Investigation of Oligomeric States, Reactivity Over Hydroperoxides and Redox Relationships with Reductant System of Ahp1 of *Saccharomyces cerevisiae*.

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2-Cys peroxiredoxins (Prxs) are antioxidant proteins able to decompose hydroperoxides using a reactive cysteine residue (peroxidatic cysteine-Cys₉-SH). Additionally, some Prx, suffers overoxidation of the catalytic cysteine (CysP-SO₂H or Cysp-SO₃H), triggering intense oligomerization into high molecular weight complex species endowed with a second activity: molecular chaperone. After hydroperoxide reduction, disulfide bond is generated in 2-Cys Prx, which in most cases is reduced by the thiol/disulfide oxidoreductase thioredoxin. Alkyl Hydroperoxide reductase1 (Ahp1p) is a peroxiredoxin very abundant in *Saccharomyces cerevisiae* able to efficiently decompose organic hydroperoxides (OHP). Indeed, disruption of the *ahp1* gene revealed that the null mutant presents high sensibility to OHP. Despite its importance, Ahp1p is poorly characterized and studies aiming its reactivity over hydroperoxides, oligomeric/functional transitions and relationships with the biological reductant (Trx) are very scarce. In this work, using size exclusion chromatography, we have demonstrated that Ahp1 is a dimeric enzyme, independent of REDOX state and very resistant to heat shock denaturation (thermal stability >60°C). Tryptophan fluorescence experiments reveal that protein presents distinct structural conformations depending of redox state. Steady-state DTT assays indicated that Ahp1 decompose H₂O₂ (7.27μM.s⁻¹) and the enzymatic parameters for OHP are in progress. Additionally, by mass spectrometry we have elucidated the electron transfer path between Ahp1 and Trx.

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