

Whole-Genome Sequence of the Fish Virulent Strain *Streptococcus iniae* IUSA-1, Isolated from Gilthead Sea Bream (*Sparus aurata*) and Red Porgy (*Pagrus pagrus*)

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***Streptococcus iniae* is a major fish pathogen that produces invasive infections that result in economic losses in aquaculture. In this study, the draft genome sequence of *Streptococcus iniae* strain IUSA-1, isolated from a natural outbreak affecting gilthead sea bream (*Sparus aurata*) and red porgy (*Pagrus pagrus*), is presented.**

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Streptococcus iniae is an important Gram-positive bacterium that is associated with acute and chronic mortality in marine and continental aquaculture (1), affecting more than 30 fish species (2, 3, 4), and has been reported in Asia, Australia, America, and Europe (3, 4). *S. iniae* causes invasive infections, producing high economic losses in aquaculture. *S. iniae* is also a zoonotic pathogen, causing soft tissue infections and sepsis in humans (5, 6). Gilthead sea bream and red porgy affected by *S. iniae* IUSA-1 showed clinical signs of hemorrhagic septicemia, lethargy, anorexia, abnormal swimming, exophthalmia, and sudden death, with mortality rates over 25% in red porgy and 10% in gilthead sea bream, and with acute meningoencephalitis as the main lesion. The strain was grown statically at 25°C in Trypticase soy agar supplemented with 0.5% (vol/vol) yeast extract. Cells were grown until the exponential phase for 24 h and harvested for the purification of genomic DNA using a DNeasy blood and tissue kit (Qiagen, Hilden, Germany). A whole-genome shotgun strategy was used with a Roche 454 GS-FLX Titanium sequencing platform (Macrogen, South Korea). A total of 137,532 reads (56,754,481 nucleotides) were generated, reaching a depth of 27.3-fold genome coverage. By using Roche's software GS *de novo* assembler (v2.6), they were assembled into 455 contigs; 296 of these were >500 bp, with bases having quality scores of ≥ 40 . The genome of *S. iniae* IUSA-1 is composed of 2.22 Mb, with an average G+C content of 36.3%.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/

GenBank under the accession no. [AOCT00000000](https://www.ncbi.nlm.nih.gov/nuclseq/AB684200). The version described in this paper is the second version, [AOCT02000000](https://www.ncbi.nlm.nih.gov/nuclseq/AB684200).

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