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Recent Work

Title

The VISTA Synteny Viewer: Navigating Whole Genome Alignments at Multiple Levels of Resolution

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<https://escholarship.org/uc/item/63k4m7kz>

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Publication Date

2009-10-27

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Overview

Comparison of whole-genome assemblies is required at all stages of their completion and analysis – from individual reads to draft and finished genomes, from assembly through finishing and annotation. We have expanded the VISTA suite of tools for comparative genomics by adding a novel interactive web application, the VISTA Synteny Viewer (VSV), for the navigation of whole genome alignments at multiple levels of resolution. The VSV uses modern web technologies to tightly wed the visualization of DNA synteny at the level of whole genomes, individual chromosomes/scaffolds, and individual aligned loci, as well to dynamically generate dot plots.

Calculation of Synteny

Synteny is derived from whole genome DNA alignments produced by the VISTA Pipeline*, which employs an efficient combination of local (BLAT) and global (Shuffle-LAGAN chaining) alignment methods.
*<http://pipeline.lbl.gov/methods.shtml>

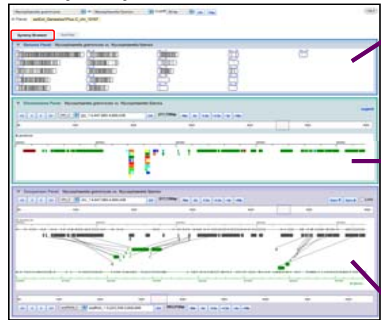
Where To Find Us

VSV: <http://genome.jgi-psf.org/vsv>

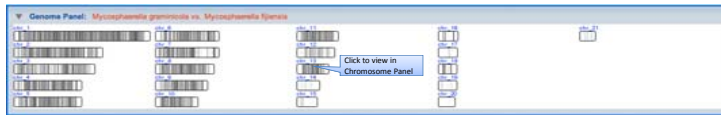
VISTA: <http://genome.lbl.gov/vista/index.shtml>

Synteny Mode

The Synteny Browser



The Genome Panel



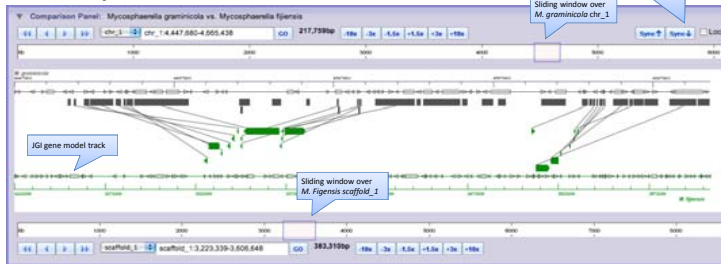
- Reference chromosomes are banded according to density of alignment with the compared genome.
- Click on a region within a chromosome to bring it into focus in the Chromosome Panel.

The Chromosome Panel



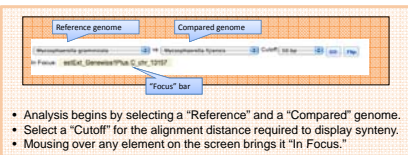
- Navigate along a single reference chromosome.
- Regions of alignment are shown as colored blocks. The color indicates the chromosome to which the region aligns in the compared genome.
- Click on a block to focus on the corresponding alignment in the Comparison Panel.

The Comparison Panel



- Independently navigate along a single reference and a single compared chromosome, viewing synteny between the two.
- Lines connected aligned regions.
- View JGI gene model annotations for each region.
- "Sync" up or down to synchronize the reference position between the Comparison and Chromosome panels. Or "Lock" the two views.

Organism Selection



- Analysis begins by selecting a "Reference" and a "Compared" genome.
- Select a "Cutoff" for the alignment distance required to display synteny.
- Mousing over any element on the screen brings it "In Focus."

Connecting to other tools

Context Menus for syntenic regions allow you to view the alignment at the sequence level or in external genome browsers.

Synteny mode



DotPlot Mode



View the reference or compared region in the JGI Genome Browser



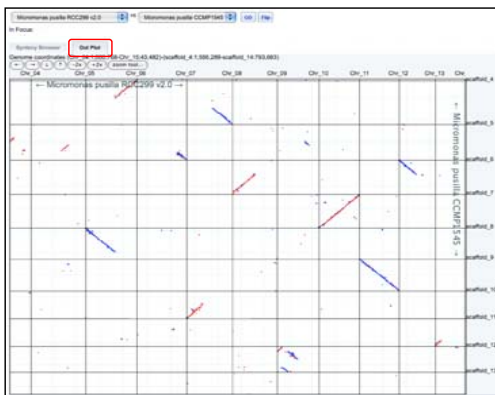
View the alignment in the VISTA browser



View a text representation of the alignment



DotPlot Mode



- Quickly identify large-scale genome rearrangement and duplication.
- Use a finished genome to help map scaffolds in a closely related organism.
- Easily identify repeats by examining a self-alignment.
- Interactive Google Maps-like navigation**
 - Click and drag to pan within Dot Plot
 - Use the Zoom tool to narrow in on a region of the alignment

