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.ADH3 is a nuclear gene that encodes the alcohol dehydrogenase isozyme of the mitochondrial matrix. Adh3p shares roughly 80% amino acid identity with Adh1p and Adh2p. The presence of glucose in the media represses ADH3 expression, although ADH3 glucose-repression is not as severe as that of ADH2. Null mutations in ADH3 do not confer a phenotype under aerobic conditions, but under anaerobic conditions mutant cells grow noticeably slower than wild type cells. This may be due to the suggested involvement of Adh3p in an ethanol-acetaldehyde redox shuttle that is involved in maintaining the mitochondrial redox balance during anaerobic growth.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