

MODELING BY HOMOLOGY AND COMPARATIVE PROFILE OF SUPEROXIDE DISMUTASE BETWEEN EXTREMOPHILES: METHYLOBACTERIUM AS A MODEL ORGANISM

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Superoxide Dismutase (SOD) is an antioxidant enzyme, which has been little studied in the genus *Methylobacterium*, a radioresistant bacterium which was our model organism in this study. The alignment of SOD sequences of all the selected extremophiles revealed a consensus motif D-[VM]-WEH-[AS]-[YF]-Y-[LI], a homology modeling of the SOD of *Methylobacterium*, the reliability of the predicted SOD model was checked using several validation metrics, including the Ramachandran plot, Z score, and energy analysis score of the normalized qualitative model.

Extremophiles are microorganisms that can withstand severe environmental conditions such as extreme levels of gamma radiation, temperature, salt stress, acidic or alkaline conditions. These types of diverse stress conditions encountered by these extremophiles result in the formation of reactive oxygen species (ROS) that cause cell death, ROS are naturally quenched by some antioxidant enzymes such as superoxide dismutase (SOD) (Priya et al. 2007). To gain a better understanding of the role of SODs, we selected *Methylobacterium radiotolerans* as the study model.

For the development of this research, 19 amino acid sequences of SOD were recovered from extremophilic organisms. These sequences were treated with different bioinformatics programs, such as ClustalW, Mega10.2.6, Modeller 10, PROSITE and Pfam. All structural analyzes, such as overlay and visualization, were carried out using the Pymol program.

Our results show that the SOD sequences of these extremophiles are very similar, finding a conserved pattern, which was D-[VM]-WEH-[AS]-[YF]-Y-[LI], which suggests that these residues could play a role in maintaining the structural and functional activity of the protein. Using pairwise alignment, ten models were designed from which the model with the highest number of residues in the allowed regions was chosen consisting of three strands, twelve helices and eleven

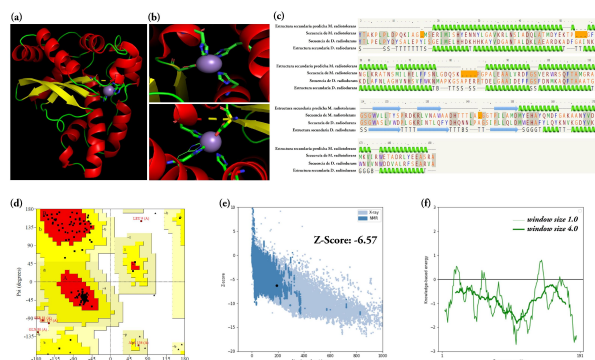


Fig. 1. Three-dimensional structure of SOD modeled by homology, with amino acids in permitted and energetically favored regions, highlighted by amino acids H25, H70, D151 and H155 that are interacting with Mn.

turns (Figure 1.a). To verify the reliability of the predicted model, different programs were used. PHYRE and the Ramachandran diagram showed that 90.4% of the residues are found in the most favored regions (Figure 1.c and Figure 1.d). The Z score found was equal to -6.57, which shows that it is energetically favored (Figure 1.e). PROSA-web demonstrates the negative energy value for all residues indicating good reliability of the predicted structure (Figure 1.f).

Various studies affirm that SOD is capable of eliminating free radicals and that this capacity is favored by binding manganese (Mn) (Wintjens et al. 2004), in our model we observe that the amino acids H25, H70, D151 and H155 are involved in the uptake of Mn (Figure 1.b top) and that are also conserved amino acids in *D. radioadurans*, with a slightly different orientation of H26 from *D. radiodurans* with respect to H25 from *M. radiotolerans* (Figure 1.b bottom), this could lead to a change in the functionality of the SOD of one organism and another.

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