Integrating Genomics and Root Crown Phenomics to Accelerate White Lupin Improvement for Edible Dual Cash–Cover Crop Use

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Take Home Message

- Root crown traits (RCT) can be phenotyped and genetically analyzed at field scale.
- RCT are heritable, polygenic, and genetically linked to agronomic traits.
- Yield trade-offs and modest genomic selection accuracy make results currently suitable for early-stage culling decisions.



Problem and opportunity

- Demand is rising for dual-purpose cover crops that deliver ecosystem services and economic value.
- White lupin (*Lupinus albus* L.; WL) is a multifunctional legume that mobilize P, fixes N and produce high-quality forage and grain.
- Breeding dual-purpose WL requires selection on root traits.
- Labor-intensive phenotyping/low-throughput, limits inclusion of root traits in breeding pipelines.

Objectives

- Establish deployable field-scale phenotyping of RCT.
- Quantify genetic signal, trade-offs, and predictability relevant to Plant breeding pipeline.

Methods

- Population and design: 232 diverse accessions evaluated across two seasons.
- Phenotyping: Field-scale shovelomics with HTP computer vision to extract RCT at pod maturity (Fig. 1).
- Analysis framework: single and bivariate mixed models, breeder-relevant CV1 genomic prediction (GBLUP) and GWAS (MLM and FarmCPU; threshold: α = 0.05/m; FDR ≤ 0.05).

Results Highlights

- RCT are heritable and stable at field-scale across years (Fig. 2).
- Genetic correlation: significant trade-offs between some RCT and yield traits(Fig.3).
- Genomic prediction accuracy: low to moderate (Fig. 4); currently supports early-stage screening.
- GWAS identified SNPs associated with variation in RCT (Fig. 5).

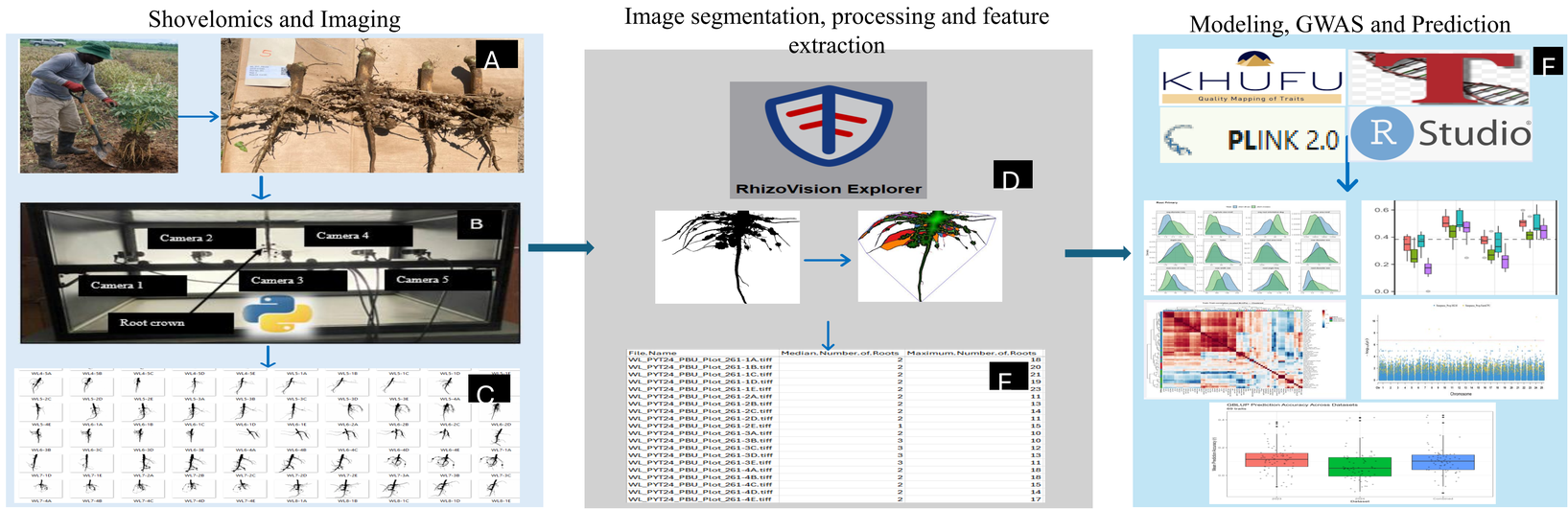

Figure 1. Shovelomics-enabled root crown phenomics pipeline in white lupin.
Root crown excavation (A), imaging (B-C), image analysis RhizoVision Explorer (D) to obtain root traits (E), statistical analysis, genomic prediction, and GWAS (F).



Figure 2. Heritability of agronomic and root crown traits.

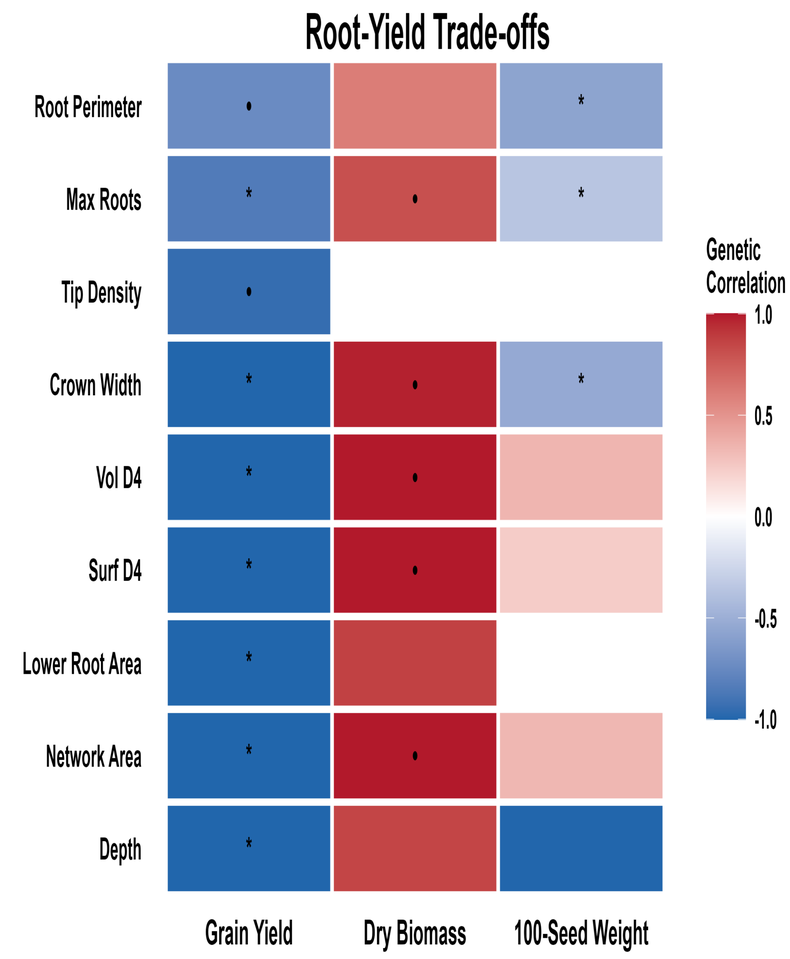

Figure 3. Heatmap of genetic correlations highlighting trade-offs and synergies between root and agronomic traits.

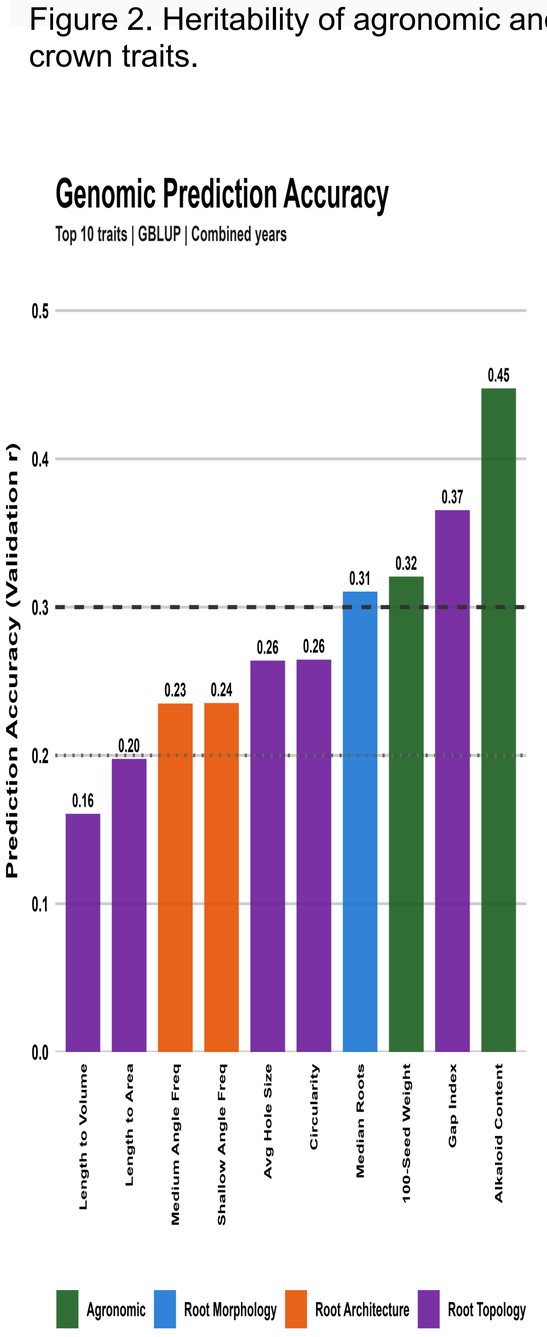

Figure 4. Genomic prediction accuracy (CV1 predicting untested genotypes)

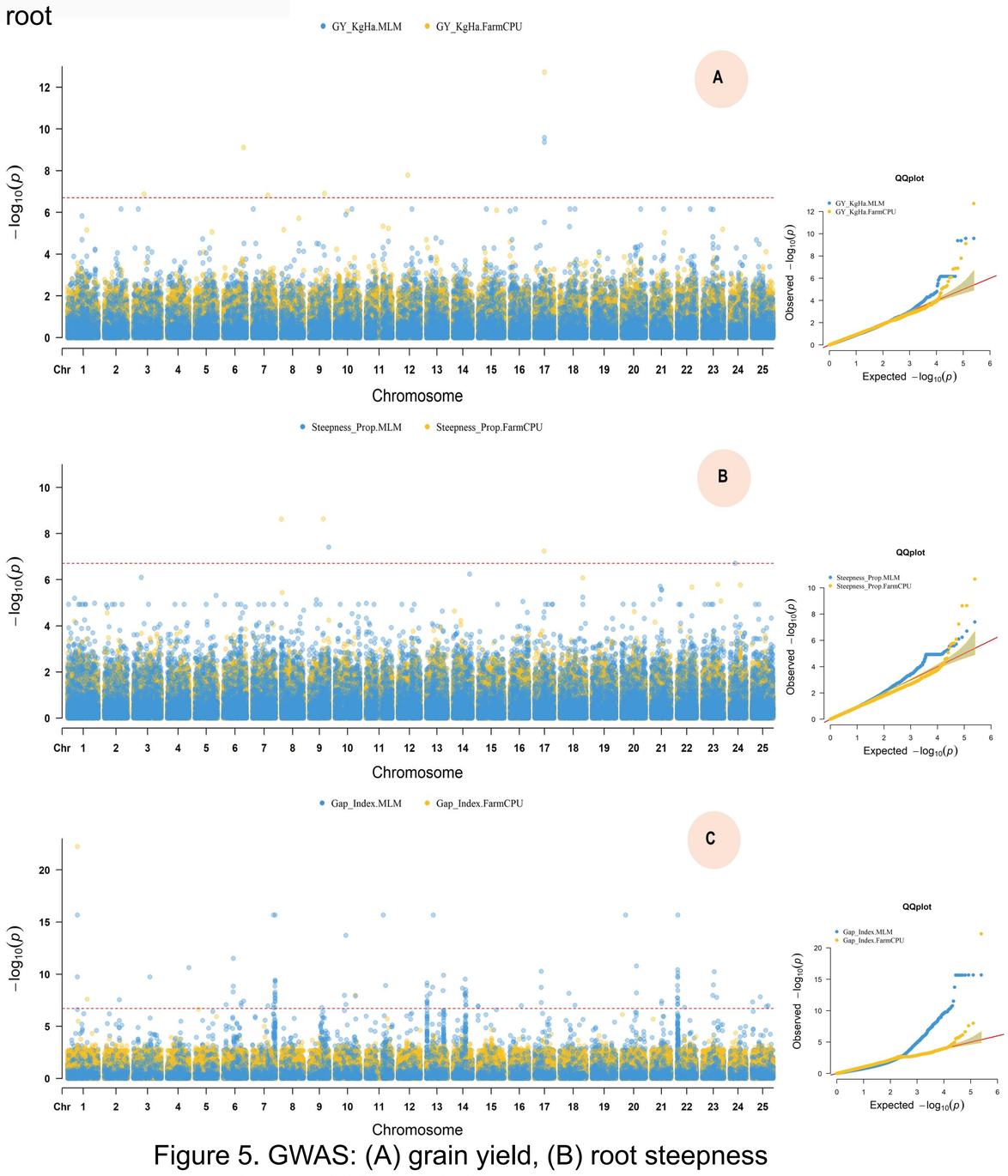

Figure 5. GWAS: (A) grain yield, (B) root steepness proportion, and (C) gap index.