

# Ancestrality and evolution of genes related with apoptosis

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Apoptosis is a process of programmed cell death that occurs in multicellular organisms. It is an essential process to maintain the development of living beings acting to eliminate unnecessary or defective cells. During apoptosis, the cell undergoes changes in morphologic characteristics leaded by biochemical events. Such changes include cell contraction, loss of adhesion to the extracellular matrix and neighboring cells, chromatin condensation, internucleosomal cleavage of DNA, formation of apoptotic bodies, nuclear fragmentation, chromosomal DNA fragmentation, and total mRNA decay. The inhibitors of apoptosis proteins or IAP (Inhibitor of Apoptosis Protein) are molecules that exert their anti-apoptotic role through the ability to inhibit the activity of the effector caspase 3, 7 and 9 modulating the transcription factor NF- $\kappa$ B. We determined the Lowest Common Ancestor (LCA) for the genes on this system to investigate their origin along the evolution. We found that members of the Bcl-2 family (called anti-apoptotic regulators), responsible for inhibit apoptosis and prevent the release of cytochrome C, are present and conserved since Metazoa. This family also includes pro-apoptotic proteins Bax, Bid and Bak. Another protein important in cell cycle is DIABLO (generally referred as Smac/Diablo), that promotes caspase-9 for binding to IAPs and by removing their inhibition activities. We observed that these proteins have origin dated in Bilateria. Thus, we can conclude that the study of the evolution of proteins involved in the apoptotic process is important for your better understanding and can be used in combination with treatment and prevention of diseases related to disorders in this process.