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Genomic prediction highlights the *aus* and *subtropical japonica* clades as reservoirs of favourable lateral root architectures in rice

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Abstract

Rice is a major staple crop of increasing importance in sub-Saharan Africa (SSA), particularly Madagascar. In Madagascar, phosphorus (P) deficiency and drought in rainfed systems are major production constraints. As rice production in Madagascar is predominantly smallholder-based, increasing production inputs is not feasible for most farmers. The rice root system comprises small (S- type) and large (L-type) lateral roots, whose abundance and length are linked to P uptake, making them targets for selective breeding. Breeding programmes rely on identifying superior donor germplasm. However, despite extensive genetic variation in gene banks, the labor-intensive nature of root phenotyping limits its application. To enable comprehensive characterisation of gene bank material for key root phenotypes, we generated root image datasets for 494 accessions grown under hydroponic and field conditions. We further developed a software tool for semi-automated, high- throughput phenotyping of lateral root traits, allowing the creation of detailed datasets for complex root characteristics in rice. Genomic prediction (GP) achieved moderate to high accuracy in predicting root phenotypes for an additional 2,076 accessions, with accuracies consistent across growth conditions for some traits. These phenotypes facilitated identification of donor germplasm with superior lateral root branching patterns without compromising potential drought adaptation. Donors for S-type lateral root traits were primarily found in the *aus* subclade, whereas L-type donors originated from the *subtropical japonica* clade. The resulting software, image datasets, and genomic estimated breeding values (GEBVs) provide valuable resources for studying root ideotypes and selecting donor germplasm for breeding in marginal environments.

Keywords: Genomic prediction , plant genetic resources, rice breeding, root research

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