Heterologous expression of laccase cDNA from Ceriporiopsis subvermispora yields copper-activated apoprotein and complex isoform patterns

Luis F. Larrondo,1 Marcela Avila,1 Loreto Salas,1 Dan Cullen2 and Rafael Vicuña1

1Departamento de Genética Molecular y Microbiología, Facultad de Ciencias Biológicas, Pontificia Universidad Católica de Chile and Instituto Milenio de Biología Fundamental y Aplicada, Santiago, Chile
2USDA Forest Products Laboratory, Madison, WI 53705, USA

Analysis of genomic clones encoding a putative laccase in homokaryon strains of Ceriporiopsis subvermispora led to the identification of an allelic variant of the previously described lcs-1 gene. A cDNA clone corresponding to this gene was expressed in Aspergillus nidulans and in Aspergillus niger. Enzyme assays and Western blots showed that both hosts secreted active laccase. Relative to the isozymic forms of the native C. subvermispora enzyme, the A. niger-produced laccase had a higher molecular mass and gave a single band on IEF gels. In contrast, A. nidulans transformants secreted several isoforms remarkably similar to those of the native system. Considered together with previously reported Southern blots and protein sequencing, expression in A. nidulans supports the view that C. subvermispora has a single laccase gene and that multiple isoforms result from post-translational processes. In addition, several lines of evidence strongly suggest that under copper limitation, A. nidulans secretes apoprotein which can be reconstituted by a short incubation with Cu(I) and to a lesser extent with Cu(II).

INTRODUCTION

Ceriporiopsis subvermispora is one of the most widely used filamentous fungi in laboratory studies of lignin biodegradation. It secretes manganese peroxidase (MnP), a haem protein that catalyses the H2O2-dependent oxidation of Mn(II) to Mn(III) (Glenn & Gold, 1985; Paszczynski et al., 1985), and laccase (EC 1.10.3.2), a member of the multicopper oxidase family of proteins, which includes ascorbate oxidase and ceruloplasmin (Mayer, 1987; Reinhammer, 1984). Laccases catalyse one-electron oxidation of a variety of phenolic compounds, with the concomitant four-electron reduction of O2 to H2O. They are involved in lignin biogenesis in higher plants, and lignin depolymerization by fungi (Eggert et al., 1997; Kirk & Farrell, 1987). Laccases also participate in a broad range of cellular processes such as sporulation (Leatham & Stahman, 1981), fruit body formation and plant pathogenesis (Choi et al., 1992; Geiger et al., 1986; Marbach et al., 1985).

The active site of laccases possesses four copper ions, which can be classified according to their spectrophotometric properties. Type I copper (blue copper) exhibits an intense absorption at about 600 nm, owing to the charge transfer between Cu(II) and a cysteine residue. Type II copper shows a very weak absorption and functions as a one-electron acceptor. Type III copper contains two copper centres absorbing at 330 nm and functions as a two-electron acceptor (Jonsson et al., 1995; Reinhammer, 1984).

Several laccase isoforms can be identified in C. subvermispora cultures depending on the composition of the medium (Salas et al., 1995). Low-stringency Southern blots (Karahanian et al., 1998) and N-terminal sequences of laccases isoenzymes (Salas et al., 1995) suggest a single laccase gene, and its expression is strongly regulated by copper at the transcriptional level (Karahanian et al., 1998). The phenomenon of isoenzyme multiplicity is commonly observed among ligninolytic fungi, although its physiological significance is not known.

To further biochemical analysis of the C. subvermispora laccase we describe here the cloning and expression of Lcs-1 cDNA in Aspergillus nidulans and Aspergillus niger. The A. nidulans system produced multiple isoforms in a pattern that was similar to the native C. subvermispora enzyme, and copper was found to play a post-transcriptional role in laccase expression.
METHODS

Strains. *Ceriporiopsis subvermispora* strain FP-105752 was obtained from the Center for Mycology Research, Forest Products Laboratory, Madison, WI, USA. *Aspergillus nidulans* A722 (pyrG89, pabaA1; fwA1; uaf9) and *Aspergillus niger* A969 (cppA1; fwaA1; pyrG5; metB10) were obtained from the Fungal Genetic Stock Center (FGSC, Kansas City, KS, USA).

Cloning and sequencing. RT-PCR was used to isolate a full-length cDNA as described by Karahanian et al. (1998). Design of primers was based on the genomic sequence of lcs-1 (GenBank accession number AF053472). The upstream primer was located at position −30 from the ATG, whereas the downstream primer was at position +7 with respect to the stop codon. The PCR product, designated Lcs-1, was directly cloned in pBluescript KSII+ as described by Lobos et al. (1998). To obtain genomic clones, lcs-1 was amplified from *C. subvermispora* homokaryons 3 and 8 (Tello et al., 2001). Nucleotide sequence was determined with the ABI-Prism Dye terminator Cycle Sequencing kit (Perkin-Elmer Applied Biosystems) with an ABI373 DNA sequencer. Sequence editing and analysis were done with DNASTar software.

*Aspergillus expression.* The expression vector pExLcs-1 was constructed by placing the Lcs-1 cDNA coding region, including the sequence for its signal sequence, under the control of the TAKA polymerase terminator (Kersten et al., 1995) by the PCR overlap extension technique (Horton et al., 1989) using proofreading polymerase *Pfu* (Stratagene). The coding region and junctions of the expression cassette were sequenced. The selection marker, ppyrG, was obtained from the Fungal Genetic Stock Center.

A. *nidulans* A722 and *A. niger* A969 cotransformations were as described by Larrondo et al. (2001), except that *A. niger* protoplasts were prepared from germinated conidia after an overnight incubation at 300 r.p.m. at 30 °C. Protoplasts were cotransformed with 5 μg ppyrG and 5 μg pExLcs-1. Selection was based on complementation of uridine auxotrophy by the selectable marker ppyrG. Transformants carrying the genetic construction pExLcs-1 were confirmed by PCR.

One hundred millilitres of *Aspergillus* minimal medium (AMM) (Cullen et al., 1987) (5% maltose) or YEM (0-5% yeast extract, 5% maltose) was inoculated with 10^7 spores and incubated for 3 days at 30 °C in an orbital shaker (250 r.p.m.). In the case of *A. niger* A969, the medium was also supplemented with 1 mM methionine. Mycelium was harvested by filtration through Miracloth, snap frozen in liquid nitrogen and stored at −70 °C. For routine cultivations, the medium was supplemented with CuSO_4 up to a final concentration of 100 μM. In copper-deficient cultures, only traces of copper were present (1–3 μM).

We screened rLcs-1 production by plate assay. Isolated transformants were inoculated and selected in agar-minimal medium plates containing maltose (5%) and 1 mM 2,2’-azino-bis-(3-ethylbenzthiazoline-6-sulfonate) (ABTS; Sigma). Characteristic ABTS oxidation could be observed after 2–3 days. Transformants were also evaluated for rLcs-1 production in liquid media by spectrophotometric measurements of ABTS oxidation.

Enzyme purification and characterization. One litre of extracellular fluid from *A. nidulans* Lcs-1 transformant (AniDL-6) culture was directly fractionated by chromatography on Q-Sepharose. One litre of supernatant from *A. niger* Lcs-1 transformant (AnigL-2) was concentrated 10-fold by filtration in a 185 ml Amicon cell possessing a 10 kDa cut-off membrane, and then dialysed twice against 300 ml 25 mM sodium acetate pH 4.5 and fractionated by chromatography on Q-Sepharose (Lobos et al., 1998). Enzyme activity was measured at 30 °C in a Shimadzu 160 UV-visible recording spectrophotometer. Reaction mixtures (1 ml) contained 50 mM glycine, pH 3-0, and 4.33 mM ABTS as substrate. *Km* values for ABTS were determined with 0-01 U laccase, using Eadie–Hofstee plots. For endoglycosidase treatment, 5 μg enzyme was treated as described by Larrondo et al. (2001).

Zymograms were as previously reported (Larrondo et al., 2001). Briefly, samples were applied with nonreducing denaturing loading buffer without boiling and subjected to SDS-PAGE at 4 °C. Gels were then fixed in a solution containing 10% acetic acid and 40% methanol for 10 min followed by incubation in 50 mM glycine buffer, pH 3-0, and 5 mM ABTS for 10 min, or until activity could be detected.

Reconstitution assays. Q-Sepharose-purified laccase (0.5 μg) from low-copper-containing media was incubated at 25 °C with various concentrations of copper as indicated in the corresponding figure legend. Thereafter, samples were withdrawn at the indicated times to measure laccase activity.

Other methods. Analytical IEF and protein concentration measurements were as described by Larrondo et al. (2001); RNA extraction and Northern blot hybridization were as described by Karahanian et al. (1998). The DNA probe corresponding to the entire coding region of Lcs-1 was labelled with [α-32P]dCTP by nick translation (Gibco-BRL).

RESULTS

Characterization of a new lcs-1 allele

In further attempts to isolate and characterize laccase genes from *C. subvermispora*, we have cloned laccase-like amplicons from homokaryotic strains. Each homokaryon harboured a highly conserved, but distinct sequence. Presumed to be allelic variants, the sequences are >99% identical with all but one mismatch occurring in non-coding regions. The single coding region mismatch occurred in the third position of an alanine codon, (GCT to GCC), located in exon X, and did not affect translation. Designated lcs-1A and lcs-1B (accession number AY219235), the former corresponds to the previously deposited lcs-1 sequence AF053472 (Karahanian et al., 1998). (Minor sequencing errors in lcs-1A have been recently corrected.)

Cloning of lcs-1 cDNA

A unique and abundant product was obtained when RT-PCR was conducted with RNA extracted from dikaryotic strain FP105752 of *C. subvermispora* grown in liquid culture containing 100 μM CuSO_4. The cDNA was cloned and sequenced, and based on the nucleotide difference mentioned above, it corresponded to lcs-1B (accession number AY219236).

Production of rLcs-1 in *Aspergillus* spp.

Transformants confirmed by PCR were screened for extracellular laccase activity when grown in minimal medium. Similar levels of enzyme activity were obtained for both *Aspergillus* hosts. No major variations in enzyme activity were detected when AMM or YEM media (both supplemented to 100 μM CuSO_4 final) were used. Laccase activity...
Lcs-1 expression in Aspergillus spp. appeared on day 2, reaching a peak of 0.23 U ml\(^{-1}\) on day 4 and then detected without major variation up to day 5 or 6. For purification purposes, cultures were routinely collected on day 3. The levels of rLcs-1 produced were about 1.5 mg per litre of culture.

**Enzyme purification.** Q-Sepharose purification of laccase from *A. nidulans*-Lcs-1 cultures yielded one major protein (Anid-rLcs-1) with the same molecular mass and immuno-reactivity as the native *C. subvermispora* enzyme (Fig. 1A). Zymograms showed the presence of only one major band, with a higher electrophoretic mobility than the enzyme under reducing conditions (Fig. 1B). The enzyme purified from *A. niger*-Lcs-1 cultures (Anig-rLcs-1) also reacted with antibodies against *C. subvermispora* laccase although its molecular mass was higher than expected. It was also detected as a single band in zymograms, with a lower electrophoretic mobility than Anid-rLcs-1 (Figs 1A and 1B, respectively).

**Isoelectric focusing.** IEF of Anid-rLcs-1 gave a pattern resembling the native *Ceriporiopsis* laccases. In contrast, Anig-rLcs-1 laccase yielded a single IEF band, which was similar in pI to the most basic isoform observed for *C. subvermispora* laccases (Fig. 2).

**Glycosylation.** Treatment of Anid-rLcs-1 with endoglycosidase H revealed N-glycosylation of about 25% of the original molecular mass, a composition similar to the native *C. subvermispora* laccase. A comparable degree of glycosylation was observed with Anig-rLcs-1, but its molecular mass after the treatment remained higher than that of native *C. subvermispora* laccase (Fig. 3) (Salas et al., 1995).

**K\(_m\) for ABTS.** The \(K_m\) values determined for the oxidation of ABTS were 0.042 mM for Anid-rLcs-1 and 0.038 mM for Anig-rLcs-1, which is in accordance with the value of 0.03 mM reported for this enzyme (Fukushima & Kirk, 1995).

**Effect of copper on rLcs-1 production**

Copper dramatically affected laccase titres in YEM cultures of *A. nidulans* Lcs-1. YEM cultures supplemented with 100 \(\mu\)M CuSO\(_4\) yielded laccase levels up to 200 U l\(^{-1}\), as compared to less than 20 U l\(^{-1}\) obtained in unsupplemented growth medium. When normalized by biomass, this represents a sixfold stimulation by copper (Fig. 4A). A similar result was observed when *A. niger* transformants were analysed (data not shown). This effect was not exerted at the transcriptional or the translational levels, as determined by Northern (Fig. 4C) and Western (Fig. 4B) blots, respectively. This suggests that apoprotein is efficiently produced and secreted at low copper levels. The effect of copper on rLcs-1 production is shown in Fig. 4.
copper was also assessed in AMM, with and without added copper. In the absence of externally added copper (copper levels of 1–3 μM), three and five times less activity was observed in A. nidulans and A. niger transformants, respectively.

Partial reconstitution of laccase activity. Copper could be incorporated into the apoprotein, giving rise to active enzyme. When supernatant or Q-Sepharose supernatant pools of Anid-Lcs1 cultures grown at low copper levels were incubated with different copper concentrations, laccase activity could be recovered in a concentration- and time-dependent manner. Concentrations up to 5 mM CuSO₄ were tested. At this copper level, a fourfold increase in activity was achieved (Fig. 5). A larger effect was observed when copper was present as Cu(II) due to incubation of Cu(II) with ascorbate. Maximal reconstitution levels were achieved after 20 min incubation of apoprotein in a solution containing 5 mM CuSO₄ and 1 mM ascorbate. Under these conditions, a ninefold increase in activity was reached, which constitutes about 75% of the maximal activity present in the Q-Sepharose pool obtained from A. nidulans-Lcs-1 grown in YEM medium in the presence of 100 μM CuSO₄ (data not shown). Incubation of the latter enzyme preparation with copper and ascorbate resulted in only a slight increase of activity (15%), which is consistent with the loss of copper during the purification procedure.

DISCUSSION

Laccase isoenzyme multiplicity is a phenomenon observed in several fungi, and in the case of Pleurotus sajor-caju (Soden & Dobson, 2001), the basidiomycete CECT 20197 (Mansur et al., 1997), Pleurotus ostreatus (Palmieri et al., 2000), Trametes villosa (Yaver & Golightly, 1996), Agaricus bisporus (Perry et al., 1993) and Rhizoctonia solani (Wahleithner et al., 1995), families of structurally related genes have been described. In the case of C. subvermispora, over four isoforms are observed, with different substrate specificity, but only one gene, lcs-1, has been identified (Karahanian et al., 1998; Salas et al., 1995). The search for a new laccase gene in C. subvermispora led to the identification of the allelic variant lcs-1B. This allele cannot contribute to the isoform multiplicity observed in this fungus, because the two alleles are predicted to encode identical proteins. Taken together with previously reported low-stringency Southern blots and N-terminal protein sequencing, the results support the existence of a single laccase gene in C. subvermispora.

We were able to successfully express Lcs-1 cDNA in A. nidulans and A. niger. To our knowledge, this is the first report of expression of a white-rot fungus laccase in A. nidulans and the second instance of using A. niger (Record et al., 2002) as a host. Enzyme titres were substantially lower than those reported for other laccases in
Aspergillus oryzae systems (Wahleithner et al., 1995; Yaver et al., 1996, 1999; Record et al., 2002; Berka et al., 1997).

The molecular mass obtained for Anid-rLcs-1 was similar to that of the native enzyme, whereas Anig-rLcs-1 had a higher molecular mass. After treatment with endoglycosidase H, the molecular mass of Anig-rLcs-1 remained higher than that of the native enzyme, which suggests that modifications other than N-glycosylation may alter molecular mass. This was also associated with an altered pI, although the K_m for ABTS remained unchanged.

The IEF pattern of Anid-rLcs-1 was strikingly similar to that obtained with laccase activity from C. subvermispora. The phenomenon of isofrom multiplicity was previously observed with recombinant Cs-MnP1, as well as recombinant Phanerochaete chrysosporium MnP1, both expressed in A. nidulans (Larrondo et al., 2001). We have also observed multiple isoforms for P. chrysosporium multi-copper oxidase when expressed in Aspergillus (L. F. Larrondo and others, unpublished). Thus, our experimental data clearly show that multiple isoforms can arise from a single cDNA, which is consistent with the presence of a single laccase gene in C. subvermispora. The precise nature of isofrom modifications in A. nidulans and C. subvermispora remains unknown. Possibilities of post-translational modification include glycosylation and phosphorylation. Notably, IEF of A. niger-produced laccase revealed a single isoform, indicating that post-translational modifications differ among species of Aspergillus. Further work is required to understand the biochemical basis of this divergence. Prior to this work, there had been a single report of laccase expression in A. niger. In that study, the recombinant protein had the same characteristics as the native enzyme (Record et al., 2002).

It has been reported that the expression of the Trichoderma reesei β-mannanase gene in yeast gives rise to two proteins with different pIs, which match the pIs described for the same activity in T. reesei (Stalbrand et al., 1995). A detailed study of T. reesei cellobiohydrolase I (CBHI) secretion revealed several pI forms during processing in the secretion pathway (Pakula et al., 2000). Both N- and O-glycans might be responsible for the final IEF pattern, but at least in the case of CBHI, it seems plausible that isofrom multiplicity is due to phosphorylation of O-glycans. In addition, sulfation of the glycopeptide region, as described in CBHI produced by the T. reesei strain ALKO2788 (Harrison et al., 1998), cannot be excluded.

Previous investigations have stressed the importance of copper in the regulation of laccase at the transcriptional level (Karahanian et al., 1998; Soden & Dobson, 2001; Palmieri et al., 2000; Galhaup et al., 2002). We previously demonstrated that under low-copper conditions, lcs-1 is not efficiently transcribed in C. subvermispora (Karahanian et al., 1998). Here, we assessed the influence of copper on the laccase titres in a foreign host. Copper limitation decreased production of fully active laccase, but transcript levels remained constant. At low concentrations of this metal, laccase activity was barely detectable. Interestingly, when AMM medium was used, the effect of copper limitation was not as striking as in YEM medium. Biomass and the total extracellular protein produced in YEM cultures were not drastically affected by supplementation with 100 μM CuSO_4. We corroborated this observation by partially recovering activity from supernatants by incubation with copper concentrations in the millimolar range. This implies that the apoprotein lacks some or all of the structural copper atoms necessary for its activity.

There has been some interest in the study of laccase copper centres, by depletion and reconstitution after addition of this metal (Hanna et al., 1988). Usually, this has been achieved by extensive dialysis against cyanide ion. In one case, apoprotein was produced under low copper levels (Bligny et al., 1986), but the activity could not be reconstituted by incubation with copper. On the other hand, reconstitution of laccase from the Chinese lacquer tree requires the addition of Cu(I) and not Cu(II) (Hauenstein & McMillin, 1978). Omura (1961) also reported that Cu(I), but not Cu(II), could be used to reconstitute the apoprotein, results that were confirmed by Ando (1970). In the case of C. subvermispora laccase produced by A. nidulans, spectroscopic studies may help to clarify whether all three types of copper or only a single one are affected in cultures with limiting concentrations of this metal.

The expression systems reported here should be useful for an array of biochemical investigations, including studies of post-transcriptional modification. The results also highlight the importance of adequate copper levels in the production of fully active laccase.

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