ABSTRACT

The mevalonate diphosphate decarboxylase is an enzyme, which converts mevalonate diphosphate to isopentenyl diphosphate, the building block of isoprenoids.

Investigation of amino acid sequences of MVDs from evolutionary diverse organisms [*C. albicans*, *S. cerevisiae*, *S. pombe*, *A. thialana,* rat and human (Dassanayake *et al,* 2002)] revealed that there are three cysteine residues conserved amongst these eukaryotes. Interestingly, a mutation (leucine to proline) adjacent to the first cysteine residue gave rise to the temperature-sensitive phenotype of *S. cerevisiae* MN19-34 mutant. Therefore we hypothezed in three strictly conserved cystein residues may be involved in forming intra- or inter-molecular disulphide linkages, as one study indicates that MVD in *S. cerevisiae* is capable of interacting with each other to form dimers (Cordier et al.1999b). Also a previous study demonstrated the biological function of *C. albicans* MVD by gene knockout experiments and complementation experiments in *S. cerevisiae* temperature-sensitive strain. *C. albicans* MVD can be immuno-detected in Western blot analysis when epitope tagged (Dassanayake et al, 2002). Although cDNAs encoding MVD have been cloned and characterized from humans, rats, yeasts, and *Arabidopsis thaliana,* MVD remains one of the less well-known enzymes in the MVA pathway (Berges *et al.,* 1997). Therefore, the main objectives of the current research project was to study the functional roll of evolutionary conserved 3-cystein residues in *C. albicans* MVD.

In this research work, biochemistry & molecular biology techniques such as PCR mutagenesis, electrophoration, DNA transformation, blunt-end ligation, restriction enzyme digestion and DNA preparation used.