Selective Reduction by Microbial Aldehyde Reductase

Youngsoo Lee and Kyungsoon Kim*

Department of Chemistry, Myong Ji University, Yongin 449-728, Korea

Received January 18, 2006 / Accepted May 30, 2006

Aldehyde reductase was purified to electrophoretic homogeneity from *Saccharomyces cerevisiae*, and then enzymatic reduction of substituted carbonyl compounds was carried out by using the purified aldehyde reductase as a biocatalyst. Under preparative scale reaction conditions, the enzymatic reduction proceeded in high chemical yield with excellent chemoselectivity. The enzymatic reduction product was identified by TLC, GC, Mass, NMR and FT-IR. Benzoic acid, an inhibitor of aldehyde reductase, also potently inhibited the reduction of substituded carbonyl compounds. This enzyme exhibited a broad substrate specificity , and can utilize both NADH and NADPH as cofactors. The enzyme was strongly inhibited by benzoic acid and quercetin. The apparent Km for 4-cyanobenzaldehyde and 3-nitrobenzamide were 4.894 mM and 0.305 mM, respectively.

Key words – Selective reduction, reductase

Introduction

A variety of carbonyl compounds such as aldehyde and ketone were reported to be highly reactive and cytotoxic. These compounds induce toxicity by the formation of DNA adducts or reacting as the cross-linker responsible for the polymerization of proteins[1,5,9,14,15,20].

Aldehyde reductase is known to be capable of inactivating xenobiotics and toxins. Protection of living organisms against the toxic and carcinogenic effects of carbonyl compounds can be achieved by detoxification enzymes such as aldehyde reductase[2,6,11,14,23,27]. Aldehyde reductase (EC 1.1.1.2) belongs to the aldo-keto reductase superfamily, which includes aldose reductase, carbonyl reductase and prostaglandin F synthase. These enzymes catalyze the reduction of carbonyl compounds to the corresponding hydroxy compounds to metabolize xenobiotics[3,7,8,13,14,24,27].

Considerable attention has recently been devoted to the biocatalyst because it may give rise to little environmental contamination in organic synthesis, and many groups carry on studies of reactions using enzymes, microorganisms and plant cell cultures as biocatalysts[10,12,17,26,28,30]. Biocatalytic reduction with enzymes or microbes is a useful method for the preparation of optically active compounds. The enzymatic reduction usually exhibited higher selectivity than the microbial reduction due to a variety of enzymes contained in the cells[16,21,22]. An additional advantage of the enzymatic reduction is the use of small amount of enzyme, which is comparable to the use of large amount of microbes of the microbial reduction[22]. Rapid and selective reduction of carbonyl compounds is of importance for the preparation of hydroxy compounds in organic synthesis, particularly when a molecule has other reducible substituents. Recently, much attention has been paid to the aldo-keto reductase superfamily due to their involvement in the pathogenesis of diabetic complications[2,23,25,29]. However, there are few reports on their potentiality as a biocatalyst.

We have reported that mammalian 1,4-benzoquinone reductase could catalyze the reduction of arylnitroso compound[18]. In the present study, we have purified aldehyde reductase from *Saccharomyces cerevisiae* and carried out enzymatic reduction of various substituted carbonyl compounds by using the purified aldehyde reductase as a biocatalyst. Under preparative scale reaction conditions, the enzymatic reduction proceeded in high chemical yield with excellent chemoselectivity for the carbonyl group over cyano, nitro and other labile substituents. The enzymatic reduction product was identified by TLC, GC, Mass, NMR and FT-IR. The selective reduction of carbonyl compounds with aldehyde reductase could be a useful method for the synthesis of hydroxy compounds.

Materials and Methods

Chemicals

Potassium bromide (FT-IR grade), chloroform-d, 4-ethyl-

*Corresponding author
Tel : +82-31-330-6183, Fax : +82-31-335-7248
E-mail : kskim@mju.ac.kr

benzaldehyde, hexanal, 3-nitrobenzamide, 4-cyanobenzaldehyde, glyceraldehyde, cyclohexanone, heptaldehyde, 3-nitrobenzaldehyde, 4-nitrobenzophenone, 4-nitroacetophenone, benzoin and benzoic acid were obtained from the Aldrich Chemical Co. (Milwaukee, USA). Coomassie brilliant blue G-250 was from the Bio-rad Chemical Co. (Richmond, USA). Bovine serum albumin, NADH, NADPH, acrylamide, ethylenediamine tetraacetic acid (EDTA), ammonium persulfate, DEAE-sephacel, N,N,N',N'-tetramethylethylenediamine (TEMED), 2-mercaptoethanol, sucrose, N,N'-methylenebisacrylamide, Sephacryl S-200-HR, glycine, lauryl sulfate, bromophenolblue, Coomassie brilliant blue R-250 and quercetin were purchased from the Sigma Chemical Co. (St. Louis, USA). TLC sheets (silica gel 60 F-254) were obtained from Merck (Darmstadt, Germany). All other chemicals were of the highest purity grade commercially available.

Activity measurement

Standard reaction mixtures consisted of 100 mM Tris-HCl buffer (pH 7.5), 100 μM glyceraldehyde, 150 μM NAD(P)H and enzyme. Reactions were initiated by the addition of the enzyme. The decrease in absorbance at 340 nm due to NADH oxidation was monitored spectrophotometrically [5]. Conditions for the specific reactions are presented in the related table or figure legends. One unit of enzyme was defined as the amount catalyzing the oxidation of 1 μmol of NADH per min.

Protein determination

Protein concentration was determined according to the method of Bradford [4], using bovine serum albumin as a standard. The protein content in fractions collected during each chromatographic procedure was determined by absorbance at 280 nm.

Enzyme purification

The aldehyde reductase was purified to electrophoretic homogeneity from *Saccharomyces cerevisiae*. All subsequent steps were carried out at 4℃. *S. cerevisiae* was mixed with glass beads (0.5 mm, Sigma) and homogenized in 20 mM Tris-HCl buffer, pH 7.5. The homogenate was centrifuged at 15,000 × g for 20 min, and the supernatant was subjected to fractional precipitation using solid ammonium sulfate. The crude extract was brought to 35 % saturation by slowly adding solid ammonium sulfate. The suspension was stirred for additional 1 hr and then centrifuged at 15,000 × g for 30 min at 4℃. The pellet was discarded, additional $(NH_4)_2SO_4$ was added to the resulting supernatant fraction to give 65% saturation, and the suspension was centrifuged as before. The supernatant was discarded and the pellet was resuspended in a minimum volume of 20 mM Tris-HCl buffer, pH 7.5, and then dialyzed against the same buffer. After centrifugation, the sample was applied to a DEAE-Sephacel anion exchange column which had been previously equilibrated with 20 mM Tris-HCl buffer (pH 7.5). The column was washed with the same buffer and then proteins were eluted from the column with a linear gradient of 0 to 0.5 M NaCl in the same buffer. Fractions were assayed for protein concentration and reductase activities as indicated. The active fractions were pooled, concentrated, and then applied to a Sephacryl S-200 column pre-equilibrated with 20 mM Tris-HCl buffer, pH 7.5. Proteins were eluted with equilibration buffer, and the active fractions were pooled and used for further study.

SDS-polyacrylamide gel electrophoresis

SDS-polyacrylamide gel electrophoresis with a 9 % running gel was carried out according to the procedure described by Laemmli[19]. The gels were stained with Coomassie brilliant blue R-250.

Thin layer chromatography

The reaction in a preparative scale was performed by mixing purified enzyme and 36 mg of 4-cyanobenzaldehyde with 210 mg of NADH in 20 mM Tris-HCl buffer (pH 7.5), then extracting the mixture with ethyl acetate. Substrates and carbonyl reduction products were analyzed by silica gel thin layer chromatography (TLC) using ethyl acetate / hexane (6:4) as the solvent system.

Gas chromatography

Gas chromatography (GC) was performed using a Hewlett-Packard 6890 Plus gas chromatograph system equipped with a HP 5 column and a flame ionization detector (FID). The oven temperature was programmed to ramp from 80 to 250℃ at 15℃/min. The injection port temperature was 250℃ and the detector temperature was 250℃. Gas flow rates were 1 ml/min for nitrogen, 30 ml/min for hydrogen, and 300 ml/min for air.

GC-mass spectrometry

Gas chromatography-mass spectrometry (GC-MS) was performed at 70 eV on a HP 5973 mass spectrometer fitted

with an HP 6890 Plus gas chromatograph.

Nuclear magnetic resonance spectrometry

Proton NMR spectra were obtained in $CDCl_3$ at 300 MHz on a Jeol-LA-300 NMR spectrometer.

Fourier-transformation infrared spectroscopy

FT-IR spectroscopy was performed with a Perkin-Elmer system 2000 FT-IR spectrometer (in KBr pellet).

Results and Discussion

The aldehyde reductase was purified to apparent homogeneity from *Saccharomyces cerevisiae* by a combination of ammonium sulfate fractionation, ion-exchange and gel permeation chromatographies (Table 1). Details of the purification procedure have been described under Materials and Methods. On polyacrylamide gel electrophoresis, the purified aldehyde reductase revealed a single band. The molecular mass of the enzyme was estimated to be 33 kDa by sodium dodecyl sulfate polyacrylamide gel electrophoresis with standard protein markers (Fig. 1). Colrat *et al.* reported that aldehyde reductase from mung bean was a monomer of 36 kDa[6].

A variety of carbonyl compounds were tested as substrates for the purified enzyme (Table 2). The enzyme catalyzed not only the reduction of substituted aryl- and alkylaldehydes, but also the reduction of substituted benzophenone, acetophenone and benzamide. This enzyme exhibited a broad substrate specificity, and the aldehyde reductase that was purified from dog thyroid also exerted a rather broad substrate specificity[25]. The purified enzyme can use both NADH and NADPH as cofactors, whereas the purified mung bean aldehyde reductase utilized only NADPH[6]. The broad substrate specificity of this enzyme suggests that this organism does not produce multiple specific aldehyde reductases.

Table 1. Purification of aldehyde reductase from *Saccharomyces cerevisiae*

Purification step	Total protein (mg)	Total activity (U)[a]	Specific activity (mU/mg)	Purification (fold)	Recovery (%)
Crude extract	3606.7	6.08	1.68	1	100
Ammonium sulfate fractionation	1338.1	4.06	3.03	1.8	66.8
DEAE-Sephacel chromatography	175.9	3.20	18.2	10.8	52.6
Sephacryl S-200-HR chromatography	16.6	1.84	110.8	66.0	30.2

[a]1U = 1 μmol of NADH oxidized min^{-1}.

The activity of the enzyme was strongly inhibited by benzoic acid and quercetin (Table 3). The kinetic constants were calculated from Lineweaver-Burk polts and summarized in Table 4. The apparent Km for glyceraldehyde, 4-cyanobenzaldehyde and 3-nitrobenzamide were 5.807 mM, 4.894 mM and 0.305 mM, respectively (Fig. 2, 3). In the

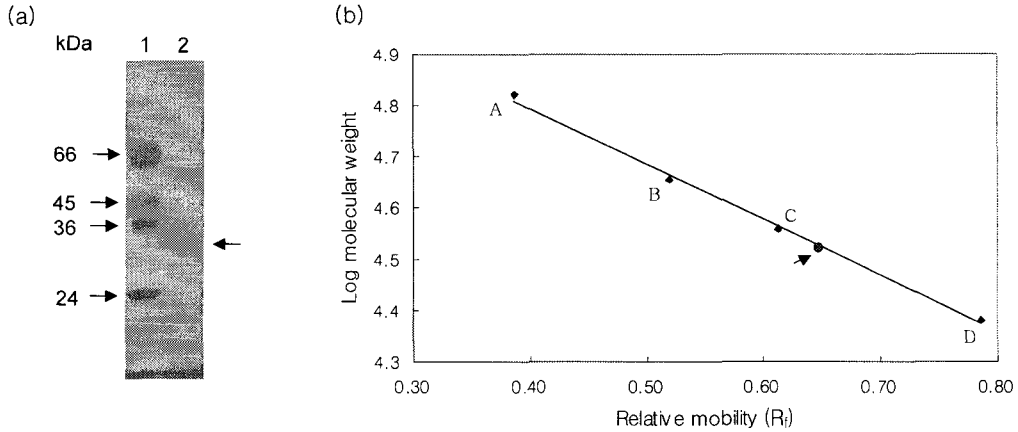

Fig. 1. Determination of molecular weight of aldehyde reductase by SDS-polyacrylamide gel electrophoresis. 9% acrylamide gel was used. (a) SDS-PAGE of purified aldehyde reductase. Lane 1 : molecular weight marker protein containging bovine serum albumin (66 kDa), egg albumin (45 kDa), glyceraldehyde-3-phosphate dehydrogenase (36 kDa) and bovine pancreas trypsinogen (24 kDa). Lane 2 : purified enzyme. (b) Determination of molecular weight. A : bovine serum albumin (66 kDa), B : egg albumin (45 kDa), C : glyceraldehyde-3-phosphate dehydrogenase (36 kDa) and D : bovine pancreas trypsinogen (24 kDa). • : purified aldehyde reductase.

Table 2. Substrate specificity of the aldehyde reductase purified from *S. cerevisiae*

Substrate (100 μM)	Relative enzyme activity (% of control)	
	NADH (150 μM)	NADPH (150 μM)
Glyceraldehyde	100	73
4-Cyanobenzaldehyde	56.8	100
4-Nitrobenzophenone	13	31
3-Nitrobenzaldehyde	13	188
3-Nitrobenzamide	10.8	20
4-Nitroacetophenone	6	30
4-Ethylbenzaldehyde	97	63
Benzoin	9	156
Hexanal	40	210
Heptaldehyde	63	94
Cyclohexanone	4	20

The reaction mixture consisted of 100 μM of the indicated substrate, 150 μM NAD(P)H, 100 mM Tris-HCl buffer (pH 7.5) and the purified enzyme. Reaction rates are expressed relative to the rate with glyceraldehyde (100 μM) and NADH (150 μM) as equal to 100.

Table 3. Inhibition of the aldehyde reductase purified from *S. cerevisiae*

Compound[a]	Residual activity (% of control)
None	100
Benzoic acid	18.9
2-Mercaptoethanol	79.0
Ammonium sulfate	70.9
Quercetin	0

The reaction mixture contained 100 mM Tris-HCl buffer (pH 7.5), 150 μM NADH, 100 μM glyceraldehyde, 1 mM inhibitor and purified aldehyde reductase. Results are expressed as a percentage of the activity without an inhibitor, with 100 representing no inhibition and 0 representing complete inhibition.

[a] Concentration of the compound was 1 mM.

Table 4. Kinetic constants for the aldehyde reductase purified from *S. cerevisiae*

Substrate	Vmax (μmol/min /mg)	Km (mM)	Vmax/Km
Glyceraldehyde	0.077	5.807	0.013
4-Cyanobezaldehyde	0.240	4.894	0.049
3-Nitrobenzamide	0.569	0.305	1.86

A fixed NADH concentration of 150 μM was used in determining the Km for the electron acceptors.
The reaction mixture contained 100 mM Tris-HCl buffer (pH 7.5), 150 μM NADH, purified enzyme,
and varied concentrations of electron acceptors.

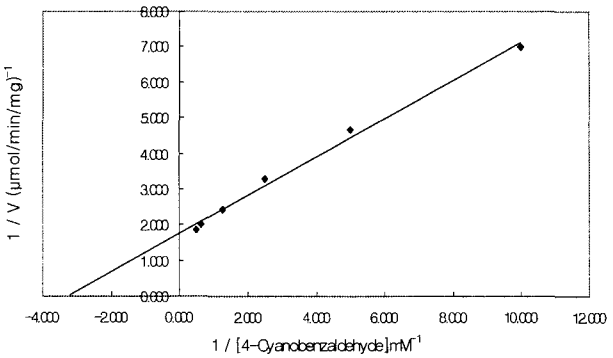

Fig. 2. The Lineweaver-Burk plot showing the aldehyde reductase activity as a function of 4-cyanobenzaldehyde concentration. The reaction mixture contained 100 mM Tris-HCl buffer (pH 7.5), 150 μM NADH, purified enzyme and varied concentrations of 4-cyanobenzaldehyde.

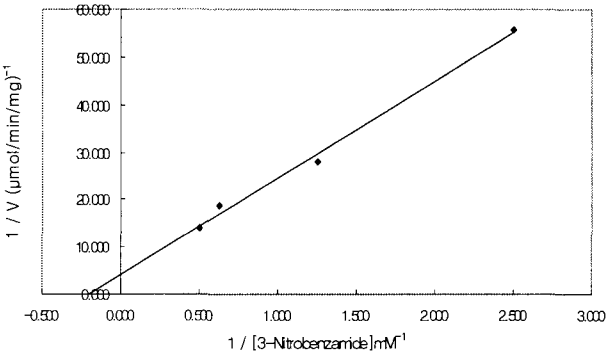

Fig. 3. The Lineweaver-Burk plot showing the aldehyde reductase activity as a function of 3-nitrobenzamide concentration. The reaction mixture contained 100 mM Tris -HCl buffer (pH 7.5), 150 μM NADH, purified enzyme and varied concentrations of 3-nitrobenzamide.

case of mung bean aldehyde reductase, the Km value of the enzyme for eutypine was previously reported to be 6.3 μM[6]. The effect of benzoic acid, an inhibitor of aldehyde reductase, on the 4-cyanobenzaldehyde and 3-nitrobenzamide reduction by aldehyde reductase is shown in Table 5. The *S. cerevisiae* aldehyde reductase was also potently inhibited by benzoic acid on the reduction of substituted aldehyde and amide.

The production of 4-cyanobenzyl alcohol from 4-cyanobenzaldehyde by purified *S. cerevisiae* aldehyde reductase was confirmed by TLC, GC (Fig. 4), Mass (Fig. 5), NMR (Fig. 6) and FT-IR (Fig. 7) analysis. The reaction in a preparative scale was performed by mixing purified enzyme and 36 mg of 4-cyanobenzaldehyde with 210 mg of NADH in 20 mM Tris-HCl buffer (pH 7.5), then extracting the mixture with ethyl acetate. 4-Cyanobenzyl alcohol in the ethyl

Table 5. Inhibition of the aldehyde reductase purified from *S. cerevisiae*

Inhibitor	Substrate	Relative enzyme activity (% of control)
Benzoic acid	Glyceraldehyde	18.9
	4-Cyanobenzaldehyde	52.4
	3-Nitrobenzamide	50.0

Results are expressed as a percentage of the activity without inhibitor, with 100 representing no inhibition and 0 representing complete inhibition for each substrate. 100 mM Tris-HCl buffer (pH 7.5), 100 μM substrate, 150 μM NADH and 1 mM inhibitor was used.

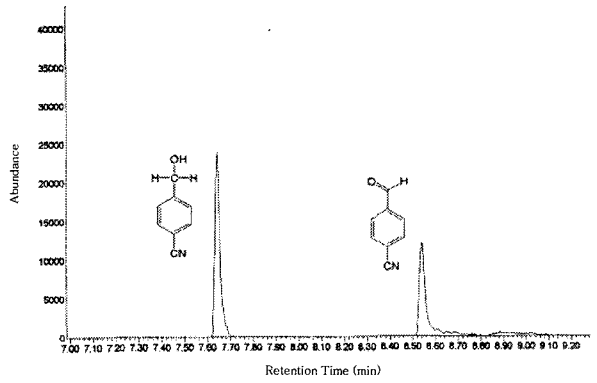

Fig. 4. GC chromatogram of the reaction mixture of 4-cyanobenzaldehyde, NADH and the purified enzyme.

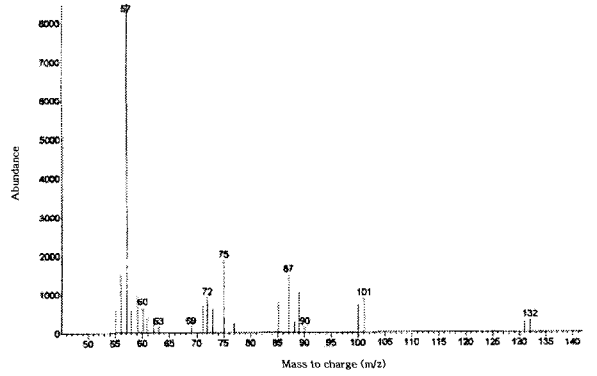

Fig. 5. Mass spectrum of the reaction product of 4-cyanobenzaldehyde, NADH and the purified enzyme. Peak abundances are reported verus mass to charge (m/z).

acetate extract was identified by comparing its retention time to that of an authentic reference compound (Fig. 4). It was also identified by comparing its Rf value to that of the authentic reference compound on TLC plate (data not shown). The ethyl acetate extract was subjected to TLC on a silica gel 60F-254 plate and developed in ethyl acetate/hexane (6:4). The major band migrated with a R_f=0.4 as did an authentic sample of 4-cyanobenzyl alcohol. Its

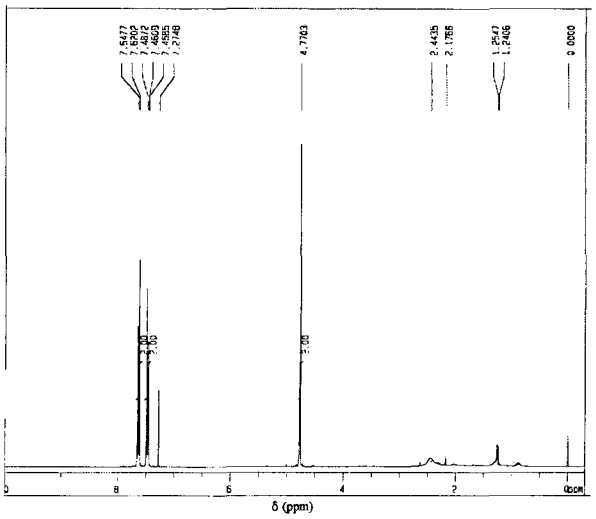

Fig. 6. NMR (300 MHz, $CDCl_3$) spectrum of the reaction product of 4-cyanobenzaldehyde, NADH and the purified enzyme.

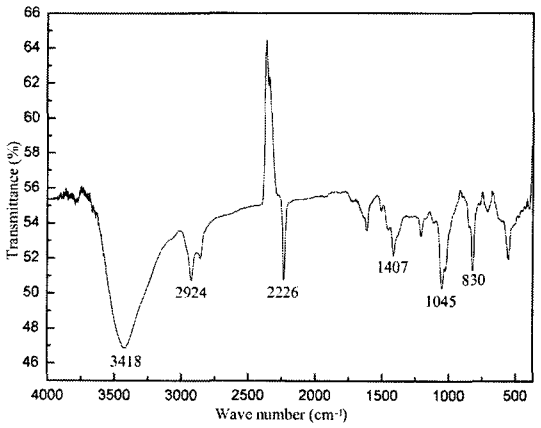

Fig. 7. FT-IR spectrum of the reaction product of 4-cyanobenzaldehyde, NADH and the purified enzyme.

mass spectrum exhibited intense peaks at m/z values of 132, 101, 87, 75 and 57 (Fig. 5). Proton NMR (300 MHz, $CDCl_3$) data was as follows : δ 4.77 (2H, S), 7.47 (2H, d, 8.4 Hz), 7.63 (2H, d, 8.4 Hz). FT-IR spectrum exhibited characteristic peaks at 830, 1045, 1407, 2226, 2924 and 3418 cm^{-1}. Consequently, the reduction product is identified as 4-cyanobenzyl alcohol on the basis of TLC, GC, Mass, NMR and FT-IR spectral comparisons with an authentic sample.

The purified enzyme selectively reduced carbonyl groups to their corresponding hydroxy compounds without reducing any other labile substituents such as cyano or nitro groups. Aromatic and aliphatic carbonyl group reduction catalyzed by biocatalyst is presently under investigation in our laboratory.

References

1. Barreiro, E., J. Gea, M. D. Falco, L. Kriazhev, S. James and S. N. A. Hussain. 2005. Protein carbonyl formation in the diaphragm. *Amer. J. Resp. Cell Mole. Biol.* **32**, 9-17.
2. Barski, O. A., K. H. Gabbay, C.E. Grimshaw and K. M. Bohren .1995. Mechanism of human aldehyde reductase : characterization of the active site pocket. *Biochemistry* **34**, 11264-11275.
3. Bohren, K. M., J. L. Page, R. Shankar, S. P Henry and K. H. Gabbay .1991. Expression of human aldose and aldehyde reductases. *J. Biol. Chem.* **266**, 24031-24037.
4. Bradford, M. M. 1976. A rapid and sensitive method for quantitation of microgram quantities of protein utilizing the principle of protein-dye binding. *Anal. Biochem.* **72**, 248-254.
5. Colrat, S., C. Deswarte, A. Latchè, A. Klaèbè, M. Bouzayen, J. Fallot and J. P. Roustan .1999a. Enzymatic detoxification of eutypine, a toxin from *Eutypa lata*, by *Vitis vinifera* cells : partial purification of an NADPH-dependent aldehyde reductase. *Planta* **207**, 544-550.
6. Colrat, S. A., Latchè, M. Guis, J.-C. Pech, M. Bouzayen, J. Fallot and J.-P. Roustan .1999b. Purification and characterization of a NADPH-dependent aldehyde reductase from mung bean that detoxifies entypine, a toxin from *Eutypa lata*. *Plant Physiol.* **119**, 621-626.
7. Cromlish, J. A. and T. G. Flynn .1985. Identification of pig brain aldehyde reductases with the high-Km aldehyde reductase, the low-Km aldehyde reductase and aldose reductase, carbonyl reductase, and succinic semialdehyde reductase. *J. Neurochem.* **44**, 1485-1493.
8. Das, B. and S. K. Srivastava .1985. Purification and properties of aldehyde reductases from human placenta. *Biochim. Biophys. Acta* **840**, 324-333.
9. Destaillats, M., R. S. Spaulding and M. J. Charles .2002. Ambient air measurement of acrolein and other carbonyls at the Oakland-San Francisco Bay Bridge toll plaza. *Environ. Sci. Technol.* **36**, 2227-2235.
10. Drescher, M., Y.-F. Li and F. Hammerschmidt .1995. Enzymes in organic chemistry, part 2. *Tetrahedron* **51**, 4933-4946.
11. Hayes, J.D., D. J. Judah and G. E. Neal .1993. Resistance to aflatoxin B_1 is associated with the expression of a novel aldo-keto reductase which has catalytic activity towards a cytotoxic aldehyde-containing metabolite of the toxin. *Cancer Res.* **53**, 3887-3894.
12. Högberg, H.-E., M. Lindmark, D. Isaksson, K. Sjödin, M. C. R. Franssen, H.Jongejan, J. B. P. A. Wijnberg and A. Groot .2000. Formation of hemiacetal esters in lipase-cytalysed reactions of vinyl esters with hindered secondary alcohols. *Tetrahedron Lett.* **41**, 3193-3196.
13. Inazu, N., Y. Nagashima, T. Satoh and T. Fujii .1994. Purification and properties of six aldo-keto reductases from rat adrenal gland. *J. Biochem.* **115**, 991-999.
14. Jagt, D. L. V., L. A. Hunsaker, B. Robinson, L. A. Stangbye and L. M. Deck .1990. Aldehyde and aldose reductases from human placenta. *J. Biol. Chem.* **265**, 10912-10918.
15. Kanazu, K., M. Shinoda, T. Nakayama, Y. Deyashiki, A. Hara and H. Sawada .1991. Aldehyde reductase is a major protein associated with 3-deoxyglucosone reductase activity in rat, pig and human livers. *Biochem. J.* **279**, 903-906.
16. Kawai, Y., S. Kondo, M. Tsujimoto, K. Nakamura and A. Ohno .1994. Stereochemical control in microbial reduction. *Bull. Chem. Soc. Jpn.* **67**, 2244-2247.
17. Kijima, T., T. Moriya, E. Kondoh and T. Izumi .2000. Lipase-mediated resolution of racemic benzo-15-crown-5 ether derivatives. *Tetrahedron Lett.* **41**, 2125-2127.
18. Kim, K. and H. Shin. 2002. Biotransformation of arylnitroso compound by mammalian 1,4-benzoquinone reductase. *Kor. J. Life Sci.* **12**, 281-287.
19. Laemmli, U. K. 1970. Cleavage of structural proteins during the assembly of the head of bacteriophage T4. *Nature* **227**, 680-685.
20. Maser, E., B. Stinner and A. Atalla .2000. Carbonyl reduction of 4-(methylnitrosamino)-1-(3-pyridyl)-1-butanone (NNK) by cytosolic enzymes in human liver and lung. *Cancer Lett.* **148**, 135-144.
21. Morgan, B., A. C. Oehlschlager and T. M. Stokes .1992. Enzyme reactions in apolar solvent. *J. Org. Chem.* **57**, 3231-3236.
22. Nakamura, K. and R. Yamanaka .2002. Light mediated cofactor recycling system in biocatalytic asymmetric reduction of ketone. *Chem. Commun.* 1782-1783.
23. Ohta, M., T. Tanimoto and A. Tanaka .1991. Localization, isolation and properties of three NADPH-dependent aldehyde reducing enzymes from dog kidney. *Biochim. Biophys. Acta* **1078**, 395-403.
24. Robinson, B., L. A. Hunsaker, L. A. Stangebye and D. L. V. Jagt .1993. Aldose and aldehyde reductases from human kidney cortex and medulla. *Biochim. Biophys. Acta* **1203**, 260-266.
25. Schaffhauser, M. A., S. Sato and P. F. Kador .1996. NADPH-dependent reductases in dog thyroid : comparison of a third enzyme "glyceraldehyde reductase" to dog thyroid aldehyde reductase. *Int. J. Biochem. Cell Biol.* **28**, 275-284.
26. Takabe, K., M. Suzuki, T. Nishi, M. Hiyoshi, Y. Takamori, H. Yoda and N. Mase .2000. Convenient route to both enantiomers of chiral 5-hydroxypyrrolidin-2-one and 5-hydroxy-1,5-dihydropyrrol-2-one. *Thtrahedron Lett.* **41**, 9859-9863.
27. Takahashi, N. 2002. Induction of cell differentiation and development of new anticancer drugs. *Yakugaku Zasshi* **122**, 547-563.
28. Takemoto, M., Y. Matsuoka, K. Achiwa and J. P. Kutney .2000. Biocatalytic dediastereomerization of dibenzylbutanolides by plant cell cultures. *Tetrahedron Lett.* **41**, 499-502.
29. Tanimoto, T., M. Ohta, A. Tanaka, I. Ikemoto and T. Machida .1991. Purification and characterization of human testis aldose and aldehyde reductase. *Int. J. Biochem.* **23**, 421-428.
30. Zouioueche, L. A. and J.-C. Fiaud .2000. Kinetic resolution of 1-acenaphthenol and 1-acetoxynaphthene through lipase-catalyzed acylation and hydrolysis. *Tetrahedron Lett.* **41**, 4085-4088.

초록 : 미생물 알데히드 환원효소에 의한 선택적 환원

이영수 · 김경순*
(명지대학교 자연과학대학 화학과)

Saccharomyces cerevisiae 로부터 알데히드 환원효소를 정제하였다. 정제된 알데히드 환원효소를 biocatalyst 로 사용하여 치환기가 있는 카르보닐 화합물의 선택적 환원을 시도하였다. 효소를 이용한 환원반응의 생성물의 구조를 TLC, GC, Mass, NMR, FT-IR 을 이용하여 확인하였으며 효소를 이용한 환원반응이 높은 선택성을 가지고 진행됨을 확인하였다. 또한 이 반응은 알데히드 환원효소의 억제제인 벤조산에 의해 크게 억제되었다. 치환기가 있는 카르보닐 화합물의 선택적 환원반응은 의약품 제조 분야에서 매우 중요한 반응이며 미생물에서 정제한 알데히드 환원효소가 biocatalyst 로서 선택적 환원반응에 이용될 수 있으리라 사료된다.