

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.