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Multicopper polyphenol oxidoreductase (laccase) – a novel laccase-mimicking protein family

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PURPOSE OF THE ABSTRACT

Enzymes that require copper essential for their catalytic action are collectively referred to as copper oxidases and include the well-known group of multicopper oxidases (MCOs) [1]. Over the past 12 years, an increasing number of bacterial enzymes have been described as 'laccases' or MCOs. However, a closer analysis of the sequence data reported in literature clearly reveals a lack of conserved sequence information that is typically associated with the MCO family. In this study, we endeavoured to gain a greater understanding of this group of enzymes that mimic MCO (laccase) activity. The sequences of 20 enzymes published as bacterial laccases and 25 structures (linked to those publications) were analysed and compared to MCOs [2]. The analysis revealed that this group of enzymes belongs to a family of proteins annotated as multicopper polyphenol oxidoreductase (MPO) or MPO laccase (MPOL). MPOLs are found in both prokaryotes and eukaryotes and exhibit biochemical properties similar to that of bacterial laccase-like MCOs, including the oxidation of the 'typical' laccase substrates, ABTS, 2,6-dimethoxyphenol, and syringaldazine - characteristics typically used to differentiate MCOs from other copper oxidases. Structural analysis also revealed that there is no similarity between MPOLs and MCOs. The systematic comparison of sequences and structures of large protein families provides an efficient approach for the identification of the structural basis of substrate recognition and catalytic activity and the prediction of activity-specific sequence fingerprints. It further highlighted the need for the incorporation of STRENDA guidelines in the description of novel enzymes, especially in this case where an enzyme of an unrelated protein family was shown to mimic the activities of laccases (and other MCOs) and subsequently erroneously described as a laccase instead of an MPOL.

FIGURE 1

FIGURE 2

KEYWORDS

Multicopper oxidase | Laccase | Multicopper polyphenol oxidoreductase | STRENDA

BIBLIOGRAPHY

[1]. Gr[]ff, M., Buchholz, P.C.F., Le Roes-Hill, M., Pleiss, J. Proteins 2020, 88, 1329 -1339
[2]. Laccase and Multicopper Oxidase Engineering Database, https://lcced.biocatnet.de/