

# Dissecting the root phenotypic and genotypic variability of the Iowa mungbean diversity panel

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## Abstract

Mung bean [*Vigna radiata* (L.) Wilczek] is a drought-tolerant, short-duration crop, and a rich source of protein and other valuable minerals, vitamins, and antioxidants. The main objectives of this research were (1) to study the root traits related with the phenotypic and genetic diversity of 375 mung bean genotypes of the Iowa (IA) diversity panel and (2) to conduct genome-wide association studies of root-related traits using the Automated Root Image Analysis (ARIA) software. We collected over 9,000 digital images at three-time points (days 12, 15, and 18 after germination). A broad sense heritability for days 15 (0.22–0.73) and 18 (0.23–0.87) was higher than that for day 12 (0.24–0.51). We also reported root ideotype classification, i.e., PI425425 (India), PI425045 (Philippines), PI425551 (Korea), PI264686 (Philippines), and PI425085 (Sri Lanka) that emerged as the top five in the topsoil foraging category, while PI425594 (unknown origin), PI425599 (Thailand), PI425610 (Afghanistan), PI425485 (India), and AVMU0201 (Taiwan) were top five in the drought-tolerant and nutrient uptake “steep, cheap, and deep” ideotype. We identified promising genotypes that can help diversify the gene pool of mung bean breeding stocks and will be useful for further field testing. Using association studies, we identified markers showing significant associations with the lateral root angle (LRA) on chromosomes 2, 6, 7, and 11, length distribution (LED) on chromosome 8, and total root length-growth rate (TRL-GR), volume (VOL), and total dry weight (TDW) on chromosomes 3 and 5. We discussed genes that are potential candidates from these regions. We reported beta-galactosidase 3 associated with the LRA, which has previously been implicated in the adventitious root development via transcriptomic studies in mung bean. Results from this work on the phenotypic characterization, root-based ideotype categories, and significant molecular markers associated with important traits will be useful for the marker-assisted selection and mung bean improvement through breeding.

# Dissecting the root phenotypic and genotypic variability of the Iowa mungbean diversity panel

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## Abstract

Mungbean (*Vigna radiata* (L.) Wilczek) is a drought-tolerant, short-season crop taking between 60-90 days from planting to harvest, with a composition of 22-28% protein, 1-1.5% fat, 60-65% carbohydrates, and valuable minerals, vitamins, and antioxidants. We explored the phenotypic and genotypic diversity of 367 mungbean genotypes in the Iowa diversity panel by analyzing over 9000 images collected at three-time points (days 12, 15, 18), generated using a hydroponic system, with root structure architecture (RSA) traits extracted using the Automated Root Image Analysis (ARIA) software. Using association studies, we identified significant markers associated with lateral root angle (LRA) and length distribution (LED). Day 15 broad-sense heritabilities (H) ranged from 0.22-0.73. Lateral Root Angle (LRA) and width (WID) had the lowest and highest heritabilities at 0.22 and 0.73 respectively. Broad sense heritabilities for days 15 and 18 were higher than those for day 12. Using root ideotype classification, genotypes PI425425 (India), PI425045 (Philippines), PI425551 (Korea), PI264686 (Philippines), PI425085 (Sri Lanka) emerged top five in the topsoil foraging category while PI425594 (Unknown origin), PI425599 (Thailand), PI425610 (Afghanistan), PI425485 (India), AVMU0201 (Taiwan) were top five in the “steep, cheap, and deep” ideotype. We identified candidate genotypes that can now be advanced to the greenhouse or field for further testing. Taken together, the wide phenotypic variation, the ideotypes after field evaluation, and the significant markers can be utilized as tools for marker-assisted selection and crop improvement for mungbean breeding.