

Environmental Science Processes & Impacts

Accepted Manuscript



This is an *Accepted Manuscript*, which has been through the Royal Society of Chemistry peer review process and has been accepted for publication.

Accepted Manuscripts are published online shortly after acceptance, before technical editing, formatting and proof reading. Using this free service, authors can make their results available to the community, in citable form, before we publish the edited article. We will replace this *Accepted Manuscript* with the edited and formatted *Advance Article* as soon as it is available.

You can find more information about *Accepted Manuscripts* in the [Information for Authors](#).

Please note that technical editing may introduce minor changes to the text and/or graphics, which may alter content. The journal's standard [Terms & Conditions](#) and the [Ethical guidelines](#) still apply. In no event shall the Royal Society of Chemistry be held responsible for any errors or omissions in this *Accepted Manuscript* or any consequences arising from the use of any information it contains.



rsc.li/process-impacts

Impacts Statements:

Bacterial laccase is multi-copper oxidase extracellular isozyme with broad range substrate range specificity. It is mainly induced in industrial waste degradation for environmental safety. Its molecular and biochemical properties in bacterial system is fragmentary and very less known in literature. Since the bacterial cell is more versatile for its nutritional and environmental adaptation. Hence the knowledge for laccase application of bioremediation for various industrial wastes will open ample opportunities for large scale application due to slight variation in the structural and functional properties of bacterial and fungal laccases. There is limitation at the large scale application. Thus, this manuscript will support to researcher for the understanding thermotolerant mechanism and application of this enzyme at alkaline conditions.

1 **Properties of Bacterial Laccases and Their Application for Bioremediation**
2 **of Industrial Wastes**

3 **Ram Chandra* and Pankaj Chowdhary**

4 *Department of Environmental Microbiology, School for Environmental Sciences*

5 *Babasaheb Bhimrao Ambedkar University (A Central University),*

6 *Vidya Vihar, Raebareli Road, Lucknow, 226025, Uttar Pradesh, India.*

7

8

9

10

11

12

13

14

15

16

17

18

19

20

21

22

23

24

25

26

27

28

29

30 ***Corresponding Author:**

31 **Prof. Ram Chandra**

32 **Telephone:** (+91) 522-2738814 (R); (+91) 522- 22998718 (O); **Fax:** (+91) 0522- 2440821

33 **E-mail address:** prof.chandrabbau@gmail.com; rc_microitrc@yahoo.co.in

34 **Abstract:**

35 The bioremediation process of industrial waste can be made more efficient by using
36 ligninolytic enzymes laccase which is obtained from fungus, bacteria, higher plant, insect and
37 also in lichen etc. Laccase are catalyzed in the mono-electronic oxidation of substrate
38 expenditure of molecular oxygen, this enzyme belong to the multicopper oxidases and
39 participate in the cross linking of monomers, involved in degradation of wide range industrial
40 pollutants. In recent years these enzyme have gained application in industries of pulp and
41 paper, textile and food industry. There are numerous reviews on laccase, however still a lot of
42 information is unknown due to their broad range of function and application. In this review
43 the bacterial laccase has been focused on the bioremediation of various industrial pollutants.
44 A brief description on structural molecular and physicochemical properties has been done.
45 Besides, the mechanism by which reaction is catalyzed, physical basis of thermostability and,
46 enantioselectivity which requires more attention for researcher, and laccase application in
47 various fields of biotechnology has been pointed out.

48

49 **Keywords:** Bacterial laccases; Biotechnological application; Industrial waste; Pulp paper
50 industry; Textile industry

51

52

53

54

55

56

57

58

59

60

61

62

63

64

65

66

67

68 1. Introduction:

69 There are many potential ligninolytic enzymes (LiP, MnP and Laccases) that are widely
70 distributed in nature in different category of taxa.^{1,2} The demand for these enzymes has
71 increased in the recent year due to their potential applications in the diverse biotechnological
72 areas. Among these laccase is most potential with broad range of specificity, and well studied
73 ligninolytic enzyme, which is highly versatile in nature with wide variety of industrial
74 applications. Laccase is an isozyme predominantly present in microbial community which are
75 encoded by different genes and expressed in different organelle and it can be readily detected
76 by gel electrophoresis. Consequently, laccase have been reported in different molecular form
77 i.e. *LCC 1*, *LCC 2*, *LCC 3* and *LCC 4* which one is obtained from *Pleurotus ostreatus*.³
78 Laccases (EC 1.10.3.2) are polyphenol oxidases that catalyze the oxidation of various
79 aromatic compounds, particularly those with electron-donating groups such as phenols (-OH)
80 and anilines (-NH₂), by using molecular oxygen as an electron acceptor.⁴ Further
81 biochemically laccases are monomeric, dimeric or tetrameric glycoproteins and have
82 ubiquitous in nature with four copper atoms and have three types of copper where Type 1
83 copper (T1Cu) is responsible for the oxidation of substrate and also responsible for the blue
84 color of enzyme, have strong electronic absorbance around 610nm and electro-paramagnetic
85 resonance (EPR) detectable, type 2 copper (T2Cu) is colorless it is also EPR detectable and
86 type 3 copper (T3Cu) gives a weak absorbance near the UV spectrum (330nm) but not
87 detectable by EPR.⁵ Laccases use molecular oxygen to oxidize a variety of aromatic and
88 non-aromatic hydrogen donors via a mechanism involving radicals. These radicals can
89 undergo further laccases catalyzed reaction and/or non- enzymatic reaction such as
90 polymerization, and hydrogen abstraction. Therefore, laccase has also the ability to oxidize
91 phenolic and nonphenolic substrate. The phenolic substrate oxidation by laccases result in
92 formation of an aryloxyradicals an active species that is converted to a quinone in the second
93 stage of the oxidation. Though, typical substrate of laccases known to be diphenol oxidase,
94 monophenol e.g. Sinapic acid or Guaiacol can also oxidize polyamines, aminophenols, lignin,
95 aryl diamine, inorganic ions and it may mitigate the toxicity of some polycyclic
96 hydrocarbon.⁶ However 2,2'-azino-bis(3-ethylbenzothiazoline-6-sulphonic acid) or ABTS is
97 substrates which are most commonly used, does not form quinone and is not pH dependent.
98 For this reason it is used to calculate international unit of laccase activity. The structurally,
99 laccases contain 15-30% carbohydrate and have molecular mass 60-90 kDa with acidic
100 isoelectric point around pH 4.0 due to this enzyme shows high stability.^{6,7} Laccase can

101 oxidize wide range of molecules and nearly 100 different types of compound have been
102 identified as substrate which varies from one laccase to another.

103 Most of study has been focused on white-rot fungus in which *Phlebia floridensis* showed
104 higher thermostability at pH 4.5⁸, *Trametes versicolor*, for dye decolorization⁹,
105 *Phanerochaete chrysosporium* has been reported for high laccase activity on solid medium¹⁰.
106 The biostimulatory effect of 2,5 xylidine has been reported in *Pholiota mutabilis*, *leurotus*
107 *ostreatus*, and *Tarmetes versicolor* for laccase production.¹¹ In another study Shingo et al.,
108 reported for degradation of phenolic lignin model compound, 4,6-di(tert-butyl)guaiacol, by
109 *Coriolus versicolor* and production of laccase.¹² Recently, in bacterial laccase polyphenol
110 oxidase activity has been reported in an *Azospirillum lipoferum*¹³, Phenol oxidases, laccase
111 were isolated from cell extracts of the soil bacterium *Pseudomonas putida* F6.¹⁴ Four strains
112 of the bacterial genus Streptomyces (*S. cyaneus*, *S. ipomoea*, *S. griseus* and *S. psammoticus*)
113 and the white-rot fungus *Trametes versicolor* were studied for their ability to produce active
114 extracellular laccase in biologically treated wastewater with different carbon sources.¹⁵
115 Similarly, *Proteus mirabilis*, *Bacillus sp.*, *Raoultella planticola* and *Enterobacter sakazakii*
116 are used for degradation of persistent organic pollutant from biomethanated distillery spent
117 wash but, it is still lacking for industrial application.¹⁶

118 The low substrate specificity makes this enzyme interesting for biotechnology in various
119 purposes, in many industries of pulp-paper and textile industries and bioremediation of
120 various industrial pollutants. Laccases have been predominantly reported in fungi for
121 reduction of colour from complex distillery waste water.¹⁷ But at large scale of laccase
122 production from fungus and applications have limitation due to its slow growth rate,
123 unfavorable submerged aquatic environment and desired low pH range. In contrast bacteria
124 have wide range of bioremediation activity by providing optimum nutrient and environmental
125 condition through biostimulation process. Recently laccases have been proficiently applied in
126 nano biotechnology due to their ability to catalyze electron transfer reaction without any
127 mediator/cofactor.¹⁸ Therefore, the bacteria is used for the different category of waste water
128 treatment containing complex pollutants. However, the information on bacterial laccase in the
129 available literature is scattered. Moreover, the detail properties of bacterial laccase and their
130 biotechnological application is very less known. Furthermore the mechanism of enzyme
131 enantioselectivity and stability at high pH and temperature is also reported in few literatures
132 only. Therefore the present review has updated on bacterial laccase molecular properties,
133 mechanism, its substrate and there thermostability has been highlighted which needs attention
134 of researcher for further study for industrial application.

135 **2. Laccase producing bacterial species:**

136 Laccases have been mostly isolated and characterized from plants and fungi, and only fungal
137 laccases are used currently in biotechnological applications for the detoxification of complex
138 industrial wastewater.¹⁷ Unfortunately, these enzymes usually work only efficiently under
139 mild acidic conditions (pH 4-6) whereas the temperature range (30-55 °C) for catalytic
140 activity is suboptimal. In contrast, little is known about bacterial laccases, which broad range
141 substrate specificity for industrial application. Although recent rapid progress in molecular
142 study the whole genome analysis revealed that these enzymes are widespread in bacteria.
143 Since bacterial genetic tools and biotechnological processes are well established, so
144 developing bacterial laccases would be much more significantly important.

145

146 **Insert table 1 here**

147 Bacterial laccases applications are still limited for industrial use but predominantly used in
148 bioremediation of various industrial wastes. The first bacterial laccases were detected in the
149 plant root associated bacterium *Azospirillum lipoferum*.⁴⁷ Thereafter, laccase has been
150 discovered in a number of bacteria including *Bacillus subtilis*, *Bordetella compestris*,
151 *Caulobacter crescentus*, *Escherichia coli*, *Mycobacterium tuberculosis*, *Pseudomonas*
152 *syringae*, γ - proteobacterium *Pseudomonas aeruginosa*, and *Yersinia pestis*.^{48,49} Recently,
153 *Stenotrophomonas maltophilia* strain has been found to be laccase producing, which has been
154 used to degrade synthetic dyes. Bacterial laccases are also reported for decolourization and
155 detoxification of post methanated distillery effluent and chlorolignin containing pulp paper
156 mill waste.^{50,51} In the table 1 the detail of bacterial species and their functions are mentioned.
157 The spore coat protein name as Cot A of *Bacillus subtilis* (Gram positive soil bacterium) is
158 copper dependent laccases, which one is best-studied bacterial laccases. This is the first
159 laccase reported from the endospore coat protein designated as endospore coat component of
160 *Bacillus subtilis* and also first bacterial laccase structurally elucidate in detail structure of
161 bacterial laccase. Cot A gene codes for a 65 kDa protein which belong to the outer spore coat.
162 Cot A gene participates in the biosynthesis of the brown spore pigment which is melanin like
163 product. Cot A protects bacterial spore from UV light and H₂O₂.
164 Further the laccase- like genes CueO has been reported from *E. coli* and CopA from the
165 *Pseudomonas syringae* and *Xanthomonas campestris* also has been considered to encode
166 Pseudo-laccase due to their dependence on 2, 4- dimethoxyphenol oxidation.⁵² A protein

167 encoded by ORF bh2082 of *Bacillus halodurans* C-125 has been identified as a potential
168 bacterium laccase by genome mining, which showed Cu²⁺ resistance properties.⁵³

169 **3. Molecular and physicochemical properties of Laccases:**

170 Laccases are monomeric, dimeric and tetrameric glycoprotein, generally having fewer
171 saccharide compounds (10-25%) in fungi and bacteria than in the plant enzymes. The
172 carbohydrate are covalently linked which are 10-45% of total molecular mass, due to this
173 property enzyme showed higher stability. Mannose is one of the major components of the
174 carbohydrate attached to laccases. The molecular weight of laccases is predicted to be in the
175 range of 50-97 kDa from various experimental reports recently in *Bacillus pumilus*, laccase
176 mol. wt. has been estimated to be 58 kDa, and also laccases molecular weight is 64.8 kDa.
177 ^{54,55} Fig. 4 showing the three dimensional structure of bacterial and fungal laccase (*Bacillus*
178 *subtilis* & *Trametes versicolor*).

179

180 **Insert figure 1 & 2 here**

181

182

183 Since laccase constitute three molecular form of isozyme where reported that *Lac I*, *Lac*
184 *II* and *Lac III*. D'souza Tielo et al. reported that Lac IInd mol. wt 56 which is isozyme of
185 laccase from *Cerrena unicolor*. Further, through SDS-PAGE analysis the molecular mass of
186 *Trametes versicolor*, \approx 97 KDa has been reported.⁵⁷ The above report showed that laccase
187 mol. wt. is varying from one organism to other. The biochemical properties of spore coat
188 protein Cot A of *Bacillus subtilis* has been reported similar with multicopper oxidase
189 including laccase.⁵⁸ Further, studies has revealed that Cot A contain all the structural feature
190 of laccase including the reactive surface-exposed copper center (T1) and two buried copper
191 centers (T2 and T3). The most thermostable laccases have been isolated from *Streptomyces*
192 *lavendulae* with half-life 100 minutes at 70 °C and in *Bacillus subtilis* for Cot A is reported
193 112 minutes at 80 °C.^{59,60} Amino acid sequence alignment of cot A with *Coprinopsis cinereus*
194 laccase and zucchini ascorbate oxidase used to generate structural model as shown in fig 3
195 which has been proposed by Ligia O. Martins et al.⁶¹ Since the redox potential of any
196 substrate also play very important role for the laccase activity. The redox potential (is a
197 measure of the tendency of a chemical species to acquire electrons and thereby be reduced) of
198 bacterial laccases ranges from 0.4-0.5 V in bacteria⁶² but they are active and stable at high
199 temperature (66 h at 60 °C), pH 7-9 and salt concentrations.^{63,64}

200

201 **Insert figure 3 here**

202

203

204 As it is known that the first gene and c-DNA sequence were recorded for laccases from
205 the fungi *Neurospora crassa*, *Aspergillus nidulans*, *Coriolus hirsutus* and *Phlebia radiata*.
206 Since then the number of laccases gene sequenced and has increased considerably. The
207 sequences mostly encode polypeptides of approximately 500 to 600 amino acid in *Bacillus*
208 *subtilis* (Cot A gene) which is 513 amino acid long and mol. wt. is 65 KDa.⁶⁰

209

210 **Insert figure 4 here**

211

212

213 Typical eukaryotic signal peptide sequences of about 21 amino acids are found at the N-
214 terminal of the protein sequences. In addition to the secretion signal sequence, laccase genes
215 from *Neurospora crassa*, *Podospora anserina*, *Myceliophthora thermophila* and *Coprinopsis*
216 *cinereus* contain regions that code for N-terminal cleavable propeptides. These laccases also
217 have C-terminal extensions of controversial function, i.e. the last amino acids from the
218 predicted amino acid sequence are not present in the mature protein. Fig. 5 shows that active
219 site of copper oxidase. Active site of CueO (T1Cu, T2Cu, and T3Cu) in ribbon form shown
220 in different colour (blue, green and orange respectively) and also shows that Asp 112 is
221 located behind the tri-nuclear copper center.

222

223 **Insert figure 5 here**

224

225

226 There are also numerous laccase isozyme are able to degraded industrial pollutants. Here
227 we have discussed about the transcript levels of laccase genes *lcc 1*, *lcc 2*, and *lcc 3*
228 (*Basidomycete sp.*) in the presence of veratryl alcohol. The *lcc1* gene is inducible in the early
229 stage of growth and *lcc 2* gene is also inducible but only when organism reaches the
230 stationary phase, where as the transcript level of *lcc 3* were un-induced and repressed by
231 glucose⁵⁶ shown in fig. 1. And also fig. 2, shows that *Basidomycete sp.* I-62 genomic DNA
232 digested with three restriction enzymes (*Pst I*, *Sca I*, and *Sam I*) and specific probe are used.
233 In fig. 2 Southern blot containing total DNA from *Basidomycetes* completely digested by
234 three restriction enzymes has been hybridized under low stringency condition, similarly in
235 highly stringent condition gave a different pattern of bands for each gene. Thus, it has been
236 confirmed that the chosen probe were specific for each laccase gene and adequate to perform
237 transcription analysis.

238 4. Substrate of Laccases and its bioassay:

239 Laccases can oxidize a wide range of molecules more than hundred different types of
240 compound have been identified as substrate for laccase. There are various natural and
241 synthetic substrates which are mentioned in table 2, used for laccase assay. All substrates
242 cannot be directly oxidized by laccases, either because of their large size which inhibit their
243 penetration into the enzyme active site or because of their particular high redox potential. To
244 overcome this hindrance, suitable chemical mediators are used which are oxidized by the
245 laccase and their oxidized forms are then able to interact with high redox potential substrate
246 targets.⁶⁵ Most commonly used substrate are the ABTS, by the free radicals. Although
247 polyphenol oxidases are copper proteins are able to oxidize aromatic compounds with
248 molecular oxygen as the terminal electron acceptor. Polyphenol oxidases are associated with
249 three types of activities.⁶⁶ Catechol oxidase or *o*-diphenol: oxygen oxidoreductase (EC
250 1.10.3.1)

251 a) Laccases or *p*-diphenol: oxygen oxidoreductase (EC 1.10.3.2)

252 b) Cresolase or monophenols monooxygenase (EC 1.18.14.1)

253 D. Faure et al., compared commercial fungal laccase and catechol oxidase, purified from
254 *Pyricularia oryzae* and *Agaricus bisporus*, respectively, with bacterial laccase from *A.*
255 *lipoferum* by using several substrates and phenol oxidase inhibitors.⁶⁷ Five classes of
256 chemical compounds were investigated as substrates for laccase:

257 (1) L-tyrosine and several substituted monophenols such as *p*-coumaric and *o*-
258 hydroxyphenylacetic or salicylic acids;

259 (2) *o*-diphenols (catechol, pyrogallol, guaiacol, and protocatechic, gallic, and caffeic acids),
260 L-3, 4- dihydroxyphenylalanine and *o*-aminophenol, which could be oxidized by both
261 laccase and catechol oxidase;

262 (3) *p*-diphenol and *p*-substituted aromatic compounds as typical *p*-phenol oxidase (*p*-PO)
263 substrates such as hydroquinone, *p*-cresol, *p*-aminophenol and *p*-phenylenediamine;

264 (4) *m*-diphenols such as resorcinol, orcinol, 4-hexylresorcinol, and 5- pentadecylresorcinol;

265 (5) Other laccase substrates such as syringaldazine, 1-naphthol, ABTS, and 4- and 5-
266 hydroxyindoles. The range of substrates used by *A. lipoferum* laccase was similar to that
267 used by *P. oryzae* laccase.

268

269 **Insert table 2 here**

270

271 In fig. 6 (a) the simplest case is the one in which the substrate molecules are oxidised to
272 the corresponding radicals by direct interaction with the copper cluster. However, the
273 substrates of interest cannot be oxidized directly by laccases, either because they are too large
274 to penetrate into the enzyme active site or because they have a particularly high redox
275 potential. By mimicking nature, it is possible to overcome this limitation with the addition of
276 “redox mediators”, which act as intermediate substrates for laccases, whose oxidized radical
277 forms are able to interact with the bulky or high redox potential substrate targets Fig. 6 (b)

278

279 **Insert figure 6 here**

280

281

282

It is very difficult to define laccases according to substrate because substrate range varies
283 from one organism to another.⁸¹ Laccase have ortho and p-diphenol activity. Immobilized
284 commercial laccase is able to degrade meta, ortho and para-substituted methoxyphenol,
285 chlorophenols and cresols, but the substituted from these three types of phenols are oxidized
286 in different orders and to different extents.⁸² Laccases are remarkably nonspecific as to the
287 including substrate from one laccases to another.⁸³ Laccases substrate specificity and its
288 affinity can also vary inhibited by various reagents such as halides (excluding iodide), azide,
289 cyanide and hydroxide.⁸⁴

290 Bioassay of laccase activity is measured based on the oxidation of various substrate in
291 presence of suitable buffer (i.e. sodium acetate) in acidic pH (5.0). The oxidation product is
292 measured by spectrophotometer taking the absorbance at 420 nm or 450 nm depending upon
293 substrate specificity. ABTS has been most commonly used substrate for laccase bioassay
294 because it acts as cooxidant that can interact with laccase to accomplish electron transfer and
295 it is chemically oxidized in two steps via $ABTS^+$ and $ABTS^{2+}$. Anisyl alcohol, and benzyl
296 alcohol can be better oxidized by $ABTS^{2+}$ than by $ABTS^+$. Assay through ABTS method
297 has been given by Bourbonnais et al. and further used by M. M. Atalla et al. In this method
298 reaction mixture contained 600 μ L sodium acetate buffer (0.1 M, pH 5.0 at 27 °C), 300 μ L
299 ABTS (5 mM), 300 μ L culture filtrate and 1400 μ L distilled water. The mixture is then
300 incubated for 2 min at 30 °C and the absorbance was measured immediately in one-minute
301 intervals. One unit of laccase activity has been defined as activity of an enzyme that catalyzes
302 the conversion of 1 mole of ABTS per minute^{85,86}. Laccase activity has been measured by
303 another substrate guaiacol described by Arora and Gill and by Arora and Sharma . In this
304 method reaction mixture contained 10 mM sodium acetate buffer (pH 5), 2 mM guaiacol and
305 0.2 ml of culture supernatant was incubated at 25°C for 2 h and the absorbance was read at

306 450 nm. The relative enzyme activity has been expressed as colorimetric units/ml (CU/ml).
307 .^{87,88}

308

309 **5. Mechanisms of bacterial laccases**

310 *5.1. Laccases Catalytic Mechanism:* The use of molecular oxygen as the oxidant and water is
311 generated byproduct are very common catalytic features. Laccases catalysis mechanism
312 occurs due to the reduction of the oxygen molecule including the oxidation of one electron
313 with the wide range of aromatic compounds which include polyphenol and also methoxyl
314 substituted monophenol and aromatic amines.^{89,90} Since, laccases have 4 copper atom known
315 as CuT1, at this site reducing substrate are bind and the trinuclear Cu cluster T2/T3, this one
316 responsible for electron transfer from T1Cu to the T2Cu and the T3Cu trinuclear cluster
317 reduction of oxygen to water at trinuclear center, T1Cu, T2Cu, T3Cu are detected by
318 UV/visible and electro-paramagnetic resonance (EPR) spectroscopy.⁹¹

319 It is believed that laccase catalysis involve following mechanism:

- 320 a) Reduction of type 1 copper by reducing substrate.
- 321 b) Internal electron transfer from the type 1 (T1Cu) to the type 2 (T2Cu) and type 3 copper
322 (T3Cu).
- 323 c) Reduction of oxygen to water at the type 2 (T2Cu) and type 3 (T3Cu) site.

324 The type 1 copper (T1Cu) gives blue color of protein (absorbance about 600 nm depends
325 on the intensity of the Scys- Cu^{II} bond and the ligand field strength^{92,93} (type 2 copper does
326 not give any colour but it is EPR detectable and type 3 copper (T3Cu) contains a pair of atom
327 in binuclear conformation that gives a weak absorbance (330nm) but not detected by EPR.⁵
328 Spectroscopy combined with crystallography has provided a detail description of the active
329 site in laccase. Type 2 copper and Type 3 copper form a trinuclear center which one is
330 involve in the catalytic mechanism. In the catalysis mechanism oxygen molecule bind to the
331 trinuclear cluster of asymmetric activation and it is postulated to restrict the access of
332 oxidizing agent. During steady state, laccase catalysis indicated that O₂ reduction takes
333 place.⁹¹ The bonds of the natural substrate, lignin, that are cleaved by laccase include C α -C β
334 cleavage and aryl cleavage. Subsequently, the lignin degradation is proceeded by phenoxy
335 radicals lead to the oxidation at α - carbon or cleavage of bond between α -carbon - β carbon.
336 This oxidation result in an oxygen-centered free radicals, which can be converted into a
337 second enzyme catalyzed reaction to quinone. Then the quione and the free radicals can then
338 undergo polymerization.⁵

339

340 **Insert figure 7 here**

341

342 The Type 2 center coordinate with two histidine ligands and water as ligands. The Type 3
343 coppers are each 4-coordinate, having three histidines (His) ligands and bridging hydroxide
344 (Fig. 7). Reduction of oxygen by laccase appears to occur in two $2e^-$ steps. The first is rate
345 determining step. In this Type 2/3 bridging mode for the first $2e^-$ reduced, the peroxide-level
346 intermediate would facilitate the second $2e^-$ reduction (from the Type 2 and 1 center) in that
347 the peroxide is directly coordinated to reduce Type 2 copper, and the reduced Type 1 is
348 coupled to the Type 3 by the covalent Cys–His linkages.

349 The above information is described about the blue copper oxidase i.e. blue laccase, but
350 there are some authors reported the yellow laccase. Both laccases (yellow and blue) have
351 similar molecular mass (70 kDa)⁹⁴ and specific activity and also it is observed that the yellow
352 laccase are obtained from culture grown on solid state medium while blue forms were
353 isolated from culture grown on liquid medium without lignin.⁹⁵ The yellow laccases are
354 formed by modification of the blue form with low molecular weight lignin decomposition
355 product, and some non- blue laccase (Yellow), have high redox potential allowing them to
356 oxidize non- phenolic compounds without any mediator.⁹⁶ Therefore, it is assumed that
357 yellow form of laccase is as a result of binding of aromatic product of lignin degradation with
358 the blue laccase. It has been postulated that yellow laccase might contain endogenous
359 mediators derived from lignin, which carry out role of exogenous mediator in the reaction of
360 non- phenolic compounds.^{97,95} Due to the insufficient information of yellow laccase it
361 requires more attention of researcher who works on this field.

362

363 *5.2. Thermostability and Enantioselectivity of bacterial Laccase:* Laccases are highly stable,
364 industrially important enzyme capable of oxidizing a large range of substrates. Thermostable
365 enzymes allow high process temperatures with associated higher reaction rates and less risk
366 of microbial contamination.^{98,99} The molecular determination of thermostability is not well
367 understood and cannot be generalized across protein families.¹⁰⁰ Thermostability is playing
368 an important role in the enzyme catalysis, several sequence and structural factor are involved
369 in this phenomenon. Some of the mechanism/indicator of increased thermostability include: a
370 more highly hydrophobic core, tighter packing (compactness), deleted loop, greater rigidity
371 (e.g. through increased Proline content in loop), higher secondary structure content, greater
372 polar surface area, fewer thermolabile residue, increased H-bonding, higher isoelectric point,
373 disulfide bridge, more salt bridge and buried polar interaction.¹⁰¹ Amino acid like Glycine,
374 Lysine, Tyrosine and Isoleucine are preferred in mesophiles.¹⁰² Isoleucine is preferred to

375 leucine in hydrophobic region of the structure because the side chain carbon can exist which
376 can result in tighter chain packing.¹⁰³ And also enhance thermostability of laccase from
377 *Bacillus* HR03 using site directed mutagenesis of surface loop. In which glutamic acid 188
378 was substituted with 2 positive (Lysine and Arginine) and 1 hydrophobic (Alanine)
379 residues.¹⁰⁴ There are some bacteria which show the thermostability at different temperatures.
380 a. Cot A from *B. subtilis* at 75 °C showed maximum activity⁶⁰ and at 80 °C wild type
381 Cot A have a life of 4 hr. whereas recombinant Cot A from *E. coli* have a half life of 2 hr.
382 b. And also *T. thermophilum* laccase have optimum activity at 92 °C with a half life of 4 hr.
383 at 80 °C attains 60% activity after incubation for 10 min. at 100 °C.

384 Enantioselectivity is the degree to which one enantiomer of a chiral product is
385 preferentially produced in a chemical reaction. In other words enantioselectivity is the result
386 of difference between the enantiomers, not only in activation enthalpy but also in activation
387 entropy.¹⁰⁵ Traditionally, an enzyme has been regarded as a lock to which only one of the
388 enantiomeric keys would fit. Later, this model has been modified to incorporate enzyme
389 flexibility and became a glove that only fits one hand. It would be important to note that
390 accrual with smaller particle sizes increases reaction rates and enantiomeric ratios during
391 biocatalyzation.¹⁰⁶ Production of enantioselective compounds for biomedical application has
392 become possible by immobilized enzymes.^{107,108} It also plays a central role within life and is
393 manifold exploit by using biocatalysis as a key step I the development of fine chemicals and
394 drug synthesis. But how it helps, mechanism is not completely known therefore it needs to
395 focus more to elucidate thermostability and enantioselectivity of laccase.

396

397 **6. Laccases Immobilization:**

398 Immobilized commercial laccase has been reported to degrade meta, ortho and para-
399 substituted methoxyphenol, chlorophenols and cresols, and also some recalcitrant compound
400 because when enzyme is immobilized, it becomes more durable, vigorous and resistant
401 towards the alteration in environment and allowing for easy recovery and multiple reuse of
402 these enzyme.

403 Laccase immobilization by alginate gel has been carried out according to the method of Lu et
404 al.¹⁰⁹ In this method 2% sodium alginate and 2% calcium chloride was used to prepare the
405 alginate immobilized laccase. *Trametes versicolor* on silica chemically modified with
406 imidazol groups, are used in the decolorization of textile dyes.¹¹⁰ Laccase immobilization
407 by gelatin has been carried out according to the method of Crecchio et al.¹¹¹ Hence 2.5%
408 gelatin was used to immobilize the laccase. Immobilization of laccase (LCC2) by

409 polyacrylamide gel has been reported by Trevan and Grover.¹¹² Buffered Monomer Solution
410 (2.0 g of acrylamide and 0.1 g of bisacrylamide in 10 ml of 100 mM sodium phosphate buffer
411 [pH 6.0]) was used to immobilize the laccase.

412 Immobilization of laccases can protect them from denaturation by organic co-solvent,
413 increase their stability.¹¹³ And also it facilitates the separation of reaction products and have a
414 good catalytic capacity over many reactions cycles.¹¹⁴⁻¹¹⁶ Laccases are well known
415 biocatalysts in transforming phenolic or aromatic amines and are considered some of the
416 most promising enzymes for future industrial applications.¹¹⁷ The immobilized spore laccases
417 are more compatible with almost all industrial processes. Laccases from the bacteria are
418 highly active and much more stable at high temperatures and high pH value.^{118,119}

419 The enzyme based biosensor, the stabilization of enzymatic activity on the biological
420 recognition element is of great importance. The fabricated an optical biosensor by using
421 staked films where 3- methyl-2 benzothiazotinone hydrazone (MBTH) has been immobilized
422 in a hybrid nafion/sol-set silicate film and laccase in a chitosan film for the detection of
423 phenolic compounds to detect catechol.¹²⁰ A disposable biosensor based on immobilization of
424 laccase with silica spheres on the multi-walled carbon nanotubes (MWCNTs)- doped screen-
425 printed electrode (SPE) has been determine DA based on a non-oxidative mechanism in a
426 rapid, selective and sensitive way.¹²¹ The magnetically separable particles have also attracted
427 much attention as a means to facilitate reuse and reduce mechanical stress during separation.

428 There are several techniques may be applied to immobilize enzymes on solid supports.
429 They are mainly based on chemical and physical mechanism.¹²² Enzyme may be immobilized
430 by a variety of method (adsorption, entrapment, cross linking and covalent bonding also self-
431 immobilization) mainly based on chemical and/or physical mechanism. Since the methods for
432 the immobilization procedures greatly influence the properties of the resulting biocatalyst,
433 immobilization strategy determines the process specifications for the catalyst. Therefore the
434 general goal of the immobilization is to obtain stable catalysts with long life times and low
435 cost, we think that the combination of these techniques will enhance: (i) the adsorption of
436 laccase on appropriate substrate, (ii) the life time of the laccase activity and (iii) reutilization
437 of the substrate/ Laccase product.

438

439 **7. Application of Laccases for industrial waste detoxification:**

440 Laccase have broad range substrate specificity due to this, it oxidized wide range of
441 pollutants present in industrial wastes. The bacterial laccases are playing important role in
442 bioremediation of industrial waste because it oxidizes both the toxic and nontoxic substrate

443 and also laccase include the cleaning of industrial effluents, mostly from industries of paper
444 and pulp, textile and distillery industries. Among the biological agents, laccases represent an
445 interesting group of ubiquitous, oxidoreductase enzymes that show promise of offering great
446 potential for biotechnological application.⁹¹ In particular, laccases from fungi have found
447 wide applications ranging from the pharmaceutical sector to the pulp and paper industry to
448 reduce the kappa number (an indication of the residual lignin content or bleach ability of
449 wood pulp) and enhance the bleaching of kraft pulp when they are used in the presence of
450 chemical mediators, such as ABTS¹²³ The role of fungal laccases for detoxification of
451 molasses distillery wastewater has been reported by Pant and Adholeya.^{17,124}
452 As well as, decontamination of phenolic pollutants in soil could be directed towards their
453 immobilization (humification) by oxidative coupling catalyzed by laccases, reducing their
454 biodisponibility so far.¹²⁵⁻¹²⁹ On the adverse, pollutants might undergo oxidative
455 transformation (degradation) by laccases to easily up-taken products by soil microflora¹³⁰
456 (Fig. 8). In the paper industries laccase are play important role, in which one of the most
457 studied application are laccase-mediator bleaching of kraft pulp and efficiency of which has
458 proven in mill-scale trials.¹³¹

459 **Insert figure 8 here**

460 *7.1. Oxidation of phenolic and non-phenolic substrate:* Laccases catalyze by subtraction of
461 one electron from phenolic hydroxyl groups of phenolic lignin model compounds, such as
462 vanillyl glycol, 4,6-di(t-butyl)guaiacol, and syringaldehyde, to form phenoxy radicals, which
463 generally undergo polymerization via radical coupling. The reaction is also accompanied by
464 demethylation, formation of quinone, resulting in ring cleavage.¹³² The degradation of
465 phenolic β -1 lignin substructure models occurs via the formation of phenoxy radicals that
466 leads to $C\alpha$ - $C\beta$ cleavage, $C\alpha$ oxidation, alkyl-aryl cleavage, and aromatic ring cleavage.¹³³
467 Laccase catalyzes oxidation of phenols, anilines, and benzenethiols correlates with the redox
468 potential difference between laccases T1 copper site and the substrate. The presence of
469 electron-withdrawing o- and p-substituents reduces the electron density at the phenoxy group
470 and, hence, more difficult to be oxidized the phenolic substrate further (less susceptible to
471 electron transfer to the T1 copper site). Bulky substituents, which impose steric interference
472 with substrate binding, cause a decrease in reactivity.
473 Laccase has been found to oxidize non-phenolic model compounds and β -1 lignin dimers in
474 the presence of a mediator, indicating that the enzyme plays a significant role in

475 depolymerization of lignin and pulp delignification.¹³⁴ The most studied mediator for laccase,
476 2,2'-azinobis-(3-ethylbenzthiazoline-6-sulfonate (ABTS), 1-hydroxybenzotriazole (HBT),
477 and 3-hydroxyanthranilic acid (HAA). The oxidation is different for ABTS and HBT involving
478 a di-cation and a benzotriazolyl-1-oxide radical, respectively¹³⁵ Oxygen uptake by laccase is
479 faster with ABTS than HBT, but the oxidation of non-phenolic substrate is comparable for
480 both mediators. ABTS-mediated oxidation of non-phenolic substrate proceeds via an electron
481 transfer mechanism.¹³⁶ In the oxidation process the ABTS is first oxidized to the radical
482 cation (ABTS.⁺) and then to the di-cation (ABTS²⁺) with redox potentials of 472 mV
483 (ABTS/ABTS.⁺) and 885 mV (ABTS.⁺/ABTS²⁺), respectively¹³⁷. The di-cation is the active
484 intermediate responsible for the oxidation of the non-phenolic substrate. HBT-mediated
485 oxidation of non-phenolic substrate involves initial oxidation of HBT to HBT.⁺ by laccase,
486 followed by immediate deprotonation to form the N-oxy radical. The latter abstracts the
487 benzylic H-atom from the substrate, converting it to a radical. The oxidation of veratryl
488 alcohol by laccase- ABTS and by laccase-HBT (radical H- abstraction mechanism) showed
489 in fig 9. HBT/HBT.⁺, with an E_o value of 1.08 V, has a mediator efficiency with laccase that
490 is higher than that of the ABTS.¹³⁶ The use of laccase/HBT for bleaching of paper pulps and
491 for the removal of lipophilic extractives has been described. Recently, two lignin-derived
492 phenols, syringaldehyde and acetosyringone, have been shown to act as effective laccase
493 mediators for the removal of lipophilic compounds from paper pulp.

494

495 **Insert figure 9 here**

496

497 The degradation of non-phenolic β -O-4 model compounds, which represent the major
498 substructure in lignin, has been studied using laccase-mediator systems. Four types of
499 reactions, β -ether cleavage, C α - C β cleavage, and C α -oxidation and aromatic ring cleavage,
500 are catalyzed by laccase- (Butylated hydroxytoluene) BHT coupled system¹³². In the
501 oxidation of a non-phenolic β -O-4 lignin model dimer, 1-(4-ethoxy-3-methoxyphenyl)-1,3-
502 dihydroxy-2-(2,6-dimethoxyphenoxy)propane, the coupled enzyme/HBT system catalyzes
503 1e⁻ oxidation of the substrate to form β -aryl radical cation or benzylic (C α) radical
504 intermediates. Electron density of the aromatic ring affects the 1e⁻ oxidation by the
505 laccase/1-HBT couple. Substrates containing electron-donating groups favor aromatic ring
506 cleavage products. The β -aryl radical cation is converted to the product via an aromatic ring
507 cleavage, and the benzylic radical is cleaved at the C α - C β bond similar to a Baeyer-Villiger
508 reaction. The β -ether cleavage of the β -O-4 lignin substructure is caused by reaction with the

509 C α -peroxy radical intermediate produced from the benzylic radical.¹³⁸ The rate of oxidation
510 depends on the k_{cat} of the laccase for the mediator and the stability of the enzyme to
511 inactivation by the free radical of the mediator. Because the nonphenolic lignin model dimer
512 is chemically oxidized by the HBT radical, it may infer that oxidation of the C α in the
513 substrate occurs more easily than that of the π electron in the aromatic ring¹³⁹. The work on
514 oxidation of veratryl alcohol may also infer that laccase/ ABTS favors the formation of aryl
515 radical intermediate, while laccase/HBP proceeds with the benzylic radical formation.

516

517 *7.2. Pulp paper industry:* Laccase has been reported for the degradation and decolourization
518 of chlorophenol, chlorolignin containing black liquor and pulp paper mill waste water.¹⁴⁰
519 Pulp paper mill effluent and black liquor containing primary mixture of all pigments, extract
520 of plant along with cellulose and some heavy metals. Lignin is an insoluble complex polymer
521 of phenolic compounds and up to 90% of the lignin is solubilized and removed during
522 pulping process. Filamentous fungi are able to efficiently degrade wastewater by the action of
523 several extract enzyme classes. The laccases have attracted considerable interest for
524 application in pulp bio-bleaching also for industrial application. During lignin degradation,
525 laccase are thought to act on small phenolic lignin fragments which substrate reacts with the
526 lignin polymer, resulting in its degradation. Conventional methods of delignifying or
527 decolourizing paper pulp involve either chlorine or oxygen based chemical oxidant (e.g. ClO₂
528 and O₂).¹⁴¹ In the pulp paper industry the chemical bleaching are very much effective but
529 these methods have serious drawbacks due to generation of hazardous chemical and
530 chlorinated by product. Hence, laccases delignification systems that overcome these
531 drawbacks and can be easily adapted to current pulp production line are attractive
532 alternatives. The direct decolourization and degradation of pulp paper mill effluent include
533 direct dechlorination, cleavage of aromatic rings, and mineralization of polycyclic aromatic
534 hydrocarbons, decolorization of pulp mill effluent. Consequently, metabolic product has been
535 detected through GC/MS-MS analysis.

536

537 *7.3. Distillery industry:* Recently the bacterial laccase also has been reported for the
538 degradation and decolourization of amino carbonyl complex containing distillery effluent.
539 Though, the distillery effluent contains the complex mixture of phenolics metals. Sulfur
540 compounds and melanoidins (amino carbonyl compounds). The detection of metabolic
541 products by GC/ MS-MS analysis from bacterial decolourization of post methanated distillery
542 effluent given strong evidence for metabolization of complex colourant by laccase.⁵⁰ Further

543 a laccase-producing white rot fungus *Trametes* sp. has been tested for bioremediation.
544 Maximum effluent decolourization of 73.3% and chemical oxygen demand (COD) reduction
545 of 61.7% was achieved after 7 days of fungal treatment to 20% v/v of distillery wastes in
546 culture medium. Under these condition, a 35-fold increase in laccase production by this
547 fungus was observed.¹⁴²

548

549 *7.4. Textile industry & Azo dye:* The textile industry containing chemical reagents used are
550 very diverse in chemical composition, ranging from inorganic compound to polymers and
551 organic products.¹⁴³ Laccase has been reported to prevent back- staining of dyed of printed
552 textiles. As part of the washing solution laccase could quickly bleach released dyestuff, thus
553 resulting in the reduction of processing time, energy, and water needed to achieve satisfactory
554 quality of the textile. Laccase-catalyzed textile dye bleaching may also be useful in finishing
555 dyed cotton fabric. Another interesting laccase application in this field is oxidative
556 transformation and consequent coupling of dye precursor to the collagen matrix in hides.
557 Under laccase catalysis, soluble dye precursor could be absorbed, oxidized, and polymerized
558 to give the desired tanning effect. The process could improve dyeing efficiency, reduced cost,
559 or provide improved hide characteristics.¹⁴⁴ Laccases have been broadly studied for the
560 degradation of azo dyes.^{145,146} (In the fig. 10 showing the proposed mechanism of laccase
561 degradation of 3-(2-hydroxy-1-naphthylazo) benzenesulfonic acid.¹⁴⁷ Laccase, manganese
562 peroxidase, lignin peroxidase, and aryl alcohol oxidase activities were found in crude extracts
563 from solid-state cultures. However, only the laccase activity has been found to correlate with
564 color removal, and the subsequently purified preparations were able to perform this reaction
565 in vitro.

566 *7.5. PAH degradation:* Polycyclic aromatic hydrocarbons (PAH) are ubiquitous
567 environmental pollutants. These are produced during the incomplete combustion of fossil
568 fuels and organic wastes and also as a result of various industrial processes.^{148,149} There have
569 been many studies on the biodegradation of various aromatic hydrocarbon, but their low
570 water solubility and subsequent low degradation rates interrupt the bioremediation of PAH
571 polluted environment.¹⁵⁰ Therefore, knowledge of microorganism having a high PAH
572 degrading capability is essential for efficient remediation of PAH contamination. White rot
573 fungi produce extracellular enzyme laccase which oxidize PAHs to corresponding PAH
574 quinones and subsequently degrade the material further to CO₂.

575 **7.6. Detection of Phenol, aniline, Oxygen:** Laccase has been used for detection of various
576 pollutants by developing of biosensor and diagnostic kits. For detecting phenol, anilines, or
577 other reducing substrates, three types of laccase based sensor have been reported. The first
578 type detects the photometric change resulted from the oxidation of a chromogenic substrate,
579 the second type monitors the O₂ concentration change that is coupled to the substrate,
580 oxidation, and the third type uses an electrode that replaces O₂ as the acceptor for the
581 electrons flown from the substrate (through laccase).¹⁴⁴

582

583 **Insert figure 10 here**

584

585

586

587 **Insert table 3 here**

588

589 Laccase has been studied intensively for myriad applications other than bioremediation.

590 These applications are discussed briefly below and summarized in Table 3.

591

592 **Insert figure 11 here**

593

594

595 Laccases have been employed for several biotechnological application showing in fig. 11 and
596 also in organic synthesis as the oxidation of functional groups, the coupling of phenol and
597 steroids, medical agents i.e. anesthetics, anti- inflammatory, antibiotics and sedatives etc.

598

599 **8. Difference of bacterial laccases from fungus**

600 The largest group of enzyme in the latter study has been indeed fungal laccase, as reported in
601 earlier section ¹²⁴, which clearly separated in two clusters of sequences from *Ascomycetes*
602 and sequences from *Basidomycetes*. The sequences were selected for the study by the
603 presence of four conserved Cu- oxidase consensus patterns and the study also included a
604 number of bacterial protein sequences. A couple of bacterial sequences were excluded, as
605 they could not be aligned without loss of resolution in phylogenetic analysis.

606 Comparison of amino acid sequences of bacterial laccases reveals a large degree of
607 diversity. This variation is reflected in several molecular parameter of the laccase to
608 approximately 65, 70, and 75 kDa for *Bacillus subtilis*, *Streptomyces lavendulae*, or
609 *Streptomyces cyaneus* laccase.^{159,60} Three dimensional structure of bacteria (*B. subtilis*), and
610 fungi (*T. versicolor*) laccases was predicted by homology modeling approach using
611 template1HL0, 1KYA and 1AOZ, respectively, by Modeller 9v6.¹⁶⁰ (Fig. 4). The qualities of

612 each modeled structure for laccases are carried out, using PROCHECK, ProSA and ProQ.
613 The PROCHECK analysis for modeled laccases shows that 90.1% (bacteria), and 89.5%
614 (fungi) residues were in favored and allowed regions in Ramachandran plot. These values
615 match well with those for experimentally determined model. Result from ProSA gave a z-
616 score (standardizing data on one scale) of -8.28 and -6.28 and protein quality predictor
617 (ProQ) analysis gave a LG score (log of a P-value and MaxSub ranges from 0-1, where 0 is
618 insignificant and 1 very significant) value of 6.006 and 5.293 respectively. These results
619 taken together suggested that the values for homology model built for bacteria and fungi fall
620 within the range of value observed for experimentally determined structure and the built
621 models are very reliable for interpretation. Three dimensional structure predictions, at
622 monomeric level, for all laccases (bacteria, and fungi) suggested that they are composed of
623 three sequentially arranged cupredoxin-like domains as presented in Fig. 4. These cupredoxin
624 domains mainly formed by β -barrels (Greek key motif) consisting of β -sheets and β -
625 strands, arranged in sandwich conformation. Comparative analysis of predicted models
626 shows, first domain present at N-terminal region (blue color) in bacteria (Fig. 4A) is
627 somewhat distorted conformation in comparison with the equivalent domain in fungi (Fig.
628 4B) Fig. 4A depicts, presence of a coiled section, which connects Domain 1 and Domain 2 in
629 bacteria, is absent in fungi. This coiled section also helps in packaging between Domain 1
630 and Domain 2 in bacteria.¹⁶¹

631 In fungi and plant, short α -helical regions connect Domain 1 to Domain 2 and Domain 2
632 to Domain 3 (Fig. 4B). These helices also connect β -strands in structure topology. By
633 comparing models, it is observed that, in bacteria a large loop segment link Domains 2 and 3
634 through external connection (Fig. 4A), whereas, in fungal laccases, the corresponding link is
635 made through internal connections (Fig. 4B). The Domain 2 (green color) acts as bridging
636 element between Domain 1 and Domain 3.¹⁶² The structure analysis revealed, tri-nuclear
637 copper cluster (T2/T3) embedded between Domains 1 and 3 with both domains provide in
638 residues for the coordination of the coppers. The copper interact in residue is highlighted in
639 all modeled structures (Fig. 4).

640 Finally, Domain 3 (red/yellow) in all modeled structures not only contains the
641 mononuclear copper center, but also contributes to the formation of the binding site of the
642 trinuclear copper center, which is located in the interface between Domains 1 and 3.
643 Moreover, in all multicopper oxidases Domain 3 includes the putative substrate binding site,
644 located at the surface of the protein, close to the Type1 mononuclear copper center. A
645 protruding section, formed by a loop and a short alpha-helix, forms a lid-like structure over

646 the substrate binding site in bacteria. There is no similar element has been found in the
647 previously analyzed 3-D structure of fungal laccases. Therefore, this structural element may
648 represent a distinctive feature of bacterial laccase. The overall structure analysis shows that, it
649 shares a common beta-barrel motif in all domains. In all laccases, the C-terminal portion is
650 characterized by short (13 residues) α -helix stretch, stabilized by two disulfide bridges, the
651 first bridge (e.g. in fungi -Cys-106–Cys-509) connects Domains 1–3 and second disulfide
652 bridge (in fungi -Cys-138–Cys-226) connects Domains 1 and 2.⁶⁴ There are various
653 significant functions carried out by bacterial and fungal laccase shown in Table 4.

654

655 **Insert table 4 here**

656

657

658

659

660

661

662

663

664

665

666

667

668

669

670

671

672

673

674

675

676

677

678

679

680

681

682 **9. Conclusions:**

683 Ligninolytic enzymes are playing important role in biotransformation of recalcitrant
684 compounds, in which laccase holds large potential for the economical treatment of waste
685 water containing phenolic compound, PHA, chemical pesticides, synthetic dyes and various
686 emerging pollutants. In some cases enzymatic oxidation of phenolic compounds can generate
687 by-product that convert the blue laccase into yellow laccase (YL), which have no requirement
688 to any mediator to degraded pollutants like blue laccase according to some author. Thus there
689 is need to more attention of researcher in this area. Laccases are highly versatile in nature and
690 they have various applications such as waste water detoxification, and textile dye
691 transformation, in food technology, personal and medical care application and biosensor and
692 analytical application. The biotechnological significance of bacterial laccase has led to
693 increase its demand in recent days.

694

695

696

697

698

699

700

701

702

703

704

705

706

707

708

709

710

711

712

713

714

715

716 **ACKNOWLEDGEMENT:**

717 Financial support from DST, DBT, New Delhi under Project and UGC fellowship to Mr.

718 Pankaj Chowdhary for Ph.D. work is highly acknowledged.

719

720

721

722

723

724

725

726

727

728

729

730

731

732

733

734

735

736

737

738

739

740

741

742

743

744

745

746

747 **References:**

- 748 1. Y. Arakane, S. Muthukrishnan, R.W. Beeman, M.R Kanost, K. J Kramer,
749 *Proceedings of The National Academy of Sciences of the United States of America.*,
750 2005, 102(32), 11337-11342.
- 751 2. S. Riva, *Trends in Biotechnology.*, 2005, 24(5), 219-226.
- 752 3. M. Mansur, M. E. Arias, J. L. Copa-Patino, M. Flardh, A. E. Gonzalez, *Mycologia.*,
753 2003, 95, 1013-1020.
- 754 4. L. Gianfreda, F. Xu, J. M. Bollag, *Bioremediation Journal.*, 1999, 3(1) 1-25.
- 755 5. C. F. Thurston, *Microbiology.*, 1994, 140, 19-26.
- 756 6. P. Baldrian, *FEMS Microbiology Reviews.*, 2006, 30(2), 215-242.
- 757 7. N. Duran, M. A. Rosa, A. D'Annibale, L. Gianfreda, *Enzyme Microb Technol.*, 2002,
758 31, 907-931.
- 759 8. D.S. Arora, P.K.Gill, *World J. Microbiol. Biotechnol.*, 2004, 21, 1021-1028
- 760 9. Diego Moldes, Maria Fernandez-Fernandez, and M. Angeles Sanroman, *The*
761 *Scientific World Journal.*, 2012, doi:10.1100/2012/398725
- 762 10. A. A. Safari Sinegani¹, G. Emtiazi and S. Hajrasuliha, *J. Agric. Sci. Technol.*, 2006,
763 9: 69-76.
- 764 11. J. M. Bollag and A. Leonowicz, *Applied and Environmental Microbiology.*, 1984, 48
765 (4), 849-854.
- 766 12. S. Kawal , T. Umezawa, M. Shimada and T. Higuchi, *FEBS.*, 1988, 236 (2) 309-311
- 767 13. G. Diamantidis, A. Effosse, P. Potier, R. Bally, *Soil Biology & Biochemistry.*, 2000,
768 32, 919-927.
- 769 14. A. M. McMahon, E. M. Doyle, S. Brooks, K. E. O'Connor, *Enzyme and Microbial*
770 *Technology.*, 2007, 40,1435-1441.
- 771 15. J. Margot, C. Bennati-Granier, J. Maillard, P. Blánquez, D. A. Barry and C. Holliger,
772 *AMB Express.*, 2013, 3:63
- 773 16. R. Chandra, R. Singh, *Biochemical Engineering.*, 2012, 61: 49-58.
- 774 17. D. Pant, A. Adholeya, *World Journal of Microbiol and Biotechnol,vol.*, 2009, 25(10),
775 1793-1800.
- 776 18. R. Shraddha Shekher, S. Sehgal, M. Kamthania, A. Kumar, *Enzyme Res.*, 2011, 2011,
777 1-11.
- 778 19. F.A. Lee, C.G. William, *J Bacteriol.*, 1987, 169, 1279-1285.
- 779 20. Y. Isono, M. Hoshino, *Agric Biol Chem.*, 1989, 53, 2197-2203.
- 780 21. J. Cha, D. A. Cooksey, *Proc Natl Acad Sci USA.*, 1991, 88, 8915-8919.

- 781 22. J. C. Freeman, P.G. Nayar, T. P. Begley, J.J. Villafranca, *Biochemistry.*, 1993, 32,
782 4826-4830.
- 783 23. G. Diamantidi, A. Effosse, P. Potier, R. Bally, *Soil Biol Biochem.*, 2000, 32, 919-27.
- 784 24. A. Givaudan, A. Effosse, D. Faure, P. Potier, M. L. Bouillant, R. Bally. *FEMS*
785 *Microbiol Lett.*, 1993, 108, 205-210.
- 786 25. Y. Lee, M. Hendson, N. J. Panopoulos, M. N. Schroth. *J Bacteriol.*, 1994, 176, 173-
787 188.
- 788 26. L. G. Van Waasbergen, M. Hildebrand, B. M. Tebo. *J Bacteriol.*, 1996, 178, 3517-
789 3530.
- 790 27. H. Claus, Z. Filip. *Microbiol Res.*, 1997, 152, 209-215.
- 791 28. S. Shashirekha, L. Uma, Subramanian. *Journal of Industrial Microbiology and*
792 *Biotechnology.*, 1997, 19, 130-133.
- 793 29. M. Okazaki, T. Sugita, M. Shimizu, Y. Ohode, K. Iwamoto, de Vrind-deJong EW, de
794 Vrind JPM, Corstjens PLAM. *Appl Environ Microbiol.*, 1997, 63, 4793-4799.
- 795 30. A. Sanchez-Amat, F. Solano, *Biochem Biophys Res Commun.*, 1997, 240, 787-792.
- 796 31. A. Sanchez-Amat, P. Lucas-Eilo, E. Fernandez, J. C. Garcia-Borron, F. Solano,
797 *Biochim Biophys Acta.*, 2001, 1547, 104-116.
- 798 32. G. Deckert, P.V. Warren, T. Gaasterland, W. G. Young, A. L. Lenox, D. E. Graham,
799 R. Overbeek, M. A. Snead, M. Keller, M. Aujay, R. Huber, R. A. Feldman, J. M.
800 Short, R. V. Swanson. *Nature.*, 1998, 393, 353-358.
- 801 33. GJ Brouwers , JPM de Vrind , PLAM Corstjens, P. Cornelis , C. Baysse , EWDV
802 DeJong . *Appl Environ Microbiol.*, 1999, 65, 1762-1768.
- 803 34. N. Bromberg, N. Duran. *Lett Appl Microbiol.*, 2001, 33, 316-319.
- 804 35. R.C. Senan, T. E. Abraham. *Biodegradation.*, 2004, 15(4), 275-280.
- 805 36. M. F. Hullo, I. Moszer, A. Danchin, I. Martin-Verstraete, *J Bacteriol.*, 2001, 183,
806 5426-5430.
- 807 37. C. Kim, W.W. Lorenz, T. Hoopes, JFD Dean, *J Bacteriol.*, 2001, 183, 4866-4875.
- 808 38. S. A. Roberts, A .Weichsel, G. Grass, K. Thakali, J.T. Hazzard, G .Tollin, C.
809 Rensing, R. William, *Proc Natl Acad Sci USA.*, 2002, 99, 2766-2771.
- 810 39. C. A. Francis, B. M. Tebo, *Appl Environ Microbiol .*, 2001, 67, 4272-4278.
- 811 40. S. T. Fitz-Gibbon, H. Ladner, U.J. Kim, K. O. Stetter, M.I. Simon, J.H. Proc Natl
812 *Acad Sci USA.*, 2002, 99, 984-989.
- 813 41. J. Bains, N. Capalash, P. Sharma. *Biotechnol Lett.*, 2003, 25, 1155-1159.
- 814 42. K. Malhotra, P. Sharma, N. Capalash. *Biotechnol Lett.*, 2004, 26, 1047-1050.

- 815 43. H.J. Ruijssenaars, S. Hartmans. *Appl Microbiol Biotechnol.*, 2004, 65, 117- 182.
- 816 44. F. Rosconi, L. F. Fraguas, G. Martinez-Drets, S. Castro-Sowinski. *Enzyme Microbial*
817 *Technol.*, 2005, 36, 800-807.
- 818 45. D. Arora, R. Sharma. *Appl. Biochem Biotechnol.*, 2010, 160 (6), 1760-1788.
- 819 46. W. Mongkolthanaruk, S. Tongbopit, and A. Bhoonobtong. *African Journal of*
820 *Biotechnol.*, 2012, 11(39), 9391-9398.
- 821 47. A.Givaudan, A. Effose, D. Faure, P. Potier, M. L. Bouillant, R. Bally, *FEMS*
822 *Microbiol Lett.*, 1993, 108, 205-210.
- 823 48. Francisco J. Enguita, LÍgia O. Martins, Adriano O. Henriques, Maria Arménia
824 Carrondo, *J. Biol. Chem.*, 2003, 278(21), 19416-19425.
- 825 49. J. Bains, N. Capalash, P. Sharma, *Biotechnol Lett.*, 2003, 25, 1155-1159.
- 826 50. S. Yadav, R. Chandra. *Biodegradation.*, 2012, 23(4), 609-20.
- 827 51. R. Chandra, R. Singh, *Biochemical Engineering.*, 2012, 61: 49-58.
- 828 52. F. Solano, P. Lucas-Elio, D. Lopez-Serrano, E. Fernandez, A. Sanchez-Amat, *FEMS*
829 *Microbiol Lett.*, 2001, 204, 175-181.
- 830 53. H. J. Ruijssenaars, S. Hartmans, *Appl Microbiol Biotechnol.*, 2004, 65, 117- 182.
- 831 54. Renate Reiss, Julian Ihssen, Linda Thony-Meyer, *BMC Biotechnology.*, 2011, 11, 9.
- 832 55. R. Jaenicke, G. Böhm, *Curr Opin Struct Biol.*, 1998, 8, 738-748.
- 833 56. M. Mansur, Teresa Suarez, E. Aldo. Gonzalez, *Appl Environ Microbiol.*, 1998, 64(2),
834 771-774.
- 835 57. D'Souza-Ticlo, D. Sharma, C. Raghukumar, *Mar Biotechnol.*, 2009, 11, 725-737.
- 836 58. Marie-Franc, Oise Hullo, Ivan Moszer, Antoine Danchin, and Isabelle Martin-
837 Verstraete. *Journal Of Bacteriology.*, 2001, 183(18), 5426-54-30.
- 838 59. T. Suzuki, K. Endo, M. Ito, H. Tsujibo, K. Miyamoto, Y. Inamori, *Biosci Biotechnol*
839 *Biochem.*, 2003, 67, 2167-2175.
- 840 60. L. O. Martins, C. M. Soares, M.M. Pereira, M. Teixeira, T. Costa, G. H. Jones, A. O.
841 Henriques, *J Biol Chem.*, 2002, 277, 18849-18859.
- 842 61. L.O. Martins, C. M. Soares, M. M. Pereira, M. Teixeira, T. Costa, George H Jones,
843 Adriano O. Henriques. *Biotechnol Lett.*, 2004, 26, 1047-1050.
- 844 62. P. Durao, I. Bento, A. T. Fernandes, E. P. Melo, P. F. Lindley, L. O. Martins. *J Biol*
845 *Inorg Chem.*, 2006, 11, 514- 526.
- 846 63. C. Held, A. Kandelbauer, M. Schroeder, Cavaco A-Paulo, G. M. Guebitz. *Environ*
847 *Chem Lett.*, 2005, 3, 74-77.

- 848 64. U. Dwivedi, P. Singh, V. Pandey, A. Kumar. *J Mol Catal B Enzym.*, 2011, 68, 117-
849 128.
- 850 65. D. Arora, R. Sharma. *Appl. Biochem Biotechnol.*, 2010, 160(6), 1760-1788.
- 851 66. M. Mayer. *Phytochemistry.*, 1987, 26, 11-20.
- 852 67. D. Faure, M. L. Bouillant, L. Bally. *Appl Environ Microbiol.*, 1995, 61, 1144-1146.
- 853 68. S. Camarero, D. Ibarra, M. J. Martinez, A.T. Martinez. *Appl. Environ. Microbiol.*,
854 2005, 71, 1775-1784.
- 855 69. S. A. Smirnov, O. V. Koroleva, V. P. Gavrilova, A. B. Belova, and N. L. Klyachko.
856 *Biochemistry (Moscow).*, 2001, 66(7), 774-779.
- 857 70. C. Johannes, A. Majcherczyk, *Appl. Environ. Microbiol.*, 2000, 66, 524-528.
- 858 71. N.N. Pozdnyakova, Rodakiewicz-Nowak, J. Turkovskaya, O.V., 2004, 30, 19-24.
- 859 72. C. Annunziatini, P. Baiocco, M.F. Gerini, O. Lanzalunga, B. Sjogren, *J. Mol. Catal.*
860 *B: Enzym.*, 2005, 32, 89-96.
- 861 73. P. Astolfi, P. Brandi, C. Galli, P. Gentili, M.F. Gerini, L. Greci, O. Lanzalunga, *New*
862 *J. Chem.*, 2005, 29, 1308-1317.
- 863 74. X. Geng, Li, K., F. Xu, *Appl. Microbiol. Biotechnol.*, 2004, 64, 493-496.
- 864 75. A. Gutiérrez, J. Rencoret, D. Ibarra, S. Molina, S. Camarero, J. Romero, J.C. Del Río,
865 A.T. Martínez, *Environmental science & technology.*, 2007, 4124-4129.
- 866 76. R.C. Minussi, G.M. Pastore, N. Duran, *Technol.*, 2007, 98, 158-164.
- 867 77. S. Mishra Salony, V.S. Bisaria, *Microbiol. Biotechnol.*, 2006, 71, 646-653.
- 868 78. H. Cabana, J.-L.H. Jiwan, R. Rozenberg, V. Elisashvili, M. Penninckx, S.N. Agathos,
869 J.P. Jones, 2007. *Chemosphere.*, 67,770-778.
- 870 79. H.Y. Alfarra, N.H.M. Hasali and M.N.Omar, *International Research Journal of*
871 *Biological Sciences.*, 2013, 2(2), 51-54.
- 872 80. I. Bratkovskaya, R. Ivanec, J. Kulys, *Biochemistry.*, 2006, 71, 550-554.
- 873 81. K. S. Shin, Y. J. Lee, *Archives of Biochemistry and Biophysics.*, 2000, 384(1), 109-
874 115.
- 875 82. Lante, A. Crapisi, A. Krastanov, P. Spettoli, *Process Biochemistry.*, 2000, 36, 51-58.
- 876 83. D. A. Wood, *J Gen Microbiol.*, 1980, 117, 339-345.
- 877 84. F. Xu, *Biochemistry.*, 1996, 35, 7608-7614.
- 878 85. R. Bourbonnais, M. G. Paice, I. D. Reid, P. Lanthier, and M. Yaguchi. *Applied and*
879 *Environmental Microbiology*, 1995, 61, (50), 1876-1880.
- 880 86. M. Mabrouk Atalla, H. Kheiralla Zeinab, R. Hamed Eman, A. Youssry Amani, A.
881 Abd El Aty Abeer. *Saudi Journal of Biological Sciences*, 2013, 20, 373-381.

- 882 87. D. S. Arora and P. K. Gill. *World Journal of Microbiology & Biotechnology.*, 2005,
883 21, 1021–1028
- 884 88. D.S. Arora and R.K. Sharma, *Journal of Animal and Feed Sciences.*, 2009, 18, 151–
885 161.
- 886 89. Dedeyan, A. Klonowska, S. Tagger, T. Tron, G. Iacazio, G. Gil, J. L. Petit, *Appl*
887 *Environ Microbio.*, 2000, 66, 925-929.
- 888 90. O. Rubilar, M. C. Diez, L. Gianfreda. *Critical Reviews in Env Sci and Technolo.*,
889 2008, 38, 227-268.
- 890 91. L. Gianfreda, F. Xu, J. M. Bollag. *Bioremediation Journal.*, 1999, 3(1) 1-25.
- 891 92. E. I. Solomon, U. M. Sundaram, T. E. Machonkin. *Chem Rev.*, 1996, 96, 2563-2605.
- 892 93. L. Quintar, C. Stoj, A. B. Taylor, P. J. Hart, D. J.Kosman, E.I. Soloan, *Acc Chem*
893 *Rev.*, 2007, 40, 455-452.
- 894 94. Augustin C. Mot, Marcel Parvu, Grigore Damian, Florin D. Irimiea, Zsuzsanna
895 Darula, Katalin F. Medzihradskyd, Balazs Brema, Radu Silaghi-Dumitrescu,
896 *Process Biochemistry.*, 2012, 47, 968-975.
- 897 95. A. A. Leontievsky, T. Vares, P. Lankinen, J. K. Shergill, N. N. Pozdny- akova, N. M.
898 Myasodeva, N. Kalkkinen, L. A. Golovleva, R. Cammack, C. F. Thurston, A.
899 Hatakka, *FEMS Microbiol Lett.*, 1997, 156, 9-14.
- 900 96. N. N. Pozdnyakova, O. V. Turkovskaya, E. N. Yudina, Rodakiewicz-Nowak Ya,
901 *Applied Biochemistry and Microbiology.*, 2006, 42, (1), 56-61.
- 902 97. J. Rodakiewicz- Nowak, J. Haber, N. Pozdnyakova, A. Leontievsky, L. A. Golovleva,
903 *Biosci Rep.*, 1999, 19, 589-600.
- 904 98. S. Kumar, C-J Tsai, R. Nussinov, *Protein Eng.*, 2000, 13, 179-191.
- 905 99. K. Hilde'n, T. Hakala, T. Lundell, *Biotechnol Lett.*, 2009, 31, 1117-1128.
- 906 100. R. Jaenicke, G. Bo'hm, *Curr Opin Struct Biol.*, 1998, 8, 738-748,.
- 907 101. I. Matsui, K. Harata, *FEBS J.*, 2007, 274, 4012-4022.
- 908 102. S. T. Farias, M. C. Bonato, *Genet Mol Res*, 2003, 2(4), 383-393.
- 909 103. R. J. Russell, J. M. Ferguson, D. W. Hough, M. J. Danson, G. L. Taylor, *A*
910 *resolution. Biochemistry.*, 1997, 36(33), 9983-9994.
- 911 104. N. Mollania, K. Khajeh, B. Raanjbar, S. Hosseinkhaanis, *Enzyme Microb*
912 *technol.*, 2011, 49 (5), 446-52.
- 913 105. R. S. Phillips, *Enzyme Microb Technol.*, 1992, 14, 417-419.
- 914 106. S. Sabbani, E. Hedenström, O. Nordin, *J Mol Catal B-Enzym.*, 2006, 42, 1-9.

- 915 107. G. Ren, X. Xu, Q. Liu, J. Cheng, X. Yuan, L. Wu, Y. Wan, *React Funct*
916 *Polym.*, 2006, 66, 1559-1564.
- 917 108. C. H. Lee, T. S. Lin, C. Y. Mou, *NANO.*, 2009, 4, 165-179.
- 918 109. Lu, L., Zhao, M., Wang, Y., *World J. Microb. Biot.*, 2007, 23, 159 - 166.
919
- 920 110. Peralta- Zamora, P., C. M. Pereira, E.R.L. Tiburtius, S.G. Moraes, M.A. Rosa,
921 R.C. Minussi and N. Duran., *Appl. Catal. B.*, 2003, 42, 131-144.
- 922 111. Crecchio, C., Ruggiero, P., Pizzigallo, M.D.R., *Biotechnol. Bioeng.* 1995, 48, 585 -
923 591.
- 924 112. Trevan, M.D., Grover, S., *Biochem. Soc. Trans.*, 1979, 7, 28 - 30.
- 925 113. A. D'Annibale, S. R. Stazi, V. Vinciguerra, G. Giovannozzi Sermanni, *J Biotechnol.*,
926 2000, 77, 265-273.
- 927 114. N. Duran, E. Esposito, *Appl Catal B Environ.*, 2000, 28, 83-99.
- 928 115. G. Palmeri, P. Giardina, G. Sannia, *Biotechnol., Prog.*, 2005, 21, 1436-1441.
- 929 116. P. Brandi, A. D'Annibale, C. Galli, P. Gentili, A. S. N. Pontes, *J Mol Catal B*
930 *Enzyme.*, 2006, 41: 61-69.
- 931 117. F. Xu, *Industrial Biotechnology.*, 2005, 1(1), 38-50.
- 932 118. G. Singh, N. Capalash, R. Goel, P. Sharma, *Enzyme Microb Technol.*, 2007, 41, 794-
933 799.
- 934 119. G. Singh, N. Ahuja, M. Batish, N. Capalash, P. Sharma, *Bioresource Technology.*,
935 2008, 99, 7472-7479.
- 936 120. K. M. Alimini Abdul, M. S. M. Annuar, *Asia Pacific Journal of Molecular Biology*
937 *and Biotechnology.*, 2009, 17(2), 47-52.
- 938 121. Li. Yuanting, Li. Zhang, Li. Meng, Zhigang Pan, Li. Dawei, *Chemistry Central*
939 *Journal.*, 2012, 6, 103.
- 940 122. O. Zaborsky, "In Immobilized enzymes," *Cleveland: CRC Press*, 1974.
- 941 123. R. Bourbonnais, M. G. Paice, B. Freiermuth, E. Bodie, S. Borneman, *Appl Environ*
942 *Microbiol.*, 1997, 12, 4627-4632.
- 943 124. D. Pant, A. Adholeya, *Bioresour Technol.*, 2007, 98, 2321-2334.
- 944 125. K. Tatsumi, S. Wada, H. Ichikawa, S. Y. Liu, J. M. Bollag, *Water Sci Technol.*,
945 1992, 26, 2157-2160.
- 946 126. J. M. Bollag, S-Y Liu, R. D. Minard, *Soil Sci Soc Am J.*, 1980, 44, 52-76.

- 947 127. G. Dawel, M. Kastner, J. Michels, W. Poppitz, W. Gunther, W. Fritsche, *Appl*
948 *Environ Microbiol.*, 1997, 63, 2560-5.
- 949 128. J. Dec, J. M. Bollag, *J Environ Qual.*, 2000, 29, 665-76.
- 950 129. Ana I. Cañas, Susana Camarero. *Biotechnol. Adv.*, 2010, 28, 694-705.
- 951 130. L. Gainfreda, M. A. Rao, *Enzyme Microb Technol.*, 2004, 35, 339-54.
- 952 131. E. Strebtonik, K. E. Hammel, *Journal of Biotechnology.*, 2000, 81(2-3), 179-188.
- 953 132. Kawai, S., Umezawa, T., & Higuchi, T. *Archives of Biochemistry and Biophysics*,
954 1999, 262, 99–110, doi: 10.1016/0003-9861(88)90172-5.
- 955 133. S. Kawai, T. Umezawa, M. Shimada, & T. Higuchi, *FEBS Letters.*, 1999, 236, 309-
956 311, doi:10.1016/0014-5793(88)80043-7.
- 957 134. R. Bourbonnais, & M. G. Paice, *FEBS Lett.*, 1990, 267, 99-102.
- 958 135. R. Bourbonnais, M. G. Paice, B. Freiermuth, E. Bodie, & S. Borneman, *Applied And*
959 *Environmental Microbiology.*, 1997, 63(12), 4627-4632
- 960 136. P. Baiocco, A. M. Barreca, M. Fabbrini, , C. Galli, & P. Gentili, *Organ*
961 *Biomolecular Chemistry.*, 2003, 1, 191-197, doi:10.1039/b208951c.
- 962 137. H. Claus , G. Faber, & H. Konig, *Applied Microbiology and Biotechnology.*, 2002,
963 59, 672-678, doi:10.1007/s00253-002-1047-z.
- 964 138. S. Kawai, M. Iwatsuki, M. Nakagawa, M., Inagaki, A. Hamabe, & H. Ohashi, 2004,
965 5, 154-160, doi:10.1016/j.enzmictec.2004.03.019.
- 966 139. H. Hirai, H. Shibata, S. Kawai, & Nishida, *TFEMS Microbiology Letter.*, 2006, 265,
967 56-59, doi:10.1111/j.1574-6968.2006.00474.x.
- 968 140. R. Chandra, A. Abhishek, M. Sankhwar. *Bioresourse Technology.*, 2011, 102, 6429-
969 6436.
- 970 141. P. Bajpai, and P. K. Bajpai, *Process Biochemistry.*, 1992, 27, 319-325.
- 971 142. T. Gonzalez, M. C. Terron, S. Yague, E. Zapico, G.C. Galletti, and A. E. Gonzalez,
972 *Rapid Communication in Mass Spectrometry*, 2000, 4, 1417-1424.
- 973 143. R.S. Juang, R.L. Tseng, F.C. Wu, S.J. Lin, *J. Environ Sci. Eng.*, 1996; 31: 325–38.
- 974 144. F. Xu, (1999) “Laccase,” In Flickinger, M.C. and Drews, S.W. (eds.), *Encyclopedia of*
975 *Bioprocess Technology: Fermentation, Biocatalysis, Bioseparation*, JohnWiley &
976 Sons Inc., New York, pp. 1545-1554.
- 977 145. M. Chivukula, V. Renganathan, *Appl Environ Microbiol.*, 1995, 61, 4374-4377.
- 978 146. P. Blanquez, N. Casas, X. Font, X. Gabarrell, M. Sarr`a, G. Caminal, T. Vicent,
979 *Water Res.*, 2004, 38, 2166-2172.

- 980 147. Andrea Zille, Barbara Gornacka, Astrid Rehorek, Artur Cavaco-Paulo, *Applied*
981 *Environmental Microbiol.*, 2005, 6711-6718.
- 982 148. M. Alcalde, T. Bulter, F. H. Arnold, *J Biomol Screen.*, 2002, 7, 547-553.
- 983 149. M. Alcalde, M. Ferrer, F. J. Plou, A. Ballesteros, *Trends Biotechnol.*, 2006, 24, 281-
984 287.
- 985 150. L. Levin, A. Viale, and A. Forchiassin, *Int. Biodet. Biodeg.*, 2003, 52, 1-5.
- 986 151. Johann F. Osma, Jose L. Toca-Herrera, and Susana Rodriguez-Couto, *Enzyme*
987 *Research.*, 2010, doi:10.4061/2010/918761
- 988 152. G. Diamantidis, A. Effosse, P. Potier, R. Bally, *Soil Biol. Biochem.*, 2000, 32, 919-
989 927.
- 990 153. A. Kunamneni, I. Ghazi, S. Camarero, A. Ballesteros, F. J. Plou, M. Alcalde, *Proc*
991 *Biochem.*, 2008, 43, 169-178.
- 992 154. Ana I. Cañas, Susana Camarero. *Biotechnol. Adv.*, 2010, 28, 694-705.
- 993 155. R. Chandra, R. Singh, *Biochemical Engineering.*, 2012, 61, 49-58.
- 994 156. S. Yadav, R. Chandra, *J. Environ. Biology.*, 2013, 34(4), 755-764.
- 995 157. R. Chandra, S. Yadav, *Biodegradation.*, 2012, 23, 609-620.
- 996 158. S. Yadav, R. Chandra, V. Rai, *Process Biochemistry.*, 46, 1774-1784.
- 997 159. M.C. Machczynski, E. Vijgenboom, B. Samyn, G.W. Canters, *Protein Sci.*, 2004,
998 13(9), 2388-97.
- 999 160. A. Sali, T.L. Blundell. *J Mol Biol.*, 1993, 234(3), 779-815.
- 1000 161. F.A. Lee, C.G. William, *J Bacteriol.*, 1987, 169, 1279-1285.
- 1001 162. F. Xu, W. Shin, S.H. Brown, J.A. Wahleithner, U.M. Sundaram, E.I. Solomon,
1002 *Biochim. Biophys. Acta.*, 1996, 1292, 303-311.
- 1003 163. J.T. Hoopes, J.F.D. Dean, *Physiol. Biochem.*, 2004, 42, 27-33.
- 1004 164. K. Langfelder, M. Streibel, B. Jahn, G. Haase, A.A. Brakhage., *Fungal Genet Biol.*,
1005 2003, 38, 143-158.
- 1006 165. G. Diamantidis, A. Effosse, P. Potier, R. Bally, *Soil Biol. Biochem.*, 2000, 32, 919-
1007 927.
- 1008 166. A. Gutiérrez, J.C. Del Rio, D. Ibarra, J. Rencoret, J. Romero, M. Speranza,
1009 S. Camarero, M.J. Martínez, A.T. Martínez, *Environ Sci Technol.*, 2006, 40(10), 3416-22.
- 1010
- 1011
- 1012
- 1013

1014 Table.1: There are some known bacterial species/ laccase- like protein and their function

S.No.	Species	Their possible function	Ref.
1.	<i>Leptothrix discophora</i> SS1	Detoxification of Mn^{2+} , destruction of toxic oxygen species	19
2.	<i>Pseudomonas maltophilia</i>	Shows nucleoside oxidase activity	20
3.	<i>Pseudomonas syringae</i> pv. <i>Tomato</i> (cop A)	Cu^{2+} resistance activity	21
4.	<i>Streptomyces antibioticus</i>	Shows phenoxazinone synthesis activity	22
5.	<i>Azospirillum lipoferum</i>	Pigmentation, oxidation of phenolic compounds, and also electron transport	23,24
6.	<i>Xanthomonas campestris</i> (copA)	Cu^{2+} resistance	25
7.	<i>Bacillus</i> sp. (mnxG)	Sporulation, Mn^{2+} oxidation	26
8.	<i>Bacillus sphaericus</i>	Sporulation and pigmentation	27
9.	<i>Phormidium valderianum</i>	Resistant to higher nitrogen concentration	28
10.	<i>Pseudomonas fluorescens</i> GB-1	Mn^{2+} oxidation, destruction of toxic oxygen species	29
11.	<i>Marinomonas</i> <i>mediterranea</i> (ppoA)	Pigmentation	30,31
12.	<i>Aquifex aeolicus</i> (suf 1)	Work as cell division protein	32
13.	<i>Pseudomonas putida</i> GB 1	Mn^{2+} oxidation	33-35
14.	<i>Bacillus subtilis</i> (cotA)	Pigmentation of spores, UV and H_2O_2 resistance	36
15.	<i>E. coli</i> (yacK)	Cu^{2+} , oxidation of phenolate- siderophores ferrooxidase activity	37,38
16.	<i>Pseudomonas</i> sp. (CumA)	Mn^{2+} oxidation	39
17.	α - <i>proteobacterium</i> SD21	Mn^{2+} oxidation	39
18.	<i>Pseudomonas aerophilum</i> (pae1888)	Unknown	40
19.	γ - <i>proteobacterium</i> JB	Oxidation of toxic compounds	41,42
20.	<i>Bacillus halodurans</i> C-125 (lbh 2082)	Cu^{2+} resistance	43
21.	<i>Shinorhizobium meliloti</i>	Thermostable	44
22.	<i>Stenotrophomonas</i> <i>maltophilia</i>	Degrade synthetic dyes	45
23.	<i>Rhodococcus</i> sp.	Reduction of synthetic dye	46

1015 Table.2: Natural and synthetic mediator of laccases

S. No.	Natural mediator	Ref.
1.	Acetosyringone	68
2.	Syringaldehyde	68
3.	Vanilin	68
4.	Acetovanillone	68
5.	Sinapic acid	69
6.	Ferulic acid	69
7.	p- coumaric acid	68
8.	Reduced glutathione	70
9.	Cystine	70
10.	Aniline	70
11.	4 hydroxybenzyl alcohol	70
	Synthetic mediator	
12.	1- hydroxylbenzotrizole (HBT)	71
13.	N- hydroxyphthalimide (HPI)	72
14.	Violuric acid (VLA)	73
15.	N- hydroxylacetanlide (NHA)	74
16.	2,2,6,6-Tetramethylpiperidine- N-oxyl (TEMPO)	75
17.	Acetohydroxamic acid	76
18.	2,2,5,5- Tetramethylpyrrolidine-N-oxyl (PROXYL)	73
20.	2,2'-Azinobis-(3-ethylbenzothiazoline 6-sulfonic acid) (ABTS)	77,78
21.	Guaicol	79
22.	Methyl syringate	80

1016

1017

1018

1019

1020

1021

1022

1023

1024

1025

1026 Table.3: Sectors where the laccases are used in various applications

S. No.	Industries	Main Application	Ref.
1.	Food industry	Brewing; Colour enhancement in tea etc. Cork modification; Wine stabilization; Oxidizing Phenolic compound in apple juice.	151
2.	Textile industry	Denim bleaching; Denim finishing; Denim bleaching and shading.	152
3.	Wood industry	Modification and polymerization of lignin; Increase the mechanical strength and thickness.	
4.	Organic synthesis, Medical, Pharmaceutical, Cosmetics and Nanotechnology	Polymers production; Coupling of phenols and Steroids; Medical agents; Carbon-nitrogen bonds construction; Complex natural products synthesis; Personal hygienic products; Biosensors and bioreporters	153
5.	Bioremediation	Polycyclic aromatic hydrocarbons (PAHs) degradation; Biodegradation of xenobiotics	154
6.	Paper industry	Pulp bleaching; Paper pulp delignification.	123,155
7.	Distillery industry	Removal of dark brown color.	156-158

1027

1028

1029 TABLE: 4. Functional difference of bacterial laccase from fungus

S. No.	Bacteria	Fungus	Reference
1.	Melanin formation, endospore coat protein synthesis	Delignification, pigmentation, fruiting body formation as well as pathogenesis	163,164
2.	Localization in bacteria most of the laccases are intracellular	Localization of fungal laccase is extracellular	165
3.	Bacterial laccase have low- redox potential	Fungal laccase (especially white rot fungi) have high redox potential	166
4.	The bacterial thermal stability is higher	The fungal laccase usually have lower thermal stability than bacterial laccase	64

1030

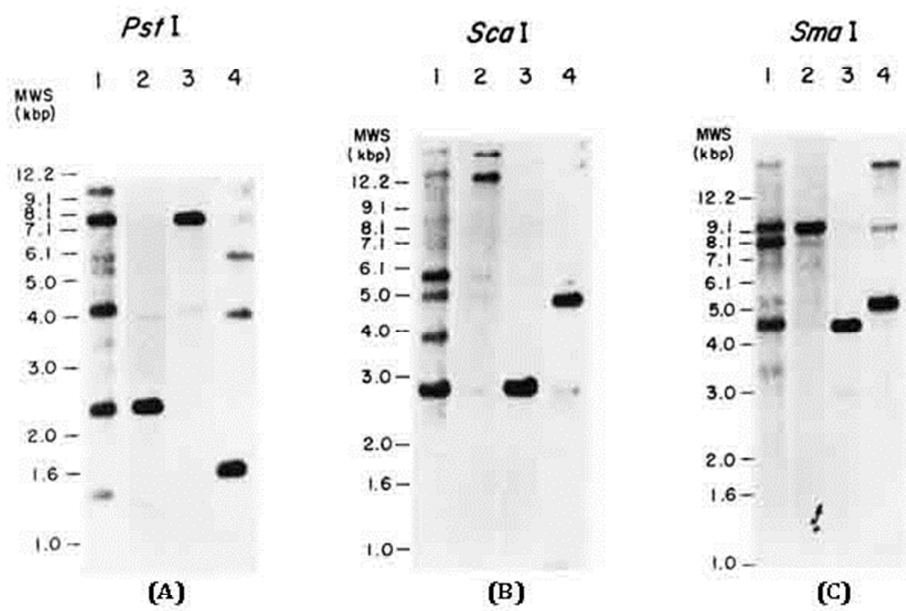


FIGURE 1: Northern analyses of *lcc1*, *lcc2*, and *lcc3* transcription patterns. (A) Total RNA samples from mycelium growing on inducing medium; (B) total RNA samples from mycelium growing on fructose medium. The actin hybridization shown in panel B corresponds to a longer exposure time. EtBr, (ethidium bromide).⁷²

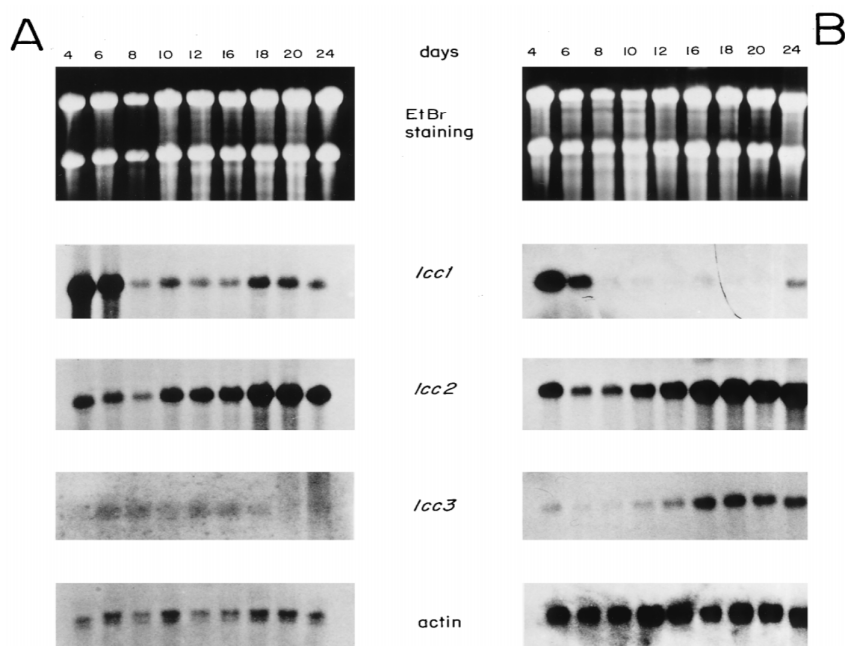


FIGURE 2: Southern analyses of *Basidiomycete* I-62 genomic DNA digested with three restriction enzymes (*PstI*, *ScaI*, and *SmaI*) and hybridized with a heterologous probe from the *Basidiomycete* PM1 *lacI* lacase gene under low-stringency hybridization conditions (lanes 1), an *lcc1*-specific probe (lanes 2), an *lcc2*-specific probe (lanes 3), and an *lcc3*-specific probe (lanes 4). MWS, molecular sizes.⁷²


```

1A0Z   SQI---RHYKWEVEYMFWAPNCNE--NIVMGINQFPGP---TIRANA-GDSVVVELTNKLHT-----EGVVIH-WH-GILQR
1A65   ---QIVNSVDIMLTIANVSPDGF--RAGILVNGVH---GPLIRGGK-NDNFELNVNDLD-NFTM-----LRPTSI-HW-HGLFQR
CotA   -----YEVMEECTHQLHRDL--PPTRLWGYNGLFPGP---TIEV-KRNENVYVKMMNLPSTHFLPIDHTIHHSDSQHEEPEVKTVVH-LH-GGVTP
      :          :          :          :          :          :          :          :          :          :
1A0Z   GTPWADGTASISQCAINPO---ETFFYNFIV-DNPOTF---FYH-QH-LQ----MQRSAGLYOSLIVDPQP-GKKE-PF-HYDGE-----INLLSDW
1A65   GTNWADGADGVNQCPISPQ---HAFLYKFTPAGHAGTF---WY-HS-HFG----TQYCDGLRQPMVIYDD---N-DPHAALYDEDDEN---TIITLADW
CotA   DDSDGYPEAWFSPKDFEQTPYFKREVYHY-PNQQRG---AILWYH-DH-A-MALTRLNVYAGLVGAYI IHDPKREKRLKLPQDEYVPLLIIDRTINEDGSL
      :          :          :          :          :          :          :          :          :          :
1A0Z   WHQSIH--KQEVGLSSKPI-RWI--GEPQTILLNGRQGF-DCSIAAKYDSNLEP---CKLKGESESC-A-PYIFHVSPKTYRIRIASTTALAALNFAIGN
1A65   YHIP--APSI-----QG-AA-QPDATL INKGGRYVG-----GPA-----AE-LSIVNVEQGKKYRMRLISLSCDPNQWQFSIDG
CotA   FYPS--APENPSPSLPNSIV--PAFCGETILVNGKV-----W-PYLEVEP-RKYRFRVINASNIRTYNLSLDN
      :          :          :          :          :          :          :          :          :          :
1A0Z   --HQLLVVEADG-NYVQPFYTSDDIYSGESYSVLIITDQNPSENYWVSV--GTRARHP--NIPP-----GLTLLNLYLPN--SVSK-LPTSPPP
1A65   --HELTIIIEVDG-ELTEPHTVDRLQIFTQQRYSFVLDANQPV-DNYWIRA--QPN---KORNOL--AGTFANOVNSAILRYAGA---ANA-DPT-TS-A
CotA   GG-DFIQIGSDGOLLPRSVKLNFSFLAPAERYDIIIDFTAYEGESIILANSA-----G-----CGGDVNP---ETDANIMQFR-VT--
      :          :          :          :          :          :          :          :          :          :
1A0Z   QTPAWDDFDRSKN-----FTYRIT-AAMGSP-KPPVK-----FNRRIFLLNTQNVINGYVVKWAINDVSLALPPTPYLGAMKYNLHA-----F
1A65   -----NPNPAQLNEADLH-AL--IDPAA---PGIPTQGAADVNLRFQLQFSG---GRFTINGTAYESPSVPTLLQIMSG---AQSandLL
CotA   -----K-PL-AQK-D-ES-----RK---PKYLASYPVQHERIQNIRTL-----KLAGTQDEYGRPVLNLLNKK-----
      :          :          :          :          :          :          :          :          :          :
1A0Z   DQNPPPEVFPEDYDIDTPPTNEK-----TRIGNG--VYQFKIGEVDVILQN-AN-MMKENLS-ETH-PWH-LH-GHDFWLVGY--G-DGKF--S-A
1A65   -----PAGSVYELPRNQVVELVPA-G-VL-----GGP-HPF-HL-HGHAFSVVRSAGSS-----
CotA   -----RWHDPVTI-----ETPKVGITTEIWSIINPTR-----GTH-PIH-LH-LVSFRVLDRRPF-DIARYQE-SG
      :          :          :          :          :          :          :          :          :          :
1A0Z   EEESSLNLKNPP-----LRNIVVIFPY-GWTAIRFVADNPGVWAFHCH---IEPH-LHMGM-GVWFAEGVEK-V--GRIPTKALA-CGGTAKSLINPFKN
1A65   ---TYNFVNPV-----KRDVSLGVTGDEVTI RFVTDNPGPWF--HCHIEF-HLMNG-LAIVFAEDMANIVDANNPPVWAQQLC-----
CotA   ELSYTOPAVPPPSEKQWKDTIQAHAGEVLRIAATFGYPSORYWHCH---ILEH-EDYDM-MRFMDITDPHK-----
      :          :          :          :          :          :          :          :          :          :
1A0Z   P-----
1A65   -EYDDLPEATSITVV
CotA   -----

```

FIGURE 3: Amino acid sequence alignment of CotA with *C. cinereus* laccase and zucchini ascobate oxidase used to generate the structural model. The CotA sequence was then aligned against the primary alignment and used to generate structural models that were checked using Modeler and PROCHECK (Laskowski et al.; see “Materials and Methods”). The alignment was changed to correct for problems detected using the above-mentioned software. Several of these cycles were performed to optimize the alignment, and the structural models were obtained. Two dots indicate similarity, whereas an asterisk indicates identity. Gaps were introduced to maximize the quality of the final structural model for CotA.⁶¹

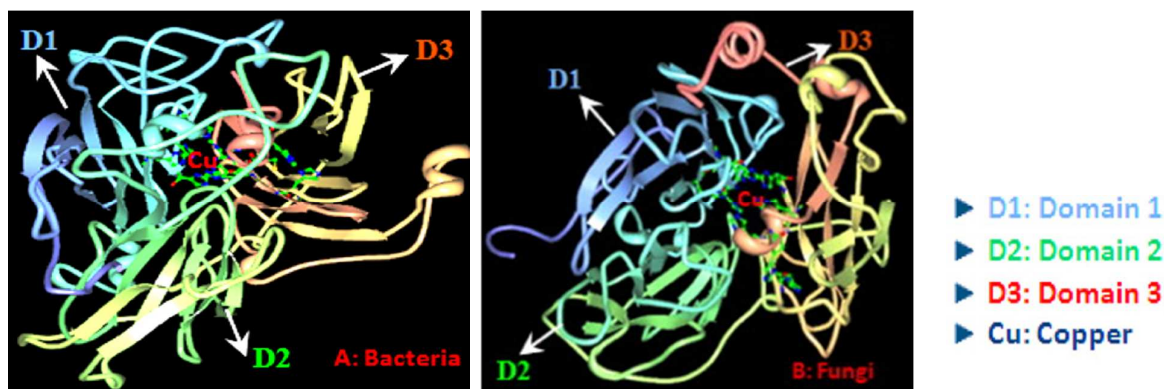


FIGURE 4: Three dimensional structure of bacterial and fungal laccase (*Bacillus subtilis* & *T. versicolor*)

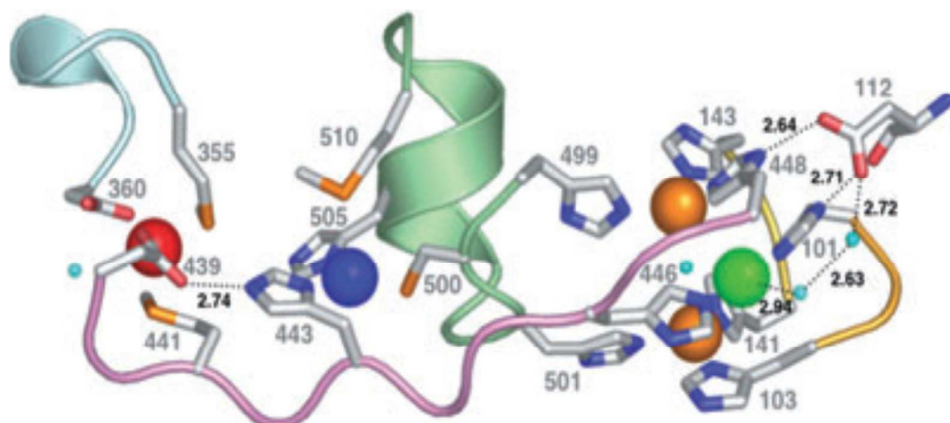


FIGURE 5: Active site of CueO. Type I Cu, type II Cu, and type III Cu's are indicated by blue, green, and orange balls, respectively. The Cu(II) bound at the substrate-binding site is indicated by the red ball. The backbone peptides colored water blue, green, magenta, orange, and yellow show that each Cu center is closely connected with each other. Asp112 is located behind the trinuclear Cu center, forming hydrogen bonds with the imidazoles coordinating to a type II and a type III Cu directly and indirectly through a water molecule. Drawn with PyMol for PDB data, 1N68.

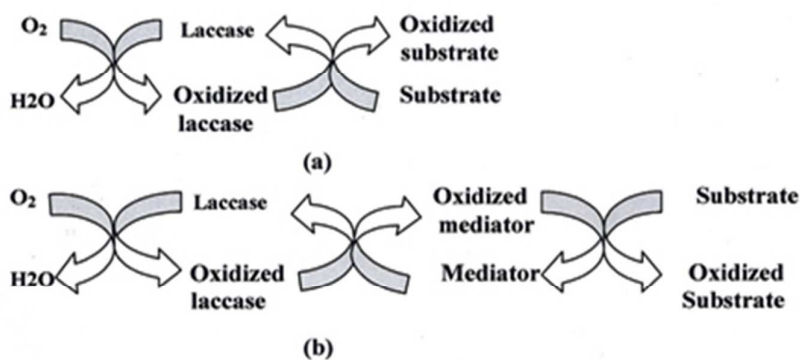


FIGURE 6: Schematic representation of laccase-catalyzed redox cycles for substrates oxidation in the absence (a) or in the presence (b) of redox mediators.

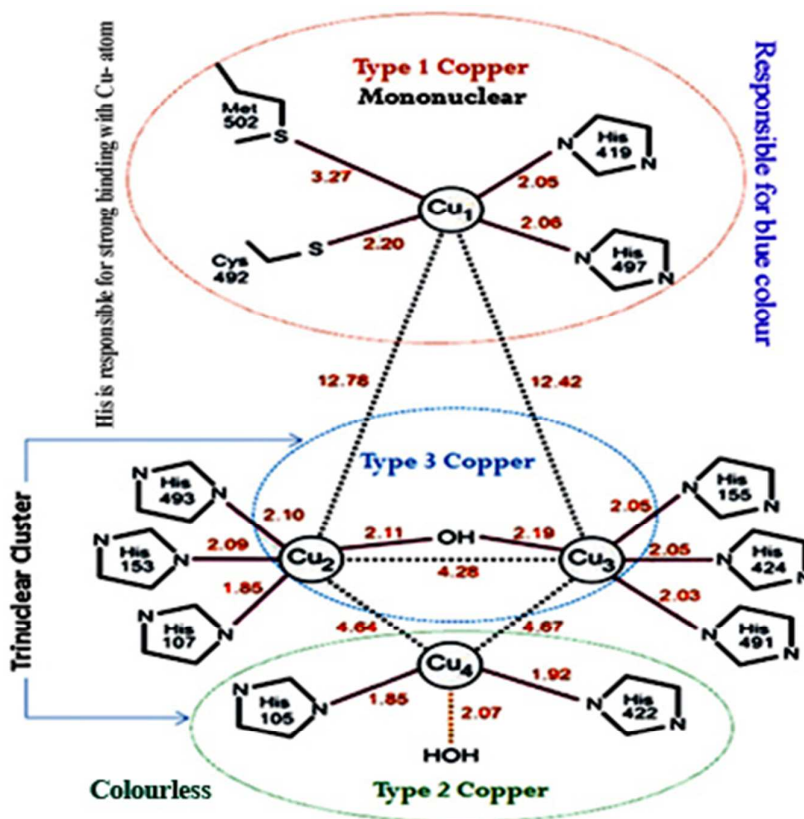


FIGURE 7: The laccase active site showing the relative orientation of the copper atoms including interatomic distances among all relevant ligands.

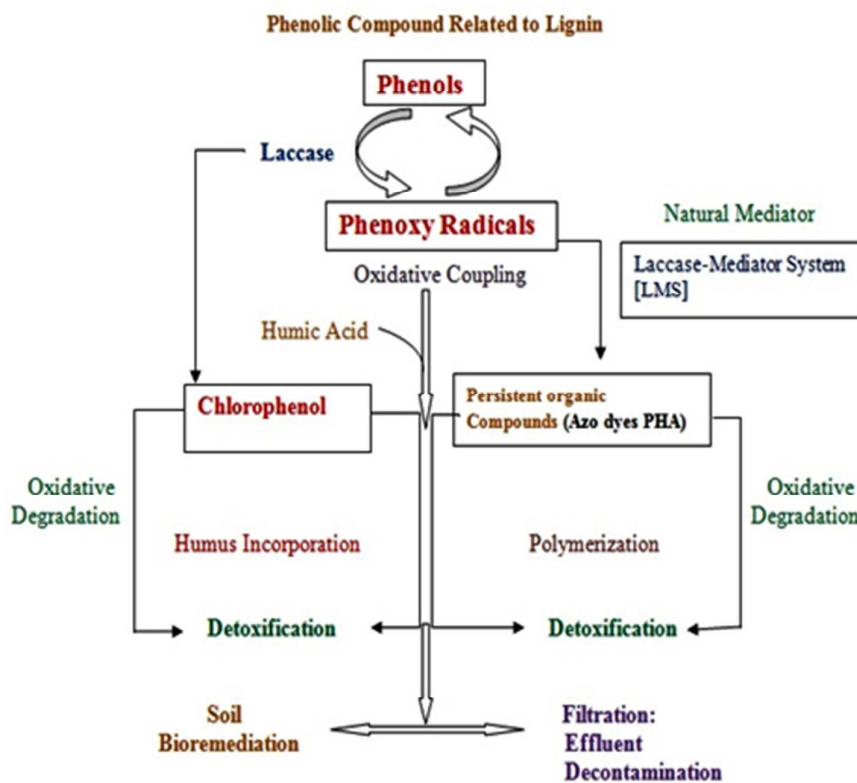


FIGURE 8: Possible role of laccase and their natural phenolic mediators in soil bioremediation and detoxification of industrial waste.¹⁵⁴

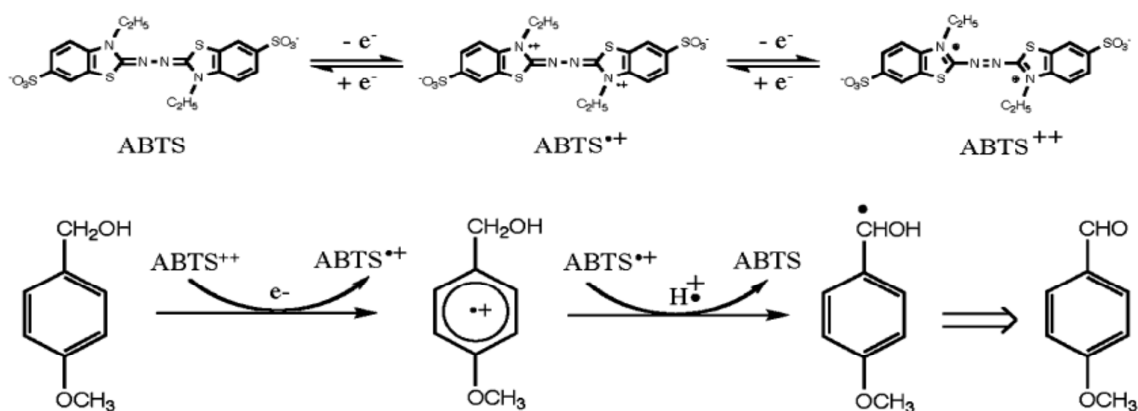


Figure 9: Radical H-atom abstraction and electron transfer mechanism

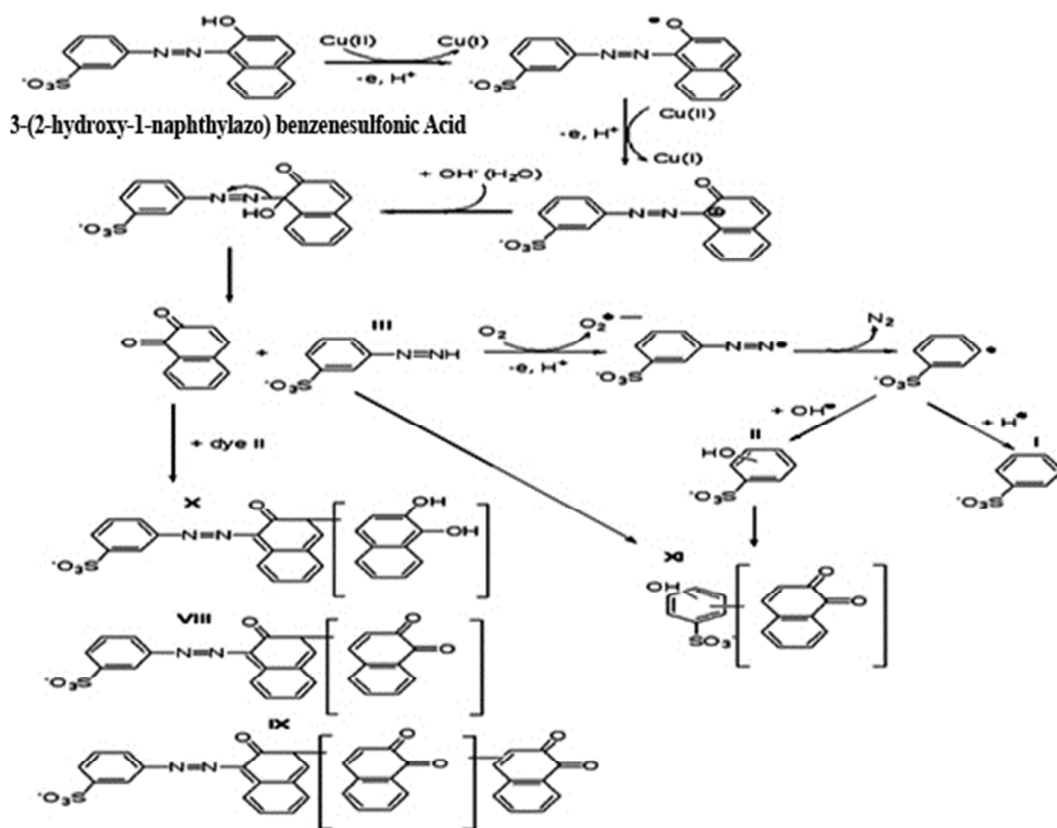


FIGURE 10: Mechanism of laccase degradation of 3-(2-hydroxy-1-naphthylazo) benzenesulfonic Acid.¹⁴⁷

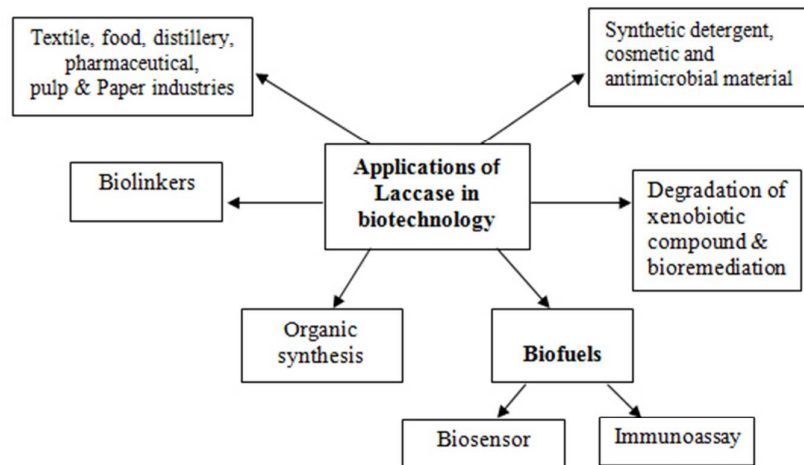


FIGURE 11: Various applications of laccases in biotechnology.