Genome Visualization and Comparison using CMap and Circos
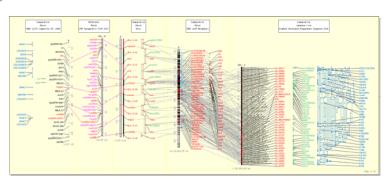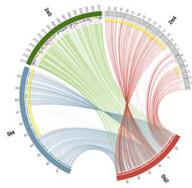
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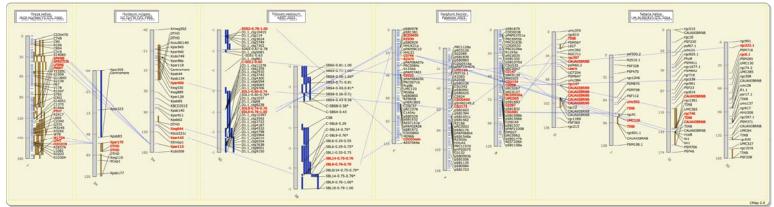[3]USDA-ARS NAA Plant, Soil & Nutrition Laboratory Research Unit, Ithaca, NY

GRAMENE

CMap[1] is a generic and extensible comparative map viewer that runs in standard web browsers and aims to assist biological researchers seeking to extrapolate known map data into unknown areas. A user can compare an unlimited number of maps, view pair-wise comparisons or known correspondences, and search for maps or for features by name, species, type and accession. Shown here is a view from the Gramene[3] website comparing genetic, bin, and sequence maps from maize and rice.

Circos[2] is a program that employs a circular layout to display relationships between genomes as scatter, line and histogram plots, heat maps, tiles, connectors and text. Shown here is a comparative mapping of protein-coding genes in an orthologous segment of the rice, sorghum, and maize genomes. Abbreviations: Osj2 = rice (japonica) chromosome 2; Sb4 = sorghum chromosome 4; Zm4 = maize chromosome 4 (AR182); Zm5 = maize chromosome 5 (homeologous region). All mappings are drawn relative to rice as a common reference. Genes are shown as tick marks in the outer radius of correspondence lines. Inversions are indicated with yellow highlighting. For Zm4 the density of repetitive sequence is shown in gray. Zm5 mappings are to individual BACs (boxes) projected onto the FPC map.

Version 2 of CMap currently in development will integrate the Circos circular genome visualization program to directly create novel views of existing CMap data.

CMap is a Perl application that runs on an Apache web server (versions a or 2) on Windows and UNIX variants. CMap has a simple relational schema that can be implemented in MySQL, Oracle, PostgreSQL or Sybase.

It relies on no proprietary software or SQL extensions, and uses all freely available software. The user interface is a basic HTML/JavaScript page that works with any modern web browser. No registration or permission is required for its use.

[1] Youens-Clark, K., et al. CMap 1.01: A comparative mapping application for the Internet. Bioinformatics (2009) doi:10.1093/bioinformatics/btp458.

[2] Krzywinski, M. et al. Circos: an Information Aesthetic for Comparative Genomics. Genome Res (2009) 19:1639-1645

[3] http://www.gramene.org/