

ACTA MARISIENSIS SERIA MEDICA

OFFICIAL PUBLICATION OF THE

GEORGE EMIL PALADE UNIVERSITY OF MEDICINE, PHARMACY, SCIENCE, AND TECHNOLOGY OF TARGU MURES



INTERNATIONAL CONGRESS FOR STUDENTS, YOUNG DOCTORS AND PHARMACISTS MARISIENSIS

22th-26th May 2024
Targu Mures, Romania

BOOK OF ABSTRACTS

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SLE activity status. **Material and methods:** A search of English literature has been performed on PubMed and Google Scholar. Inclusion criteria for the selected articles consisted of publication between the year 2004 and 2024, and presence of the keywords "monomeric C-reactive protein", "Systemic Lupus Erythematosus", "anti-mCRP antibodies", "Autoimmune Diseases". **Results :** A study including 160 patients diagnosed with SLE showed that serum pCRP did not discriminate between active and quiescent disease, however the ratios of mCRP/pCRP reached statistical significance in paired samples, with lower values displayed in active disease as opposed to the dormant state. Furthermore, the mCRP/pCRP ratio was higher during remission. Serially collected sera of 10 patients involved in a prospective control program demonstrated anti-mCRP positivity for 60% of the SLE individuals at flare, whereas all the participants with active lupus nephritis had anti-mCRP positivity at flares. In addition, SLE disease activity index (SLEDAI) scores positively correlated with anti-mCRP levels. A recently conducted study aimed to investigate the prevalence of both pCRP and mCRP on extracellular vesicles (EVs), as the latter are implicated in SLE pathogenesis by exposing nuclear antigens on their external surface, therefore promoting autoantibodies generation. Plasma mCRP+ but not pCRP+ EVs were significantly increased in patients with active SLE state and in anti-mCRP positive participants. **Conclusions:** The interrelationship between pCRP and mCRP appears to discriminate SLE activity states. Anti-mCRP antibodies correlated with SLE disease activity, nevertheless, further research exploring their generation by mCRP opsonized EVs and effects are needed.

Keywords: Monomeric C-Reactive Protein, Lupus Erythematosus Systemicus, Anti-mCRP Antibodies, Autoimmune Diseases

THE ROLE OF ARTIFICIAL INTELLIGENCE IN PREDICTING PROTEIN-PROTEIN INTERACTIONS FOR INVESTIGATING ARYLSULFATASE B IN THE DEVELOPMENT OF COLORECTAL CANCER

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Background: The investigation of protein-protein interactions is crucial for comprehending various biological mechanisms, cellular processes, and the pathogenesis of different diseases. While some studies have suggested a potential link between the arylsulfatase B (ARSB) protein and malignant colorectal tumours, the molecular mechanisms behind this are still poorly understood. Recent technological advancements have made it possible to have several databases that store our current information on protein-protein interactions and based on this knowledge, with the use of artificial intelligence to predict new interactions. This has made in silico interaction studies significantly more accessible compared to experimental methods. **Objective:** Our research attempts to analyse the possible involvement of arylsulfatase B in the pathogenesis of colorectal cancer, while using various bioinformatics tools and databases to predict protein-protein interactions. **Material and methods:** For the analysis of arylsulfatase B interaction network the STRING online database was utilised with a confidence score of 0.400, as suggested by the database. Following this, the proteins from the most effective interaction pathway were selected and individually examined using two machine learning software. The PEPPI system predicted interactions based on the protein's amino acid sequence, while the HDock Server online tool utilised the protein's tertiary structure for this purpose. **Results :** Based on the results of STRING database, the GUSB and HSP90AB1 proteins are the most strongly associated with ARSB in the development of colorectal cancer, with an overall confidence score of 0.778 and 0.626 respectively. According to the PEPPI system, the HSP90AB1 protein is most likely to interact with the AKT1 ($\log(\text{LR}) = 1.787$), TP53 ($\log(\text{LR}) = 0.965$), and EGFR ($\log(\text{LR}) = 0.874$) proteins. Furthermore, the HDock Server showed a high confidence score of interacting with HSP90AB1 for the RAF1 (0.9208), BRAF (0.9141), and EGFR (0.9020) proteins. **Conclusions:** The PEPPI system predicts the AKT1, while the HDock Server predicts the RAF1 protein to be the most likely interaction partner of HSP90AB1. It is noteworthy that both software found a significant interaction probability between the HSP90AB1 and EGFR protein. The difference in results can be attributed to the distinct prediction methods and the differences in information carried by the primary and tertiary structures input. These results demonstrate the wide availability and applicability of in silico prediction of protein-protein interactions. This method holds a significant place in future biomedical research, including the potential to better understand the role of arylsulfatase B in the development of colorectal cancer.

Keywords: arylsulfatase B, colorectal cancer, protein-protein interaction, artificial intelligence