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A systems genetics approach to deciphering the effect of dosage variation on leaf morphology in Populus

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摘要 Gene copy number variation is frequent in plant genomes of various species, but the impact of such gene dosage variation on morphological traits is poorly understood. We used a large population of Populus carrying genomically characterized insertions and deletions across the genome to systematically assay the effect of gene dosage variation on a suite of leaf morphology traits. A systems genetics approach was used to integrate insertion and deletion locations, leaf morphology phenotypes, gene expression, and transcriptional network data, to provide an overview of how gene dosage influences morphology. Dosage-sensitive genomic regions were identified that influenced individual or pleiotropic morphological traits. We also identified cis-expression quantitative trait loci (QTL) within these dosage QTL regions, a subset of which modulated trans-expression QTL as well. Integration of data types within a gene co-expression framework identified co-expressed gene modules that are dosage sensitive, enriched for dosage expression QTL, and associated with morphological traits. Functional description of these modules linked dosage-sensitive morphological variation to specific cellular processes, as well as candidate regulatory genes. Together, these results show that gene dosage variation can influence morphological variation through complex changes in gene expression, and suggest that frequently occurring gene dosage variation has the potential to likewise influence quantitative traits in nature.

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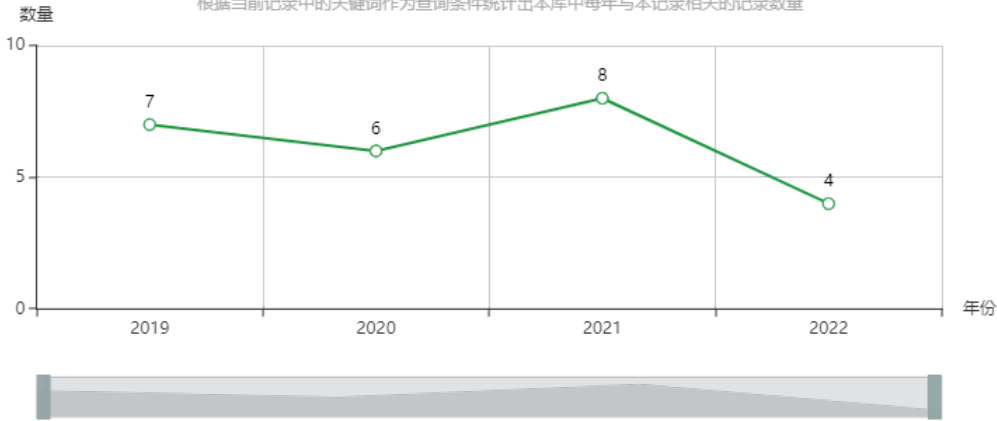
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