# Structural Bioinformatic Study of wBm-Wsp-an anti-filarial Drug Target

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Wolbachia is a common and the obligate intracellular α-proteobacteria, which are found in insects, mites, and arthropods species. The parasitic nematodes cause lymphatic filarial disease in human. The current treatment approach for lymphatic filariasis is chemotherapy with the drugs, namely diethylcarbamazine (DEC), ivermectin, tetracycline, doxycycline and albendazole. The existing drugs are efficient only for microfilariae stages of parasites not for adult worms and also it needs a prolonged treatment procedure with the higher dosage which causes unwanted side effects especially for children and breastfeeding women. Wolbachia has endosymbiont activity that is essential for worm fertility and survival of nematodes. Wolbachia resides in nematodes' host and it helps to transfer the essential substances for nematodes survival. So, Wolbachia may be the promising drug target to develop antibacterial drugs against lymphatic filariasis. The Wolbachia genome suggested many drug targets, which are playing an indispensable role in nematode survival and reproduction. Wolbachia surface protein (Wsp) is one among them, which is observed in the outer membrane surface of the cell and helps to transfer small chemical molecules which are absent in nematodes through porin activity. Brugia malayi is one of the infectious filarial nematodes which is most prevalent parasite observed in India and South East Asia. So, our interest is the structural study of wolbachia surface protein (Wsp) from B. malayi, a promising drug target to eradicate the filarial disease by stopping the porin activity. Since Wsp structure hasn't been reported from any nematode species, we have chosen Wsp gene from B. malayi (wBm-Wsp) for structural investigation by X-ray crystallographic method. In this view, the wBm-Wsp gene is cloned and respective protein has been expressed in E.coli. The homogeneity of this protein was observed using SDS- PAGE analysis, which indicates the molecular weight nearly 26KDa. In addition, bioinformatics study of this wBm-Wsp protein shares sequence identity just18.4% with NspA structure from Neisseria meningitidis (PDB Id: 1p4t) and homology modelling structure confirms that both these NspA and wBm-Wsp proteins have similar structural features (beta barrel) with the porin type activity. The lack of Wsp structure from any parasites increased our interest to study the wBm-Wsp structure, hence the purified protein of the same is in crystal optimisation condition to facilitate X-ray crystallographic structure determination. Further investigation of this protein structure is in under progress.

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