Draft genome sequence of *Vibrio vulnificus* H1828/94, a clinical isolate of multidrug-resistant emerging pathogenic isolates

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Dear Editor,

Here we report the draft genome of *V. vulnificus* H1828/94, a clinical isolate from Hamburg, Germany. Based on the genome we predicted 16 potential antimicrobial resistant genes including multidrug resistance and 43 virulence genes.

The genus *Vibrio* belongs phylogenetically to the Gammaproteobacteria and consists typically of facultative anaerobic, motile, curved rods with single polar flagellum. Among the members of this genus, twelve species have been reported to be pathogenic to humans. From those, only *Vibrio cholerae* serotypes O1/O139 cause the disease cholera. Other most important potentially pathogenic *Vibrio* species are subtypes of *V. cholera* (different non-O1/O139 serotypes NOVC), *V. vulnificus*, *V. parahaemolyticus* and *V. alginolyticus*. These organisms are common planktonic and benthic bacteria found in the freshwater-saltwater transitions and can cause infections in humans which are usually associated with the consumption of raw or undercooked shellfish or by direct contact with water. In contrast to other pathogens are infections caused by *V. vulnificus* currently strongly increasing since it prefers to grow in brackish, (< 25 g/L NaCl) warmer (> 15°C) water and therefore profit from current climate change [1].

A paired-end library was prepared from the genomic DNA of *V. vulnificus* H1828/94, which was isolated from an infected patient. The high number of virulence genes is expected since *V. vulnificus* H 1828/94, was isolated from an infected patient.

Determining whether *Vibrio vulnificus* is a potential pathogen when isolated from the environment is difficult since also strains that phylogenetically belong to the species *Vibrio vulnificus* can be nonpathogenic despite different biotypes. A commonly used gene for phylogenetic assignment is HSP60 [3]. The HSP60 phylogeny of revealed a high identity with *V. vulnificus* FDAARGOS 119, *V. vulnificus* CG27, *V. vulnificus* CG62, *V. vulnificus* MO6-24/O and *Vibrio vulni* H1828/94, was isolated from an infected patient.

In conclusion, the genome of *V. vulnificus* H1828/94 carries clinically significant genes associated with pathogenicity and antimicrobial resistance. HSP60 gene analysis of *V. vulnificus* H1828/94 supports the assumption that *Vibrio vulnificus* lineage (based on HSP60) contains strains with a significant potential for infection [5].
H1828/94 revealed a close relationship to environmental and clinical strains that all contain essential pathogenicity factors.

**Transparency declaration**

The authors state no conflict of interest.

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