

## The prediction of MHC-binder and conformational epitope of *Campylobacter jejuni*: A combine approach

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**C**ampylobacter is a major cause of acute bacterial diarrhea in humans worldwide (Altekruse 1999). It is a slim, caprophilic, microaerophilic, spiral, Gram-negative, bacterium with a polar flagellum at one or both ends (Bolton & Coates, 1983; Ketley, 1997; Smibert, 1978). Infections occur from drinking unpasteurized milk and contaminated water but livestock and poultry remain a major risk in the transmission of *Campylobacter* in most developed countries (Yamazaki et al., 2009). The consumption of undercooked poultry and uncooked meat products are leading risk factors for human campylobacteriosis. Campylobacteriosis constitutes a serious medical and socioeconomic problem worldwide. The use of antibiotics for the treatment of *Campylobacter* infections is controversial. This study, thus, sought to screen the OMP of *C. jejuni* to identify epitopes present in silico sequence analysis. In advances in bioinformatics technologies will enable more detailed molecular studies. Such studies combined with better integration of host and pathogen research driven by epidemiological findings may truly advance our understanding of *Campylobacter* infection in humans. Molecular and proteomics approaches in the study of host-pathogen interactions, combined with host and pathogen driven epidemiological findings are important in elucidating the pathogenesis of *Campylobacter* infection for effective control strategies to be developed. Attempts have been made to provide the implication on the basis of predicted epitopes in the outer membrane proteins from *C. jejuni* may be useful in the formulation of immunodiagnostic kit and the peptides based safe subunit vaccine design against the diarrhea.

### Biography

A. G. Ingale obtained Ph.D in Biotechnology from Sant Gadge Baba Amravati University, Amravati (India). He was the founder Head, Department of Biotechnology, Dr. Babasaheb Ambedkar Marathwada University, Aurangabad (MS) India. Dr. Ingale is president of Society for Biotechnology and Bioinformatics, India. He is also the editor in-chief of the Journal of Biotechnology and Bioinformatics (JBB) and International Journal of Modern Biotechnology. He has received the award as a Fellow of Society of Sciences (FSSc), Dumka. His primary field is immunology with research emphasis on CD antigens and the structure-function prediction using Bioinformatics approach. He has recently entered the developing field of Lectin Biosensor and GlycoNanobiotechnology research. In Genomics research area he has been working on constructions of transgenic Okra against pest (*Lipidopteron*) and pigeon pea against bollworm. In proteomics research area he is working on proteomics of lectin and other plant and microbial proteins. Finally, His main research area is bioinformatics. In this, he has developed a database of CD markers and Toxin database is on completion. He has published several research papers in national and International journal of repute. He has submitted protein and nucleotide sequences on NCBI and viral protein models are being submitted in PDB database. Currently, Dr. Ingale is holding Major research projects as a Principal Investigator and Head Department of Biotechnology, North Maharashtra University, Jalgaon (MS) India.

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