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Emergence of fosfomycin resistance gene *fosZ* in carbapenem and fosfomycin–resistant *Pseudomonas juntendi* isolates in China

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With the emergence and spread of plasmid-mediated fosfomycin resistance genes[1–3], fosfomycin has been moved up to the highest priority critically important antimicrobials in the 2024 *World Health Organization list of medically important antimicrobials*[4,5]. Due to the reduction in treatment options for multidrug resistant bacterial infections, fosfomycin has been reintroduced to treat infections caused by multidrug-resistant *Pseudomonas* (*P.*) *aeruginosa* and carbapenem-resistant Enterobacteriaceae. Carbapenem-resistant-*P. aeruginosa* have been listed in the high-priority pathogens in the 2024 *World Health Organization Bacterial Priority Pathogens List*. The increasing prevalence of fosfomycin resistance genes has become a serious challenge in both animals and clinical environments[1–3,6,7]. Recently, a novel plasmid-mediated fosfomycin resistance mechanism, *fosZ*, has been described in a conjugative *IncP–2* plasmid recovered from a carbapenem-resistant *P. aeruginosa* strain in China[8]. It shows less than 70% amino acid identity with known *fosA* proteins and displays a fosfomycin minimum inhibitory concentration (MIC) of 128 mg/L. Although the *fosZ* gene has been identified in six species, including *P. aeruginosa*, *P. putida*, *P. fulva*, *P. asiatica*, *P. oleovorans*, and *P. defluvii*, there are gaps in our understanding of the host range of *fosZ*.

Here, we report the first identification of *fosZ* from a *P. juntendi* isolate of human origin in China. A *Pseudomonas* spp. strain DS24IMWYN200_XXB469 was isolated from the urine sample of a 79-year-old male in a nursing home in Qingpu District, Shanghai, on July 2, 2024, using a Columbia blood agar plate. The species was identified by matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) and whole-genome sequencing. Antimicrobial susceptibility testing was performed using broth microdilution and interpreted according to the Clinical and Laboratory Standards Institute 2023 standards and the European Committee on Antimicrobial Susceptibility Testing. DS24IMWYN200_XXB469 was resistant to ampicillin, ceftazidime, cephalexin, cefoxitin, cefazolin, cefotaxime, cefuroxime, ceftazidime/avibactam, ampicillin/sulbactam, amoxicillin/clavulanate, ertapenem, meropenem, imipenem, chloramphenicol, florfenicol, nalidixic acid, ciprofloxacin, fosfomycin, gentamicin, streptomycin, trimethoprim/sulfamethoxazole, tetracycline, and tigecycline, while non- susceptible to polymyxin, colistin, and cefepime, but susceptible to amikacin, and azithromycin (Figure 1A and Supplementary Table 1). The exact MIC values and corresponding CLSI 2023 and EUCAST interpretive criteria were determined for imipenem, meropenem, and tigecycline (Supplementary Table 1).

The genomic DNA of DS24IMWYN200_XXB469 was extracted and sequenced by the DNBSEQ-T7 platform and assembled by Unicycler v0.5.0 (https://github.com/rrwick/Unicycler), and then generated a total length of 6070833 bp with an N50 of 59046 bp and GC content of 62%. The species was identified by both gtdb-Tk v2.6.1 (https://github.com/Ecogenomics/GTDBTk) and MetaPhlAn v4.2.4 (https://github.com/biobakery/MetaPhlAn), indicating that DS24IMWYN200_XXB469 belongs to *P. juntend*. DS24IMWYN200_XXB469 harbored one chromosome and one

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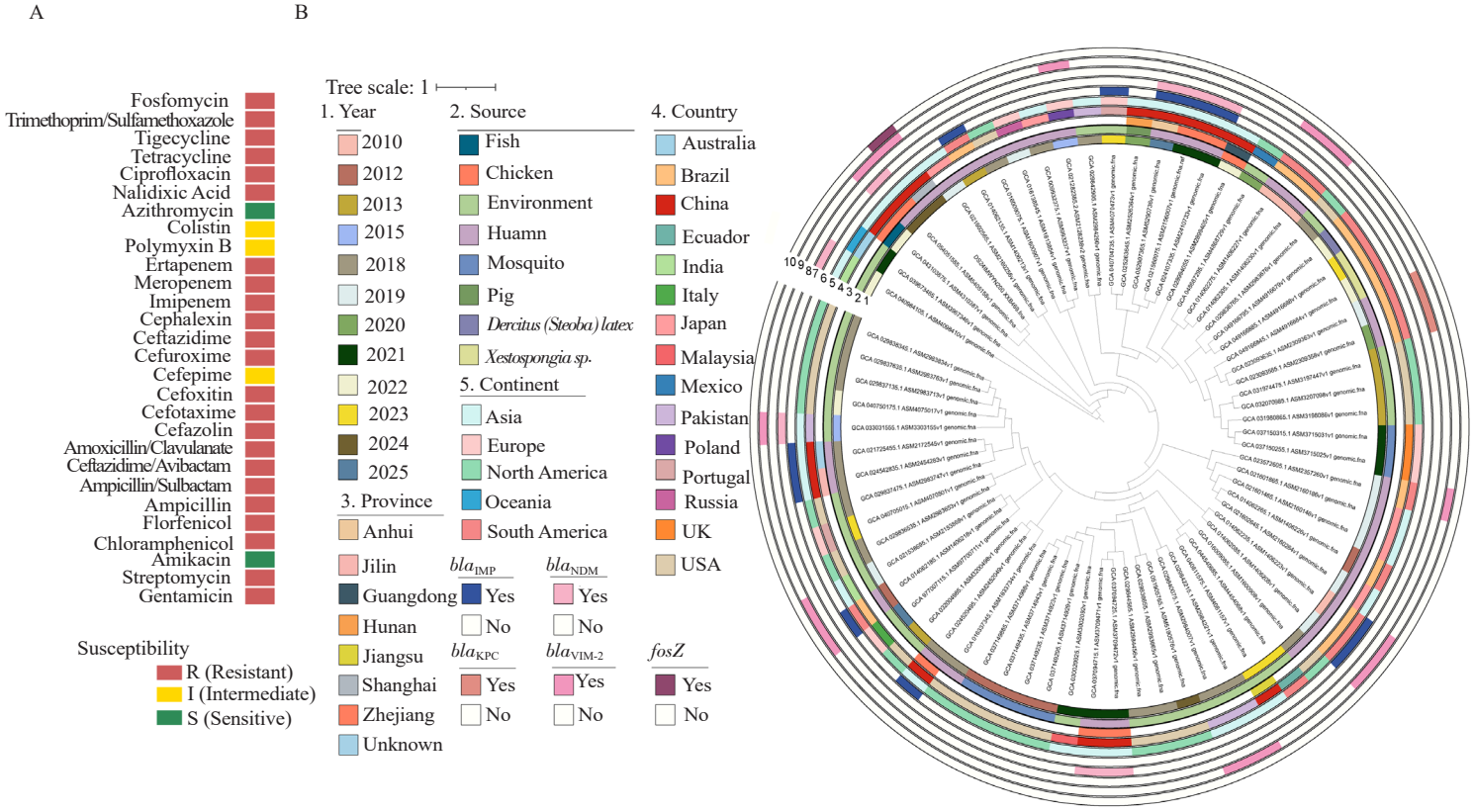
plasmid using MOB-suite v3.1.9 (https://github.com/phac-nml/mob-suite). The completeness and contamination of the genome was 99.94% and 0.55%, respectively, according to CheckM2 (https://github.com/chklovski/CheckM2). A total of 5719 predicted coding sequences were identified.

BLAST analysis showed that DS24IMWYN200_XXB469 harbored multiple antibiotic resistance genes (ARGs), including *fosZ*, bla_{VIM-2}, *aph(3´´)–Ib*, *aac(6´)–Ib3*, *aac(6´)–IIa*, *aph(6)–Id*, *CmlA9*, *qnrVC6*, *tet(G)*, *sul1*, *dfrB1*, and transferable resistance-nodulation-division pump gene cluster *tmexCD3–toprJ3*, using ResFinder (https://github.com/genomicepidemiology/resfinder) and the Comprehensive Antibiotic Resistance Database (https://card.mcmaster.ca/). Notably, *aac(6´)–IIa*, *CmlA9*, and *tet(G)* were predicted in the plasmid; other ARGs were predicted in the chromosome.

Phylogenetic analysis indicated that the *fosZ*-positive strain was clustered together with a genome from human urine in Jinhua, Zhejiang, in 2024, and a genome from a fish intestinal isolate in Wenzhou, Zhejiang, in 2022 (Figure 1B and Supplementary Table 2). The strains from different regions of China have significant genetic differences and are distributed on different branches, clustering separately from other regions (for example, Europe and Australia). Among these 70 *P. juntendi* isolates used in this work, only one fosfomycin resistance gene, *fosZ*, was identified in DS24IMWYN200_XXB469. To the best of our knowledge, this is the first report of the identification of new discovered fosfomycin resistance gene, *fosZ*, in a carbapenem- and fosfomycin-resistant *P. juntendi* isolate. In addition, a total of 35 carbapenem resistance genes, including bla_{VIM-2} (n=13), bla_{IMP-1} (n=4), bla_{IMP-15} (n=3), bla_{IMP-16} (n= 3), bla_{IMP-8} (n=1), bla_{NDM-1} (n= 7), bla_{NDM-14} (n=1), bla_{KPC-2} (n=2), and bla_{BKC-1} (n=1) were identified in *P. juntendi* genomes (Supplementary Table 2). Further analysis showed that the *fosZ*-positive strain harbored multiple virulence factors (Supplementary Table 3). Genetic environment analysis revealed that *fosZ* is located next to an insertion sequence (IS) of the IS*66* family. The genetic context of *fosZ* in carbapenem- and fosfomycin-resistant *P. juntendi* isolate is *TnpA–TnpB–ISPa75–fosZ* (Figure 1C), which is similar to those reported previously[8]. The genetic context of bla_{VIM-2} located on the chromosome of *P. juntendi* was *dfrB1–aac(6´)–Ib3–*bla_{VIM-2}*–TniR–TniQ–TniB–TniA* (Figure 1D), which was similar to the previous report that bla_{VIM-2} was in a *P. putida* plasmid of migratory bird origin[9]. The genetic context of the RND-type efflux pump gene cluster *tmexC3–tmexD3–toprJ3* is similar to clinical *P. fulva* strains isolated from the bile specimen of a liver transplant patient in Zhengzhou, Henan Province, on May 4, 2019[10], that carry plasmid-mediated bla_{VIM-24} and *tmexCD3–toprJ3*. No other mobile genetic elements were observed around *tmexC3–tmexD3–toprJ3* (Figure 1E).

In summary, to our knowledge, this is the first report of the convergence of *fosZ*, bla_{VIM-2}, and *tmexC3–tmexD3–toprJ3* in *P. juntendi* isolated from a human, which expanded our knowledge of the host reservoir of *fosZ*. To better protect human, animal, and environmental health worldwide, a continuous surveillance of carbapenem, tigecycline, and fosfomycin resistance in different environments is urgently needed to fight the emergence and



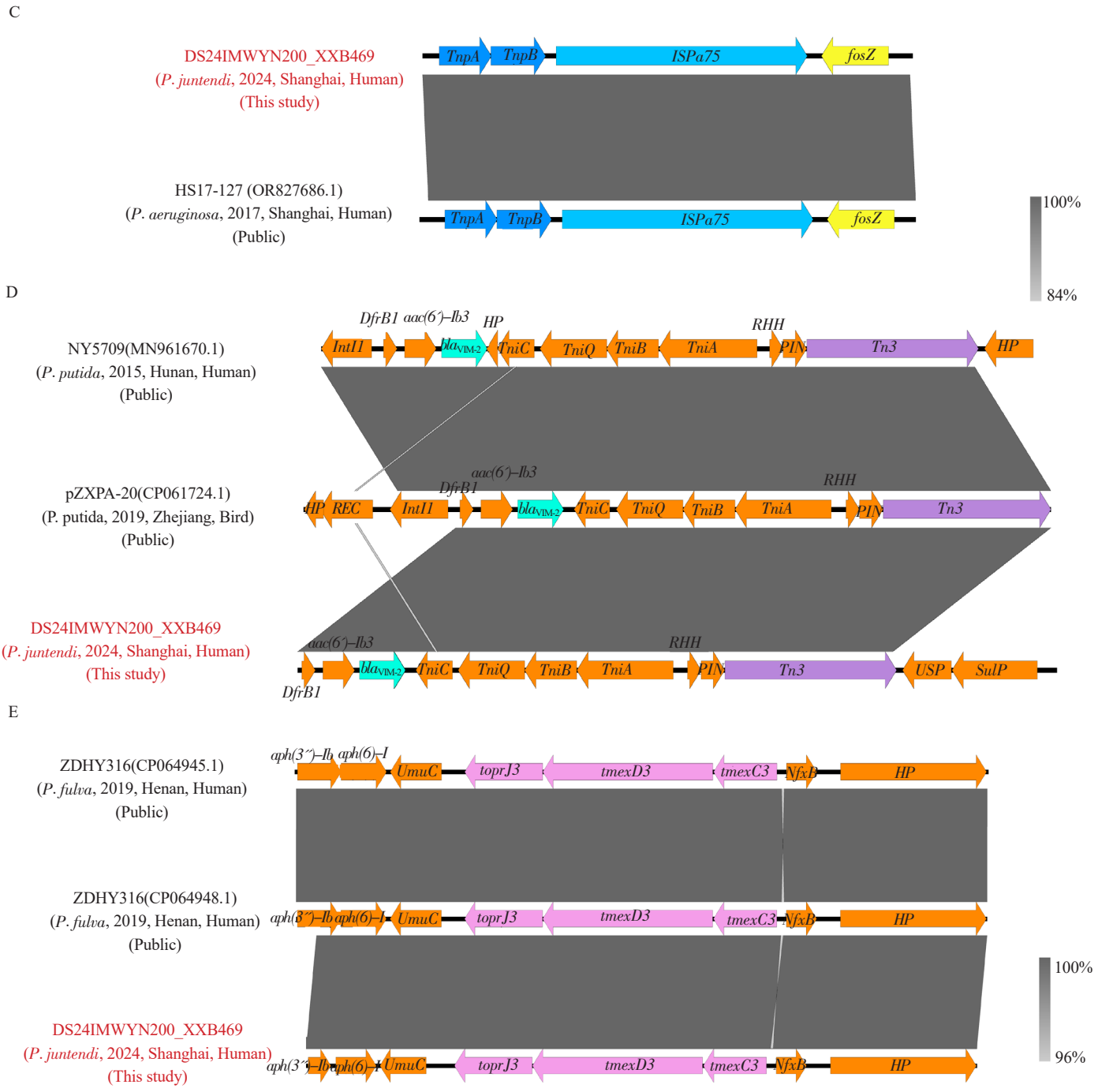


Figure 1. Comparative analysis of *fosZ*-harbor *P. juntendi* genomes and comparison of the genetic context of *fosZ*. A: Susceptibility of the *fosZ*-positive strain of *P. juntendi* to commonly used antibiotics. R: resistant; I: intermediate; S: sensitive. B: Phylogenetic analysis of *fosZ*-harbor *P. juntendi* and 69 publicly available genomes. From the inner to outer circles are year, source, province (only isolates in China), country, continent, bla_{IMP}, bla_{NDM}, bla_{KPC}, bla_{VIM-2}, and *fosZ*. The *P. juntendi* PP_2463 (GCA_021560075.1) was used as the reference genome. C: Genetic environment of the *fosZ* gene in *P. juntendi* and *P. aeruginosa* HS17-127 (OR827686.1). Different genes are shown in different colors. Arrows indicate: insertion sequence (light blue), transposase genes *tnpA/tnpB* (dark blue), resistance gene *fosZ* (yellow). Regions of >84% identity are indicated by dark grey shading. D: Genetic environment of the bla_{VIM-2} gene in *P. juntendi* genome. *P. putida* NY5709 (MN961670.1) and *P. putida* ZXPA-20 (CP061724.1). Different genes are shown in different colors. Arrows indicate: bla_{VIM-2} (green), *Tn3* transposon (purple), and other genes (orange). E: Genetic context of t*mexC3–tmexD3–toprJ3* in the *fosZ*-positive *P. juntendi* genome. *P. fulva* ZDHY316 (CP064945.1), and *P. fulva* ZDHY414 (CP064948.1). Different genes are shown in different colors. Arrows indicate: *tmexC3–tmexD3–toprJ3* (pink), and other genes (orange).

dissemination of these resistant pathogens. Overall, our study highlights the emergence of bla_{VIM-2}, *fosZ*, and *tmexC3–tmexD3–toprJ3*, which are predicted to be associated with resistance to the last-line antibiotics, carbapenem, fosfomycin, and tigecycline, and may pose a huge challenge to clinical therapy in the future.

Ethical approval

The participant provided written informed consent and allowed analysis of strains and data for medical case report.

Conflict of interest statement

The authors declare that there is no conflict of interest.

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Data availability statement

The data supporting the findings of this study are available from the corresponding author upon request.

Authors' contributions

Wang YN and Xu XB conceived and designed the project. Xu XB collected samples, strains, and epidemiological data. Yang ZR performed bioinformatics analysis, created the figures and tables. Wang YN, Yang ZR, and Xu XB drafted and revised the manuscript.

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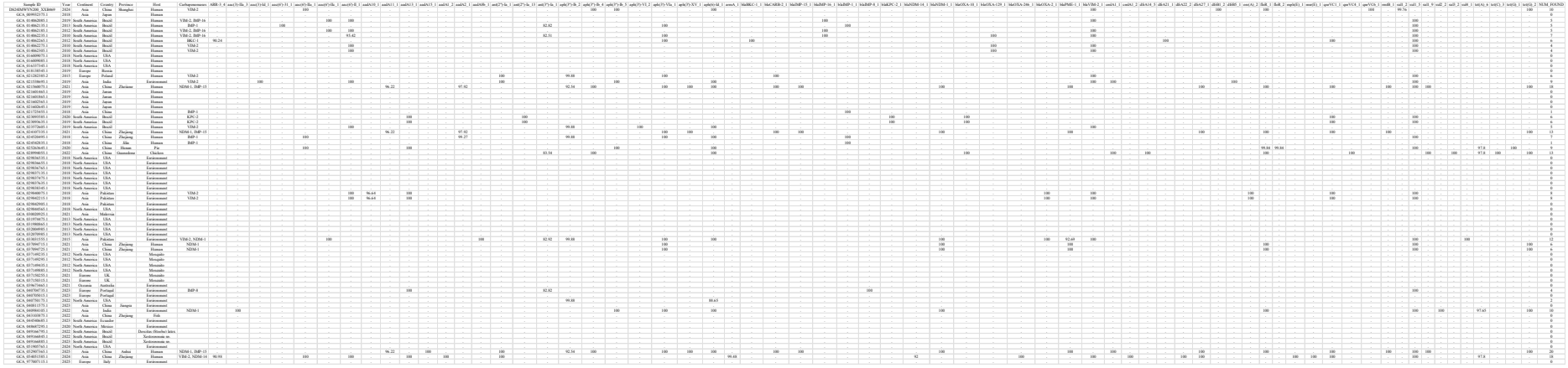
Supplementary Table 1. MIC values and resistance phenotypic interpretation according to CLSI M100-S33 (2023) and EUCAST.

Antibiotic	MIC (μg/mL)	Susceptibility Interpretation	Note
Fosfomycin	200 μg DISC	R	Kirby-Bauer (K-B) disk diffusion met
Gentamicin	8	R	
Streptomycin	32	R	
Amikacin	2	S	
Chloramphenicol	64	R	
Florfenicol	32	R	
Ampicillin	64	R	
Ampicillin/Sulbactam	64	R	
Ceftazidime/Avibactam	8	R	
Amoxicillin/Cavulanic Acid	64	R	
Cefazolin	32	R	
Cefotaxime	16	R	
Cefoxitin	64	R	
Cefepime	8	I	
Cefuroxime	32	R	
Ceftazidime	32	R	
Ceftiofur	16	R	
Imipenem	8	R	
Meropenem	4	R	
Ertapenem	8	R	
Polymyxin B	1	I	
Colistin	1	I	
Nalidixic Acid	64	R	
Ciprofloxacin	16	R	
Azithromycin	4	S	
Tetracycline	32	R	
Tigecycline	8	R	
Sulfamethoxazole/Trimethoprim	8	R	

Supplementary Table 2. Background of *P. juntendi* from this study and public sources for phylogenetic tree analysis with annotated resistance genes.



Supplementary Table 3. Virulence factors identified in *P. juntendi* strains.

Sample ID	alg8	algA	algB	algC	algD	algI	algU	algW	fleN	fleQ	flgC	flgG	flgH	flgI	flhA	fliA	fliE	fliF	fliG	fliI	fliM	fliN	fliP	fliQ	mbtH-like	motA	motB	motC	mucD	pilH	pvdH	pvdM	pvdS	waaF	waaG	NUM_FOUND
DS24IMWYN200_XX	96.3	97.16	.	94.97	.	82.09	100	.	95.49	97.9	99.77	97.71	93.53	96.76	99.2	90.99	.	.	99.51	96.98	99.69	91.77	93.49	99.63	97.26	.	.	99.46	93.89	98.91	.	.	93.62	94.32	.	25
GCA_009932375.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	97.9	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	.	.	.	.	97.72	.	.	99.46	93.96	98.63	.	90.05	93.62	94.32	.	22
GCA_014062085.1	96.3	97.23	.	.	.	81.7	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.72	.	.	99.46	93.96	.	.	.	93.62	94.22	98.31	24
GCA_014062135.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	97.9	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.07	91.14	93.49	99.63	97.26	.	.	99.46	93.96	98.63	.	90.05	93.62	94.22	.	26
GCA_014062185.1	96.3	97.23	.	.	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	24
GCA_014062235.1	96.3	97.23	.	.	.	81.7	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.72	.	.	99.46	93.96	.	.	.	93.62	94.22	98.31	24
GCA_014062265.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.98	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	.	24
GCA_014062275.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	96.76	99.2	91.4	.	.	99.51	96.98	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	90.05	93.62	94.32	.	25
GCA_014062305.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	96.76	99.2	91.4	.	.	99.51	96.98	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	90.05	93.62	94.32	.	25
GCA_016009075.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	97.9	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.72	.	.	99.46	93.96	98.63	.	90.05	93.62	94.32	.	26
GCA_016009085.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	.	24
GCA_016337345.1	96.3	97.23	.	.	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	.	93.96	.	.	.	93.62	94.32	98.31	23
GCA_018138545.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	97.9	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.72	.	.	99.46	93.96	98.63	.	90.05	93.62	94.32	.	26
GCA_021282385.2	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.07	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	93.12	90.05	93.62	94.32	98.31	27
GCA_021538695.1	96.3	97.23	.	.	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	24
GCA_021560075.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	93.12	90.05	93.62	94.32	98.31	27
GCA_021601465.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	.	24
GCA_021601865.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	.	24
GCA_021602565.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	97.9	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	98.63	.	90.05	93.62	94.22	98.31	27
GCA_021602645.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	.	24
GCA_021725455.1	96.3	97.23	.	.	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	24
GCA_023093585.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.55	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	93.12	90.05	93.62	94.32	.	26
GCA_023093635.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.55	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	90.05	.	94.32	.	24
GCA_023572605.1	96.3	97.23	.	94.9	.	81.89	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	.	24
GCA_024107335.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	93.12	90.05	93.62	94.32	98.31	27
GCA_024520495.1	96.3	97.23	.	.	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	24
GCA_024542835.1	96.3	97.23	.	.	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	24
GCA_025263645.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.1	99.63	97.26	.	.	99.46	93.96	.	.	90.05	93.62	94.32	98.31	26
GCA_028994055.1	96.23	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	93.12	90.05	93.62	94.32	.	26
GCA_029836535.1	96.3	97.23	.	.	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	24
GCA_029836655.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	25
GCA_029836765.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.55	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	93.12	90.05	93.62	94.32	.	26
GCA_029837135.1	96.3	97.23	.	.	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	24
GCA_029837475.1	96.3	97.23	.	.	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	24
GCA_029837635.1	96.3	97.23	.	.	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	24
GCA_029838345.1	96.3	97.23	.	.	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	24
GCA_029840075.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	25
GCA_029842215.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	25
GCA_029842905.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	93.12	90.05	93.62	94.32	.	26
GCA_029844565.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.72	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	25
GCA_030020925.1	96.3	97.23	.	94.83	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.24	.	.	99.41	91.89	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.44	94.22	.	24
GCA_031974475.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.55	97.71	93.53	99.73	99.2	90.59	.	.	99.51	.	99.69	.	93.49	99.63	.	.	.	99.46	.	.	.	90.05	.	.	.	19
GCA_031980865.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.55	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	93.12	90.05	.	94.32	.	25
GCA_032004985.1	96.3	97.23	.	.	.	82.09	100	.	95.49	.	99.77	97.71	93.53	96.76	99.2	96.37	.	.	99.51	96.98	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	23
GCA_032070985.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.55	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	93.12	90.05	.	94.32	.	25
GCA_033031555.1	96.3	97.23	.	.	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	24
GCA_037094715.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.72	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	25
GCA_037094725.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.72	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	25
GCA_037149235.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.72	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	25
GCA_037149295.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.72	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	25
GCA_037149435.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.72	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	25
GCA_037149885.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.80-99.80	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.72	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	25
GCA_037150255.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.55	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	93.12	90.05	93.62	94.32	.	26
GCA_037150315.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	89.12	97.71	90.66	99.73	89.64	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	93.12	89.98	93.62	94.32	.	26
GCA_039673465.1	96.09	97.16	98.52	95.04	.	82.09	100	.	95.73	97.76	.	98.85	99.55	99.55	99.34	92.2	99.09	.	100	91.96	99.59	91.77	93.36	99.63	97.72	.	.	99.33	94.81	88.52	.	.	91.49	93.55	98.4	26
GCA_040704735.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	93.12	90.05	93.62	94.32	98.31	27
GCA_040705015.1	96.3	97.23	.	.	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	24
GCA_040750175.1	96.3	97.23	.	.	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	24
GCA_040811575.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	.	24
GCA_040984105.1	97.51	97.23	98.59	94.47	99.47	82.09	100	97.86	95.85	99.66	99.77	97.46	93.39	97.39	99.53	95.16	99.09	94.32	100	91.96	99.59	91.35	92.19	100	92.24	99.88	80.94	99.46	93.75	90.98	91.77	89.09	93.09	92.87	99.11	35
GCA_043103875.1	96.3	97.16	.	94.97	.	82.09	100	.	95.49	.	99.77	97.71	93.53	99.73	99.2	90.99	.	.	99.51	96.98	99.69	91.77	93.49	99.63	97.26	.	.	99.46	93.89	.	.	.	93.62	94.22	.	23
GCA_044540685.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	.	24
GCA_048687295.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	96.76	99.2	91.4	.	.	99.51	96.98	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	93.12	90.05	93.62	94.32	.	26
GCA_049166795.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.55	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	90.05	.	94.32	.	24
GCA_049166845.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.55	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	93.12	90.05	.	94.32	.	25
GCA_049166885.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.55	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	90.05	.	94.32	.	24
GCA_051905765.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	25
GCA_052907365.1	96.3	97.23	.	94.9	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	96.37	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	93.12	90.05	93.62	94.32	98.31	27
GCA_054051585.1	96.3	97.16	.	94.97	.	82.09	100	.	95.49	97.9	99.77	97.71	93.53	96.76	99.2	90.99	.	.	99.51	96.98	99.69	91.77	93.49	99.63	97.26	.	.	99.46	93.89	98.91	.	.	93.62	94.32	.	25
GCA_977007115.1	96.3	97.23	.	.	.	82.09	100	.	95.49	99.8	99.77	97.71	93.53	99.73	99.2	91.4	.	.	99.51	91.96	99.69	91.14	93.49	99.63	97.26	.	.	99.46	93.96	.	.	.	93.62	94.32	98.31	24