Genome of a European Fresh-Vegetable Food Safety Outbreak Strain of *Salmonella enterica* subsp. *enterica* Serovar Weltevreden[∇]

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The genome of *Salmonella enterica* subsp. *enterica* serovar Weltevreden strain 2007-60-3289-1 was sequenced. The genome sequence of this fresh-vegetable isolate from Scandinavia will be useful for the elucidation of plant host factors in comparison to other serovars of *S. enterica* subsp. *enterica*.

Food-borne *Salmonella enterica* subsp. *enterica* serovars are a major cause of human gastroenteritis worldwide. Outbreaks have been traced to consumption of meat, egg, dairy, and plant products that have been contaminated during the production or processing stage. A diversity of serovars has been implicated (5). *Salmonella enterica* subsp. *enterica* serovar Weltevreden has emerged as an important food-borne pathogen in Southeast Asia (2, 6, 8) and Europe. *S.* Weltevreden was identified as the cause of a recent gastroenteritis outbreak in Scandinavia associated with contaminated alfalfa sprouts and fresh salad (3). Here, we report the complete genome of this *S.* Weltevreden outbreak strain, 2007-60-3289-1 (1).

Whole-genome shotgun sequencing was performed with a combined strategy using 454 single-end sequencing technology and Illumina paired-end technology (GATC, Konstanz, Germany). Totals of 270,589 and 6,442,668 reads were used to generate a draft assembly using Lasergene NGen version 2.2.0 (DNASTAR, Madison, WI), with overall coverages of 19.0- and 47.1-fold, respectively. Contigs were linked using complementary information from the draft genome sequences of *S.* Weltevreden SL484 and *Salmonella enterica* subsp. *enterica* serovar Dublin CT_02021853, followed by realignment using both sets of reads to confirm linkage. Final genome assembly after linkage resulted in 67 contigs with, in total, 4,922,273 bp ($N_{50} = 196,931$ bp). The *S.* Weltevreden 2007-60-3289-1 genome has a G+C content of 52.1%, with an estimated 4,858 coding sequences (CDS). Putative functions of encoding genes were automatically assigned using the GenDB annotation pipeline (7).

Salmonella pathogenicity islands (SPI) 1 to 6, 9, 11, 13, 14, 17, and 19 were detected in this strain, containing genes necessary for host-cell invasion and intracellular pathogenesis (4). The genome contains several phage-gene-containing regions and genomic islands unique for *S.* Weltevreden. These genomic islands encode mainly hypothetical proteins or conserved proteins with unknown function. A novel *Salmonella* plasmid, pSW82 (81,965 bp, with 48.8% G+C content), which contains 93 CDS, including genes encoding typical plasmid maintenance and stability proteins, (remnants of) transposases and integrases, and a two-gene type II nonribosomal peptide synthase/polyketide synthase, was identified.

The genome sequence of *S.* Weltevreden strain 2007-60-3289-1 will be used for comparative genomic analysis of this fresh produce isolate with the scallop isolate *S.* Weltevreden SL484 and other publically available *S. enterica* subsp. *enterica* serovar genomes. Serovar-discriminatory sequences from the *Salmonella* pan-genome will be developed as targets for specific detection of *S.* Weltevreden strains.

Nucleotide sequence accession numbers. The 66 contigs of the draft chromosome of *S. enterica* subsp. *enterica* serovar Weltevreden strain 2007-60-3289-1 were deposited in the EMBL database under accession numbers FR775188 through FR775253; the plasmid pSW82 sequence was deposited under accession number FR775255.

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