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Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our [Editorial Policies](#) and the [Editorial Policy Checklist](#).

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- ☐ ☒ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- ☐ ☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- ☐ ☒ The statistical test(s) used AND whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- ☒ ☐ A description of all covariates tested
- ☐ ☒ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- ☐ ☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- ☐ ☒ For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- ☒ ☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- ☒ ☐ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- ☐ ☒ Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection

Ultra-high-performance liquid chromatography–diode array detection–quadrupole time-of-flight mass spectrometry (UHPLC–DAD–QTOFMS) was carried out on the Agilent Infinity 1290 UHPLC system (Agilent Technologies, Santa Clara, CA, USA). LC-MS data were collected by Agilent 6545 QTOF MS equipped with Agilent Dual Jet Stream electrospray ion source. NMR spectra were recorded on an 800 MHz Bruker Avance III spectrometer equipped with a TCI CryoProbe using standard pulse sequences. Specific rotations were acquired using Perkin-Elmer 241 polarimeter. IR data were acquired on Bruker Alpha FTIR spectrometer using OPUS version 7.2. X-ray data collection was performed on an Agilent Supernova Diffractometer using CuK α radiation.

Data analysis

Raw LC-MS/MS data were analyzed with Agilent MassHunter software. The annotation of known secondary metabolites in *Streptomyces* was conducted using GNPS. The X-ray data were processed and scaled using the CrysAlisPro software (Agilent Technologies) and the structure was solved using SHELXS and refined using SHELXL. The identification and annotation of all BGCs of *Streptomyces* secondary metabolites were carried out with antiSMASH 6.0. The BiG-FAM database and BiG-SCAPE software were used to identify the distribution of pta gene clusters in different bacteria and generate the pta-gene cluster family similarity network. The alignment of pta-containing *Streptomyces* genome sequences was performed using the whole-genome alignment plugin of the CLC Genomics Workbench version 22.0.2 (Qiagen). The networks of BiG-SCAPE and GNPS analysis were visualised using Cytoscape 3.9. The phylogenetic analysis was conducted by the online multiple sequence alignment tool MAFFT and visualised by iTOL v5. Significant analysis was performed with GraphPad Prism 9.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

The metabolomics data in this study were deposited at <https://massive.ucsd.edu> with the identifier MSV000090745. The genome sequence of each *Streptomyces* strain is available at NCBA and the accession number is noted in the supplementary information. Other data supporting the findings of this study are included in this published article and supplementary information. All raw and processed data will be made available upon request.

Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research](#).

Reporting on sex and gender

This information has not been collected and is not related to this study.

Population characteristics

This information has not been collected and is not related to this study.

Recruitment

This information has not been collected and is not related to this study.

Ethics oversight

This information has not been collected and is not related to this study.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size

Sample size was predetermined based on standard practices in this field. No statistical analysis was performed to select sample size.

Data exclusions

No data were excluded from the analyses

Replication

Replicate experiments were successful.

Randomization

Randomization was not relevant to this study. The production of these three *Streptomyces* strains we studied was stable during fermentation.

Blinding

As our investigation objects are bacteria and plant, blinding was not relevant to our study.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

Methods

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging