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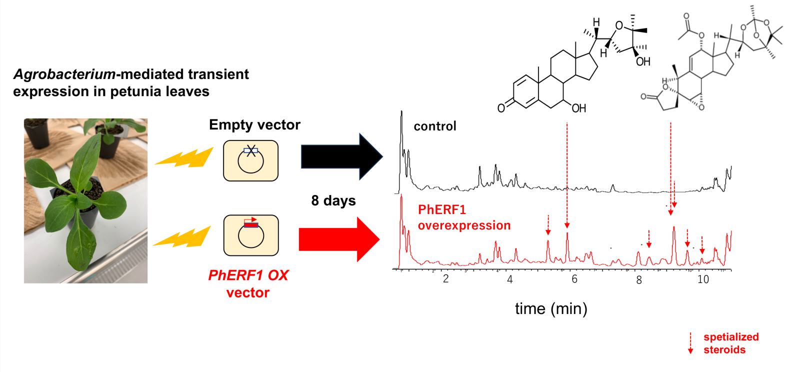
A single regulatory factor sufficient to induce the accumulation of complex specialized steroids in plants

TOYAMA, JAPAN, November 1, 2023 /EINPresswire.com/ -- A research group led by Professor Tsubasa Shoji at the University of Toyama's Institute of Natural Medicine, in collaboration with the RIKEN Center for Sustainable Resource Science and the University of Tsukuba, has successfully induced a significant accumulation of plant steroid compounds in a short period using a single transcription factor from plant-specific AP2/ERF family.



Induced production of bioactive steroids by reprograming transcription in petunia leaves

Natural products with complex chemical structures, such as steroids, which possess physiological activities, are widely used in medicine and other applications. However, these effective ingredients are present in only trace amounts within plant organisms. If it were possible to significantly increase the accumulation of these trace plant compounds, it would enable stable production and supply for pharmaceuticals and their raw materials.

In plants, natural compounds are synthesized through multiple steps of enzyme-catalyzed reactions, starting from simple precursor compounds. In this study, the researchers enhanced the function of a transcription factor PhERF1 by transiently overexpressing its gene, which acts as a central regulator for the expression of numerous enzyme genes. This led to the induction of over 100 metabolic enzyme genes, resulting in a substantial increase in the accumulation of highly toxic steroid compounds unique to petunia plants, called petuniolites and petuniasterones, in their leaves in a short period (within 8 days after the introduction of PhERF1 gene).

The homologous factors to petunia PhERF1 used in this study exist in nearly all dicotyledonous plants and are believed to act as "versatile" regulatory factors that oversee the synthesis of specific plant compounds in each plant species. The use of this technique, which employs a single universal factor, can be applied to various plant species, promoting advances in plant-based bioproduction. Their findings highlight the potential use of evolutionarily conserved factors as genetic tools to effectively elicit the production of bioactive natural products by reprogramming transcription, without requiring prior knowledge of downstream metabolic pathways.

This research achievement was published in the electronic version of the Proceedings of the National Academy of Sciences Nexus on October 31, 2023 (https://academic.oup.com/pnasnexus/article/2/10/pgad326/7321481?searchresult=1).

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