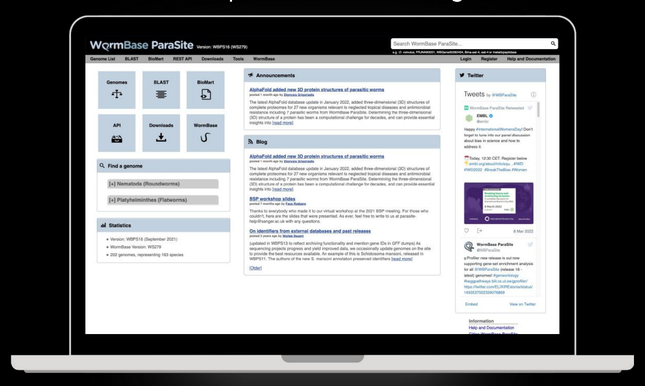
WormBase ParaSite

EMBL-EBI | University of Glasgow

www.parasite.wormbase.org



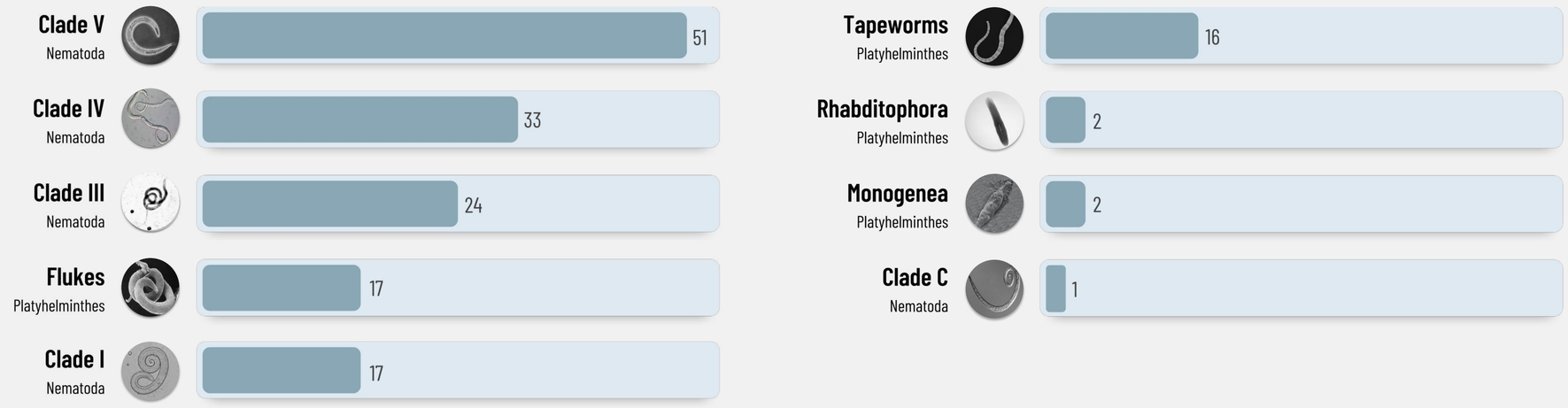
A comprehensive online resource for helminth genomics.

Publicly available genomes are imported from the European Nucleotide Archive (ENA).

Further value is added by systematic and consistent functional annotation, as well as presentation of comparative analysis in a user-friendly format.

We are aiming to interrogate data for nearly all nematode and platyhelminth genomes!

WormBase ParaSite hosts 202 genomes from 163 species including all major parasitic worms and their free-living relatives:



Genome browsers | Functional annotation | Gene Expression Portal | Gene set analysis | Comparative Genomics | Variant Effect Predictor | BLAST/BLAT | BioMart | Rest API | Downloads

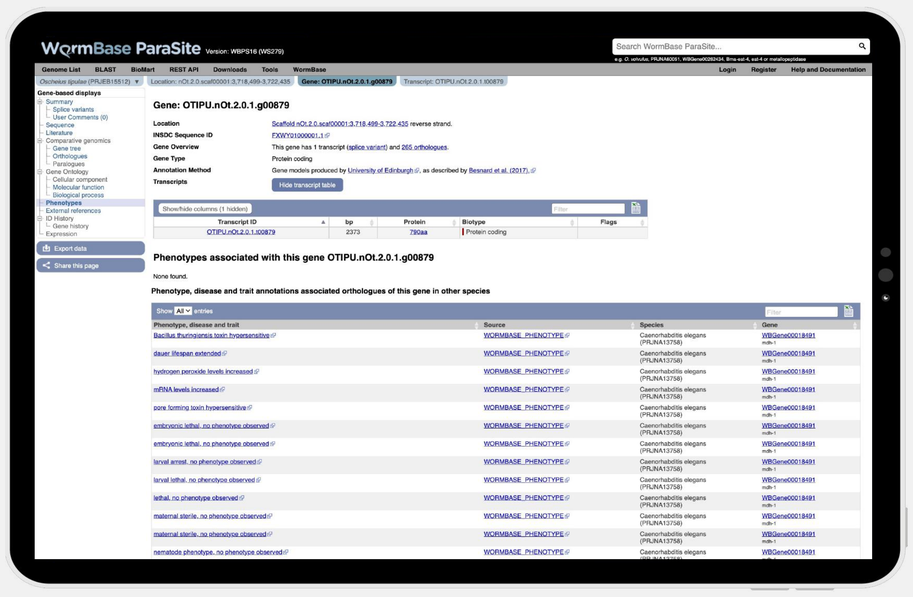
Gene-Phenotype Association Data

We have developed a system for capturing and presenting published gene-phenotype associations for well-studied genomes.

More than 360,000+ gene-phenotype associations for *Schistosoma mansoni* and *Caenorhabditis elegans* have been added and we anticipate more studies of this type for helminths to be published in the future.

These associations have been propagated between orthologs to all our hosted species.

Although there are no phenotypic studies for this *Oscheius tipulae* gene, the user is able to browse a list of phenotypic associations with its orthologues in other species.

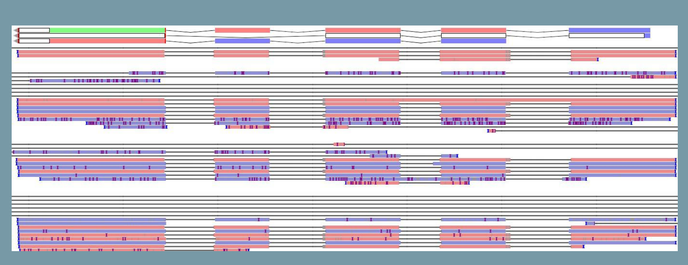


Community Annotation

We supplement our in-house gene curation platform by hosting Web Apollo instances for an increasing number of genomes.

Web Apollo is an instantaneous, collaborative genomic annotation editor available on the web.

Users can request relevant Web Apollo instances to be deployed from us; training can be provided.



Other Updates

An archiving service has been introduced so older WormBase ParaSite releases will remain available for browsing.

ARCHIVED

New improved assembly/annotation quality metrics have been introduced: CEGMA has been deprecated and replaced by BUSCO annotation.

Future Development Highlights

WormBase ParaSite will continue to expand by including new genomes and replacing deprecated ones.

AlphaFold Protein Structure Database's new predicted 3D protein models of WormBase ParaSite's species will be integrated into our next release 17.

We are expanding our in-house gene curation platform by deploying Web Apollo instances for more genomes.

We are creating multi-genome alignments which will be fully browsable from our gene pages.

WormBase ParaSite would like to hear from you! Please tell us about your use-cases and make suggestions for improvements, to help us prioritise future work.

D Grigoriadis[1], F Rodgers[2], T Le[1], M Zarowiecki[1], S Dyer[1], KL Howe[1], M Berriman[3]

1) European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI), UK
2) Wellcome Trust Sanger Institute, UK
3) Institute of Infection, Immunity & Inflammation, University of Glasgow, UK

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