

NPASS database update 2023: quantitative natural product activity and species source database for biomedical research

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ABSTRACT

Quantitative activity and species source data of natural products (NPs) are important for drug discovery, medicinal plant research, and microbial investigations. Activity values of NPs against specific targets are useful for discovering targeted therapeutic agents and investigating the mechanism of medicinal plants. Composition/concentration values of NPs in individual species facilitate the assessments and investigations of the therapeutic quality of herbs and phenotypes of microbes. Here, we describe an update of the NPASS natural product activity and species source database previously featured in NAR. This update includes: (i) new data of ~95 000 records of the composition/concentration values of ~1 490 NPs/NP clusters in ~390 species, (ii) extended data of activity values of ~43 200 NPs against ~7 700 targets (~40% and ~32% increase, respectively), (iii) extended data of ~31 600 species sources of ~94 400 NPs (~26% and ~32% increase, respectively), (iv) new species types of ~440 co-cultured microbes and ~420 engineered microbes, (v) new data of ~66 600 NPs without experimental activity values but with estimated activity profiles from the established chemical similarity tool Chem-

ical Checker, (vi) new data of the computed drug-likeness properties and the absorption, distribution, metabolism, excretion and toxicity (ADMET) properties for all NPs. NPASS update version is freely accessible at <http://bidd.group/NPASS>.

INTRODUCTION

Natural products (NPs) are important sources of modern drug discovery (1,2). NP research facilitates the mechanistic investigation of herbal medicines (3,4). In particular, the knowledge of activity values of NPs and their derivatives against specific targets is important for structure-activity studies in drug discovery (5). This knowledge is also needed to assess the therapeutic effects of individual NPs (6), NP combinations (7) and medicinal herbs (8). The composition/concentration values of NPs in individual species facilitate the assessments and investigations of foods, medicinal herbs, and microbes. These include the nutritional, flavor, and beneficial quality of foods (9) and teas (10), the therapeutic potential of medicinal herbs (11), and the phenotype of microbial communities (12).

These investigations can be facilitated by the establishment of the quantitative NP activity and content databases, which include the NP activity and species sources database NPASS (13), the USDA Database for the Flavonoid Content of Selected Foods (<https://data.nal.usda.gov/dataset/usda-database-flavonoid->

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Table 1. Accumulation of NPs, source organisms, quantitative composition and biological activities in the latest and previous version of NPASS database

		NPASS-2018	NPASS-2023
Natural products (NPs)	NP (with activity values)	30 926	43 285 (increased by 40.0%)
	NP (without activity values)	–	51 128 (new)
	Total NPs	30 926	94 413 (increased by 205.3%)
Organisms	Natural organisms	25 041	31 690 (increased by 26.6%)
	Co-culture organisms	–	444 co-culture combinations (new)
	Engineered organisms	–	427 engineered species (new)
	Total organisms	25 041	32 561 (increased by 30.0%)
Organism-NP pairs	298 106	872 723 (increased by 192.8%)	
Activity records	446 552	958 866 (increased by 114.7%)	
Targets	5 863	7 753 (increased by 32.2%)	
The composition/concentration of NPs in individual species	–	95 004 quantity records (new)	
			- 398 organisms
			- 1 490 NP/NP Clusters
			- 15 292 NP-Organism pairs
Bio- and Chem-properties of NPs		1 Category	7 Categories
		- Physicochemical property	- Physicochemical properties
			- Medicinal chemistry properties (new)
			- ADMET properties (new)
NP similarity metrics		1 Category	2 Categories
		- Chemically structural similarity	- Chemically structural similarity
			- Biological similarity (new)

content-selected-foods-release-32-november-2015), the Unified Food Composition Database for the European Project ‘Stance4Health’ (14) and Flavonoid Database Based on Indonesian Foods (15). The usefulness of these databases can be further enhanced by expanded data coverage of activity values, species sources, and composition/content values for more variety of NPs and species. Moreover, there are a large number of NPs for which experimental activity values are not yet available. Nonetheless, computational methods such as chemical similarity have been established for estimating molecular activity values (16). Methods for evaluating the drug-likeness and the absorption, distribution, metabolism, excretion and toxicity (ADMET) properties have been developed to assess the drug development potential of active molecules (17–19). These tools may be employed for providing estimated activity values and drug-likeness scores of NPs.

Expanding the diversity of NP-producing sources is the fundamental driving force for the discovery of novel NPs (20). To this end, intensive efforts have been made for decades to explore new natural organisms (e.g. organisms of underexplored taxonomic space or novel organisms from extreme living environments like deep-sea sediments) (20). In recent years, new strategies are emerging as attractive lines of NP research, and these include: (i) co-cultures of multiple organisms for mimicking their natural living ecosystems (also termed as microbial consortia or co-cultivation), e.g. fermenting producer and inducer species together to mimic cell-cell communications for induction of novel NPs (21); (ii) genetic engineering of microorganisms through synthetic biology strategies, e.g. introducing synthetic genes to model strains, reprogramming their metabolic pathways, and activating silenced synthetic pathways (22,23). These new NP-producing sources provide either highly-expanded NP chemical diversity or optimized metabolic profiles, contributing to the discovery of many novel NPs or increased production yields of high-value NPs

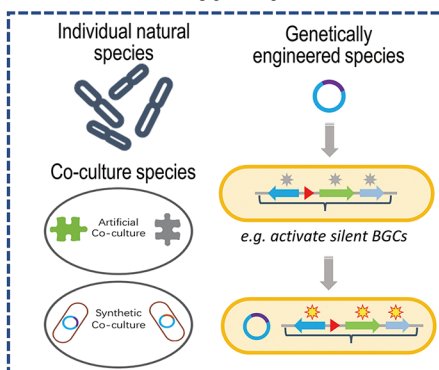
(e.g. biofuel, pharmaceuticals and industrial chemicals). However, current bioinformatics resources basically focus on NPs isolated from naturally individual species. There is a lack of an open-access database for data on NPs from species co-cultivations and engineered microorganisms.

We therefore conducted several major updates of the NPASS database (Table 1). The first is the addition of ~95 000 new records of the composition/concentration values of ~1 500 NPs/NP clusters in ~400 species. The second is the extended data of activity values of ~43 200 NPs against ~7 700 targets (~40% and ~32% expansion, respectively). The third is the expanded data of ~31 600 species sources of ~94 400 NPs (~26% and ~32% increase, respectively). The fourth is the new data of species types of ~440 co-cultured microbes and ~420 engineered microbes. The fifth is the new data of ~67 000 NPs without experimental activity values but with estimated activity profiles from the established bioactivity similarity tool Chemical Checker (16). The sixth is the computed drug-likeness properties and the absorption, distribution, metabolism, excretion and toxicity (ADMET) properties for all NPs using the established tool ADMETlab 2.0 (17). The key features of these updates were illustrated in Figure 1. A comparison of NPASS with several representative NP databases, including StreptomeDB (24), The Natural Products Atlas (25), CMNPD (26) and COCONUT (27) was provided in Table 2. NPASS is freely accessible at <http://bidd.group/NPASS>.

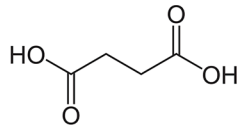
COMPOSITION/CONCENTRATION VALUES OF NATURAL PRODUCTS

Knowledge of the composition/concentration values of natural products is valuable in assessing the nutrition and health-beneficial quality of foods and medicinal plants. For instance, the plant family *Brassicaceae* includes well-known vegetables such as broccoli, cabbage, cauliflower, mustard, rapeseed, rocket and turnip, which were among the first plants cultivated and domesticated by humanity (28). These

A Different type species sources



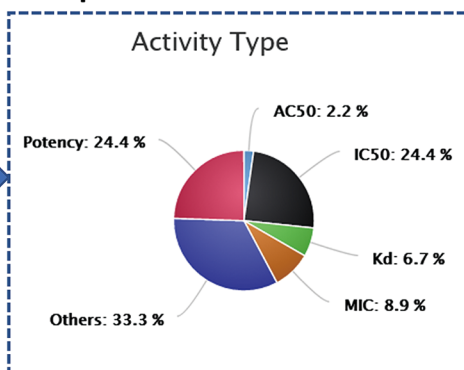
Succinic Acid



» Natural Product: [NPC236709](#)

Natural Product ID:	NPC236709
Common Name:	Succinic Acid
IUPAC Name:	butanedioic acid
Synonyms:	E363; Succinic Acid
Standard InChIKey:	KDYFGRWOOYBRFD-UHFFFAOYSA-N
Standard InChI:	InChI=1S/C4H6O4(CS-3(6)1-2-4(7)(8)1-2H2)(H,5,6)(H,7,8)
Canonical SMILES:	OC(=O)CCC(=O)O
Synthetic Gene Cluster:	CHEMBL578
CHEMBL Identifier:	1110-21952380
PubChem CID:	1110-21952380

B Experimental Bioactivities



C NP properties

Physi-Chem Properties	
Molecular Weight	118.07
MedChem Properties	
ADMET: Absorption score:	0.544
Caco-2	ADMET: Distribution
ADMET: Metabolism	
CYP1A2	ADMET: Excretion
ADMET: Toxicity	(CL): 4.976
hERG Blockers:	0.004
Human Hepatotoxicity (H-HT):	0.123
	T(1/2): 0.842

D NP concentration

» NP Quantity Composition/Concentration

Show 5 entries

Organism ID	NP ID	Organism Material Preparation	Organism Part	NP Quantity (Standard)	NP Quantity (Minimum)	NP Quantity (Maximum)	Quantity Unit	Reference
NPO10300	NPC236709	n.a.	Flowers	0.44 ± 0.01	n.a.	n.a.	mg/g	PMID[32156350]
NPO10300	NPC236709	n.a.	Flowers	0.52 ± 0.04	n.a.	n.a.	mg/g	PMID[32156350]
NPO42031	NPC236709	n.a.	Flowers	0.37 ± 0.01	n.a.	n.a.	mg/g	PMID[32156350]
NPO623	NPC236709	n.a.	Flowers	0.11 ± 0.00	n.a.	n.a.	mg/g	PMID[32156350]
NPO7269	NPC236709	n.a.	Fruits	0.478-0.977	n.a.	n.a.	g/L	PMID[31619015]

Showing 1 to 5 of 7 entries

Previous 1 2 Next

E Chemical & Bioactivity similarity landscape

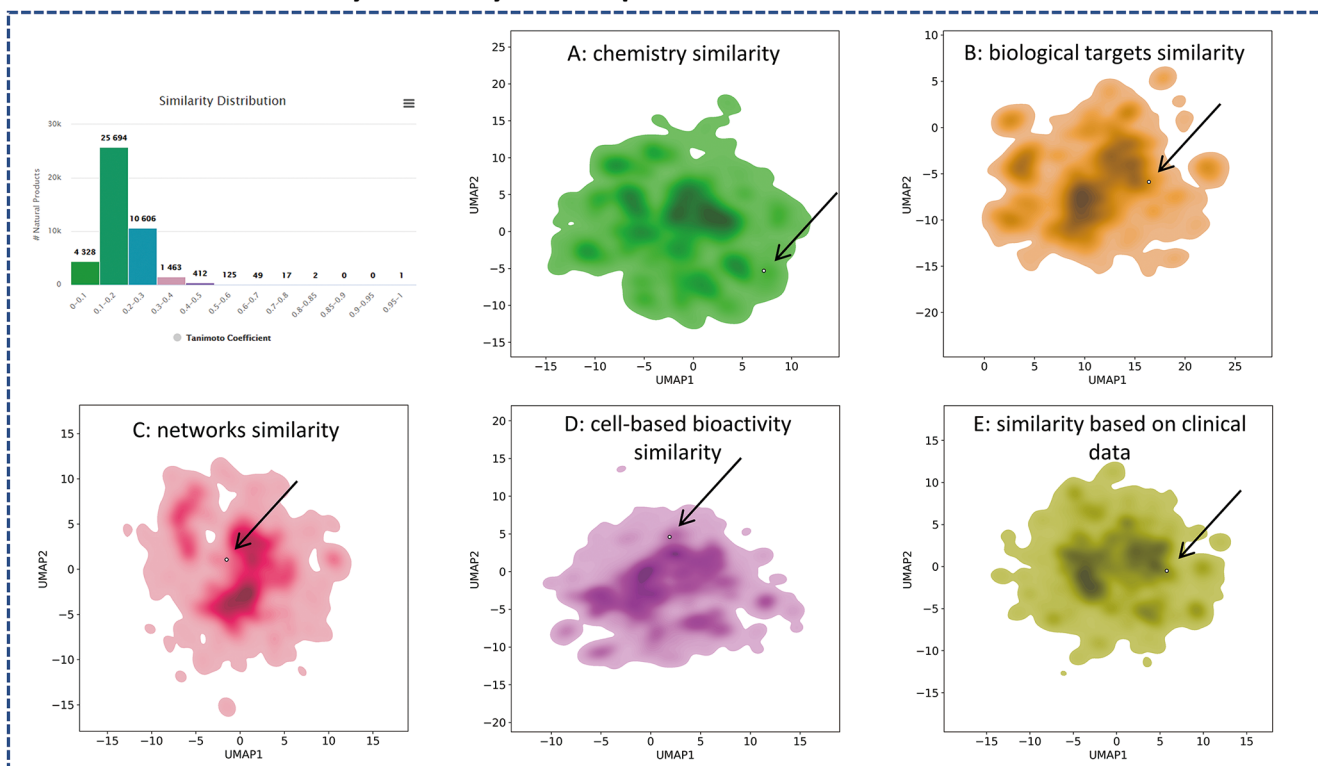


Figure 1. Illustration of key features of NPASS-2023 was shown using the example NP succinic acid. (A) Several types of species sources are included: individual natural species, co-cultured species and genetically engineered species. (B) Experiments-derived biological activities of NPs were significantly expended in this update. (C) In addition to physico-chemical properties, new property layers were calculated by ADMETlab 2.0. (D) Quantitative composition/concentration data of NPs in their producing species was included in this update. (E) In addition to traditional structure-based similarity, a five-level bioactivity similarity distribution was built based on Chemical Checker descriptors and visualized in 2D UMAP projection. The current NP was labeled with a small circle (indicated by those long arrows) in UMAP projections.

Table 2. Different features of representative NP databases

Database name		NPASS	StreptomeDB	The natural products atlas	CMNPD	COCONUT
Coverage of organism category		Diverse (plants, bacteria, metazoan, fungi)	Specialized (Streptomyces genus)	Specialized (bacteria, fungi)	Specialized (marine species, e.g. bacteria, fungi, algae, sponges)	Diverse (plants, bacteria, fungi, marine species, animals)
No. of organisms	Natural organisms	31 690	3302	1200	3354	n.a.
	Co-culture Organisms	444	n.a.*	n.a.	n.a.	n.a.
	Engineered Organisms	427	n.a.	n.a.	n.a.	n.a.
	Total organisms	32 561	3302	1200	3354	n.a.
No. of NPs		94 413	6524	32 552	31 561	1 136 517
No. of activity records		958 866	1 031	n.a.	72 349	n.a.
No. of quantity records		95 004	n.a.	n.a.	n.a.	n.a.
No. of organism-NP pairs		872 723	10 912	n.a.	n.a.	n.a.
No. of targets		7753	n.a.	n.a.	2652	n.a.
Properties of NPs	physicochemical properties	Y*	Y	N*	Y	N
	Medicinal chemistry properties	Y	N	N	N	N
	ADMET properties	Y	Y	N	Y	N
	Chemically structural similarity	Y	N	N	N	N
Similarity metrics	Biological similarity	Y	N	N	N	N
		2.0 (2023)	3.0 (2021)	2.0 (2022)	1.0 (2021)	1.0 (2022)
Latest version		2.0 (2023)	3.0 (2021)	2.0 (2022)	1.0 (2021)	1.0 (2022)

*Note: n.a. means not available; Y means this data category was included; N means this data category was not included.

vegetables contain chemical ingredients of high nutritional and health beneficial value. In particular, glucosinolates are one of the most important classes of secondary metabolites in the *Brassicaceae* family, and the compositions of these metabolites influence the level of protective and preventive effects against several cancer (28). Moreover, *Brassicaceae* plants contain an important inorganic micronutrient, Se, which serves as part of the active site of the antioxidant enzyme glutathione peroxidase, and the content of Se affects the antioxidant effects of the vegetables (28). Therefore, the experimentally determined composition/content of individual NPs in plants and microbes was searched from the PubMed database (29). These search results were obtained by using the keywords ‘composition’, ‘content’, ‘chemical characterization’, ‘biochemical characterization’, ‘phytochemical characterization’, ‘abundance’ or ‘profile’ in combination with ‘plant’, ‘herb’, ‘vegetable’, ‘fruit’, ‘microbe’ and ‘bacterium’.

CO-CULTURED AND ENGINEERED ORGANISMS FOR ENHANCED NP-PRODUCTION

In the genomic and synthetic biology era, strategies for the discovery of novel NPs are rapidly evolving (1). Optimization of cultivation systems and genetic modification of species are emerging strategies to expand the sources of NP discovery from traditional models (individual natural organisms) to more sophisticated ones (co-cultivation of multiple species and unnatural organisms). Naturally, microorganisms grow and function (e.g. producing specialized metabolites) in concert within their surrounding microbial ecosystem, rather than as individual/isolated species. Species communities can exert positive microbial interactions that benefit community members through several

mechanisms such as syntrophy, cooperation, mutualism, and commensalism (30). By recovering or designing specialized positive microbial interactions, co-culture systems can produce novel NPs or increase the yield of existing NPs through reshaping metabolic profiles of individual organisms (21,31). In addition, many synthetic gene clusters for high-value NPs biosynthesis are silenced in natural organisms. By activating silenced synthetic pathways or introducing synthetic enzyme genes, natural species can be engineered to produce high-value NPs more efficiently (22,32).

These strategies represent promising trends in NP research, which leverages large-scale mining of synthetic gene clusters to exploit biosynthetic potential and manipulate key genes or metabolic parameters to enable the production of novel NPs or increased NP yields (33–35). Therefore, we compiled NP yields or yield changes of NPs in co-cultured species and engineered species through an extensive search of PubMed. Finally, NPASS included 444 co-culture species combinations and 427 engineered species/strains manually extracted from 221 and 382 publications, respectively. During data curation, key manipulation parameters, such as the taxonomic background of parent species, the synthetic genes regulated/introduced, the fold-changes of NP yields and other information, were also extracted from the original references when available. As shown in Figure 2, diverse co-culture combinations were curated in NPASS. Phylogenetic trees were generated based on NCBI taxonomy (36) and visualized using the iTOL web server (37) to present the landscape of co-culture combinations. These curated engineered species (Figure 2B) and co-culture combinations (Figure 2C) contributed to both the discovery of novel NPs (4% and 36%, respectively) and yield increase of existing high-value NPs (89% and 40%, respectively).

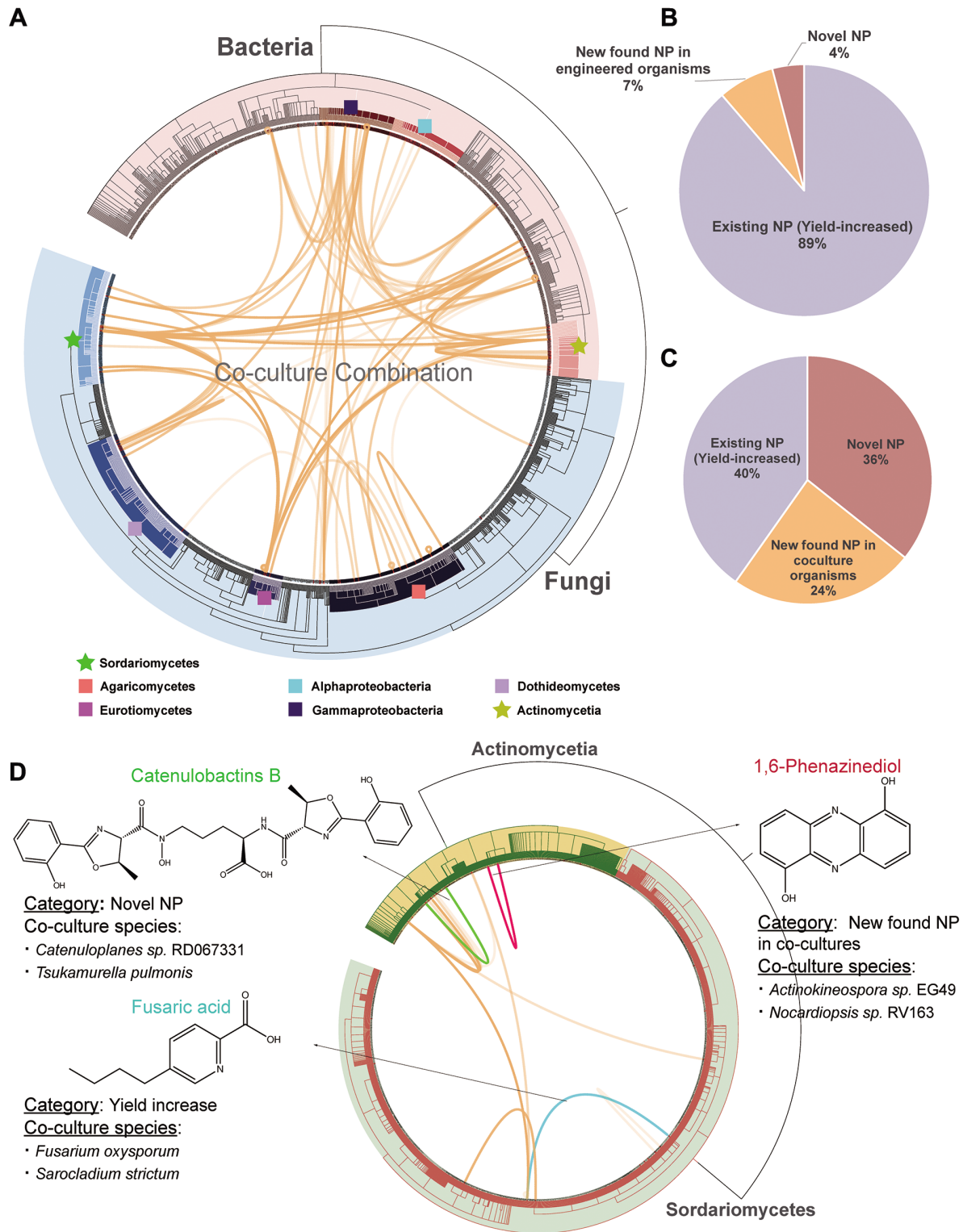


Figure 2. An overview of co-cultured and engineered species for optimized NP production. (A) An overview of co-culture combinations was projected on a family-level phylogenetic tree of bacteria and fungi. Taxonomic classes that enriched co-cultured species were highlighted with different colors and labeled with different shapes. The phylogenetic tree was built using phyloT-v2 (<https://phyloT.biobyte.de/>) based on NCBI taxonomic identifiers and visualized using iTOL. Connection lines between taxonomic tree leaves indicate co-culture combinations. NPs produced by engineered or co-cultured species were classified into three categories: (i) novel NP: novel structure that reported for the first time; (ii) new found NP: NPs that produced by engineered species but not found in wild type parent species; (iii) existing NP (Yield-increased): NPs produced by both parent species and engineered species but have increased yield in engineered species. The percentages of NPs produced by engineered species (B) and co-cultured species (C) were shown in pie charts. (D) The family-level phylogenetic tree in (A) was zoomed in at genus-level for *Actinomycetia* and *Sordariomycetes* class to illustrate typical examples of NP production in co-culture combinations. NCBI Taxonomic IDs used to generate phylogenetic trees were provided in Supplementary Table S1.

ESTIMATING ACTIVITY PROFILES OF NATURAL PRODUCTS WITH THE MOLECULAR SIMILARITY PRINCIPLE

NPs are the most significant source for drug discovery, while the majority of isolated NPs have not been subjected to bioactivity evaluation against broad therapeutic targets. Characterizing the bioactive space of NP is critical for more efficient NP-based research and drug discovery. The molecular similarity principle has become a driving force of drug discovery, particularly in molecular activity prediction and activity profile estimation (16,38). This principle has also been applied for charting and navigating NP chemical space (39), probing clustered patterns of NP drugs against privileged molecular target sites (40), and developing NP likeness scores (41).

Recently, these chemical structure-centric similarity metrics have been extended to a broad level of biology, aiming to capture more comprehensive representations of biological properties/behaviors of chemical compounds at different biological levels. For example, a five-levels (chemistry, targets, networks, cells, and clinics) Chemical Checker bioactivity descriptor was proposed (16), and it exhibits enhanced performance in predicting the biological activity of compounds that lack experimental bioactivity evaluation (42). This provides clues for revealing the bioactive space of NPs. In the updated NPASS database, we employed the Chemical Checker (16) to generate bioactivity descriptors for all NPs and subsequently constructed the NPs' bioactivity similarity space for NPASS. In detail, continuous descriptor vectors generated by Chemical Checker were subjected to Uniform Manifold Approximation and Projection (UMAP) manifold learning for dimension reduction. Five 2D sub-spaces A, B, C, D and E (represent chemistry, targets, networks, cells, and clinics levels, respectively) were built (based on the first two dimensions learned by UMAP) and visualized as density maps generated by ChemPlot Python package (43). For each NP, its locations in density maps were highlighted using a small circle. Biological similarities of all NP pairs were calculated using Euclidean distance based on UMAP projection coordinates (UMAP distance) to navigate the NP biological similarity space. A smaller UMAP distance between NPs indicated a closer bioactivity similarity, which allowed us to explore top-N similar NPs of an individual NP in each bioactivity sub-spaces. Due to the inherent differences between Chemical Checker sub-spaces, for a specific NP, the lists of top-N similar NPs in different bioactivity sub-spaces are not necessarily consistent (16). This may be useful for inferring activity profiles of those NPs which have no experimental activity record via exploring their top similar active NPs in each sub-space.

DRUG-LIKENESS AND ADMET PROFILING OF NATURAL PRODUCTS

The drug development potential of active molecules can be partly judged by the drug-likeness properties (18,19). In particular, drug-likeness rules have been developed and widely used in drug discovery (19,44,45). These rules exploit the drug's distinguished physicochemical properties, such as

molecular weight and the number of hydrogen bond donors, as the basis for drug-likeness evaluations (46). The therapeutic effectiveness and safety of drugs are also strongly influenced by the absorption, distribution, metabolism, excretion (ADME) and toxicity (T) profiles of these drugs (47). Early evaluation of ADMET properties of molecules, including NPs, is useful for selecting promising candidates in drug discovery (48). We therefore used the ADMETlab 2.0 (17) web server for computing physical-chemical properties, medicinal chemistry properties, and ADMET properties for each NP.

CONCLUDING REMARKS

There has been increasing interest in NP drug discovery (1), new nutrition sources from plant diversity (49), and the exploration of beneficiary effects of herbs (50). These extensive investigations are generating data on a wider variety of NP activity (51,52) and on the composition/concentration of NPs in various species (53,54). The rich information generated from these and future investigations can be incorporated into the NPASS database and other established databases (<https://data.nal.usda.gov/dataset/usda-database-flavonoid-content-selected-foods-release-32-november-2015>) (14,15). These databases with extended data collectively provide enriched resources for facilitating drug discovery (1), functional food development (55), and investigations and explorations of herbal medicines (3).

DATA AVAILABILITY

No new data were generated or analysed in support of this research.

SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online.

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Conflict of interest statement. None declared.

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