

Characterization of *Serratia* species isolated from fresh vegetables using genomics

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Bacteria of the genus *Serratia* (*S.*) are motile and non-endospore forming gram-negative rods. They belong to the gamma-proteobacteria and are members of the *Enterobacteriaceae* family. At the time of writing, 19 species of the genus *Serratia* have been described, with *S. oryzae* as the latest novel species of this genus [1]. *Serratia* strains have been isolated from various sources, including water [2], plants [3] and animals [4]. Some species, i.e. *S. marcescens*, *S. liquefaciens* and *S. odorifera* are considered to be opportunistic pathogens and have been associated with various human infections [5]. Among the *Serratia* species, *S. marcescens* is particularly well-known to be a common clinical isolate [6]. Some of the clinical isolates of *S. marcescens* were found to carry resistance genes toward quinolone antibiotics and beta lactam antibiotics, including genes encoding extended-spectrum beta lactamases (ESBL [7]. In this study, we isolated 17 *Serratia* strains from fresh produce including herbs, salads, cucumbers, carrots and mixed salads. Most of the strains (> 60 %) showed resistance to either ampicillin or cefotaxime. 58.8% of strains were resistant to tetracycline, while < 30% of strains showed resistances to streptomycin, tobramycin and chloramphenicol. Strains were generally sensitive to meropenem, ofloxacin and gentamicin. The genomes of 7 of the 17 strains were sequenced using an Illumina MiSeq and genome sizes ranged from 5.0 to 5.4 Mbp. One of the strains was also completely sequenced using PacBio sequencing. Genome sequence analysis showed that tetracycline resistance generally relied on the presence of *tet(41)* genes. Although some quinolone (*qnrS* and *qnrB*-types) and aminoglycoside (*aac(6')-Ic*) resistance genes could be identified, these genes also could occur in species which were phenotypically not resistant, indicating that other resistance genes (mechanisms) might also play a role. Phylogenomics done with whole genome sequences showed that most species belonged to *S. marcescens*, but a potentially novel species and one *S. liquefaciens* strain were also identified.

1. Zhang CW, Zhang J, Zhao JJ, Zhao X, Zhao DF, Yin HQ, Zhang XX: ***Serratia oryzae* sp. nov., isolated from rice stems**. *Int J Syst Evol Microbiol* 2017, **67**(8):2928-2933.
2. Kampfer P, Glaeser SP: ***Serratia aquatilis* sp. nov., isolated from drinking water systems**. *Int J Syst Evol Microbiol* 2016, **66**(1):407-413.
3. Grimont PAD, Grimont F, Starr MPJCM: ***Serratia ficaria* sp. nov., a bacterial species associated with Smyrna figs and the fig wasp *Blastophaga psenes***. 1979, **2**(5):277-282.

4. Garcia-Fraile P, Chudickova M, Benada O, Pikula J, Kolarik M: **Serratia myotis sp. nov. and Serratia vespertilionis sp. nov., isolated from bats hibernating in caves.** *Int J Syst Evol Microbiol* 2015, **65**(Pt 1):90-94.
5. Grimont F, Grimont PAD: **The Genus Serratia.** In: *The Prokaryotes: Volume 6: Proteobacteria: Gamma Subclass.* Edited by Dworkin M, Falkow S, Rosenberg E, Schleifer K-H, Stackebrandt E. New York, NY: Springer New York; 2006: 219-244.
6. Iguchi A, Nagaya Y, Pradel E, Ooka T, Ogura Y, Katsura K, Kurokawa K, Oshima K, Hattori M, Parkhill J *et al*: **Genome evolution and plasticity of Serratia marcescens, an important multidrug-resistant nosocomial pathogen.** *Genome Biol Evol* 2014, **6**(8):2096-2110.
7. Moradigaravand D, Boinett CJ, Martin V, Peacock SJ, Parkhill J: **Recent independent emergence of multiple multidrug-resistant Serratia marcescens clones within the United Kingdom and Ireland.** *Genome research* 2016, **26**(8):1101-1109.