Apoptotic Proteins

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The main purpose of the research project was to identify if there were any prevalent nucleotide patterns associated with excess expression pro-apoptotic genes (orthologous or paralogous) in neuronal cells. The project also aimed to isolate specific proteins could be modeled based on these sequences, and what scientists could learn about the interactions within them (i.e. hydrophobic interactions, disulfide bridges, etc.). The hypothesis is that such sequences existed and the functions that these proteins may have based on homologous relationships. To test this, model organisms were used, and BLAST sequence procedures were ran to identify FASTA amino sequences of these proteins (i.e. amyloid beta), as well as their related E-values (13 of which were under 1e-48) that could suggest homology. Comparing them with known proteins, it was observed that they had certain functions in common, such as release of cytochrome c from mitochondria. Running Clustal Omega procedures strengthened the relationship between the genes coding these proteins. Using Sequence Alignment in Molecular Operating Software prototypes, it was found that there were some steric clashes within some of the modeled proteins (based on a combination of the obtained FASTA sequences), suggesting that there may be some incompatibility in these protein homologs which is why some may not be as effective in inducing apoptosis. DNA sequences coding for these ineffective proteins tended to have CG dense areas near their enhancers and promoter regions as well. In summary, these pro-apoptotic-protein-encoding genes had similarities that suggest homology.

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