

B.oleracea genomic resources



a comprehensive genomics database for *Brassica oleracea*



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Version 1.0

Data Usage Policy

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Brassica oleracea Genomics Project

Brassica oleracea is one of the most important vegetables in the world. As a member of *Brassica* family, *Brassica oleracea* is the closest crop relatives to *Brassica napus* and *Brassica juncea*. So, it's very meaningful to get genome of *Brassica oleracea* for *Brassica* family. In this project, whole-genome shotgun (WGS) sequencing strategy, based on paired short reads generated by second-generation Illumina GA sequencing technology, was used to assemble the draft genome of *Brassica oleracea*. So far, 630Mb genome sequence was obtained, with scaffold N50 size 1.457Mb and contig N50 size 26.828Kb.

Until now, the nine psuedochromosomes of genome assembly, gene prediction and function annotation are already completed. The study of biological function is under going. Via the genomic and genetic information of *Brassica oleracea*, to study the genus *Brassica* becoming very conveniently. Hence, ***Brassica oleracea* genetics project** not only improve development of genetics and molecular biology but also can accelerate process of molecular breeding.

Introduction to Bolbase

The *Brassica oleracea* Genome Database (Bolbase) was designed to provide users a useful and unique genome data source in the field of studying *Brassica oleracea*. In this database, it contained two important sections. First, it supplied genomic data and genomic components data, for genomic data, it mainly contains genome structure, scaffold sequences, and psuedochromosome sequences; for genomic components data, it mainly includes putative protein-coding genes (gene location, gene structure, protein feature, gene functional annotation, orthologs and syntenic regions), repeats elements (type, classification, location and sequences) and predicted non-coding RNAs (type, classification, location, description and sequences), and so on. Second, it provides thorough analysis on syntenic regions and triplicated blocks for *Brassica oleracea*, *Brassica rapa* and *Arabidopsis thaliana*. All of the data can be downloaded on line very conveniently. This

Resources Links

- NCBI
- EMBL-EBI
- DDBJ
- KEGG
- JGI
- Phytozome
- InterproScan
- TAIR
- BRAD
- CPAN
- MySQL
-

Journals Links

Search Bolbase

WWW SITE
Google Search

B.oleracea (chromosome v1.0) 2013-06-08: 5.001 kbp from C01:80,000..85,000

Browser Select Tracks Snapshots Custom Tracks Preferences

Search

Landmark or Region:

C01:80,000..85,000 Search

Examples: C01:80000..85000, Bol040365.

Data Source

B.oleracea (chromosome v1.0) 2013-06-08

Overview

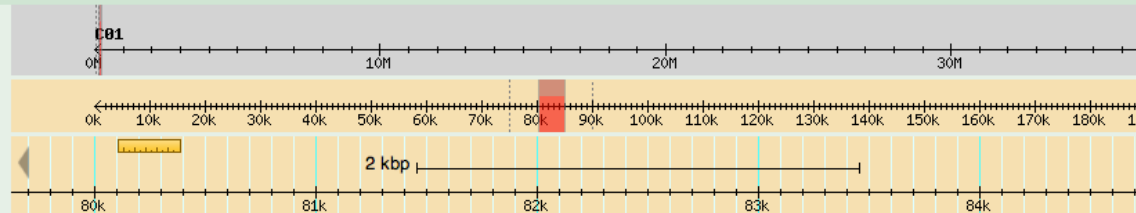
Region

Details

Annotate Restriction Sites Configure... Go

Save Snapshot Load Snapshot


Scroll/Zoom: Show 5.001 kbp



Select Tracks Clear highlighting

Brassica oleracea var. capitata, whole genome shotgun sequencing project

GenBank: AOIX00000000.1

 This entry is the master record for a whole genome shotgun sequencing project and contains no sequence data.

[Go to:](#)

LOCUS AOIX01000000 42466 rc DNA linear PLN 01-APR-2014
DEFINITION Brassica oleracea var. capitata, whole genome shotgun sequencing project.
ACCESSION AOIX000000000
VERSION AOIX000000000.1 GI:601087403
DBLINK BioProject: [PRJNA174731](#)
BioSample: [SAMN01173935](#)
KEYWORDS WGS.
SOURCE Brassica oleracea var. capitata (cabbage)
ORGANISM [Brassica oleracea var. capitata](#)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Brassiceae; Brassica.
REFERENCE 1 (bases 1 to 42466)
AUTHORS Liu,S., Hua,W., Yang,X., Liu,Y., Hu,Q., Wang,X., Fang,Z., Lu,C., Yu,J., Tong,C., Wu,J., Huang,S., Zhou,Q., Wang,W., Yang,L., Yue,Z., Cheng,F., Wang,J., Dong,C., Wu,Z., Huang,J., Yang,L., Hu,Z., Zhao,S., Liu,J., Zhuang,M., Wang,X., Wang,Z., Huang,Y., Zhang,Y., Shi,J., Min,J., Mei,D., Sun,P., Liang,X. and Li,Z.

TO1000Dh

Table 2. Genetic anchoring of TO1000 assembly to *B. oleracea* pseudomolecules (C1-C9)

Pseudo-molecule	No. linked scaffolds	No. bps anchored	% bps anchored	No. anchored scaffolds	No. (%) bps in pseudomolecules
C1	154	44,537,578	9.1%	106	43,754,388 (9.0)
C2	161	53,780,918	11.0%	111	52,875,895 (10.8)
C3	142	65,831,836	13.5%	102	64,974,595 (13.5)
C4	235	55,258,765	11.3%	138	53,705,393 (11.0)
C5	141	48,366,635	9.9%	99	46,892,785 (9.6)
C6	132	40,383,462	8.3%	79	39,814,676 (8.1)
C7	129	49,639,853	10.2%	64	48,360,397 (9.9)
C8	124	43,398,395	8.9%	63	41,752,485 (8.5)
C9	192	56,144,286	11.5%	121	54,667,868 (11.2)
Total	1,410	457,341,728	93.6%	883	446,798,482 (91.5)
Total assembled bases			488,535,107		
% genetically linked (RAD mapping)			93.61%		
% anchored to pseudomolecules			91.46%		