

An alternative direction involved engineering *O. polymorpha* for L-lactic acid production by expression of heterologous lactate dehydrogenase genes. The most efficient recombinant strain accumulated up to 72 g/L L-lactic acid from glucose, whereas production from xylose reached 9.6 g/L.

The obtained results demonstrate that *O. polymorpha* metabolism can be redirected toward either ethanol or L-lactic acid production using complementary strain-development strategies. The identified genetic targets and constructed strains provide a basis for further improvement of both processes.

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SILVERFISH-ASSOCIATED YEASTS LINK ENVIRONMENTAL PERSISTENCE WITH EPITHELIAL-INTERACTION PHENOTYPES.

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Abstract. Synanthropic insects may represent overlooked reservoirs of viable yeasts in the built environment. Fungal profiling and culture-based characterization of the silverfish *Lepisma saccharinum* revealed a yeast-dominated mycobiota and yielded isolates of *Nakaseomyces glabratus* and *Candida zeylanoides*. The isolates differed markedly in stress tolerance, biofilm formation, and interactions with human keratinocytes. Importantly, environmental robustness did not consistently predict epithelial-interaction phenotypes, indicating distinct and isolate-specific combinations of traits relevant to environmental persistence and potential host interactions.

Keywords: *Lepisma saccharinum*, *Nakaseomyces glabratus*, *Candida zeylanoides*, fungal microbiota, epithelial interaction.

Synanthropic insects represent a largely overlooked microbial niche within the built environment, yet little is known about the viable fungi they harbor and their functional properties. We characterized the fungal microbiota associated with the silverfish *Lepisma saccharinum* and examined phenotypic diversity among cultivable yeasts recovered from the insects. ITS1 amplicon profiling of a pooled silverfish sample revealed a strongly yeast-dominated fungal community, with *Candida* accounting for approximately 83 % of assigned reads. Culture-dependent analysis yielded two *Candida glabrata* (currently *Nakaseomyces glabratus*) isolates, LS1 and LS6, and one *Candida zeylanoides* isolate, LS4. The isolates displayed pronounced strain-dependent differences in carbon-source utilization, thermotolerance, halotolerance and biofilm formation. LS1 and LS6 grew at temperatures up to 42 °C, showed greater tolerance to osmotic stress than LS4 and produced more biofilm than the *Saccharomyces cerevisiae* reference strain. Imaging flow cytometry further demonstrated association of all

three isolates with HaCaT keratinocytes and internalization-associated signals, while yeast exposure was accompanied by increased IL-6- and IL-8-associated fluorescence. Importantly, environmental robustness did not directly parallel epithelial-interaction phenotypes: LS4 showed the narrowest stress-tolerance profile and the lowest internalization-associated fraction, yet elicited the strongest IL-8-associated signal. Together, these findings reveal substantial isolate-specific functional diversity among silverfish-associated yeasts and identify *L. saccharinum* as a previously underexplored potential reservoir of viable, clinically relevant yeasts in the built environment.

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ENHANCING BIOACTIVE COMPOUND AND ENZYME PRODUCTION IN *PSEUDOPESTALOTIOPSIS THEAE* THROUGH EPIGENETIC MODIFICATION

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Abstract. The chemical modifier BRD4770 treatment enhanced secondary metabolite production, cellulase and antioxidant activity. *Pseudopestalotiopsis theae* SAL1 compared to both the control and 5-azacytidine. The treated cultures exhibited stronger ABTS⁺ radical-scavenging activity ($EC_{50} = 66.6 \mu\text{g/mL}$) and increased cellulase production, with a 22 mm hydrolysis zone and $71.33 \mu\text{g/mL}$ glucose release. GC-MS and LC-ESI-MS/MS analyses revealed the induction of several previously undetected metabolites, indicating activation of silent biosynthetic gene clusters. Montelukast-like antioxidant compounds were identified in BRD4770-treated extracts and confirmed by RP-HPLC. These findings demonstrate that BRD4770 effectively enhances the metabolic diversity and bioactive potential of *P. theae*.

Keywords: Endophytic fungus, Microbial epigenetics, Chemical epigenetic modulator, Histone modification, Cryptic Metabolites, Metabolite profiling.

Endophytic fungi are a rich but less explored source of biologically active metabolites, particularly those associated with medicinal plants. In this study, the endophytic fungus *Pseudopestalotiopsis theae* isolate SAL1 was isolated from *Saraca asoca* (Roxb.). Using the DNA methyltransferase inhibitor 5-azacytidine ($25 \mu\text{M}$) and the histone H3K9 methyltransferase inhibitor BRD4770 (100 nM), cryptic secondary metabolite synthesis was increased by epigenetic regulation. Compared to 5-azacytidine, BRD4770 significantly increased metabolite production, enzyme activity and antioxidant potential, demonstrating its greater capacity to activate cryptic metabolic pathways. ABTS⁺ radical-scavenging activity was markedly enhanced in BRD4770-treated cultures, with an EC_{50} of $66.6 \mu\text{g/mL}$, compared with $> 133.3 \mu\text{g/mL}$ in the control. Additionally, cellulase synthesis increased, with wider hydrolysis zones (22 mm) and higher glucose release ($71.33 \mu\text{g/mL}$), peaking between 72 and 120 h. While LC-ESI-MS/MS detected six additional compounds in BRD4770 and BRD4770 + 5-azacytidine-treated cultures, including fatty acids, phytohormones, phenolics, heterocyclic and fluorinated derivatives, indicating activation of previously silent biosynthetic gene clusters, GC-MS analysis demonstrated the induction of new metabolites following epigenetic treatment. Montelukast-like antioxidant molecules were also found in extracts treated with BRD4770 by LC-ESI-MS/MS. The increased antioxidant activity shown following BRD4770 therapy was supported by reverse-phase HPLC, which revealed retention durations similar to those of a