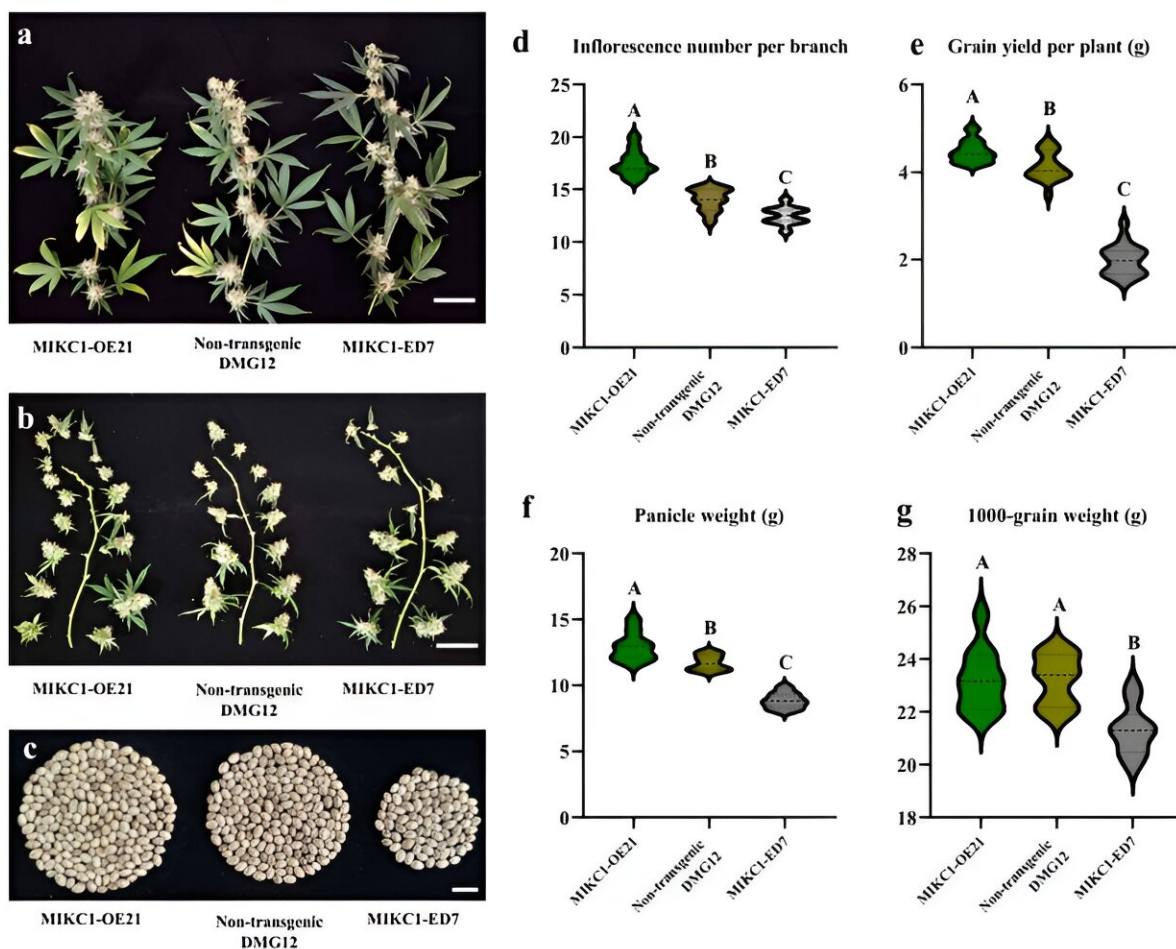


Boosting cannabis production: The science behind bud abundance

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Performance of CsMIKC1-overexpressing transgenic plants and CsMIKC1 mutants in the greenhouse. Credit: *Horticulture Research* (2024). DOI: 10.1093/hr/uhae161

Cannabis sativa is highly valued for its cannabinoids, which are primarily produced in female inflorescences. However, the genetic control of inflorescence development remains largely unexplored, posing a significant challenge to optimizing flower and grain yield.

As demand for Cannabis-derived products grows, understanding the underlying regulatory mechanisms is critical for enhancing production. Current cultivation practices often fall short due to this knowledge gap.

Addressing these challenges necessitates detailed research into the genetic factors influencing [inflorescence](#) growth, providing a foundation for strategies that can meet the increasing global demand.

A research team from the Chinese Academy of Agricultural Sciences and other institutions published their [findings](#) on June 12, 2024, in *Horticulture Research*. The study identifies CsMIKC1, a MIKC-type MADS-box transcription factor, as a pivotal regulator of inflorescence development in Cannabis sativa.

Using CRISPR-Cas9 [gene editing](#), the team examined how CsMIKC1 mutations and overexpression influence flower and grain production. Their findings offer fresh insights into the genetic architecture of inflorescence, underscoring the gene's significant role in enhancing [crop yields](#) and presenting new avenues for genetic improvement.

The study pinpointed a major quantitative trait locus (QTL) on chromosome 8 linked to inflorescence number per branch, leading to the discovery of the CsMIKC1 gene. CsMIKC1 functions as a transcription factor that modulates inflorescence development by interacting with proteins CsBPC2 and CsVIP3.

Transgenic plants overexpressing CsMIKC1 exhibited a substantial increase in inflorescence numbers, flower production, and grain yield,

while CsMIKC1 mutants showed diminished growth and yield, highlighting the gene's regulatory importance.

The researchers also found that CsMIKC1 is influenced by ethylene signaling pathways, as seen in the reduced ethylene sensitivity of CsBPC2 mutants. Applying external ethylene stimulated CsMIKC1 expression, enhancing flower production and suggesting practical applications in commercial Cannabis farming.

By identifying key genes regulated by CsMIKC1, the study maps a comprehensive genetic network governing inflorescence formation, offering critical insights for future crop enhancement strategies.

Dr. Jianguang Su, a co-author of the study, stated, "The identification of CsMIKC1 as a regulator of inflorescence development marks a significant step forward in Cannabis genetics. This gene is crucial in determining flower yield, which has profound implications for both medicinal and industrial uses.

"By utilizing genetic modification techniques, we can develop targeted approaches to optimize crop performance, enhancing the Cannabis industry's potential. This research not only deepens our understanding but also opens up exciting possibilities for developing high-yielding strains."

The discovery of CsMIKC1's influence on inflorescence development offers a new target for genetic engineering to boost Cannabis yields. This knowledge could drive the creation of novel cultivars with improved flower and [grain production](#), maximizing farming efficiency.

Furthermore, the involvement of ethylene signaling pathways presents opportunities for refined agronomic practices, such as ethylene treatments, to further increase flower yield.

These advances hold significant promise for scaling up Cannabis production to meet the growing demand for medicinal and industrial applications worldwide.

More information: Gencheng Xu et al, CsMIKC1 regulates inflorescence development and grain production in Cannabis sativa plants, *Horticulture Research* (2024). DOI: [10.1093/hr/uhae161](https://doi.org/10.1093/hr/uhae161)

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