

IN SILICO ANALYSIS OF GOAT (CAPRA HIRCUS) HEAT-SHOCK PROTEINS HSP70 AND HSP 90
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Abstract / Resumo:

Heat-shock proteins play important role on cellular processes and are divided in numerous families. Two important families are the 70kDa (Hsp70) and 90kDa (Hsp90) molecular chaperones. Hsp70 acts at multiple steps in a protein's life cycle, including the processes of folding, trafficking, remodeling and degradation. The function of Hsp90 also includes assistance in protein folding, cell signaling, and tumor repression. Hsp90 chaperone activity range from interacting with the specific proteins/chaperones involved in cell cycle control and hormone signaling, to more general interaction such as binding to metastable cellular proteins following stress. Whereas Hsp90 beta is expressed constitutively to a high level, Hsp90 alpha is stress-inducible and is over-expressed in many cancerous cells. Both Hsp70 and Hsp90 seem to be related to cancer. In this study, we analyzed in silico one predicted Hsp70 protein isolated from goat, and two partial Hsp90 proteins from goat and sheep. Both goat and sheep Hsp90 partial proteins (282 and 722 amino acids respectively) presented the conserved amino acids among Hsp90 α isoform related in literature (10 and 26 amino acids respectively). It was identified one conserved ATP-binding site and one steroid receptor-binding domain on goat partial protein, and three ATP-binding sites on sheep partial protein. Phylogenetic analysis of cDNA and amino acid sequences were consistent between them. Hsp90 primary sequence seems to be very conservative according to comparative analysis between other mammals. Predicted Hsp70 protein of goat (841 total amino acids) possesses 82 strongly basic (+) amino acids (K,R) and 92 strongly acidic (-) amino acids (D, E), 220 hydrophobic amino acids and 151 amino acids are polar in nature, and showed isoelectric point as 5.611. Goat Hsp70 protein showed conserved catalytically essential acidic residues in the active site region of the ATPase fragment (Asp-10, Asp-199, Asp-206 and Glu-175). Comparison among Hsp70 protein of goat, sheep (partial), cattle and buffalo nucleotide sequences showed 96-99% similarity, and 95-100% on amino acid level. Comparison between goat and cattle secondary structure showed high similarity as expected. This is an initial study for understand the systematic work of molecular chaperones on goat under stress environment.