Nucleotide sequence of a new lignin peroxidase gene *GLG3* from the white-rot fungus, *Phanerochaete chrysosporium*

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Phanerochaete chrysosporium, a wood-degrading basidiomycete, produces a family of 6 to 10 closely related extracellular, glycosylated, heme proteins, designated lignin peroxidases (LIPs) which are a key component of the lignin degrading system of this organism (1). Sequence data with *LIP* cDNAs (2, 3, 6) and genes (4-6) indicated that the *LIP* gene family contains a number of closely related genes. We present here the complete nt sequence and the deduced aa sequence of a new *LIP* gene *GLG3*. The gene is interrupted by 8 introns ranging in size from 50-60 bp. The gene encodes a 372 aa protein including a 28 aa signal peptide which ends in a Lys-Arg cleavage site. The sequence of the protein encoded by *GLG3* is identical to that of the *LIP* isozyme H8 except for minor aa substitutions. The coding region of this gene has > 96% homology to the gene encoding the *LIP* isozyme H8 and to its allelic variant *ML-4*. Using differences in restriction fragment length polymorphism between *GLG3* and the other two genes, we analyzed the DNA from basidiospore-derived homokaryotic strains and these results showed that *GLG3* is non-allelic to the gene encoding H8. Northern blotting analyses

showed that *GLG3* is expressed only during secondary metabolism.

ACKNOWLEDGEMENTS

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REFERENCES

1. Kirk, T.K. and Farrell, R.L. (1987) *Annu. Rev. Microbiol.* **41**, 465-505.
2. de Boer, H.A., Zhang, Y.Z., Collins, C. and Reddy, C.A. (1987) *Gene* **60**, 93-102; Corrigendum (1988), **69**, 369.
3. Tien, M. and Tu, C.-P.D. (1987) *Nature (London)* **326**, 520-523. Corrigendum (1987) *Nature (London)* **328**, 74.
4. Zhang, Y.Z., Reddy, C.A. and Rasooly, A. (1990) *Gene* (In press).
5. Schalch, H., Gaskell, J., Smith, T.L. and Cullen, D. (1989) *Mol. Cell. Biol.* **9**, 2743-2747.
6. Andrawis, A., Pease, E.A., Kuan, I.-C., Holzbaur, E. and Tien, M. (1989) *Biochem. Biophys. Res. Commun.* **162**, 673-680.

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CGTCATTGCGACTGCTTCT -120
ACGGCGAACAATATCAGGAACGTCGACCAACGCTAGGGTATAAAAGGGCGACAGGACCAACGCGAGTCCCTCAGACATCCAGTCTCTTCCAGTCCCACTCAG - 20
CACCAGCAACACAGCGCATGGCCCTCAAGCAGCTCTTCGACGATCTCTCTCGCTCTCGCTCTCGGCTGCGAAG\GTACGCCCATCGCAGTTAT 80
MetAlaPheLysGluLeuPheAlaAlaIleSerLeuAlaLeuSerLeuSerAlaAlaAsnA 20
CGTTGACCAGTGGAGCTGCTGAAAGTCTGTGTCAG\CGGCTGCGGTTATTCGAGAAGCGCGCCACCTGTTCACCGGCAAGACCGTCGGCGATGC 179
IVS1 laAlaAlaValIleGluLysArgAlaThrCysSerAsnGlyLysThrValGlyAspAl 40
GTGCTCGTGGCTTGGTTCGAGCTCCTGGATGATATCCAGCAGAACCTGTTCCAGCGGCGCCAGTGGCGGCTGAGGCGCAGAGTCGATCTCT\GTG 278
aSerSerCysAlaTrpPheAspValLeuAspAspIleGlnGlnAsnLeuPheHisGlyGlyGlnCysGlyAlaGluAlaHisGluSerIleArgLe 72
AGTGATCCCGTCGCGACCTCTGCTATGATGTTTGAACGCGCCGCCAG\CGTCTTCCACGACTCCATCGCAATTCGCCCGCGCATGGAGGCACAGGG 377
IVS2 eValPheHisAspSerIleAlaIleSerProAlaMetGluAlaGlnG1 88
CAAGTTCGG\GTAAGTTGCCACCGCGTTCGCCACCTAGTCTGTTGCTGATCCCTCCTTGAC\CGGCGGTGGTGTGACGGCTCCATCATGATCTTCGA 475
yLysPheG1 IVS3 yGlyGlyGlyAlaAspGlySerIleMetIlePheAs 103
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IleAlaPheAlaGlyAlaValAlaLeuSerAsnCysProGlyAlaProGlnMetAsnPhePheThrGlyArgAlaProA 162
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IVS4 laThrGlnAlaAlaProAspGlyLeuValProGluProPheH 176
TAGGTGCGGTCTACTAGTCATGTCAG\ACACTGTGCGACCAATCATCAACCGTGTCAACGACGCGAGGCGAGTTCGATGAGCTCGAGCTTGTCTGGA 871
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etLeuSerAl1 IVS6 aHisSerValAlaAlaValAsnAspValAspProThrV 215
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IVS7 CysAlaGluThrProPheProThrLeuThrLeuProGlyProGluThrSerValG 363
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lnArgI1 IVS8 eProProProProGlyAla*** 372
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