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Editorial

Crop improvement driven by pangenomics and genomic diversity exploration

Pangenomics is the study of the entire set of genes (the pangenome) within a species, encompassing the core genome shared by all individuals and the dispensable, variable accessory genome. By using multiple genomes instead of a single linear reference, pangenomics captures comprehensive genetic diversity, including structural variations and presence-absence variations. Pangenomics improves crops by analyzing the entire set of genes within a species including core and dispensable (variable) genes rather than relying on a single reference genome. This approach identifies structural variations (SVs) like deletions, inversions, and insertions, facilitating the discovery of trait-related genes. Pangenomes are utilized to enhance climate resilience, improve nutritional value, and accelerate breeding, especially for underutilized "orphan crops". Pangenomics represents a critical shift in crop breeding from relying on a single, linear reference genome to using a comprehensive, multi-genome framework that captures the full genetic diversity within a species. As climate change, population growth, and reduced genetic diversity in elite cultivars threaten food security, pangenomics is essential for identifying "lost" genes (such as those for stress tolerance) in landraces and wild relatives, enabling the development of more resilient, high-yielding, and nutritious crops. In soybean pangenomes approach identified 3621 protein-coding genes not present in the reference genome, highlighting genes for adaptability in wild relatives. In rice crop studies on 3010 accessions identified core and variable gene families linked to grain size and plant height. Whereas in wheat crop pangenome analysis revealed that roughly 35% of genes are variable among cultivars, providing new sources for disease resistance. In tomato, this approach identified a rare allele that improves flavor, which had been lost during modern, high-yield selection. Pangenomics, while revolutionizing our understanding of genetic diversity beyond a single reference genome, carries significant hidden risks, primarily centered on computational complexity, data bias, and technical limitations. The shift from a single linear genome to complex graph-based structures introduces challenges in data interpretation, increased storage requirements, and the risk of exacerbating health inequalities if diverse populations are not represented. Key hurdles include managing massive, complex datasets, developing efficient graph-based assembly algorithms, and handling high-repetition eukaryotic genomes. Additionally, the field struggles with standardizing annotations and translating vast genetic diversity into actionable insights for medicine or breeding. Key pangenomics solutions for crop improvement includes, identification of lost traits e.g., disease resistance, drought tolerance from wild relatives. Enhanced genomic selection (GS), precise genome editing (CRISPR/Cas), "Super-Pangenome" for genus-wide breeding and graph based pangenome representations. It revolutionizes biology by capturing the full genetic spectrum of a species both core and accessory genes using multiple individual genomes instead of a single reference. This approach advances personalized medicine, crop improvement, and evolutionary studies, with, AI, and super-pangenomes accelerating discoveries across species and complex traits. In conclusion, the transition to pangenome based breeding is essential to reverse the loss of genetic diversity and ensure agriculture can meet future environmental and food security challenges. The integration of pangenomics with machine learning and other omics data (transcriptomics, proteomics) will further accelerate the development of next-generation, climate ready crop and further growth.