing blast resistant finger millet varieties through genomics assisted breeding.

T6PP022:

Rapid mapping of genomic regions and candidate genes governing seed protein content in chickpea using QTL-seq

Goura M[1,2], Macha MR[3], Kanuganahalli V[1], Padherla LK[2], Barmukh R[1], Mangala RS[2], Gangashetty P[1] and Kudapa H[1]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India

[2]Acharya N.G Ranga Agricultural University, S.V Agricultural College, Tirupati, India

[3]Malla Reddy University, Hyderabad, India

*Correspondence: himabindu.kudapa@icrisat.org

Protein is an important component of nutrition in human diet. It can be obtained from plants and animals, but protein obtained from plants is cheaper and healthier than from animals. Inadequate intake of protein leads to Protein Energy Malnutrition (PEM). Vulnerable people from South-Asia and Sub-Saharan Africa cannot afford animal-based protein and hence they often experience PEM. To combat PEM, consumption of plant-based protein is an affordable and more sustainable approach. Chickpea (*Cicer arietinum* L.) is a major legume crop cultivated in the semi-arid tropics and is a rich source of seed protein content (SPC) which varies from 17-25% among different accessions. Improvement of SPC in high yielding chickpea varieties will meet the demand of food and nutritional security. Identification of candidate genes/ alleles governing SPC is crucial in genomics assisted breeding for chickpea quality trait improvement. In the present study, we intend to identify genomic regions and candidate genes governing SPC in chickpea using QTL-seq approach. Crossing the parental lines (ICCV 10 × ICC 9848 and NBeG 119 × ICC 6263) for SPC yielded 49 and 15 F1 seeds, respectively. Hybridity confirmation is in progress and true F1s will be advanced to F2:3 generations. Phenotyping for SPC will be performed using F2:3 seeds, and lines with high and low protein bulks will be identified. WGS of bulks and parental lines, followed by a comprehensive analysis of sequencing data will facilitate the identification of genomic regions associated with SPC in chickpea. Furthermore, potential genes underlying the genomic regions and SNPs/indels associated with SPC will be identified. This study facilitates understanding of molecular mechanisms underlying SPC and marker development for use in molecular breeding program for development of high yielding and protein rich chickpea varieties.