

【Grant-in-Aid for Scientific Research (S)】

Broad Section H



Title of Project : Genomic origin of chemodiversity in medicinal plants

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Research Project Number : 19H05652 Researcher Number : 00146705

Keyword : medicinal plants, genome, metabolome

【Purpose and Background of the Research】

The diversity of the plant metabolome, which is the source of medicine, far surpasses animals and so on, but its genomic origin is an unknown subject and is a fundamental issue. In addition, 90% of physicians still prescribe Kampo, and expectations for botanical medicine are high for extension of healthy lifespan in the aging society. While many herbal medicines depend on imports, the Nagoya Protocol came to seek fair profit distribution, but it is rather a great opportunity for genomic elucidation and intellectual property defense of domestically grown medicinal plants. In addition, in the “Sustainable Development Goals” SDGs (Sustainable Development Goals) adopted by the United Nations in 2015, conservation of biodiversity resources and its sustainable use are issues of global concern. In addition, there is a rapid development of genomic science related technology as a technical background.

In this study, we decipher the genome and metabolome of medicinal resource plants, clarify the origin of their chemical diversity, and apply their findings to the sustainable use of plant resources.

【Research Methods】

Regarding licorice most important as a herbal medicine, which is most frequently used for Kampo prescriptions and so on, we determined high-quality genome sequences of plant species containing and not containing glycyrrhizin, its main active ingredient. Variant strains with different component patterns are resequenced to obtain mutational information. Next, transcriptome and metabolome data are also acquired, and genes, genome regions and mutations that determine component patterns are identified by co-occurrence network analysis or genome wide association study (GWAS) of these. Next, along with functional identification of these genes, biotechnologies such as genome editing and synthetic biology are applied to molecular breeding of licorice and production of active ingredients. At the same time, we will extend this basic method to functional genomics of important medicinal plants other than licorice.

【Expected Research Achievements and Scientific Significance】

It is possible to decipher genomes and metabolomes and clarify the origin of their chemical diversity in medicinal plants of increasing importance in the fields of medicines and medical field. This can be applied to the sustainable

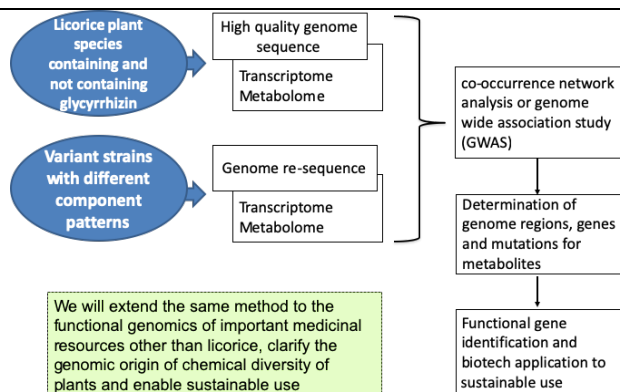


Figure 1 Outline of research

use of plant resources that contributes to "Sustainable Development Goals" SDGs, and at the same time, it can extend the horizon of human knowledge. Furthermore, it will open up a new path to medicinal plant resource development in the next 10 to 20 years.

【Publications Relevant to the Project】

- Mochida, K., *et al.*: Draft genome assembly and annotation of *Glycyrrhiza uralensis*, a medicinal legume. *Plant J.*, **89**, 181–194, (2017)
- Rai, A., Saito, K., Yamazaki, M.: Integrated omics analysis of specialized metabolism in medicinal plants. *Plant J.*, **90**, 764–787 (2017)
- Knoch, E., *et al.*: The third DWF1 paralog in Solanaceae, sterol Δ^{24} -isomerase, branching withanolide biosynthesis from the general phytosterol pathway. *Proc. Natl. Acad. Sci. USA*, **115**, E8096–E8103 (2018)
- Tsugawa, H., Nakabayashi, R., *et al.*: A cheminformatics approach to characterize metabolomes in stable-isotope-labeled organisms. *Nature Methods*, **16**, 295–298 (2019)

【Term of Project】 FY2019–2023

【Budget Allocation】 154,600 Thousand Yen

【Homepage Address and Other Contact Information】

<http://www.riken.jp/research/labs/csrs/metabolom/>
<http://metabolomics.riken.jp/>