ICLGG 2024

Brisbane/Meanjin, Australia

11th International Conference on Legume Genetics and Genomics (ICLGG)

30 September – 3 October 2024
Brisbane Convention & Exhibition Centre

POSTER
ABSTRACT BOOK

www.iclgg2024.org

P193

Genomic selection for different agronomic traits in ICARDA chickpea breeding program

Hamwieh A1, Jighly A2, Kaur S3, Istanbuli T1
1. International Center for Agricultural Research in the Dry Aras (ICARDA PO Box. 114/5055, Beirut, Lebanon.
2. SuSTATability statistical solutions, Melbourne, Australia
3. Agriculture Victoria, AgriBio, Centre for AgriBioscience, Department of Energy, Environment and Climate Action, 5
Ring Road, Bundoora, VIC 3803, Australia

Chickpea (Cicer arietinum) is a crucial legume crop for food security and agricultural sustainability. Genomic selection (GS), an emerging breeding approach, enables early selection by predicting the genetic value of individuals using genome-wide markers. This study investigated the prediction accuracy of key agronomic traits using ICARDA chickpea breeding germplasm. The training population for this study was comprised of 297 genotypes, where 48% were breeding lines, 22% recombinant inbred lines (RILs), 14% of varieties, landraces, and wild types. Approximately 8% of the training population represented materials imported From Australia and India. The germplasm was genotyped using 1,922 single nucleotide polymorphism (SNP) markers covering the eight chromosomes. Field evaluation was conducted over two years (2023 and 2024) at Terbol station, Lebanon, using a replicated Alpha Lattice design. Key agronomic traits assessed included 100 seed weight (100SW), flowering time (FLWR), maturity time (MAT), and plant height (PLHT). Grain and biological yield were also measured. The prediction accuracy was calculated with and without fitting the genotype by environment interaction in the prediction model with two cross-validation strategies (CV1: predicting new individuals; and CV2: predicting complete data across environments from unbalanced field trials). The results demonstrated moderate heritability values for 100SW, FLWR, MAT, and PLHT, and high prediction accuracy values ranging from 0.51 to 0.81 for CV1, and from 0.63 to 0.90 for CV2. However, yield and yield component traits exhibited relatively lower heritabilities and accuracies ranging from 0.38 to 0.48 for CV1, and from 0.37 to 0.51 for CV2. These findings underscore the potential of GS to enhance the efficiency and accuracy of chickpea breeding programs to achieve better yield stability and adaptability in chickpea across diverse growing conditions.