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Protein-surfactant interaction: Selective unfolding in hemeproteins

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Denaturation of proteins by surfactant has been known for long and this aspect is employed extensively in SDS-gel electrophoresis. In spite of wide applications of various surfactants in biochemical studies, studies directed at understanding the nature of interaction at the molecular level are limited. We have studied the effect of different types of surfactants on a series of hemeproteins using various spectroscopic techniques. Ionic surfactants were found to be quite effective for unfolding the structure of O_2-carrier (myoglobin and hemoglobin) and electron carrier (cytochrome c) proteins. They caused depletion of heme from myoglobin and hemoglobin. However, peroxidases (horseradish peroxidase and lactoperoxidase) exhibited more resistance towards denaturation. Evidence from optical spectra, circular dichroism, ^{1}H-NMR, tryptophan fluorescence and stopped flow kinetic measurements suggests that the primary process of unfolding is the weakening of the proximal histidine-heme(N[ε]-Fe) bond. In case of CTAB-induced unfolding of metmyoglobin, the kinetic mechanism suggests that apart from the heme-dissociation process, there are at least two other transitions related to changes in global conformation of the protein. However, denaturation of cytochrome c by SDS occurred through a single transition with $\Delta E = 5{\cdot}4$ kcal/mol.

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