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Discovery of lipid-degrading enzymes through functional metaproteomics

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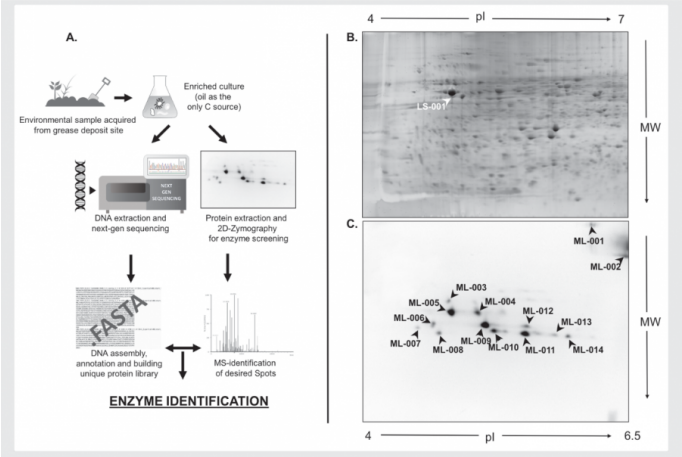
PURPOSE OF THE ABSTRACT

Lipolytic enzymes are important biocatalysts and are one of the few enzymes that are produced in large-scale. They are widely used as industrial catalyst, e.g. in the detergent, food and leather industries. Lipases are generally resilient against harsh conditions due to their broad pH profile, temperature stability, halotolerance and activity in various organic solvents. They also show characteristics like enantioselectivity, which can be an advantage in the production of fine chemicals. We have developed a functional metaproteomics approach combining the immediacy of an activity-based screening with the independence from lab-cultivability of ?meta-omic? approaches to screen different soil samples for lipolytic enzymes with desirable properties like enantioselectivity (Sukul et al., 2017).

In this work we tested 9 commercial available lipases for their chain-length specificity with fluorogenic substrates. We can show that all tested enzymes had the highest activity with heptanoate (C7). It was also possible to demonstrate in-gel activity with a particularly long chain-length (C16). Moreover, we could detect lipolytic enzymes which showed a high activity for specific substrates, which, e.g. had a very bulky structure.

FIGURES



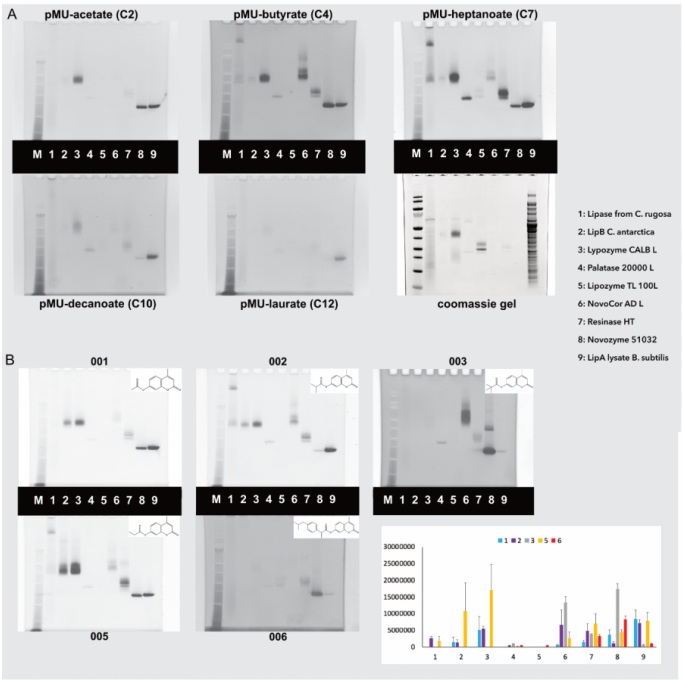


FIGURE 1

Discovery of lipase through functional metaproteomics

Functional metaproteomics as a tool to discover biocatalysts [1]. A. Schematic representation of the functional metaproteomics workflow. B. 2DGEL analysis of the metaproteome. C. In-Gel zymography to identify lipolytic enzymes.

FIGURE 2

In-Gel zymography: a fast and convenient tool

A. 9 known lipolytic enzymes were successfully tested for their substrate-specifity (chain-length) through in-gel zymography. B. It was possible to detect lipolytic enzymes from the lipase panel which showed a high activity for specific substrates.

KEYWORDS

Zymography | Lipase | Metaproteomics | Screening

BIBLIOGRAPHY

[1] Sukul, P., et al., Microbiome, 2017, 5 (1), 28.