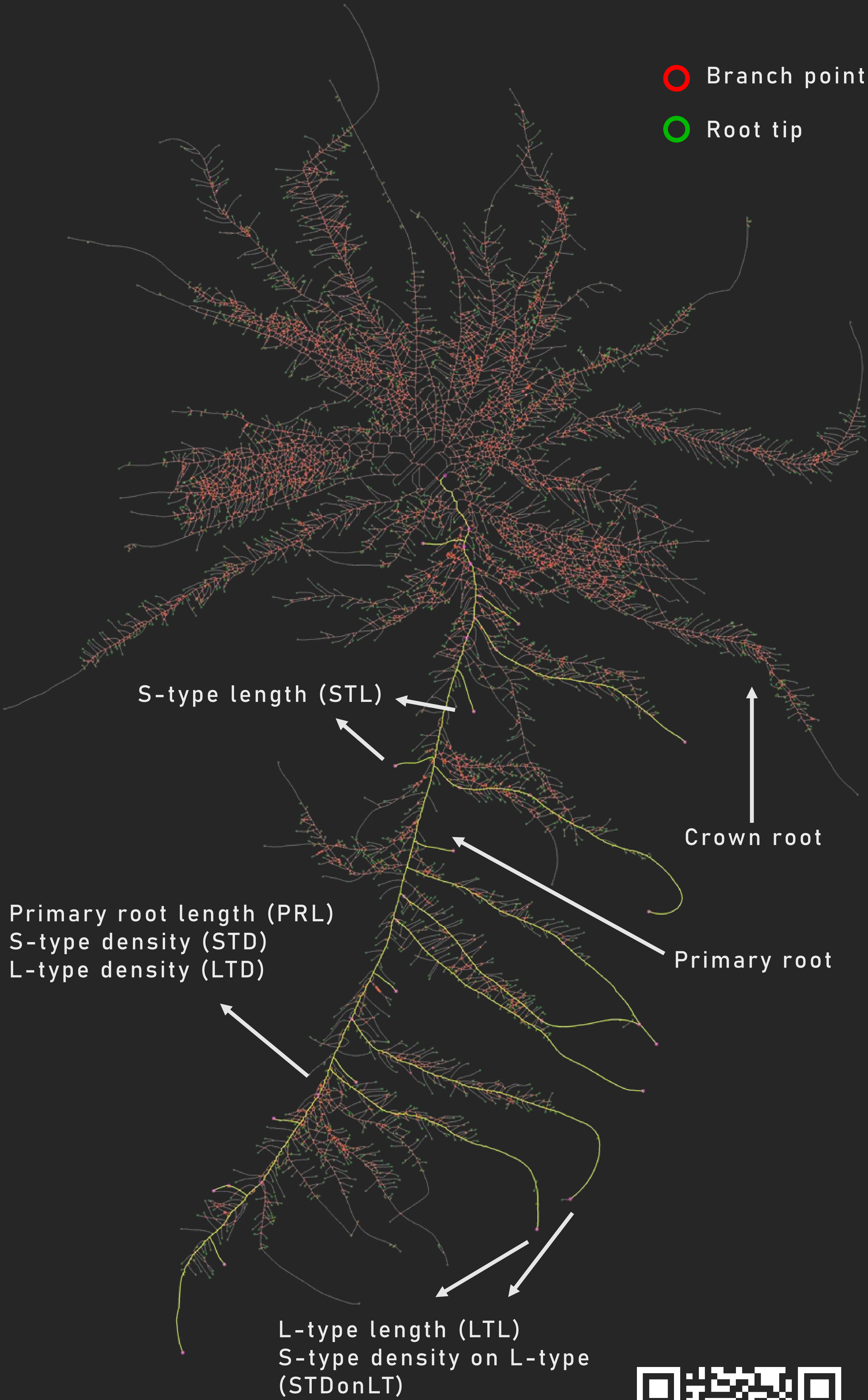


GENOMIC PREDICTION HIGHLIGHTS THE *AUS* AND *SUBTROPICAL JAPONICA* CLADES AS RESERVOIRS OF FAVORABLE LATERAL ROOT ARCHITECTURES IN RICE



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Use our software:

1. Rice Roots for Marginal Soils

Rice S- and L-type lateral roots contribute to phosphorus (P) uptake under nutrient-limiting conditions on smallholder farms and are promising targets for selective breeding. However, phenotyping traits related to lateral root branching has so far been too laborious for large-scale studies. Consequently, their variation across the rice gene pool remains largely unknown.

2. Scalable Root Phenotyping

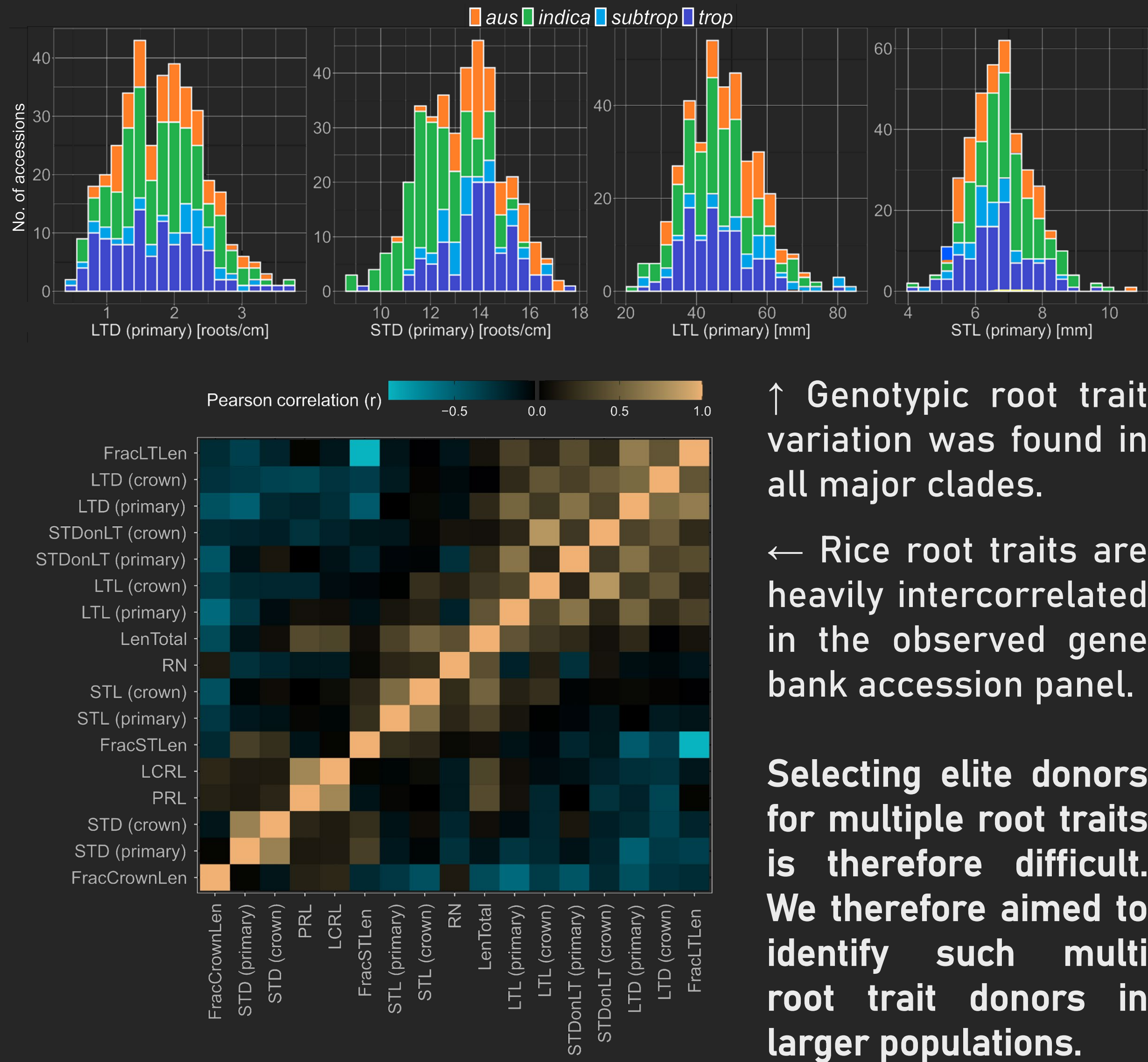


A total of 494 rice accessions (3-k rice genomes project) were grown both in hydroponics and rainfed upland fields in Madagascar. Root scans were obtained and made publicly available. →

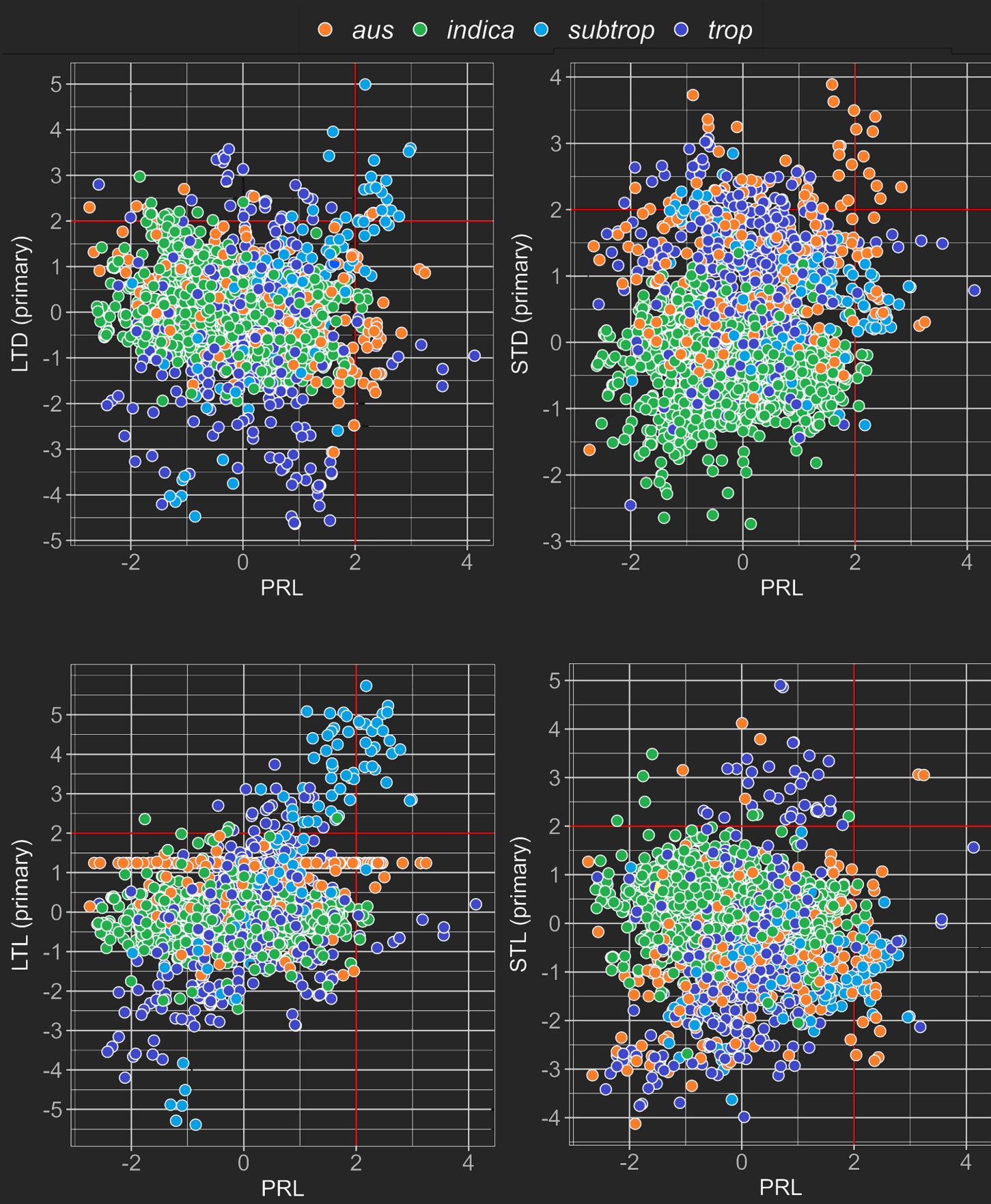


Our novel software tool estimates the geometry of individual roots using A* search and automatically counts class-specific lateral roots, enabling scalable root phenotyping. (*Bottom left panel*)

3. Root Trait Diversity



4. Donor Discovery



We have established genomic predictions of root traits for a total of 2,076 additional gene bank accessions.

The *sub trop. japonica* and *aus* clades provide promising donors for rare trait combinations relevant to P uptake.

Best-case accuracy [*r* in testset]

	Hydro	Upland
PRL	0.58	NA
LTD _(primary)	0.57	0.33
STD _(primary)	0.34	0.34
LTL _(primary)	0.62	0.56
STL _(primary)	0.51	0.29

* Accuracy estimates vary across clades.