Resource Summary Report

Generated by dkNET on Apr 29, 2025

DBM-DB

RRID:SCR_006258
Type: Tool

Proper Citation

DBM-DB (RRID:SCR_006258)

Resource Information

URL: http://iae.fafu.edu.cn/DBM/

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Description: Database storing and integrating genomic data of diamondback moth (DBM), Plutella xylostella (L.). It provides comprehensive search tools and downloadable datasets for scientists to study comparative genomics, biological interpretation and gene annotation of this insect pest. DBM-DB contains assembled transcriptome datasets from multiple DBM strains and developmental stages, and the annotated genome of P. xylostella (version 2). They have also integrated publically available ESTs from NCBI and a putative gene set from a second DBM genome (KONAGbase) to enable users to compare different gene models. DBM-DB was developed with the capacity to incorporate future data resources, and will serve as a long-term and open-access database that can be conveniently used for research on the biology, distribution and evolution of DBM. This resource aims to help reduce the impact DBM has on agriculture using genomic and molecular tools.

Abbreviations: DBM-DB

Synonyms: Diamondback moth Genome Database

Resource Type: data or information resource, database

Defining Citation: PMID:24434032

Keywords: genome, rna-seq, gene expression profiling, micrornas, metagenomics, blast, gbrowse, FASEB list

Funding:

Availability: Free, Public

Resource Name: DBM-DB

Resource ID: SCR_006258

Alternate IDs: OMICS_02235

Alternate URLs: http://59.79.254.1/DBM/

Record Creation Time: 20220129T080235+0000

Record Last Update: 20250429T055041+0000

Ratings and Alerts

No rating or validation information has been found for DBM-DB.

No alerts have been found for DBM-DB.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 30 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Zhang Z, et al. (2022) Optimization and Application of CRISPR/Cas9 Genome Editing in a Cosmopolitan Pest, Diamondback Moth. International journal of molecular sciences, 23(21).

Guo Z, et al. (2021) The regulation landscape of MAPK signaling cascade for thwarting Bacillus thuringiensis infection in an insect host. PLoS pathogens, 17(9), e1009917.

Xiong L, et al. (2021) A Novel Reference for Bt-Resistance Mechanism in Plutella xylostella Based on Analysis of the Midgut Transcriptomes. Insects, 12(12).

Harvey-Samuel T, et al. (2020) Identification and characterization of a Masculinizer homologue in the diamondback moth, Plutella xylostella. Insect molecular biology, 29(2), 231.

Gong L, et al. (2020) Reduced Expression of a Novel Midgut Trypsin Gene Involved in Protoxin Activation Correlates with Cry1Ac Resistance in a Laboratory-Selected Strain of Plutella xylostella (L.). Toxins, 12(2).

You M, et al. (2020) Variation among 532 genomes unveils the origin and evolutionary history of a global insect herbivore. Nature communications, 11(1), 2321.

Han G, et al. (2019) Characterization of a novel Helitron family in insect genomes: insights into classification, evolution and horizontal transfer. Mobile DNA, 10, 25.

Zhao Q, et al. (2019) Genome-wide profiling of the alternative splicing provides insights into development in Plutella xylostella. BMC genomics, 20(1), 463.

Zhang LL, et al. (2019) Host Plant-Derived miRNAs Potentially Modulate the Development of a Cosmopolitan Insect Pest, Plutella xylostella. Biomolecules, 9(10).

Wang Y, et al. (2018) Genome-wide identification and characterization of putative lncRNAs in the diamondback moth, Plutella xylostella (L.). Genomics, 110(1), 35.

Lin J, et al. (2018) Gene expression profiling provides insights into the immune mechanism of Plutella xylostella midgut to microbial infection. Gene, 647, 21.

Yasukochi Y, et al. (2018) Conservation and lineage-specific rearrangements in the GOBP/PBP gene complex of distantly related ditrysian Lepidoptera. PloS one, 13(2), e0192762.

Herfurth AM, et al. (2017) ?-Cyanoalanine Synthases and Their Possible Role in Pierid Host Plant Adaptation. Insects, 8(2).

Kumar S, et al. (2017) An endoparasitoid wasp influences host DNA methylation. Scientific reports, 7, 43287.

He P, et al. (2017) A reference gene set for sex pheromone biosynthesis and degradation genes from the diamondback moth, Plutella xylostella, based on genome and transcriptome digital gene expression analyses. BMC genomics, 18(1), 219.

Baa-Puyoulet P, et al. (2016) ArthropodaCyc: a CycADS powered collection of BioCyc databases to analyse and compare metabolism of arthropods. Database : the journal of biological databases and curation, 2016.

Wu Y, et al. (2016) Systematic Identification and Characterization of Long Non-Coding RNAs in the Silkworm, Bombyx mori. PloS one, 11(1), e0147147.

Kumar S, et al. (2016) Glyceraldehyde-3-phosphate dehydrogenase is a mediator of hemocyte-spreading behavior and molecular target of immunosuppressive factor CrV1. Developmental and comparative immunology, 54(1), 97.

Yin C, et al. (2016) InsectBase: a resource for insect genomes and transcriptomes. Nucleic acids research, 44(D1), D801.

Qi W, et al. (2016) Characterization and expression profiling of ATP-binding cassette transporter genes in the diamondback moth, Plutella xylostella (L.). BMC genomics, 17(1), 760.