Draft genome sequences of two Kocuria isolates, K. salsicia G1 and K. rhizophila G2, isolated from a slaughterhouse in Denmark

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Kocuria rhizophila and Kocuria salsica are Gram-positive, cocoid, spherical saprotrophic bacteria belonging to the family Micrococccinaceae. Kocuria species are ubiquitous and highly adapted to their ecological niches (1) and are mainly identified in soil samples (2), clinical specimens (3, 4), fermented food (5, 6), and as members of the oral and skin flora (7). K. rhizophila is also commonly used as a standard quality control strain for antimicrobial susceptibility testing (2). Currently, there is one complete genome and one draft genome sequence publicly available of K. rhizophila: K. rhizophila DC2201 (2) and K. rhizophila P7-4 (1). Here, we present the draft assembly of K. salsica G1 and K. rhizophila G2, isolated from a slaughterhouse in Denmark (8).

The whole-genome sequencing libraries were prepared using the Nextera XT kit (Illumina, USA), according to the manufacturer’s recommendations, and then sequenced as part of the flow cell, as 2 \times 250-base paired-end reads using the Illumina MiSeq (Illumina) technology. The reads were cleaned and trimmed using CLC Genomics Workbench 7 (CLC bio, Denmark). Quality-filtered reads were assembled using SPAdes version 3.5.0 (9). The annotations on the resulting contigs were performed on the RAST server (10) and RNAmer 1.2 (11) to check and screen for non-coding RNAs.

The assembly of K. salsica G1 resulted in 199 contigs at 27× coverage, with an average G+C content of 70.43%. K. rhizophila G2 is assembled into 87 contigs at 126× coverage, with an average G+C content of 70.81%. The annotated results from G1 predicted 2,565 coding sequences, with an average length of 971 bp (1,172 coding sequences [CDSs] have functional predictions), 19 tRNA-coding genes, and 5 rRNA-coding genes. The predictions from G2 included 2,531 coding sequences, with an average length of 955 bp (1,154 CDSs have functional predictions), 18 tRNA-coding genes, and 7 rRNA-coding genes. Both strains had single predicted copies of 16S and 23S rRNA genes, with the only difference in 5S rRNA gene copies, with 3 for G1 and 5 for G2. There are 359 and 358 predicted subsystems in the genomes of G1 and G2, respectively. Metabolic network comparisons revealed 1,774 putative protein-encoding genes (PEGs) conserved in both G1 and G2 genomes. In a function-based comparison to the genome of DC2201, the genomes of G1 had 179 unique PEGs and 147 PEGs in G2. The main differences observed in a comparison of K. salsica G1 to K. rhizophila DC2201 and K. rhizophila G2 were the presence of sequences encoding clustered regularly interspaced short palindromic repeat (CRISPR) elements, iron acquisition, and metabolism subsystems identified in G1 only. These suggest a prominent influence of phage exposure and possible adaptation mechanisms of isolate G1 to a more densely populated environment, such as the animal gut. Further work with these genomes is expected to facilitate the identification and understanding of genes associated with adaptive mechanisms of these strains and biofilm formation.

**Nucleotide sequence accession numbers.** The whole-genome sequencing (WGS) projects for K. salsica G1 and K. rhizophila G2 have been deposited at the European Nucleotide Archive (ENA) under the contig accession numbers CZJU01000001 to CZJU01000199 and CZJW01000001 to CZJW01000087, respectively. The versions described in this paper are the first versions.

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**REFERENCES**

1. Kim WJ, Kim YO, Kim DS, Choi SH, Kim DW, Lee JS, Kong HJ, Nam BH, Kim BS, Lee SJ, Park HS, Chae SH. 2011. Draft genome sequence of Kocuria rhizophila 7-4. J Bacteriol 193:4286–4287.
2. Takarada H, Sekine M, Kosugi H, Matsuo Y, Fujisawa T, Osumi S, Kishi E, Shimizu A, Tsukatani N, Tanikawa S, Fujita N, Harayama S. 2008. Complete genome sequence of the soil actinomycete Kocuria rhizophila. J Bacteriol 190:4139–4146. http://dx.doi.org/10.1128/JB.01853-07.
3. Becker K, Rutsch F, Uekötter A, Kipp F, König J, Marquardt T, Peters G, Von Eiff C. 2008. Kocuria rhizophila adds to the emerging spectrum of micrococcal species involved in human infections. J Clin Microbiol 46:3537–3539. http://dx.doi.org/10.1128/JCM.00823-08.
4. Dunn R, Bares S, David MZ. 2011. Central venous catheter-related bacteremia caused by Kocuria kristinae: case report and review of the literature. Ann Clin Microbiol Antimicrob 10:31. http://dx.doi.org/10.1186/1476-0711-10-31.
5. Yun JH, Roh SW, Jung MJ, Kim MS, Park EJ, Shin KS, Do Nam YD, Bae JW. 2011. Kocuria salsica sp. nov., isolated from salt-fermented seafood. Int J Syst Evol Microbiol 61:286–289. http://dx.doi.org/10.1099/ijsem.0.021469-0.
6. Park EJ, Kim MS, Roh SW, Jung MJ, Bae JW. 2010. Kocuria atrinae sp.
nov., isolated from traditional Korean fermented seafood. Int J Syst Evol Microbiol 60:914–918. http://dx.doi.org/10.1099/ijs.0.014506-0.
7. Szczerba I. 2003. Occurrence and number of bacteria from the Micrococcus, Kocuria, Nesterenkonia, Kytococcus and Dermacoccus genera on skin and mucous membranes in humans. Med Dosw Mikrobiol 55:67–74.
8. Røder HL, Raghupathi PK, Herschend J, Brejnrod A, Knochel S, Sørensen SJ, Burmølle M. 2015. Interspecies interactions result in enhanced biofilm formation by co-cultures of bacteria isolated from a food processing environment. Food Microbiol 51:18–24. http://dx.doi.org/10.1016/j.fm.2015.04.008.
9. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 19:455–477.
10. Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, Edwards RA, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R. 2014. The SEED and the rapid annotation of microbial genomes using subsystems technology (RAST). Nucleic Acids Res 42:D206–D214. http://dx.doi.org/10.1093/nar/gkt1226.
11. Lagesen K, Hallin P, Rødland EA, Staerfeldt H-H, Rognes T, Ussery DW. 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Res 35:3100–3108. http://dx.doi.org/10.1093/nar/gkm160.