

CHARACTERIZATION OF A SYRINGIC AND VANILLIC ACID-INDUCIBLE GENE EXPRESSION SYSTEM IN *SPHINGOBIUM* SP. SYK-6

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Phenolic acids such as syringic and vanillic acids are recognized as key intermediates in lignin depolymerization and are considered valuable bioactive compounds with applications in biotechnology, biorefinery processes, and synthetic biology. The aerobic alphaproteobacterium *SPHINGOBIUM* sp. SYK-6 is widely employed for the study of lignin-derived aromatic compound degradation because monoaryl and biaryl substrates can be utilized by this organism as sole carbon and energy sources. Despite the extensive characterization of lignin catabolic pathways in this bacterium, the transcriptional regulation of genes involved in syringic and vanillic acid metabolism has not been sufficiently understood [1,2]. In *SPHINGOBIUM* sp. SYK-6, syringic acid is converted to 3-methylgallic acid and is subsequently metabolized via the gallate cleavage pathway.

A powerful platform for the development of genetically encoded whole-cell biosensors is provided by transcription factor (TF)-based inducible gene expression systems, through which the detection and quantification of small molecules relevant to metabolic engineering and strain optimization can be achieved. Although biosensors responsive to several phenolic compounds have been reported, the development of a robust and specific syringic acid-inducible system has remained challenging [3].

In this study, a DesR-dependent inducible gene expression system from *SPHINGOBIUM* sp. SYK-6 that responds to syringic and vanillic acids was characterized. Genetic constructs containing *desR* and the promoter region upstream of *desB* were assembled and were evaluated in both native and heterologous bacterial hosts. New insights into the regulation of lignin-derived aromatic compound metabolism are provided by these results, and a foundation for the future design of syringic acid-responsive biosensors with potential applications in biotechnological and environmental monitoring platforms is established.

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- [1] T. Araki et al., "Regulation of vanillate and syringate catabolism by a MarR-type transcriptional regulator DesR in *Sphingobium* sp. SYK-6," *Scientific Reports*, vol. 9, no. 1, p. 18036, Dec. 2019, doi: 10.1038/s41598-019-54490-7.
- [2] Kamimura, N. et al., "Bacterial catabolism of lignin-derived aromatics: new findings in a recent decade," *Environmental Biotechnology Reports*, vol. 9, no. 6, pp. 679–705, Dec. 2017, doi: 10.1111/1758-2229.12597.
- [3] E. Augustiniene, I. Kutraite, E. Valanciene, P. Matulis, I. Jonuskiene, and N. Malys, "Transcription factor-based biosensors for detection of naturally occurring phenolic acids," *New Biotechnology*, vol. 78, pp. 1–12, Sep. 2023, doi: 10.1016/j.nbt.2023.09.004.