BGDMdocker: an workflow base on Docker for analysis and visualization pan-genome and biosynthetic gene clusters of Bacterial

Gong Cheng[1,2] ,Zongshan Zhou[1]*, Ling Ma[3],Guocai Zhang[3],Yilei WU[4], Chao Chen[5]
[1]Research Institute of Pomology, Chinese Academy of Agricultural Sciences, Xingcheng 125100, Liaoning, China,[2]Forest Protection Research Institute of Heilongjiang Province,Harbin,China,[3]Northeast Forestry University,Harbin 150040,[4]Beijing Hygenoimcs CO.,LTD,Beijing,China,[5]TangTangTianxia Biomedical Information Technology CO.,LTD,BeiJing , China

ABSTRACT

Motivation: At present Docker technology is increasing level of attention throughout the bioinformatics community,but Docker technology implementation details have not been mastered by most biologist and applied in biological research, In order to apply this technology in the popularization and sufficient use plenty of free academic resources of bioinformatics tools images(community, official, and private) in Docker Hub Registry and other Docker sources base on Docker, In this article, we introduced full and accurate instance of an bioinformatics workflow base on Docker of analysis and visualization pan-genome and biosynthetic geneclusters of Bacterial, provides the solutions for the data mining bioinformatics big data from various free biology databases of Bacterial. we'll guide you step-by-step through the process from dockerfile building your own image and run an container fast creating an workflow.

Results: We present BGDMdocker(bacterial genome data ming docker-based) workflow based on docker of pan-genome and biosynthetic geneclusters analysis and visualization can be fully reusable immediately in different computing platforms(Linux, Windows , Mac and deployed in the cloud),achieved cross platform deployment flexibility, rapid development integrated software packag.The workflow consists of three integrated toolkit Prokka v1.11, panX, antiSMASH3.0 and its dependencies are all write in Dockerfile,and we use Dockerfile build docker image and run container for anlysis pan-genome of total 44 *B.amyloliquefaciens* strains, that is an open pan-genome, total 172,432 gene, 2,306 Core gene cluster , and visualized pan-genomic data such as alignment, a phylogenetic tree, maps mutations within that cluster to the branches of the tree, infers loss and gain of genes on the core-genome phylogeny for each gene cluster, besides, mining 997 known(MIBiG database) and 553 unknown (antiSMASH-predicted clusters and Pfam database) total 1550 biosynthesis geneclusters types and orthologous groups in all strains.This workflow can also be used for other species pan-genome vis analysis and ualization, you can completely duplicate the display of visual data as well as in this paper.all data of result have been upload in our website,no need to register you can download all tools ,data and files.

Availability and implementation:BGDMdocker is available at http://42.96.173.25/bapgd/ and the source code under GPL license is available at https://github.com/cgwyx/debian_prokka_panx_antismash_docker

Contact: chenggongwyx@foxmail.com

Supplementary information: Supplementary data are available at biorxiv online.

Keywords: Docker, pan-genome,biosynthesis geneclusters, Bacterial, *Bacillus amyloliquefaciens*,

1 INTRODUCTION

Bioinformatics academic free software difficulty installing,configuration,and large dependencies and several online server programs limit size of the data upload and so on. therefore a lot of excellent software not make full use of biological problems by biologists. Sharing bioinformatics tools with Docker can reproducibility, convenience build all kind of bioinformatics workflow. It gives programmers, development teams and biologist of bioinformatics the common toolbox they need to take advantage of the use, and building, shipping and running any app, anywhere your distributed applications.

Thus,Dockers technology is very suitable for the application in the field of bioinformatics, because of its advantages and characteristics that allows applications to run in an isolated, self-contained package that can be efficiently distributed and executed in a portable manner across a wide range of computing platforms,etc.(Peter Belmann,2015; Abdelrahman Hosny,2016; Aranguren ME,2015), At present, there are a lot of bioinformatics tools based on docker are developed and published,such as perl and bioperl(Peter Martini ,2016),python and biopython(Moghedrin *et al*. ,2016), R and Bioconductor(Eddelbuettel et al. ,2016), contribute their Official Docker image;famous Galaxy also contribute docker galaxy(Björn A. Grüning, 2016). docker will become very extensive in the field of bioinformatics.we use docker technology that rapid construction of pan-genome analysis process, this process can be set up in the Linux , windows and MAC system, can also be deployed in the cloud such as Amazon EC2 or other cloud providers. greatly facilitate biologists apply to biological field. Docker containers have only a minor impact on the performance of common genomic pipelines(Di Tommaso et al. 2015)

B.amyloliquefaciens has been researched and explored more and more widely with the a-bilities to inhibit fungi and bacteria,there by it has high research values and potential for development,which was widely used in biological control (Nam H-S, 2016;).Based on the Docker we quickly run an container (ubuntu 16.04 and win10 platform) of analysis workflow and reveal the pan-genome and biosynthetic geneclusters basic features of 44 strains *B.amyloliquefaciens*, achieve result visualizations. The analytical workflow consists of three toolkit: genome annotation Prokka v1.11 (Seemann, 2014),panX (Wei Ding *et al*. 2016) anlanysi and visualization of pan genome and antiSMASH3.0 (Weber T *et al*. 2015)biosynthesis geneclusters,which we write script file and with all of the application and its dependencies in Dockerfile of BGDMdocker (we also write standlone Dockerfile of Prokka,panX,antiMASH in order to meet different application requirements of user), here we detailed how to build workflow and manipulate of the analysis.

2 METHODS AND Implementation details

2.1 Install docker

Docker containers can be run anywhere:Linux kernels, Windows and Mac(64-bit), can also be deployed in the cloud such as Amazon EC2 or other cloud providers. in this

instance we installation docker-engine on Ubuntu Xenial 16.04 (LTS) and win10 Enterprise operating system.Docker requires a 64-bit installation regardless of your Ubuntu version. Additionally, your kernel must be 3.10 at minimum.more operating systems installation see here,

Installation latest docker(docker-engine 1.12.5-0~ubuntu-xenial) on Ubuntu Xenial 16.04 (LTS) (Install Docker on Ubuntu,2016):

Copy the following commands is meant for quick & easy install via latest docker-engine (ubuntu, debian,raspbian,fedora,centos,redhat, suse and oraclelinux *et al*. all applicable):

```
$    curl -sSL https://get.docker.com/ | bash -x
```

or:

```
$    wget -qO- https://get.docker.com/ | bash -x
```

Type the following commands at your shell prompt, If output for docker version it means your installation is successful:

```
$ docker version
```

Installation latest docker on Windows 10 Enterprise(Install Docker on Windows,2016):

The current version of Docker for Windows runs on 64bit Windows 10 Pro, Enterprise and Education.

Step 1.Download Docker InstallDocker.msi (https://download.docker.com/win/stable/InstallDocker.msi)

Step 2. Install Docker(1.12.0-rc2) for Windows

Double-click InstallDocker.msi to run the installer.Follow the install wizard to accept the license, authorize the installer, and proceed with the install.

Type the following commands at your shell prompt(cmd.exe or PowerShell),will output for docker version it means your installation is successful.

```
$ docker version
```

2.2 build images of workflow and run container login interaction patterns

Dockerfile of BGDMdocker workflow have submit github (https://github.com).on your host type the following commands line will login an BGDMdocker container:

```
$ git clone https://github.com/cgwyx/debian_prokka_panx_antismash_docker.git
```

or

```
$ unzip BGDMdocker.zip (Download BGDMdocker.zip)
$ cd ./debian_prokka_panx_antismash_docker/prokka_panx_antismash_dockerfile
```

Build images of workflow:

```
$ sudo docker build -t BGDMdocker:latest .
```

Run an container from image of BGDMdocker:atest:

```
$ sudo docker run -it --rm -v home:home --name=BGDMdocker BGDMdocker:latest
```

“-v home:home” parameter, Docker will mount the local folder /home into the Container under /home, Store all your data in one directory of home of host operating system, then you may access theose directory of home inside of container .

Check out local images and container:

```
$ sudo docker images
$ sudo docker ps –a
```

2.2.1 Run Prokka annotation genome in container in interaction patterns (if you have own sequene of genome need this step generates .gbff annotation files):

Check out help documentation and command parameters:

$ prokka --help

Copy the following commands run the analysis instances of annotation genome of Ba_xx strains in command-line interface of container (boldface please enter your data):

```
$ prokka --kingdom Bacteria --gcode 11 --genus Bacillus \
  --species Amyloliquefaciens \
  --strain Ba_xx --locustag Ba_xx --prefix Ba_xx --rfam \
  --rawproduct --outdir /home/manager/PRJNA291327 \
  /home/manager/Ba_xx.fasta
```

"Ba_xx.fasta" is sequene of genome, "PRJNA291327" is output folder of result.

2.2.2 Run panX anlanysi pan-genome in container in interaction patterns:

panX starts with a set of annotated sequences files .gbff(.gbk)(e.g. NCBI RefSeq or GenBank) of a bacterial species genomes, If using own GenBank files(or you have download these files), step02 can be skipped. detail parameters see here.

Check out help documentation and command parameters:

$ sh run.sh

Copy the following commands run the analysis instances of pan-genome of 44 *B.amyloliquefaciens* strains in command-line interface of container (boldface please enter your data):

```
$ cd /pan-genome-analysis
$ python ./scripts/run-pipeline.py -fn ./data/B_amy -sl B_amy-RefSeq.txt \
  -st 1 3 4 5 6 7 8 9 10 11
```

*.gbff(GenBank files) and B_amy-RefSeq.txt(accession list for strains) should reside in "./data/B_amy" folder,result will also output "./data/B_amy" folder.

2.2.3 Run antiSAMSH search geneclusters of every strain in container in interaction patterns:

Check out help documentation and command parameters:

$ run_antismash.py --help

Copy the following commands run the analysis instances of Biosynthesis geneclusters of Y2(Y2.gbff) strains in command-line interface of container (boldface please enter your data):

```
$ cd /antismash-3.0.5/antismash/
$ run_antismash.py /home/manager/input/Y2.gbff \
  --outputfolder /home/manager/output/Y2 _out \
  --dbgclusterblast ./generic_modules/clusterblast \
  --pfamdir ./generic_modules/fullhmmer --input-type nucl --knownclusterblast \
  --clusterblast --subclusterblast --inclusive --full-hmmer --smcogs --verbose --asf \
  --borderpredict
```

*.gbff (GenBank files) reside in "input"folder, "Y2 _out" is output folder of result.

3 Conclusion

3.1 Fast and repeatable build BGDMdocker workflow based on Docker across computing platform

Based on docker technology, useing Dockerfile script file,build images and run an Containers in seconds or milliseconds on Linux and Windows(also can be deployed in Mac,cloud such as Amazon EC2 or other cloud providers), Dockerfile is just a small plain text file that can be easily stored and shared. The user does not have to deal with installing and configuring.

In this instance, all image based on Debian 8.0(Jessie),Establishment of a novel Docker-based bioinformatics platform for the study of microbes genomes.The use of workflow containers with standardised interfaces has the potential make the work of biologists easier by creating simple to use, inter-changeable tools to excavate the biological meaning contained in data from biological experiments and Studied on the biological sequence data obtained from biological database through internet. Depending on the sequence obtained, we focused on the information mining in the sequence. We have upload this dockerfile to GitHub for the use of relevant scientific researchers.

3.2 result of pan genomes of *B.amyloliquefaciens*

BGDMdocker workflow analyze pan genomes of *B.amyloliquefaciens*. Inorder to exploration High Dimensional Data We built Website for interactive exploration of the pan-genome and biosynthetic geneclusters. The visualization allows rapid filtering of and searching for genes. For each gene cluster, panX displays an alignment, a phylogenetic tree, maps mutations within that cluster to the branches of the tree, and infers loss and gain of genes on the core-genome phylogeny,in this paper we only lists Summary statistics of result of pan genomes(Table 1),Phylogenetic tree of 44 *B.amyloliquefaciens* strains (Figure 1), no need to register all detail data can be visualization and download.

Table 1. summary statistics of pan-genome of 44 *B.amyloliquefaciens* strains

Accession	Strains	Gene of strains in pan-genome of *B.amyloliquefaciens* (172,432 Total gene ;2306 Core gene cluster)				Gene of strains genome	
		Total gene	Core gene	Acc gene	Uni gene	All gene	All protein
CYHL01000001	JRS5	3856	2310	1546	57	3870	3863
CYHP01000001	JRS8	3994	2311	1683	118	4016	4006
NC_014551	DSM7	3935	2307	1628	21	4030	3811
NC_017188	TA208	3935	2307	1628	1	3974	3847
NC_017190	LL3	3981	2308	1673	19	4037	3887
NC_017191	XH7	3942	2307	1635	6	3983	3846
NC_017912	Y2	4099	2310	1789	46	4148	3983
NC_020272	IT-45	3803	2310	1493	4	3832	3678
NC_022653	CC178	3754	2310	1444	19	3795	3641
NC_023073	LFB112	3761	2308	1453	19	3801	3637
NZ_AUNG01000001	Lx-11	3700	2309	1391	5	3742	3619
NZ_AUWK01000001	HB-26	3797	2311	1486	30	3842	3714
NZ_AVQH01000001	EGD-AQ141	4079	2311	1768	54	4121	3995
NZ_AWQY01000001	UASWS BA1	3794	2309	1485	8	3806	3681
NZ_CP006058	UMAF6639	3825	2311	1514	20	3879	3716
NZ_CP006960	UMAF6614	3804	2311	1493	13	3850	3695
NZ_CP007242	KHG19	3775	2310	1465	19	3816	3658
NZ_CP010556	L-H15	3724	2309	1415	6	3769	3615
NZ_CP011278	L-S60	3728	2310	1418	7	3773	3611
NZ_CP013727	MBE1283	3794	2314	1480	24	3856	3681
NZ_CP014700	S499	3776	2310	1466	5	3819	3671
NZ_CP014783	B15	3820	2315	1505	13	3875	3704
NZ_CP016913	RD7-7	3597	2308	1289	39	3656	3483
NZ_DF836091	DNA	3771	2311	1460	128	3901	3706
NZ_JCOC01000001	EBL11	3733	2308	1425	20	3773	3682
NZ_JMEG01000001	B1895	3824	2306	1518	167	4026	3623
NZ_JQNZ01000001	X1	3724	2309	1415	3	3766	3619
NZ_JTJG01000001	JJC33M	3888	2309	1579	121	3952	3796
NZ_JXAT01000001	LPL-K103	3709	2309	1400	15	3743	3637
NZ_JZDI01000001	12B	8166	2354	5812	4040	8194	7985
NZ_KB206086	DC-12	3910	2311	1599	50	3984	3842
NZ_KN723307	TF281	3640	2312	1328	5	3782	3571

NZ_LGYP01000001	629	3536	2313	1223	11	3785	3427
NZ_LJAU01000001	Bs006	4042	2312	1730	46	4074	3969
NZ_LJDI01000020	XK-4-1	3799	2310	1489	14	3821	3701
NZ_LMAG01000001	RHNK22	3781	2309	1472	37	3837	3698
NZ_LMAT01000001	Jxnuwx-1	3930	2309	1621	246	4008	3870
NZ_LMUC01000016	H57	3816	2310	1506	42	3859	3732
NZ_LPUP01000011	11B91	3790	2311	1479	49	3892	3702
NZ_LQQW01000001	M49	3694	2311	1383	21	3741	3617
NZ_LQYO01000001	B4140	3771	2307	1464	49	3847	3713
NZ_LQYP01000001	B425	3921	2310	1611	39	4034	3844
NZ_LYUG01000001	SRCM101266	3724	2306	1418	15	3781	3628
NZ_LZZO01000001	SRCM101294	3946	2308	1638	175	3982	3850

Genome sequences of 44 *B.amyloliquefaciens* strains (download genbank RefSeq dadabase) used in this study,strains name, accession numbers, and gene numbers of pan-genome and genome summary statistics. “Acc gene” is accessory gene(dispensable gene), “Uni gene” is unique gene(strain-specific gene) “All genes” is genes of *.gbff files recoder,incloud Pseudo Genes, “Total genes” is involved in the pan genome analysis, not Pseudo Genes.

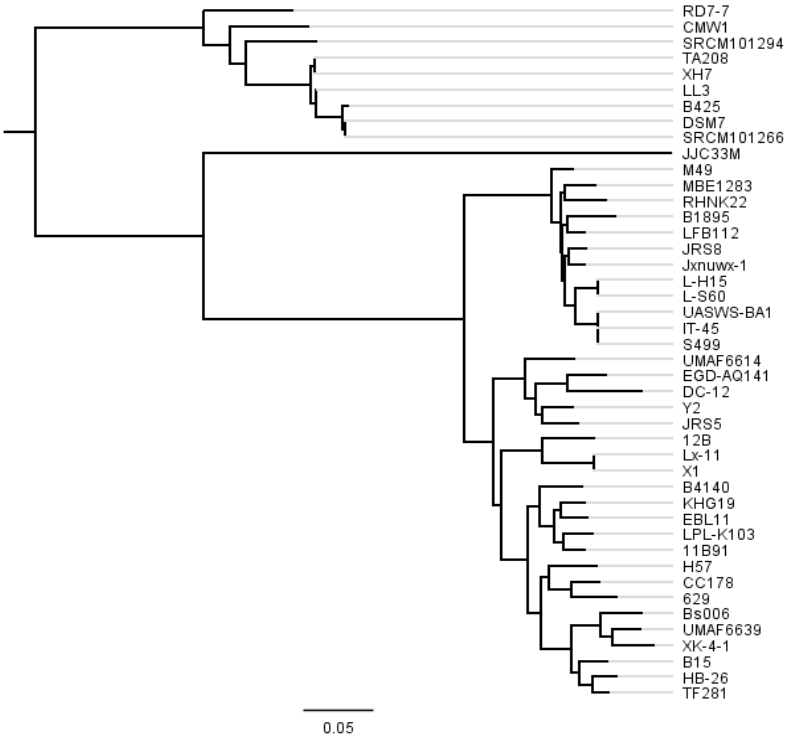

Fig.1. Phylogenetic tree of 44 *B.amyloliquefaciens* strains. The tree was constructed using all of the genes shared between all 44 strains (2306 core genes).

3.3 result of Analysis of biosynthetic geneclusters result

BGDMdocker workflow identification and analysis results of biosynthetic gene clusters of genomes of 44 strain *B. amyloliquefaciens* have been upload in our website,no need to register and vis and download all detail data.

In this paper we only give a brief summary statistics of biosynthetic geneclusters of all 44 strains(Table 2),and shows an instance of biosynthetic geneclusters type and number result of Y2 strain,there are total 31 geneclusters in Genome of Y2 strain， 21 geneclusters show similarity known cluster MIBiG,like this Surfactin,Mersacidin, Fengycin,and so on ,others 10 geneclusters is unknown(Table 3).

Table 2. summary statistics of biosynthetic geneclusters of 44 *B.amyloliquefaciens* strains

Accession	Strains	Biosynthesis geneclusters				Genome of strains			Host
		Total	known	Unknown	Type	Size(Mb)	Gene	Protein	
CYHL01000001	JRS5	38	27	11	12	4.03148	3870	3863	-
CYHP01000001	JRS8	42	26	16	11	4.0909	4016	4006	-
NC_014551	DSM7	31	18	13	9	3.9802	4030	3811	-
NC_017188	TA208	29	17	12	10	3.93751	3974	3847	-
NC_017190	LL3	29	17	12	9	4.00199	4037	3887	-
NC_017191	XH7	29	17	12	10	3.9392	3983	3846	-
NC_017912	Y2	31	21	10	11	4.23862	4148	3983	-
NC_020272	IT-45	32	19	13	11	3.93687	3832	3678	-
NC_022653	CC178	35	19	16	9	3.91683	3795	3641	-
NC_023073	LFB112	35	20	15	10	3.94275	3801	3637	-
NZ_AUNG01000001	Lx-11	37	25	12	11	3.88689	3742	3619	-
NZ_AUWK01000001	HB-26	45	30	15	9	3.98936	3842	3714	-
NZ_AVQH01000001	EGD-AQ141	36	26	10	12	4.22259	4121	3995	-
NZ_AWQY01000001	UASWS BA1	37	25	12	11	3.94409	3806	3681	-
NZ_CP006058	UMAF6639	35	21	14	10	4.03464	3879	3716	-
NZ_CP006960	UMAF6614	32	20	12	10	4.00514	3850	3695	-
NZ_CP007242	KHG19	32	20	12	10	3.95336	3816	3658	-
NZ_CP010556	L-H15	32	19	13	10	3.90597	3769	3615	-
NZ_CP011278	L-S60	32	19	13	10	3.90302	3773	3611	-
NZ_CP013727	MBE1283	35	22	13	12	3.97993	3856	3681	-
NZ_CP014700	S499	33	19	14	11	3.93593	3819	3671	Plant
NZ_CP014783	B15	29	19	10	10	4.00675	3875	3704	Grape
NZ_CP016913	RD7-7	31	17	14	8	3.68821	3656	3483	-
NZ_DF836091	DNA	30	20	10	11	3.90857	3901	3706	-
NZ_JCOC01000001	EBL11	35	23	12	11	3.92932	3773	3682	-
NZ_JMEG01000001	B1895	38	24	14	12	4.10728	4026	3623	-
NZ_JQNZ01000001	X1	40	28	12	10	3.9211	3766	3619	-
NZ_JTJG01000001	JJC33M	36	25	11	12	3.96166	3952	3796	-
NZ_JXAT01000001	LPL-K103	36	23	13	9	3.87327	3743	3637	-
NZ_JZDI01000001	12B	69	49	20	11	7.59676	8194	7985	-
NZ_KB206086	DC-12	28	19	9	11	4.01656	3984	3842	-
NZ_KN723307	TF281	31	20	11	11	3.98764	3782	3571	Glycine max
NZ_LGYP01000001	629	31	18	13	10	3.90337	3785	3427	Theobroma cacao
NZ_LJAU01000001	Bs006	45	30	15	10	4.17309	4074	3969	Musa acuminata
NZ_LJDI01000020	XK-4-1	37	24	13	12	3.94181	3821	3701	Cotton
NZ_LMAG01000001	RHNK22	38	27	11	12	3.97818	3837	3698	-
NZ_LMAT01000001	Jxnuwx-1	40	27	13	10	4.08932	4008	3870	-
NZ_LMUC01000016	H57	34	23	11	11	3.95883	3859	3732	Lucerne
NZ_LPUP01000011	11B91	33	20	13	10	4.02366	3892	3702	-
NZ_LQQW01000001	M49	41	30	11	11	3.88665	3741	3617	-
NZ_LQYO01000001	B4140	39	25	14	11	4.01425	3847	3713	-
NZ_LQYP01000001	B425	29	20	9	9	3.9682	4034	3844	-
NZ_LYUG01000001	SRCM101266	31	19	12	11	3.76536	3781	3628	-
NZ_LZZO01000001	SRCM101294	32	20	12	10	3.96275	3982	3850	-

“Total” of Biosynthesis geneclusters is include “Known”and“Unknown”.“Known” of Biosynthesis geneclusters from the MIBiG (Minimum Information about a Biosynthetic Gene cluster). “Unknown” of Biosynthesis geneclusters detected by Cluster Finder are further categorized into putative (‘Cf_putative’) biosynthetic types. A full integration of the recently published Cluster Finder algorithm now allows using this probabilistic algorithm to detect putative gene clusters of unknown types, “-” of host is unrecorded.

Table 3. biosynthetic geneclusters of Y2 strains

Cluster	Type	Most similar known cluster	MIBiG BGC-ID
Cluster 1	Nrps	Surfactin_biosynthetic_gene_cluster (43% of genes show similarity)	BGC0000433_c1
Cluster 2	Cf_putative	-	-
Cluster 3	Cf_putative	-	-
Cluster 4	Cf_fatty_acid	-	-
Cluster 5	Phosphonate	Pactamycin_biosynthetic_gene_cluster (3% of genes show similarity)	BGC0000119_c1
Cluster 6	Cf_saccharide	Plantathiazolicin_/_plantazolicin_biosynthetic_gene_cluster (33% of genes show similarity)	BGC0000569_c1
Cluster 7	Cf_putative	-	-
Cluster 8	Otherks	-	-

Cluster 9	Cf_fatty_acid	-	-
Cluster 10	Cf_putative	-	-
Cluster 11	Terpene	-	-
Cluster 12	Cf_fatty_acid	-	-
Cluster 13	Cf_putative	-	-
Cluster 14	Cf_putative	-	-
Cluster 15	Transatpks	Macrolactin_biosynthetic_gene_cluster (90% of genes show similarity)	BGC0000181_c1
Cluster 16	Nrps-Transatpks	Bacillaene_biosynthetic_gene_cluster (85% of genes show similarity)	BGC0001089_c1
Cluster 17	Nrps-Transatpks	Fengycin_biosynthetic_gene_cluster (93% of genes show similarity)	BGC0001095_c1
Cluster 18	Terpene	-	-
Cluster 19	Cf_saccharide-T3pks	-	-
Cluster 20	Transatpks	Difficidin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000176_c1
Cluster 21	Cf_putative	-	-
Cluster 22	Nrps-Bacteriocin	Bacillibactin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000309_c1
Cluster 23	Cf_saccharide	-	-
Cluster 24	Nrps	-	-
Cluster 25	Cf_saccharide	Teichuronic_acid_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0000868_c1
Cluster 26	Cf_putative	-	-
Cluster 27	Cf_saccharide	Bacilysin_biosynthetic_gene_cluster (100% of genes show similarity)	BGC0001184_c1
Cluster 28	Cf_putative	-	-
Cluster 29	Lantipeptide	Mersacidin_biosynthetic_gene_cluster (90% of genes show similarity)	BGC0000527_c1
Cluster 30	Cf_saccharide	-	-
Cluster 31	Cf_putative	-	-

“Cf putative” is putative biosynthetic types (unknown types) detected by Cluster Finder are further categorized, known types from the MIBiG (Minimum Information about a Biosynthetic Gene cluster , http://mibig.secondarymetabolites.org).

4 DISCUSSION

Docker advantages and limitations:

Docker advantages as follow:

1.Dockerfile convenient for deployed and shared; make it is easy for other users to customize the image by editing the Dockerfile directly.It very unlikely Makefile and other installation that the resulting build will differ when being built on different machines(Boettiger C. 2014).Through Dockerfile, can maintain and update related adjustment, further more rapid rollback in the event of failure of System, according to the demand to control version and build the best application environment.

2.Portability, Modular reuse; Most bioinformatics tools is written in different languages, require different operating environment configuration and cross platform, Docker provide the same functions and services in different environments without additional configuration(Folarin, A. *et al*. 2015), so it is possible that the results of repetition and reuse tools. By constructing pipelines with different tools, bioinformatics can automatically and effectively analyze scientific problem they are concern at of biological.

3.Application solation,efficiency,exible:Docker can be run independently containers of every applications,and Management operations (start, stop,boot, etc.) of Containers in seconds or milliseconds;we may run more than hundreds of containers on a single host (Ali, A. A. *et al*. 2016). This ensure that the failure of one task does not cause disruption of the entire process, and quickly start a new container to continue to perform this task until the completion of the whole process, improve the overall efficiency.

Docker limitations as follow:

1.Docker is limited to 64-bit host machines, then making it can not to run on 32-bit older hardware.

2.On Mac and Windows OS,Docker must run boot2docker tool in a fully virtualized environment.

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