GRAIN YIELD STABILITY AND GENETIC DIVERSITY AMONG 30 ACCESSIONS OF COMMON BEAN (*Phaseolus vulgaris* L.) USING AGROMORPHOLOGICAL CHARACTERS AND DArT SEQUENCING

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ABSTRACT

Common bean (*Phaseolus vulgaris* L.) is an important crop planted for its edible dry seeds, immature pods and fodder. The potentials of common bean accessions in the Genebank have not been fully explored. This study assessed the grain yield stability of common bean accessions, evaluated the representativeness and discriminatory ability of locations in multi-environment trials, and assessed the genetic diversity among Thirty (30) common bean accessions using Diversity Array Technology (DArTSeq). Field trials were conducted at three International Institute of Tropical Agriculture research fields, Ibadan (7°48'N3°89'E), Ikenne (6°92'N3°73'E) and Mokwa (9°29'N 5°06'E), using a Randomized Complete Block Design in three replications. Seventeen agro-morphological traits were measured from five randomly selected plants per accession. The agro-morphological data were subjected to combined analysis of variance, principal component analysis (PCA), FASTCLUS, Genotype plus Genotype by Environment biplot and Additive Main Effects and Multiplicative Interaction models. Deoxyribonucleic acid extraction and Diversity Array Technology Sequence Single Nucleotide Polymorphism marker analysis were performed to evaluate molecular genetic diversity. Out of 30,893 SNPs identified, 13,735 SNPs were retained after filtering and distributed across all eleven common bean chromosomes. The study revealed significant Genotype by Environment Interaction and variability among the accessions for measured characters under the three environmental conditions. The broad sense heritability values were observed to be 95.98% for seed width, 89.88% for 100-seed weight, 85.05% for physiological maturity, and 82.07% for days to harvesting. These figures suggest a significant genetic influence and underscore their reliability for selection in a breeding

programme. Results identified six accessions (TPv-791, TPv-769, TPv-759, TPv-928, TPv-773 and TPv-902) that have consistent yield performance. The DArTseq analysis identified significant genetic diversity, with PCA revealing four distinct clusters among the accessions. TPv-866 and TPv-882 from Cluster 1 showed high positive values in PC2, while accessions TPv-784 and TPv-902 from Cluster 3 exhibited negative values in PC2 and PC3, indicating significant genetic divergence. Two accessions (TPv-781 and TPv-834) in Cluster 4 had high positive PC1 values, suggesting the potential for desirable agronomic traits. The study revealed significant genetic diversity and genotype by environment interaction among common bean accessions from Burundi, with six stable accessions identified for breeding programme. These findings underscore the potential for enhancing yield stability. This study effectively explored genetic diversity and yield stability in common bean accessions, identifying six stable varieties with desirable traits, which can enhance future breeding programme. The result recommended that identified key agro-morphological traits that contributed to generic variation in the PCA be targeted for breeding efforts while the stable accessions can be focused on for future breeding programme aimed at further enhancing yield stability. In conclusion, by integrating both genetic diversity and yield stability analyses, this study provides essential insights for developing improved common bean varieties with enhanced adaptability and productivity.