Database Resources for Small Fruit Research

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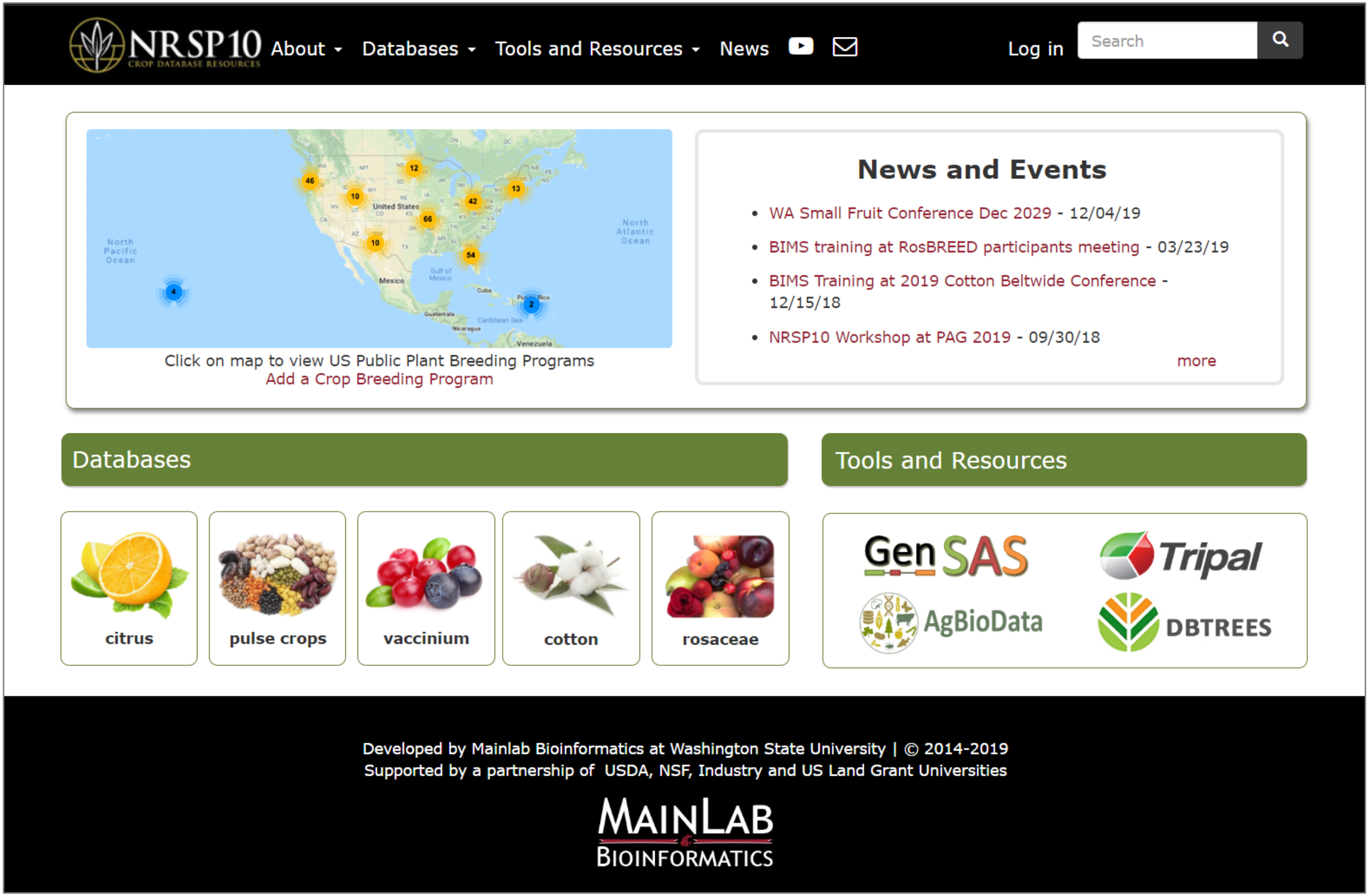
WA Small Fruit Washington Small Fruit Conference
Dec 4-6, 2019, Lynden, WA

NRSP10 CROP DATABASE RESOURCES
USDA
ars
NIFA
NSF
VacCAP



Click on map to view US Public Plant Breeding Programs
Add a Crop Breeding Program

News and Events

- WA Small Fruit Conference Dec 2029 - 12/04/19
- BIMS training at RosBREED participants meeting - 03/23/19
- BIMS Training at 2019 Cotton Beltwide Conference - 12/15/18
- NRSP10 Workshop at PAG 2019 - 09/30/18

more

Developed by Mainlab Bioinformatics at Washington State University | © 2014-2019
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NIFA Hatch Funded: 2014-2024 ($4.5 million)
USDA SCRI and NSF Funding: 2009-2023 ($5 million)

Small Fruit Crop Databases

NRSP10 databases for small fruit research

2.1 m pages accessed over 300,000 visits (2014-19)

- Fragaria: strawberry
- Rubus: red raspberry, black raspberry and blackberry

SCRI GDR & RosBREED (20 M)

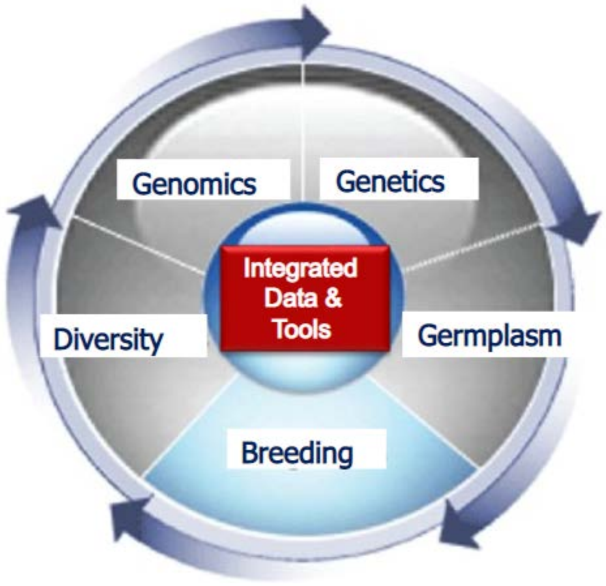
100,000 pages accessed over 17,500 visits (2014-19)

- Blueberry and cranberry

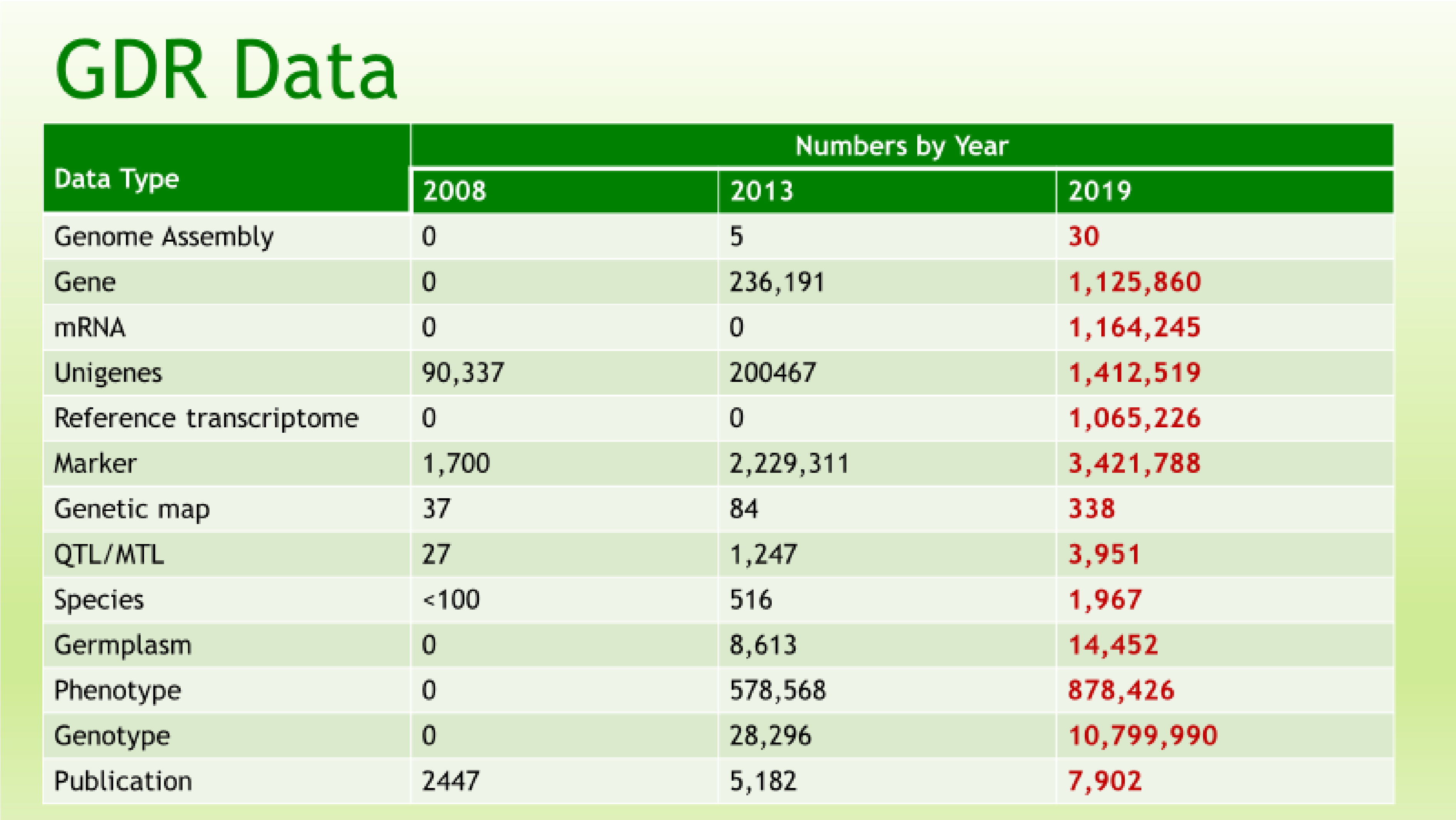
SCRI VacciniumCAP (6.5 M)

Crop Community Databases

Recent advances in sequencing, genotyping, and phenotyping technologies have led to a paradigm shift in crop science research – “Big Data” driven



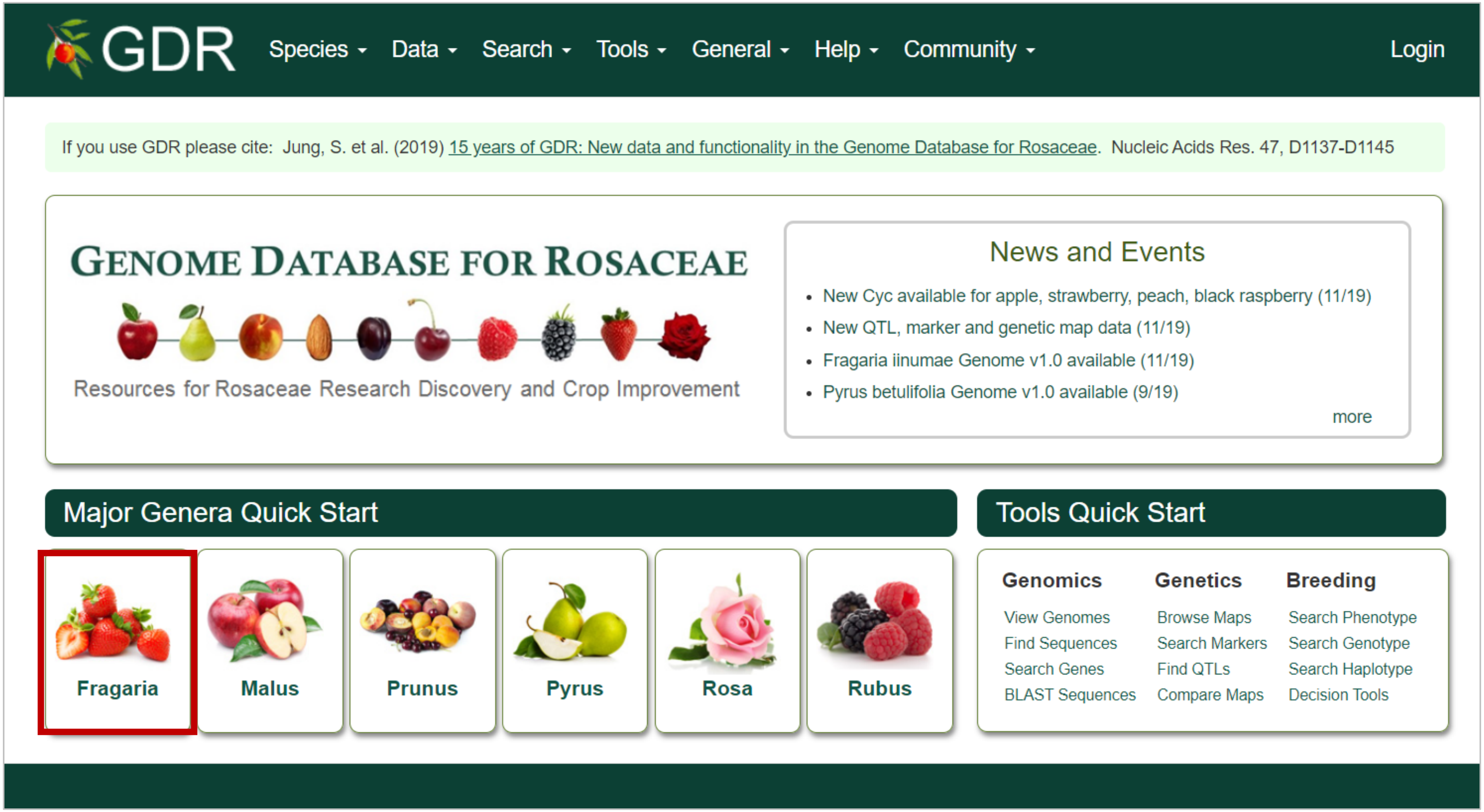
1. Collect, curate and distill data
2. Integrate data and tools
3. Facilitate research discovery
4. Facilitate translation and application in crop improvement
5. Build research communities



GDR Data

Data Type	Numbers by Year		
	2008	2013	2019
Genome Assembly	0	5	30
Gene	0	236,191	1,125,860
mRNA	0	0	1,164,245
Unigenes	90,337	200467	1,412,519
Reference transcriptome	0	0	1,065,226
Marker	1,700	2,229,311	3,421,788
Genetic map	37	84	338
QTL/MTL	27	1,247	3,951
Species	<100	516	1,967
Germplasm	0	8,613	14,452
Phenotype	0	578,568	878,426
Genotype	0	28,296	10,799,990
Publication	2447	5,182	7,902

Billions of data points condensed into re-useable, integrated data with added value



If you use GDR please cite: Jung, S. et al. (2019) 15 years of GDR: New data and functionality in the Genome Database for Rosaceae. Nucleic Acids Res. 47, D1137-D1145

GENOME DATABASE FOR ROSACEAE

Resources for Rosaceae Research Discovery and Crop Improvement

News and Events

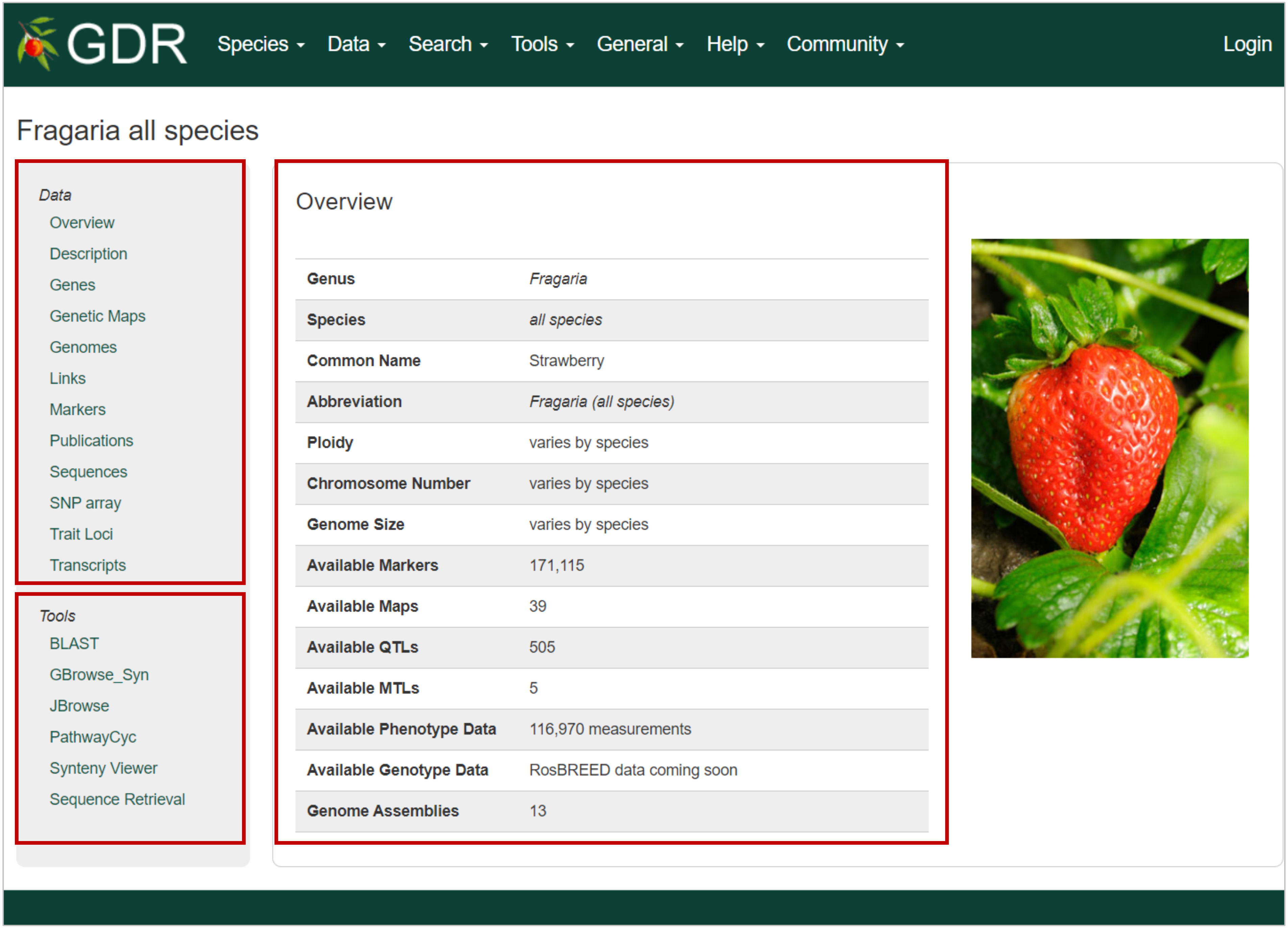
- New Cyc available for apple, strawberry, peach, black raspberry (11/19)
- New QTL, marker and genetic map data (11/19)
- Fragaria iinumae Genome v1.0 available (11/19)
- Pyrus betulifolia Genome v1.0 available (9/19)

more

Major Genera Quick Start

Tools Quick Start

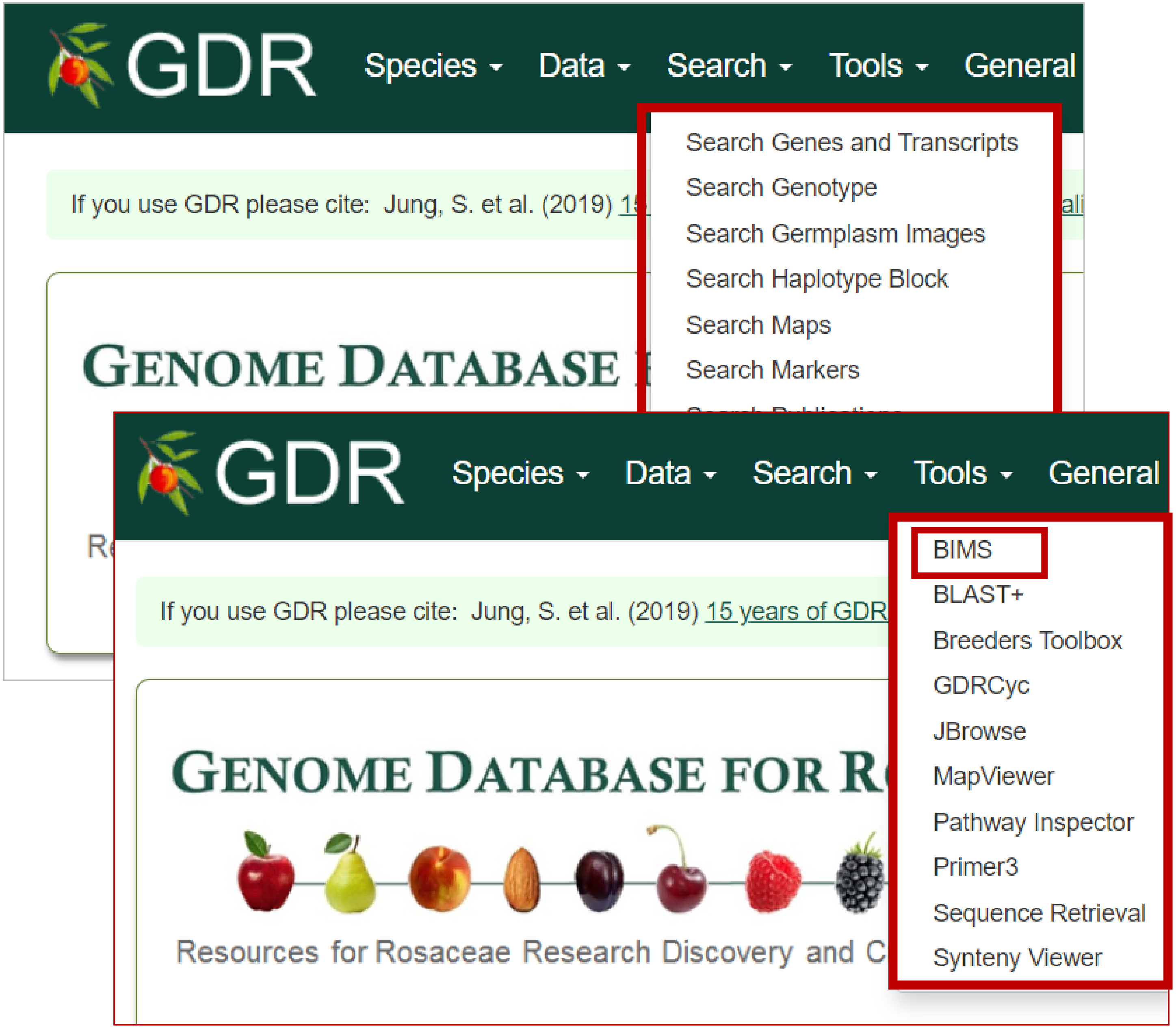
Genomics	Genetics	Breeding
View Genomes	Browse Maps	Search Phenotype
Find Sequences	Search Markers	Search Genotype
Search Genes	Find QTLs	Search Haplotype
BLAST Sequences	Compare Maps	Decision Tools



Fragaria all species

Overview

Genus	*Fragaria*
Species	*all species*
Common Name	Strawberry
Abbreviation	*Fragaria (all species)*
Ploidy	varies by species
Chromosome Number	varies by species
Genome Size	varies by species
Available Markers	171,115
Available Maps	39
Available QTLs	505
Available MTLs	5
Available Phenotype Data	116,970 measurements
Available Genotype Data	RosBREED data coming soon
Genome Assemblies	13



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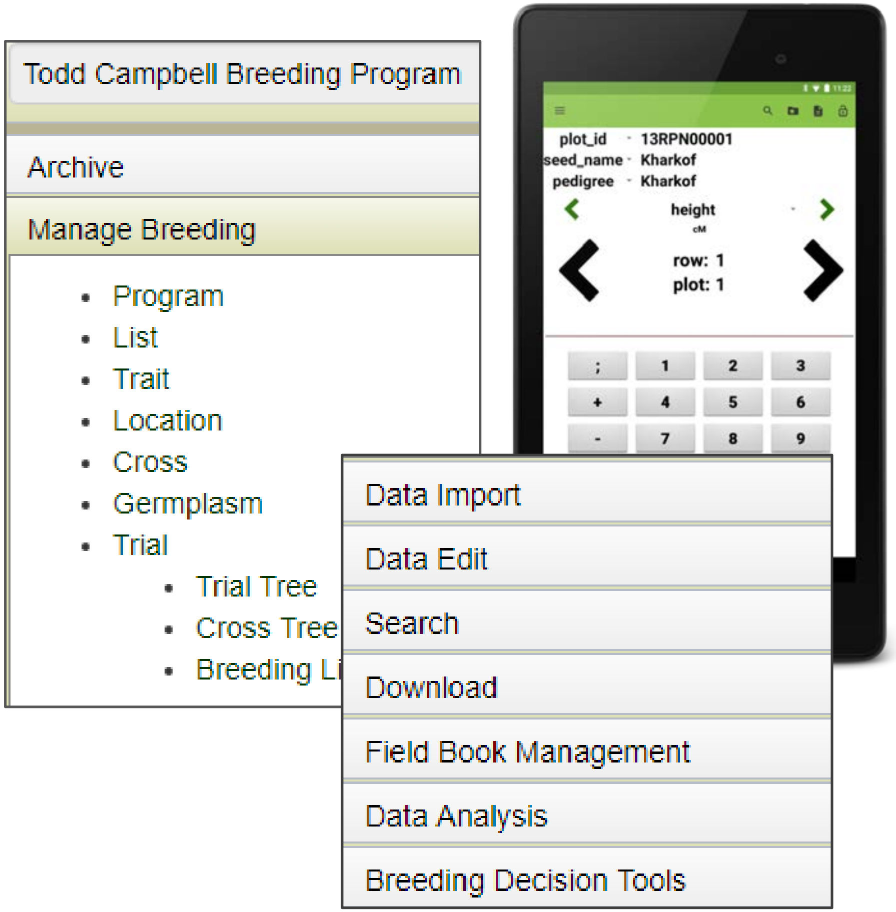
GENOME DATABASE FOR R

Resources for Rosaceae Research Discovery and C

Breeding Information Management

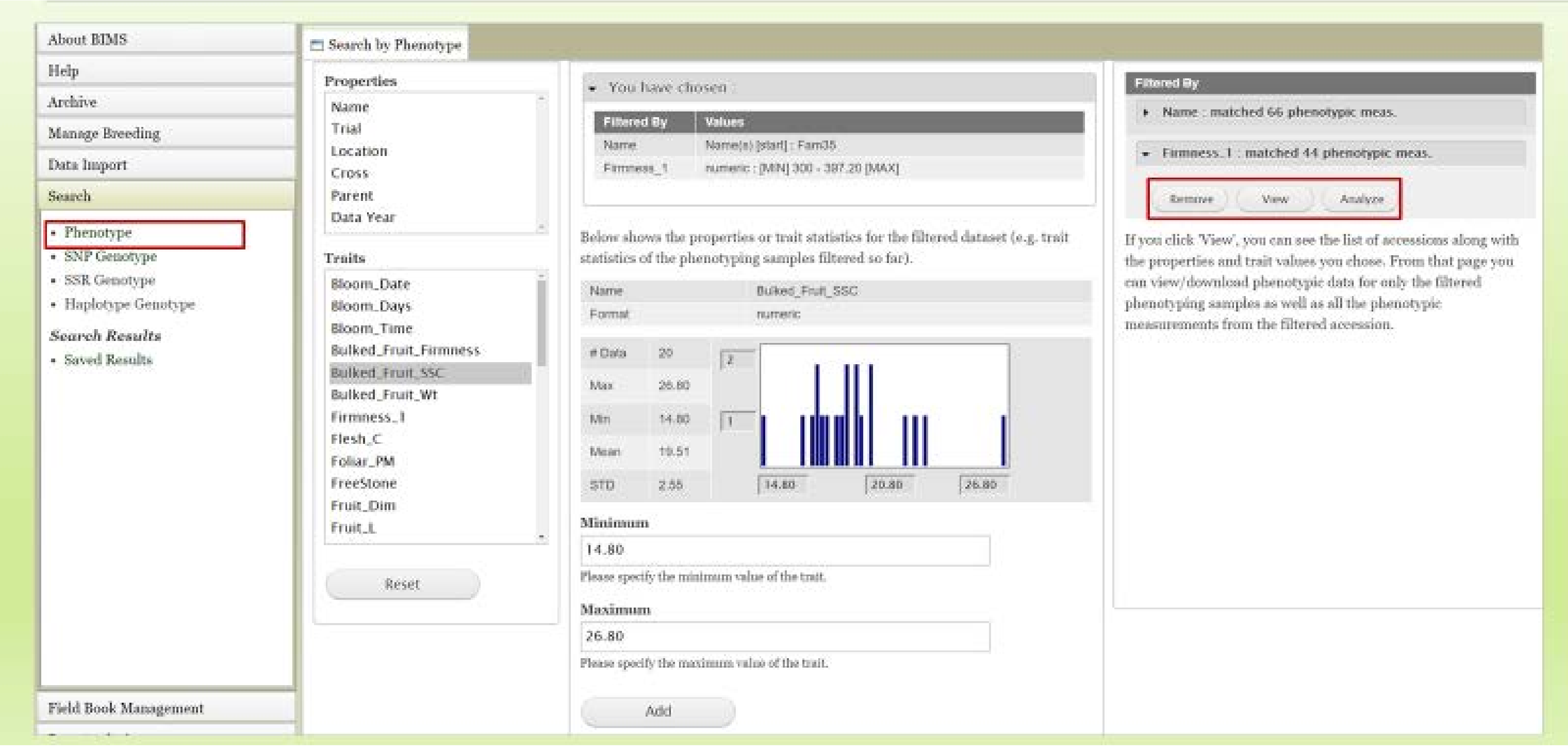


plot_id · 13RPN00001
seed_name · Kharkof
pedigree · Kharkof
row: 1
plot: 1

BIMS and Field Book

- Archive
- Manage Breeding
- Data Import
- Data Edit
- Search and Download
- Field Book App Management
- Data Analysis Tools
- Breeding Decision Tools

Search/Filter/Analyze



Filtered By	Values
Name	Name(s) [start] : Fam35
Firmness_1	numeric : [MIN] 300 - 397.20 [MAX]

Below shows the properties or trait statistics for the filtered dataset (e.g. trait statistics of the phenotyping samples filtered so far).

Name	Bulked_Fruit_SSC
Format	numeric

# Data	20
Max	26.80
Min	14.80
Mean	19.51
STD	2.55

Minimum: 14.80

Please specify the minimum value of the trait.

Maximum: 26.80

Please specify the maximum value of the trait.

Name : matched 66 phenotypic meas.

Firmness_1 : matched 44 phenotypic meas.

If you click 'View', you can see the list of accessions along with the properties and trait values you chose. From that page you can view/download phenotypic data for only the filtered phenotyping samples as well as all the phenotypic measurements from the filtered accession.

Acknowledgements

- The Bioinformatics Team and CoPI’s (all are co-authors)
- The Rosaceae and Vaccinium Community for their support and data ☺
- The Bioinformatics community for open-source software
- Funding Sources

Thank you for your attention ☺

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