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Raghupathi, Prem Krishnan; Herschend, Jakob; Røder, Henriette Lyng; Sørensen, Søren Johannes; Burmølle, Mette

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Genome Sequence of Kocuria varians G6 Isolated from a Slaughterhouse in Denmark

Prem K. Raghupathi, Jakob Herschend, Henriette L. Røder, Søren J. Sørensen, Mette Burmølle
Section for Microbiology, Department of Biology, University of Copenhagen, Copenhagen, Denmark

We report here the first draft genome sequence of Kocuria varians G6, which was isolated from a meat chopper at a small slaughterhouse in Denmark. The 2.90-Mb genome sequence consists of 95 contigs and contains 2,518 predicted protein-coding genes.

Kocuria varians is a Gram-positive bacterium belonging to the family Micrococccineae. Kocuria species are ubiquitous and are highly adapted to their ecological niches (1). K. varians is predominately isolated from different food-processing plants, e.g., milk-processing (2), fermented meat (3), and beef-processing plants (4). In these industrial settings, K. varians is often found in biofilms, and it is reported to favor both attachment and detachment including 10 genes coding for antibiotic resistance and 7 clustered regularly interspaced short palindromic repeat (CRISPR) elements, indicating the influence of phage exposure on the adaptation of this strain. Sixty-eight genes are involved in the stress responses of the bacterium. Functional comparison on the RAST server revealed the closest neighbors of K. varians to be Kocuria rhizophila DC2201, followed by K. rhizophila P7-4, Rothia dentocariosa ATCC 17931, and Arthrobacter aurescens TC1. Further work with this genome and comparisons to other Kocuria species will give more insights into the adaptation and evolution of K. varians to different environments.

Nucleotide sequence accession numbers. The whole-genome shotgun project for K. varians G6 has been deposited at the European Nucleotide Archive (ENA) under the contig accession numbers CZJX01000001 to CZJX01000095. The version described in this paper is the first version.

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REFERENCES

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