Looking beyond the QTL peak

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ABSTRACT

AAGI is developing *QTL2Pan,* a computational toolbox to uncover biologically meaningful variation behind trait-associated genomic signals. Using pangenomes to look beyond conventional marker-based approaches, it aims to strengthen candidate functional allele discovery and deliver more informative targets for crop breeding. Sorghum provides the initial proof of concept, with the approach designed for broader application across crops.

Navigating the pangenome

Pangenomes capture genomic diversity beyond a single reference. *QTL2Pan* provides a modular computational toolbox to explore this diversity within trait-associated regions and identify biologically relevant variation.

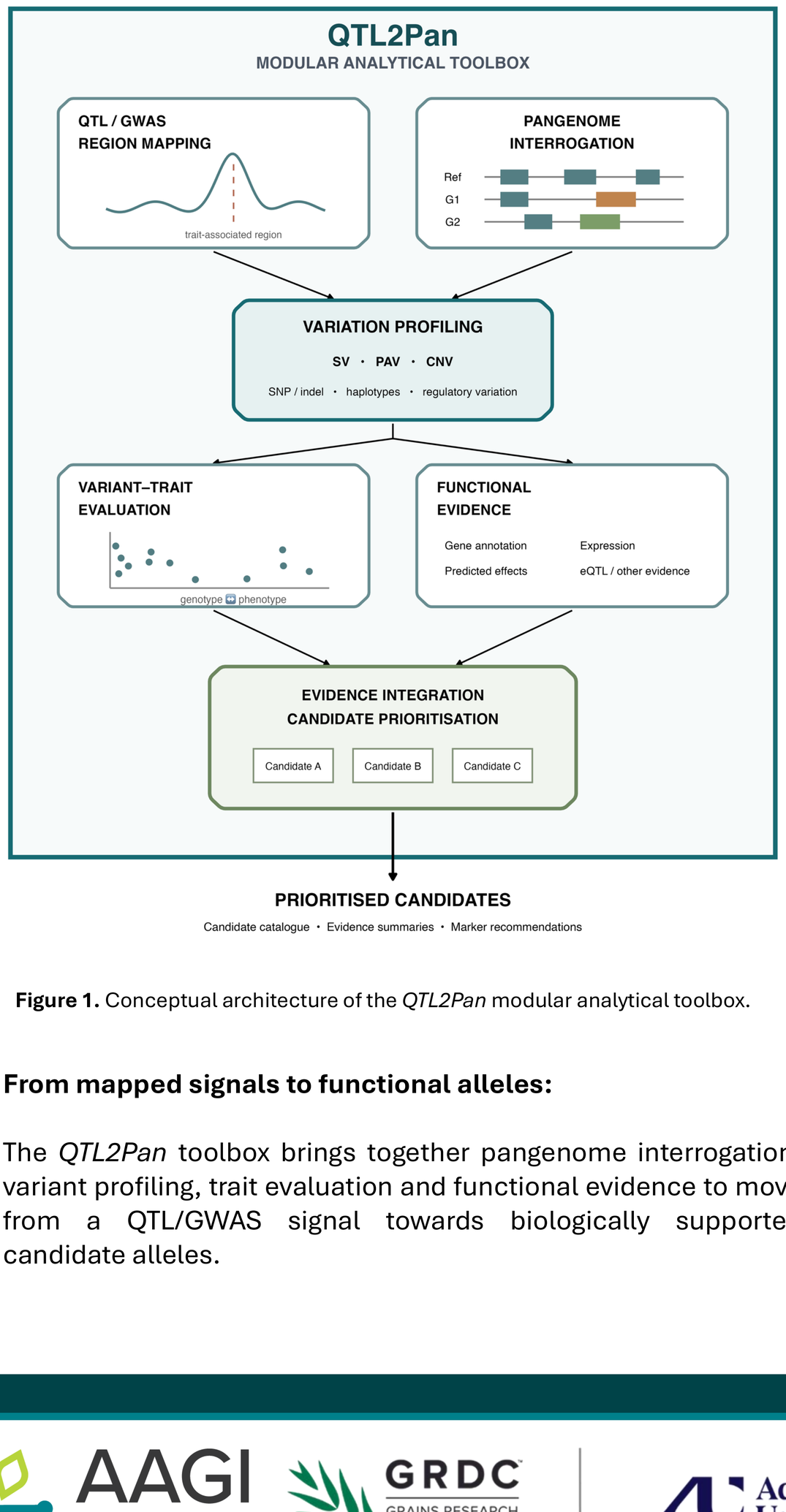


Figure 1. Conceptual architecture of the *QTL2Pan* modular analytical toolbox.

From mapped signals to functional alleles:

The *QTL2Pan* toolbox brings together pangenome interrogation, variant profiling, trait evaluation and functional evidence to move from a QTL/GWAS signal towards biologically supported candidate alleles.

What lies beneath the peak?

A pangenome perspective

Identifying a genomic region associated with a trait is only the first step. The key challenge is to pinpoint the biological variation within that region that contributes to the trait. QTL and genome-wide association study (GWAS) signals can localise trait-associated regions, but the markers defining these peaks may tag rather than represent the functional variation. Relevant variation extends beyond SNPs to structural and gene-content differences that may not be represented by a single reference genome (Monat et al., 2022; Bayer et al., 2022).

Pangenomes provide a broader view of variation within these regions, revealing structural, gene-content and regulatory diversity that may help resolve the biology underlying trait-associated signals (Tao et al., 2021; Morris et al., 2026).

❖ Objective

To develop a pangenome-enabled analytical approach to prioritise biologically relevant candidate functional alleles underlying complex traits.

Starting with sorghum, but designed to go further

QTL2Pan will be developed through co-design with end users to ensure the approach addresses breeding-relevant needs. Following consultation with GRDC, sorghum was identified as a valuable proof-of-concept system, supported by established pangenome, QTL, genotype, phenotype and functional resources (Tao et al., 2021; Morris et al., 2026).

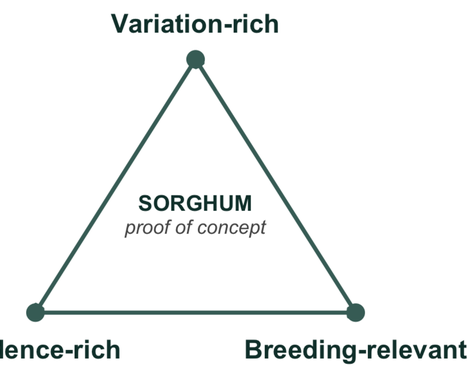


Figure 2. Rationale for using sorghum as the QTL2Pan proof-of-concept system.

The *QTL2Pan* toolbox is designed to extend across traits, populations and crop species.

❖ Impact

If successful, *QTL2Pan* will provide stronger targets for validation and crop improvement.

References

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