DOES PECTIN METHYLATION MODULATE ITS ANTIMICROBIAL POTENTIAL? INSIGHTS FROM MOLECULAR DOCKING

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ABSTRACT

Pectin is widely studied due to its favorable physicochemical properties, biocompatibility, and non-toxic nature. Methylation of pectin represents a natural structural modification occurring within plant cell walls and is considered part of the defense mechanism against microbial pathogens.

In this study, molecular docking analysis was performed to evaluate whether the degree of methylation influences the predicted antimicrobial activity of pectin derivatives. Four model compounds consisting of three α-1,4-linked D-galacturonic acid units were investigated: non-methylated, mono-methylated, di-methylated and fully methylated derivatives. The negatively charged derivatives (pKa ≈ 3.5) differ in the number of esterified carboxyl groups, while the fully methylated compound is neutral due to complete esterification. Prior to docking, all structures were optimized at the ωB97XD/def2-TZVP level of theory. Docking simulations were carried out against selected microbial protein targets, including *Salmonella Typhi* TtsA, *Pseudomonas aeruginosa* Earp, *Streptococcus mutans* MetE, and *Staphylococcus aureus* Cas9. The analysis focused on predicted binding modes, interaction patterns, and the potential influence of methylation on ligand–protein recognition. The results suggest that variations in methylation do not significantly alter binding site preference or predicted binding affinity among the investigated derivatives. Notably, the fully methylated derivative exhibited distinct binding behavior in the case of *Streptococcus mutans* MetE.

Keywords: pectin; methylation; antimicrobial activity; molecular docking.

Acknowledgment

This work was supported by the Ministry of Science, Technological Development and Innovation of the Republic of Serbia (Contracts No. 451-03-136/2025-03/200026 and 451-03-137/2025-03/200162).