THE PYRROLOQUINOLINE-QUINONE (PQQ)-DEPENDENT QUINOHEMOPROTEIN PYRANOSE DEHYDROGENASE FROM *COPRINOPSIS CINEREA* (*CC*PDH), BELONGING TO THE AA12 FAMILY, DRIVES LYTIC POLYSACCHARIDE MONOOXYGENASE (LPMO) ACTION

Aniko Varnai, NMBU, Norway
aniko.varnai@nmbu.no
Kiwamu Umezawa, Tokyo University of Agriculture and Technology, Japan
Vincent G.H. Eijsink, Norwegian University of Life Sciences (NMBU), Norway
Makoto Yoshida, Tokyo University of Agriculture and Technology, Japan

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Fungi secrete a set of glycoside hydrolases and oxidoreductases, including lytic polysaccharide monooxygenases (LPMOs), for the degradation of plant polysaccharides. LPMOs accelerate the decomposition of cellulose by cellulases by catalyzing the oxidative cleavage of glycosidic bonds after activation by an external electron donor (1-3). LPMOs procure electrons from non-enzymatic electron donors, such as ascorbic acid, lignin and other plant biomass-derived phenols (1-3), or they can be activated by flavin-dependent oxidoreductases, directly or through plant-derived diphenols and quinones acting as redox mediators (3-7). Cellobiose dehydrogenase, in particular, efficiently transfers electrons from its AA3_1 dehydrogenase domain to LPMOs via an appended AA8 cytochrome domain (7). Here we show that LPMOs can be activated by a quinohemoprotein, namely the pyrroloquinoline-quinone (PQQ)-dependent pyranose dehydrogenase *Cc*PDH from *Coprinopsis cinerea,* the founding member of the recently discovered AA12 family (8). *Cc*PDH has a domain composition similar to that of cellobiose dehydrogenases (CDHs) but contains a central catalytic AA12 dehydrogenase domain, rather than an AA3_1 domain. We have studied the ability of full length *Cc*PDH and its truncated variants to drive catalysis by two *Neurospora crassa* LPMOs, *Nc*LPMO9F and *Nc*LPMO9C. Our study shows that both the AA8 and CBM1 domains of *Cc*PDH have a positive effect on the *Cc*PDH-*Nc*LPMO system. The interplay between the PDH and LPMOs seemed also to depend on whether the LPMO contained a CBM. Unlike the single dehydrogenase domain of *Mt*CDH from *Myriococcum thermophylum*, the AA12 dehydrogenase domain of *Cc*PDH could drive the LPMO reaction, which is due to the non-covalently bound PQQ co-factor acting as a diphenol/quinone redox mediator. *Cc*PDH does not oxidize cello-oligosaccharides, which makes this enzyme a useful tool in future studies of LPMOs and redox enzyme systems involved in cellulose degradation.

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