

## Heterologous Expression of *Pleurotus eryngii* Peroxidase Confirms Its Ability To Oxidize $Mn^{2+}$ and Different Aromatic Substrates

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Received 6 May 1999/Accepted 16 July 1999

**A versatile ligninolytic peroxidase has been cloned from *Pleurotus eryngii* and its allelic variant MnPL2 expressed in *Aspergillus nidulans*, with properties similar to those of the mature enzyme from *P. eryngii*. These include the ability to oxidize  $Mn^{2+}$  and aromatic substrates, confirming that this is a new peroxidase type sharing catalytic properties of lignin peroxidase and manganese peroxidase.**

The ligninolytic enzymes lignin peroxidase (LiP) and manganese peroxidase (or manganese-dependent peroxidase) (MnP) were described in 1983 and 1984 in the fungus *Phanerochaete chrysosporium* (6, 9, 24). Their corresponding cDNA were cloned, and recombinant enzymes were obtained in 1987 to 1989 (11, 15, 18, 25), and the molecular structure of both proteins was reported in 1993 and 1994 (16, 17, 23). A third type of ligninolytic peroxidase has been described in several species of the genera *Pleurotus* and *Bjerkandera*, characterized by sharing catalytic properties of MnP (efficient oxidation of  $Mn^{2+}$  to  $Mn^{3+}$ ) and LiP (oxidation of veratryl alcohol, *p*-dimethoxybenzene, and non-phenolic lignin model dimers) and a high affinity for substituted hydroquinones (2, 7, 8, 12, 13, 20). Recently, two peroxidases produced in solid-state fermentation and liquid cultures of *Pleurotus eryngii* have been cloned, the latter appearing as two 99% identical variants (MnPL1 and MnPL2) encoded by two alleles of the same gene (3, 19). These versatile enzymes have higher sequence and structural homology with *P. chrysosporium* LiP than with MnP, but their molecular models showed a putative  $Mn^{2+}$  interaction site near the internal propionate of heme, accounting for their ability to oxidize low concentrations of this cation. Expression of the gene encoding the peroxidase isolated from *P. eryngii* liquid cultures, allelic variant MnPL2 (19), in *Escherichia coli* (by using the T7 *lac* promoter and terminator) resulted in a recombinant protein detected by immunoblotting (unpublished results). However, all attempts to obtain active peroxidase by protocols described previously (21) for refolding denatured proteins were unsuccessful. In order to obtain an active recombinant enzyme, the expression of *P. eryngii* peroxidase in *Aspergillus nidulans*, as a model organism for fungal genetics studies, was attempted.

A cDNA fragment encoding the whole protein with its signal peptide was amplified, cloned, and used to transform an *A. nidulans* *arg* mutant strain. For this purpose, two PCR primers (5'-CGggatccCCCATGTCTTTCAAGACGC-3' and 5'-GgaattcTTACGATCCAGGGACGGG-3') were synthesized (restriction sites shown in lowercase), and a *Bam*HI-*Eco*RI fragment corresponding to MnPL2 cDNA (GenBank accession no. AF007222) was amplified by using MnPL2 cDNA cloned into pBSK+/- as a template (19). The PCR products were separated on 0.8% agarose and purified, and the *Bam*HI-

*Eco*RI fragment was cloned into *palcA1* (5) (containing the *alcA* promoter inducible by ethanol or threonine and repressed by glucose [10], the *trpC* terminator, and the *argB* gene encoding ornithine carbamoyltransferase as a selection marker), yielding *pALMP2*. Automatic sequencing of the PCR fragment, with synthetic oligonucleotides as primers, confirmed that the sequence matched that of MnPL2 cDNA exactly. Mycelia of *A. nidulans* (*biA1 methG1 argB2*) (IJFM A729, derived from FGSC A89 and A219) were grown at 28°C and 180 rpm in a minimal medium (4) containing 10 µg of D-biotin per liter, 74.5 mg of L-methionine per liter, and 0.53 g of L-arginine per liter. Protoplasts were obtained by incubating washed mycelia (1 g [wet weight]) with Novozym 234 (20 mg) in 1.2 M  $MgSO_4$  (buffered at pH 5.8) containing serum albumin (24 mg) and separated by centrifugation at 4,000 × *g* with an overlay of 0.6 M sorbitol in 0.1 M Tris-HCl (pH 7.5). They were transformed (1 to 2 µg of *pALMP2*) in 10 mM Tris-HCl (pH 7.5) containing polyethylene glycol 6000, sorbitol, and  $CaCl_2$  (26), inoculated in a selective minimal medium with 10 µg of D-biotin per liter, 74.5 mg of L-methionine per liter, and 1 M sucrose, in a soft agar overlay, and incubated at 37°C. Southern blot analysis after DNA digestion (with the *argB* gene as a probe) showed that the plasmid containing *mnpl2* cDNA was integrated in the genome of *A. nidulans*, occupying a position different from that of *argB* of the host fungus, and no evidence for multiple integration was obtained.

Different growth conditions for the recombinant *A. nidulans* strain containing *mnpl2* DNA were investigated for peroxidase production. Since peroxidase expression was under the *alcA* promoter, it was induced by substituting threonine for glucose. The fungus was grown in minimal or complete media (4) containing 10 µg of D-biotin per liter and 74.5 mg of L-methionine per liter at 28°C and 180 rpm for 24 h. Then, washed mycelia were transferred to induction media with the same composition but containing 0.05% glucose and 100 mM threonine, with or without 0.5 g of hemin per liter. Peroxidase activity in culture samples collected during incubation (96 h) was estimated by the formation of  $Mn^{3+}$ -tartrate complex (12). The addition of hemin to the medium was required for peroxidase production in both minimal and complete media, the latter yielding the highest peroxidase activity (up to 150 U/liter). It had already been reported that the addition of hemin to media increased the activities of other peroxidases expressed in ascomycetes (1, 22).

The recombinant peroxidase MnPL2\* from *A. nidulans* was purified from cultures in a hemin-containing complete medium. Maximal peroxidase activity was observed 43 h after

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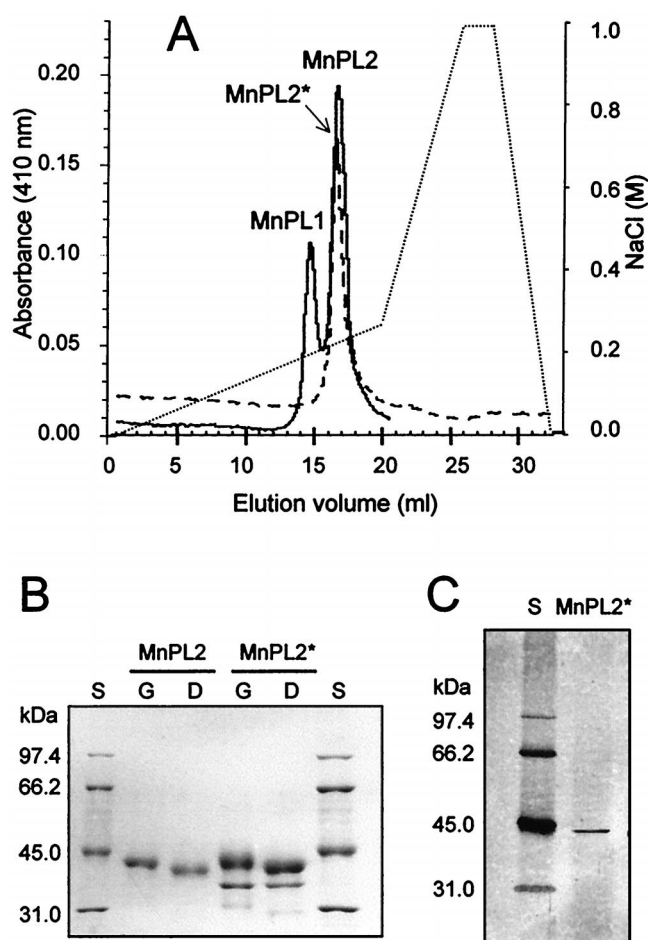


FIG. 1. Purification of peroxidase MnPL2\* from recombinant *A. nidulans*. (A) Superimposition of Mono-Q profiles (410 nm) of protein MnPL2\* from *A. nidulans* (dashed line) and proteins MnPL1 and MnPL2 from *P. eryngii* (solid line) showing the same elution volume for wild-type and recombinant MnPL2 (NaCl gradient shown as a dotted line). (B) SDS-PAGE of proteins in peaks MnPL2\* and MnPL2, showing similar molecular masses before (G) and after (D) deglycosylation; lane S, low-molecular-mass standards from Bio-Rad. (C) SDS-PAGE of glycosylated protein MnPL2\* after a final purification step with ConA, which removed any contaminating protein.

induction, and protein MnPL2\* was purified from concentrated and dialyzed (against 10 mM sodium tartrate, pH 4.5) culture liquid by using the protocol described for *P. eryngii* MnPL2 (12) with an additional step. As shown in Fig. 1A, Mono-Q chromatography yielded a single peak with high absorbance at 410 nm and peroxidase activity corresponding to protein MnPL2\*. This peak showed the same elution volume as allelic variant MnPL2 from *P. eryngii* CBS 613.91 (IJFM A169) grown in glucose-peptone medium (12) (Fig. 1A). Proteins MnPL2 and MnPL2\* were N deglycosylated with endo- $\beta$ -N-acetylglucosaminidase, and sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) of native and deglycosylated proteins was performed in 12% polyacrylamide gels, which were stained with  $\text{AgNO}_3$ . As shown in Fig. 1B, both proteins showed the same molecular mass before (43 kDa) and after (41 kDa) deglycosylation. In the case of protein MnPL2\*, a contaminant protein representing 13% of the peak collected from Mono-Q was detected. Since this protein did not seem to be N glycosylated, a purification step was performed based on affinity for concanavalin A (ConA). The peroxidase peak from Mono-Q chromatography was concentrated, dialyzed against

TABLE 1. Purification of peroxidase MnPL2\* from recombinant *A. nidulans*

Purification step	Amt of protein (mg)	Recombinant peroxidase			
		Total (U)	Specific (U/mg)	Yield (%)	Purification Factor (fold)
Culture liquid	294.3	157	0.5	83	
Ultrafiltered	147.1	190	1.3	100	1
Q-cartridge	66.1	150	2.3	79	2
Sephacryl S-200	28.1	134	4.8	71	4
Mono-Q	0.5	79	161.8	41	126
ConA-Sepharose	0.4	62	148.5	33	115

10 mM sodium tartrate (pH 5) containing 0.5 M NaCl, 1 mM  $\text{MnCl}_2$ , and 1 mM  $\text{CaCl}_2$ , and applied to a ConA-Sepharose column. The retained protein MnPL2\* was eluted with 0.2 M  $\alpha$ -D-methylglucoside, dialyzed, and stored at  $-20^\circ\text{C}$ . In this way, electrophoretically homogeneous MnPL2\* protein was obtained, as shown in Fig. 1C. N-terminal sequencing of the recombinant protein by automated Edman degradation revealed the same sequence obtained for mature protein MnPL2 from *P. eryngii*. The whole process used to purify peroxidase MnPL2\* is summarized in Table 1. The purification yield and factor are relative to peroxidase activity after ultrafiltration, but they should be higher if referred to activity in the culture liquid, where an unknown reaction seemed to partially interfere with the activity assay. Despite the fact that recombinant peroxidase activity in cultures of *A. nidulans* was at a lower level than peroxidase activity in cultures of *P. eryngii* (12), the specific activity of purified protein MnPL2\* was similar to that of protein MnPL2 from *P. eryngii*. Expression in other fungal systems, such as *Aspergillus oryzae* or *Pichia pastoris* (14, 22), will be attempted in the future when high peroxidase levels are required.

Finally, steady-state kinetic constants for oxidation of  $\text{Mn}^{2+}$ , veratryl alcohol, and methoxyhydroquinone by peroxidases MnPL2\* and MnPL2 were compared, under the conditions described for *P. eryngii* peroxidase (8). The apparent  $K_m$  and turnover numbers ( $t$ ) are shown in Table 2, revealing that both peroxidases have similar enzymatic activities oxidizing  $\text{Mn}^{2+}$  to  $\text{Mn}^{3+}$  as well as phenolic and nonphenolic aromatic substrates with high affinity on both  $\text{Mn}^{2+}$  and substituted hydroquinones. The recombinant peroxidase also oxidized 2,6-dimethoxyphenol, although no kinetic constants were calculated. The  $K_m$  for  $\text{H}_2\text{O}_2$  (around 10  $\mu\text{M}$ ) was similar to that of the *P. eryngii* enzyme.

In summary, the *P. eryngii* peroxidase (allelic variant MnPL2) could be successfully expressed and secreted in *A. nidulans* under the *alcA* promoter with the *mnpl2* cDNA including its signal sequence, and electrophoretically homogeneous perox-

TABLE 2. Steady-state kinetic constants of recombinant peroxidase expressed in *A. nidulans* and the corresponding protein produced by *P. eryngii*

Substrate	$K_m$ ( $\mu\text{M}$ )		$t$ ( $\text{s}^{-1}$ )	
	MnPL2* ( <i>A. nidulans</i> )	MnPL2 ( <i>P. eryngii</i> )	MnPL2* ( <i>A. nidulans</i> )	MnPL2 ( <i>P. eryngii</i> )
$\text{Mn}^{2+}$	20	12	99	110
Veratryl alcohol	1,780	2,170	12	13
Methoxyhydroquinone	23	19	10	17

idase MnPL2\* was isolated with a final purification factor of 115. This recombinant protein exhibited the same molecular mass (determined by SDS-PAGE) of peroxidase MnPL2 before and after deglycosylation, as well as the same catalytic properties of the *P. eryngii* enzyme. The latter finding confirms that the enzyme produced by *P. eryngii*, the biochemical and molecular characteristics of which have been recently reported (19), represents a new type of versatile peroxidase sharing catalytic properties of both LiP and MnP of *P. chrysosporium*. Site-directed mutagenesis studies are in progress, to confirm the involvement of several key residues in the catalytic properties of this enzyme, by using the heterologous expression system described here.

We thank M. A. Peñalva (CIB, CSIC, Madrid, Spain) for valuable suggestions and for providing the *A. nidulans* strain and the plasmid palcA1. J. Varela and A. Díaz contributed to protein and DNA sequencing, respectively.

This work was partially supported by the Agro-Industry programme of the EU and the Spanish Biotechnology programme.

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