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In-silico genomic characterization of *Vibrio alginolyticus* on a global scale: lineages, resistome, and virulome

Inhalt

Vibrio alginolyticus is a halophilic marine bacterium and an opportunistic pathogen for humans and marine organisms. Recently, it has been increasingly associated with outbreaks in aquaculture, impacting fish, shrimp, and shellfish production, particularly in Asia and Europe, while also posing zoonotic risks through contaminated seafood. Rising seawater temperatures and intensive farming practices may favor its persistence and dissemination worldwide. Here, we performed a genomic characterization of 1,250 *V. alginolyticus* genomes, including isolates recovered from sharks (n=5) and coastal upwelling events (n=9) in Rio de Janeiro/Brazil, together with publicly available genomes from GenBank. An SNP-based phylogenomic tree revealed the existence of spatiotemporally distributed lineages spanning the three One Health axes. Importantly, several lineages circulating among clinical, environmental, and animal sources harbored a complete Type III Secretion System, its effectors, and genes related to adhesion/colonization, indicating a potentially pathogenic profile. Moreover, we identified an integrative conjugative element carrying multiple antibiotic resistance genes (*ant*, *aph*, *veb-1*, *vim-71*, *arr-2*, *floR*, and *sul2*) in a genome belonging to a lineage detected in China, Canada, and Brazil (2014-2024) from different sources. Our findings show that this opportunistic pathogen has the potential to emerge with virulence and antibiotic resistance traits across One Health axes worldwide.

Keywords

Vibrio; genomic epidemiology; ARG; virulence; T3SS; ICE

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Postdoc

Junior Scientist Status

No, I am not a Junior Scientist.

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