

Shanghai Cooperation Organization- 1st Young Scientists Conclave (SCO-YSC 2020) A virtual event organsied in India at CSIR-IICT, Hyderabad Theme: Shaping SCO-STI Partnership: Young Scientists Perspectives

SCO-Young Scientist Profile

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Details of research work carried out in S&T (limit to 200 words)

The research work in the field of S&T and Innovation encompasses major contribution towards chickpea genomics-assisted breeding. These include various genetic and genomic resources development and devising of different efficient integrated genomic strategies for implementation towards genome-wide genetic dissection of complex quantitative yield-component pod number (PN), seed number (SN) and 100-seed weight (SW) traits for marker-assisted chickpea improvement. Developed genetic resources include an association panel (365 chickpea accessions) and three advanced generation bi-parental mapping populations; while, genomic resources comprise larger set of experimentally validated transcription factor (TF) genes-derived microsatellite markers and genotyping-by-sequencing (GBS) assay-based SNPs (single nucleotide polymorphisms) at genome wide level. The devised and successfully implemented various novel efficient cost-effective integrated genomic strategies on the other hand entail combination of different association (genome-wide and candidate gene-based association study) and genetic mapping approaches coupled with transcript profiling and high-resolution molecular haplotyping through deployment of developed genetic and genomic resources. Collectively, all these delineated several functionally relevant novel allelic variants and multiple genomic regions harboring PN, SN- and SW-associated candidate QTLs (quantitative trait loci)/ genes and alleles (haplotypes), including superior haplotypes-containing TFs and other trait-regulatory genes for marker-assisted chickpea improvement. These results are now being translated into improved high-PN/SN-yielding chickpea cultivars

Associated SCO-YSC Theme: Agriculture and Food Processing

Statement of Innovation (Brief information on new innovative ideas including startup / entrepreneurs-limit to 150 words)

Currently, deploying integrative genomics, genetics and physiology approaches to dissect drought tolerance for improving chickpea yield potential. Chickpea is an important food legume crop that complements protein and other essential nutrient requirement of humans. It is predominantly rain-fed crop, mostly grown on marginal lands with residual soil moisture in arid/semi-arid regions. The crop therefore is largely affected by terminal drought stress of varying intensities and frequencies that hit the very crucial reproductive stage, determining its yield. Evidences suggest that physiological traits (e.g. canopy conductivity and leaf canopy architecture traits) which allow water conservation during early cropping cycle and makes soil water available for use at grain filling stage can potentially increase yield under drought. However, limited efforts are underway towards chickpea genomics-assisted breeding based on physiological approaches to improve their yield. Henceforth, this work aims to improve tolerance and achieve higher yield stability under drought through application of integrative physiological and genomics-assisted breeding approaches in chickpea.

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Major awards/ Achievements (Upto 3 awards)

- 1. Jawaharlal Nehru Award for P.G. Outstanding Doctoral Thesis Research in Agricultural and Allied Sciences (Biotechnology)-2019 by the Indian Council of Agricultural Research (ICAR), New Delhi.
- 2. NASI-Young Scientist Platinum Jubilee Award 2019 in Plant Sciences, Agriculture and Environment from the National Academy of Sciences, India (NASI), Prayagraj.
- 3. INSPIRE (Innovation in Science Pursuit for Inspired Research) Faculty Fellowship Award-Jan 2018, sponsored by the Department of Science & Technology, Ministry of Science and Technology, Government of India (GoI), New Delhi, for 5 years (2018-2023).

Possible collaboration with SCO countries (limit to 100 words)

Grain legumes offers an unparalleled solution for ensuring worldwide adequate nutritional food security at an affordable rate through efficient and sustainable food production system. However, global climate variabilities heavily impact their productivity which requires attention for sustainable and balanced production This widens the scope for legume genetic improvement through multidisciplinary research approaches. Keeping these in view, we are into generation of various genomic resources including high-throughput genome assemblies and genotyping datasets useful for genomics-assisted breeding applications. Nonetheless, genomics-assisted crop improvement requires high-throughput precise multi-locational phenotyping datasets for fruitful prediction of various biotic and abiotic traits. This provides avenues for collaboration with several institutes within India as well as other SCO countries.

Key words (relevant to research work conducted as well as proposed innovation, 5-6 words)

Chickpea, transcription factor genes-derived microsatellite markers, genotyping-by-sequencing (GBS) assay-based SNPs, genome-wide association study, physiological traits, genomics-assisted crop improvement