



Decoding the Genetic Blueprint of Grass Skyscrapers

The skyscraping bamboos are actually a type of grass. Bamboo flowers infrequently, often blooming only once every 60-120 years for some species, which is an extreme example of the cyclical flowering habit seen in many grasses. (Image by Pixabay)

In the lush forests of Asia, towering bamboos stand tall, defying the folk expectations for grassy plants. These woody giants, some reaching the staggering height of nearly 40 meters, are the world's largest members of the grass family.

A joint team led by Dr. LI Dezhu from the Kunming Institute of Botany of the Chinese Academy of Sciences has now unraveled the genomic mysteries behind the evolution and remarkable traits of these colossal grasses, shedding light on their ancient polyploid origins and the dynamic interplay between their subgenomes.

Polyploidy, the condition of having more than two sets of chromosomes, has long been recognized as a driving force for plant evolution, providing a wellspring of genetic novelty. However, the interactions between the parental genomes within a polyploid nucleus, often involving the dominance of one subgenome over others, have remained poorly understood, particularly in ancient polyploids that have undergone extensive species diversification.

In a breakthrough study published in *Nature Genetics*, researchers assembled and analyzed 11 high-quality genome sequences representing the major clades of bamboos, spanning herbaceous diploids, tetraploids (four subgenomes), and hexaploids (six subgenomes). Their findings paint a remarkable picture of the reticulate evolution and genomic architecture of these iconic plants.

Through meticulous genomic analyses, the researchers traced the origins of woody bamboos to a complex history of hybridization events between extinct diploid ancestors, followed by two independent tetraploidizations and a subsequent hexaploidization, all occurring around 20 million years ago. Remarkably, despite the passage of over 12 million years since the most recent polyploidization event, the subgenomes of woody bamboos have maintained stunning karyotype stability, with little to no large-scale reshuffling of chromosomes.

One of the most intriguing discoveries is the phenomenon of subgenome dominance, where one or more subgenomes exert a disproportionate influence

on gene expression and trait evolution. In the tetraploid woody bamboo clades, the researchers uncovered parallel dominance of the 'C' subgenome, characterized by higher gene expression, more conserved genes, and enrichment in genes associated with vegetative growth and development.

Interestingly, in the hexaploid clade, the researchers observed a gradual shift in dominance from the 'C' subgenome to the 'A' subgenome over evolutionary time, a remarkable example of the dynamic nature of subgenome interactions.

The researchers also delved into the genomic underpinnings of the unique traits that define woody bamboos, such as their lignified culms (stems), rapid growth, and synchronous flowering cycles that can span decades. They identified numerous genetic alterations, including expanded gene families, new genes, and positively selected genes, many of which were enriched in the dominant subgenomes. Of particular note is the caffeic acid O-methyltransferase (COMT) gene, which plays a crucial role in lignin biosynthesis and the development of the massive woody culms.

Beyond the scientific insights into bamboo studies, this research has far-reaching implications for diverse fields. For ecologists and conservationists, understanding the genomic basis of woody bamboo traits could inform efforts to preserve these ecologically vital species, which provides habitats for numerous organisms and plays a crucial role in carbon sequestration.

In the realm of agriculture and biotechnology, the findings open avenues for engineering crops with desirable traits, such as rapid growth or improved lignin content, by leveraging the genetic toolbox uncovered in bamboos.

In summary, this study represents a significant leap in our understanding of polyploid evolution and subgenome dynamics. The insights gleaned from bamboos could serve as a model for investigating other ancient polyploid lineages and unraveling the intricate interplay between subgenomes that shape the incredible diversity of plant life on our planet.

Reference

Ma, P. F., Liu, Y. L., Guo, C., Jin, G., Guo, Z. H., Mao, L., . . . Li, D. Z. (2024). Genome assemblies of 11 bamboo species highlight diversification induced by dynamic subgenome dominance. *Nature Genetics*. doi:10.1038/s41588-024-01683-0