What is GDV?

GDV is a centralized location for genomics, genetics, and breeding data for *Vaccinium* sp. Genome sequences are available to view and search and there is also information about genetic maps, molecular markers, and QTL. If you are a breeder who needs to manage a private breeding program data, access to the Breeding Information Management System (BIMS) can be requested through GDV. Visit us at www.vaccinium.org to see everything that is available. Each issue of the newsletter will focus on a different type of data and what features are available.

New Cranberry, Bilberry, and Blueberry Genomes

In the last year, multiple genomes have been added to GDV. These genomes join the *V. corymbosum* genome assembly on GDV. For all the genomes, you can view the genome sequence and annotations in JBrowse; search the scaffold, transcripts, and protein sequences using the BLAST tool; view the different biochemical pathways using PathwayCyc; and view the synteny between the genome sequences with the Synteny Viewer tool.

Bilberry Genome

The *V. myrtillus* genome is available on GDV thanks to Chen Wu, Richard Espley and David Chagne of New Zealand Institute for Plant and Food Research.

Genome	V. mytrillus
Total size	524 Mbp
Scaffold number	1418
N50	38 Mbp
BUSCO score	97.6%

Cranberry Genomes

Thanks to Luis Diaz-Garcia and Juan Zalapa from the University of Wisconsin-Madison, the genomes of *V. macrocarpon* cv. Stevens and *V. microcarpum* are available on GDV.

Genome	V. macrocarpon	V. microcarpum
Total size	490 Mbp	623 Mbp
Scaffold number	350	4820
N50	38 Mbp	176 Kbp
BUSCO score	93.4%	87.4%

More Cranberry Genomes

Two additional cranberry genomes were just recently made available pre-publication thanks to Joseph Kawash, Todd Michael, and James Polashock. You now can find the *V. macrocarpon* cv. Ben Lear and *V. oxycoccos* NJ96-20 genomes on GDV.

Genome	V. macrocarpon	V. oxycoccos
Total size	485 Mbp	484 Mbp
Scaffold number	13	1692
N50	39 Mbp	1.8 Mbp
BUSCO score	96.9%	95.3%

Darrow's Blueberry Genome

Primary and secondary haplotype assemblies of *V. darrowii* were provided by Jiali Wu and Meg Staton from the University of Tennessee, Knoxville.

Genome	Primary, v1.2	Secondary, v2.4
Total size	583 Mbp	481 Mbp
Scaffold number	107	384
N50	47 Mbp	40 Mbp
BUSCO score	94.0%	85.3%

Genome Synteny Viewer

One of the additional analyses that GDV does with provided genome data is a synteny (gene order) comparison between the genomes. The analysis is conducted with [MCScanX](#) and displayed using the [Tripal Syntenic Viewer](#) module.

Using the [simple web interface](#), select the first genome and a chromosome or scaffold, and then select one or more genomes to compare against. The pairwise comparison data is displayed in a circus plot and syntenic blocks can be selected and viewed in a more detailed, linear side-by-side view.

In the detailed view, there is also an accompanying table that lists the corresponding mRNAs and has hyperlinks to the corresponding mRNA feature page on GDV. Each mRNA feature page has the associated sequences and details about homology to the Swiss-Prot protein and InterPro protein family databases.
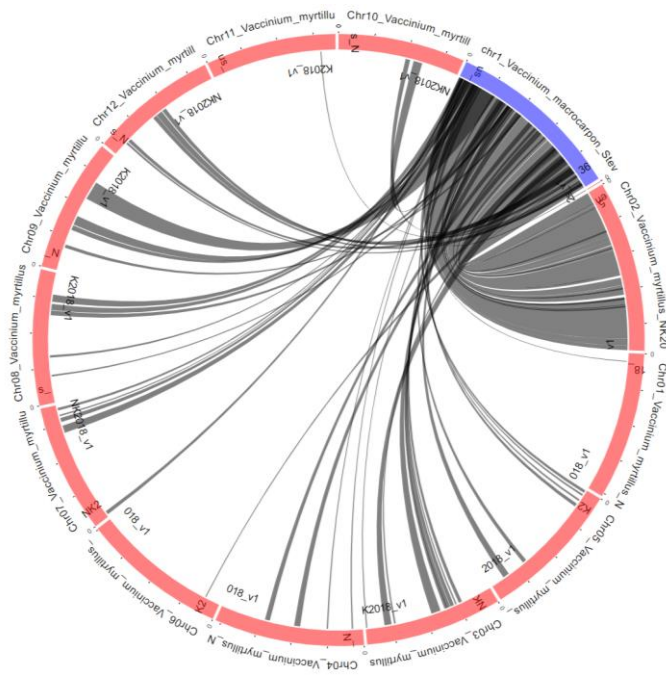
Synteny plot of Chromosome 1 from *V. macrocarpon* cv. Stevens compared to the *V. myrtillus* genome.

PathwayCyc
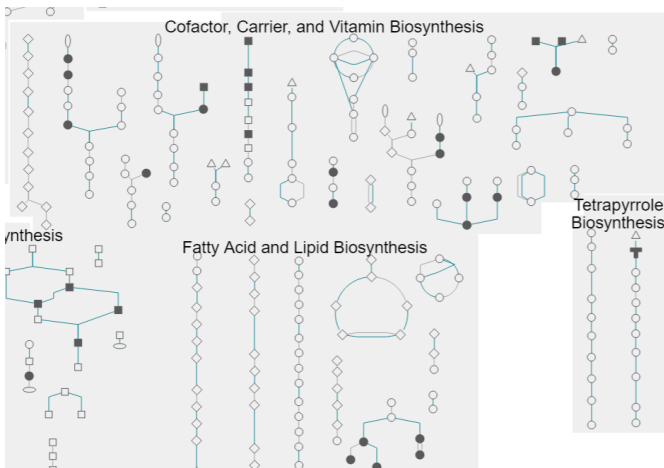
Section of the Cellular Overview diagram from the *V. macrocarpon* cv. Stevens genome.

Genomes added to GDV are also analyzed with [Pathway Tools](#) to identify metabolic pathways. The data is then displayed with an embedded instance of the software on GDV under the [PathwayCyc tool](#).

Users can also overlay data from transcriptomics or metabolomics experiments onto the cellular overview graphic. The pathways that have corresponding data are color coded to show over- or under-expression.

PathwayCyc accounts can also be requested to allow users to upload, sort, and save data using the SmartTables feature. For more details on how to use the PathwayCyc tool, watch the video on the MainLab Bioinformatics [YouTube channel](#).

Join the [GDV Mailing List](#) and follow us on [Twitter](#)