Dissecting the genetics of canopy dynamics in mungbean using longitudinal modelling of UAV-derived traits

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Mungbean is a high-value export pulse crop grown in subtropical farming systems globally. Their indeterminate growth behaviour is a major physiological constraint negatively impacting yield, as it results in the accumulation of vegetative and reproductive components simultaneously. Understanding canopy dynamics can provide new insight to increase yield potential by improving resource accumulation, remobilisation, and light interception. Additionally, understanding the genetics underpinning these complex traits would allow breeders to strategically target improved phenotypes that could enhance mungbean productivity. However, due to the current phenotyping bottleneck that exists, screening these traits particularly at a large-scale remains a challenge, thereby limiting our understanding of their genetics. In this study, a diverse nested association mapping (NAM) population was evaluated across three environments in QLD, Australia and imaged using a drone fitted with a multi-spectral camera flown regularly throughout development. Several vegetative indices and geometric traits were extracted from each flight and used to establish biomass prediction models. Spline curve fitting was used to integrate the predicted values from single flights into a continuous time course to calculate canopy dynamic traits such as canopy accumulation rate. A multi-environment trial analyses was undertaken to understand the Genotype x Environment interactions influencing these traits to generate overall best linear unbiased estimates (BLUEs). Haploblocks associated with these dynamic traits were identified and can be explored to develop cultivars with optimised canopy development patterns. The identification of these haploblocks establishes a catalogue of chromosome segments that can be leveraged for the enhancement of mungbean breeding and crop performance.