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BRIEF REPORT

OysterDB: A Genome Database for Ostreidae

Xinchun Li[1] · Yitian Bai[1] · Chengxun Xu[1] · Shikai Liu[1] · Hong Yu[1] · Lingfeng Kong[1] · Shaojun Du[3] · Qi Li[1,2]

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Abstract
The molluscan family Ostreidae, commonly known as oysters, is an important molluscan group due to its economic and ecological importance. In recent years, an abundance of genomic data of Ostreidae species has been generated and available in public domain. However, there is still a lack of a high-efficiency database platform to store and distribute these data with comprehensive tools. In this study, we developed an oyster genome database (OysterDB) to consolidate oyster genomic data. This database includes eight oyster genomes and 208,923 protein-coding gene annotations. Bioinformatic tools, such as BLAST and JBrowse, are integrated into the database to provide a user-friendly platform for homologous sequence searching, visualization of genomes, and screen for candidate gene information. Moreover, OysterDB will be continuously updated with ever-growing oyster genomic resources and facilitate future studies for comparative and functional genomic analysis of oysters (http://oysterdb.com.cn/).

Keywords Oyster · Genome · Database · Bioinformatic tools

Introduction

The family Ostreidae belongs to the phylum Mollusca and the class Bivalvia (WoRMS Editorial Board 2024; Li et al. 2020). This family contains 16 genera and 74 species, with the mostly oyster species belonging to *Magallana*, *Crassostrea*, *Ostrea*, *Saccostrea*, and *Dendostrea* (Salvi et al. 2014; WoRMS Editorial Board 2024). Oysters are distributed across various marine environments globally, including estuarine areas with species like the *C. virginica* (euryhaline and eurythermal), *O. edulis* (euryhaline and eurythermal), *M. hongkongensis* (thermophilic and oligohaline), and *M. ariakensis* (eurythermal and oligohaline). They are also found in intertidal zones, such as the *M. gigas* (euryhaline and eurythermal) and *M. angulata* (thermophilic and euryhaline), as well as in the high-salinity subtidal zones, exemplified by *M. nippona* and *O. denselamellosa* (Casas et al. 2018; Eymann et al. 2020; Perry et al. 2023). Oysters are characterized by their left–right shell asymmetry, with the flat right valve and the convex left valve. As filter-feeding benthos, oysters attach their left valve to a substrate and sieve plankton and organic particulates from the water (Salvi et al. 2014). Oysters play a crucial role as ecosystem engineers. Oyster reefs serve vital ecological functions by maintaining the environmental stability of the coastline and providing essential habitats for marine organisms (Searles et al. 2022; Barbier et al. 2011; Davis and Kidd 2012). Moreover, the oyster aquaculture industry holds a considerable economic importance globally. The major commercial oyster species include the Pacific oyster (*M. gigas*), European oyster (*O. edulis*), Hong Kong oyster (*M. hongkongensis*), Portuguese oyster (*M. angulata*), Eastern oyster (*C. virginica*), and Sydney rock oyster (*S. glomerata*) (Jiang et al. 2024). Over the past seven decades, the global oyster aquaculture production has increased from 0.2 million in 1950 to 6.67 million tons in 2021 (FAO 2024). However, wild populations of some oyster species, such as the European oyster, had nearly been extinct by the mid-twentieth century along the coastlines of Europe, due to the impacts of overfishing, pollution, invasive species, and disease (Airoldi and Beck

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✉ Qi Li
qili66@ouc.edu.cn

[1] Key Laboratory of Mariculture, Ministry of Education, Ocean University of China, Qingdao 266003, China

[2] Laboratory for Marine Fisheries Science and Food Production Processes, Qingdao National Laboratory for Marine Science and Technology, Qingdao 266237, China

[3] Institute of Marine and Environmental Technology, Department of Biochemistry and Molecular Biology, University of Maryland School of Medicine, Baltimore, MD, USA

2007; Beck et al. 2011; Thurstan et al. 2013; Stechele et al. 2022). The Pacific oyster, introduced as an economic species on every continent except Antarctica, may fundamentally alter local ecosystems and disrupt local biodiversity (Beck et al. 2024; King et al. 2020). Therefore, it is of significant importance to gain a deeper understanding of the biological characteristics and ecological functions of oysters for the conservation of marine resources and the promotion of sustainable development.

With the rapid development of high-throughput sequencing technologies, 25 oyster genomes have been sequenced over the past decade (Powell et al. 2018; Bai et al. 2023; Qi et al. 2022; Li et al. 2021a, 2023; Zhang et al. 2022; Dong et al. 2023; Boutet et al. 2022; Gundappa et al. 2022 Adkins et al. 2023). These genomic and transcriptomic studies have deepened our knowledge of the environmental adaptation (Zhang, et al. 2012), such as parasite resistance, stress response, and osmotic pressure regulation (Li et al. 2023), as well as molecular genetic of shell formation (Zhang et al. 2012; Bai et al. 2023) and evolution (Bai et al. 2023) of this group. However, the genomic resources of Ostreidae are currently scattered across multiple public databases, including NCBI, CNGBdb, Figshare, and dbSROG databases, presenting a significant challenge for researchers to fully leverage the genomic potential. Recently, many genomic databases focusing on specific biological taxa have been constructed, such as GDR database for Rosaceae (Jung et al. 2019, 2004), HeveaDB for Rubber tree (Cheng 2020), and MolluscDB for molluscs (Caurcel et al. 2021; Liu et al. 2021). These databases have incorporated various types of high-throughput sequencing data, which are essential for maximizing the utilization of valuable datasets. However, a comprehensive oyster genomic database has yet to be established with powerful and inclusive bioinformatic tools.

For biological researchers, acquiring the necessary powerful computer information technology for establishing an accessible database requires a substantial investment of resource and effort in learning. Thus, Drupal (https://www.drupal.org/) has emerged as a solution in the past decades. It is an open-source, popular content management system (CMS) with an active community that allows users to freely download from thousands of user-contributed extensions, as well as to customize and upload new extension modules. Concurrently, Chado (http://gmod.org/wiki/Chado_-_Getting_Started) is built to handle complex representations of biological knowledge, including sequence, phenotypes, genotypes, ontologies, publications, and other useful information. Based on the above two tools, Tripal was designed as a versatile toolkit for the streamlined development of online genomic databases (Ficklin et al. 2011). It is a freely accessible and open-source suite of modules within Drupal for managing and visualizing data housed in the Generic Model Organism Database (GMOD) Chado database (Ficklin et al. 2011). Nowadays, Tripal provides the primary support for at least 31 public databases, covering a wide range of taxa including plants, animals, and humans, with plants comprising the majority (Staton et al. 2021). This technology allows non-technical biologists to quickly establish databases and reduce the costs of building and maintaining them.

In this study, we constructed the Oyster Genome Database (OysterDB; http://oysterdb.com.cn/) with Tripal (Staton et al. 2021; Ficklin et al. 2011). This database integrates oyster genomic resources and developed bioinformatic tools, providing researchers with a convenient and user-friendly online platform for molecular genetic studies on oysters.

Material and Methods

Genomic Data

A total of 12 published oyster genome assemblies were collected and integrated in the OysterDB (Table 1). The genome assemblies of *M. gigas* (GCF_902806645.1 and GCF_000297895.1), *C. virginica* (GCF_002022765.2), *M. angulata* (GCF_025612915.1), and *O. edulis* (GCA_024362745.1, GCA_023158985.1 and GCF_947568905.1) were obtained from the National Center for Biotechnology Information (NCBI) database (Adkins et al. 2023; Boutet et al. 2022; Gundappa et al. 2022; Peñaloza et al. 2021; Teng et al. 2023; Modak et al. 2021; Zhang et al. 2012), and those of *M. nippona*, *O. edulis*, and *O. denselamellosa* were downloaded from the Figshare database (Bai et al. 2023; Dong et al. 2023; Li et al. 2023). *M. ariakensis* genome (CNA0022698) was downloaded from the China National GeneBank (CNGB) database (Wu et al. 2022). In addition, the *S. glomerata* genome was collected form the dbSROG database (Powell et al. 2018).

Gene Function Annotation

For the functionally well-annotated species by NCBI, including *M. gigas* (GCF_902806645.1 and GCF_000297895.1), *M. angulata*, *C. virginica*, and *O. edulis* (GCA_023158985.1 and GCF_947568905.1), we utilized the version annotated with GenBank or RefSeq features. For the other oyster genomes that have only structural annotations but lack of functional annotations, we performed functional annotations for the protein-coding genes using eggNOG-mapper software (version 2.1.12) against the EggNOG database (version 5.0) with the default parameters (Huerta-Cepas et al. 2019).

Data Integration and Website Construction

The database was developed and deployed using the Tencent Cloud Linux servers and the Apache Web server software.

Table 1 Statistics of oyster genomes in the OysterDB

Species	Genome size (Mb)	Scaffold N50	GC percent (%)	Data source
Crassostrea virginica	684.7	75.9 Mb	35	GCF_002022765.2 (NCBI)
Magallana gigas	647.9	58.5 Mb	33.5	GCF_902806645.1 (NCBI)
Magallana gigas	557.7	401.7 kb	35.5	GCF_000297895.1 (NCBI)
Magallana angulata	624.3	60.5 Mb	33.5	GCF_025612915.1 (NCBI)
Magallana nippona	529.0	50.9 Mb	34	Figshare website
Magallana anriakensis	663.1	66.3 Mb	33.6	CNA0022698 (CNGB)
Saccostrea glomerata	788.1	804.2 kb	33.5	dbSROG
Ostrea densekamellosa	635.9	71.8 Mb	35	Figshare website
Ostrea edulis	946.0	94.8 Mb	35.5	Figshare website
Ostrea edulis	1035.8	95.8 Mb	35.5	GCA_024362745.1 (NCBI)
Ostrea edulis	935.1	95.6 Mb	35.4	GCA_023158985.1 (NCBI)
Ostrea edulis	894.8	94.3 Mb	35.5	GCF_947568905.1 (NCBI)

The front-end web development technologies for the database include HTML, CSS, and JavaScript languages. This is complemented by the Bootstrap framework that facilitates rapid development of websites and web applications. The content management system Drupal (version 7), the relational database schema Chado, and the open-source relational database PostgreSQL were installed on the Linux server. These components were seamlessly integrated and aggregated through the Tripal toolkit. After the data mentioned above had been converted to a standardized format, they were stored in PostgreSQL using the data loaders provided by Tripal. An online sequence comparison tool, BLAST, was constructed using the Tripal BLAST software, with additional support from the Tripal Job Daemon for managing the BLAST requests submitted by users. This setup ensures the automated execution of the request and swift delivery of the results. The integration of JBrowse (Diesh et al. 2023) software with Drupal Bioinformatic Server Framework provides a fast-responsive and high-performance genome browser for visualizing genome sequences and corresponding annotation information of the oyster genomes.

Results and Discussion

Overview of the Database

The Homepage of OysterDB

The homepage of the OysterDB is primarily divided into the navigation bar, the phylogenetic tree of the Ostreidae family, and a footer containing the affiliated institutions (Fig. 1). Located at the top of the homepage, the navigation bar consists of eight labels: home, species, search, download, BLAST, JBrowse, login, and register. The modules of "register" and "login" are intended for administrator use only. Public ordinary users are not required to log in to access all functionalities of the database. Below the navigation bar is the phylogenetic tree of the Ostreidae family obtained from a previous study (Li et al. 2021b), through which users can visually find the classification of oysters.

Species and Download

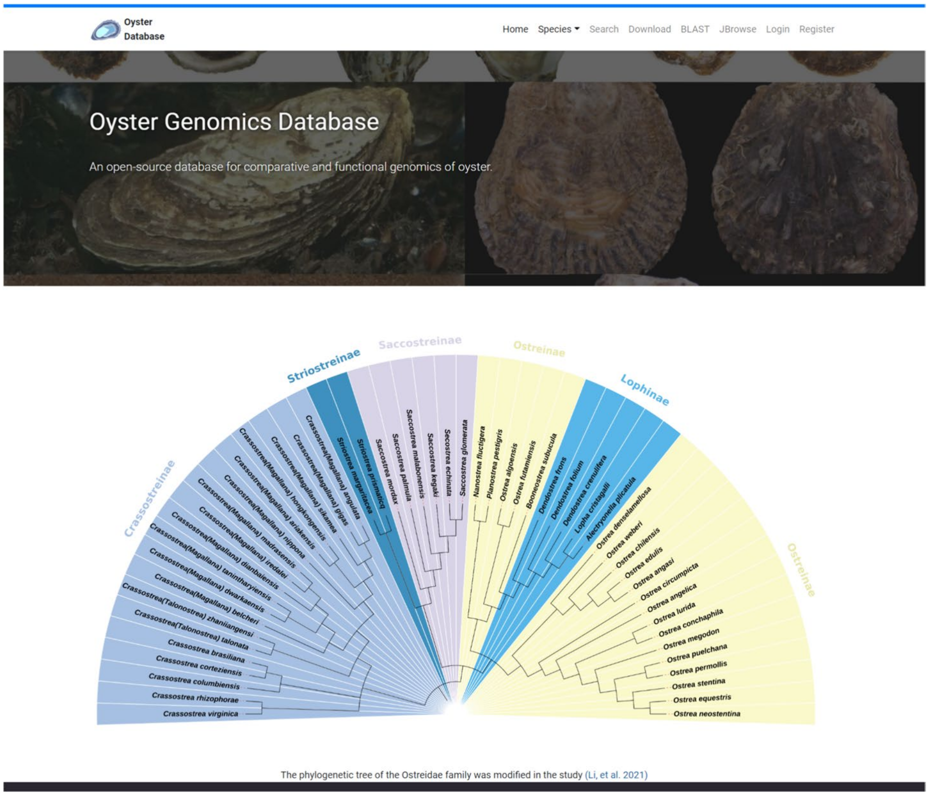
Clicking on the "Species" dropdown menu in the navigation bar displays information for eight oyster species, including common name, genus, species, images, description, genome assembly statistics, and distribution map (Fig. S1). In addition, we provide the link to the publications utilized the genome of each species under "Publication" tab. All data in OysterDB are available for users to download, including the genome assembly (FASTA), the gene annotation (GFF3/GBFF), the protein sequences, and CDS sequences. Upon clicking the "Download" button in the navigation bar, users are directed to the download page to access the information of interest (Fig. S2).

With the rapid increase of oyster genomic and other omics data, we will continually update the database and enhance this database with more annotated information. Furthermore, we will also augment the database with additional omics data such as transcriptomics, proteomics, molecular markers for genome breeding, as well as practical tools including synteny analysis, gene expression, gene networks, and gene families. Furthermore, tools capable of deeply mining omics data based on machine learning will be integrated into the OysterDB in the future.

Statistical Overview of the Data

Currently, OysterDB stores genome data of eight oyster species. The genome size of *C. virginica* is 684.7 Mb,

Fig. 1 The homepage of OysterDB



An open-source database for comparative and functional genomics of oyster.

The phylogenetic tree of the Ostreidae family was modified in the study (Li, et al. 2021)

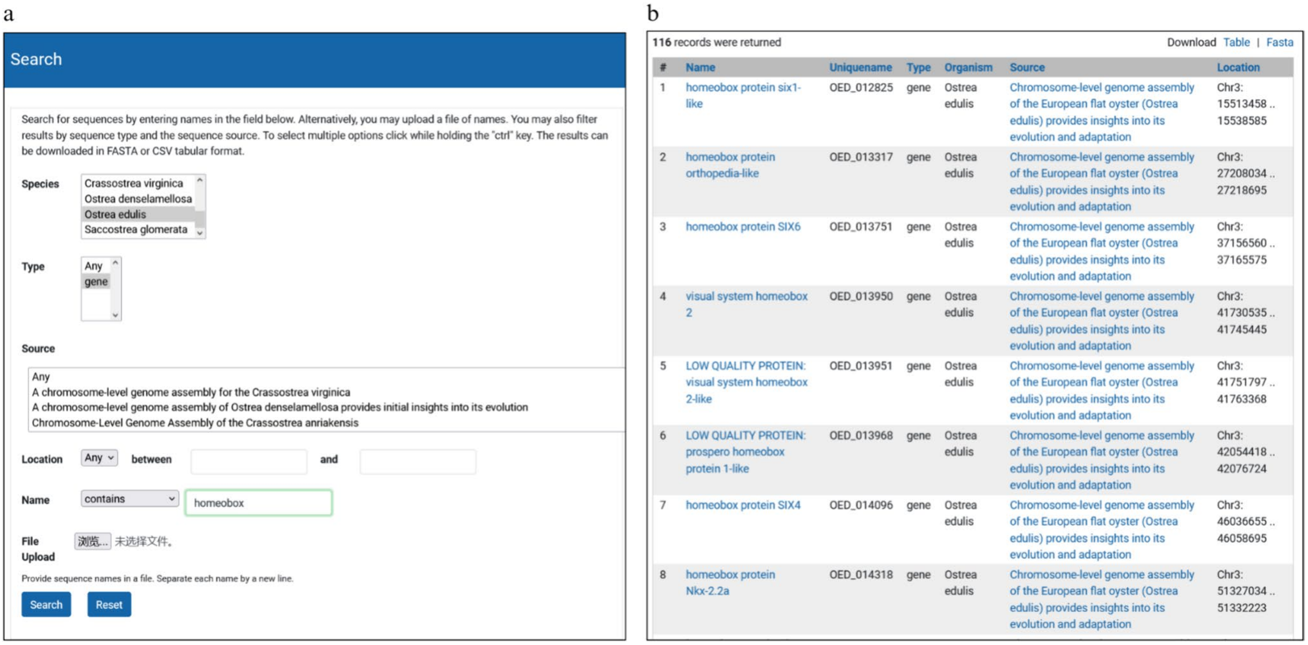
and the scaffold N50 is 75.9 Mb. In the genus *Magallana*, three species (*M. angulata*, *M. nippona*, and *M. ariakensis*) have genome sizes of 624.3 Mb, 529.0, and 663.1 Mb, with the scaffold N50 lengths of 60.5 Mb, 50.9 Mb, and 66.3 Mb, respectively. The sizes of the two genomes (GCF_902806645.1 and GCF_000297895.1) of *M. gigas* are 627.9 Mb and 557.7 Mb with the scaffold N50 lengths of 58.5 Mb and 401.7 kb, respectively. For the genus *Ostrea*, the genome size of *O. denselamellosa* is 635.9 Mb, and the scaffold N50 is71.8 Mb. The sizes of the four genomes (Figashere, GCA_024362745.1, GCA_023158985.1, and GCF_947568905.1) of *O. edulis* are 946.0 Mb,1035.8 Mb, 935.1 Mb, and 894.8 Mb, respectively, with the respective scaffold N50 lengths of 94.8 Mb, 95.8 Mb, 95.6 Mb, and 94.3 Mb. The genome size of *S. glomerata* is 788.1 Mb, and the scaffold N50 is 804.2 kb (Table 1).

A total of 17,780 protein-coding genes with functional annotations were collected from the well-annotated genomes. These include 34,076 genes from *M. ariakensis*, 60,162 genes from *M. gigas* (GCF_902806645.1 and GCF_000297895.1), 34,579 genes from *C. virginica*, and 36,693 genes from *O. edulis* (GCA_023158985.1 and GCF_947568905.1). In addition, we have performed functional annotations for the genomes that have only structural annotations without the functional annotations. In total, we annotated 106,232 protein-coding genes, including 24,398 genes from *M. ariakensis*, 27,407 genes from *M. nippona*, 30,899 genes from *O. edulis* (Figshare), and 23,528 genes from *O. denselamellosa*.

Bioinformatic Tools

Search

A search tool is presented on the menu "Search," which provides a method for users to easily access information on genes across eight oyster species, including gene annotations, gene IDs, species, the gene source, and the gene location. The search tool facilitates precise searches based on the start and end positions of genes, gene annotation keywords, and supports broad searches based on species names and gene source. Users can select the species or the gene source from the menu and enter the gene annotation keyword and gene positions as searching criteria, then click the search button. The search results are presented directly below on the search page, in a list format that includes gene annotation, gene ID, gene source, and gene location. For example, if the user chooses "*Ostrea edulis*" from the "Species" dropdown list and enter "homeobox" in the input box next to "Name," then clicks on the search button (Fig. 2a), a list of genes from *O. edulis* with functional annotations containing "homeobox" will be returned (Fig. 2b). The search results can be downloaded as a CSV file. This search tool helps users in quickly retrieving essential information about target



Search

Search for sequences by entering names in the field below. Alternatively, you may upload a file of names. You may also filter results by sequence type and the sequence source. To select multiple options click while holding the "ctrl" key. The results can be downloaded in FASTA or CSV tabular format.

Species
Crassostrea virginica
Ostrea denselamellosa
Ostrea edulis
Saccostrea glomerata

Type
Any
gene

Source
Any
A chromosome-level genome assembly for the Crassostrea virginica
A chromosome-level genome assembly of Ostrea denselamellosa provides initial insights into its evolution
Chromosome-Level Genome Assembly of the Crassostrea ariakensis

Location Any between and

Name contains homeobox

File Upload 浏览... 未选择文件。

Provide sequence names in a file. Separate each name by a new line.

Search Reset

116 records were returned Download Table | Fasta

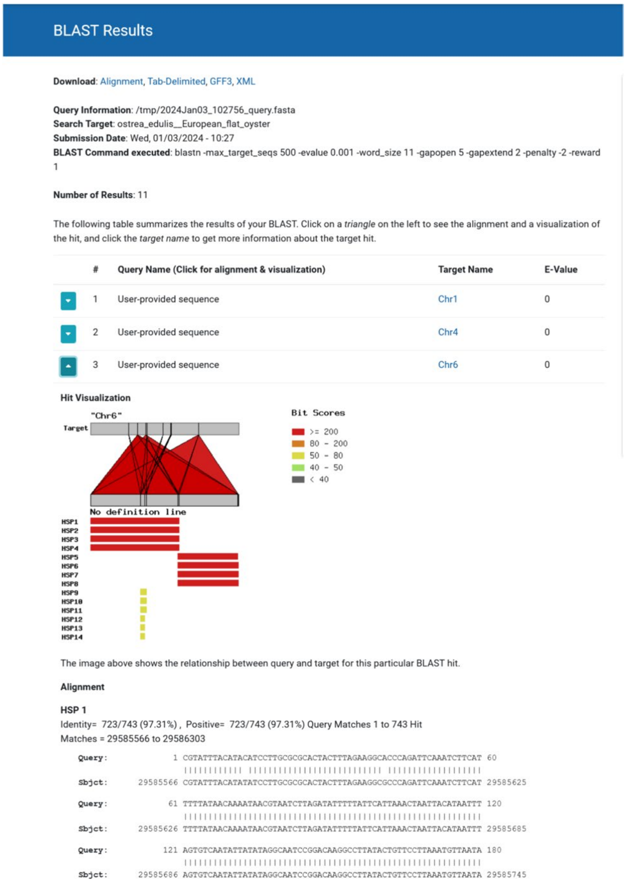
#	Name	Uniquename	Type	Organism	Source	Location
1	homeobox protein six1-like	OED_012825	gene	Ostrea edulis	Chromosome-level genome assembly of the European flat oyster (Ostrea edulis) provides insights into its evolution and adaptation	Chr3: 15513458 .. 15538585
2	homeobox protein orthopedia-like	OED_013317	gene	Ostrea edulis	Chromosome-level genome assembly of the European flat oyster (Ostrea edulis) provides insights into its evolution and adaptation	Chr3: 27208034 .. 27218695
3	homeobox protein SIX6	OED_013751	gene	Ostrea edulis	Chromosome-level genome assembly of the European flat oyster (Ostrea edulis) provides insights into its evolution and adaptation	Chr3: 37156560 .. 37165575
4	visual system homeobox 2	OED_013950	gene	Ostrea edulis	Chromosome-level genome assembly of the European flat oyster (Ostrea edulis) provides insights into its evolution and adaptation	Chr3: 41730535 .. 41745445
5	LOW QUALITY PROTEIN: visual system homeobox 2-like	OED_013951	gene	Ostrea edulis	Chromosome-level genome assembly of the European flat oyster (Ostrea edulis) provides insights into its evolution and adaptation	Chr3: 41751797 .. 41763368
6	LOW QUALITY PROTEIN: prospero homeobox protein 1-like	OED_013968	gene	Ostrea edulis	Chromosome-level genome assembly of the European flat oyster (Ostrea edulis) provides insights into its evolution and adaptation	Chr3: 42054418 .. 42076724
7	homeobox protein SIX4	OED_014096	gene	Ostrea edulis	Chromosome-level genome assembly of the European flat oyster (Ostrea edulis) provides insights into its evolution and adaptation	Chr3: 46036655 .. 46058695
8	homeobox protein Nkx-2.2a	OED_014318	gene	Ostrea edulis	Chromosome-level genome assembly of the European flat oyster (Ostrea edulis) provides insights into its evolution and adaptation	Chr3: 51327034 .. 51332223

Fig. 2 Gene search page of the OysterDB. **a** Search for gene annotation and location **b** the results page of gene search

genes, providing a convenient and efficient tool for gene analysis. In this study, the Mainlab Chado Search module utilizes pre-built local index tables to deliver high-performance search results and searches any sequence within the Chado database, such as gene, mRNA, and CDS. Therefore, the Mainlab Chado Search module offers easy scalability when new sequence types are added to the database. Currently, databases such as Citrus Genome Database (https://www.citrusgenomedb.org), CottonGen (Yu et al. 2021), and GDR (Jung et al. 2019) have been incorporated into this module to construct the search function.

Blast

Comparing newly obtained nucleotide and amino-acid sequences with previously known ones underpins modern biological research (Camacho et al. 2009). BLAST search is a well-established and user-friendly tool for sequence alignment (Priyam et al. 2019). The Tripal BLAST UI module facilitates nucleotide and amino acid sequence similarity searches through a user-friendly interface provided by BLAST. Users can align query nucleotide or protein sequences with BLASTN, BLASTX, TBLASTN, or BLASTP, respectively. BLAST submissions result in the creation of Tripal jobs which need to run from the command line, leading to increased waiting time for users and management overhead for administrators. To mitigate this problem, we have enabled the Tripal Jobs Deamon to automate running the Tripal Jobs, aiming to reduce user waiting times and enhance efficiency. The BLAST result page



BLAST Results

Download: Alignment, Tab-Delimited, GFF3, XML

Query Information: /tmp/2024Jan03_102756_query.fasta
Search Target: ostrea_edulis__European_flat_oyster
Submission Date: Wed, 01/03/2024 - 10:27
BLAST Command executed: blastn -max_target_seqs 500 -evalue 0.001 -word_size 11 -gapopen 5 -gapextend 2 -penalty -2 -reward 1

Number of Results: 11

The following table summarizes the results of your BLAST. Click on a *triangle* on the left to see the alignment and a visualization of the hit, and click the *target name* to get more information about the target hit.

	#	Query Name (Click for alignment & visualization)	Target Name	E-Value
▾	1	User-provided sequence	Chr1	0
▾	2	User-provided sequence	Chr4	0
▴	3	User-provided sequence	Chr6	0

The image above shows the relationship between query and target for this particular BLAST hit.

Alignment

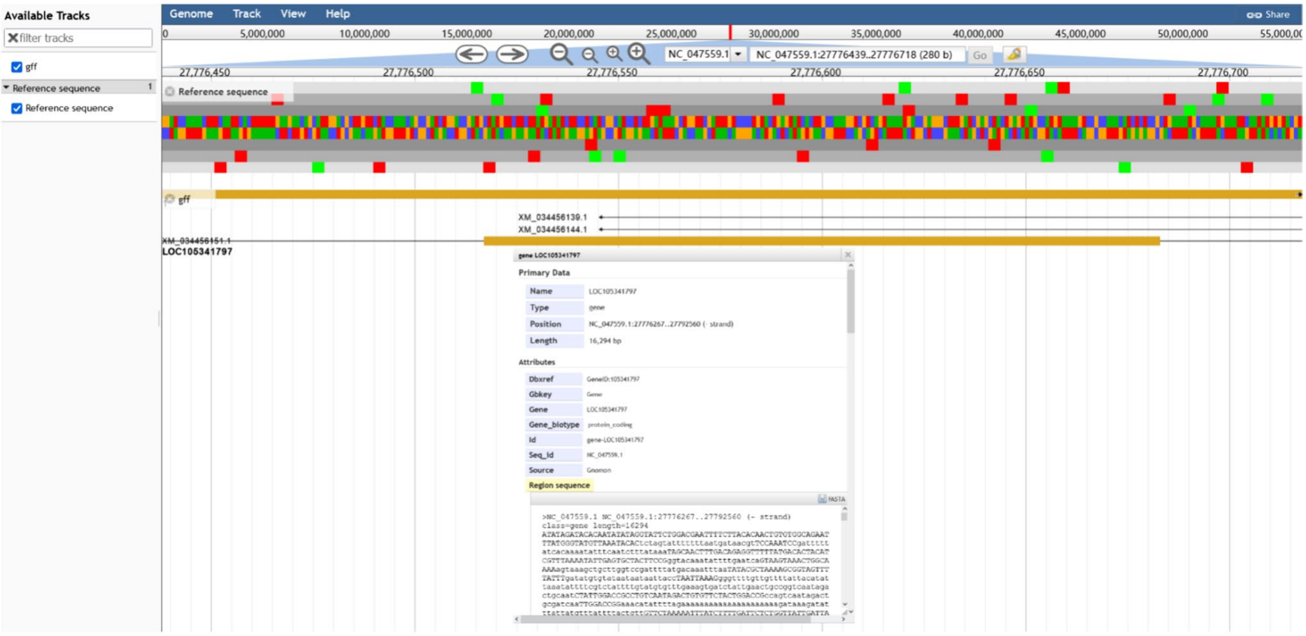
HSP 1
Identity= 723/743 (97.31%) , Positive= 723/743 (97.31%) Query Matches 1 to 743 Hit Matches = 29585566 to 29586303

```
Query:          1 CGTATTTACATACATCCTTGCGCGCACTACTTTAGAAGGCACCCAGATTCAAATCTTCAT 60
                  |||||||||||| ||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct:   29585566 CGTATTTACATATATCCTTGCGCGCACTACTTTAGAAGGCGCCCAGATTCAAATCTTCAT 29585625

Query:         61 TTTTATAACAAAATAACGTAATCTTAGATATTTTTATTCATTAAACTAATTACATAATTT 120
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   29585626 TTTTATAACAAAATAACGTAATCTTAGATATTTTTATTCATTAAACTAATTACATAATTT 29585685

Query:        121 AGTGTCAATATTATATAGGCAATCCGGACAAGGCCTTATACTGTTCCTTAAATGTTAATA 180
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   29585686 AGTGTCAATATTATATAGGCAATCCGGACAAGGCCTTATACTGTTCCTTAAATGTTAATA 29585745
```

Fig. 3 Results of nucleotide sequence alignment



Primary Data

Name	LOC105341797
Type	gene
Position	NC_047559.1:27776267..27792560 (- strand)
Length	16,294 bp

Attributes

Dbxref	GeneID:105341797
Gbkey	Gene
Gene	LOC105341797
Gene_biotype	protein_coding
Id	gene-LOC105341797
Seq_id	NC_047559.1
Source	Gnomon

```
>NC_047559.1 NC_047559.1:27776267..27792560 (- strand)
class=gene length=16294
ATATAGATACACAATATATAGGTATTCTGGACGAATTTTCTTACACAACTGTGTGGCAGAAT
TTATGGGTATGTTAAATACACtctagtattttttaatgataacgtTCCAAATCCgatttttt
atcacaaaatatttcaatctttataaaTAGCAACTTTGACAGAGGTTTTTATGACACTACAT
CGTTTAAAATATTGAGTGCTACTTCCGggtacaaatattttgaatcaGTAAGTAAACTGGCA
AAAagtaaagctgcttggtccgattttatgacaaatttaaTATACGCTAAAAGCGGTAGTTT
TATTTgatatgtgtataataataattaccTAATTAAAGggttttgttgttttattacatat
taaatattttcgtctattttgtatgtgtttgaaagtgatctattgaactgccggtcaataga
ctgcaatCTATTGGACCGCCTGTCAATAGACTGTGTTCTACTGGACCGccagtcaatagact
gcgatcaaTTGGACCGGaaacatatttttagaaaaaaaaaaaaaaaaaaaaagataaagatat
ttattatgtttattttactgttGTTCTAAAAATTTATCTTTTGATTCTCTGGTTATTGATTA
```

Fig. 4 Visualization of genomic regions using the genome browser and detailed gene information

is an expandable summary table with query, positions, and e-value (Fig. 3). Users can click on the dropdown box menu to view additional sequence information, including the alignment and download the results as Tab-Delimited text, GFF3, and XML files.

JBrowse

We have collected the genome assembly and annotation information, of eight oysters, and created a JBrowse page for each species. In the left pane, titled "Available Tracks," all the file types available for display are provided. On the right side of the window, visualizations of the selected files are displayed, including gene sequences, gene structures, and genome annotation files. Users can freely and smoothly drag, zoom in, and zoom out of the visualization window. For example, if the user selects the genomic region of 27,842,301 bp to 27,961,700 bp on the chromosome "NC_047559.1" for browsing, all the genes in this zone will be displayed (Fig. 4). If the user clicks on the gene ID "LOC105341797," the subsequent level of specific gene data, such as mRNAs, the CDS and other gene features will be presented (Fig. 4).

The genome browser is an analysis tool for fundamental visualization of high-throughput sequencing data. JBrowse is a browser base on JavaScript, constituting a complete rewrite of GBrowse (Stein et al. 2002), adopting the architecture of modern web software to enhance the scalability, portability of the software, and reduce dependencies on older software libraries. JBrowse excels in visualizing genomic structural variations and illustrating the evolutionary relationships among genes and genomes through syntenic visualizations. This feature makes this tool especially valuable for future expansion of gene variation modules (Diesh et al. 2023). The Tripal JBrowse (https://github.com/tripal/tripal_jbrowse) module provides integration between Drupal/Tripal sites and pre-existing JBrowse instances (Diesh et al. 2023; Buels et al. 2016). This module creates a "JBrowse Instance" content type with fields for specifying the URL of the pre-existing JBrowse instance and a new page for each JBrowse instance. In the future, we aim to integrate JBrowse instances into Tripal pages, and merge them with other relevant information to provide users a more comprehensive browsing experience.

Conclusion

The web address of our database is as follows: http://oysterdb.com.cn/. The OysterDB integrates eight genome assemblies and 208,923 protein-coding gene annotations of eight Ostreidae species, presented via an interactive and user-friendly platform that provide efficient and practical tools for data analysis. This database aids researchers in rapidly retrieving, analyzing, and browsing genomic data, thereby facilitating in-depth studies and the advancement of oyster genomics in the future. As more advancements in biotechnology, OysterDB will progressively evolve into an integrative and comprehensive platform that enables the community to manage the increasing oyster genomic resources efficiently and accelerate new scientific discoveries for understanding the molecular genetics and evolution of oysters.

Supplementary Information The online version contains supplementary material available at https://doi.org/10.1007/s10126-024-10327-7.

Author Contribution Xinchun Li: completion of the experiment, data analysis, and manuscript drafting. Yitian Bai: data analysis and manuscript drafting. Chengxun Xu: resources. Shikai Liu: investigation. Hong Yu: resources. Lingfeng Kong: resources. Shaojun Du: manuscript revision. Qi Li: experimental design and coordination, manuscript revision, and funding acquisition.

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Data Availability No datasets were generated or analyzed during the current study.

Declarations

Conflict of Interest The authors declare no competing interests.

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