





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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Sabarinath Subramaniam, Phoenix Bioinformatics

AgBioData Sustainability Workgroup

OVERVIEW

- AGBIODATA
- Sustainability Roadmap for AgBioData databases
 - Goals
 - Work to Date
- Research Impact of Crop Community Databases Case study

HTTPS://www.AGBIODATA.ORG



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
- Conduct a detailed analysis and modeling of sustainability solutions for representative $A_GB_{IO}D_{ATA}$ 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

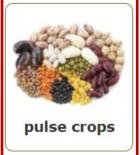
- WHAT IS IMPACT?
 - "HAVE A STRONG EFFECT ON SOMEONE OR SOMETHING"
 - "Exert Influence"
- How do we measure Impact of AgBioData Databases?
 - Usage metrics
 - Publications citing use of the databases
 - PRIMARY CITATIONS
 - Secondary Citations
- How do we interpret Impact?

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











Tools and Resources



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

1						Citation numbers by date
	Citation	Author	Country	Email	Cited by link	2/21/2024
3	Jung, S., Bassett, C., Bielenberg, D. G., Cheng, C. H., Dardick, C., Main, D., & Schaffer, R. J. (2015). J			robert.schaffer@plantandfood.co.nz	Cited By	23
4	Darwish, O., Shahan, R., Liu, Z., Slovin, J. P., & Alkharouf, N. W. (2015). Re-annotation of the woodla	Nadim W Alkharouf	USA	NALKHAROUF@TOWSON.EDU	Cited By	81
5	Hanada, T., Nashima, K., Kato, M., Takashina, T., Ikeda, K., Sakamoto, Y., & Isuzugawa, K. (2015). I	K. Isuzugawa	Japan	isuzugawak@pref.yamagata.jp	Cited By	4
6	Donoso, J. M., Eduardo, I., Picañol, R., Batlle, I., Howad, W., Aranzana, M. J., & Arús, P. (2015). High-	Pere Arús	Spain	pere.arus@irta.cat	Cited By	41
7	Ru, S., Main, D., Evans, K., & Peace, C. (2015). Current applications, challenges, and perspectives of n	Sushan Ru	USA	sru@bioinfo.wsu.edu	Cited By	114
8	Cova, V., Bandara, N. L., Liang, W., Tartarini, S., Patocchi, A., Troggio, M., & Komjanc, M. (2015). F	Riccardo Velasco	Italy	riccardo.velasco@fmach.it	Cited By	28
9	Salazar, J. A., Rubio, M., Ruiz, D., Tartarini, S., Martínez-Gómez, P., & Dondini, L. (2015). SNP develop	edro Martínez-Góme	Spain	pmartinez@cebas.csic.es	Cited By	27
10	Kaja, E., Szcześniak, M. W., Jensen, P. J., Axtell, M. J., McNellis, T., & Makałowska, I. (2015). Identific	Izabela Makałowska	Poland	izabel@amu.edu.pl	Cited By	32
11	Jia, Y., Yuan, Y., Zhang, Y., Yang, S., & Zhang, X. (2015). Extreme expansion of NBS-encoding genes in	Xiaohui Zhang	China	xiaohuizhang@nju.edu.cn	Cited By	73
12	Kang, C., & Liu, Z. (2015). Global identification and analysis of long non-coding RNAs in diploid straw	Zhongchi Liu	USA	zliu@umd.edu	Cited By	110
13	Wilde, H. D., Gandhi, K. J., & Colson, G. (2015). State of the science and challenges of breeding lands	H Dayton Wilde	USA	dwilde@uga.edu	Cited By	61
14	Bassil, N. V., Davis, T. M., Zhang, H., Ficklin, S., Mittmann, M., Webster, T., & van de Weg, E. (2015)	Nahla V Bassil	USA	nahla.bassil@ars.usda.gov	Cited By	220
15	Lashbrooke, J., Aharoni, A., & Costa, F. (2015). Genome investigation suggests MdSHN3, an APETALA	Fabrizio Costa	Italy	fabrizio.costa@fmach.it	Cited By	90
16	Dereeper, A., Bocs, S., Rouard, M., Guignon, V., Ravel, S., Tranchant-Dubreuil, C., & Droc, G. (2015)	Alexis Dereeper	France	alexis.dereeper@ird.fr	Cited By	73
17	Song, C., Ring, L., Hoffmann, T., Huang, F. C., Slovin, J., & Schwab, W. (2015). Acylphloroglucinol bios	Wilfried Schwab	Germany	wilfried.schwab@tum.de	Cited By	32
18	Bai, Y., Dougherty, L., Cheng, L., & Xu, K. (2015). A co-expression gene network associated with deve	Kenong Xu	USA	kx27@cornell.edu	Cited By	34
19	Kim, T., Dreher, K., Nilo-Poyanco, R., Lee, I., Fiehn, O., Lange, B. M., & Rhee, S. Y. (2015). Patterns	Seung Y. Rhee	USA	srhee@carnegiescience.edu	Cited By	27
20	Shin, J., & Lee, I. (2015). Co-inheritance analysis within the domains of life substantially improves ne	Insuk Lee	Korea	insuklee@yonsei.ac.kr	Cited By	21
21	Davik, J., Eikemo, H., Brurberg, M. B., & Sargent, D. J. (2015). Mapping of the RPc-1 locus for Phytopl	Jahn Davik	Norway	jahn.davik@nibio.no	Cited By	20
22	Dossett, M., Bushakra, J. M., Gilmore, B., Koch, C. A., Kempler, C., Finn, C. E., & Bassil, N. V. (2015). D	Michael Dossett	Canada	Michael.Dossett@agr.gc.ca	Cited By	11
23	Afanador-Kafuri, L., Mejía, J. F., González, A., & Álvarez, E. (2015). Identifying and analyzing the diver	E. Alvarez	Colombia	e.alvarez@cgiar.org	Cited By	5
24	Fernandez-Pozo, N., Menda, N., Edwards, J. D., Saha, S., Tecle, I. Y., Strickler, S. R., & Mueller, L. A	Lukas A. Mueller	USA	lam87@cornell.edu	Cited By	628
25	Adal, A. M., Demissie, Z. A., & Mahmoud, S. S. (2015). Identification, validation and cross-species tra	Soheil S. Mahmoud	Canada	soheil.mahmoud@ubc.ca	Cited By	41
26	Song, Z., Guo, S., Zhang, C., Zhang, B., Ma, R., Korir, N. K., & Yu, M. (2015). KT/HAK/KUP potassium tra	Mingliang Yu	China	mly1008@aliyun.com	Cited By	29
27	Song, Z. Z., Yang, Y., Ma, R. J., Xu, J. L., & Yu, M. L. (2015). Transcription of potassium transporter ger	M. L. Yu	China	mly1008@aliyun.com	Cited By	24
28	Uncu, A. O., Uncu, A. T., Celık, İ., Doganlar, S., & Frary, A. (2015). A primer to molecular phylogenetic	Anne Frary	Turkey	annefrary@iyte.edu.tr	Cited By	13
29	Park, H. Y., Cho, I. H., Jung, S., & Main, D. (2015). Information and communication technology and us	II-Hyung Cho	USA	icho@svsu.edu	Cited By	21
30	Koning-Ramarinan C.F. Faralink G.D. Vinkaranlian M. Uan't Wastanda M. B. Girama V. W. Krait	tarinne i M. Smilitan	Garage	rene smulders@wur nl	Cited By	70
*	2024 2023 2022 2021 2020 2019 2018 2017 2016 2015 2	2014 2013 2012	2011 20	010 🕂 🕴 🚺		10
100						The second secon

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		.W

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					

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GENOME DATABASE FOR ROSACI



Resources for Rosaceae Research Discovery and Crop Improv

About

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Presentations

Steering Committee

Usage

Work Completed

Work in Progress

me Database for Rosaceae. Nucleic Acids Res. 47, D1137-D1145

News and Events

Delicious haplotype-resolved genome available (6/24)

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

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

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

Genomics		Genetics	Breeding		
	View Genomes	Search Maps	Search Phenotyp		
	VIew Pan-Genomes	Search Markers	Search Genotype		
	Search Genes	QTLs and GWAS	Search Haplotype		
	BLAST Sequences	Compare Maps	BIMS		

DATABASE CITATION PAGE: GDR

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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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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Figures

res References

Abstract

Sections

Background

Results and discussion

Conclusions

Methods

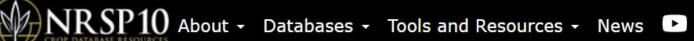
References

<u>Acknowledgements</u>

Author information

Additional information

Rights and permissions



- 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









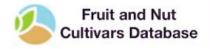




Tools and Resources







FUNDING AND ACKNOWLEDGEMENTS

FUNDERS



US Land Grant Universities Industry

COMMUNITY SUPPORT



Database Community
Database Research Users