

Evaluating Deep Learning-Based UAV Phenotyping for Genetic Mapping of Southern Leaf Blight Resistance in Maize

Southern leaf blight (SLB), caused by the necrotrophic fungal pathogen *Cochliobolus heterostrophus*, is an important foliar disease of maize (*Zea mays* L.), for which genetic resistance is a primary management strategy. Genetic dissection of disease resistance, however, depends on accurate and reproducible phenotyping, and conventional SLB assessment relies on visual severity ratings that are labor-intensive, subjective, and difficult to scale across large breeding populations. Unmanned aerial vehicle (UAV)-based imaging coupled with deep learning offers an opportunity to increase phenotyping throughput while reducing reliance on manual disease assessment. Yet, whether automated phenotypes retain the genetic signal captured by conventional field ratings remains largely untested for SLB. Previously, we developed EVA-02-B, a deep learning model trained on more than 26,000 UAV-acquired plot images collected across three field seasons and paired with contemporaneous expert disease severity ratings. EVA-02-B generalized to previously unseen growing seasons ($R^2 = 0.697$). Its performance was comparable to the precision of expert raters, demonstrating its potential for high-throughput SLB disease phenotyping. In this study, we test whether these automated severity estimates can support genetic mapping as effectively as conventional phenotyping. Using the intermated B73 $\times$ Mo17 (IBM) maize population, we perform QTL mapping for SLB resistance independently using deep learning-derived and manually scored disease severity. By evaluating automated phenotyping at the level of downstream genetic inference, rather than prediction accuracy alone, this study addresses a critical requirement for integrating AI-based phenotyping into genetic studies and breeding pipelines. Concordance between QTL identified from automated and manual phenotypes would provide evidence that UAV-based deep learning can serve as a scalable, objective alternative to conventional disease scoring without compromising the detection of loci underlying disease resistance.