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Identification of Candidate Genes Associated with Yield in Potato (*Solanum tuberosum* L.)

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Yield in potato (*Solanum tuberosum* L.) is a complex quantitative trait influenced by multiple genetic, physiological, and environmental factors. With the advent of high-throughput genomic tools such as quantitative trait loci (QTL) mapping, genome-wide association studies (GWAS), and transcriptome analyses, researchers have made significant progress in identifying candidate genes and genomic regions linked to yield and yield-related traits. This review synthesizes recent findings on candidate gene identification for potato yield, discusses diverse genetic strategies, and highlights opportunities for marker-assisted selection (MAS) and molecular breeding to enhance yield potential.

Introduction

Potato is among the world's most important food crops, with global yield potential constrained by complex genetic architecture and major environmental influences. Yield is typically defined by traits such as tuber number, tuber weight, and total tuber yield per plant. The genetic basis of these traits involves numerous small-effect loci, epistatic interactions, and pleiotropic effects, making candidate gene identification a central challenge in potato breeding programs.

Genetic Architecture of Yield in Potato

Early efforts in identifying genetic components of yield in potato used linkage mapping approaches. For example, QTL mapping in diploid and tetraploid populations revealed several loci for yield and its components, although most exhibited modest phenotypic effects individually. Classical interval mapping identified multiple yield-related QTLs across different chromosomes, noting the influence of genetic background and environmental interactions on yield expression. A study in a diploid mapping population revealed 14 QTLs underpinning tuber yield, average tuber weight, and tubers per plant, many of which displayed epistatic interactions and co-localized with regions of residual heterozygosity, suggesting complex genetic controls beyond additive effects.

Genome-wide Association Studies (GWAS) for Yield Traits

GWAS has become a powerful strategy to detect genomic regions associated with complex traits in diverse germplasm panels. Unlike traditional linkage mapping, GWAS leverages historical recombination and higher marker densities to pinpoint loci and putative candidate genes. Several GWAS have identified SNPs significantly associated with yield and yield-related traits in potato. For instance, one large-scale SNP association study detected markers linked to starch yield and granule morphology, which are indirectly related to overall yield potential. Importantly, many of these significant SNPs reside within or near coding regions that may harbour yield-influencing genes such as those involved in starch biosynthesis and carbohydrate metabolism.

A review of GWAS findings in potato highlights several hotspot regions for agronomic and yield components, notably on **chromosomes 5, 4, 9, and 11**, demonstrating that different genomic regions contribute distinctly to yield and quality traits.

Integrating Transcriptomics for Candidate Gene Discovery

Beyond genotype-phenotype associations, transcriptome analyses provide functional insights into gene expression patterns correlated with high yield. RNA-sequencing of tuber and leaf tissues across contrasting yield phenotypes revealed numerous differentially expressed genes (DEGs) involved in sugar metabolism, phytohormone signaling, stress responses, and transcriptional regulation. Examples of candidate genes include UDP-glucose glucosyltransferase, phytohormone biosynthesis regulators (e.g., GA20 oxidase), and transcription factors such as MYB and WRKY families. Integration of RNA-seq data with GWAS or QTL maps enhances the confidence of candidate gene identification by aligning expression profiles with genomic loci associated with yield phenotypes.

Challenges and Future Perspectives

While significant progress has been made, several challenges remain:

- **Polyploidy and complex inheritance:** Potato’s autotetraploid nature complicates allele dosage estimation and association mapping resolution.
- **Epistatic interactions:** Many yield QTLs interact epistatically, making simple candidate gene identification difficult without large-scale population studies.
- **Environmental influence:** Gene-environment interactions significantly modulate yield, requiring multi-environment trials to validate candidate genes.

Emerging tools such as fine-mapping, functional validation via gene editing (e.g., CRISPR/Cas), and integrative multi-omics approaches are expected to accelerate candidate gene characterization and breeding application.

Conclusion

Identification of candidate genes for potato yield traits has advanced through high-density SNP genotyping, GWAS, QTL mapping, and transcriptomics. These combined approaches have uncovered multiple genomic regions and candidate genes associated with yield components. The integration of genomic markers with physiological and transcriptomic data paves the way for effective **marker-assisted selection** and precision breeding strategies to improve potato yield under diverse environmental conditions.

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