Characterization of peroxide detoxification pathways will be described here, with emphasis in peroxiredoxins (prx). Prx and glutathione peroxidases are thiol dependent peroxidases that share no amino acid sequence similarity but possess a common structural characteristic: the thioredoxin fold (central core of four-stranded mixed beta-sheet, flanked by three alfa-helices). Our studies have demonstrated that although all five peroxiredoxins from Saccharomyces cerevisiae possess thioredoxin-dependent peroxidase activity, their functions are not completely redundant. In an attempt to better characterize peroxiredoxins and related proteins, we are performing structural studies. In one of these studies, glutaredoxin 2, the main glutathione-dependent oxidoreductase of yeast, had its structure solved by molecular replacement using a homologous protein from Sus scrofa as a model. The structure of thioredoxin reductase 1 from Saccharomyces cerevisiae was also solved by molecular replacement from crystals obtained by the hanging drop method. We are also studying antioxidant proteins from Xylella fastidiosa. In this regard, we were able to show for the first time that Ohr (‘Organic Hydroperoxide Resistance protein) is a dithiol-dependent peroxidase. The crystal structure of Ohr was elucidated and it is composed of two six-stranded β-sheets surrounded by two-helices, forming a barrel-like structure. Contrary to other classes of thiol-dependent peroxidases, Ohr does not possess the thioredoxin fold. Furthermore, the mechanism by which the reactive cysteine is stabilized appeared to be different among the three classes of thiol-dependent peroxidases. Therefore, Ohr from Xylella fastidiosa is a member of a new class of antioxidant proteins exclusively present in bacteria, most of them pathogenic.

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