

Abstract

Genetic diversity, characterized by single-nucleotide polymorphisms (SNPs) and significant structural variations (SVs), plays a crucial role in shaping the gene content within a species. Pangenomic investigations reveal the impact of SVs on crop domestication, enhancement, and evolution, providing insights into a species' complete genomic repertoire. The pan-genome, comprising core and dispensable genes, unveils novel genes and alleles linked directly to phenotypes through a Pangenomic approach. Utilizing an iterative mapping strategy, a chickpea pan-genome captures genetic diversity across cultivated and wild accessions, identifying unique genes with defense and adaptation mechanisms. Similarly, rice pan-genome analysis highlights deletions in key genes contributing to blast resistance and environmental adaptation. Overall, pan-genomics enhances our understanding of genetic diversity, facilitating trait dissection, broadening access to genetic resources for breeding programs, and accelerating crop improvement strategies for creating resilient and high-yielding varieties.

Introduction

Single-nucleotide polymorphisms (SNPs) and big structural variations (SVs) are examples of genetic diversity that can result in differences in gene content between members of the same species. Pangenome study identifies structural variations (SVs) as having contributed to crop domestication, improvement, and evolution. The exploration of a species' complete genome repertoire is aided by pan-genome analysis.

An entire gene set from a biological group, such as a species, is referred to as a pan-genome. This gene set can be divided into a set of core genes that are shared by all individuals and a collection of dispensable genes that are either partially shared or individual specific (Tettelin *et al.*, 2005). Finding new genes and alleles directly connected to phenotype using a Pangenomic method.

By using an iterative mapping strategy, a chickpea pan-genome was constructed to represent the genetic diversity found in both cultivated and wild accessions of the crop. 29,870 genes in total, 1,582 of which were unique genes with numerous defence and adaption mechanisms, were found. More gene-gain copy number variations (CNVs) and gene-loss CNVs have been found in *C. reticulatum* than in cultivated accessions, indicating a higher degree of divergence between wild and domesticated cousins (Varshney *et al.*, 2021).

A pangenome analysis in rice revealed those two independent deletions in the OsWAK112d gene, which is a negative regulator of blast resistance in rice, contributed to environmental adaptation by improving blast resistance. This deletion is located 643 bp upstream of the OsGLP2-1 gene, which was shown to block seed dormancy and strongly increase seed dormancy upon overexpression. Additionally demonstrated that OsVIL1 copy number variation (CNV) is probably related to grain number and blooming period (Qin *et al.*, 2021).

During tomato domestication and improvement, there was significant gene loss and strong negative selection of genes and promoters, according to presence/absence variation analyses of the tomato pangenome. discovered an uncommon allele in the TomLoxC promoter that is linked to the formation of apocarotenoid, which contributes to the desired tomato flavour and was selected against during domestication (Gao *et al.*, 2016).

Brassica napus accessions were found to have presence and absence variations (PAVs) ranging from 77.2-149.6 metabases. In a nested association mapping population with ZS11 (the reference line) as the donor, PAV-based genome-wide association study (PAV-GWAS) directly identified causal structural variations for silique length, seed weight, and flowering time that were not detected by single-nucleotide polymorphisms-based GWAS (SNP-GWAS), demonstrating that PAV-GWAS was complementary

to SNP-GWAS in identifying associations to traits (Ming *et al.*, 2021).

Analysis of the genome Soybean revealed that genes producing an amino acid transporter, a -SNAP protein, and a WI12 (wound inducible protein) are involved in soybean cyst nematode (SCN) resistance in a 31 kb section at rhg1-b. Additionally, this segment's copy number variation improves the SCN resistance (Cook *et al.*, 2016).

Conclusion

Overall, pan genomics aids in a better understanding of the genetic diversity of the gene pool which can facilitate trait dissection applications to identify structural variations, allow breeding programmes to access a wider range of genetic resources, aid in the adoption of the best breeding programme strategies, and ultimately accelerate crop improvement to create varieties with stab.

References

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