World Academy of Science, Engineering and Technology
International Journal of Bioengineering and Life Sciences
Vol:11, No:03, 2017

# In silico Analysis towards Identification of Host-Microbe Interactions for Inflammatory Bowel Disease Linked to Reactive Arthritis

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**Abstract :** Reactive Arthritis (ReA) is a disorder that causes inflammation in joints due to certain infections at distant sites in the body. ReA begins with stiffness, pain, and inflammation in these areas especially the ankles, knees, and hips. It gradually causes several complications such as conjunctivitis in the eyes, skin lesions in hand, feet and nails and ulcers in the mouth. Nowadays the diagnosis of ReA is based upon a differential diagnosis pattern. The parameters for differentiating ReA from other similar disorders include physical examination, history of the patient and a high index of suspicion. There are no standard lab tests or markers available for ReA hence the early diagnosis of ReA becomes difficult and the chronicity of disease increases with time. It is reported that enteric disorders such as Inflammatory Bowel Disease (IBD) that is inflammation in gastrointestinal tract namely Crohn's Disease (CD) and Ulcerative Colitis (UC) are reported to be linked with ReA. Several microorganisms are found such as Campylobacter, Salmonella, Shigella and Yersinia causing IBD leading to ReA. The aim of our study was to perform the in-silico analysis in order to find interactions between microorganisms and human host causing IBD leading to ReA. A systems biology approach for metabolic network reconstruction and simulation was used to find the essential genes of the reported microorganisms. Interactomics study was used to find the interactions between the pathogen genes and human host. Genes such as nhaA (pathogen), dpyD (human), nagK (human) and kynU (human) were obtained that were analysed further using the functional, pathway and network analysis. These genes can be used as putative drug targets and biomarkers in future for early diagnosis, prevention, and treatment of IBD leading to ReA.

**Keywords :** drug targets, inflammatory bowel disease, reactive arthritis, systems biology
**Conference Title :** ICMSB 2017 : International Conference on Metabolomics and Systems Biology
**Conference Location :** Singapore, Singapore
**Conference Dates :** March 29-30, 2017