Genome Warehouse: A Public Repository Housing Genome-scale Data

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Abstract

The Genome Warehouse (GWH) is a public repository housing genome assembly data for a wide range of species and delivering a series of web services for genome data submission, storage, release, and sharing. As one of the core resources in the National Genomics Data Center (NGDC), part of the China National Center for Bioinformation (CNCB, https://bigd.big.ac.cn/), GWH accepts both full genome and partial genome (chloroplast, mitochondrion, and plasmid) sequences with different assembly levels, as well as an update of existing genome assemblies. For each assembly, GWH collects detailed genome-related metadata including biological project and sample, and genome assembly information, in addition to genome sequence and annotation. To archive high-quality genome sequences and annotations, GWH is equipped with a uniform and standardized procedure for quality control. Besides basic browse and search functionalities, all released genome sequences and annotations can be visualized with JBrowse. By December 2020, GWH has received 17,264 direct submissions covering a diversity of 949 species, and has released 3370 of them. Collectively, GWH serves as an important resource for genome-scale data management and provides free and publicly accessible data to support research activities throughout the world. GWH is publicly accessible at https://bigd.big.ac.cn/gwh/.

KEYWORDS: Genome submission; Genome sequence; Genome annotation; Genome warehouse; Quality control

Introduction

Genome sequences and annotations are fundamental information for a wide range of genome-related studies, including various omics data analysis such as genome [1], transcriptome [2], epigenome [3,4], and genome variation [5,6]. China, as one of the most biodiverse countries in the world, harbors more than 10% of the world's known species [7]. In the past decades, a large number of genome assemblies of featured and important animals and crops in China have been sequenced [1, 8–11], most of which were submitted to International Nucleotide Sequence Database Collaboration (INSDC) members (National Center for Biotechnology Information (NCBI), European Bioinformatics Institute (EBI), and DNA Data Bank of Japan (DDBJ)) [12]. With the rapid growth of genome assembly data, in China for example, large genome data size, slow data transfer rate due to limited international network transfer bandwidth, and language barrier for communication of technical issues have obstructed researchers from efficiently submitting their data to INSDC members. All these call for a centralized genomic data repository within China to complement the INSDC.

Here, we report the Genome Warehouse (GWH, https://bigd.big.ac.cn/gwh/), a centralized resource housing genome assembly data and delivering a series of genome data services. As one of the core resources in the National Genomics Data Center (NGDC), part of the China National Center for Bioinformation (CNCB, https://bigd.big.ac.cn/) [13], the aim of GWH is to accept data submissions worldwide and provide an important resource for genome data quality control, data archive, rapid release, and public sharing (*e.g.*, with INSDC) in support of research activities from all over the world. To date, GWH has received a total of 12,366 genome submissions (including 14 international submissions), demonstrating its increasingly important role in global genome data management and sharing.

Data model

Designed for compatibility with the INSDC data model, each genome assembly in GWH is linked to a BioProject (https://bigd.big.ac.cn/bioproject) and a BioSample (https://bigd.big.ac.cn/biosample), which are two fundamental resources for metadata description in CNCB-NGDC. Full or partial (chloroplast, mitochondrion, and plasmid) genome assemblies with different assembly levels (complete, draft in chromosome, scaffold, and contig) are all acceptable and existing genome assemblies are allowed to be updated. Accession numbers are assigned with the following rules (**Figure 1**): (1) each genome assembly has an accession number prefixed with "GWH", followed by four capital letters and eight zeros (*e.g.*, GWHAAAA00000000); (2) genome sequences have the same accession number format as their corresponding genome assembly, with the exception that the eight digits start from 00000001 and increase in order (*e.g.*, GWHAAAA00000001); (3) genes have similar accession pattern as those of genome sequences, with the addition of letter "G" between the GWH prefix and the four capital letters, and there are six digits at the end instead of eight (*e.g.*, GWHGAAAA000001); (4) transcripts use the letter "T" to replace "G" in accession numbers for genes (*e.g.*, GWHTAAAA000001); (5) proteins use the letter "P" to replace "G" in accession numbers for genes (*e.g.*, GWHPAAAA000001); (6) if the submission is an update of existing submission in GWH, it will be assigned a dot and an incremental number to represent the version (*e.g.*, GWHAAAA00000000.1).

Database components

GWH is a centralized resource housing genome-scale data, with the purpose to archive high-quality genome sequences and annotation information. GWH is equipped with a series of web services for genome data submission, release, and sharing, accordingly involving three major components, namely, data submission, quality control, and archive and release (Figure 2).

Data submission

GWH not only accepts genome assembly associated data through an on-line submission system but also allows off-line batch submissions. Users need to register first and then to provide complete description on submitted genome sequences. Biological project and sample information should be provided (through BioProject and BioSample, respectively) together with genome assembly sequence, annotation, and associated metadata. Metadata mainly consist of a variety of information about submitter, general assembly, file(s), sequence assignment, and publication (if available). After submission, GWH runs an automated quality control pipeline to check the validity and consistency of submitted genome sequence and genome annotation files. Accession numbers are assigned to assemblies and sequences upon the pass of quality control. The updated assembly data can also be submitted to GWH. It should be noted that compatible with the INSDC members (*e.g.*, NCBI GenBank), it is the responsibility of the submitters to ensure the data quality, completeness, and consistency and GWH does not warrant or assume any legal liability or responsibility for the data accuracy.

Quality control

After metadata and file(s) are received, GWH automatically runs standardized quality control (QC) to check 45 different types of errors in submitted genome sequences and annotations, and to scan for contaminated genome sequences (see details at https://bigd.big.ac.cn/gwh/documents) if needed (Figure 2), which roughly falls into 5 QC steps: (1) The component will check the consistency of file(s) according to filename and md5 code. (2) For genome sequences, the component will check the legality of genome sequence ID and sequence content, *e.g.*, unique sequence ID, sequence composition (A/T/C/G or degenerate base), sequence length (≥ 200 bp). (3) For genome annotations, the component will check gene structure completeness and consistency, *e.g.*, unique ID, a exon/CDS/UTR coordinate falling within the corresponding gene coordinate, strand consistency for all features (including gene/transcript/exon/CDS/UTR), codon validity (*e.g.*, valid start/stop codon, no internal stop codon). (4) Finally, it will check the internal consistency of genome sequence and annotation, *e.g.*, sequence ID in genome annotation must match genome sequence ID, a feature coordinate falling within the range of the corresponding genome sequence. (5) Genome sequences will also be scanned to check vectors, adaptors, primers, and indices (collected from UniVec database, ftp://ftp.ncbi.nlm.nih.gov/pub/UniVec/) using NCBI's VecScreen (https://www.ncbi.nlm.nih.gov/tools/vecscreen/). If there is an error, a report will be automatically sent to the submitter by email. To finish a successful submission, the submitter needs to fix all errors and resubmit files until they pass the QC process.

Archive and release

GWH will assign a unique accession number to the submitted genome assembly upon the pass of quality control, allot accession numbers for each genome sequence, gene, transcript, and protein, generate and backup downloadable files of genome sequence and annotation in FASTA, GFF3, and TSV formats. Data generation is performed with in-house-writing scripts based on submitted genome sequence and annotation files. In order to ensure the security of submitted data, a copy of backup data is stored on a physically separate disk. GWH will release sequence data on a user-specified date, unless a paper citing the sequence or accession number is published prior to the specified release date, in which case the sequence will be released immediately. For the released data, GWH will generate web pages containing two primary tables: genome and assembly. The former shows species taxonomy information and genome assemblies, and the latter contains general information of the assembly (including external links to other related resources), statistics of genome assembly and its corresponding annotation. All released data are publicly available at GWH FTP site (ftp://download.big.ac.cn/gwh/). GWH provides data visualization for both genome sequence and genome annotation using JBrowse [14]. It offers statistics and charts in light of total holdings, assembly levels, genome representations, citing articles, submitting organizations, sequencing platforms, assembly methods, and downloads. GWH provides user-friendly web interfaces for data browse and query using BIG Search [13], in order to help users find any released data of interest. For a released genome assembly, GWH also provides machine-readable APIs (Application Programming Interfaces) for publicly sharing and automatically obtaining information on its associated BioProject, BioSample, genome, and assembly metadata and file paths.

Global sharing of SARS-CoV-2 and coronavirus genomes

During the COVID-19 outbreak, GWH, in support of the 2019 Novel Coronavirus Resource (2019nCoVR) [15, 16] has received worldwide submissions of more than a thousand SARS-CoV-2 genome assemblies with standardized genome annotations [17], and has released 134 of them. To expand the international influence of data, 62 of the released sequences have been shared, with the submitters' permission, in GenBank [18] through a data exchange mechanism established with NCBI. In this model, GWH accessions are represented as secondary accessions in NCBI GenBank records, which are retrievable by the NCBI Entrez system. This model sets a good example for data sharing among different data centers.

In addition, GWH offers sequences of the Coronaviridae family to facilitate researchers to reach the data conveniently and thus to study the relationship between SARS-CoV-2 and other coronaviruses. To promote the data sharing and make all relevant information of the Coronaviridae readily available, GWH integrates genomic and proteomic sequences as well as their metadata information from NCBI [19], China National GeneBank Database (CNGBdb) [20], National Microbiology Data Center (NMDC) [21] and CNCB-NGDC. Duplicated records from different sources are identified and removed to gain a non-redundant dataset. As of December 31, 2020, the dataset has 83,095 nucleotide and 575,438 protein sequences of the Coronaviridae. Filters are implemented to narrow down the required Coronaviridae sequences using multiple conditions, including country/region, host, isolation source, length, and collection date. Both the metadata and sequences of the filtered results can be selected and downloaded as a separate file. The daily updated sequences and all sequences can also be downloaded from FTP (ftp://download.big.ac.cn/Genome/Viruses/Coronaviridae/).

Data statistics

By December, 2020, GWH has received 17,264 direct submissions covering a broad diversity of species (**Table 1**) with different assembly levels (Figure 3). These genome assemblies link to 301 BioProjects and 16,538 BioSamples, and are submitted by 231 submitters from 61 institutions (including 5 international submitters from 2 countries). There are a total of 3370 released submissions, which were reported in 83 articles from 44 journals. GWH has over 135,000 visits from 153 countries/regions, with ~891,000 downloads. The amount of data, visits, and downloads in the GWH has been on the dramatic increase over the past years, clearly showing its great utility in genome-scale data management.

Summary and future directions

Collectively, GWH is a user-friendly portal for genome data submission, release, and sharing associated with a matched series of services. The rapid growth of genome assembly submissions demonstrates the great potential of GWH as an important resource for accelerating the worldwide genomic research. With the aim to fully realize the findability, accessibility, interoperability, and reusability (FAIR) of genome data [22], GWH has made ongoing efforts, including but not limited to, improvement of web interfaces for data submission, presentation, and visualization, continuous integration of newly sequenced genomes, and development of useful online tools to help users analyse genome data (such as BLAST [23]). Therefore, we will put in more efforts to provide genome annotation services, especially for bacteria and archaea genomes, with the particular consideration that uniform standardized annotation determines the accuracy of downstream data analysis. Besides, we will expand the Coronaviridae dataset to other important pathogens to improve the ability of public health emergency response. Finally, we plan to share and exchange all public genome assembly data with the INSDC members to provide comprehensive data for researchers globally.

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Competing interests

The authors have declared no competing interests.

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Figure legends

Figure 1 Data model in GWH

Genome assembly accession number is prefixed with "GWH", followed by four capital letters (represented by XXXX) and 8 zeros. For genome sequence accessions, eight digits increase in order. For gene sequence, transcript sequence, and protein sequence accessions, G, T, and P are followed by the GWH prefix, respectively, with six digits at the end that increase in order.

Figure 2 Major components in GWH data processing workflow

Figure 3 Statistics of genome assembly in GWH (as of December 31, 2020)

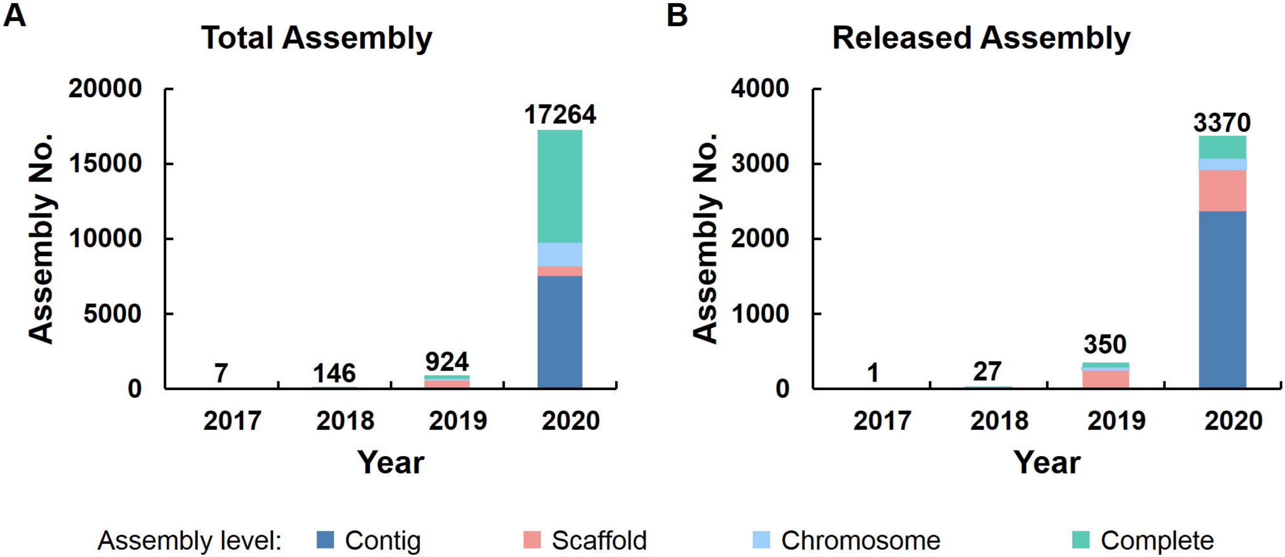
Tables

Table 1 Total data holdings in GWH

Status	Type	Animals	Plants	Fungi	Bacteria	Archaea	Viruses	Metagenomes	Others	Total
Released	Assembly	187 (5.55%)	210 (6.23%)	13 (0.39%)	220 (6.53%)	73 (2.17%)	701 (20.80%)	1957 (58.07%)	9 (0.27%)	3370
	Species	72 (19.41%)	139 (37.47%)	12 (3.23%)	106 (28.57%)	11 (2.96%)	19 (5.12%)	3 (0.81%)	9 (2.43%)	371
Unpublic	Assembly	6783 (48.82%)	926 (6.66%)	5 (0.04%)	68 (0.49%)	13 (0.09%)	939 (6.76%)	4702 (33.84%)	458 (3.30%)	13,894
	Species	22 (3.67%)	549 (91.50%)	5 (0.83%)	7 (1.17%)	2 (0.33%)	6 (1.00%)	5 (0.83%)	4 (0.67%)	600
Total	Assembly	6970 (40.37%)	1136 (6.58%)	18 (0.10%)	288 (1.67%)	86 (0.50%)	1640 (9.50%)	6659 (38.57%)	467 (2.71%)	17,264
	Species	92 (9.69%)	675 (71.13%)	16 (1.69%)	110 (11.59%)	13 (1.37%)	24 (2.53%)	7 (0.74%)	12 (1.26%)	949

Genome Assembly
GWHXXXX00000000
Genome Sequence 1
GWHXXXX00000001
...
Genome Sequence m
GWHXXXX0000000m
Gene Sequence 1
GWHGXXXX000001
...
Gene Sequence i
GWHGXXXX00000i
...
Gene Sequence j
GWHGXXXX00000j
...
Gene Sequence n
GWHGXXXX00000n
Transcript Sequence 1
GWHTXXXX000001
...
Transcript Sequence k
GWHTXXXX00000k
...
Transcript Sequence l
GWHTXXXX00000l
Transcript Sequence l+1
GWHTXXXX00000(l+1)
...
Transcript Sequence x
GWHTXXXX00000x
Protein Sequence 1
GWHPXXXX000001
...
Protein Sequence k
GWHPXXXX00000k
...
Protein Sequence l
GWHPXXXX00000l
...
Protein Sequence y
GWHPXXXX00000y

Data Submission
Register account
Register BioProject
Register BioSample
Create a submission
Fill meta-data
Upload files
Quality Control
Filename & md5 code
Genome sequence
• Sequence ID
• Sequence content
Genome annotation
• Gene structure completeness
• Gene structure consistency
Data internal consistency
Sequence contamination
(optional)
Archive & Release
Accession assignment
• Genome assembly
• Genome sequence
• Gene
• Transcript
• Protein
Generation of downloadable files & backup
• Genome sequence
• Genome annotation
• Gene feature
• RNA sequence
• CDS sequence
• Protein sequence
Release & sharing
• Genome
• Assembly
• Download files
• Genome browser
• BIG Search


A
Total Assembly
Assembly No.
20000
15000
10000
5000
0
7
146
924
17264
2017
2018
2019
2020
Year
B
Released Assembly
Assembly No.
4000
3000
2000
1000
0
1
27
350
3370
2017
2018
2019
2020
Year
Assembly level:
Contig
Scaffold
Chromosome
Complete