



GENOME DATABASE FOR VACCINIUM

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

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What's new in GDV?

Outreach

- [How to view correspondences between genomes and genetic maps](#) (2:47 mins)
- Presentations in NRSP10 Database Workshop at PAG

New Data and Functionality

- 232 genetic markers, 299 GWAS and 3 QTL added in last quarter
- Image management added to BIMS – breeders can now load images into BIMS

Recap of data added in 2023

Below is information about the data we added in 2023. A huge 'Thank You' to the Vaccinium community for contributing this data!

New expression datasets

- Aligned to *V. corymbosum* cv. *Draper* genome
 - [Monotropein biosynthesis in blueberry](#) from the manuscript: Lawas et al. 2023. [Transcriptome-based identification and functional characterization of iridoid synthase involved in monotropein biosynthesis in blueberry](#).
 - [UV-B treatment of blueberry calli](#) from the manuscript: Song et al. 2022. [UV-B induces the expression of flavonoid biosynthetic pathways in blueberry \(*Vaccinium corymbosum*\) calli](#).

New markers, genetic maps, GWAS and/or QTL added from these manuscripts:

- Erndwein et al. 2023. [Cranberry fruit epicuticular wax benefits and identification of a wax-associated molecular marker](#).
- Herniter et al. 2023. [Trait Mapping of Phenolic Acids in an Interspecific \(*Vaccinium corymbosum* var. *caesariense* × *V. darrowii*\) Diploid Blueberry Population](#).
- Jacobs et al. 2023. [Uncovering genetic and metabolite markers associated with resistance against anthracnose fruit rot in northern highbush blueberry](#).
- Njuguna et al. 2023. [Impact of genotype-calling methodologies on genome-wide association and genomic prediction in polyploids](#).
- Ferrao et al. 2018. [Insights Into the Genetic Basis of Blueberry Fruit-Related Traits Using Diploid and Polyploid Models in a GWAS Context](#).

GDV by the Numbers

The database has seen growth in the number of users, citations, and data over the years. Let's look at the numbers! First, let's look at [usage](#). The number of users has grown and the number of times they visit the site (Session) and the number of pages they view (Pageviews) each visit is growing.

GDV Usage by Year

Year	Sessions	Pageviews	Users	Countries
2023	13,292	334,692	5,660	117
2022	11,235	95,163	6,136	90
2021	10,922	101,998	5,643	94
2020	9,110	66,694	5,465	88
2019	6,832	39,904	4,746	92
2018	4,723	30,437	3,006	88
2017	3,549	21,781	2,267	91
2016	2,054	6,393	1,560	83
2015	1,669	6,875	1,221	71
2014	1,708	5,271	1,320	86
2013	1,735	5,834	1,329	84
2012	1,651	5,898	1,120	84
2011	1,463	8,810	835	75

Last, let's look at the amount of data that has been added over the last 4 years. The amount of genetic data (markers, maps, QTL) has grown steadily. This year we started adding GWAS data. We are adding data as it is published and feature newly curated data in the News section of the homepage.

Genome data had a very large increase in 2022 thanks to the [Vaccinium Pangenome Project](#). We thank the [VacCAP project](#) for generating that data.

The number of [manuscripts that cite GDV](#) has also grown over the years and will continue to grow as more data, analyses, and tools are added. Primary citations refer to manuscripts that cite GDV directly. Secondary citations are the number of times the primary citations were cited. We would like to thank our users for citing GDV!

GDV Peer-Reviewed Citations by Year

Year	Primary Citations	Secondary Citations
2011	2	110
2012	2	180
2013	4	161
2014	1	70
2015	0	0
2016	1	38
2017	1	10
2018	6	142
2019	5	106
2020	6	73
2021	22	216
2022	23	172
2023	14	38
Total	87	1,316

Total GDV Data by Year

Year	Genomes	Genes	mRNA	Maps	Markers	QTL	GWAS
2023	42	3193094	3235659	39	247457	836	308
2022	42	3193094	3235659	38	245127	816	NA
2021	8	466354	476613	34	136212	465	NA
2020	4	245382	253280	31	89951	403	NA

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