In S. cerevisiae, there are five genes that encode alcohol dehydrogenases involved in ethanol metabolism, ADH1 to ADH5. Four of these enzymes, Adh1p, Adh3p, Adh4p, and Adh5p, reduce acetaldehyde to ethanol during glucose fermentation, while Adh2p catalyzes the reverse reaction of oxidizing ethanol to acetaldehyde.The five ethanol dehydrogenasesas well as the bifunctional enzyme Sfa1p are also involved in the production of fusel alcohols during fermentation. Fusel alcohols are end products of amino acid catabolismvia the Ehrlich pathway and contribute to the flavor and aroma of yeast-fermented foods and beverages. They may also have physiological roles. For example, exposing cells to isoamyl alcohol, derived from catabolism of leucine, stimulates filamentous growth. Similarly, other fusel alcohols also stimulate filamentous growth in S. cerevisiae and biofilm formation in the pathogens Candida albicans and Candida dubliniensis.When glucose becomes depleted from the environment, Adh2p is responsible for catalyzing the initial step in the utilization of ethanol as a carbon source. S. cerevisiae cells lacking alcohol dehydrogenase activity are unable to grow when ethanol is the sole carbon source and these cells also accumulate high levels of glycerol. Although ADH1 and ADH2 share 89% sequence similarity, their gene products differ in metabolic directionality due to their differences in substrate affinity; Adh2p has a ten-fold lower Km for ethanol than all the other alcohol dehydrogenases.Two cis-acting elements in the ADH2 promoter, UAS1and UAS2/CSRE, are both necessary for maximal ADH2 expression. In the absence of a fermentable carbon source, these sites are bound cooperatively by the transcriptional activators Adr1p and Cat8p; Adr1p binds to the UAS1 site while Cat8p binds to the UAS2/CSRE site. The presence of glucose downregulates the levels of these transcription factors which in turn results in ADH2 expression being repressed by several hundred-fold.About the medium-chain dehydrogenase/reductasefamily Medium-chain dehydrogenase/reductases, sometimes referred to as long-chain dehydrogenases, constitute an ancient and widespread enzyme superfamily with members found in Bacteria, Archaea, and Eukaryota. Many MDR members are basic metabolic enzymes acting on alcohols or aldehydes, and thus these enzymes may have roles in detoxifying alcohols and related compounds, protecting against environmental stresses such as osmotic shock, reduced or elevated temperatures, or oxidative stress. The family also includes the mammalian zeta-crystallin lens protein, which may protect the lens against oxidative damage and enzymes which produce lignocellulose in plants. MDR enzymes typically have subunits of about 350 aa residues and are two-domain proteins, with a catalytic domain and a second domain for binding to the nicotinamide cofactor, either NADor NADP. They contain 0, 1, or 2 zinc atoms. When zinc is present, it is involved in catalysis at the active site. Based on phylogenetic and sequence analysis, the members of the MDR superfamily can be further divided into more closely related subgroups. In families which are widespread from prokaryotes to eukaryotes, some members appear conserved across all species, while others appear to be due to lineage specific duplications. Some subgroups are only found in certain taxa. S. cerevisiae contains fifteenor twenty-onemembers of the MDR superfamily, listed below. The difference in number is due to six sequences that were included as members of the quinone oxidoreductase family by Riveros-Rosas et al.but not by Nordling et al.. Zinc-containing enzyme groups: - PDH; \"polyol\" dehydrogenase family - BDH1, BDH2, SOR1, SOR2, XYL2 - ADH; class III alcohol dehydrogenase family - SFA1 - Y-ADH; \"yeast\" alcohol dehydrogenase family - ADH1, ADH2, ADH3, ADH5 - CADH; cinnamyl alcohol dehydrogenase family - ADH6, ADH7 Non-zinc-containing enzyme groups: - NRBP; nuclear receptor binding proteinor MRF; mitochondrial respiratory functionfamily - ETR1 - QOR; quinone oxidoreductase family - ZTA1, AST1, AST2, YCR102C, YLR460C, YMR152W, YNL134C- LTD; leukotriene B4 dehydrogenases - YML131W - ER; enoyl reductasesor ACR; acyl-CoA reductasefamily - no members in S. cerevisiae