



Plant Bioinformatics Resources for FAIR Agricultural Data Discovery and Reuse Workshop
Plant Biology 2024, June 22, 2024

Research Impact of Plant Community Databases

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AgBioData Sustainability Workgroup

OVERVIEW

- AgBioData
- SUSTAINABILITY ROADMAP FOR AgBioData DATABASES
 - GOALS
 - WORK TO DATE
- RESEARCH IMPACT OF CROP COMMUNITY DATABASES – CASE STUDY



AgBioData

Toward enhanced genomics, genetics, and breeding research outcomes through standardization of practices and protocols across agricultural databases

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Welcome to AgBioData!

We are a consortium of agricultural biological databases with the mission of consolidating standards and best practices for acquiring, displaying, and reusing genomic, genetic, and breeding (GGB) data ([Harper et al., 2018](#)). Formed in 2015, our consortium involves 44 GGB databases (the complete list [here](#)) and over 200 members, including database curators, researchers, librarians, and anybody that works with agricultural data.

The AgBioData consortium embraces the **Findable, Accessible, Interoperable, and Reusable (FAIR) principles** to facilitate and maximize the accessibility and reuse of large-scale data in agricultural research. We recently received funding for a **National Science Foundation (NSF) for Research Coordination Network** project that aims to:

1. define community-based standards for FAIR agricultural data;
2. expand our network by recruiting anybody that generates, uses, curate, archive, and publish data;
3. provide educational material to train scientists on FAIR data sharing;
4. develop a roadmap for a sustainable GGB database ecosystem.

News & Events

August 7th webinar

Seth Murray on Temporal Field Phenomics

Posted: 06/20/2024

AgBioData at the Plant Biology 2024 conference

Join us at booth #406, and for the Plant Bioinformatics Resources for FAIR Agricultural Data Discovery and Reuse Workshop on June 22 (10 AM)

Posted: 06/12/2024

Bringing FAIR data to the classroom

Join us on June 4 at 1 PM EDT at the Virtual Plant Biology 2024 conference!

ROADMAP FOR SUSTAINABLE DATABASES

1. SELF-ASSESSMENT OF THE LONG TERM FINANCIAL STABILITY OF MEMBER DATABASES
2. CONDUCT A DETAILED ANALYSIS AND MODELING OF SUSTAINABILITY SOLUTIONS FOR REPRESENTATIVE **AgBioData** MEMBER DATABASES.
3. DEVELOP A ROADMAP FOR **GENOMIC, GENETIC AND BREEDING (GGB) DATABASE** SUSTAINABILITY TO ENSURE DATA PERSISTENCE AND RESOURCE LONGEVITY

ASSESSMENT OF MEMBER DATABASES: GOALS

1. CAPTURE COST OF OPERATIONS, STAFF LEVEL, SOURCES OF FUNDING, USAGE LEVEL, DATA TYPES, SPECIES AND STRAINS, STAKEHOLDERS SERVED AND ANTICIPATED FUTURE NEEDS.
2. COLLECT INFORMATION ON EACH GGB DATABASE'S VIEW OF ITS SUSTAINABILITY AND APPROACHES TO IMPROVE THAT SUSTAINABILITY.
3. GATHER DATA THROUGH WRITTEN SURVEYS AND INTERVIEWS WITH STAFF AT ALL MEMBER DATABASES.
4. UNDERSTAND THE CURRENT FUNDING SITUATION AND THE ANTICIPATED FUTURE NEEDS.

AgBioData MEMBER DATABASES: IMPACT

- WHAT IS IMPACT?
 - “HAVE A STRONG EFFECT ON SOMEONE OR SOMETHING”
 - “EXERT INFLUENCE”
- HOW DO WE MEASURE IMPACT OF AgBioData DATABASES?
 - USAGE METRICS
 - PUBLICATIONS CITING USE OF THE DATABASES
 - PRIMARY CITATIONS
 - SECONDARY CITATIONS
- HOW DO WE INTERPRET IMPACT?

Crop Community Databases

- Provide access to integrated and curated data, and analysis tools
- Promote FAIR data sharing and community building
- Enable genomics, genetics and breeding research

Databases



citrus



pulse crops



vaccinium



cotton



rosaceae

Tools and Resources

 GenSAS

AgBioData

 TripalFruit and Nut
Cultivars Database

NRSP10 IMPACT: PUBLICATIONS

- DATA COLLECTED
 - CROPS ECONOMIC VALUE (VALUE OF PRODUCTION)
 - PEER-REVIEWED CITATIONS TO THE DATABASES (GOOGLE SCHOLAR)
 - PRIMARY
 - TO OUR DATABASE PAPERS **AND** DATABASE NAME
 - RECORD TITLE (WITH LINK), JOURNAL, CORRESPONDING AUTHOR AND EMAIL, COUNTRY
 - SECONDARY
 - PEER-REVIEWED PAPERS CITING THE PRIMARY CITATIONS
 - LINK TO CITATION QUERY

DATABASE CITATION DATA: GDR 2015

Citation	Author	Country	Email	Citation numbers by date	
				Cited by link	2/21/2024
Jung, S., Bassett, C., Bielenberg, D. G., Cheng, C. H., Dardick, C., Main, D., ... & Schaffer, R. J. (2015). Jung et al. (2015)	Robert J. Schaffer	New Zealand	robert.schaffer@plantandfood.co.nz	Cited By	23
Darwish, O., Shahan, R., Liu, Z., Slovin, J. P., & Alkharouf, N. W. (2015). Re-annotation of the woodlouse genome. Darwish et al. (2015)	Nadim W Alkharouf	USA	NALKHAROUF@TOWSON.EDU	Cited By	81
Hanada, T., Nashima, K., Kato, M., Takashina, T., Ikeda, K., Sakamoto, Y., ... & Isuzugawa, K. (2015). Hanada et al. (2015)	K. Isuzugawa	Japan	isuzugawak@pref.yamagata.jp	Cited By	4
Donoso, J. M., Eduardo, I., Picañol, R., Batlle, I., Howad, W., Aranzana, M. J., & Arús, P. (2015). High-throughput genotyping of olive. Donoso et al. (2015)	Pere Arús	Spain	pere.arus@irta.cat	Cited By	41
Ru, S., Main, D., Evans, K., & Peace, C. (2015). Current applications, challenges, and perspectives of next-generation sequencing in plant breeding. Ru et al. (2015)	Sushan Ru	USA	sru@bioinfo.wsu.edu	Cited By	114
Cova, V., Bandara, N. L., Liang, W., Tartarini, S., Patocchi, A., Troggio, M., ... & Komjanc, M. (2015). Fingerprinting of olive varieties using microsatellites. Cova et al. (2015)	Riccardo Velasco	Italy	riccardo.velasco@fmach.it	Cited By	28
Salazar, J. A., Rubio, M., Ruiz, D., Tartarini, S., Martínez-Gómez, P., & Dondini, L. (2015). SNP development and validation for olive. Salazar et al. (2015)	Pedro Martínez-Gómez	Spain	pmartinez@cebas.csic.es	Cited By	27
Kaja, E., Szcześniak, M. W., Jensen, P. J., Axtell, M. J., McNellis, T., & Makałowska, I. (2015). Identification of novel genes in the olive genome. Kaja et al. (2015)	Izabela Makałowska	Poland	izabel@amu.edu.pl	Cited By	32
Jia, Y., Yuan, Y., Zhang, Y., Yang, S., & Zhang, X. (2015). Extreme expansion of NBS-encoding genes in the olive genome. Jia et al. (2015)	Xiaohui Zhang	China	xiaohuizhang@nju.edu.cn	Cited By	73
Kang, C., & Liu, Z. (2015). Global identification and analysis of long non-coding RNAs in diploid strawberry. Kang et al. (2015)	Zhongchi Liu	USA	zliu@umd.edu	Cited By	110
Wilde, H. D., Gandhi, K. J., & Colson, G. (2015). State of the science and challenges of breeding landslide-resistant crops. Wilde et al. (2015)	H Dayton Wilde	USA	dwilde@uga.edu	Cited By	61
Bassil, N. V., Davis, T. M., Zhang, H., Ficklin, S., Mittmann, M., Webster, T., ... & van de Weg, E. (2015). Genome investigation suggests MdSHN3, an APETALA3-like gene, is involved in the regulation of the apple fruit shape. Bassil et al. (2015)	Nahla V Bassil	USA	nahla.bassil@ars.usda.gov	Cited By	220
Lashbrooke, J., Aharoni, A., & Costa, F. (2015). Genome investigation suggests MdSHN3, an APETALA3-like gene, is involved in the regulation of the apple fruit shape. Lashbrooke et al. (2015)	Fabrizio Costa	Italy	fabrizio.costa@fmach.it	Cited By	90
Dereeper, A., Bocs, S., Rouard, M., Guignon, V., Ravel, S., Tranchant-Dubreuil, C., ... & Droc, G. (2015). The olive genome. Dereeper et al. (2015)	Alexis Dereeper	France	alexis.dereeper@ird.fr	Cited By	73
Song, C., Ring, L., Hoffmann, T., Huang, F. C., Slovin, J., & Schwab, W. (2015). Acylphloroglucinol biosynthesis in olive. Song et al. (2015)	Wilfried Schwab	Germany	wilfried.schwab@tum.de	Cited By	32
Bai, Y., Dougherty, L., Cheng, L., & Xu, K. (2015). A co-expression gene network associated with development of olive fruit. Bai et al. (2015)	Kenong Xu	USA	kx27@cornell.edu	Cited By	34
Kim, T., Dreher, K., Nilo-Poyanco, R., Lee, I., Fiehn, O., Lange, B. M., ... & Rhee, S. Y. (2015). Patterns of gene expression in olive. Kim et al. (2015)	Seung Y. Rhee	USA	srhee@carnegiescience.edu	Cited By	27
Shin, J., & Lee, I. (2015). Co-inheritance analysis within the domains of life substantially improves network reconstruction. Shin et al. (2015)	Insuk Lee	Korea	insuklee@yonsei.ac.kr	Cited By	21
Davik, J., Eikemo, H., Brurberg, M. B., & Sargent, D. J. (2015). Mapping of the RPl-1 locus for Phytophthora resistance in olive. Davik et al. (2015)	Jahn Davik	Norway	jahn.davik@nibio.no	Cited By	20
Dossett, M., Bushakra, J. M., Gilmore, B., Koch, C. A., Kempler, C., Finn, C. E., & Bassil, N. V. (2015). Divergence of olive and other Rosaceae species. Dossett et al. (2015)	Michael Dossett	Canada	Michael.Dossett@agr.gc.ca	Cited By	11
Afanador-Kafuri, L., Mejía, J. F., González, A., & Álvarez, E. (2015). Identifying and analyzing the divergence of olive and other Rosaceae species. Afanador-Kafuri et al. (2015)	E. Alvarez	Colombia	e.alvarez@cgiar.org	Cited By	5
Fernandez-Pozo, N., Menda, N., Edwards, J. D., Saha, S., Tecle, I. Y., Strickler, S. R., ... & Mueller, L. A. (2015). The olive genome. Fernandez-Pozo et al. (2015)	Lukas A. Mueller	USA	lam87@cornell.edu	Cited By	628
Adal, A. M., Demissie, Z. A., & Mahmoud, S. S. (2015). Identification, validation and cross-species transferability of microsatellites in olive. Adal et al. (2015)	Soheil S. Mahmoud	Canada	soheil.mahmoud@ubc.ca	Cited By	41
Song, Z., Guo, S., Zhang, C., Zhang, B., Ma, R., Korir, N. K., & Yu, M. (2015). KT/HAK/KUP potassium transporter gene family in olive. Song et al. (2015)	Mingliang Yu	China	mly1008@aliyun.com	Cited By	29
Song, Z. Z., Yang, Y., Ma, R. J., Xu, J. L., & Yu, M. L. (2015). Transcription of potassium transporter genes in olive. Song et al. (2015)	M. L. Yu	China	mly1008@aliyun.com	Cited By	24
Uncu, A. O., Uncu, A. T., Celik, I., Doganlar, S., & Frary, A. (2015). A primer to molecular phylogenetic analysis of olive. Uncu et al. (2015)	Anne Frary	Turkey	annefrary@iyte.edu.tr	Cited By	13
Park, H. Y., Cho, I. H., Jung, S., & Main, D. (2015). Information and communication technology and its application in olive. Park et al. (2015)	Il-Hyung Cho	USA	icho@svsu.edu	Cited By	21
Koning, R.,	70

DATABASE CITATION DATA: GDR 2015

Year	Primary	Secondary	Collection-Date	Updated citations
2024	100	11	2/26/2024	3/22/2024
2023	289	592	2/14/2024	3/22/2024
2022	336	2407	2/15/2024	3/22/2024
2021	255	3820	2/15/2024	3/22/2024
2020	175	4607	2/16/2024	3/22/2024
2019	170	7463	2/17/2024	3/22/2024
2018	154	6077	2/20/2024	3/22/2024
2017	152	7581	2/20/2024	3/22/2024
2016	143	7371	2/21/2024	3/22/2024
2015	135	6920	2/22/2024	3/22/2024
2014	111	7335	2/22/2024	3/22/2024
2013	116	9318	2/22/2024	3/22/2024
2012	98	13236	2/22/2024	3/22/2024
2011	48	4436	2/22/2024	3/22/2024
2010	17	837	2/22/2024	3/22/2024
2009	14	1452	2/23/2024	3/22/2024
2008	14	1957	2/23/2024	3/22/2024
2007	9	794	2/23/2024	3/22/2024
2006	6	435	2/23/2024	3/22/2024
2005	1	96	2/23/2024	3/22/2024
2004	1	45	2/23/2024	3/22/2024
Total	2344	86790		

Journal Name										Impact factor		2024	2023	2022	2021	2020	2019						
3 Biotech										3.1						1							
Acta Ecologica Sinica										1.111				1									
Acta Physiologiae Plantarum										2.63				2	1		1						
Advances in Botanical Research										2.2													
Agriculture										3.6				1	1								
Agronomy										2.24		1	3	6	3	2	1						
Agronomy Journal										2.24				1									
American Journal of Botany										3					1								
Anais da Academia Brasileira de Ciências										1.73				1									
Annual Review of Plant Biology										30.5						1							
Antioxidants										7.675				2	1								
AoB Plants										3.138													
Applications in Plant Sciences										3.6					1								
Arabian Journal for Science and Engineering										2.7													
Australasian Plant Pathology										1.4													
Biochemical and Biophysical Research Communicat										3.1						1							
Biochemical Genetics										2.22				1			1						
Biochemical Systematics and Ecology										1.6													
Tree Physiology										4.196				2	2		1						
Trees										2.888				1									
Trends in Biotechnology										18.1													
Trends in Plant Science										22.5													
Tropical Plant Biology										1.9				1									
Turkish Journal of Agriculture and Forestry										2.3													
Total Journals by Year												40	300	338	264	179	179						
Total Journals cited												2310											
▶ ...										2015	2014	2013	2012	2011	2010	2009	2008	2007	2006	2005	2004	GDR-journal-log	

If you use GDR please cite: Jung, S. et al. (2019) [15 years of GDR: New data and](#)

[ome Database for Rosaceae](#). Nucleic Acids Res. 47, D1137-D1145

GENOME DATABASE FOR ROSACEAE



Resources for Rosaceae Research Discovery and Crop Improvement

- About
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- People
- Presentations
- Steering Committee
- Usage
- Work Completed
- Work in Progress

News and Events

Delicious haplotype-resolved genome available (6/24)

Genome data for *Fragaria x ananassa* FL 20.82-27 available (5/24)

Genome data for *Prunus dulcis* Texas Genome v3.0 available (5/24)

Workshop to be held on May 6-9th, 2025 at Costa Brava, Spain

[more](#)

Major Genera Quick Start



Fragaria



Malus



Prunus



Pyrus



Rosa



Rubus

Tools Quick Start

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[Search Genotype](#)
[Search Haplotype](#)
[BIMS](#)

GDR Citations

Below is a list of peer-reviewed publications that cite GDR using Google Scholar. Links are provided to **each publication and to secondary citations**. As of 1/13/2024, GDR was cited in 2,177 primary publications and 79,253 secondary publications. **List of journals with primary citations to GDR.**

- **2024** (100 citations)
- **2023** (266 citations)
- **2022** (320 citations)
- **2021** (231 citations)
- **2020** (176 citations)
- **2019** (173 citations)
- **2018** (156 citations)
- **2017** (154 citations)
- **2016** (142 citations)
- **2015** (135 citations)
- **2014** (111 citations)
- **2013** (116 citations)
- **2012** (98 citations)
- **2011** (47 citations)
- **2010** (17 citations)
- **2009** (14 citations)

2015 Peer-reviewed publications citing the use of GDR

2015 Peer-reviewed papers citing GDR (135)

1. Jung, S., Bassett, C., Bielenberg, D. G., Cheng, C. H., Dardick, C., Main, D., ... & Schaffer, R. J. (2015). A standard nomenclature for gene designation in the Rosaceae. *Tree genetics & genomes*, 11, 1-7.
Cited By
2. Darwish, O., Shahan, R., Liu, Z., Slovin, J. P., & Alkharouf, N. W. (2015). Re-annotation of the woodland strawberry (*Fragaria vesca*) genome *BMC genomics*, 16(1), 1-9.
Cited By
3. Hanada, T., Nashima, K., Kato, M., Takashina, T., Ikeda, K., Sakamoto, Y., ... & Isuzugawa, K. (2015). Molecular cloning and expression analysis of the WEE1 and CCS52A genes in European pear (*Pyrus communis* L.) and their possible roles in a giant fruit mutant. *The Journal of Horticultural Science and Biotechnology*, 90(5), 511-517.
Cited By
4. Donoso, J. M., Eduardo, I., Picañol, R., Batlle, I., Howad, W., Aranzana, M. J., & Arús, P. (2015). High-density mapping suggests cytoplasmic male sterility with two restorer genes in almond× peach progenies. *Horticulture research*, 2.
Cited By
5. Ru, S., Main, D., Evans, K., & Peace, C. (2015). Current applications, challenges, and perspectives of marker-assisted seedling selection in Rosaceae tree fruit breeding. *Tree Genetics & Genomes*, 11, 1-12.
Cited By
6. Cova, V., Bandara, N. L., Liang, W., Tartarini, S., Patocchi, A., Troggio, M., ... & Komjanc, M. (2015). Fine mapping of the Rvi5 (Vm) apple scab resistance locus in the 'Murray' apple genotype. *Molecular Breeding*, 35, 1-12.
Cited By
7. Salazar, J. A., Rubio, M., Ruiz, D., Tartarini, S., Martínez-Gómez, P., & Dondini, L. (2015). SNP development for genetic diversity analysis in apricot. *Tree Genetics & Genomes*, 11, 1-9.
Cited By
8. Kaja, E., Szcześniak, M. W., Jensen, P. J., Axtell, M. J., McNellis, T., & Makałowska, I. (2015). Identification of apple miRNAs and their potential role in fire blight resistance. *Tree Genetics & Genomes*, 11, 1-11.

BMC Genomics

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Research article | [Open access](#) | Published: 27 January 2015

Re-annotation of the woodland strawberry (*Fragaria vesca*) genome

[Omar Darwish](#), [Rachel Shahan](#), [Zhongchi Liu](#), [Janet P Slovin](#) & [Nadim W Alkharouf](#) 
[BMC Genomics](#) **16**, Article number: 29 (2015) | [Cite this article](#)
5497 Accesses | **54** Citations | **5** Altmetric | [Metrics](#)

Abstract

Background

Fragaria vesca is a low-growing, small-fruited diploid strawberry species commonly called woodland strawberry. It is native to temperate regions of Eurasia and North America and while it produces edible fruits, it is most highly useful as an experimental perennial plant system that can serve as a model for the agriculturally important *Rosaceae* family. A draft of the *F. vesca* genome sequence was published in 2011 [Nat Genet 43:223,2011]. The first generation annotation (version 1.1) were developed using GeneMark-ES+[Nuc Acids Res

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Re-annotation of the woodland strawberry (*Fragaria vesca*) genome

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A roadmap for research in octoploid strawberry

[VM Whitaker](#), [SJ Knapp](#), [MA Hardigan](#)... - *Horticulture ...*, 2020 - [academic.oup.com](#)


The cultivated strawberry (*Fragaria* × *ananassa*) is an allo-octoploid species, originating nearly 300 years ago from wild progenitors from the Americas. Since that time the strawberry ...

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Developmental mechanisms of fleshy fruit diversity in Rosaceae

[Z Liu](#), [H Ma](#), [S Jung](#), [D Main](#)... - *Annual Review of Plant ...*, 2020 - [annualreviews.org](#)

Rosaceae (the rose family) is an economically important family that includes species prized for high-value fruits and ornamentals. The family also exhibits diverse fruit types, including ...

☆ Save  Cite Cited by 48 Related articles All 5 versions

- Average Annual Value of Production, 2016-21 = **\$26.4 billion**
- # Primary Citations, 2004-2024 = 3634
- # Secondary Citations, 2004-2024 = **118,244**
- # pages served viewed by users in 2023 = **2.61 million**
- Cost of these databases in 2023 = **\$1.5 M (0.55% of VoP!!)**

Databases



citrus



pulse crops



vaccinium



cotton



rosaceae

Tools and Resources



AgBioData

Fruit and Nut
Cultivars Database

FUNDING AND ACKNOWLEDGEMENTS

FUNDERS



US Land Grant Universities
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COMMUNITY SUPPORT



Database Community
Database Research Users