

## IDT7-073 | Phenotypic variability of drought-avoidance shoot and root phenes and their relationships with yield under drought and low P conditions in cowpea

Belko N<sup>1\*</sup>, Boukar O<sup>1</sup>, Fatokun C<sup>2</sup>, Togola A<sup>1</sup>, Chamarthi S<sup>1</sup>, Moukoumbi Y<sup>1</sup>, Abberton M<sup>2</sup>

<sup>1</sup> International Institute of Tropical Agriculture, IITA Kano Station, Nigeria

<sup>2</sup> International Institute of Tropical Agriculture, IITA-HQ Ibadan, Nigeria

\*E-mail: N.Belko@cgiar.org

Cowpea (*Vigna unguiculata* (L.) Walp.) is the most important grain legume crop cultivated by resource-limited farmers in marginal lands of Sub-Saharan Africa's dry savannahs. Although the crop is well adapted to this region, it could benefit from genetic improvement aimed at enhancing its tolerance to drought and low soil fertility. Cowpea minicore collection and breeding lines were phenotyped under both screenhouse and field conditions to (i) assess genotypic differences in water-saving shoot traits and root system architecture and (ii) evaluate the contributions of these traits to crop yield and adaptation to drought and low phosphorus. The parameters considered included whole plant transpiration rates, canopy temperature, chlorophyll content, ad-

ventitious and basal root numbers and growth angle. Correlation analysis revealed significant positive relationships between the plant shoot and root traits and the crop yield under stress conditions. Overall, Dan'lla, IT86D-1010, IT98K-205-8, IT97-499-35, IT99K-573-2-1, TVu-9486, TVu-14788, TVu-15391, TVu-11986, and TVu-14676 with conservative soil water-use attributes and steep root systems as well as IT98K-1111-1, IT07K-318-33, IT99K-494-6, TVu-9797, TVu-11982 and TVu-15055 with shallow root systems are potential for adaptation to drought and low P, respectively. These results reveal the possibility for improving the productivity of cowpea in water deficit and poor soil environments by exploiting its genetic potentials.

## IDT7-074 | Molecular mapping of seed protein content in pigeonpea – a drought tolerant crop of the semi-arid tropics

Obala J<sup>1,2</sup>, Saxena RK<sup>1</sup>, Singh VK<sup>1</sup>, Kale SM<sup>1</sup>, Garg V<sup>1</sup>, Kumar V<sup>1</sup>, Sameerkumar CV<sup>1</sup>, Tongoona P<sup>2</sup>, Sibiyi J<sup>2</sup>, Saxena KB<sup>1</sup>, Varshney RK<sup>1\*</sup>

<sup>1</sup> International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India

<sup>2</sup> School of Agricultural, Earth and Environmental Sciences, University of KwaZulu-Natal, Pietermaritzburg, South Africa

\*E-mail: r.k.varshney@cgiar.org

Pigeonpea is a uniquely drought and heat tolerant crop that provides a major source of dietary protein to nearly a billion people in the tropical and semi-arid tropics of the world. Despite its importance as a source of dietary protein the genetic control of its seed protein content (SPC) is poorly understood. The present study used high density linkage maps to identify quantitative trait loci (QTL) associated with SPC and its relationship with 100-seed weight (HSW), seed yield (SY), days to first flower (DTFF) and growth habit (GH). Five F2 mapping populations segregating for SPS including ICP 11605 × ICP 14209, ICP 8863 × ICP 11605, HPL 24 × ICP 11605, ICP 5529 × ICP 11605 and ICP 8863 × ICPL 87119 were genotyped using genotyping-by-sequencing and phenotyped for the traits. The average inter-marker distance on the population-specific maps varied from 1.6cM to 3.5cM. On the basis of the population-specific and consensus

linkage maps, 48 main effect QTLs (M-QTLs) with phenotypic variance explained (PVE) ranging from 0.7 to 23.5% were detected across five populations, of which 15 M-QTLs were major (PVE ≥ 10). Twenty seven of the M-QTLs could be collapsed into six consensus QTL regions. In addition, 34 epistatic QTLs (E-QTLs) with PVE ranging from 6.3% to 69.8% were detected across populations. Co-localization of M-QTLs and E-QTLs affecting SPC and the agronomic traits explained the genetic basis of the significant (P < 0.05) correlations of SPC with HSW (r<sup>2</sup> = 0.22 to 0.30), SY (r<sup>2</sup> = -0.18 to -0.28), DTFF (r<sup>2</sup> = -0.17 to -0.31) and GH (r<sup>2</sup> = 0.18 to 0.34). The quantitative nature of genetic control of SPC and its relationship with agronomic traits suggest that marker-assisted recurrent selection or genomic selection would be effective for the simultaneous improvement of SPC and other important traits.