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 *Gammproteobacteria* 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 ordered from the German Collection of Microorganisms and Cell Cultures GmbH, and sequenced using a V3 kit on a NextSeq400 platform (Illumina, Inc.,). *De novo* assembly of the *V. vulnificus* H1828/94 genome was prepared as described previously [2] and annotated using the online platform IMG (https://img.jgi.doe.gov/cgi-bin/mer/main.cgi). The draft genome of *V. vulnificus* H1828/94 is about 4.8 Mbp long and has a GC content of 46.9%. A total of 4264 coding genes were identified in the genome, consisting of 3593 proteins coding genes with functional prediction and 671 new genes. Moreover, 96 RNA genes were detected, consisting of 85 transfer RNA and 8 ribosomal RNA genes. PathoFact identified 43 virulence genes of the category 1 and 2 and 16 antimicrobial genes including multidrug resistance. 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 *HSP*60 [3]. The *HSP*60 phylogeny of revealed a high identity with *V. vulnificus* FDAARGOS 119, *V. vulnificus* CG27, *V. vulnificus* CG62, *V. vulnificus* MO6-24/O and *Vibrio vulnificus* Vv18080 (Fig. 1). The *Vibrio vulnificus* strains MO6-24/O, FDAARGOS 119, Vv18080 were all clinically isolated from infected humans whereas CG27, and CG62 are derived from oysters and seawater. However, CG62, and CG27 have been shown to contain the main virulence factors including *pil*F, *Viu*B and *Vuu*A [4] supporting that this *Vibrio vulnificus* lineage (based on *HSP*60) contains strains with a significant potential for infection [5].

In conclusion, the genome of *V. vulnificus* H1828/94 carries clinically significant genes associated with pathogenicity and antimicrobial resistance. *HSP*60 gene analysis of *V. vulnificus*

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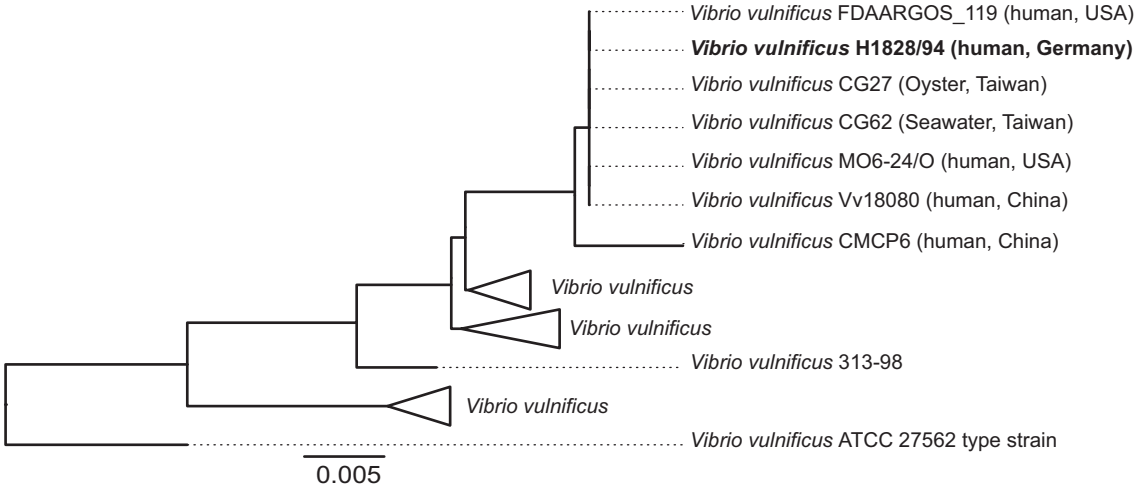

FIG. 1. Neighbor joining tree of the *HSP*60 gene based on 262 unambiguously aligned DNA columns. In bold is the strain H1828/94 all other strains are retrieved from Genbank, the type strain *Vibrio vulnificus* ATCC 27562 was set root. Sequence definition was complemented by the host and the country of origin.

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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