The genus *Weissella* consists of Gram-positive, catalase-negative, non-spore-forming, nonmotile bacteria with irregular or cocoid heterofermentative rod morphologies (1). *Weissella* species are common in diverse nutrient-rich environments, including fermented foods, soil, and the intestines of many animals, including humans (2). *Weissella confusa* strains have infrequently been reported to cause infections in both humans (3–5) and non-human primates (6); however, members of the genus are not typically associated with disease. Novel *Weissella* sp. bacteria have recently been associated with disease outbreaks in rainbow trout (*Oncorhynchus mykiss*) at commercial farms in China, Brazil, and the United States. Each of these outbreaks occurred at commercial rainbow trout farms and caused high levels of morbidity and mortality. The origin of the bacteria associated with these outbreaks is unknown, but 16S rRNA sequences from the Brazilian, Chinese, and U.S. isolates are >99% identical, suggesting a high level of genetic similarity among strains (Welch and Good, submitted). The trout isolates also show >99% 16S sequence similarity to *W. ceti* sp. nov., which was recently isolated from beaked whales (9), and therefore, the whale and fish isolates may constitute a single species. The occurrence of this pathogen on three continents over a relatively short period (5 years) suggests that weissellosis is a rapidly emerging disease of farmed rainbow trout. Comparison of the genome sequences of the U.S., Brazilian, and Chinese strains will therefore, the whale and fish isolates may constitute a single species, isolated from the southeastern United States.

**Results of comparative analysis highlighted several putative virulence factors, which do not have homologs encoded in any of the other sequenced *Weissella* genomes. These include five collagen adhesins (WCNC_00912, WCNC_00917, WCNC_00922, WCNC_05547, and WCNC_06207), a platelet-associated adhesin (WCNC_01820), and a mucus-binding protein (WCNC_01840).**

**Nucleotide sequence accession numbers.** This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number ANCA00000000. The version described in this paper is the first version, ANCA01000000.

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