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 salsicia are Gram-positive, coc- 
coidal, spherical saprotrophic bacteria belonging to the family 
Micrococccineae. Kocuria species are ubiquitous and highly adapted 
to their ecological niches (1) and are mainly identified in soil sam-
ples (2), clinical specimens (3, 4), fermented food (5, 6), and as 
members of the oral and skin flora (7). K. rhizophila is also com-
monly 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 
report here the draft genome sequences of Kocuria salsicia G1 and 
Kocuria rhizophila G2, isolated from a meat chopper at a small slaughterhouse in Denmark. The two annotated genomes are 2.99 Mb and 2.88 Mb in size, respectively.

The whole-genome sequencing libraries were prepared using the Nextera XT kit (Illumina, USA), according to the manufactur-
er’s recommendations, and then sequenced as part of the flow cell, 
as 2 × 250-base paired-end reads using the Illumina MiSeq (Illu-
mina) 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. salsicia 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 cop-
ies 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, respect-
ively. Metabolic network comparisons revealed 1,774 putative 
protein-encoding genes (PEGs) conserved in both G1 and G2 
ge
domes. 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. salsicia 
G1 to K. rhizophila DC2201 and K. rhizophila G2 were the pres-
ence of sequences encoding clustered regularly interspaced short 
palindromic repeat (CRISPR) elements, iron acquisition, and me-
tabolism subsystems identified in G1 only. These suggest a prom-
inent influence of phage exposure and possible adaptation mech-
isms of isolate G1 to a more densely populated environment, 
such as the animal gut. Further work with these genomes is ex-
pected 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. salsicia 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, respec-
tively. The versions described in this paper are the first versions.

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