

Structural basis for enhanced MHET degrading activity of engineered feruloyl esterase

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Abstract

Enzymatic degradation offers a promising solution to the persistent accumulation of synthetic plastics in the environment [1]. Since 2000, numerous Poly(ethylene terephthalate) (PET) hydrolases, or PETases, have been identified. These enzymes cleave the ester bonds of the polymer, producing mono-(2-hydroxyethyl) terephthalate (MHET), as primary degradation product [2]. MHET hydrolases (MHETases) further cleave MHET into terephthalic acid (TPA) and ethylene glycol, enabling their reuse as chemical feedstocks. Ferulic acid esterases (E.C. 3.1.1.73, FAEs) are a class of esterases with biotechnological relevance, as they can hydrolyze the ester linkages between hydroxycinnamic acids and arabinose in the plant cell walls. A FAE from *Fusarium oxysporum* (*FoFaeC*, PDB ID: 6FAT) [3], belonging to the tannase-like family, is a structural homolog of the bacterial MHETase from *Ideonella sakaiensis* (PDB ID: 6JTT), [4,5]. *FoFaeC* shows activity on PET oligomers and acts synergistically with PETases to enhance PET degradation [6]. The present study focuses on an *FoFaeC* variant, *FoFaeC_G122S*, engineered by structure-guided mutagenesis to mimic the MHETase active site. This variant displays improved catalytic activity against MHET compared to the native enzyme [6]. Its crystal structure in both apo and benzoic acid-bound forms (PDB IDs: 9I50 and 9HUN) were determined at 1.90 and 1.71 Å resolution, respectively. MHET was subsequently docked into the active site of unmodified *FoFaeC* and G122S variant, followed by molecular dynamics (MD) simulations, to acquire deeper understanding of the observed biochemical findings. The engineered mutation resulted in increased active site flexibility, providing a possible explanation for improved catalytic efficiency. The combined crystallographic and computational analysis provide mechanistic insights into the molecular determinants of PET-active enzymes and their potential for biotechnological applications.

References

[1] Urbanek et al. (2021) *Front Bioeng Biotech.*, 9, 771133., [2] Yoshiba et al. (2021) *Meth Enzym.*, 687, 9, 187-205. [3] Dimarogona et al. (2020) *FEBS Let.*, 594, 1738-1749. [4] Ferousi et al. (2023) *FEBS Let.*, 597, 1415-1427. [5] Sagong et al. (2020) *ACS Cat.*, 10, 4805-4812. [6] Makryniotis et al. (2025) *Int. J. Bion. Macromol.*, 333, 148892.

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