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The Possible Role of Heat-shock proteins (HSPs) on Inflammatory Bowel Disease (IBD): Peptide Motif Analysis as an Immunoinformatic Technique

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Abstract

Inflammatory bowel disease (IBD) is classified as Ulcerative Colitis and Crohn's Disease, both of which affect the gastrointestinal system and are caused mainly by gut dysbiosis. There is a lack of data available regarding inflammatory bowel disease pathogenesis. This encouraged us to look into whether or not any protein of microorganisms has a potential relationship in the immunopathogenesis of inflammatory bowel disease. Therefore the bioinformatic evaluation of host-microbe interactions would be a crucial approach in identifying the mentioned target. Using the basic local alignment search tool for protein (BLASTP) tool from National Center for Biotechnology Information (NCBI) and T-coffee expresso, the proteome of the mentioned microorganisms of the literature review linked to IBD was analyzed for protein sequences with identities exceeding 35%. The phylogenetic tree and degree of relationship between the protein sequences of microorganisms and the human proteome were determined using Multiple Sequence Alignment from Protein Data Bank (PDB). In this study, Campylobacter, Clostridium, Escherichia coli, Klebsiella, Listeria, Mycobacterium, Salmonella, Shigella, and Yersinia were identified as microorganisms associated with IBD. This study found traces of molecular mimicry (molecular-level similarity between microbial antigens and host proteins). Due to their high conservation in evolution, the 60, 70, and 90 kilo Dalton heat shock proteins (HSP) of the microorganisms and humans were identified as possible molecular targets, followed by autoreactive T lymphocytes against heat shock proteins in humans. It can be a possible pathogenesis in IBD through a dysbiotic gut microbiome. Finally, cytotoxic T lymphocytes and helper T lymphocyte epitopes with high homology between 60, 70, and 90 kilo Dalton heat shock proteins were extracted with Immune Epitope Data Base (IEDB) tool. Last but not least, by using in silico immunoinformatic approach, this study supports the concept that bacteria and the human proteome likely share many cross-reactive T cell epitopes.

Keywords: Immunoinformatic, Molecular mimicry, Auto-inflammatory, Heat-shock proteins (HSPs), Inflammatory Bowel Disease (IBD)