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Quantitative trait loci mapping for drought tolerance in an Andean recombinant inbred population of common bean (*Phaseolus vulgaris*)

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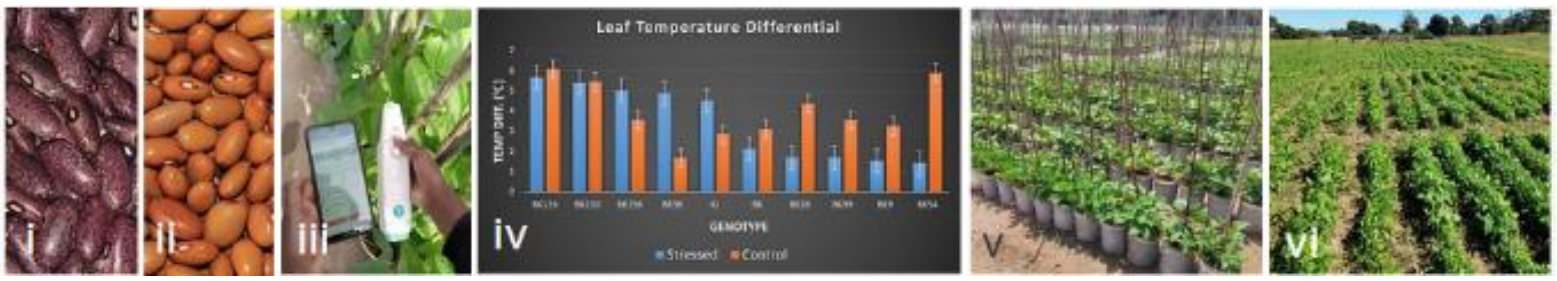
Abstract

Drought is a major abiotic common bean (Phaseolus vulgaris L.) production constraint worldwide. There is limited knowledge on the role and relative importance of agronomic and morphophysiological traits as well as the genetic architecture of drought tolerance of Andean common bean. The objectives of this study were to (i) determine the role and relative importance of agronomic and morpho-physiological traits in drought tolerance of the Andean gene pool of common beans, and (ii) identify common bean genomic regions associated with these traits. In this study, field and pot experiments were conducted at the University of Zambia (UNZA) (28˚20′ E, 15˚ 25′ S) research farm, Golden Valley Research Trust (GART) (28″ 10′ E, 14″ 50′ S), and Zambia Agricultural Research Institute - Kabwe (28° 50′ E S, 14° 39′ S). In the first objective, 20 Andean genotypes were evaluated with three field trials and one pot experiment. Significant correlations of seed yield with Harvest index (HI), pod harvest index (PHI), and carbon isotope discrimination (CID) under drought stress (DS) were observed, which suggested the important role of photo-assimilate partitioning efficiency (measured by PHI and HI) and water use efficiency (measured by CID) in the observed drought tolerance. The genotypes Kibala, OAC Inferno and Kijivu showed high seed yield and low CID under DS, and were categorized as water savers and recommended for use in environments prone to severe intermittent or terminal

drought. Nine genotypes (Pink Panther, Kardinal, H9659-27-10, Mrondo, PI638816, G17913, PR0737, Krimson, and H9659-27-1) showed high seed yield and high CID under DS, and were categorized as water spenders and recommended for use in environments prone to intermittent drought. Drought tolerant genotypes including Krimson, OAC Inferno and SEQ11 showed significantly lower electrolyte leakage than the drought tolerant checks under DS indicating that these genotypes had lower cell membrane damage under DS, which could be one of the physiological mechanism that could explain their observed drought tolerance. In the second objective, 155 F4:5 recombinant inbred lines (RILs) derived from a cross of Kijivu, which was identified as drought tolerant in this study and Bukoba, a drought susceptible Andean genotype were used to map the quantitative trait loci (QTL) for drought tolerance. These RILs were evaluated for drought tolerance in four field experiments conducted in three locations. In addition, a pot trial was conducted to assess the photosynthetic response of the 155 RILs under drought stress. The RIL population was genotyped with 12,000 Single Nucleotide Polymorphism (SNP) markers and composite interval mapping was conducted. QTL "hotspots" for drought tolerance were identified on chromosomes Pv06 (21.0 Mbp -25.0 Mbp), Pv07 (2.0 Mbp - 9.0 Mbp) and Pv10 (37.0 Mbp - 41.0 Mbp). These three genomic regions showed extensive co-localization of seed yield, geometric mean, seed weight, partitioning indices, photosynthetic traits, pod load, and drought susceptibility index. These QTL overlapped with previously identified genomic regions for drought tolerance, suggesting that genes underlying these QTL have stable expression from drought tolerance in diverse environments and genetic backgrounds. Some of the identified QTL are novel. In this study, it is evident that there is complex genetic architecture of drought tolerance in the Andean gene pool of common bean involving several loci with additive gene action. The three "QTL hotspots" could be targeted for use in marker-assisted selection to enhance selection efficiency for drought tolerance in the Andean gene pool of common bean.

Publication

Hamabwe, S.M., Otieno, N.A., Soler-Garzón, A., Miklas, P.N., Parker, T., Kramer, D.M., Chattopadhyay, A., Cheelo, P., Kuwabo, K. and Kamfwa, K., 2023. Identification of quantitative trait loci for drought tolerance in Bukoba/Kijivu Andean mapping population of common bean. *Theoretical and Applied Genetics*, *136*(11), pp.1-17.



Parental lines for the genetic mapping population: kijvu (i) and Bukoba (ii); Ms Swivia measuring leaf temperature of different bean varieties under water stresses conditions and non stressed conditions (control; iii); results of the leaf temperature meaurments (iv); pot trials (v) and field trials (vi).