

# In-silico identification of the putative internalin (pIn) Group B *Streptococcus* (GBS) ST283 as a putative zoonotic virulence factor (PZVF) via whole genome sequence (WGS) data of diseased fish and human GBS isolates

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## ABSTRACT

**Introduction:** Group B *Streptococcus* (GBS) ST283 caused bacteremia and meningitis in freshwater fish. Alarmingly, consuming contaminated fish products led to foodborne infection in humans, who also presented bacteremia and meningitis. A previous proteomic study identified internalin protein for the first time in the proteome of GBS from fish and humans, suggesting it as a putative zoonotic virulence factor (PZVF). Therefore, this study intended to identify and characterize the structure of putative internalin (pIn) of GBS ST283 by comparing it to those of other GBS lineages, other streptococcal species and non-streptococcal species' proteins. **Materials and Method:** This study analyzed five Malaysian GBS ST283 WGS data from diseased fish and humans which are available in NCBI; BioProject PRJNA 293392 from a previous study. The WGS assembly, annotation, and identification of pIn were performed via The Bacterial and Viral Bioinformatics Research Center (BV-BRC). The homologous pIn was mined from the BV-BRC database, UniprotKb, NCBI, and literature. A phylogenetic tree was constructed using MEGA software. **Results:** pIn was identified among a total of 1426 identical proteins. The phylogenetic tree showed that pIn was inferred to be related to group B leucine-rich (Blr) and conserved in GBS isolated from fish and humans. pIn was also associated with homologous proteins of *L. monocytogenes*, *S. pyogenes*, and *S. suis*. **Conclusion:** pIn of GBS ST283, homologous to Blr is structurally related to zoonotic streptococcal and non-streptococcal species, suggesting that pIn may have zoonotic potential. Therefore, pIn can be proposed as a molecular target for treatment and prevention at the fish farm level which eventually can curb the infection in the human population.