**Genome mining reveal secondary metabolites of antarctic bacterium *Streptomyces albidoflavus* ANT\_B131 related to antimicrobial and antiproliferative activities.**

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**SUPPORT INFORMATION**



Supplementary Figure. 1. Phylogenetic tree based on the phylogenetic analysis of the 16S ribosomal RNA gene sequence of the ANT\_B131 bacteria isolated from Antarctic and related microorganisms. Bootstrap values (1000 repetitions, showed as %) are listed. Scale bar represents 1 nucleotide substitution per 100 nucleotides position. *Saccharopolyspora gregorii* NCIB 12823 was used as outgroup.



Supplementary Figure 2. MS/MS match for surugamide A between GNPS database (green) and *S. albidoflavus* ANT\_B131 extracts (black).



Supplementary Figure 3. MS/MS match for surugamide D between GNPS database (green) and *S. albidoflavus* ANT\_B131 extracts (black).



Supplementary Figure 4. MS/MS match for desferrioxamine B between GNPS database (green) and *S. albidoflavus* ANT\_B131 extracts (black).



Supplementary Figure 5. MS/MS match for desferrioxamine E between GNPS database (green) and *S. albidoflavus* ANT\_B131 extracts (black).

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Supplementary Figure 6. Extracted ion chromatograms of *m/z* 143.08 for extracts of (A) culture media (control) and (B) *S. albidoflavus* ANT\_B131. (C) Mass spectrum obtained for ectoine. (D) MS/MS spectrum of ion [M+H]+ *m/z* 143.0816. (E) MS/MS spectrum of ectoine in Mass MassBank of North America database (adapted from https://mona.fiehnlab.ucdavis.edu/spectra/display/CCMSLIB00005435933 - acessed 18th September of 2020).



Supplementary Figure 7. Extracted ion chromatograms of *m/z* 912.62 for (A) culture media (control) and (B) *S. albidoflavus* ANT\_B131. (C) Mass spectrum obtained for surugamide A.(D) MS/MS spectrum of ion [M+H]+ *m/z* 912.6295. (E) Typical mass fragments of surugamide A.



Supplementary Figure 8. Extracted ion chromatograms of *m/z* 898.61 for (A) culture media (control) and (B) *S. albidoflavus* ANT\_B131. (C) Mass spectrum obtained for surugamide D.(D) MS/MS spectrum of ion [M+H]+ *m/z* 898.6117. (E) Typical mass fragments of surugamide D.



Supplementary Figure 9. Extracted ion chromatograms of *m/z* 585.32 for (A) culture media (control) and (B) *S. albidoflavus* ANT\_B131. (C) Mass spectrum obtained for desferrioxamine B.(D) MS/MS spectrum of ion [M-2H+Al]+ *m/z* 585.3204. (E) Typical mass fragments of desferrioxamine B + Al.



Supplementary Figure 10. Extracted ion chromatograms of *m/z* 623.34 for (A) culture media (control) and (B) *S. albidoflavus* ANT\_B131. (C) Mass spectrum obtained for desferrioxamine E.(D) MS/MS spectrum of ion [M+Na]+ *m/z* 623.3403.

Supplementary Table 1. Sequence accession number of genes used in Multilocus Sequence Analysis

|  |  |  |
| --- | --- | --- |
| **Name** | **Strain** | **Accession number GenBank**  |
| **atpD** | **gyrB** | **recA** | **rpoB** | **trpB** |
| *Streptomyces daghestanicus* | NRRL B-5418 | KJ137021 | KJ137038 | KJ137055 | KJ137072 |  KJ137089 |
| *Streptomyces albidoflavus* | NRRL B-1271 | KT384451 | KT384800 | KT385148 | KT388770 | KT389120 |
| *Streptomyces violascens* | NRRL B-2700 | KT384752 | KT385100 | KT385454 | KT389072 | KT389421 |
| *Streptomyces violaceochromogenes* | NRRL B-5427 | KT384748 | KT385096 | KT385450 | KT389068 | KT389417 |
| *Streptomyces purpurascens* | NRRL B-12230 | KT384696 | KT385046 | KT385397 | KT389017 | KT389365 |
| *Streptomyces luteogriseus* | NRRL B-12422 | KT384632 | KT384981 | KT385332 | KT388952 | KT389301 |
| *Streptomyces hawaiiensis* | NRRL B-1988 | KT384592 | KT384941 | KT385290 | KT388912 | KT389261 |
| *Streptomyces levis* | NRRL B-16370 | KT384621 | KT384970 | KT385320 | KT388941 | KT389290 |
| *Streptomyces violaceus* | JCM 4533 | LC381981 | LC381982 | LC381983 | LC381984 |  |
| *Streptomyces iakyrus* | NRRL B-3317 | KT384600 | KT384949 | KT385298 | KT388920 | KT389269 |
| *Streptomyces massasporeus* | NRRL B-3300 | KT384636 | KT384985 | KT385336 | KT388956 | KT389305 |
| *Streptomyces roseoviolaceus* | NRRL B-12177 | KT384710 | KT385060 | KT385411 | KT389031 | KT389379 |
| *Streptomyces janthinus* | NRRL B-3365 | KT384604 | KT384953 | KT385303 | KT388924 | KT389273 |
| *Streptomyces carpinensis* | NRRL B-16921 | KT384503 | KT384852 | KT385200 | KT388822 | KT389172 |
| *Streptomyces cinerochromogenes* | NRRL B-16928 | KT384514 | KT384863 | KT385211 | KT388833 | KT389183 |
| *Streptomyces parvulus* | NRRL B-1628 | KJ196367 | KJ196369 | KJ196371 | KJ196373 | KJ196375 |
| *Streptomyces muensis* | JCM 17576 | KX784758 |  | KX784760 | KX784762 | KX784764 |
| *Streptomyces asterosporus* | NRRL B-24328 | KT384471 | KT384820 | KT385168 | KT388790 | KT389140 |

Supplementary Table 2. Pairwise correlation between whole genome of *S. albidoflavus* ANT\_B131 and phylogenetic closest strains *S. albidoflavus* SM254 and *S. albidoflavus* J1074.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Pairwise correlation between strains | ANIb (%) | ANIm (%) | TETRA | isDDH | Difference in %G+C |
| ANT\_B131 x SM254 | 97.41 | 97.78 | 0.99961 | 79.50 | 0.17 |
| ANTB\_131 x J1074 | 97.02 | 97.80 | 0.99952 | 79.60 | 0.15 |