Spring 1989

Identification of the functional regions of the yeast activator ADR1

Lynne Taylor Bemis

University of New Hampshire, Durham

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Identification of the functional regions of the yeast activator

ADRI

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University of New Hampshire, 1989
IDENTIFICATION OF THE FUNCTIONAL REGIONS OF THE YEAST ACTIVATOR \textit{ADR1}

BY

Lynne Taylor Bemis
Bachelor of Science, University of New Hampshire, 1979

DISSERTATION

Submitted to the University of New Hampshire
in Partial Fulfillment of
the Requirements for the Degree of

Doctor of Philosophy
in
Biochemistry

May, 1989
This dissertation has been examined and approved.

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February 22, 1989  
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ABSTRACT

IDENTIFICATION OF THE FUNCTIONAL REGIONS OF THE YEAST

ACTIVATOR ADR1

by

Lynne T. Bemis
University of New Hampshire, May, 1989

ADR1, a transcriptional activator from the yeast *Saccharomyces cerevisiae*, is required for activation of the glucose-repressible alcohol dehydrogenase, ADH II (encoded by the *ADH2* gene). The *ADR1* gene encodes a protein which binds to an upstream activation sequence in the *ADH2* promoter. Several methods were used to locate functional regions of the ADR1 protein.

The *adr1-1* mutation was identified as a C to G transversion resulting in a nonsense codon at the eleventh codon of ADR1. tRNA-suppressors which substituted an amino acid at the eleventh codon of *adr1-1* resulted in a functional *adr1-1* protein, indicating that the translational start of *ADR1* occurs at the first AUG of the
ADR1 transcript. The adr1-1 5.1 kb RNA was found to be two- to three-fold less abundant than the ADR1 transcript. This observation is a further instance of a nonsense mutation early in a gene leading to decreased stability of the RNA and confirms that the 5.1 kb transcript is the ADR1 mRNA.

A series of C-terminal truncations of the ADR1 gene were constructed and used to investigate functional regions of ADR1. A C-terminal truncation leaving only 151 N-terminal amino acids (ADR1-151) and deleting part of a "Zn-binding" DNA-binding finger motif was not capable of transcriptional activation. In contrast, the ADR1-220 protein containing the complete "Zn-binding" DNA-binding finger motif was capable of transcriptional activation. However, none of the truncated ADR1 proteins were as transcriptionally active as the entire ADR1 protein.

An ADR1 protein containing at least 506 N-terminal amino acids was required for glycerol growth. Mutations in the GLP1 gene were identified that allowed strong glycerol growth, while remaining dependent on the presence of a functional ADR1 gene. This newly identified function of ADR1 suggests that ADR1 has a more extensive role in the regulation of nonfermentative growth in S. cerevisiae than previously expected.
To All My Family

especially

Mary and Ken Taylor

Kristen and Gordon Bemis
Acknowledgments

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TABLE OF CONTENTS

DEDICATION........................................................................ iii
ACKNOWLEDGMENTS...................................................... iv
TABLE OF CONTENTS...................................................... v
LIST OF TABLES..................................................................... vii
LIST OF FIGURES................................................................... viii
ABSTRACT........................................................................ ix

SECTION PAGE

INTRODUCTION................................................................. 1

I. CHARACTERIZATION OF THE \textit{adr1-1} MUTATION 20
    Introduction.................................................................. 20
    Materials and Methods.............................................. 23
    Results......................................................................... 32
    Discussion.................................................................... 41

II. IDENTIFICATION OF FUNCTIONAL REGIONS OF \textit{ADR1}.... 45
    Introduction.................................................................. 45
    Materials and Methods.............................................. 46
    Results......................................................................... 49
    Discussion.................................................................... 50
LIST OF TABLES

<table>
<thead>
<tr>
<th>TABLE</th>
<th>PAGE</th>
</tr>
</thead>
<tbody>
<tr>
<td>Table 1. ADH activities of strains carrying regulatory mutations</td>
<td>7</td>
</tr>
<tr>
<td>Table 2. <em>Saccharomyces cerevisiae</em> strains used in Section 1</td>
<td>22</td>
</tr>
<tr>
<td>Table 3. ADH II enzyme activities (Section 1)</td>
<td>28</td>
</tr>
<tr>
<td>Table 4. ADH activities of strains carrying UGA-suppressors</td>
<td>31</td>
</tr>
<tr>
<td>Table 5. ADH II enzyme activities (Section 2)</td>
<td>50</td>
</tr>
<tr>
<td>Table 6. Strains used for glycerol growth studies</td>
<td>57</td>
</tr>
<tr>
<td>Table 7. Segregation of glycerol growth</td>
<td>63</td>
</tr>
<tr>
<td>Table 8. Glycerol growth is independent of <em>ADH2</em></td>
<td>64</td>
</tr>
<tr>
<td>Table 9. Diploid Strains</td>
<td>66</td>
</tr>
</tbody>
</table>
# LIST OF FIGURES

<table>
<thead>
<tr>
<th>FIGURE</th>
<th>PAGE</th>
</tr>
</thead>
<tbody>
<tr>
<td>Figure 1. ADH in metabolic pathways</td>
<td>4</td>
</tr>
<tr>
<td>Figure 2. Regulatory regions of the <em>ADH2</em> gene</td>
<td>9</td>
</tr>
<tr>
<td>Figure 3. Regulators of <em>ADH2</em></td>
<td>11</td>
</tr>
<tr>
<td>Figure 4. Functional domains of <em>ADR1</em></td>
<td>14</td>
</tr>
<tr>
<td>Figure 5. Plasmids (Section 1)</td>
<td>26</td>
</tr>
<tr>
<td>Figure 6. Northern analysis of <em>adr1-1</em> mRNA levels</td>
<td>38</td>
</tr>
<tr>
<td>Figure 7. Northern analysis of <em>ADR1/adr1-1</em> mRNA levels</td>
<td>40</td>
</tr>
<tr>
<td>Figure 8. Internal deletion of amino acids 220-253 of <em>ADR1</em></td>
<td>48</td>
</tr>
<tr>
<td>Figure 9. Strains isogenic to 43-2B on 3% glycerol</td>
<td>59</td>
</tr>
<tr>
<td>Figure 10. Strains isogenic to 411-40 on 3% glycerol</td>
<td>60</td>
</tr>
<tr>
<td>Figure 11. Strains isogenic to 411-40 on 3% acetate</td>
<td>69</td>
</tr>
<tr>
<td>Figure 12. Strains isogenic to 411-40-B on 3% acetate</td>
<td>70</td>
</tr>
<tr>
<td>Figure 13. Strains isogenic to 43-2B on 3% acetate</td>
<td>72</td>
</tr>
<tr>
<td>Figure 14. Strains isogenic to 43-2B on 2% lactate</td>
<td>73</td>
</tr>
<tr>
<td>Figure 15. Strains isogenic to 43-2B on 2% pyruvate</td>
<td>74</td>
</tr>
<tr>
<td>Figure 16. Strains isogenic to 411-40 on 2% lactate</td>
<td>76</td>
</tr>
<tr>
<td>Figure 17. Strains isogenic to 411-40-B on 2% lactate</td>
<td>77</td>
</tr>
<tr>
<td>Figure 18. Strains isogenic to 411-40-B on 1% lactate</td>
<td>78</td>
</tr>
<tr>
<td>Figure 19. Strains isogenic to 411-40 on 2% pyruvate</td>
<td>79</td>
</tr>
<tr>
<td>Figure 20. Strains isogenic to 411-40-B on 2% pyruvate</td>
<td>80</td>
</tr>
</tbody>
</table>
INTRODUCTION

Regulatory mechanisms have been studied in many eukaryotic and prokaryotic organisms. *Saccharomyces cerevisiae* is an organism particularly amenable to the study of regulatory mechanisms because it has a short generation time and a well-characterized genome. One of the most well studied systems of cellular control is that of carbon catabolite repression and the regulatory mechanisms necessary for that control. Carbon catabolite repression, in both prokaryotes and eukaryotes, is a regulatory mechanism used to block the use of alternative carbon sources until the bulk of available glucose is utilized. Systems regulated by carbon catabolite repression in the yeast *Saccharomyces cerevisiae*, include the galactose utilization pathway (Matsumoto et al., 1983; Oshima, 1982), the sucrose utilization pathway (Grossman and Zimmerman, 1979) cytochrome C (Zitomer et al., 1979) and the glucose-repressible alcohol dehydrogenase II (Ciriacy, 1975a).
There are four NAD-linked alcohol dehydrogenase isozymes: ADH I, II, III (Lutstorf and Megnet, 1968) and ADH IV (Paquin and Williamson, 1986) in yeast. ADH I and ADH II are cytoplasmic enzymes while ADH III is found in the mitochondria (Fowler et al., 1971; Ciriacy, 1975a). The recently identified enzyme, ADH IV, is not well characterized at this time. The ADH I isozyme, encoded by the ADH1 gene, converts acetaldehyde to ethanol under fermentative growth conditions (Figure 1). The glucose-repressible isozyme, ADH II, is encoded by the ADH2 gene which is transcribed only in the absence of glucose (Denis et al., 1981). ADH2 is therefore a gene subject to carbon catabolite repression. In the absence of glucose and under aerobic conditions, ADH II converts the ethanol accumulated during fermentative growth to acetaldehyde (Wills, 1976). Although, ADH I and ADH II are 95% identical at the protein level (Wills and Jornvall, 1979) the glucose-repressible isozyme ADH II has a lower Km for both ethanol and NAD+ than does ADH I (Wills, 1976). ADH III, the mitochondrial isozyme, is encoded in the nucleus and is targeted to the mitochondrial membrane by a leader sequence (Young and Pilgrim, 1987). The mitochondrial ADH is 85% homologous to ADH I and ADH II at the protein level.

The availability of yeast strains lacking one or more of the ADH isozymes has facilitated the characterization of individual ADH
Isozymes and the factors which control their expression. Mutated ADH isozymes have been identified by growth on allyl alcohol, an unsaturated alcohol which is nontoxic to yeast. In the presence of ADH activity allyl alcohol is readily oxidized to acrolein, a toxic unsaturated aldehyde (Figure 1) (Lutstorf and Megnet, 1968; Ciriacy, 1975a). Only cells possessing a reduced level of ADH activity can grow in the presence of allyl alcohol. ADH isozymes have been separated and identified by electrophoresis of crude extracts. Analysis of mutant strains have been used to identify three classes of mutations, \textit{adh}1, \textit{adh}2, \textit{adh}3 (originally called \textit{adc}1, \textit{adr}2, and \textit{adm}, respectively) (Ciriacy, 1975a). A fourth mutation \textit{adr}1-1, initially thought to be an ADH2 mutation, was later identified to occur in the regulatory allele \textit{ADR}1 (Ciriacy, 1975b). All four genes \textit{ADH}1, \textit{ADH}2, \textit{ADH}3, and \textit{ADR}1, were found to be unlinked and observed to show Mendelian segregation. Yeast strains were constructed which contained mutations in both \textit{adh}1 and \textit{adh}3 but not in \textit{ADH}2. The only ADH activity in these strains is derived from the glucose-repressible ADH. These strains were used to select for mutations at \textit{ADH}2 and mutations in regulatory genes controlling \textit{ADH}2 expression.
Figure 1  ALCOHOL DEHYDROGENASES IN METABOLIC PATHWAYS

GLUCOSE → NAD⁺ NADH → PYRUVATE → CO₂

Aerobic conditions

HEXOSE-P ← GLYOXYLATE CYCLE

Acrolein toxic (results in cell death)

ADH I

NAD⁺ NADH → ACETALDEHYDE → ETHANOL

ADH II

NAD⁺ NADH → ACETALDEHYDE → ETHANOL

Acetyl / Cyanide

TCA CYCLE

Antimycin A - Respiratory Inhibitor
The increase in ADH II activity under nonfermentative growth conditions was shown to result from an increase in ADH2 mRNA levels (Denis et al., 1981). In contrast, the ADH1 mRNA was repressed about fivefold during growth in medium containing a nonfermentable carbon source (Denis et al., 1983).

The ADH1 and ADH2 genes have been cloned (Williamson et al., 1980; Williamson et al., 1981) and sequenced (Bennetzen and Hall, 1982; Russell et al., 1983a). Comparison of DNA sequence analysis shows 90% homology between ADH1 and ADH2 confirming earlier evidence that at the protein level ADH I and ADH II are 95% homologous. The structural genes and parts of the promoter regions of ADH I and ADH II are similar. The TATAA boxes of ADH1 and ADH2 are located 91 to 107 base pairs prior to the mRNA start sites and the sites of translational initiation are located 40 to 60 base pairs to the 3' side of either the ADH1 or ADH2 mRNA (Bennetzen and Hall, 1982; Russell, et al., 1983a). The location of the TATAA box and the mRNA start site of ADH1 and ADH2 are similar to the location of these transcriptional elements in other known yeast genes (Sentenac and Hall, 1982; Russell et al., 1983a).

The sequences 5' to the TATAA box of the ADH2 gene, originally
designated ADR3 (Ciriacy, 1976), are significantly different from those 5' to the ADH1 gene (Russell et al., 1983b). The ADR3° mutations located cis to ADH2 block catabolite repression of ADH2. The ADR3° mutations were later sequenced and shown to result from Ty (yeast transposable element) insertions in the promoter region of ADH2 (Williamson et al., 1981; Williamson et al., 1983) or from an increase in the number of A residues in a poly A tract upstream of the ADH2 transcriptional start site (Russell et al., 1983b) (Table 1). The Ty insertions alter the regulation of ADH2 such that it is no longer under the control of glucose-repression. Ty insertions have been shown to disrupt the normal regulation of other structural genes, including Ty insertions that were localized upstream from the iso-2-cytochrome C gene (Errede et al., 1980). The Ty insertions and the mutations at the polyA tract in the upstream region of ADH2 identify a region required for normal regulation of ADH2.

The upstream region of ADH2 required for the glucose-repression phenomenon was further characterized by placing the ADR3 region (ADH2 upstream) upstream from a reporter gene.
Table 1. ADH activities for strains containing mutations at one or more regulatory allele.

<table>
<thead>
<tr>
<th>Relevant genotype</th>
<th>ADH II activities (mU/mg)\textsuperscript{a}</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>glucose</td>
</tr>
<tr>
<td>\textit{ADR1}</td>
<td>8</td>
</tr>
<tr>
<td>\textit{adr1-1}</td>
<td>3</td>
</tr>
<tr>
<td>\textit{ADR1-5C}</td>
<td>280</td>
</tr>
<tr>
<td>\textit{ADR1, ADR3C (Ty)}\textsuperscript{b}</td>
<td>783</td>
</tr>
<tr>
<td>\textit{ADR1, ADR3C (+poly dA)}\textsuperscript{b}</td>
<td>463</td>
</tr>
<tr>
<td>\textit{ADR1, ccr1}</td>
<td>2</td>
</tr>
<tr>
<td>\textit{ADR1, cre1}</td>
<td>175</td>
</tr>
<tr>
<td>\textit{adr1-1, cre1}</td>
<td>155</td>
</tr>
<tr>
<td>\textit{ADR1, cre2}</td>
<td>77</td>
</tr>
<tr>
<td>\textit{adr1-1, cre2}</td>
<td>70</td>
</tr>
<tr>
<td>\textit{ADR1, ccr4}</td>
<td>12</td>
</tr>
<tr>
<td>\textit{ADR1, ccr4, cre1}</td>
<td>23</td>
</tr>
<tr>
<td>\textit{ADR1, ccr4, cre2}</td>
<td>6</td>
</tr>
</tbody>
</table>

\textsuperscript{a}One unit of ADH activity reduced 1 \textmu M of NAD in one minute at 22\textdegree C (Denis \textit{et al.}, 1981). All enzyme activities are taken from (Denis, 1984) except as noted.

\textsuperscript{b}Values taken from Ciriacy, 1979.

All activities are taken from strains which are \textit{adh1}, \textit{adh3}, and \textit{ADH2}. 


The reporter gene encoded the fermentative ADH, ADH1 (Beier and Young, 1982). Synthesis of the reporter gene (ADH1) was shown to depend upon the presence or absence of glucose. These experiments confirmed that the upstream region of ADH2 is required for the glucose repression signal. Deletion analysis of ADR3 sequences upstream from the reporter gene identified a region necessary for activation of the reporter gene but did not detect a region that when deleted releases ADH2 from glucose repression (Beier and Young, 1985). These analyses support the hypothesis that a trans-activating element acts through the ADR3 (ADH2 upstream) sequences as opposed to a trans-repressing element.

Upstream Activation Sites (UAS) have been characterized in many inducible systems in yeast (Guarente and Ptashne, 1981; Guarente, Yocum, and Gifford, 1982; Struhl, 1982). The region of ADH2 (-210 to -320 base pairs) containing the upstream activation sites of ADH2 has seven copies of the sequence A/TGGAGA, a 22 base pair dyad, and a poly dA tract of 20 base pairs (Figure 2). The 22 bp dyad is required for ADR1-dependent activation of ADH2 transcription (Shuster et al., 1986; Eisen et al., 1988). Deletions of the poly dA tract did not affect ADH2 expression and thus may not be important to transcriptional regulation of ADH2 (Shuster et al., 1986).
Figure 2. Regulatory regions of the ADH2 gene

ATCTCCAACTTATAAGTGAGA
TAGAGGTGAATATTCAACCTCT

Dyad

TCTCC
AGAGG

UAS2

UAS1

TATAA

-280

-160

Poly dA tract

ADR3 C mutations localized to this region

ADH2
A variety of regulators that control ADH2 expression have been identified by genetic means. ADR1, an activator of ADH2 transcription, was identified by recessive atr1 mutations that block ADH2 expression (Ciriacy, 1975b) and by semi-constitutive ADR1C mutations that allow low levels of ADH II expression on glucose (Ciriacy, 1975a). The ADR6 allele is an activator of ADH2 expression and was identified by recessive atr6 mutations that blocked Ty-induced ADH2 expression. ADR6 is thought to act downstream from the TATAA box of ADH2 (Taguchi and Young, 1987) and appears to be a DNA binding protein (O’Hara et al., 1988). ADR6 is not specific to ADH2 expression since it is required for sporulation (Taguchi and Young, 1987). The CCR1 gene (Ciriacy, 1977), allelic to SNF1(Denis, 1984), encodes a protein kinase required for the expression of several glucose-repressible genes (Carlson and Celenza, 1986). It has been suggested that CCR1 acts through or with ADR1 to exert its regulatory effect on ADH2 (Denis, 1984; Denis, 1987) (Figure 3). More recent evidence suggests that CCR1 acts independently of ADR1 (D. Audino, pers. comm.). Other regulators of ADH2 expression include CRE1,CRE2, and CCR4. These genes are pleiotropic regulators which appear to act at the ADH2 TATAA sequence or downstream from the TATAA sequence (Denis and Malvar, in prep.). CCR4 is an
Figure 3. Regulators of ADH2

-400 -300 -200 -100 +1

TATAA ATG

ADH2 mRNA

CCR1

UAS

ADR1

TDS

CCR4

CRE2 (SPT6) (SSN20)

CRE1

SUC2

hls4-912

X
activator of ADH2 and is controlled by the negative effectors CRE1 and CRE2 (Denis, 1984). CRE2 is allelic to SPT6, which acts to regulate his4-912 delta, and to SSN20, a regulator of the SUC2 gene. The effects of the CRE genes on ADH2 expression are mediated through CCR4 as are their effects on his4-912 delta expression (Denis and Malvar, in preparation). ADR1 and CCR4 are independent activators of ADH2 expression and both are required for the full activation of ADH2 (Table 1). cre1 mutations result in altered cell morphology and the ccr4 allele in combination with the cre1 allele can restore normal cell morphology. Other than CRE1 and CRE2, a repressor specific to ADH2 has yet to be conclusively identified although the ADR4 gene may act as a repressor. The phenotype of ADR4 is not clearly understood because adr4 relieves glucose repression only in the presence of the ADR1-5C allele but not in the presence of the ADR1 allele (Ciriacy, 1979).

The most well studied of these regulators is ADR1. The ADR1 allele has been cloned (Denis and Young, 1983) and sequenced (Hartshorne et al., 1986). The open reading frame encodes a protein of 153 Kilodaltons (1323 amino acids, 3969 base pairs). The ADR1 protein has been identified by antibody precipitation and corresponds to the size predicted by sequence analysis of the open reading frame.
(R. Vallari, pers. comm.). DNA sequence analysis and comparison with other proteins have identified several potentially important regions.

These include, an acidic amino acid region which may be important to transcriptional activation, a DNA binding domain, and multiple potential phosphorylation sites (Hartshorne et al., 1986). Mutations that fall within the DNA binding domain at amino acids 102-159 (Blumberg et al., 1987, Denis in prep.) have been characterized (Figure 4) and reduce or block activation of ADH2.

The acidic amino acid region of ADR1 has been identified by analogy to regions found in other yeast activators. This region of eleven amino acid residues (between residues 29 and 39, Figure 4) contains six acidic residues, 4 Glu and 2 Asp. Transcriptional activating segments separate from DNA binding regions have been characterized in the yeast transcriptional activators GAL4 (Ma and Ptashne 1987a) and GCN4 (Hope and Struhl 1986; Hope et al., 1988), and these regions are noted for their abundance of acidic residues. In other experiments, random DNA fragments from E. coli were ligated in place of the yeast GAL4 transcriptional activation region. Several of the fragments were able to allow GAL4 to activate transcription (Ma and Ptashne, 1987a). These E. coli DNA fragments were found to encode peptide regions with a relatively large concentration of acidic amino acids.
Figure 4. Functional domains of ADR1

Transcriptional Activation region
amino acids 29-39

synthetic peptide

Phosphorylation site-230
Amino Acids 227-231

DNA-Binding region
Amino acids 102-159
acid residues. A deletion of one or more of the GCN4 acidic residues in its transcriptional activation region did not completely disrupt activation. However, a gradual loss of transcriptional activation was observed with the increasing deletion of this region of GCN4 (Hope and Struhl, 1986). Similar results were observed with mutations in the GAL4 acidic segment (Gill and Ptashne, 1987). The deletion experiments suggest that a decrease in negative charge results in a corresponding decrease in transcriptional activation and that overall acidity of the region is important, not the specific amino acid content. The absence of identified mutations in the acidic region of *ADR1* could result from the fact that single amino acid changes in this region would not result in a detectable phenotype due to the lack of a rigid sequence requirement for this region.

Several *adr1*-type mutations suppressing the *ADR1*-5C mutation have been cloned and sequenced (Denis, in prep.). These mutations occur in a region of *ADR1* homologous to the DNA binding region of transcription factor IIIA (TFIIIA) of *Xenopus laevis* (Hartshorne *et al.*, 1986; Blumberg *et al.*, 1987; Denis, in prep.) (Figure 4). TFIIIA has nine repeat units of a finger motif which has been shown to bind DNA (Fairall, *et al.*, 1986). Each finger has two cysteines and two histidines which act as ligands to bind Zn$^{2+}$ (Diakun *et al.*, 1986). The twelve
amino acids between the cysteines and histidines are thought to loop out to form the DNA-binding finger (Miller et al., 1985). ADR1 contains two such DNA-binding finger motifs in tandem located between amino acid 102 and 159 (Figure 4). C-terminal truncations leaving only 151 amino acids and disrupting the second Zn$^{2+}$ coordination site block ADH II activity (Bemis and Denis, 1988). Mutations in the finger region of ADR1 have been characterized (Blumberg et al. 1987; Denis, in prep.). The mutations were selected by their ability to suppress the ADR1-5C mutation (Denis, in prep.) or by their ability to reduce ADH II activity in strains carrying an ADR1-β-galactosidase fusion protein (Blumberg et al., 1987). The amino acids which have been mutated are designated with an arrow and the amino acid replacement is noted in Figure 4. The mutations found in the conserved DNA-binding finger region blocked or reduced ADR1 activation of ADH2. DNA binding studies using a synthesized peptide modeled on the finger region of ADR1 show that a single finger motif is capable of binding DNA in a nonspecific manner and binding of DNA is enhanced by coordination with Zn$^{2+}$ (Parraga et al., 1988). Moreover, a single finger is not capable of sequence specific binding.

The ADR1$^{C-}$ type mutations which result in increased ADH II expression under glucose-repressed conditions have also been
sequenced. Each point mutation occurs at a cAMP-dependent protein kinase (cAPK) consensus sequence in which serine-230 is the presumed phosphoacceptor (Denis and Gallo 1986; Cherry et al., 1989). ADR1C mutations have been shown to result in decreased phosphorylation of residue 230 by cAPK (Cherry et al., 1989), suggesting that ADR1 is more active when it is less phosphorylated.

The focus of this thesis is the identification of the functional regions of ADR1. Functional regions are the areas of this large protein (153 Kd) responsible for a specific action or interaction of the protein. The following questions were addressed in this dissertation:

Does the adr1-1 mutation inactivate a specific domain required for ADR1 control over ADH2 expression? This was the first question, broached at a time when it was still unclear whether ADR1 specified a protein product. Cloning and sequencing of the adr1-1 allele identified the adr1-1 mutation as a nonsense mutation and confirmed that ADR1 encoded a protein product. The adr1-1 mutation was found to be a serine codon mutated to a stop codon at amino acid 11. The translational start of ADR1 was inferred by the identification of the adr1-1 mutation. It was concluded that the first possible AUG codon is the translational start site as predicted by the nucleic acid sequence (Hartshorne et al., 1986). The serine residue at amino acid eleven was
found not to be important to ADR1 function since it could be replaced by several other amino acids without affecting ADR1 activity. The instability of the *adr1-1* mRNA as compared to the *ADR1* mRNA was also analyzed (Section I).

The second question addressed by this thesis concerned the separation of the functional domains of ADR1. In multifunctional proteins it is often possible to identify separate regions of the protein responsible for individual functions. This method was used with much success in regulatory proteins such as the glucocorticoid receptor (Danielsen *et al.*, 1986) and the yeast regulatory proteins GAL4 (Keegan *et al.*, 1986) and GCN4 (Hope and Struhl, 1986). C-terminal truncations of ADR1 were used to identify functional regions. Using this technique the transcriptional activation region, a DNA-binding domain, a site required for activation on glucose, and a region required for growth on glycerol were all identified.

The last questions asked in this thesis involved further characterization of the sites involved with activation on glucose and the region required for glycerol growth. An internal deletion of the phosphorylation site at amino acid 230 was constructed to determine if the loss of this site affected glucose activation. The role of *ADR1* in glycerol growth was addressed by genetic methods to determine which
factor or factors were being affected by ADR1 during growth of yeast on glycerol.
SECTION 1

CHARACTERIZATION OF THE \textit{adr1-1} MUTATION

Introduction

The \textit{adr1-1} mutation was first identified by Ciriacy (1975b). The mutation was identified following growth of yeast on medium containing allyl alcohol. Allyl alcohol, which is nontoxic, is converted to the toxic aldehyde acrolein by ADH. Only strains that are deficient in ADH activity are able to survive in the presence of allyl alcohol. The \textit{adr1-1} mutation has since been found to inhibit transcription of \textit{ADH2} (Denis \textit{et al.}, 1981). Yeast cells containing the \textit{adr1-1} mutation are thus able to grow on allyl alcohol, providing that the ADH isozymes ADH I and ADH III are also absent (Table 1). Recessive mutations that suppress \textit{ADR1-5C} function and recessive mutations in \textit{ADR1-lacZ} fusion genes have also been isolated (Blumberg \textit{et al.}, 1987; Denis, in prep.). Characterization of different \textit{ADR1} clones often made use of the \textit{adr1-1} phenotype and thus it
was imperative that the mutation be analyzed. The first chapter in this thesis focuses on the characterization of the *adr1-1* allele and discusses the implications resulting from its identification.
Table 2. *Saccharomyces cerevisiae* strains used to characterize the *adr1-1* allele

<table>
<thead>
<tr>
<th>Strain</th>
<th>Genotype</th>
</tr>
</thead>
<tbody>
<tr>
<td>43-2B</td>
<td>MATa adh1-11 adh3 ura1 his4</td>
</tr>
<tr>
<td>411-40</td>
<td>MATa adh1-11 adr1-1::YRp7-ADR1-411 adh3 ura1 his4</td>
</tr>
<tr>
<td>500-16</td>
<td>MATa adh1-11 adr1-1 adh3 ura1 trp1 his4</td>
</tr>
<tr>
<td>3C4</td>
<td>same as 500-16 except <em>adr1-1::YRp7-adr1-1-23A</em></td>
</tr>
<tr>
<td>4B1</td>
<td>same as 500-16 except <em>adr1-1::YRp7-adr1-1-4-23A</em></td>
</tr>
<tr>
<td>11-2</td>
<td>same as 500-16 except <em>adr1-1::YRp7-5'adr1-1-3'ADR1</em></td>
</tr>
<tr>
<td>C9</td>
<td>same as 500-16 except <em>adr1-1::YRp7-5'ADR1-3'adr1-1</em></td>
</tr>
<tr>
<td>17-3c</td>
<td>MATa leu2-u trp1 ade5,7-u adh1-11 adr1-1</td>
</tr>
<tr>
<td>19-6d</td>
<td>MATa leu2-u trp1 ade5,7-u his5-u adh1-11</td>
</tr>
<tr>
<td>21-5c</td>
<td>MATa leu2-u trp1 ade5,7-u adh1-11 adr1-1</td>
</tr>
<tr>
<td></td>
<td>SUP79</td>
</tr>
</tbody>
</table>
Materials and Methods

Strains and conditions of growth

Yeast strains are described in Table 2. Yeast were grown overnight in YEP medium (2% Bacto-Peptone [Difco Laboratories, Detroit, Mich.], 1% yeast extract, 20 mg each of adenine and uracil, per liter) supplemented with either 8% glucose or 3% ethanol. YD plates contained YEP medium, 2% glucose, and 2.5% agar. Minimal plates lacking tryptophan contained synthetic complete media, 2% glucose, 2.5% agar, and amino acids except tryptophan (Williamson et al., 1981).

Localization of the \textit{adr1-1} mutation

The \textit{adr1-1} mutation was mapped within the 5 to 6 kb of \textit{ADR1} DNA using methods similar to those described by Denis and Gallo (1986). Two gapped plasmids were used (Plasmids A and B, Figure 5). The plasmid YRp7-ADR1-5C-23A (Denis and Young, 1983), which contains the upstream region of \textit{ADR1} and 2982 bp of the \textit{ADR1} open reading frame, was deleted between base pairs +440 and +1075 upon cleavage with BclI (Plasmid A, Figure 5). Deletion of the 635 bp fragment removes the \textit{ADR1-5C} point mutation at base pair 683 (Denis and Gallo, 1986). Plasmid YRp7-ADR1-411-BA, which contains a 4.8 kb \textit{ADR1} insert including approximately 1600 bp of sequences upstream from \textit{ADR1} to
+3200 bp of the \textit{ADR1} structural gene, was cleaved with Bcil which deleted a 2.2 kb region of \textit{ADR1} extending from about -1200 bp to +1075 bp (Plasmid B, Figure 5).

The gapped plasmids were site-specifically targeted for integration (Orr-Weaver \textit{et al.}, 1981) into the \textit{adr1-1} allele in strain 500-16 (Denis and Gallo, 1986). Transformants carrying integrated copies of plasmids A and B were identified on minimal plates lacking tryptophan, followed by successive growth on non-selective YEP plates containing 2% glucose. Those colonies which did not lose the TRP+ phenotype conferred by the plasmid, and which presumably contained integrated plasmid, were analyzed further. Southern analysis (Southern, 1975) was used to determine the number of plasmid copies integrated into the genome while tetrad analysis (Mortimer and Hawthorne, 1969) verified integration at the \textit{adr1-1} locus. The ADH II activities of all integrants were determined following growth on medium containing either glucose or ethanol and were compared to the activities of strains carrying the \textit{ADR1} or \textit{adr1-1} allele (strain 43-2B or 500-16, Table 3).
Figure 5. Plasmids Section 1.

*ADR1* sequences are represented by solid black boxes. Sequences from *adr1-1* plasmids are designated by grey boxes. Solid black lines designate the *TRP1* marker gene from *S. cerevisiae*. Thin black lines represent pBR322 sequences and are not drawn to scale. Numerical designations refer to *ADR1* sequences only.
Figure 5. Plasmids (Section 1)

A  YRp7-ADR1-5^C-23A-BclI

B  YRp7-ADR1-411BA-BclI

C  YRp7-adr1-1-23A

D  YRp7-5'adr1-1-3'ADR1

E  YRp7-5'ADR1-3'adr1-1
The **adr1-1** allele was cloned by plasmid rescue (Orr-Weaver *et al.*, 1983), from the integrant 3C4 (Table 2). Subsequent transformation of the strain 500-16 (**adr1-1**) with the recovered plasmid demonstrated that the recovered plasmid (YRp7-adr1-1-23A, Plasmid C, Figure 5) was indeed carrying the **adr1-1** allele (strain 4B1, Table 3).

The YRp7-adr1-1-23A and the YRp7-ADR1-411-BA plasmids were used to construct two hybrid plasmids for further localization of the **adr1-1** mutation. Plasmid D (Figure 5) contained the 5' region of the **adr1-1** plasmid (YRp7-adr1-1-23A) to base pair +48 and the 3' region of the **ADR1** plasmid (YRp7-ADR1-411-BA). Plasmid E (Figure 5) contained the 5' region of the **ADR1** allele from plasmid YRp7-ADR1-411-BA to base pair +48 and the 3' region of the **adr1-1** allele from plasmid YRp7-adr1-1-23A.

The **adr1-1** mutation was identified by sequence analysis (Sanger *et al.*, 1977) following digestion of YRp7-adr1-1-23A plasmid DNA with PvuII and EcoRI and subcloning the fragments into M13 phage mp18 and mp19.
**Table 3. ADH II enzyme activities (Section 1)**

<table>
<thead>
<tr>
<th>Strain</th>
<th>ADR1 genotype</th>
<th>Integrated ADR1 plasmid</th>
<th>ADH II activity mU/mg&lt;sup&gt;a&lt;/sup&gt; glucose</th>
<th>ADH II activity mU/mg&lt;sup&gt;a&lt;/sup&gt; ethanol</th>
</tr>
</thead>
<tbody>
<tr>
<td>43-2B</td>
<td>ADR1</td>
<td>none</td>
<td>5</td>
<td>2500</td>
</tr>
<tr>
<td>500-16</td>
<td>adr1-1</td>
<td>none</td>
<td>2</td>
<td>9</td>
</tr>
</tbody>
</table>

13 integrants<sup>b</sup>
- **adr1-1**
  - Plasmid A
  - 635 bp deletion
  - ADH II activity: 5 mU/mg<sup>a</sup> glucose, 2200 mU/mg<sup>a</sup> ethanol

2 integrants<sup>b</sup>
- **adr1-1**
  - Plasmid A
  - 635 bp deletion
  - ADH II activity: 3 mU/mg<sup>a</sup> glucose, 20 mU/mg<sup>a</sup> ethanol

11 integrants<sup>c</sup>
- **adr1-1**
  - Plasmid B
  - 2200 bp deletion
  - ADH II activity: 2 mU/mg<sup>a</sup> glucose, 10 mU/mg<sup>a</sup> ethanol

4B1<sup>d</sup>
- **adr1-1**
  - Plasmid C
  - (adr1-1)
  - ADH II activity: nd<sup>g</sup> mU/mg<sup>a</sup> glucose, 4 mU/mg<sup>a</sup> ethanol

11-2<sup>f</sup>
- **adr1-1**
  - Plasmid D
  - 5'adr1-1/3'ADR1
  - ADH II activity: nd<sup>g</sup> mU/mg<sup>a</sup> glucose, 4 mU/mg<sup>a</sup> ethanol

C9<sup>g</sup>
- **adr1-1**
  - Plasmid E
  - 5'ADR1/3'adr1-1
  - ADH II activity: nd<sup>g</sup> mU/mg<sup>a</sup> glucose, 2500 mU/mg<sup>a</sup> ethanol

---

<sup>a</sup>Yeast that were inoculated into YEP medium containing 8% glucose had been pregrown on YEP plates supplemented with 8% glucose, while yeast inoculated into YEP medium containing 3% ethanol had been pregrown on YEP plates supplemented with 2% glucose.
b Integrants derived from transformation of strain 500-16 with Plasmid A.
c Integrants derived from transformation of strain 500-16 with Plasmid B.
d Strain 4B1 carrying rescued plasmid YRp7-adr1-1-23A (Plasmid C) integrated at adr1-1.
e nd - not determined
f Strain 11-2 carrying hybrid plasmid D, 5' region of adr1-1 to base pair +48 ligated to the 3' region of ADR1 at base pair +49.
g Strain C9 carrying hybrid plasmid E, 5' region of ADR1 to base pair +48 ligated to the 3' region of adr1-1 at base pair +49.
tRNA-Suppressors

Strains carrying the *adr1-1* allele and the UGA-tRNA-suppressors *SUP88* and *SUP79* (D. Hawthorne personal communication) were constructed using standard yeast genetic techniques (Table 4). The *SUP4* (E. Schmidt, pers. comm.) and *SUP3e* (Hottinger *et al.*, 1982) alleles, present on shuttle vectors containing the *S. cerevisiae TRP1* gene and pBR322 sequences, were used to transform strains carrying the *adr1-1* allele.
Table 4. ADH II activities in the presence and absence of UGA-tRNA suppressors

<table>
<thead>
<tr>
<th>Strain</th>
<th>UGA suppressor (amino acid insert)</th>
<th>ADH II activity (ethanol)\textsuperscript{a} mU/mg</th>
</tr>
</thead>
<tbody>
<tr>
<td>segregants (adr1-1)\textsuperscript{b}</td>
<td>no SUP</td>
<td>12</td>
</tr>
<tr>
<td>segregants (adr1-1)\textsuperscript{b}</td>
<td>SUP\textsuperscript{88} leucine</td>
<td>96</td>
</tr>
<tr>
<td>19-6D (ADR1)</td>
<td>SUP\textsuperscript{88} leucine</td>
<td>2500</td>
</tr>
<tr>
<td>segregants (adr1-1)\textsuperscript{c}</td>
<td>no SUP</td>
<td>4</td>
</tr>
<tr>
<td>segregants (adr1-1)\textsuperscript{c}</td>
<td>SUP\textsuperscript{79} arginine</td>
<td>44</td>
</tr>
<tr>
<td>500-16</td>
<td>no SUP</td>
<td>10</td>
</tr>
<tr>
<td>500-16-1AS (adr1-1)\textsuperscript{d}</td>
<td>SUP\textsuperscript{3e} serine</td>
<td>216</td>
</tr>
<tr>
<td>500-16-5A (adr1-1)\textsuperscript{e}</td>
<td>SUP\textsuperscript{4} tyrosine</td>
<td>205</td>
</tr>
</tbody>
</table>

The ADH II activities were shown to be statistically significant at the 0.95 confidence level for the leucine inserting genomic tRNA-suppressors and at the 0.99 confidence level for the arginine inserting tRNA-suppressor using the t-test.

\textsuperscript{a} Yeast were pregrown on YEP plates supplemented with 2% glucose before inoculation into YEP medium containing 3% ethanol.

\textsuperscript{b} Average of ten segregants from the cross 19-6d with 17-3c.

\textsuperscript{c} Average of eleven segregants from the cross of 21-5c with 17-3c.

\textsuperscript{d} Strain 500-16 transformed with SUP\textsuperscript{3e}-UGA inserting serine.

\textsuperscript{e} Strain 500-16 transformed with SUP\textsuperscript{4}-UGA inserting tyrosine.
Northern analysis

Northern analysis of total RNA was conducted as previously described (Denis and Gallo, 1986). Densitometric analysis of the \( ADR1 \) mRNA, rRNA, and \( URA1 \) mRNA was conducted using an EC-210 densitometer. The amount of rRNA and \( URA1 \) mRNA were used as internal standards of the RNA present.

Fragments of DNA were isolated from agarose gels following restriction digestion and electrophoresis and used as hybridization probes. Probes were labeled with \([\delta - ^{32} P]dATP\) using a Random Primed DNA labeling kit from Boehringer Mannheim (Indianapolis, IN).

Results

Localization and identification of the \( adr1-1 \) mutation

The \( adr1-1 \) mutation was localized by transformation of yeast harboring the \( adr1-1 \) allele. Two plasmids with different size deletions of the \( ADR1 \) DNA sequences (Materials and Methods) were targeted for site-specific integration. Upon integration of the plasmid into the \( adr1-1 \) locus the plasmid deleted sequences would be filled in with information from the genomic \( adr1-1 \) allele (Orr-Weaver et al., 1981). Fifteen transformants
containing an integrated copy of plasmid A (Figure 5), the YRp7-ADR1-5C-23A BclI deleted plasmid, were characterized. Thirteen displayed the wild-type ADR1 phenotype (Table 3), while two failed to derepress ADH II, a characteristic of the adr1-1 phenotype (Table 3). These results indicate that the adr1-1 mutation is not located in the deleted region (+440 bp to +1075 bp), but is located either to the 5' or 3' side of the deletion. The two transformants displaying the adr1-1 phenotype probably resulted from plasmid integrations in which the size of the original 635 bp gap had been increased (Clancy et al., 1984).

The location of the adr1-1 mutation was further investigated by transforming strain 500-16 with linearized plasmid B (Figure 5) lacking ADR1 sequences from -1200 bp to +1075 bp. Eleven transformants carrying integrated copies of the plasmid were identified. All transformants were deficient in ADH II activity (Table 3), indicating that the adr1-1 mutation was located within the -1200 bp and +1075 bp gap. The mutation causing the adr1-1 phenotype was thus localized to the 5' side of the BclI site at base pair +440. Further localization was conducted using YRp7-adr1-1-23A (Plasmid C, Figure 5), a plasmid rescued from integrant 3C4 (Table 2). Hybrid plasmids were constructed using plasmid YRp7-adr1-1-23A and YRp7-ADR1-411-BA (Materials and Methods). Transformants carrying plasmid D integrated into the genome (Figure 5: adr1-1
sequences 5' to +48 bp) expressed low ADH II activities (strain 11-2, Table 3) while those carrying plasmid E (Figure 5: ADR1 sequences 5' to +48 bp) expressed wild type ADH II activities (strain C9, Table 3). The hybrid plasmid experiments indicated that the adr1-1 mutation was contained either within the 5' noncoding region or within the first 48 base pairs of the putative adr1-1 open reading frame.

The nucleotide sequence of the adr1-1 allele between base pairs -121 and +54 was determined to correspond to that previously observed for the ADR1 gene (Hartshorne et al., 1986) with one exception: a C to G transversion was observed at base pair +32 in adr1-1. Such an alteration would lead to the replacement of a UCA serine triplet with a UGA stop signal.

UGA-tRNA-suppressors are capable of suppressing the adr1-1 mutation

UGA-tRNA-suppressor studies were undertaken to confirm that the C to G transversion and the resultant nonsense codon were the cause of the adr1-1 phenotype. Two UGA-suppressors of genomic origin were combined with the adr1-1 allele by making the appropriate crosses. SUP88 would result in the insertion of leucine (Hawthorne, 1981) while SUP79 is thought to insert arginine (D. Hawthorne, pers. comm.). In addition, plasmid borne tyrosine-inserting (E. Schmidt, pers. comm.) and
serine-inserting (Hottinger et al., 1982) UGA-tRNA-suppressors were also combined with the *adr1-1* allele. The results of the *adr1-1* UGA-tRNA-suppressor studies are compiled in Table 4. In all cases the presence of a UGA-tRNA-suppressor caused an increase in ADH II activity, indicating that the *adr1-1* allele did in fact contain a UGA nonsense mutation. In contrast, no increase of *ADR1*-dependent ADH II activity was found in the presence of the UGA-tRNA-suppressors (Table 4, 19-6D). The arginine UGA-tRNA-suppressor appeared to restore the *ADR1* phenotype to the lowest extent, whereas the tyrosine and serine suppressors were the most effective in restoring *ADR1* function (Table 4).

RNA analysis

Nonsense mutations which occur early in a translated sequence may result in less stable mRNAs (Chang and Kan, 1979; Losson and Lacroute, 1979; Kinniburgh et al., 1982; Pelsy and Lacroute, 1984). In order to analyze the effect of *adr1-1* on the stability of the putative 5.1 kb *ADR1* mRNA, total yeast RNA from strains 500-16 (*adr1-1*) and 411-40 (*ADR1*) grown on glucose-containing medium was examined by Northern analysis. Figure 6 shows a typical Northern blot in which the levels of *adr1-1* and *ADR1* mRNA are compared. *ADR1* mRNA was found to be two-to three-fold more abundant than *adr1-1* mRNA (Figure 6). The decrease in the amount of *adr1-1* mRNA was not due to defective ADH II expression, for
yeast containing the ccr1-1 allele, which also blocks ADH II synthesis, express normal levels of ADR1 mRNA (Denis and Gallo, 1986). A similar decrease in adr1-1 mRNA levels relative to ADR1 mRNA levels was also observed when yeast strains were grown on ethanol containing medium (Figure 7).
Figure 6. Northern analysis of *adr1-1* mRNA levels.

Total cellular RNA was loaded in each lane and probed with an *ADR1* probe as described in Materials and Methods (Section 1): A-RNA from strain 500-16 (*adr1-1*) B-RNA from strain 411-40 (*ADR1*) C-duplicate of lane A at higher concentration D-duplicate of lane B at higher concentration. The inserts show the amount of rRNA or *URA1* RNA in each lane and these were used to standardize the levels of total *ADR1/adr1-1* RNA loaded.
Figure 6

ADR1

rRNA

25S

18S

URA1
Figure 7. Northern analysis of $ADR1/adr1-1$ mRNA levels from cells grown on glucose- or ethanol-containing medium.

Total cellular RNA was loaded in each lane and probed with an $ADR1$ probe as described in Materials and Methods (Section 1): A and B- RNA from strain 500-16 ($adr1-1$) from cells grown overnight in 3% ethanol-containing medium  C- RNA from strain 500-16 ($adr1-1$) from cells grown overnight in 8% glucose-containing medium  D and E- RNA from strain 411-40 ($ADR1$) grown overnight in 3% ethanol-containing medium  F- RNA from strain 411-40 ($ADR1$) grown overnight in 8% glucose-containing medium. The insert shows the amount of rRNA in each lane. The amount of rRNA was used to standardize the levels of total $ADR1/adr1-1$ RNA loaded.
Discussion

Cloning and sequencing of the *adr1-1* allele identified a UGA nonsense mutation at the 11th codon of *ADR1*. The identification of the *adr1-1* mutation was confirmed by the use of UGA-tRNA-suppressors to restore *ADR1* function. These results indicate that the *ADR1* gene does in fact encode a protein product and that the first AUG codon in the *ADR1* sequence is the site of translational initiation. The *adr1-1* mRNA is less stable than the *ADR1* mRNA, this observation allowed confirmation that the previously identified 5.1 kb transcript (Denis and Gallo, 1986) is the *ADR1* transcript.

There are two explanations which could account for the low level of ADH II activity in strains carrying both the *adr1-1* mutation and the UGA-tRNA-suppressors. One possibility is that read-through of the normal UGA stop codon at base pair +3970 (Hartshorne *et al*., 1986) yields a larger than normal protein having diminished *ADR1* function. This seems unlikely since the UGA-tRNA-suppressors were observed to have no effect on wild-type *ADR1* activity. An alternative explanation is that suppressors have variable efficiencies for individual nonsense codons. The variability of suppression by tRNA-suppressors is influenced by the context surrounding the nonsense codon, the acceptability of the amino acid inserted at the mutation site, the position of the mutant codon within the
locus, and the level of expression of the suppressor (Sherman, 1982). A serine inserting UGA-tRNA-suppressor, which restores the original ADR1 sequence, did suppress the mutation with the highest efficiency (10% of wild-type). The tyrosine inserting UGA-tRNA-suppressor suppressed the adr1-1 mutation at levels roughly similar to the serine suppressor, while leucine and arginine suppressors resulted in somewhat lower ADH II activities. The inherent variability of tRNA-suppressors would indicate that all four amino acid substitutions resulted in functional ADR1 proteins. The placement of a serine residue at codon 11 in the ADR1 protein is thus believed nonessential for ADR1 function.

The first 5' AUG codon is normally the one used for translational initiation in eukaryotes (Kozak, 1983), although there are exceptions in which one or more small open reading frames are present prior to the site of translational initiation. The mechanism which allows reinitiation of translation at internal open reading frames is not clear at this time (Kozak, 1987). Translation could reinitiate at an AUG following the adr1-1 mutation. The next closest AUG is out of frame at base pair +83 and 5 triplets away is a UAG stop codon. Following the second AUG is a third AUG that is in-frame with ADR1. If reinitiation occurred here, an ADR1 protein with an N-terminal deletion of 34 amino acids would result. Because the first 34 amino acids contain part of an acidic region proposed...
to be involved in transcriptional activation (Bemis and Denis, 1988; Figure 1) an \textit{adr1-1} reinitiation product is likely to be nonfunctional.

The reduced levels of the 5.1 kb \textit{adr1-1} transcript confirm that the previously identified 5.1 kb transcript (Denis and Gallo, 1986) is indeed the \textit{ADR1} mRNA. The ability of nonsense mutations to decrease the level of mRNA appears to be a common phenomenon. Several alleles of the human $\beta^G$ globin gene have been identified which contain nonsense mutations within the first 180 bp of the structural gene (Chang and Kan, 1979; Orkin and Goff, 1981; Kinniburgh \textit{et al.}, 1982). These mutations also show reduced levels of mRNA as compared to the normal allele. Nonsense mutations in N-terminal regions resulting in unstable mRNAs have also been identified in the \textit{ura1} (Pelsy and Lacroute, 1984), \textit{ura3} (Losson and Lacroute, 1979), and \textit{cyc1} (Zitomer \textit{et al.}, 1979) genes of \textit{S. cerevisiae}. Nonsense mutations in the C-terminal region of \textit{ura1} have no effect on its mRNA stability (Pelsy and Lacroute, 1984). A mechanism similar to transcriptional polarity in \textit{E. coli} has been suggested to explain the translational protection evidenced by the comparison of mRNA stability in \textit{ura1} alleles which contain polar nonsense codons (Pelsy and Lacroute, 1984). A single base pair change resulting in a nonsense codon would block further translation of the mRNA and further protection of the mRNA by ribosomes or by the newly formed protein product (Maquat and Daar,
1988). The ADR1 mRNA is normally present at very low levels (less than 0.01% mRNA) in the cell and may represent a class of rapidly degraded transcripts (Santiago et al., 1986).
SECTION 2

IDENTIFICATION OF FUNCTIONAL REGIONS OF ADR1

Introduction

Transcriptional activators have several functions in common. They must be capable of interacting with DNA and they must also be able to interact with the transcriptional machinery. Transcriptional activators may also interact with other protein factors. GAL4, for example, binds the repressor GAL80 which prevents GAL4 transcriptional activation of the galactose utilization genes (Ma and Ptashne, 1987b). The various functions required by a transcriptional activating protein are often carried out by distinct regions of the protein. Deletion analysis of transcriptional activators may be used to define the location of such domains.

Early investigations suggested that deletion of the C-terminus of ADR1 (amino acids 305 to 1323) results in a truncated version of the ADR1 protein which is still capable of activating ADH2 transcription (Denis and
Young, 1983). Further deletions of ADR1 from the C-terminus were constructed to identify functional regions of ADR1 (these experiments are described in the Appendix). An internal deletion of ADR1 was also constructed that spanned the region of ADR1 suggested to be required for bypassing glucose control.

**Methods and Materials**

**Internal deletion of amino acids 220 to 262**

Plasmids were constructed by ligation of fragments from plasmid YRp7-ADR1-23A (Denis and Gallo, 1986), pUC18 (obtained from New England Biolabs, Beverly MA), and pTRP1 (obtained from M. Wigler, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY).

A fragment of ADR1 extending from the XmnI site at base pair +786 to the SstI site at base pair +1713 was ligated into the pUC18 polylinker region at the SmaI and SstI sites to generate plasmid LBp45. Plasmid LBp45 was cleaved at the unique SalI site and the 5' overhang was filled in to form blunt ends. The resultant plasmid was then restricted with the enzyme HindIII. Restriction of the YRp7-ADR1-23A plasmid with HindIII and Scal allowed the isolation of a fragment containing 346 bp of pBR322 and the entire 5' region of ADR1 to base pair +661. The fragment containing the 5' region of ADR1 was then ligated into the LBp45 plasmid which had
been filled in and restricted as described above. The resulting plasmid, LBp8, contains the 5' region of \textit{ADR1} at the HindIII site of pUC18 to the Scal site of \textit{ADR1} at base pair 661, the polylinker region of pUC18 from the filled in Sall site, 19 base pairs of the pUC18 polylinker to the Smal site, and base pairs 786 to 1713 of \textit{ADR1} (Figure 8). The LBp8 plasmid contains a deletion that would result in an ADR1 protein lacking amino acid residues 220 to 262. Seven additional amino acids are added after amino acid 220 due to the polylinker of pUC18 (Figure 8).

Expression of plasmid LBp8 in yeast required the addition of the yeast autonomously replicating sequence (ARS) contained on the \textit{TRP1} gene fragment (Tschumper and Carbon, 1980). Plasmid pTRP1 carries the \textit{TRP1} gene inserted at the EcoRI site of pUC18. A fragment extending from the XmnI site to the SstI site containing the entire \textit{ADR1} gene from plasmid LBp8 was ligated into the pTRP1 plasmid at the SstI and XmnI sites. The ligation of these two fragments repairs the ampicillin gene of the pUC18 vector and forms LBp6. Plasmid LBp6 contains the \textit{TRP1} gene, all of the 5' \textit{ADR1} sequences, and the \textit{ADR1} open reading frame to base pair 1713 with a deletion between base pairs 661 and 786 (Figure 8).

Transformation of plasmid LBp6 into the yeast strain 500-16 was by the lithium acetate method (Ito \textit{et al.}, 1983). Plasmid LBp6 was restricted with
Figure 8: Internal deletion of amino acids 220-253 of ADR1

*ADR1 sequences are underlined

**Plasmid LBp8 is the same as LBp6 except that it lacks the TRP1 fragment.
the enzyme NruI at base pair 1411 (in wild type ADR1 the NruI site is at base pair 1517) to allow site directed integration into the ADR1 gene (Orr-Weaver et al., 1981; Denis and Gallo, 1986).

Results

Expression of the internally deleted plasmid LBp6 in yeast strain 500-16

Plasmid LBp6 was transformed into strain 500-16 and transformants carrying free plasmid or integrated plasmid were identified (Denis and Gallo, 1986). The presence of plasmid LBp6 in yeast strain 500-16 allowed growth on antimycin A. This result suggests that when present in high copy, plasmid LBp6 allows activation of ADH2 expression under glucose growth conditions (Table 5). This observation is in contrast to our previous result which suggested that the phosphorylation region is required for ADR1 to bypass glucose control.

A single integrant of plasmid LBp6 in strain 500-16 were also isolated. The ADH II activity of these strains have been determined under glucose growth conditions and is similar to that of a strain carrying an ADR1C allele (Table 5).
Table 5. ADH II enzyme activities (Section 2)

<table>
<thead>
<tr>
<th>Plasmid</th>
<th>ADH II activity mU/mg</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>glucose</td>
</tr>
<tr>
<td>ADR1-5C</td>
<td>none</td>
</tr>
<tr>
<td>plasmid LBp6</td>
<td>LBp6</td>
</tr>
<tr>
<td>integrated LBp6</td>
<td>LBp6</td>
</tr>
</tbody>
</table>

\(^a\)and-not determined

Discussion

The goal of the internal deletion experiments described in this section was to obtain a better understanding of the role of the region defined by amino acids 220 to 253 of ADR1. The results presented in Appendix for ADR1-220 and ADR1-253 suggested that the region between residues 220 and 253 was necessary for enhancing ADR1 activity but was not required for ADR1 activity. Mutations in the region between amino acids 227 and 231 (a phosphorylation site) (Cherry et al., 1989) allow ADH II to bypass glucose repression. Two models have been proposed to explain the function of this region: this region may be required to enhance ADR1 activity or these mutations prevent a repressor from binding to this region. Other models are also possible as described below. The deletion leaving
just the N-terminal 220 amino acids of ADR1 was subject to glucose repression but was also capable of transcriptional activation (Bemis and Denis, 1988; Appendix). These results suggest that the absence of the phosphorylation region does not allow escape from a negative effector.

The internal deletion removing just the region between amino acids 220 and 262 leaves the C-terminus of ADR1 intact. Therefore the region of ADR1 to which constitutive mutations have been localized is deleted. ADH II activity in strains carrying the internally deleted ADR1 was no longer subject to glucose repression which was similar to what was observed in strains carrying an ADR1C mutation.

The above results suggest that the phosphorylation region may in fact interact with a negative effector and when this region is absent the negative effector can not act through this portion of ADR1.

Another plausible role for this region is that it could be required for dimerization of ADR1. Foot print analysis of ADR1 bound to the promoter region of ADH2 is consistent with the supposition that ADR1 binds as a dimer to this region (Eisen et al., 1988). ADR1 monomers may bind separately to UAS1 but once bound may interact, possibly through the phosphorylation region. This hypothesis is supported by the fact that ADR1 can bind to one half of the inverted repeat sequence but only half of UAS1 is inactive as a UAS (Yu et al., 1989).
The phosphorylation region could be required for proper folding of the ADR1 protein. The complete deletion of this region results in a less active protein than does a point mutation in this region. A point mutation might be expected to have a different effect upon the folding of the protein than the deletion of a large region. This model suggests that the phosphorylation region is required for interactions within the ADR1 protein rather than interaction with a repressor or another monomer of ADR1.

The contrasting evidence between the ADR1 protein containing only 220 amino acids and the internal deletion of the region between amino acids 220 and 262 could be due to the low level of $ADH2$ activation detected in strains carrying ADR1-220. The ADH II activity in these strains is very low under derepressed conditions and any bypassing of glucose repression (typically at a level 5-10% of derepressed activity) may not be detectable under glucose growth conditions. The addition of the C-terminus may assist the N-terminal 220 amino acids to a higher level of $ADH2$ activation. In agreement with this, we previously determined that no C-terminal truncation of ADR1 is as active as the entire ADR1 protein (Appendix).

Further experiments involving this region are planned and include the creation of internal deletions throughout this region. The LBp6 plasmid has seven amino acids present due to the pUC18 polylinker region which
would not be present in ADR1. The seven amino acids include an Asp which would provide a negative charge and might be expected to reduce the activity of ADR1 in a manner similar to that of a phosphorylated serine. This, however, could not account for the observed increase in activity.

Another consideration when planning future experiments is the recent identification of several other ADR1C mutations in this region. The recently identified mutations were not localized to the phosphorylation site between 227 and 231. These mutations include a serine to an arginine change at amino acid 232 and a tyrosine to an asparagine or a cysteine change at amino acid 239 (pers. comm. Dan Chase and Susan Fontaine). The sites of these newly characterized mutations have also been deleted in the LBp6 plasmid. Internal deletions and studies of the actual ADR1 protein will help to clarify the remaining questions concerning the regulation of ADR1 through the region C-terminal to amino acid 220.
SECTION 3

THE EFFECT OF ADR1 ON GLYCEROL GROWTH

Introduction

The transcriptional activator ADR1 has been shown to be required for the use of glycerol as a carbon source (Bemis and Denis, 1988; Appendix). The previously described C-terminal truncation analysis of ADR1 indicated that ADR1-truncated proteins capable of transcriptional activation could grow on ethanol-containing medium (Table 2, Appendix). In contrast, only ADR1-truncated proteins which contained at least 506 N-terminal amino acids could utilize glycerol-containing medium (Table 2, Appendix). A yeast strain with constitutive ADH II activity and an adr1-1 allele (Figure 3, Appendix) could not grow on glycerol-containing medium although it could grow on ethanol-containing medium. These results suggest that ADR1 is
required for growth on glycerol-containing medium regardless of ADH II activity. The requirement of ADR1 for glycerol growth is the first indication that ADR1 acts in a metabolic pathway other than that directly regulating ADH2.

Catabolism of glycerol is poorly understood in S. cerevisiae although two glycerol catabolizing enzymes, glycerol kinase and glycerol 3-phosphate dehydrogenase, have been identified (Sprague and Cronan, 1977). The glucose repressible enzymes glycerol kinase and glycerol 3-phosphate dehydrogenase are not regulated by ADR1 (Bemis and Denis, 1988; Appendix).

Evidence presented here suggests that ADR1 is required for glycerol growth and that a recessive mutation at the GLP1 locus must be present for strong glycerol growth.

Materials and Methods

Yeast Strains

Glycerol growth characteristics were studied using strains isogenic to 43-2B and 411-40. The genotypes of these strains are given in Table 6.
Growth Conditions

Strains were tested for growth on glycerol by inoculation into YEP media (1% yeast extract, 2% Bacto-Peptone, 20 mg/l adenine, and 20 mg/l uracil) supplemented with 3% glycerol. Strains that were able to grow in YEP 3% glycerol after two days were considered "strong glycerol growers". Strains able to grow in YEP 3% glycerol after 4-7 days of incubation were classified as "glycerol growers". Strains unable to grow on glycerol after 10 days of incubation in YEP 3% glycerol were termed "glycerol-non-growers". Strains were initially tested on YEP 3% glycerol plates (YEP 3% glycerol media and 2% bacto agar) in which the same glycerol growth characteristics were detected. Plate analysis was not definitive and needed to be confirmed by growth in liquid glycerol-containing medium. All growth conditions were conducted at 30°C.

Medium containing alternative carbon sources was prepared as described above by substituting either 2% lactate, 2% pyruvate, or 3% acetate for the 3% glycerol.
Table 6. Isogenic strains used for characterization of glycerol growth.

<table>
<thead>
<tr>
<th>Strain</th>
<th>Relevant genotype</th>
</tr>
</thead>
<tbody>
<tr>
<td>43-2B*</td>
<td>MATα adh1-1 adh3 ura1 his4</td>
</tr>
<tr>
<td>43-2B-R*</td>
<td>MATα adh1-11 adh3 ura1 his4 glp1</td>
</tr>
<tr>
<td>R234*</td>
<td>MATα adh1-11 adh3 ura1 his4 ADR1-5C</td>
</tr>
<tr>
<td>R234-R*</td>
<td>MATα adh1-11 adh3 ura1 his4 ADR1-5C glp1</td>
</tr>
<tr>
<td>R234-7*</td>
<td>MATα adh1-11 adh3 ura1 his4 adr1-5C</td>
</tr>
<tr>
<td>411-40**</td>
<td>MATα adh1-11 adh3 adr1-1:YRp7-ADR1-411 ura1 his4</td>
</tr>
<tr>
<td>660**</td>
<td>MATα adh1-11 adh3 adr1-1:YRp7-ADR1-5C-23A ura1 his4</td>
</tr>
<tr>
<td>500-16**</td>
<td>MATα adh1-11 adh3 adr1-1 trp1 ura1 his4</td>
</tr>
<tr>
<td>68-3D</td>
<td>MATα adh1-11 adh3 trp1 ura1 his4</td>
</tr>
<tr>
<td>68-3D-R</td>
<td>MATα adh1-11 adh3 trp1 ura1 his4 glp1</td>
</tr>
</tbody>
</table>

* Strains isogenic to 43-2B

** Strains isogenic to 411-40
Results

Glycerol Growth of Isogenic Strains in Liquid Culture

Figure 3 (Appendix) shows the pattern of glycerol growth for 411-40 (ADR1, ADH2) and the isogenic strain ΔSPH6 (adr1-1, ADH2-S6). Strains having a functional ADR1 (411-40) were found to be capable of slowly utilizing glycerol. In contrast strains lacking a functional ADR1 (ΔSPH6) were observed to be unable to utilize glycerol as a carbon source (Figure 3, Appendix).

The isogenic strains 43-2B and R234 (Table 5) could not grow on glycerol at first but could adapt to growth on glycerol after 5-7 days (Figure 9). Thus, adaptation to glycerol growth by 43-2B and R234 appears to be a different phenotype than that observed in the 411-40 isogenic series which grows slowly on glycerol (Figure 3, Appendix; Figure 10). Single colonies from adapted cultures of 43-2B and R234 were isolated to determine if the ability to grow on glycerol is reversible. The putative glycerol-adapted strains isolated in this manner were then grown on nonselective media (glucose containing) for several generations. The glycerol-adapted phenotype did not revert back to being poor glycerol growers after several generations of nonselective growth. This result
Figure 9
Growth of strains isogenic to 43-2B on 3% glycerol

![Graph showing growth of different strains on 3% glycerol.](image-url)
Figure 10

Growth of strains isogenic to 411-40-B on 3% glycerol

<table>
<thead>
<tr>
<th>Time (days)</th>
<th>0</th>
<th>2</th>
<th>4</th>
<th>6</th>
<th>8</th>
<th>10</th>
</tr>
</thead>
<tbody>
<tr>
<td>log of cells/ml</td>
<td>6</td>
<td>7</td>
<td>8</td>
<td>9</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- 411-40
- 411-40-B
- B19
- B19-B
- 500-16
suggests a genetic alteration had occurred in those strains (43-2B-R and R234-R). The strains that were "strong glycerol growers" were called 43-2B-R and R234-R (R indicates revertant on glycerol). These strains grew strongly on glycerol after two days (Figure 9). The isogenic strain R234-7 (ADR1-5C-7) lacking a functional ADR1 could not adapt to glycerol growth (Figure 9), suggesting that ADR1 is required for reversion to the strong glycerol growth phenotype.

**Strong glycerol growth is due to genetic alteration**

To confirm that strong glycerol growth was due to a nuclear genetic alteration and not a cytoplasmically inherited alteration genetic studies were undertaken. The strains 43-2B-R and R234-R were crossed to 567-5d, a "strong glycerol grower". Glycerol growth segregated 4:0 in tetrads from these crosses (Diploids 111 and 112, Table 7) suggesting that the strong glycerol growth observed in 567-5d and in 43-2B-R and R234-R is of a similar nature. In another cross the strong glycerol growth seen in 567-5d segregated 2:2 against the "glycerol grower" phenotype of 43-2B-m1 (Table 8).

In the cross 411-40 to 43-2B-R (Diploid 68, Table 7) "strong glycerol growers" segregated 2:2 further indicating that the mutation which allows glycerol growth is a nuclear mutation rather than a cytoplasmically inherited trait.
The segregant 68-3d was used in further studies because it is adaptable to glycerol growth on plates and in liquid culture. The strain 68-3d-R was isolated following growth of 68-3d in liquid glycerol containing media. The culture of 68-3d was monitored daily by cell counts. When cells were counted after 6 days of growth in glycerol media, two different cell types were detectable, one round and the other elongate. The two cell types were separated by micromanipulation and allowed to grow on YEP 2% glucose. The isolates were screened for ability to grow on glycerol. The cells that were elongate were found to be "strong glycerol growers". The round cells were determined to be "glycerol-non-growers". The "strong glycerol grower" isolate was designated 68-3d-R and subjected to further analysis.
Table 7. Segregation of glycerol growth

<table>
<thead>
<tr>
<th>Cross</th>
<th>Parental strains</th>
<th>genotype</th>
<th>Glycerol nongrowers/Glycerol growers</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>complete tetrads</td>
</tr>
<tr>
<td>65</td>
<td>411-40 / 43-2B</td>
<td>GLP1/GLP1*</td>
<td>4:0 3:1 2:2 1:3 0:4</td>
</tr>
<tr>
<td></td>
<td>612-4A / 68-3D</td>
<td>GLP1/GLP1</td>
<td>8</td>
</tr>
<tr>
<td></td>
<td>43-2B / 567-5D</td>
<td>GLP1/glpl</td>
<td>7</td>
</tr>
<tr>
<td></td>
<td>43-2B-R / 567-5D</td>
<td>glp1/glpl</td>
<td>2 4</td>
</tr>
</tbody>
</table>

* glp1 is the designation of the mutation allowing strong growth on glycerol.
Table 8. Glycerol growth is independent of ADH2 but not ADR1.

<table>
<thead>
<tr>
<th>Strain</th>
<th>relevant genotype</th>
<th>Growth on ethanol</th>
<th>Growth on glycerol</th>
</tr>
</thead>
<tbody>
<tr>
<td>411-40</td>
<td>ADR1/ADH2</td>
<td>+</td>
<td>+/-</td>
</tr>
<tr>
<td>500-16</td>
<td>adr1-1/ADH2</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>ΔSPH6</td>
<td>adr1-1/ADH2-S6</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>216-2a</td>
<td>ADR1/ADH2</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>216-2b</td>
<td>ADR1/ADH2</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>216-2c</td>
<td>ADR1/adh2-m1</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>216-2d</td>
<td>ADR1/adh2-m1</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>216-7a</td>
<td>ADR1/adh2-m1</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>216-7b</td>
<td>ADR1/adh2-m1</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>216-7c</td>
<td>ADR1/ADH2</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>216-7d</td>
<td>ADR1/ADH2</td>
<td>+</td>
<td>-</td>
</tr>
</tbody>
</table>
Strong glycerol growth is the result of a recessive mutation.

Segregation of the mutation resulting in strong glycerol growth indicated that the mutation was in a nuclear gene but it was unclear if the mutation was recessive or dominant. In order to answer this question the following crosses were conducted. Strain 68-3d-R and strain 612-4a (glycerol grower) were crossed to form diploid 78. Diploid 78 did not grow strongly on glycerol (Table 9). In addition, tetrad analysis of diploid 78 yielded a strong glycerol growth segregation pattern of 2:2 (Table 7). When strain 612-4a was crossed to 68-3d to form diploid 77, the diploid grew slowly on medium-containing glycerol (Table 9). Upon tetrad analysis of diploid 77 no segregants were "strong glycerol growers" (Table 7). These results confirm that a recessive nuclear mutation results in ability to grow well on glycerol-containing medium. Segregants from two tetrads of diploid 78 were back crossed to 68-3d-R or 43-2B-R in order to show that strong glycerol growth was recessive (diploids of tetrads 78-11 and 78-16, Table 9). The nuclear mutation resulting in strong glycerol growth was designated *glp1* because it allows strong growth on glycerol, lactate, and pyruvate. The wild type allele is designated *GLP1*. Diploids listed in table 9 are "strong glycerol growers" if both parents carry the *glp1* allele.
Table 9. Diploid Strains used to characterize recessivity of GP1.

<table>
<thead>
<tr>
<th>Diploid</th>
<th>Parent strains</th>
<th>Genotype</th>
<th>Growth on Glycerol</th>
</tr>
</thead>
<tbody>
<tr>
<td>77</td>
<td>68-3d/612-4a</td>
<td>GLP1/GLP1</td>
<td>-</td>
</tr>
<tr>
<td>78</td>
<td>68-3d-R/612-4a</td>
<td>glp1/GLP1</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>68-3d-R/78-11a</td>
<td>glp1/glp1</td>
<td>+</td>
</tr>
<tr>
<td></td>
<td>43-2B-R/78-11b</td>
<td>glp1/GLP1</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>68-3d-R/78-11c</td>
<td>glp1/glp1</td>
<td>+</td>
</tr>
<tr>
<td></td>
<td>43-2B-R/78-11d</td>
<td>glp1/GLP1</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>43-2B-R/78-16a</td>
<td>glp1/glp1</td>
<td>+</td>
</tr>
<tr>
<td></td>
<td>68-3d-R/78-16b</td>
<td>glp1/glp1</td>
<td>+</td>
</tr>
<tr>
<td></td>
<td>68-3d-R/78-16c</td>
<td>glp1/GLP1</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>43-2B-R/78-16d</td>
<td>glp1/GLP1</td>
<td>-</td>
</tr>
<tr>
<td>101</td>
<td>43-2B-R/612-1d-2</td>
<td>glp1/GLP1, ccr4</td>
<td>-</td>
</tr>
<tr>
<td>102</td>
<td>43-2B-R/612-1d</td>
<td>glp1/GLP1, CCR4</td>
<td>-</td>
</tr>
<tr>
<td>103</td>
<td>78-16b/553-4b</td>
<td>glp1/GLP1, CCR4</td>
<td>-</td>
</tr>
<tr>
<td>104</td>
<td>78-16b/553-4b-10</td>
<td>glp1/GLP1, ccr4</td>
<td>-</td>
</tr>
<tr>
<td>107</td>
<td>78-16b/B19-B*</td>
<td>glp1/?</td>
<td>+</td>
</tr>
<tr>
<td>108</td>
<td>78-16b/411-40-B</td>
<td>glp1/glp1</td>
<td>+</td>
</tr>
<tr>
<td>113</td>
<td>78-17a/411-40</td>
<td>GLP1/GLP1</td>
<td>-</td>
</tr>
<tr>
<td>114</td>
<td>78-17a/411-40-B</td>
<td>GLP1/glp1</td>
<td>-</td>
</tr>
<tr>
<td>115</td>
<td>78-17a/B19*</td>
<td>GLP1/?</td>
<td>+</td>
</tr>
<tr>
<td>116</td>
<td>78-17a/B19-B*</td>
<td>GLP1/?</td>
<td>+</td>
</tr>
</tbody>
</table>

*Strain B19 carries 21 copies of ADR1-642 integrated into the genome.
Mutation to strong glycerol growth on YEP 3% glycerol plates

Strains isogenic to 411-40 and to 43-2B were plated to single colonies on YEP 3% glycerol plates. Two colony types were observed in those strains containing a completely functional *ADR1* or *ADR1-5C* allele. Strains lacking *ADR1* could not mutate to strong glycerol growth and displayed only small colonies. Strains carrying the *glp1* allele *ie. 43-2B-R*, contained only large colonies. Strains that could revert to strong glycerol growth formed two colony types: those that were larger like those that carried the *glp1* allele and smaller colonies as found in strains carrying the *GLP1* allele.

Large colonies from strains 411-40 and 500-16:B19 (B19) were isolated and found to result in strong glycerol growth. When strains isolated as big colonies, designated (B for big or larger), were crossed to the strain 78-16b (*glp1*) the diploids were "strong glycerol growers" indicating that they failed to complement the *glp1* allele. Diploids formed by crossing 78-17a (*GLP1*) with 411-40-B or 411-40 were poor growers on glycerol (Table 9). The diploids formed when 78-17a (*GLP1*) was crossed to 500-16:B19 (B19) and B19-B, however, were strong glycerol growers. This latter result is puzzling since strain B19 by itself is not a strong glycerol grower. The lack of complementation between 411-40-B and 78-16b indicates that the mutation in 411-40-B allowing strong glycerol growth is at the *GLP1* locus.
Glycerol growth is independent of ADH2 but requires ADR1

Previous studies indicate that strain 411-40 (ADR1, ADH2) grows weakly on glycerol containing medium (Appendix). Strain ΔSPH6 (adr1-1, ADH2-S6) which has constitutive ADH II activity due to deletion of the ADH2 promoter does not utilize glycerol as a carbon source (Appendix). Further indication that ADH II enzyme activity is not linked to glycerol growth was derived from strains lacking ADH II activity (containing the adh2-m1 allele). Two tetrads from diploid 216 formed between strains 43-2B-m1 (adh2-m1, GLP1) and 567-5d (ADH2, glp1) were analyzed. Strong glycerol growth segregated 2:2 and did so independently of the adh2-m1 allele (Table 8). The suggestion that ADR1, and not ADH2, is required for glycerol utilization was therefore confirmed by the independent segregation of adh2-m1 and strong glycerol growth.

Effect of the glp1 mutation on Lactate, Pyruvate, and Acetate growth

The effect of the glp1 mutation on growth on other nonfermentative carbon sources was also tested. Strains isogenic to 411-40 which carried a functional or non-functional ADR1 gene grew equivalently on medium containing acetate (Figure 11 and 12). Although strain 411-40-B appears by cell counts to grow almost as well on acetate-containing medium as its isogenic counterparts the cells appeared small and irregularly shaped
Figure 11

Growth of strains isogenic to 411-40 on 3% acetate

- strain 411-40
- strain 660
- strain 500-16
- strain ΔSPH6
Figure 12
Growth of strains isogenic to 411-40B on 3% acetate

- 411-40
- 411-40-B
- B19
- B19-B
- 500-16
suggesting that these growth conditions were stressful. Strain B19-B grew slightly better than its parental strain on acetate-containing medium (Figure 12).

Strains 43-2B-R and R234-R which carry the *glp1* alleles grew slightly better than their respective parental strains when grown on acetate-containing medium (Figure 13). The *glp1* mutation in these strains may augment growth on acetate containing medium.

Strains isogenic to 43-2B grown on lactate-containing medium show growth similar to that observed when these strains were grown on glycerol-containing medium (Figure 14 as compared to Figure 9). Strains 43-2B and R234 which carry the *GLP1* allele did not grow as well on medium containing lactate as did strains 43-2B-R and R234-R which carry the *glp1* allele. After 5-7 days of growth in lactate-containing medium strains carrying the *GLP1* allele adapt in a manner similar to that observed for the same strains in glycerol-containing medium (Figure 14 as compared to Figure 9).

Growth in pyruvate-containing medium of strains isogenic to 43-2B carrying either the *GLP1* allele or the *glp1* allele was similar to growth in glycerol- or lactate-containing medium. However, adaptation of strains carrying the *GLP1* allele was observed after 7 days of growth in pyruvate-
Figure 13
Growth of strains isogenic to 43-2B on 3% acetate

- strain 43-2B
- strain R234
- strain 43-2BR
- strain R234-R
Figure 14

Growth of strains isogenic to 43-2B on 2% lactate

- strain 43-2B
- strain R234
- strain 43-2BR
- strain R234-R
Figure 15
Growth of strains isogenic to 43-2B on 2% pyruvate

- strain 43-2B
- strain R234
- strain 43-2BR
- strain R234-R

log of cells/ml

Time (days)
containing medium rather than 5-7 days observed for the same strains in glycerol- or lactate-containing medium (Figure 15).

Strains isogenic to 411-40 carrying a GLP1 allele grown on lactate did not adapt to growth but grew slowly similar to glycerol growth in the same strains (Figures 16, 17, and 18 as compared to Figure 10). Strain B19-B (glp1) grew strongly on lactate-containing medium as it did on glycerol-containing medium. In contrast, strain 411-40-B (glp1) which grew strongly on glycerol-containing medium could not grow on 2% lactate and grew weakly on 1% lactate (Figures 17 and 18). Independent selection of the mutant glp1 alleles may explain the discrepancy between lactate growth and glycerol growth of strain 411-40-B as compared to strain 43-2B-R.

Growth of strains isogenic to 411-40 on pyruvate-containing medium suggested that a functional ADR1 gene was needed for growth, a result similar to that found for these strains in glycerol and lactate-containing medium (Figure 19 as compared to Figure 16). B19-B (glp1) grew slightly better than its respective parental strains (GLP1) in pyruvate-containing medium (Figure 20).
Figure 16

Growth of strains isogenic to 411-40 on 2% lactate

- strain 411-40
- strain 660
- strain 500-16
- strain ΔSPH6

log of cells/ml vs. Time (days)
Figure 17

Growth of strains isogenic to 411-40-B on 2% lactate

- 411-40
- 411-40B
- B19
- B19-B
- 500-16
Figure 18
Growth of strains isogenic to 411-40-B on 1% lactate

<table>
<thead>
<tr>
<th>Strain</th>
<th>Time (days)</th>
</tr>
</thead>
<tbody>
<tr>
<td>411-40</td>
<td>0, 2, 4, 6, 8, 10</td>
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<tr>
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<td>0, 2, 4, 6, 8, 10</td>
</tr>
<tr>
<td>B19</td>
<td>0, 2, 4, 6, 8, 10</td>
</tr>
<tr>
<td>B19-B</td>
<td>0, 2, 4, 6, 8, 10</td>
</tr>
<tr>
<td>500-16</td>
<td>0, 2, 4, 6, 8, 10</td>
</tr>
</tbody>
</table>
Figure 19
Growth of strains isogenic to 411-40 on 2% pyruvate
Figure 20

Growth of strains isogenic to 411-40-B on 2% pyruvate

- 411-40
- 411-40-B
- B19
- B19-B
Discussion

A mutation allowing *S. cerevisiae* to grow well when the sole carbon source is either glycerol, lactate, or pyruvate has been identified. The mutation, designated "glp1" is recessive and allows glycerol growth only in the presence of a functional *ADR1* gene encoding at least 506 N-terminal amino acids (Bemis and Denis, 1988; Appendix). Furthermore, a functional *ADR1* gene was required for growth in either lactate- or pyruvate-containing medium.

Previous studies of glycerol growth in wild type *S. cerevisiae* present conflicting evidence as to whether wild type yeast can grow on glycerol. Sprague and Cronan (1977) state that wild type yeast can utilize glycerol as a sole carbon source while Wills et al., (1984) find that wild type yeast can not grow on glycerol as a sole carbon source. Earlier confusion may stem from variations in growth conditions and different genetic backgrounds among strains. In our hands, strain 567-5d grew very well on glycerol whereas most of our other strains did not grow well. Strain 567-5d was found to already carry a *glp1* mutation (Table 7). All results presented in this study were conducted with isogenic strains under growth conditions of YEP media plus 3% glycerol at 30ºC. The results included here suggest that *S. cerevisiae* is able to rapidly metabolize glycerol as a carbon source when the strain carries at least 506 amino acids of *ADR1* and the recessive
mutation glp1. Wild type strains utilize glycerol at a very slow rate unless a mutation occurs in the GLP1 gene.

ADR1 has not been implicated in the regulation of glycerol kinase and glycerol 3-phosphate dehydrogenase because the enzyme activities of these two proteins were not altered in a strain carrying the adr1-1 allele (Bemis and Denis, 1988; Appendix). The GLP1 allele is thought to act at a later stage of glycerol metabolism because metabolism of lactate and pyruvate can be affected by the glp1 mutation.

In contrast to the requirement of a functional ADR1 gene for growth on glycerol-, lactate-, and pyruvate-containing medium, a functional ADR1 gene is not required for growth on ethanol-containing medium as long as there is constitutive ADH activity (Bemis and Denis, 1988). Similarly, a functional ADR1 gene is not required for growth on acetate containing medium. The presence of the GLP1 allele or a mutated glp1 allele does not affect growth on ethanol-containing medium. However, the presence of the glp1 mutation may enhance growth on acetate-containing medium.

Ethanol is metabolized to acetaldehyde by ADH, the acetaldehyde is then metabolized to acetate by acetaldehyde dehydrogenase. Acetate is metabolized directly into acetyl CoA and used as an energy and carbon source in the TCA cycle (tricarboxylic acid). The fact that yeast readily metabolize ethanol and acetate regardless of the presence of ADR1 or
GLP1 suggests that the newly identified function of ADR1 is probably not involved with the regulation of enzymes that are required to metabolize ethanol and acetate. The increase in growth on acetate in strains containing the glp1 mutation may be due to increased transport across the mitochondrial membrane but does not require ADR1.

The GLG mutations previously characterized by Wills et al. (1984) may be allelic to GLP1 but it is unclear if any of the GLG mutations require ADR1 for activity or if they are recessive. The GLG mutations do allow growth on glycerol, lactate, and pyruvate (C. Wills, per. comm.).

The GLG mutations may be involved in a mitochondrial shuttle mechanism necessary for transport of reducing equivalents across the mitochondrial membrane. If the glp1 mutation increases transport of metabolites into the mitochondria, growth on glycerol, lactate, pyruvate, and acetate might be enhanced.

It has previously been observed that when the mitochondrial porin gene is disrupted yeast slowly adapt to glycerol growth and an 86 kd protein accumulates (Dihanich et al., 1987). The adaptation to glycerol growth by yeast with a disrupted porin gene is not permanent. Porin minus yeast grown on nonselective media must readapt to glycerol growth in the absence of other carbon sources. Alleles required to regulate porin have not been identified although they are postulated to exist. The porin gene
encodes the only known mitochondrial pore for entry of metabolites, of molecular weight 6000 or less. The 86-kd protein that accumulates is not porin nor is it the 90-kd heat shock protein of yeast (Dihanich et al., 1987). ADR1 is required for yeast to adapt to glycerol growth in strains isogenic to 411-40 and 43-2B. ADR1 could be one of the as yet unidentified regulators of genes involved with mitochondrial transport.

Heat shock proteins and glucose-repressible proteins have been implicated in translocation of proteins across membranes when cells are stressed (Deshaies et al., 1988). Growth on glycerol is a metabolic stress to yeast and thus might be expected to invoke one of the known stress responses.

One model for the function of ADR1 in the utilization of glycerol is as a transcriptional activator of a gene (Y) necessary for interaction with GLP1. GLP1 would be the repressor of gene (Y) which ADR1 activates or it could be a repressor of a gene (X) needed to interact with gene (Y). ADR1 would not directly interact with GLP1 but would regulate some factor (Y) that was in turn needed for growth on glycerol.

Future experiments are required to determine how ADR1 influences glp1 and what role GLP1 normally plays in the metabolism of S. cerevisiae. The disruption of ADR1 in a glp1 strain would confirm that ADR1 is required for glycerol growth. The disruption of ADR1 in a glp1
strain would provide a strain necessary for further experiments. This \textit{adr1} strain with the \textit{glp1} mutation could be mutagenized and screened for "strong glycerol growers". These mutations would be in either the gene (Y) or gene (X) of the above model. Isolation of the \textit{glp1} allele would be very difficult because of the recessive nature of the mutation and the absence of a good method for identifying differences between strong and slow glycerol growers. The gene (Y) of the model could also be cloned by overexpression using an appropriate plasmid library. It would be expected that overproduction of Y would bypass the need for \textit{ADR1}. Another experimental approach would be to search a yeast gene library with the \textit{ADH2} dyad sequence which is required for \textit{ADR1} binding. This would be an interesting approach because \textit{ADR1} may activate other genes that have yet to be identified.
SECTION 4

GENERAL DISCUSSION

The goal of this research was to identify functional regions of the transcriptional activator ADR1. This was accomplished by analyzing several facets of ADR1 function.

The \textit{adr1-1} mutation, which blocks \textit{ADR1} activation of \textit{ADH2}, was identified as a nonsense codon at amino acid 11. This result confirms that the \textit{ADR1} open reading frame encodes a protein product and that translation of the ADR1 protein begins at the first AUG in the \textit{ADR1} transcript. The \textit{adr1-1} mutation was found to be suppressible by tRNA-suppressors carrying serine, tyrosine, leucine, or arginine aminoacyl residues, indicating that serine-11 is not essential to ADR1 function.

The second section of this thesis used C-terminal deletions of the \textit{ADR1} gene to detect functional regions of the ADR1 protein. Such analyses have been conducted for other transcriptional activators including
the E1A protein (Kriplı et al., 1985), GAL4 (Johnston et al. 1986), and GCN4 (Hope and Struhl. 1986). The C-terminal deletion analyses led to the identification of a transcriptional activation domain and identification of a region of ADR1 required for glycerol growth.

The third section of this thesis concerned the requirement of ADR1 for growth on glycerol. Previous observations suggested that the sole function of ADR1 was the transcriptional activation of ADH2. The requirement of ADR1 for growth on glycerol suggests that ADR1 may also be involved in some function other than ADH2 regulation.

The upstream region of ADR1 had been sequenced to base pair -610 by Hartshorne et al., in 1986. The 5' end of the ADR1 mRNA had been mapped to base pair -509 (Blumberg et al., 1988) and found to contain an unusually long untranslated leader sequence relative to the translational start site identified in this thesis. Other long 5' untranslated leader sequences have been identified on yeast genes. The GCN4 mRNA contains small open reading frames in its 5' untranslated sequence which have been implicated in translational control of GCN4 (Mueller and Hinnebusch, 1986). Translational regulation of ADR1 in a manner similar to that found for GCN4 has been ruled out by the lack of small open reading frames in the ADR1 untranslated region. The ADR1 mRNA could be regulated by another translational regulatory mechanism or through the
stability of its mRNA.

The possibility that ADR1 is translationally regulated or is controlled by differences in RNA stability has not been extensively analyzed. Little variation in total ADR1 RNA levels under glucose or ethanol growth conditions suggests that differences in mRNA stability are not controlling ADR1 function. It has been shown using an ADR1-β-galactosidase hybrid protein that β-galactosidase protein levels do not vary between glucose and ethanol growth conditions (Blumberg et al., 1988). More recent data suggest that actual ADR1 protein levels may vary by five- to -ten-fold under the two growth conditions (R. Vallari, pers. comm.). It is also possible that the 5' untranslated region plays no regulatory role but may act in slowing general translation of the ADR1 mRNA under all growth conditions.

Santiago et al., (1986) have classified mRNA of S. cerevisiae into two groups on the basis of mRNA stability. The first group, very stable transcripts, include transcripts having a half life greater than ca. 20 minutes. The class of less stable mRNAs have stabilities less than 20 minutes. While function does not appear to be related to stability, stability was inversely proportional to transcript length. For example, the actin mRNA has a half life of 77 minutes and is 1.3 kb in length. The PPR1 mRNA has a half life of 2 minutes and is 2.9 kb in length, 1 kb smaller than ADR1. If ADR1 belongs to this less stable class of mRNA it is likely that
the $ADR1$ half life would be less than 2 minutes. Overall stability of the transcript may be a mechanism by which mRNA species are maintained at desired levels in the yeast cell. Too high of an $ADR1$ concentration is known to cause mitochondrial DNA loss and petite formation (Cherry and Denis, 1989).

The presence of the nonsense mutation at codon 1.1 in the $adr1-1$ mRNA results in decreased stability of the $ADR1$ mRNA. Decreased stability of mRNA by nonsense mutations has been characterized for several other alleles containing nonsense mutations in the 5' region of the structural gene. It is unclear at this time if the instability results from a translational block due to the ribosomes being stalled or if it is due to increased nuclease action on the mRNA. The most likely explanation is a combination of ribosomal stalling and nuclease degradation (Daar and Maquat, 1988).

Transcriptional activating proteins require a region of acidic nature that may be important for interaction with the transcriptional machinery (Ptashne, 1986; Struhl, 1987). Amino acid sequence homology comparison of $ADR1$ to other transcriptional activators suggests an acidic transcriptional activation region at amino acids 29 through 39 (Figure 3). Initial studies suggested that the commonality between the transcriptional activation regions in GCN4 and GAL4 is the overall acidic nature of the
regions. Recent evidence suggests that not only must the amino acids be of an acidic nature, but the acidic region must form an amphipathic alpha helix (Giniger and Ptashne, 1987). The acidic region of ADR1 has not been characterized by deletion analysis or by mutational analysis. It is possible that single mutations occurring at the acidic region in ADR1 would not destroy the phenotype if the overall shape or charge of the region is important.

Regulation of transcription by proteins which bind specifically to DNA is a common regulatory mechanism well studied in both eukaryotes and prokaryotes alike. The ADR1 "Zn-binding" DNA-binding finger motif has been characterized by sequence analysis (Hartshorne et al., 1986), mutational analysis (Blumberg et al., 1987; Denis et al., in prep.), deletion analysis (Bemis and Denis, 1988), and DNA binding gel retardation studies (Eisen et al., 1988). The "Zn-binding" DNA-binding finger domain was originally identified in transcriptional factor TFIIIA from Xenopus oocytes (Miller et al., 1985). The binding fingers of TFIIIA have nine repeats of a 30 amino acid finger that are coordinately stabilized by cysteine and histidine residues through Zn$^{2+}$ linkages (Diakun et al., 1986; Frankel et al., 1987). A "Zn-binding" DNA-binding finger of ADR1 (amino acids 130-159) was synthesized and studies confirm that metal binding occurs and drives the folding of the peptide (Parraga et al., 1988). These results agree with
similar experiments on synthesized peptides of TFIIIA finger regions
(Frankel et al., 1987) and with studies that suggest \( \text{Zn}^{2+} \) is tetrahedrally coordinated between histidine and cysteine residues in peptides of this nature (Diakun et al., 1986). ADR1 has two "Zn-binding finger" regions. The presence of both of these regions are required for ADR1 binding to the \( \text{ADH2} \) gene (Bemis and Denis, 1988; Appendix; Parraga et al., 1988).

Mutations localized to the DNA-binding domain of \( \text{ADR1} \) have been characterized. Mutations of the amino acids proposed to be directly involved in "Zn-binding" block ADR1 activity while mutations in other residues of the finger reduce activity to varying degrees (Blumberg et al., 1987; Denis et al., in prep.).

The \( \text{adr}1-5^\text{C}-x \) mutations (Figure 3) which were isolated as second site mutations of the \( \text{ADR}1-5^\text{C} \) allele have been identified. The \( \text{adr}1-5^\text{C}-7 \) mutation was identified at amino acid 117 in the finger tip of the first DNA-binding finger and blocks activity of \( \text{ADR1} \). The \( \text{adr}1-5^\text{C}-5 \) mutation was localized to amino acid 129 which is in the linker region between the two fingers. This change causes a less severe effect on \( \text{ADR1} \) function with respect to its ability to activate \( \text{ADH2} \). The \( \text{adr}1-5^\text{C}-2,-3, \) and -6 mutations were all localized to amino acid 97 causing a proline to a serine change in all three alleles (D. Mullaney, 1988). A proline residue is commonly found 8 amino acids from the first finger in "Zn-binding" DNA-
Binding proteins. The proline at amino acid 97 is nine residues away from
the first finger region in ADR1, but other than the possibility of creating a
bend in the polypeptide chain, little is known about the importance of this
residue.

Several cAMP-dependent protein kinase phosphorylation consensus
sequences have been identified in ADR1 by sequence analysis
(Hartshome et al., 1986). The ADR1-2C, 5C, and 7C mutations which
allow ADH2 expression during glucose growth were localized to the
phosphorylation sequence near amino acid 230 (Figure 3) (Denis and
Gallo, 1986; Cherry et al., 1989). ADR1 mutations localized to the
phosphorylation sequence allow partial ADH2 activation during glucose
repression (Strains R234, Table 1). In vitro phosphorylation studies of
ADR1, ADR1-2C, 5C, and 7C fusion proteins confirm that the mutations near
the phosphorylation site at amino acid 230 reduce the phosphorylation of
ADR1 (Cherry et al., 1989). The ADR1-7C mutation completely blocks
phosphorylation at this site because the phosphoacceptor serine-230 is
mutated to a leucine (Figure 3). The ADR1-2C and 5C mutations cause a
phenylalanine to serine conversion at amino acid 231 and an arginine to
lysine substitution at amino acid 228, respectively. Both changes appear to
increase the Km of phosphorylation but do not completely block possible
phosphorylation at serine-230 (Cherry et al., 1989). The in vitro
phosphorylation studies of the ADR1 and ADR1C fusion proteins indicate that ADR1 is also phosphorylated by cAMP-dependent protein kinase at a site other than the site at amino acid 230 because even the ADR1-7C protein is a phosphoprotein (Cherry et al., 1989).

The C-terminal truncated ADR1 protein (220 amino acids, Appendix) lacking the phosphorylation site at amino acid 230 was found to be capable of transcriptional activation of ADH2 but not able to allow escape of ADH2 from glucose repression. Alternative explanations for this result may be that the deletion of such a large region (1103 amino acids) of ADR1 may alter interactions necessary for the escape from glucose repression or that the increase in ADH II activity during glucose growth conditions may be undetectable due to the reduced function of the ADR1-220 protein. In contrast to the C-terminal truncation leaving only 220 amino acids, a small internal deletion removing the amino acids between 220 and 262 of ADR1 results in an ADR1 protein able to escape glucose repression. The deletion of this region may remove a site required for interaction with a repressor or this region could have another function. Other functions proposed for this region are that it may be required to block dimerization of ADR1 monomers or that it may block the proper folding of the ADR1 protein until dephosphorylation occurs. Further experiments are planned to study the existence of a repressor. One experiment is to over express the
proposed repressor site on ADR1 in the expectation of titrating out the repressor.

CCR1 is not a cAMP-dependent protein kinase and is proposed to be an activator of ADH2. CCR1 would therefore not be the kinase directly phosphorylating ADR1, but might be required for the regulation of a phosphatase that controls ADR1. Alternatively CCR1 may phosphorylate a protein that ADR1 acts with.

The cAMP-dependent protein kinase of yeast is composed of regulatory subunits encoded by BCY1 (Toda et al., 1985) and catalytic subunits encoded by the TPK alleles, TPK1, TPK2, and TPK3 (Toda et al., 1987). A mutation at BCY1 (bcyl) blocks regulation of the catalytic subunits allowing unregulated phosphorylation at cAMP-dependent phosphorylation sites. In strains carrying a bcyl allele, one functional TPK gene, and the ADR1 gene ADH II activity was reduced under nonfermentative growth as compared to wild type ADH II activity. In strains of similar genotype except that an ADR1C allele was present the effect of unregulated cAMP dependent protein kinase activity was diminished. In strains in which all three cAMP dependent protein kinases are mutated or disrupted (bcy1, tpk1, tpk2, tpk3w) there was no effect on ADR1 regulated ADH2 activity. This result supports the hypothesis that ADH2 may be regulated by complex mechanisms including both cAMP dependent and independent protein kinases. ADR1 is suggested to be a
phosphoprotein (Cherry et al., 1989; R. Vallari and D. Audino, pers. comm.) and may be phosphorylated by a complex and interactive method between several protein kinases under various conditions.

Phosphorylation may act as a signal for degradation of ADR1 as it does for fructose-1,6-bisphosphatase (Lamponi et al., 1987). Phosphorylation as a degradation signal is a model supported by the fact that under glucose growth conditions ADR1 is found to be present at very low levels as compared with ethanol growth conditions (R. Vallari, pers. comm.). This hypothesis is also consistent with the observation that ADR1\(^C\) type mutations augment the activity of ADR1 under glucose repression but never to fully derepressed levels. It is possible that ADR1\(^C\)-type mutations may contain phosphorylation sites other than serine-230 which might allow altered protein degradation under glucose growth conditions.

Phosphorylation is the signal for many regulatory mechanisms. When the 60 kD protein pp60 from Xenopus laevis oocytes is phosphorylated it binds mRNA and blocks translation (Kick et al., 1987). Upon dephosphorylation binding is destabilized and translation occurs. A mechanism of translational regulation for ADR1 has purportedly been excluded because ADR1-β-galactosidase fusion proteins appear to be equally abundant under glucose and ethanol growth conditions (Eisen et al., 1988). However, the fusion proteins are capable of some escape from
glucose repression so the possibility of autoregulation of translation by
ADR1 is not completely ruled out.

Phosphorylation of the CREB protein, a protein isolated from rat brain
and required to bind cAMP response elements, controls its dimerization
and transcriptional activation (Yamamoto et al., 1988). Phosphorylation of
CREB enhances dimerization and transcriptional activation while
phosphorylation of ADR1 is thought to inhibit activation of ADH2. The
effect on dimerization of ADR1 by phosphorylation is unknown. The
general trend for DNA-binding phosphoproteins is the more
phosphorylated the protein the less able to bind nucleic acids (Radtke and
Unteregger, 1988). ADR1 appears to follow this trend based on genetic
evidence. However, it has not been determined if phosphorylation affects
ADR1 binding to ADH2 DNA.

A previously unidentified function of ADR1, involvement in utilization of
glycerol, has been characterized. The natural environment of S.
cerevisiae, grapes, would provide sugars as the major carbon source
available for yeast metabolism. In the absence of glucose S. cerevisiae
can use ethanol which has been excreted following the fermentation of
glucose. Metabolism of glucose and ethanol are thus highly regulated
processes in yeast. Growth on nonfermentative carbon sources uncommon
outside of the laboratory probably were not important enough for yeast to
develop separate highly controlled pathways for utilization. Growth of wild-type yeast on glycerol as the sole carbon source is a very stressful condition for yeast and the cells grow slowly (Wills et al. 1984; Bemis and Denis, 1988). Strains capable of rapid growth on glycerol were identified and isolated (approximately 1 in $1 \times 10^6$ cells). These strains were shown to carry the glp1 mutation, a mutation which allows growth on glycerol, lactate, pyruvate, and acetate. glp1 is a nuclear gene requiring ADR1 for activity. The GLP1 gene may be allelic to one of the glg mutations previously characterized by Wills et al., (1984). The glg mutations are putative enhancers of transport across the mitochondrial membrane (Wills et al. 1984). Transport is thought to be important in the adaptation to glycerol growth in the porin minus yeast described by Dihanich et al., (1987).

Isolation of the GLP1 gene may be difficult because the mutation is recessive. Genetic studies are in progress and cloning strategies to isolate the gene or genes regulated by ADR1 or GLP1 are being contemplated. The isolation of the GLP1 gene itself would be complicated because the only detectable phenotype would be loss of glycerol growth. Another important experiment would be to disrupt the ADR1 gene in a glp1 strain to confirm the requirement of ADR1 to glycerol growth.

GLP1 has been proposed to be important in transport across the
mitochondrial membrane. The porin gene and the 86 Kd protein gene (Dihanich et al., 1987) have been cloned. Increased information about the mitochondrial membrane proteins may provide insight into the role of GLP1.

The results of this thesis extend our understanding of the various functions of ADR1 and suggest further avenues of exploration. Investigations of ADR1 and its interactions with other alleles will be of great interest to the subject of transcriptional activators and their universal role in gene regulation.
REFERENCES


APPENDIX
Identification of Functional Regions in the Yeast Transcriptional Activator ADRI

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The transcriptional activator ADRI from Saccharomyces cerevisiae is a postulated DNA-binding protein that controls the expression of the glucose-repressible alcohol dehydrogenase (ADH2). Carboxy-terminal deletions of the ADRI protein (1, 233 amino acids in length) were used to localize its functional regions. The transcriptional activation region was localized to the N-terminal 228 amino acids of ADRI containing two DNA-binding zinc finger motifs. In addition to the N terminus, a large part of the ADRI sequence was shown to be essential for complete activation of ADH2. Deletion of the putative phosphorylation region, defined by ADRI' mutations that overcome glucose repression, did not render ADH2 expression insensitive to glucose repression. Instead, this region (amino acids 220 through 253) was found to be required by ADRI to bypass glucose repression. These results suggest that ADRI' mutations enhance ADRI function, rather than block an interaction of the putative phosphorylation region with a repressor molecule. Furthermore, the protein kinase CCR1 was shown to affect ADH2 expression when the putative phosphorylation region was removed, indicating that CCR1 does not act solely through this region. A functional ADRI' gene was also found to be necessary for growth on glycerol-containing medium. The N-terminal 506 amino acids of ADRI were required for this newly-identified function, indicating that ADH2 activation and glycerol growth are controlled by separate regions of ADRI.

Eucaryotic transcriptional regulators tend to be large proteins having molecular masses greater than 70,000 daltons (20, 24, 27, 35). Their large size suggests the presence of multiple domains, each being wholly or partly responsible for imparting one or more biological activities to the protein. Deletion and mutation analyses, together with sequence homology comparisons, have proven useful in identifying and localizing functional regions. These approaches have been notably successful in studying the human virus 40 T antigen (19, 32), the glucocorticoid receptor (18, 26), GAL4 (17, 21, 26), and GCN4 (14).

The transcriptional activator ADRI, a protein of 151, 000 daltons (12), functions in controlling the expression of the glucose-repressible alcohol dehydrogenase (ADH2). When encoded by the ADH2 gene on Saccharomyces cerevisiae (14). Two functional regions of ADRI have been identified by sequence comparisons and mutation analysis. One of these regions is highly homologous to the zinc-containing DNA-binding fingers previously identified in transcription factor HLF of Xenopus laevis (29). This region lies between amino acids 99 and 155 of ADRI (12) and contains two such zinc fingers. Although not yet demonstrated to be a DNA-binding protein, ADRI is located in the nucleus (21) and has been shown to control ADH2 expression through a 22-base-pair (bp) segment of dyad symmetry upstream of the ADH2 gene (31). Deletion analysis indicates that the first 104 N-terminal amino acids of ADRI are sufficient to cause partial derepression of ADH2 (101), whereas the first 151 amino acids are not sufficient (12). Furthermore, most mutations that inactivate ADRI occur in the zinc finger region (12, L. Dem et al., manuscript in preparation). These results confirm the importance of the finger region to ADRI function.

The second functional region in ADRI consists of a CAMP-dependent protein kinase phosphorylation recognition site, located between amino acids 227 and 231 (22). Mutations which allow ADRI to bypass glucose control and activate ADH2 transcription have been localized to this region (9). This region (amino acids 220 through 253) was found to be required by ADRI to bypass glucose repression. These results suggest that ADRI' mutations enhance ADRI function, rather than block an interaction of the putative phosphorylation region with a repressor molecule. Furthermore, the protein kinase CCR1 was shown to affect ADH2 expression when the putative phosphorylation region was removed, indicating that CCR1 does not act solely through this region. A functional ADRI' gene was also found to be necessary for growth on glycerol-containing medium. The N-terminal 506 amino acids of ADRI were required for this newly-identified function, indicating that ADH2 activation and glycerol growth are controlled by separate regions of ADRI.

We have undertaken a series of progressive carboxy-terminal deletions of ADRI to obtain a clearer understanding of its structure and function. The questions which we address include the following: (1) What part of ADRI is required for ADH2 activation? (2) Is the putative phosphorilation region the site through which the glucose signal is mediated? and (3) Does CCR1 act through the phosphorilation region of ADRI? We report here that ADRI contains several functional regions, and identify a region specifically required for growth on glycerol. We also present data showing that the putative phosphorylation region, while not being absolutely required for ADRI' activation of ADH2, does play a positive role in ADRI function.

MATERIALS AND METHODS

Yeast strains. Strain 500-16 (MATa adh2-11 asd1-11 aux5-1 leu2-3, 112 trp1-3) was used for yeast transformations. Other strains used in this study are: S288S (MATa adh2-11 asd1-11 leu2-3 trp1-3), 150-5d (MATa adh2-11 trp1-3 leu2-3 aux5-1), and 500-16-C3 (same as...
ADRI plasmids. All ADRI genes were derived from plasmids YRp7-ADRI-111, YRp7-ADRI-22A, and YRp7-ADRI-3119.19 and were present on YRp7 vectors. Each contains at least 1.2 kilobases of ADRI upstream DNA, which is sufficient for normal ADRI expression (80). Truncated ADRI gene sequences end at the restriction sites and have paired numbers shown in Fig. 1. Each gene is designated by the number of amino acids of ADRI protein sequence it encodes (i.e., ADRI-282 encodes the first 282 N-terminal amino acids of ADRI). In most cases, non-ADRI amino acids are present on the carboxy terminus of the truncated ADRI polypeptides: ADRI-123 encodes the wild-type coding sequence. ADRI-180 encodes an extra 81 amino acids derived from pBR322 bp 859 to 1232. ADRI-30 encodes an extra 18 amino acids derived from the complementary strand of pBR322 from bp 376 to 394. ADRI-237 encodes a single 18 amino acid derived from pBR322 sequences from bp 975 to 1011. ADRI-206 encodes an extra 2 amino acids from the complementary strand of pBR322 that runs from bp 274 to 275. ADRI-242 encodes an extra 22 amino acids derived from bp 185 to 251 of the TRPI gene. ADRI-272 encodes 23 extra amino acids that run from bp 2038 to 2165 of pBR322. ADRI-253 encodes 10 extra amino acids from bp 192 to 155 of pBR322. ADRI-268 encodes 18 extra amino acids, and ADRI-151 encodes an extra 235 amino acids derived from pBR322 sequences extending from bp 869 to 1232.

RESULTS

Carboxy-terminal deletions of the ADRI gene were used to localize functional regions of the ADRI protein (Fig. 1). Truncated ADRI genes, present either as plasmid vectors or as stable integrants at the rpl locus, were analyzed. Genes were stably integrated into the genome so that the gene dosage per cell could be accurately determined. This approach allows the ADRI dosage dependence of ADH2 expression to be studied (81). Five criteria were used to compare the functionalities of the truncated ADRI genes:

A abilities to allow derepression of ADH2 to its maximal level of ADH2 expression, run as a means for eliminating non-functional ADH2 alleles, to allow growth on a non-fermentative carbon source, and to allow one copy of a defect in the CDC1 gene. ADH2 activating region. Wild-type and deleted ADRI genes were stably integrated at the rpl locus and assayed for their abilities to activate ADH2 expression (Table I). ADRI genes coding for activation expressed vary in their relative ability to activate ADH2 expression. ADRI-220 lacks the putative phosphorylation site implicated in glucose control of ADRI. All functional ADRI genes at a single or low dosage contained an ADH2 phenotype that remained glucose repressed (Table II). Conversely, no region of ADRI was identified which, when removed, rendered ADH2 derepressed. ADRI-220 containing only one complete DNA-binding zinc finger did not allow ADH2 expression. Increases in ADRI gene size did not show a proportional increase in the ability to activate ADH2. This feature is observed most clearly when single dosage of the different genes are compared (Table I). These variations could be the result of differences in protein or mRNA stability between the various ADRI constructs.

To better estimate the relative function of the various-sized ADRI genes in a way that would eliminate possible differences in their protein and mRNA stability, the maximal ability of the ADRI genes to activate ADH2 was measured. The maximal activation ability of ADH2 was observed to be very high in ADRI plasmids. This observation is in agreement with previous observations that high ADRI dosage levels result in high ADH2 expression during non-fermentative growth in which ADH2 copy number is the limiting factor (88). By using the value for maximal activation of ADH2, a comparison could be made between the functions of different-sized ADRI proteins that are independent of their relative protein stability. A range of dosages for the activating ADRI was integrated at the rpl locus and assayed. The results of these experiments are shown in Table II. ADH2 expression was measured in the presence of glucose or ethanol. The results of these experiments are shown in Table II.

FIG. 1 Comparison of deleted ADRI genes. Each ADRI construct is designated on the left by the number of amino acids present in its coding sequence. To the right are given the restriction sites and base pair numbers at which ADRI DNA sequences and ADRI-1112 sequences are represented by the complete ADRI gene present on YRp7-ADRI-111.
TABLE 1. Effect of truncated ADR1 gene on ADR2 expression

<table>
<thead>
<tr>
<th>Gene</th>
<th>Genes</th>
<th>Glucose</th>
<th>ADR2 Activity (mol mg)</th>
</tr>
</thead>
<tbody>
<tr>
<td>ADR1-122</td>
<td>1</td>
<td>66</td>
<td>2,000</td>
</tr>
<tr>
<td>ADR1-109</td>
<td>1</td>
<td>66</td>
<td>400</td>
</tr>
<tr>
<td>ADR1-96</td>
<td>1</td>
<td>9</td>
<td>1,400</td>
</tr>
<tr>
<td>ADR1-82</td>
<td>2</td>
<td>21</td>
<td>4,100</td>
</tr>
<tr>
<td>ADR1-70</td>
<td>2</td>
<td>12</td>
<td>1,000</td>
</tr>
<tr>
<td>ADR1-40</td>
<td>1</td>
<td>5</td>
<td>800</td>
</tr>
<tr>
<td>ADR1-75</td>
<td>5</td>
<td>5</td>
<td>600</td>
</tr>
<tr>
<td>ADR1-72</td>
<td>5</td>
<td>29</td>
<td>1,000</td>
</tr>
<tr>
<td>ADR1-77</td>
<td>2</td>
<td>20</td>
<td>1,000</td>
</tr>
<tr>
<td>ADR1-55</td>
<td>1</td>
<td>56</td>
<td>1,000</td>
</tr>
<tr>
<td>ADR1-20</td>
<td>1</td>
<td>5</td>
<td>120</td>
</tr>
<tr>
<td>ADR1-15</td>
<td>6</td>
<td>2</td>
<td>10</td>
</tr>
<tr>
<td>ADR1-14</td>
<td>1</td>
<td>2</td>
<td>10</td>
</tr>
</tbody>
</table>

The number after the ADR1 gene designates the number of ADR1-coded amino acids present. All values are means of triplicate determinations for ADR1-220 and are significantly different (p < 0.05) from the ADR1-220 activities determined by Dennis and Young. (12)

Note: All values are means of triplicate determinations for ADR1-220 and are significantly different (p < 0.05) from the ADR1-220 activities determined by Dennis and Young. (12)

1) As determined by Dennis and Young. (12)
2) The ADR1-151 gene was deleted from the TRP1 plasmid.
3) ND: Not done

The above results obtained using plasmid-bearing ADR1
only required for CCR1 control.

220. ADRI-304.

putative phosphatase activity at which CCR1 does not transmit its signals solely through amino acids 220 through 1225 and suggest that the putative phosphatase site at amino acid 220 is not the only requirement for CCR1 control.

adds cells to grow on ethanol-containing medium (Table 2).

ADRI domain required for growth on glycerol as a carbon source. Each of the ADRI genes described in the legend to Fig. 1. Strains ADRI-272, ADRI-282, ADRI-292, and ADRI-304 grow on YEP medium containing 2\% glycerol, lacking glucose (Fig. 1). Further growth, to densities 3 x 10^9 to 5 x 10^9 cells per ml, required the presence of glucose and an ADRI gene having at least 706 N-terminal amino acids (Fig. 1, Table 2). Strains containing an adri-I allele but also having ADH II enzyme activity due to the ADRI-220 allele were unable to grow on glycerol-containing medium (Table 2), indicating that growth on glycerol was independent of ADH II activity levels. Recombination of cells grown to 3 x 10^8 to 5 x 10^9 cells per ml on glycerol-containing medium into fresh glycerol-containing medium resulted in growth patterns identical to those described above, indicating that glycerol growth is not due to mutation or adaptation. Glycerol kinase and glyceraldehyde 3-phosphate dehydrogenase, two enzymes responsible for glycerol metabolism (133), were assayed in cells containing the ADRI or the adri-I allele, but no differences were observed (data not shown).

![FIG. 1](image)

**TABLE 2**: ADRI regions involved in bypassing glucose control and in growth on nonfermentable carbon sources

<table>
<thead>
<tr>
<th>Genes</th>
<th>ADRI II activity</th>
<th>Relative growth</th>
<th>ADRI II activity</th>
<th>Relative growth</th>
</tr>
</thead>
<tbody>
<tr>
<td>ADRI-272</td>
<td>2000</td>
<td>4</td>
<td>200</td>
<td>8</td>
</tr>
<tr>
<td>ADRI-282</td>
<td>100</td>
<td>4</td>
<td>100</td>
<td>8</td>
</tr>
<tr>
<td>ADRI-292</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>ADRI-304</td>
<td>100</td>
<td>4</td>
<td>200</td>
<td>8</td>
</tr>
</tbody>
</table>

*See Table 1.*
DISCUSSION

The large size of the transcriptional activator ADR1 suggests that it contains multiple domains, each potentially having one or more functions. Several of the regions which have been identified are depicted in Fig. 4. The deletion analysis experiments described in this paper confirm the importance of the putative DNA-binding region of ADR1 (amino acids 99 through 155) to ADR1 function. Deletion into this region resulted in an ADR1 polypeptide unable to allow ADR2 derepression. While this result is consistent with a previous deletion analysis of ADR1 (12), the possibility remains that such an observation could be the result of decreased levels of ADR1-151 protein in the cell, rather than intrinsic inactivity of ADR1-151. However, this is probably not the case. When an ADR1-151-β-galactosidase fusion protein was expressed to the same levels as longer ADR1-β-galactosidase fusions, as measured by β-galactosidase activity, the ADR1-151-β-galactosidase protein was unable to activate ADR2, whereas the longer fusion polypeptides were able to (R. Wallin and J. Cherry, personal communication). Our results thus support the hypothesis that ADR1-151 is inactive as a result of its lack of two complete zinc finger regions. In this regard, it is interesting to note that all proteins which share homology to the DNA-binding fingers of transcription factor IIIA contain at least two such fingers (13, 29, 30, 36), implying that multiples of such regions are required for function.

Although we have not been able to show directly that ADR1 binds to ADR2 DNA, it is probable that it does bind DNA on the basis of its homology to transcription factor IIIA. If this were the case, the first 220 amino acids of ADR1 must contain at least the recognition sites for binding and the ability to activate transcription. Transcriptional activation regions have been mapped relative to the DNA-binding regions for several other eucaryotic regulators. For the yeast GCN4 (14) and GAL4 (15) activators, the two regions are physically distinct. For the glucocorticoid receptor, however, it appears that both regions may occur in the same or overlapping segments of the protein (13, 28). The GCN4 and GAL4 activation regions coincide with an acidic part of the polypeptide that has been postulated to be a contact point with RNA polymerase II or another transcriptional component (14). ADR1 also contains a single acidic region, amino acids 29 through 40 (50% acidic), within the first 220 amino acids (Fig. 4).

Whereas the first 220 amino acids of ADR1 were sufficient to cause at least some derepression of ADR2, no shortened ADR1 protein was as functional as ADR1-1323 (Fig. 2B). Progressive carboxy-terminal deletions caused progressive decreases in the ability of ADR1 to maximally activate ADR2. These differences in maximal activation of ADR2 are not due to differences in protein stability, indicating that a large part, if not all, of ADR1 is required for normal modulation of its transcriptional function. These findings are in contrast to the results of a previous study using plasmid ADR1 gene constructs, which suggested that an ADR1-106 polypeptide retained wild-type function (12). The interpretation of the earlier results was complicated, however, by the fact that not all cells contained plasmids and that ADR1 dosage per cell was not known. Although we are unable to define the function of amino acids 220 through 1323 of ADR1 as they pertain to ADR1 control, it is possible that this region provides contact points to itself or other regulatory proteins that improve the efficiency of ADR1 activation but are not required for transcriptional activation. It is also possible that parts of the C terminus are required to ensure proper folding of the N terminus. Without the whole original C terminus, the N-terminal domain, although partially active, would form a functionally impaired structure.

A second region of importance to ADR1 function has been defined by characterization of ADR1 mutations that allow ADR1 to bypass glucose control. These mutations occur within the cAMP-dependent protein kinase phosphorylation recognition sequence (22) between amino acids 227 and 231.
growth than had previously been thought. However, the ADR1 phosphorylation region did not render ADR2 depressed independent of the CCR1 mutation (Table 3). This result implies that CCR1 may control ADR1 through the first 220 amino acids at other potential phosphorylation sites or that CCR1 does not act through ADR1 at all.

The requirement of ADR1 for growth on glycerol implicates ADR1 as a more global regulator of nonfermentative growth than had previously been thought. However, the identity of the factor through which ADR1 controls growth on glycerol is unknown. A more important role in growth on glycerol, other than the enzymatic activities of glycerol kinase and glycophosphate dehydrogenase, could be the process of transporting reducing equivalents or other molecules across the mitochondrial membrane 54, 111. Amino acids 364 through 506 of ADR1 are required for growth on glycerol, though they are not essential for ADR2 activation. These results suggest that ADR1 control of growth on glycerol is modulated by the binding of ADR1 to specific regions of the ADH2 gene, which require this region of the ADR1 protein.

ACKNOWLEDGMENTS

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