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ACTIVITY OF CURCUMIN METAL COMPLEXES AGAINST MATURE *PSEUDOMONAS AERUGINOSA* BIOFILMS

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Abstract. The aim of this study was to evaluate the antibiofilm activity of curcumin complexes with zinc, neodymium, ytterbium, and dysprosium against mature biofilms formed by *Pseudomonas aeruginosa* strains. The results demonstrated that the curcumin metal complexes had antibiofilm activity against mature biofilms formed by some *Pseudomonas aeruginosa* strains.
Keywords: *Pseudomonas aeruginosa,* curcumin, biofilm, antibiofilm activity, metal–curcumin complexes

Biofilm formation is an important stage in the development of many chronic infections, with the formation of the extracellular matrix being a key factor in this process. Together with the metabolic reprogramming of cells, the extracellular matrix provides protection to microorganisms (Osondu-Chuka et al., 2026). During biofilm maturation, cells form microcolonies and secrete an extracellular matrix, which may account for more than 90 % of the biofilm mass. Matrix components can bind antimicrobial compounds or promote their enzymatic degradation, thereby reducing the concentration of antimicrobial agents reaching bacterial cells. Thus, the matrix acts as a functionally active environment that maintains biofilm integrity and protects bacteria from environmental factors, particularly antimicrobial agents (Flemming et al., 2025). Given the high tolerance of mature biofilms to antimicrobial agents, the search for compounds capable of affecting their functioning is of particular relevance. Curcumin is one promising natural compound, and its metal-modified derivatives have been reported to exhibit antibacterial and antibiofilm activity against *P. aeruginosa* (Shariati et al., 2024; Mittal et al., 2024).

The antibiofilm activity of curcumin complexes with zinc, ytterbium, neodymium, and dysprosium was evaluated against strains of *P. aeruginosa* ATCC 15692, ATCC 10145, and ATCC 9027. Mature biofilms were formed for 48 h in polystyrene microplates, after which the studied compounds were added to the culture medium. Following an additional 24 h of incubation, biofilm biomass was determined spectrophotometrically using crystal violet staining (Haney et al., 2022).

None of the studied compounds exhibited antibiofilm activity against *P. aeruginosa* ATCC 15692 or ATCC 10145. In contrast, a reduction in biofilm biomass was observed for *P. aeruginosa* ATCC 9027. The most pronounced inhibitory effect was observed for the dysprosium complex, which reduced biofilm biomass by 32 % at 25 μM and 37 % at 50 μM

compared with the control. Zinc- and neodymium-containing complexes also exhibited activity at 5 μM, showing a higher inhibitory effect, whereas at 50 μM their activity was approximately twofold lower.

The increased sensitivity of the *P. aeruginosa* ATCC 9027 biofilm to the studied compounds may be primarily associated with strain-specific features of quorum-sensing regulation. A functional defect in the transcriptional regulator LasR, which plays a central role in the quorum-sensing regulatory hierarchy and the regulation of virulence, has been described in this strain (García-Reyes et al., 2020). Reduced LasR functionality may affect the expression of QS-dependent genes and the interplay between the Las, Rhl, and Pqs regulatory systems. Since quorum sensing contributes to the regulation of the biofilm phenotype, maturation, and spatial organization, atypical QS regulation in *P. aeruginosa* ATCC 9027 may contribute to differences in the physiological state of cells and the architecture of the resulting biofilm, which, in turn, may affect its susceptibility to the studied compounds (Chadha et al., 2022).

Another factor potentially contributing to the differential efficacy of the studied compounds against the biofilm of *P. aeruginosa* ATCC 9027 may be the specific composition of its extracellular matrix. The matrix of *P. aeruginosa* biofilms contains the polysaccharides Psl, Pel, and alginate, whose relative contributions and interactions may vary considerably among strains (Böhning et al., 2024). For *P. aeruginosa* ATCC 9027, the absence of the *mucA* gene, which encodes a negative regulator of alginate biosynthesis, has been described, providing a genetic basis for alterations in the polysaccharide profile of the matrix (Neubauer et al., 2021). Such differences may affect the spatial organization of the biofilm, the physicochemical properties of the matrix, and the accessibility of bacterial cells to external antimicrobial agents.

Therefore, the results obtained indicate the potential of curcumin metal complexes as promising antibiofilm agents capable of affecting mature *P. aeruginosa* biofilms. Further investigation of the matrix composition, spatial architecture, and physicochemical properties, combined with studies of the interactions between its components and metal complexes, may elucidate the basis of the identified differences, determine the factors underlying the varying susceptibility of individual strains, and provide a framework for developing more effective antibiofilm compounds.

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POTENTIAL PROBIOTIC PROPERTIES AND IN VIVO EFFECTS OF *SACCHAROMYCES CEREVISIAE* CL4

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Abstract. *Saccharomyces cerevisiae* CL4 was evaluated as a potential probiotic strain based on stress tolerance, safety-related properties, microbial interactions, and effects in rats. The strain grew at 37 °C and showed 71.0 % survival at pH 2.5 and 83.2 % survival under simulated gastric conditions. No hemolytic activity was detected. CL4 did not inhibit *Candida albicans*, but altered the phenotype of *Pseudomonas aeruginosa*, an effect also reproduced by cell-free culture fluid. In rats with metabolic syndrome, CL4 administration increased superoxide dismutase activity and affected other antioxidant defense parameters.
Keywords: *Saccharomyces cerevisiae*, probiotic yeast, antioxidant defense, tolerance assay, microbial interactions.

Probiotic yeasts are gaining increasing attention because of their ability to survive gastrointestinal conditions and potentially modulate host physiology. However, these properties are strongly strain-dependent, emphasizing the need for individual characterization of candidate strains (Ruchała, et al., 2026; Nenciarini, et al., 2024). Some studies using animal models also indicate the ability of probiotic yeasts to influence metabolic processes in the host organism, including carbohydrate and lipid metabolism and antioxidant defense (Egea, et al, 2023). The present study evaluated selected probiotic-associated properties of *Saccharomyces cerevisiae* CL4 and its effects on metabolic and antioxidant parameters in laboratory rats.

The obtained results indicate the tolerance of the studied strain to physiological temperatures of 28 and 37 °C, but not that of 42 °C, and to modeled conditions of the internal environment of the organism, the viability of cells being 71.0 % and 83.2 % after exposure to low pH and modeled gastric conditions respectively, compared with 45.7 % and 71.9 % for the reference strain *S. cerevisiae* BY4742.