

Evolutionary Aspects of the DNA Damage Response system: BRCT Triplet example

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INTRODUCTION: The DNA structure is subjected to damage and its integrity depends of the DNA damage response system (DDR), a system that recognizes, repair and prevent damage propagation. The major DDR pathways are base excision repair (BER), nucleotide excision repair (NER), mismatch Repair (MMR), homologous recombination (HR) and non-homologous end joining (NHEJ). Several proteins involved in DDR enclose the BRCT motifs, which can contain from 1 to 3 BRCT units. This domain mediates protein-protein and protein-nucleic acid interactions, and is able to recognize phosphopeptides. **OBJETIVES:** The aim of this work was to study the evolution of the DDR, determining the conservation of DNA repair pathways and BRCT triplet along the evolutionary scale. MATERIAL AND **METHODS:** KEGG was used to identify DDR proteins in chosen taxa. The absent proteins were searched in nr database using MolFuncs, a program that uses a reciprocal BLAST strategy. BRCT triplets of TOPBP1 and ECT2 from each taxon were analyzed using multiple alignments and the secondary structure was predicted by JNET. **RESULTS AND DISCUSSION:** The DNA repair pathways are conserved in eukaryotes while in prokaryotes, most of the pathways seemed to be carried out by analogous proteins. MMR seems to be the most conserved pathway in eukaryotes. TOPBP1 and ECT2 were identified in most eukaryotes taxa but not in prokaryotes. The BRCT-triplet was always present despite truncated in minor cases. **CONCLUSION:** The distributions of the DNA repair pathways proteins as those from TOBP1 and ECT2 are wide and indicate that DDR is conserved in eukaryotes. Moreover, the presence of analogous proteins in prokaryotes highlights the conservation of DNA repair function. The evolutionary distribution of TOPBP1 and ECT2 suggests that both proteins (with BRCT triplet) possibly originated in unicellular eukaryotes.

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