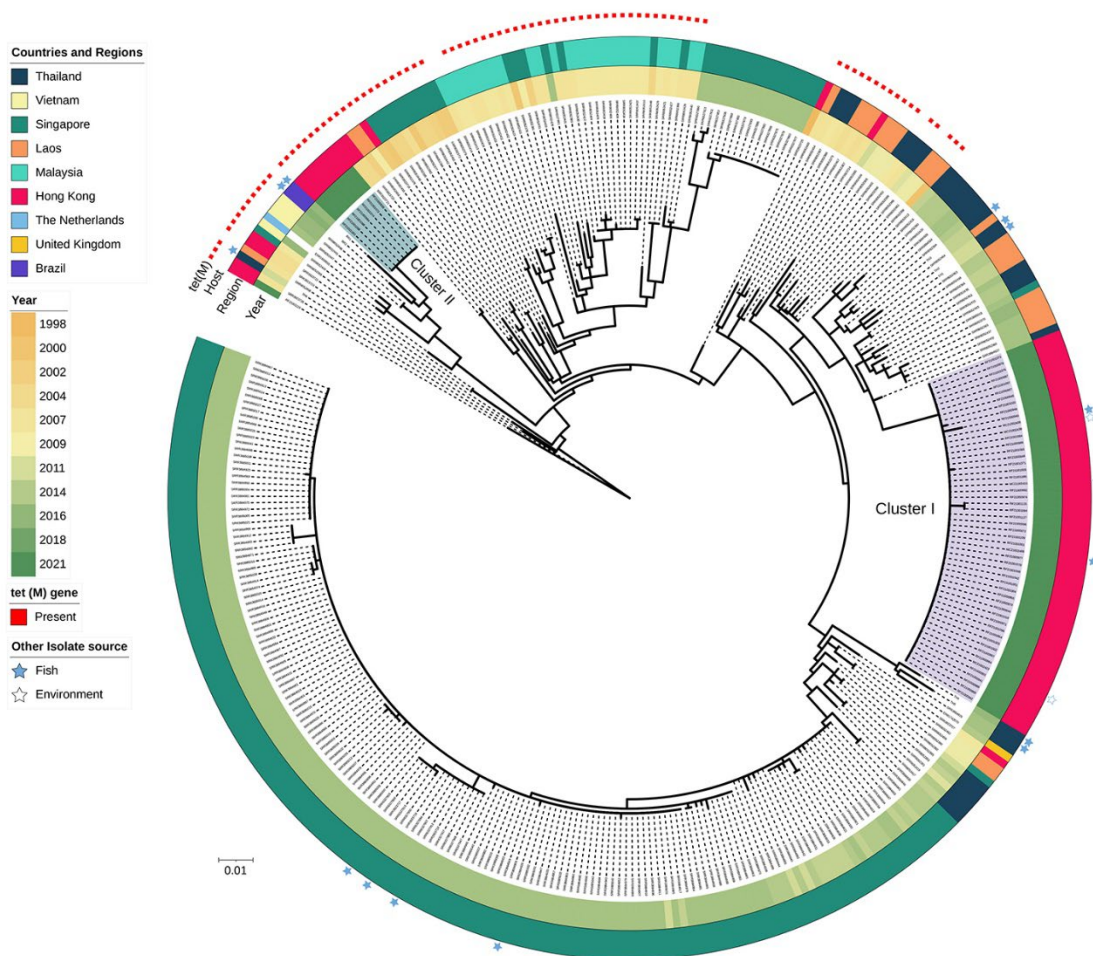


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# Invasive Group B *Streptococcus* Infections Caused by Hypervirulent Clone of *S. agalactiae* Sequence Type 283, Hong Kong, 2021

## Appendix 2



**Appendix 2 Figure.** Phylogeny of iGBS ST283 in Hong Kong Special Administrative Region, People's Republic of China from our study and global ST283 sequence data. GBS ST283 strains from our study were compared with ST283 sequence data across the globe (n = 303). The country/ region, and year of

isolation were noted. Isolates from fish (solid blue star) and the environment (hollow blue star) were marked under Host, while the remaining strains with no marking were clinical isolates. Presence of *tetM* gene (red square) was noted. Our two isolate clusters were highlighted (Cluster I and Cluster II with shadows of purple and blue shades respectively). Cluster I is the predominant group with the absence of *tetM*, and cluster II is the minor group that carries *tetM* gene.