

## IDT7-065 | Identification of climate resilient pigeonpea [*Cajanus cajan* (L.) Millsp.] genotypes

Muniswamy S<sup>1\*</sup>, Ramesh<sup>1</sup>, Mahalinga D.M<sup>1</sup>

<sup>1</sup>All India Coordinated Research Project on Pigeonpea, ARS Kalaburagi, Karnataka, India.

\*E-mail: muniswamygp@gmail.com

Pigeonpea [*Cajanus cajan* (L.)] is the important grain legume crop under rainfed Agriculture. The goal of this study was to identify climate resilient pigeonpea genotypes. During *kharif*-2011 evaluated 443 genotypes under both irrigated and rainfed condition and recorded various quantitative traits. Based on the *per se* performance under stress conditions 50 genotypes were promoted for evaluation during *kharif*-2012 and evaluated for various quantitative traits. During *kharif*-2013, based on their *per se* performance 40 genotypes were evaluated and were divided in to two groups based on the maturity *viz.*, <170 days and > 170 days maturity group. Each group consist of 21 and 19 genotypes respectively both were sown under irrigated and rainfed condition and evaluated for various quantitative traits. The same two

maturity groups consisting of total 40 genotypes were evaluated during *kharif*-2014 and *kharif*-2015 to study stability in their performance. Out of 40 genotypes 18 genotypes were identified as well performing and stable lines. These 18 genotypes seeds will be multiplied during *kharif*-2016 and they will be evaluated for irrigated and rainfed condition. The best performing lines are Bennur local, JKM-189, JKM-7, RVK-275, WRP-1, AKT-9913 *etc.* which we can call as climate resilient genotypes. Two years field screening for *Fusarium* wilt and SMD yielded resistant genotypes for these diseases. However only one (JSA 59) out of these genotypes showed multiple disease resistance reaction for both *Fusarium* wilt and SMD Hence, this genotype can be used directly as a variety or choice of parent for hybridization programme.

## IDT7-066 | Phenotypic and genetic dissection of water stress adaptations in pearl millet (*Pennisetum glaucum*)

Murugesan Tharanya<sup>1,2</sup>, Jana Kholova<sup>1</sup>, Kaliamoorthy Sivasakthi<sup>1,2</sup>, Vincent Vadez<sup>1\*</sup>, Deepmala Seghal<sup>3</sup>, Charles Tom Hash<sup>4</sup>, Basker Raj<sup>1</sup>, Rekha Baddam<sup>1</sup>, Thiyagarajan Thirunalasundari<sup>2</sup>, Rattan Yadav<sup>3</sup>

<sup>1</sup>International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Crop Physiology Laboratory, Patancheru 502324, Telangana, India.

<sup>2</sup>Bharathidasan University, Tiruchirappalli 620 024, Tamilnadu, India.

<sup>3</sup>Institute of Biological, Environmental and Rural Sciences (IBERS), Aberystwyth University, Aberystwyth SY23 3EB, UK.

<sup>4</sup>International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), ICRISAT Sahelian Center, Pearl Millet Breeding, BP 1204, Niamey, Niger.

\* E-mail: v.vadez@cgiar.org

Pearl millet is an important staple food for farming communities across semi-arid tropical systems of South Asia and Sub-Saharan Africa where production suffers uncertain precipitation. This work is undertaken under the premise that maximizing grain yield under water-limited conditions depends on both maximizing water use and ensuring water availability for the grain filling period. Here we discuss the phenotyping methods targeting the variability in plant water use strategies which determine the crop production success in water-limited environments. A fine-mapping population of pearl millet, segregating within the previously identified drought tolerance quantitative trait locus (QTL) on chromosome 2 (LG02), was tested across different experimental environments (pot culture, high-throughput phenotyping platform (LeasyScan), Lysimeter, and Field). Recombinants were then analyzed for traits

at different levels of plant organization, ranging from water-use traits (transpiration rate, leaf area, plant organ dry weights, etc.) to crop production and agronomic traits (grain yield, tiller number, harvest index, etc.) The linkages between traits across the experimental systems were analyzed, using principal component analysis (PCA) and QTL co-localization approach. The functional relevance of the phenotyping systems was traced by PCA analysis. Furthermore, we found four regions within the LG02-QTL underlying substantial co-mapping of water-use related and agronomic traits. These regions were identified across the experimental systems and justified linkages between water-use traits were phenotyped at lower level of plant organization to the agronomic traits assessed in the field. Therefore, the phenotyping systems at ICRISAT are validated and well set to accelerate crop breeding for drought adaptations.