



GENOME DATABASE FOR VACCINIUM

Genomics, genetics, and breeding resources for blueberry, cranberry, bilberry, and lingonberry research

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What is GDV?

GDV is a centralized database for genomics, genetics, and breeding data and analysis tools 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.

More GDV training and tools

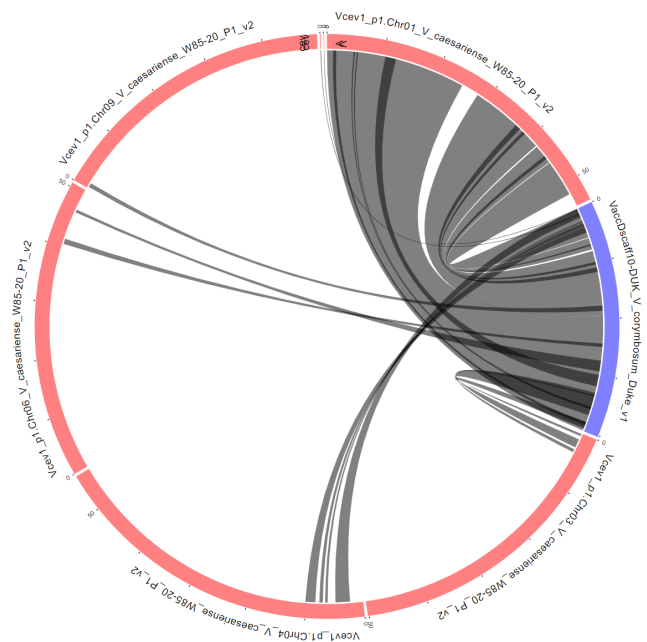
Thanks to a new award from the USDA-SCRI, GDV and the other MainLab specialty crop databases will continue to grow to provide the tools, data, and training that breeders and researchers need. You can read more about the award here: [Enabling Genomics-Assisted Specialty Crop Breeding and Research Through Advanced Database Resources](#).

The continued funding will provide new tools and resources for big data, data management, and staff for in-person training with GDV users. We will be announcing all the new developments via the GDV mailing list, so please [subscribe](#) if you have not done so already.

Vaccinium Pangenome Data

Thanks to the VacCAP project and Patrick Edger and collaborators, [22 new blueberry and 10 new cranberry genomes](#) have been added to GDV. The genomes are available to view in [JBrowse](#), available in the [BLAST Tool](#), and the gene and mRNA annotations can be searched with [MegaSearch](#). Three of the blueberry (Duke, Earlie Blue, Elliot) and three of the cranberry (Budd's Blues, Garwood Bell, Native Budd's Blues) genomes will be added to [PathwayTools](#) and [Synteny Viewer](#) over the next couple weeks.

And the most exciting news is that the pangenome graph provided by the authors will be available on GDV soon. The needed visualization files are being created and watch the News and Events section of the homepage and the Vaccinium Pangenome Project page for the link!



Scaffold of *V. corymbosum* cv. Duke compared to *V. caesariense* W85-20 P1 genome in Synteny Viewer.

Ortholog/Paralog MegaSearch

We have made a new MegaSearch for the data that is stored during the [Synteny Viewer](#) analysis. Now you can search that data without going through the Synteny Viewer.

The new [Ortholog/Paralog Search](#) interface is simple to use. First select the primary genome and chromosome/scaffold of interest. Or provide a single gene/transcript ID or a file of them.

Once parameters are set, you can preview the number of results by clicking “Refresh Count”. And then you can configure what data will be returned and available for download.

When viewing the results on the website, there are green hyperlinks that open details about the associated transcripts including the annotated terms, homology to SwissProt, InterPro results, and mRNA and protein sequences.

Tripal MegaSearch

Tripal MegaSearch is a tool for downloading biological data. (Current limit per download: 1,000,000 records. 200,000 FASTA sequences.)
Video tutorial: [2020 presentation](#) | [2021 tutorial \(Gene/Transcript\)](#) | [2022 tutorial \(QTL\)](#)

Select a data type to start building your own query and download data in bulk:

Data Type

413 Ortholog/Paralog. Note: actual rows in downloaded file depend on the selected fields.

Query

Clear Refresh Count

Genome

Chromosome/Scaffold

Start

Stop

Gene/Transcript Name

No file chosen

Compare to
Vaccinium corymbosum cv. Draper v1.0 genome sequence
Vaccinium darrowii clone NJ8810/NJ8807 v1.2 genome sequence
Vaccinium darrowii clone NJ8810/NJ8807 v2.4 genome sequence

Chromosome/Scaffold

Options to view and download data

Downloadable Fields

All Fields

- Genome1
- Chromosome1
- Location1
- Ortholog1
- Genome2
- Chromosome2
- Location2
- Ortholog2
- Associated Gene

419 records were returned

#	Genome1	Chromosome1	Location1	Ortholog1	Genome2	Chromosome2	Location2	Ortholog2
1	<input type="checkbox"/> Vaccinium macrocarpon cv. Ben Lear v1.0 genome sequence	Vmac_chr01	Vmac_chr01:10030571..10031776	Vmac_004665-T1	Vaccinium macrocarpon cv. Stevens v1.0 genome sequence	chr1	chr1:38607153..38616510	vmacro00514-RA
2	<input type="checkbox"/> Vaccinium macrocarpon cv. Ben Lear v1.0 genome sequence	Vmac_chr01	Vmac_chr01:1023682..1025168	Vmac_003648-T1	Vaccinium macrocarpon cv. Stevens v1.0 genome sequence	chr1	chr1:47672677..47676938	vmacro00012-RA

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