**Evolution, development, and application of the DArTag common bean mid-density platform in a breeding program to develop rapid cooking beans in Africa**

Male AS.1, Saradadevi R2, Amongi W1, Nkalubo S3, Tumsa K4, Misango S5, Ndabashinze B6, Uwera A7, Mbiu J8, Rubyogo JC9, Suarez D10, Huttner E11, Siddique K2, Cowling WA2, Mukankusi C1,

*E-mail of corresponding author: a.m.ssekamate@cgiar.org*

*1 Alliance of Bioversity International & CIAT, Kawanda, Uganda*

*2 The UWA Institute of Agriculture, The University of Western Australia, Perth, Australia*

*3 National Crop Resources Research Institute (NaCRRI), Namulonge, Uganda*

*4 Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, Ethiopia*

*5 Kenya Agricultural and Livestock Research Organization (KALRO), Kakamega, Kenya*

*6 Institut des Sciences Agronomiques du Burundi (ISABU), Bujumbura, Burundi*

*7* *Rwanda Agriculture and Animal Resources Development Board (RAB), Kigali, Rwanda*

*8 Tanzanian Agricultural Research Institute (TARI), Maruku, Bukoba, Tanzania*

*9 Pan Africa Bean Research Alliance (PABRA), Nairobi, Kenya*

*10 Molecular Plant Breeding, Institute of Agricultural Sciences, ETH Zurich, Switzerland*

*11 Australian Centre for International Agricultural Research (ACIAR), Canberra, Australia*

The common bean mid-density single nucleotide polymorphism (SNP) panel was developed from whole genome re-sequencing (WGS) and genotyping by sequencing (GBS) of more than 1,700 breeding lines and landraces from Africa and America. These lines were characterised for various biotic and abiotic stresses, agronomic and commercial qualities, and inter-specific introgressions. A matrix of more than 40 million SNPs was generated making it suitable for drought and heat tolerance, pest and disease resistance, cooking time, and diversity studies. This matrix was later filtered using biological and technical replicates to remove defective markers resulting in a DArTag SNP array of 1,862 markers in the mid-density SNP genotyping panel (MDSG)1.

Genomic selection with MDSG for rapid cooking biofortified common beans is underway in an East African breeding program based at the Alliance of Bioversity International and CIAT, Uganda, with regional testing at national agricultural research systems in six countries. A genomic relationship matrix based on MDSG markers has been used to develop accurate genomic breeding values for cooking time, seed iron and zinc, grain yield, and other traits2. These accurate genomic breeding values have been incorporated into an optimised selection index for optimal contributions selection to optimise crossing designs, and results show significant genetic gains in these traits (see Saradadevi et al, abstract at this conference). Thus, MDSG is helping to overcome the biggest barrier to common bean consumption in Africa - the long soaking and cooking times of beans.

***References:***

*[1] Ariza-Suarez, D., et al. (2023). Genetic analysis of resistance to bean leaf crumple virus identifies a candidate LRR-RLK gene. Plant J, 114: 23-38. https://doi.org/10.1111/tpj.15810*

*[2]**Saradadevi, R., et al. (2021). Multivariate genomic analysis and optimal contributions selection predicts high genetic gains in cooking time, iron, zinc, and grain yield in common beans in East Africa. Plant Genome 14(3): e20156.*