

Supplemental Data

Material & Methods

Phage gene annotation

Prophage regions were derived from the web tool PHASTER (PHAge Search Tool - Enhanced Release, <http://phaster.ca>) which is a more efficient and faster version of PHAST [1]. The columns “COMPLETENESS (score)” and “SPECIFIC_KEYWORD” of the summary file were screened for a score > 90 and for the main structural phage components (portal, capsid/head, tail) to distinguish between prophage and prophage-like regions. Additionally, NCBI based annotation, BLASTn based comparison against the NCBI nt-database and functional assignments to KEGG and GO terms, using BlastKOALA (version 2.1, <https://www.kegg.jp/blastkoala/>) and InterProScan 5 (version 5.32-70.0, <https://www.ebi.ac.uk/interpro/interproscan.html>), respectively, were considered to identify tailocins and its most common phage [2,3,4].

Detection of orthologous protein clusters

Orthologous clusters of phage proteins were obtained with an in-house pipeline, aligning the respective protein sequences of the strain *Kosakonia radicincitans* DSM16656 against the proteins of the nine closely related strains of its genus: *K. radicincitans* Ola 51, GXGL-4A, YD4, UMEnt01/12; *K. oryziphila* REICA_142; *K. oryzendophytica* REICA_082; *K. sacchari* SP1, BO-1; and *K. oryzae* KO348 in a pairwise manner using BLASTp+ with thresholds for identity of 35%, for coverage of 60% and for an e-value cut-off of $1e^{-5}$ [4]. Finally, reciprocal best hits (RBH) were selected and their genomic location verified. To visualize the detected and manual

revised syntenic gene clusters of the considered orthologous protein clusters in each genome a SVG file was generated.

Transmission electron microscopy of K. radicincitans DSM 16656 tailocins

Bacterial cultures were grown on LB (Luria-Bertani) agar over night at 28°C [5]. For electron microscopy, 1 cm from the colonies' outer border was homogenized in 0.1 M phosphate, pH 7.0 containing 2% polyvinylpyrrolidone MW 11.000 and 0.2% sodium sulfite. Bacteria and tailocins were adsorbed by floating a pioloform carbon-coated copper grid for 5 min on the preparation. After incubation the grids were washed with deionized water. For negative contrast the grids were stained with 1% uranyl acetate in ultrapure water and dried. Grids were examined in a Tecnai G2 Spirit electron microscope at 80 kV. Images were taken with a 2K Veleta camera. Brightness and contrast were adjusted when necessary using Adobe Photoshop CS6.

References

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3. Kanehisa M, Sato Y, Morishima K. BlastKOALA and GhostKOALA: KEGG tools for functional characterization of genome and metagenome sequences. *J. Mol. Biol.* 2016; 428, 726-731.
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