

N°1359 / PC

TOPIC(s) : Enzyme discovery and engineering

Unveiling the structural determinants for substrate recognition and catalysis of bacterial C-glycoside oxidases

AUTHORS

André TABORDA / ITQB NOVA, AV REPÚBLICA, OEIRAS

Tomás FRAZÃO / ITQB NOVA, AV. REPÚBLICA, OEIRAS

Miguel RODRIGUES / ITQB NOVA, AV REPÚBLICA, OEIRAS

Xavier FERNÁNDEZ-LUENGO / DEPARTMENT OF CHEMISTRY, UNIVERSITAT AUTÒNOMA DE BARCELONA, BELLATERRA

Ferran SANCHO / ZYMVOL BIOMODELING, C/ PAU CLARIS, 94, 3B, BARCELONA

Carlos FRAZÃO / ITQB NOVA, AV. REPÚBLICA, OEIRAS

Laura MASGRAU / DEPARTMENT OF CHEMISTRY, UNIVERSITAT AUTÒNOMA DE BARCELONA, BELLATERRA

Rita VENTURA / ITQB NOVA, AV. REPÚBLICA, OEIRAS

Patricia BORGES / ITQB NOVA, AV. REPÚBLICA, OEIRAS

Llgia MARTINS / ITQB NOVA, AV. REPÚBLICA, OEIRAS

Corresponding author : Lígia O. MARTINS / lmartins@itqb.unl.pt

PURPOSE OF THE ABSTRACT

C-glycosides are a class of natural products with biological activities but are recalcitrant to degradation, making their catabolic pathway a topic of interest. C-glycoside 3-oxidases (G3Oxs) are a newly identified group of bacterial flavo-oxidases from the glucose-methanol-choline (GMC) superfamily, which catalyze the oxidation of C-glycosides with the concomitant reduction of O₂ to H₂O₂. Physiologically, this oxidative step is followed by the C-C cleavage through the action of a deglycosylation complex, which releases the sugar and the free aglycone. Despite the high sequence similarity between G3Oxs and the well-studied pyranose-2-oxidases (P2Oxs), which oxidize monosaccharides at the C2 position, these two groups belong to distinct phylogenetic clades. This work shows that a bacterial G3Ox, previously known as AsP2Ox [1], has a 4-order magnitude higher catalytic efficiency (kcat/Km) to the C-glycoside mangiferin compared to D-glucose, which is the preferred substrate of fungal P2Ox. NMR analysis shows that mangiferin is oxidized to 3-keto-mangiferin, and we have renamed AsP2Ox to PsG3Ox [2]. The crystal structure was solved, showing a higher similarity to previously characterized bacterial monomeric G3Oxs [3] than to fungal tetrameric P2Oxs. The combination of mutagenesis, X-ray studies, molecular simulations, and substrate dockings revealed (i) a substrate loop located inside the active site that modulates substrate regioselective recognition, and (ii) a new structural motif, an insertion segment, with a key role for the catalysis. The joint articulation of these two regions is essential for the access and proper accommodation of the substrates in the active site. This work advances our understanding of the structure-function relationships among this family of enzymes and the mechanisms underlying the different substrate specificity between P2Ox and G3Ox.

Aknowledgements: This work was supported by the Fundação para a Ciência e Tecnologia, Portugal, by project grants (PTDC/BII-BBF/29564/2017, EXPL/BIA-BQM/0473/2021 and 2022.02027.PTDC), and PhD fellowships for AT (2020.07928.BD), TF (2022.13872.BDANA) and MVR (2022.09426.BD). B-Ligzymes (GA 824017) from the European Union's Horizon 2020 Research and Innovation Program is acknowledged for funding T.F. secondment at Zymvol.

FIGURES

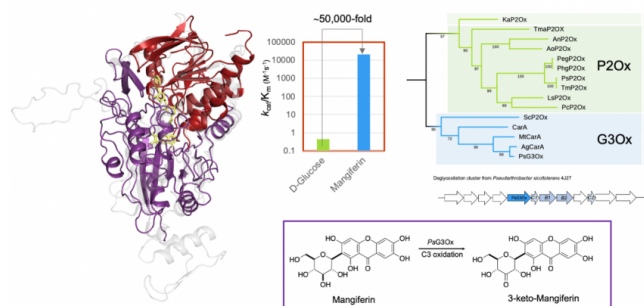


FIGURE 1

Glycoside 3-oxidases: New Bacterial Enzymes With Distinctive Phylogenetic, Functional And Structural Features

FIGURE 2

KEYWORDS

Flavoenzymes | Carbohydrate oxidases | Auxiliary active family AA3 | Glycosides

BIBLIOGRAPHY

1. Mendes, S., et al., Characterization of a bacterial pyranose 2-oxidase from *Arthrobacter siccitolerans*. *Journal of Molecular Catalysis B: Enzymatic*, 2016. 133: p. S34-S43.
2. Taborda, A., et al., Mechanistic Insights into Glycoside 3-Oxidases Involved in C-Glycoside Metabolism in Soil Microorganisms. PREPRINT (Version 1) available at Research Square 2023.
3. Kumano, T., et al., FAD-dependent C-glycoside-metabolizing enzymes in microorganisms: Screening, characterization, and crystal structure analysis. *Proceedings of the National Academy of Sciences*, 2021. 118(40): p. e2106580118.