
ABC opening remarks
Travis Parker
2023 KT annual meeting

2019…

2020 - 2022…


UNZA BEAN BREEDING
FUNDED BY:
KIRKHOUSE TRUST

Gaining new skills…

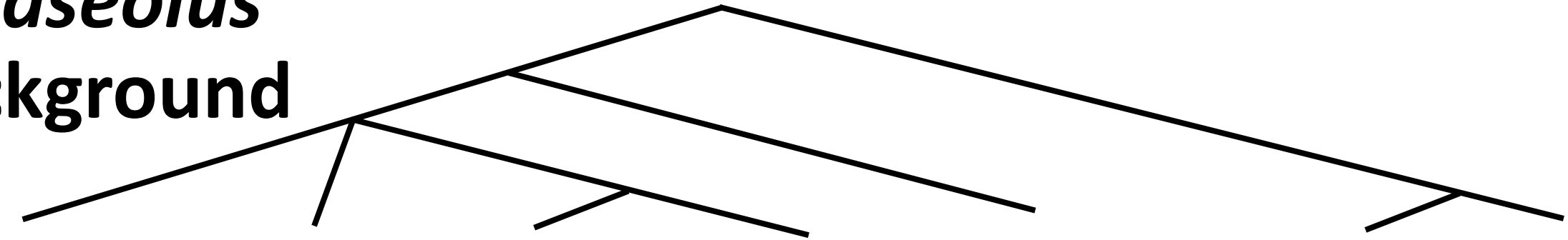
Impending releases…

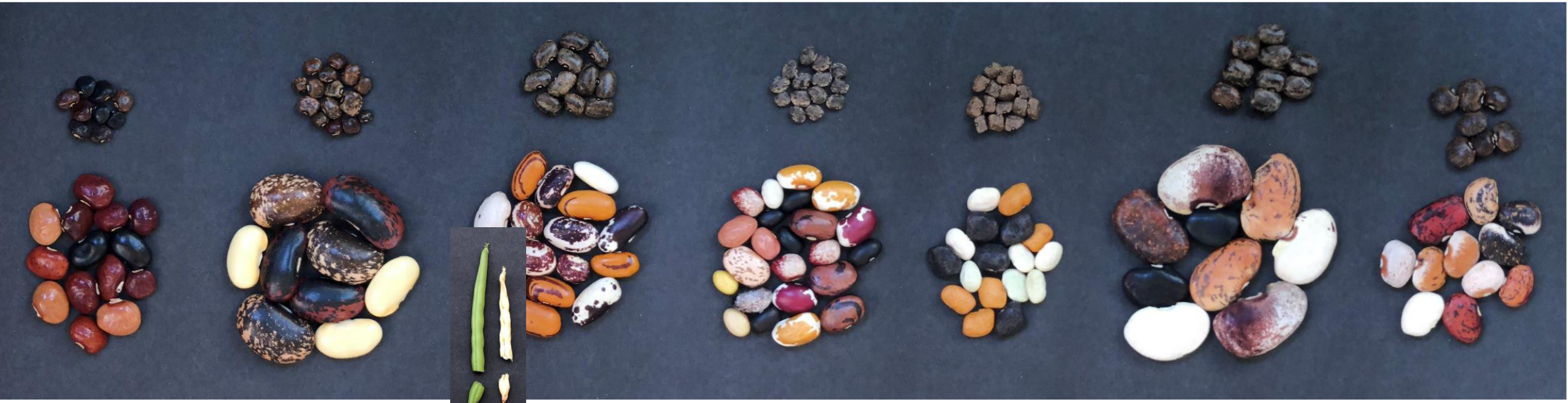
Kelvin Kamfwa and team

Stanley Nkalubo and team

Yayis Rezene and team

Phaseolus background





Year bean
Phaseolus dumosus
Middle American

Runner bean
Phaseolus coccineus
Middle American

Common bean
Phaseolus vulgaris
Andean

Common bean
Phaseolus vulgaris
Middle American

Tepary bean
Phaseolus acutifolius
Middle American

Lima bean
Phaseolus lunatus
Andean

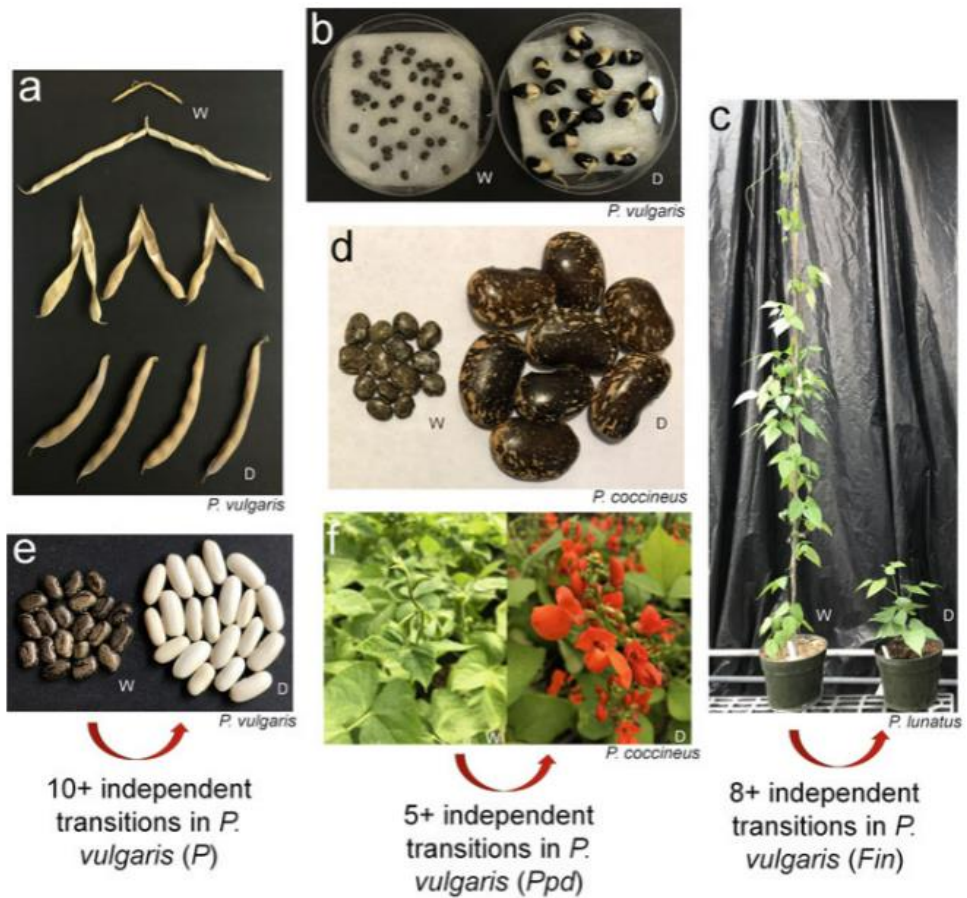
Lima bean
Phaseolus lunatus
Middle American

Population Genomics of *Phaseolus* spp.: A Domestication Hotspot

Travis A. Parker and Paul Gepts

T. A. Parker · P. Gepts (✉)
Department of Plant Sciences/MS1, Section of Crop and Ecosystem Sciences, University of California, Davis, CA, USA
e-mail: plgepts@ucdavis.edu

Om P. Rajora (ed.), *Population Genomics: Crop Plants*,
Population Genomics [Om P. Rajora (Editor-in-Chief)],
https://doi.org/10.1007/13836_2021_89,



NCGR

I. Migration of PhaseolusGenes to the Legume Information System (LIS, legumeinfo.org)

PHASEOLUSGENES
Bean Breeder's Molecular Marker Toolbox

→

LIS: Legume Information System
Information about legume traits for crop improvement

Andrew Farmer

Steven Cannon

Sam Hokin

LIS - Legume Information System

Information about legume traits for crop improvement

Newsletter signup

Marker Search

Search for markers in *Phaseolus vulgaris* using the form below.

Species – Any –

Marker name (can be partial)

Publication

Search Example

Organism	Marker	Alt names used on maps	Synonyms
Phaseolus vulgaris	(ACTG)4_850		
Phaseolus vulgaris	0205G		
Phaseolus vulgaris	1-Gm		
Phaseolus vulgaris	118M3		
Phaseolus vulgaris	11M-Gm		
Phaseolus vulgaris	11M1		
Phaseolus vulgaris	129M2		
Phaseolus vulgaris	12M-Gm		
Phaseolus vulgaris	12M1		
Phaseolus vulgaris	13-Gm		

Data Collections

Arachis
Cajanus
Cicer
Glycine
Lotus
Lupinus
Medicago
Phaseolus
Pisum
Trifolium
Vigna

Phaseolus data collections

Phaseolus lunatus

Genomes

G27455.gnm1.7NXX
Phaseolus lunatus accession G27455 genome assembly V1

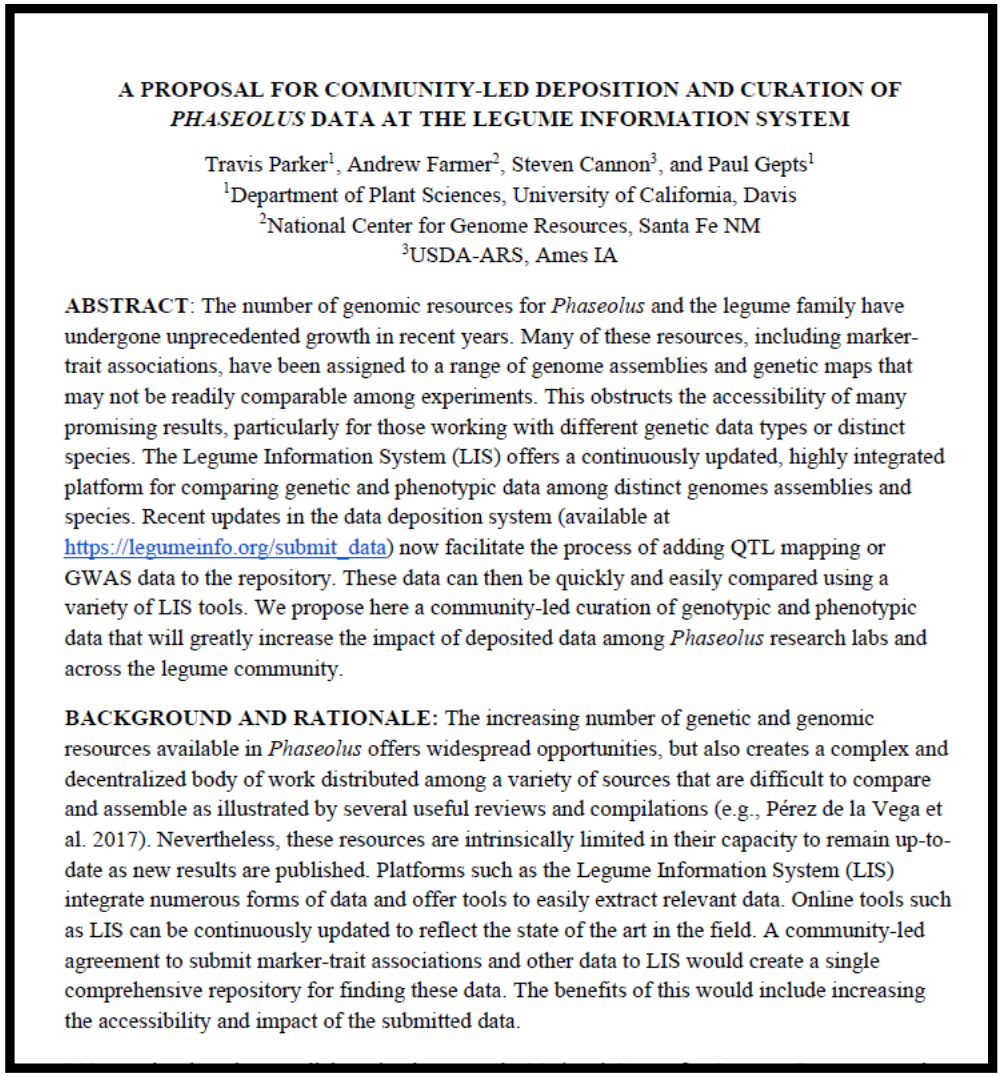
Annotations

G27455.gnm1.ann1.JD7C
Phaseolus lunatus accession G27455 annotation files from genome assembly V1

Phaseolus vulgaris

Genomes

5-593.gnm1.1P7P
Phaseolus vulgaris accession 5-593 (Middle American race), genome assembly v1.
G19833.gnm1.zBnF
Phaseolus vulgaris accession G19833 genome assembly v1.0



A PROPOSAL FOR COMMUNITY-LED DEPOSITION AND CURATION OF *PHASEOLUS* DATA AT THE LEGUME INFORMATION SYSTEM

Travis Parker[1], Andrew Farmer[2], Steven Cannon[3], and Paul Gepts[1]
[1]Department of Plant Sciences, University of California, Davis
[2]National Center for Genome Resources, Santa Fe NM
[3]USDA-ARS, Ames IA

ABSTRACT: The number of genomic resources for *Phaseolus* and the legume family have undergone unprecedented growth in recent years. Many of these resources, including marker-trait associations, have been assigned to a range of genome assemblies and genetic maps that may not be readily comparable among experiments. This obstructs the accessibility of many promising results, particularly for those working with different genetic data types or distinct species. The Legume Information System (LIS) offers a continuously updated, highly integrated platform for comparing genetic and phenotypic data among distinct genomes assemblies and species. Recent updates in the data deposition system (available at https://legumeinfo.org/submit_data) now facilitate the process of adding QTL mapping or GWAS data to the repository. These data can then be quickly and easily compared using a variety of LIS tools. We propose here a community-led curation of genotypic and phenotypic data that will greatly increase the impact of deposited data among *Phaseolus* research labs and across the legume community.

BACKGROUND AND RATIONALE: The increasing number of genetic and genomic resources available in *Phaseolus* offers widespread opportunities, but also creates a complex and decentralized body of work distributed among a variety of sources that are difficult to compare and assemble as illustrated by several useful reviews and compilations (e.g., Pérez de la Vega et al. 2017). Nevertheless, these resources are intrinsically limited in their capacity to remain up-to-date as new results are published. Platforms such as the Legume Information System (LIS) integrate numerous forms of data and offer tools to easily extract relevant data. Online tools such as LIS can be continuously updated to reflect the state of the art in the field. A community-led agreement to submit marker-trait associations and other data to LIS would create a single comprehensive repository for finding these data. The benefits of this would include increasing the accessibility and impact of the submitted data.

LIS - Legume Information System
Information about legume traits for crop improvement

PhaseolusMine v5.1.0.2 Phaseolus species data from the Legume Information System

Home | Templates | Lists | QueryBuilder | Regions | Data Sources | API | MyMine

Other LIS Mines | LIS Home | Log in

Search: e.g Phvul.002G040500 GO

Search

Search this mine. Enter **names**, **identifiers** or **keywords**. Examples: Phvul.002G040500, Phvul.002G040500.1, Seed weight 3-2.

e.g. X, Y, Z

SEARCH

Analyze

Enter a **list** of identifiers.

Gene

Phvul.002G040500

advanced

ANALYZE LIST

Welcome back to PhaseolusMine!

This mine integrates genomic and genetic data for Phaseolus species. It is being developed by the Legume Information System, and is built from the LIS datastore. Contact Sam Hokin shokin at

Description *Click here to enter a description for your list*

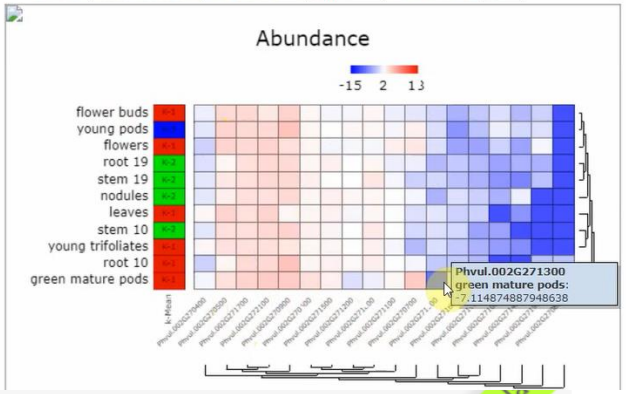
Date Created: 2023-01-26 20:25

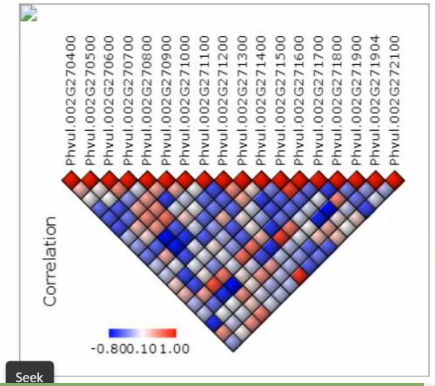
Cufflinks Gene Expression

The plotted values and are log2 of the recorded FPKM. FPKM values exactly 0 are thresholded to -10 in this plot.
Heatmap visualization powered by canvasXpress, learn more about the display options.

Click to see/hide the expression maps

FPKM Expression Clustering - Hierarchical: Single and K-means: 3





Seek

5.1.0.2 (January, 2022)

PhaseolusMine is sourced from files found on the LIS datastore (https://data.legumeinfo.org/).

GENOMICS | COMPARISON | FUNCTION | EXPRESSIC

Genomic queries, leading to genes and other chromosome features. Read more

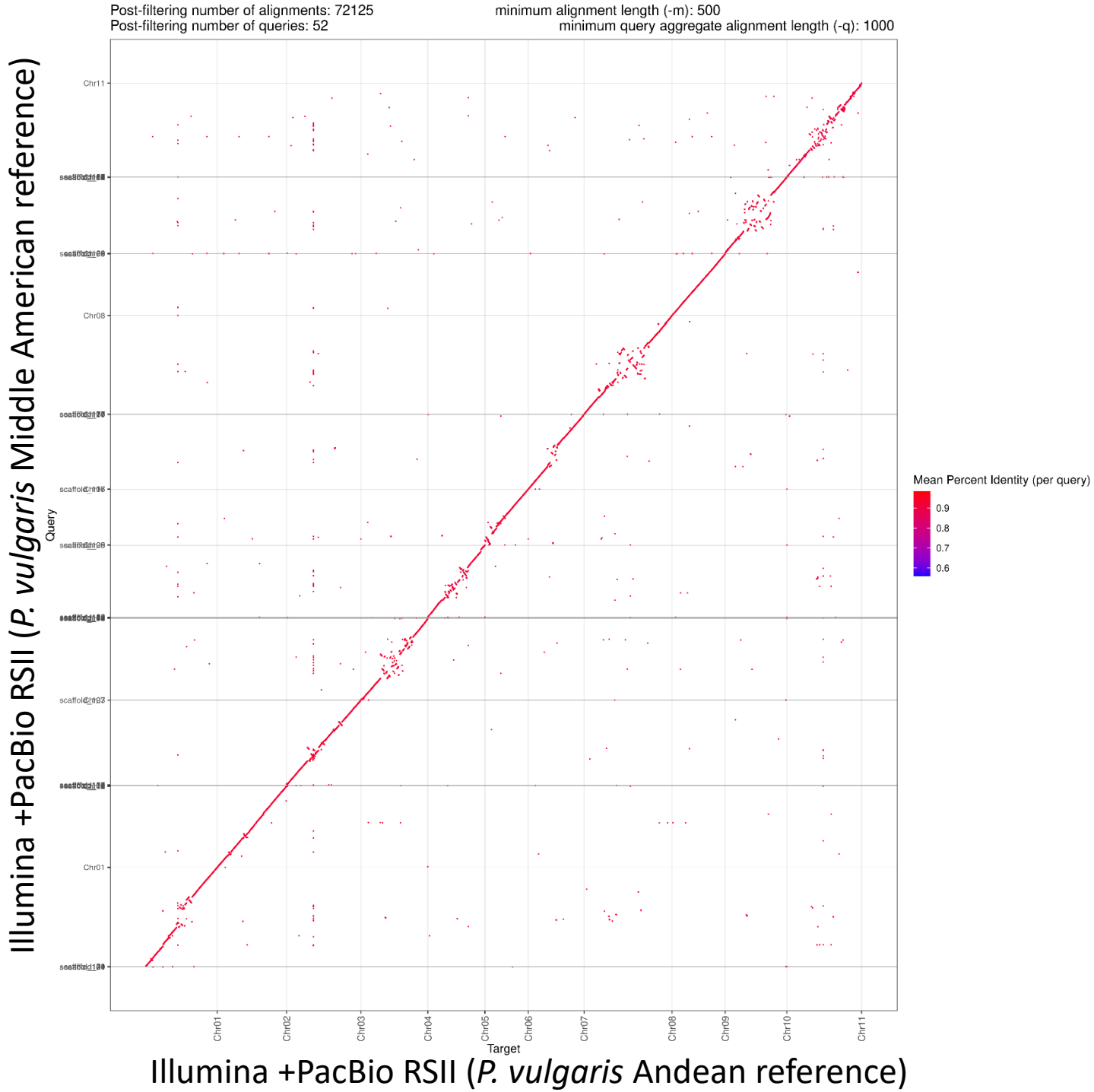
Query for genomics:

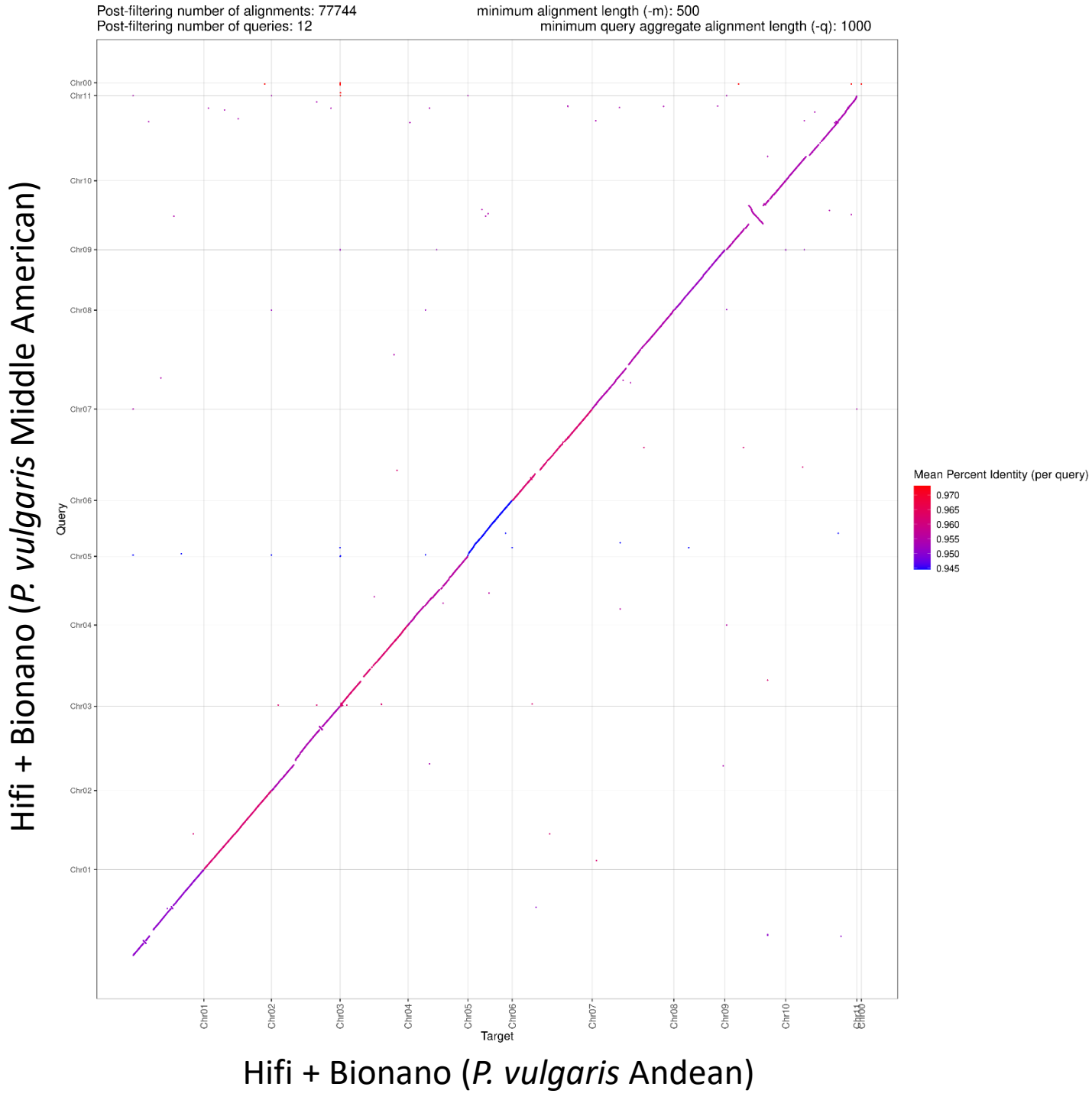
- Gene → Transcripts and Sequences
- Region → Genes
- Region → Genetic Markers
- Gene → Protein sequences

» More queries

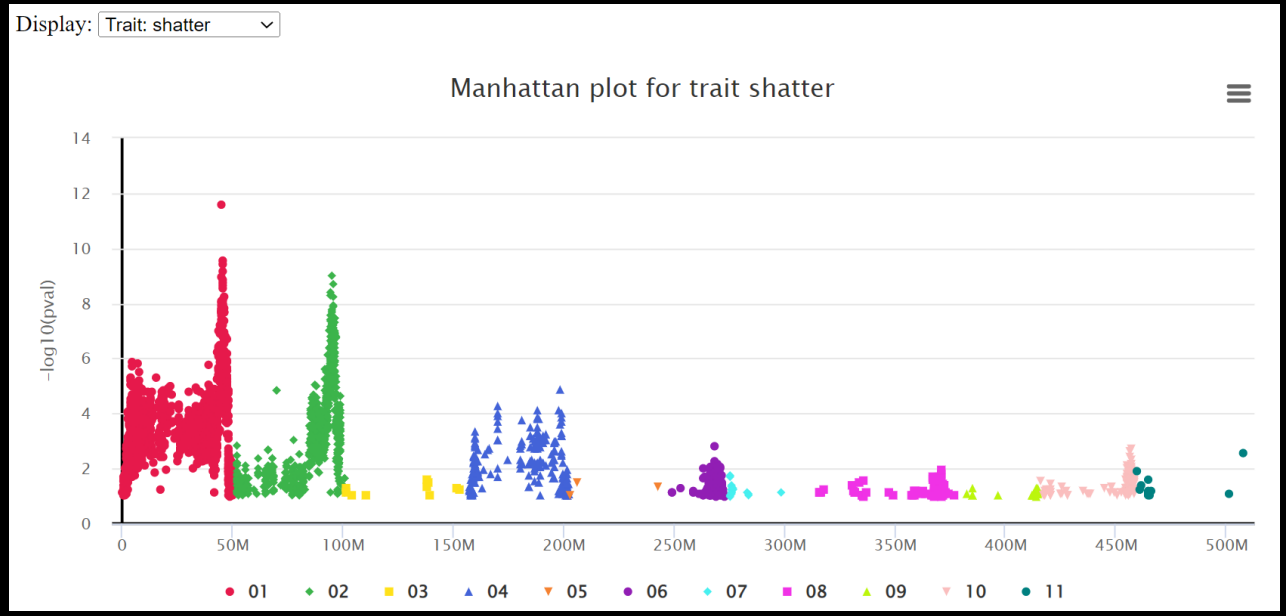
popular templ

II. Developing improved genome assemblies and associated resources


Post-filtering number of alignments: 72125
Post-filtering number of queries: 52
minimum alignment length (-m): 500
minimum query aggregate alignment length (-q): 1000
Illumina +PacBio RSII (P. vulgaris Middle American reference)
Query
Chr11
Chr08
Chr01
Target
Chr01
Chr02
Chr03
Chr04
Chr05
Chr06
Chr07
Chr08
Chr09
Chr10
Chr11
Illumina +PacBio RSII (P. vulgaris Andean reference)
Mean Percent Identity (per query)
0.9
0.8
0.7
0.6

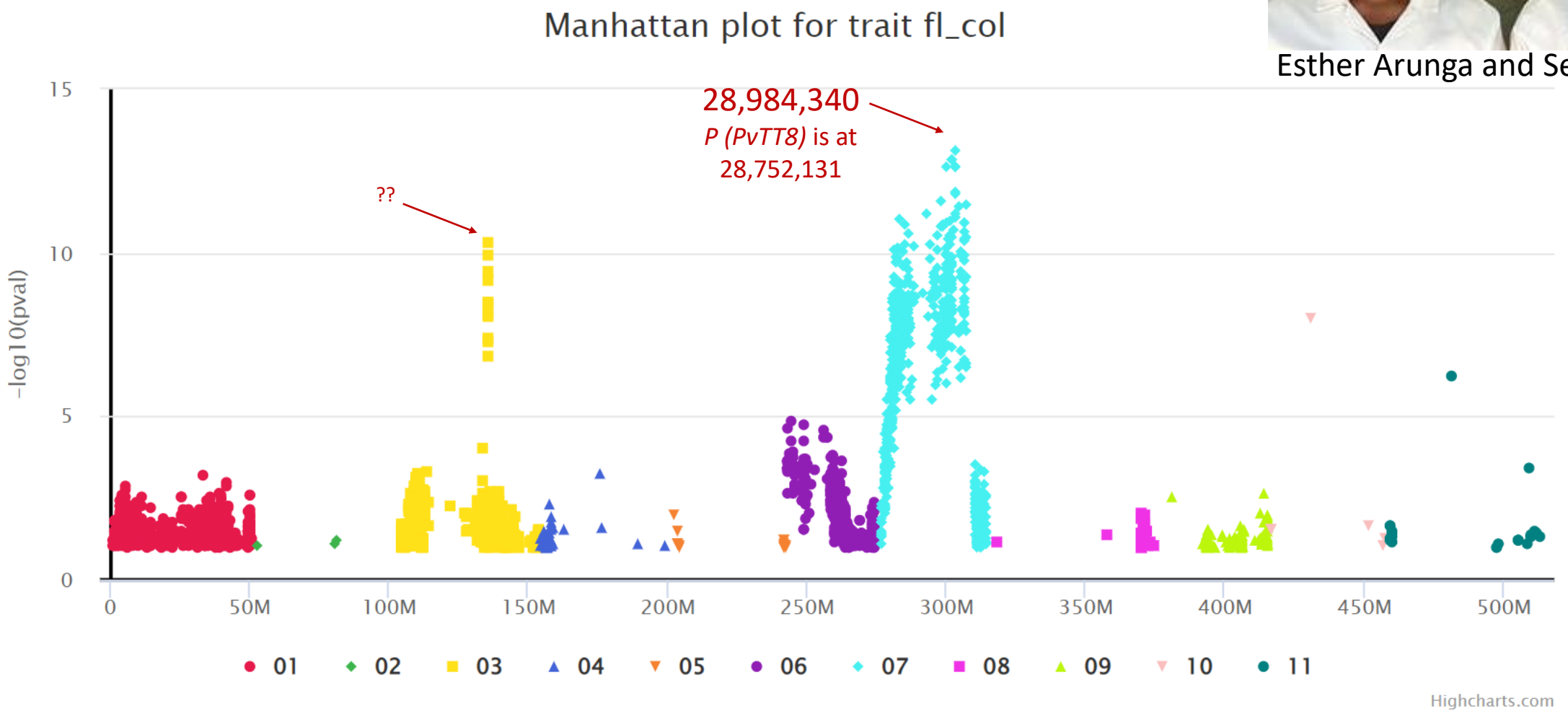

Post-filtering number of alignments: 77744
Post-filtering number of queries: 12
minimum alignment length (-m): 500
minimum query aggregate alignment length (-q): 1000
Hifi + Bionano (P. vulgaris Middle American)
Query
Chr00
Chr11
Chr10
Chr09
Chr08
Chr07
Chr06
Chr05
Chr04
Chr03
Chr02
Chr01
Target
Chr01
Chr02
Chr03
Chr04
Chr05
Chr06
Chr07
Chr08
Chr09
Chr10
Chr11
Mean Percent Identity (per query)
0.970
0.965
0.960
0.955
0.950
0.945
Hifi + Bionano (P. vulgaris Andean)

Value for mapping



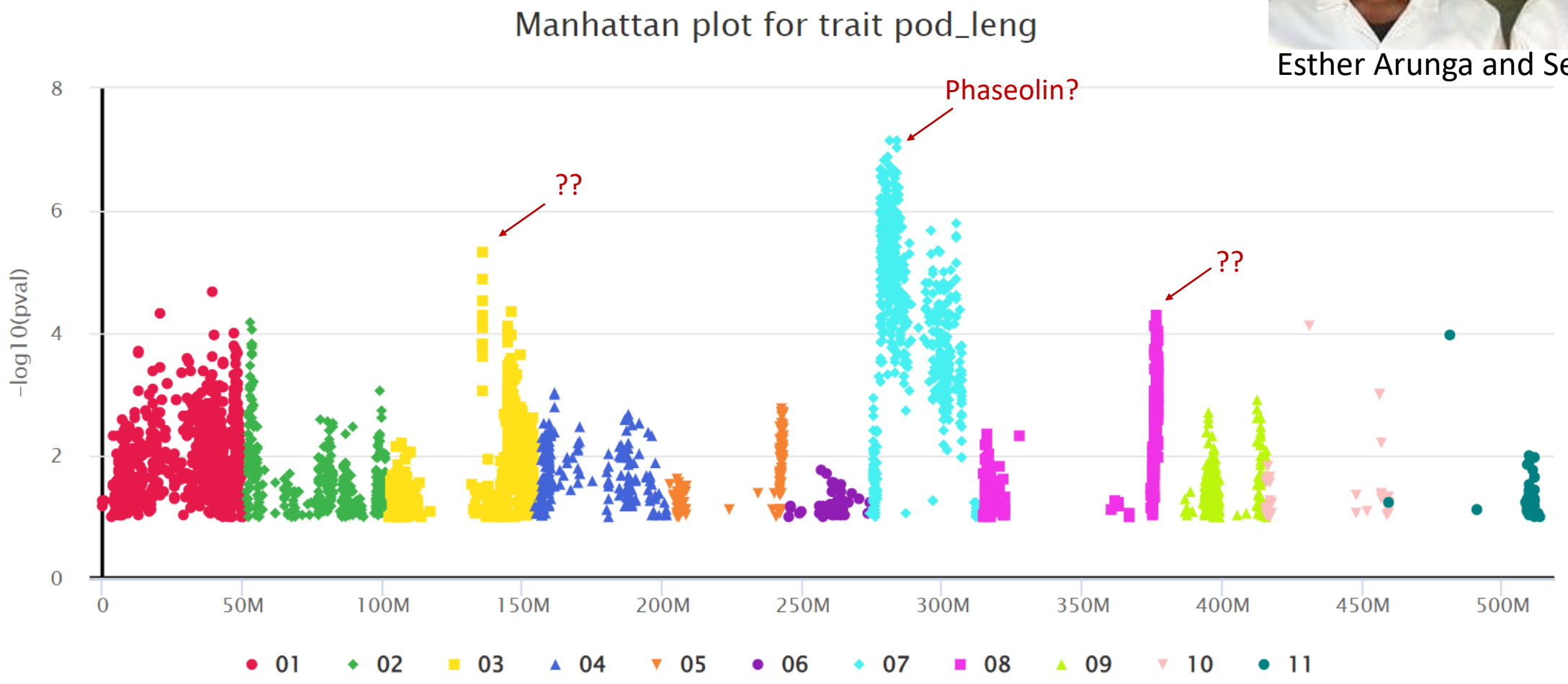
Esther Arunga and Serah Njau

Display: Trait: fl_col



Esther Arunga and Serah Njau

Display: Trait: pod_leng



Complex structural variation

Wall fiber absent (0)

Wall fiber present (10)

Strings absent (0)

Strings present (10)

Both traits spontaneously and heritably revert!

New Phytologist

FULL PAPER

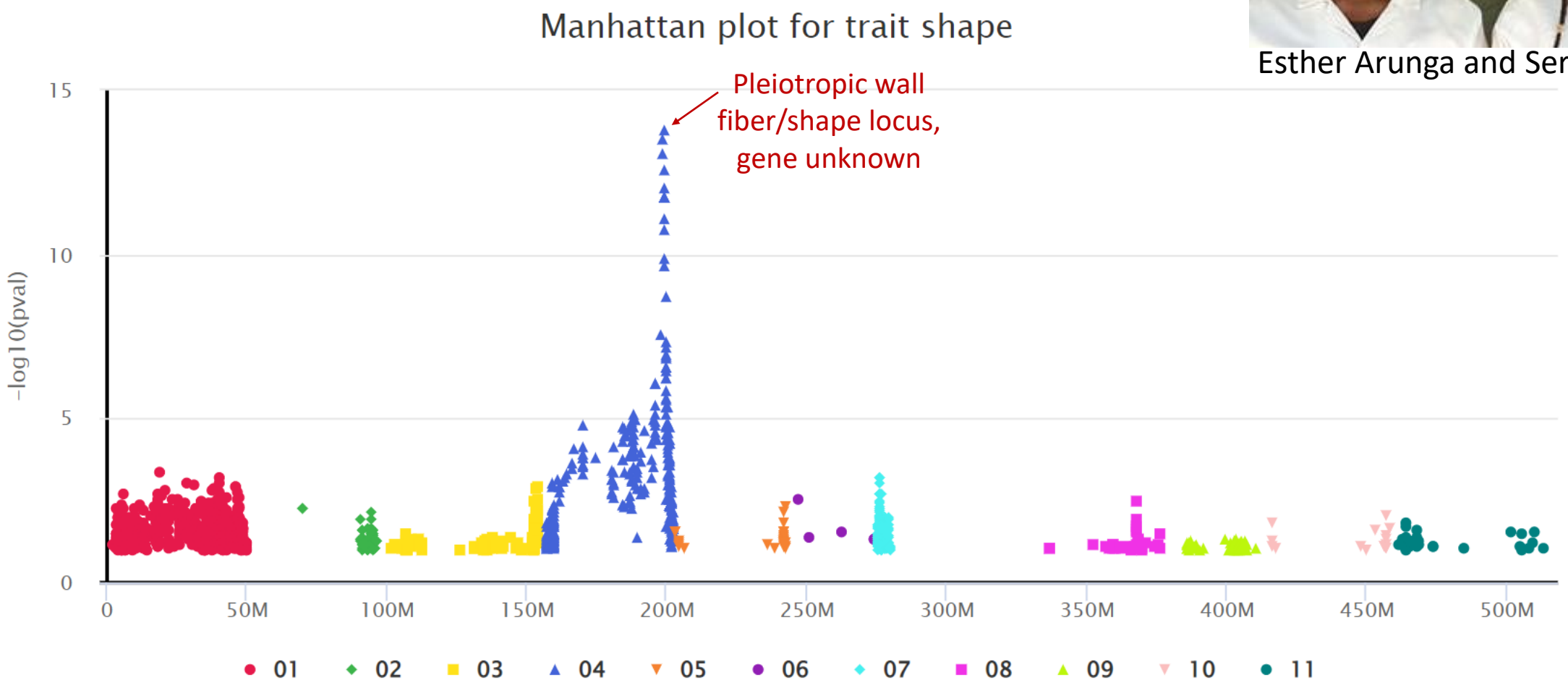
Loss of pod strings in common bean is associated with gene duplication, retrotransposon insertion, and overexpression of *PvIND*

Travis A. Parker, Jose Cetz, Lorenna Lopes de Sousa, Saarah Kuzay, Sassoum Lo, Talissa de Oliveira Floriani, Serah Njau, Esther Arunga, Jorge Duitama, Judy Jernstedt, James R. Myers, Victor Llaca, Alf Herrera-Estrella, Paul Gepts ... See fewer authors

First published: 16 June 2022 | https://doi.org/10.1111/nph.18319

Esther Arunga and Serah Njau

Display: Trait: shape



Other reports

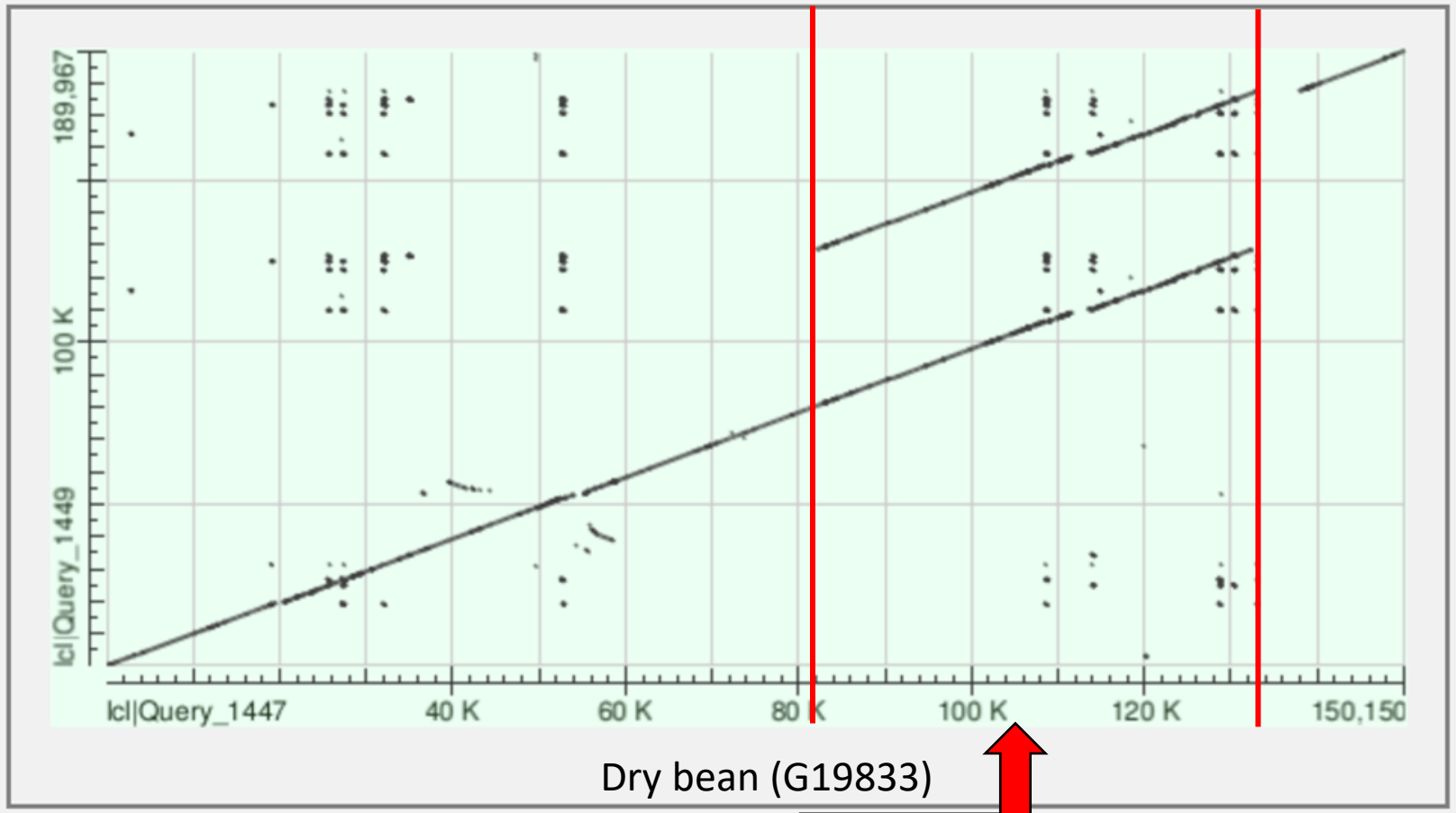
MSA viewer

Spontaneous excision → reversion to wall fiber?

Compare with the *Bar* gene of *Drosophila*

Descriptions | Graphic Summary | Alignments | **Dot Plot**

Plot of lcl|Query_1447 vs lcl|Query_1449



Only one gene in duplicated region

Feedback

Poster

The 'I Gene' for Resistance to Bean Common Mosaic Virus in Phaseolus vulgaris was Identified within a Cluster of NLR Genes

January 2023

Conference: Plant & Animal Genome Conference: PAG 30 · At: San Diego, CA, USA

Labs: Valérie Geffroy's Lab · Phillip N. Miklas's Lab

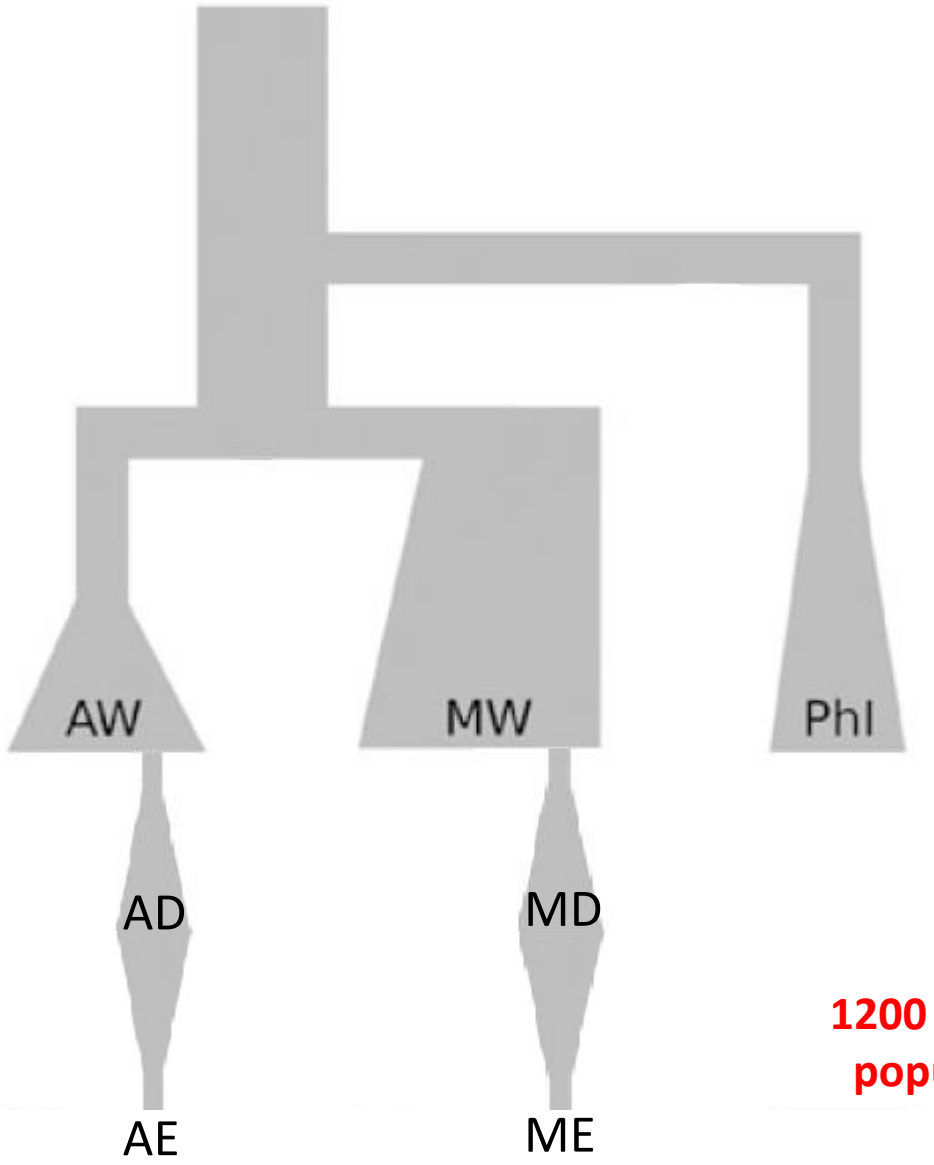
Álvaro Soler-Garzón · Juan camilo Alvarez · Timothy G. Porch · Show all 9 authors · Phillip N. Miklas

See also APA, many more

Takeaway: high-quality assemblies important for many traits

Description

Bean common mosaic virus (BCMV) and related Bean common mosaic necrosis virus (BCMNV) limit common bean (Phaseolus vulgaris L.) production worldwide.



1200 RILs, five populations

Table 3 Genetic diversity and divergence statistics for *Phaseolus vulgaris*

Comparison	Marker	Metric	Value	Reference
Genetic diversity, Andean vs. Middle American wild				
Diversity AW/MW	SSR	H_e	0.34	Kwak and Gepts (2009)
Diversity AW/MW	AFLP	H_e	0.55	Rossi et al. (2009)
Diversity AW/MW	Nucleotide	*Pi*	0.094	Bitocchi et al. (2012)
Diversity AW/MW	Nucleotide	*Pi*	0.096	Bitocchi et al. (2013)
Diversity AW/MW	Nucleotide	*Hd*	0.685	Mamidi et al. (2013)
Diversity AW/MW	Nucleotide	*Pi*	0.23	Schmutz et al. (2014)
Diversity AW/MW	Nucleotide	H_e	0.46	Rodriguez et al. (2016)
Diversity AW/MW	Nucleotide	*Pi*	0.45	Ariani et al. (2018)
Genetic diversity, PhI vs. Middle American wild				
Diversity PhI/MW	SSR	H_e	0.55	Kwak and Gepts (2009)
Diversity PhI/MW	AFLP	H_e	0.59	Rossi et al. (2009)
Diversity PhI/MW	Nucleotide	*Pi*	0.25	Bitocchi et al. (2012)
Diversity PhI/MW	Nucleotide	*Pi*	0.95	Schmutz et al. (2014)
Diversity PhI/MW	Nucleotide	H_e	0.28	Rodriguez et al. (2016)
Diversity PhI/MW	Nucleotide	*Pi*	0.73	Ariani et al. (2018)
Divergence time, Andean vs. Middle American wild				
Divergence time AW/MW	Nucleotide	Age (years)	110,706	Mamidi et al. (2013)
Divergence time AW/MW	Nucleotide	Age (years)	165,000	Schmutz et al. (2014)
Divergence time AW/MW	Nucleotide	Age (years)	87,410	Ariani et al. (2018)
Divergence time, PhI vs. Middle American wild				
Divergence time PhI vs. AW+MW	Nucleotide	Age (years)	260,000	Rendón-Anaya (2017a)
Divergence time PhI vs. AW+MW	Nucleotide	Age (years)	373,060	Ariani et al. (2018)
Genetic diversity, Middle American domesticate vs. wild				
Diversity MD/MW	AFLP	H_e	0.68	Rossi et al. (2009)
Diversity MD/MW	Nucleotide	*Pi*	0.28	Bitocchi et al. (2013)
Diversity MD/MW	Nucleotide	*Pi*	0.83	Schmutz et al. (2014)
Genetic diversity, Andean domesticate vs. wild				
Diversity AD/AW	AFLP	H_e	1.00	Rossi et al. (2009)
Diversity AD/AW	Nucleotide	*Pi*	0.73	Bitocchi et al. (2013)
Diversity AD/AW	Nucleotide	*Pi*	1.21	Schmutz et al. (2014)
Diversity AD/AW	Nucleotide	H_e	0.74	Rodriguez et al. (2016)

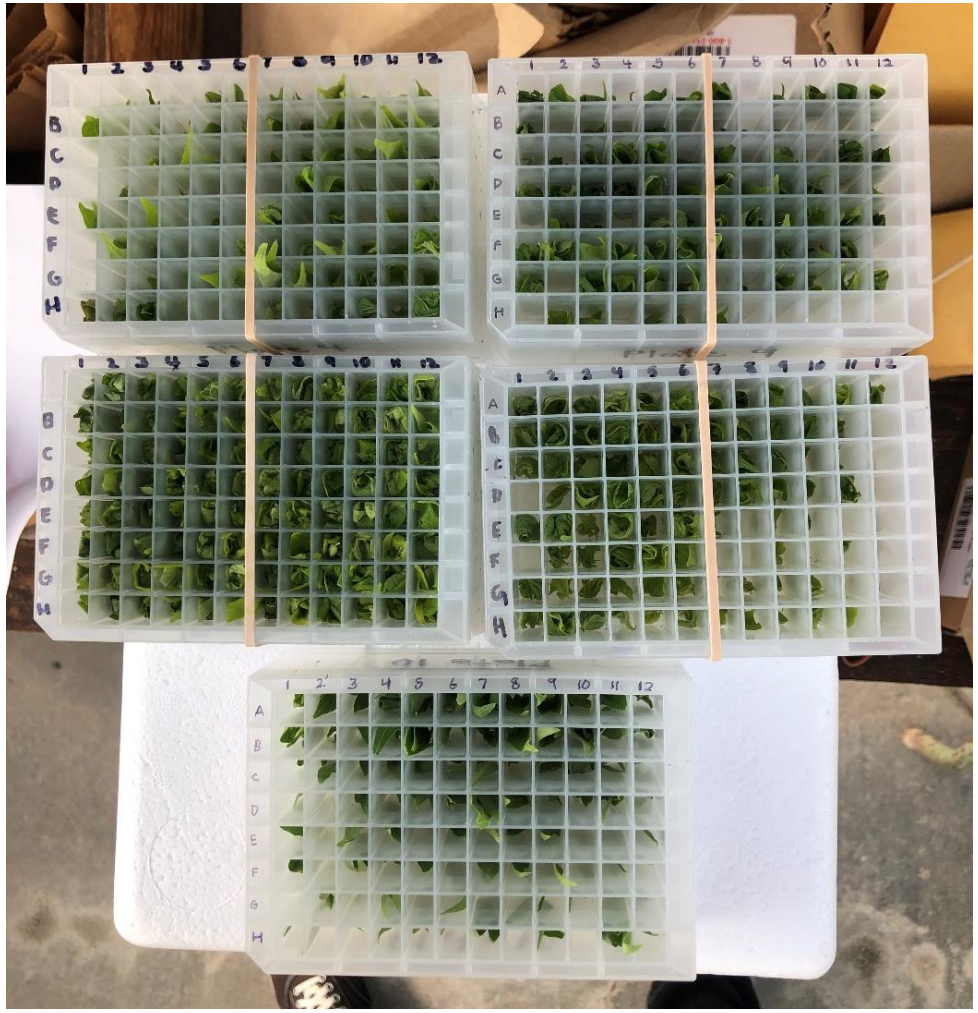
Table 3 (continued)

Comparison	Marker	Metric	Value	Reference
Genetic diversity, Andean vs. Middle American domesticate				
Diversity AD/MD	AFLP	H_e	0.81	Rossi et al. (2009)
Diversity AD/MD	Nucleotide	*Pi*	0.25	Bitocchi et al. (2013)
Diversity AD/MD	Nucleotide	*Pi*	0.34	Schmutz et al. (2014)
Diversity AD/MD	Nucleotide	H_e	0.56	Rodriguez et al. (2016)

AW Andean Wild, *MW* Middle American Wild, *PhI* Inca Phaseolin (*P. debouckii*), *MD* Middle American Domesticated, *AD* Andean Domesticated, H_e Expected heterozygosity, *Hd* Haplotype diversity, *Pi* Nucleotide diversity

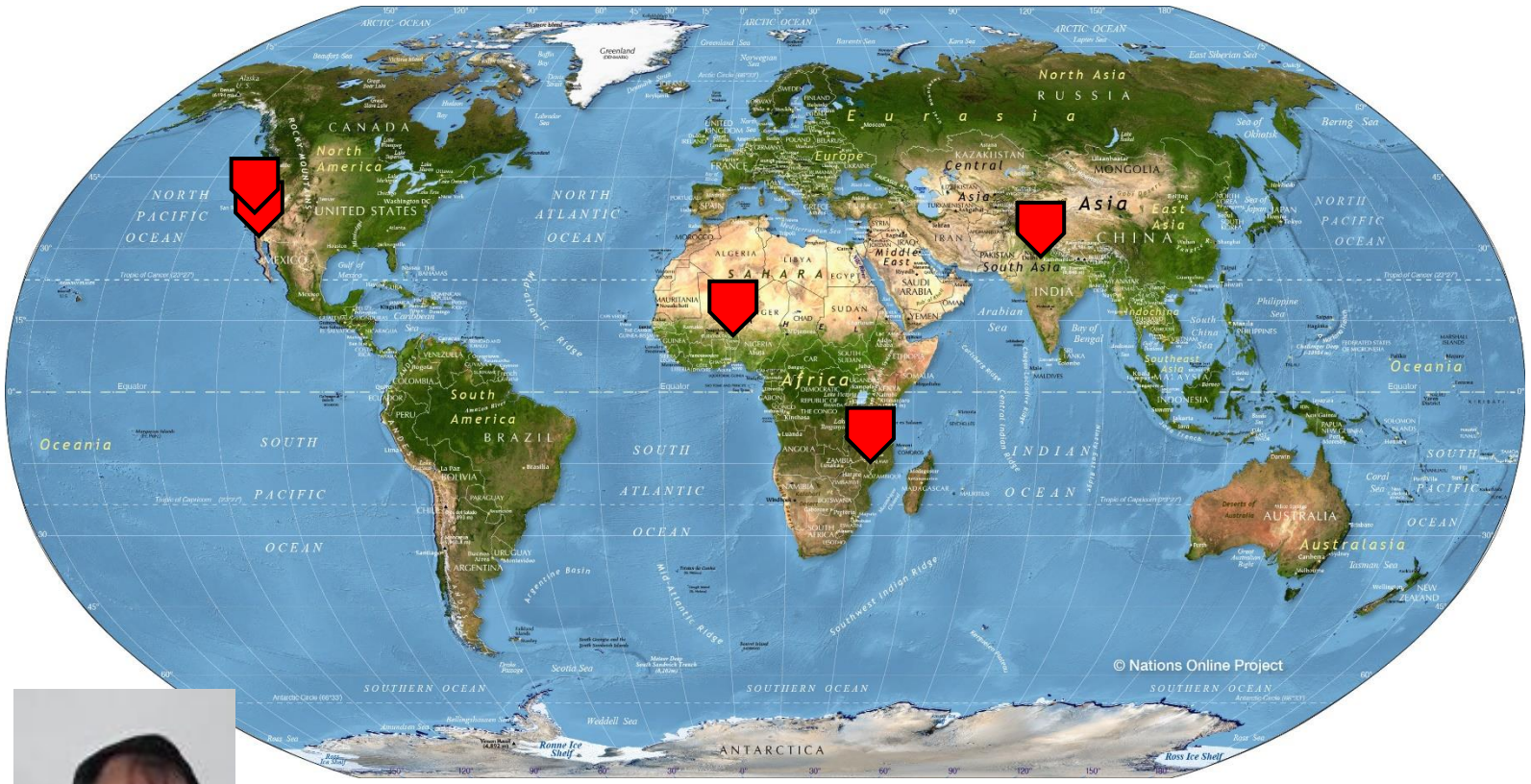
Quantitative component

Interested in adding KT lines of interest to WGS study? Let's talk!

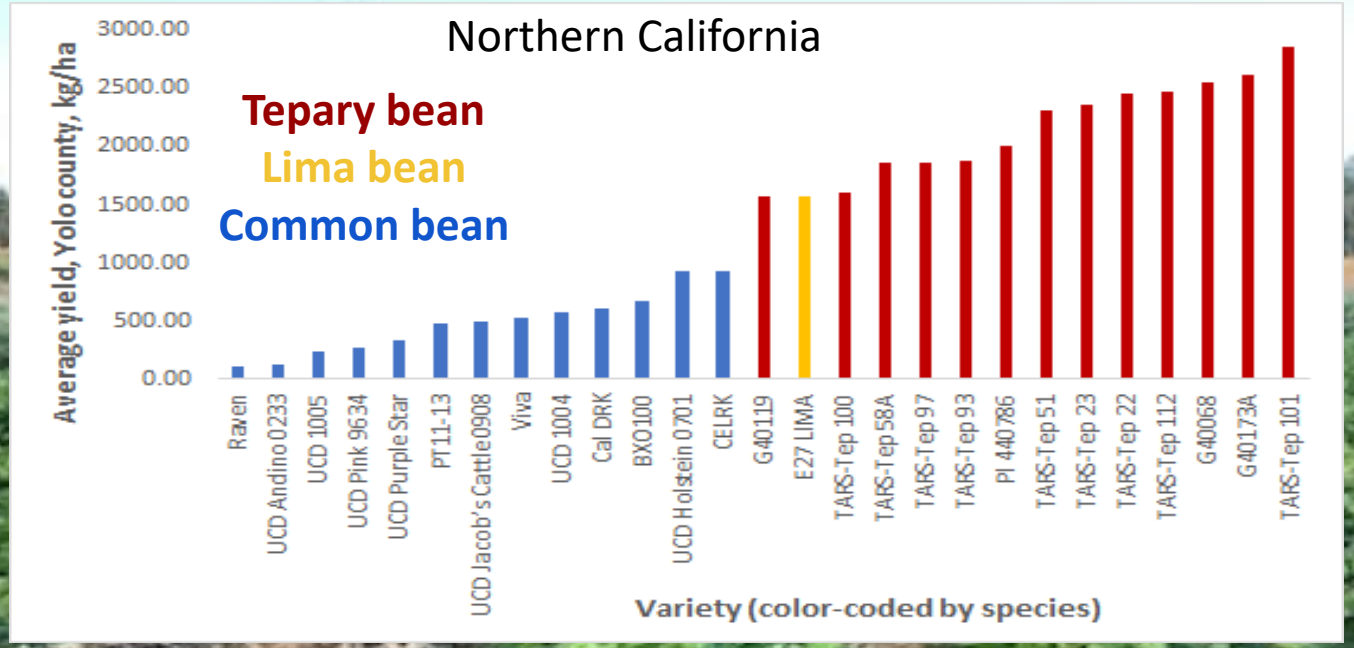


Tepary bean evaluations, 2022*

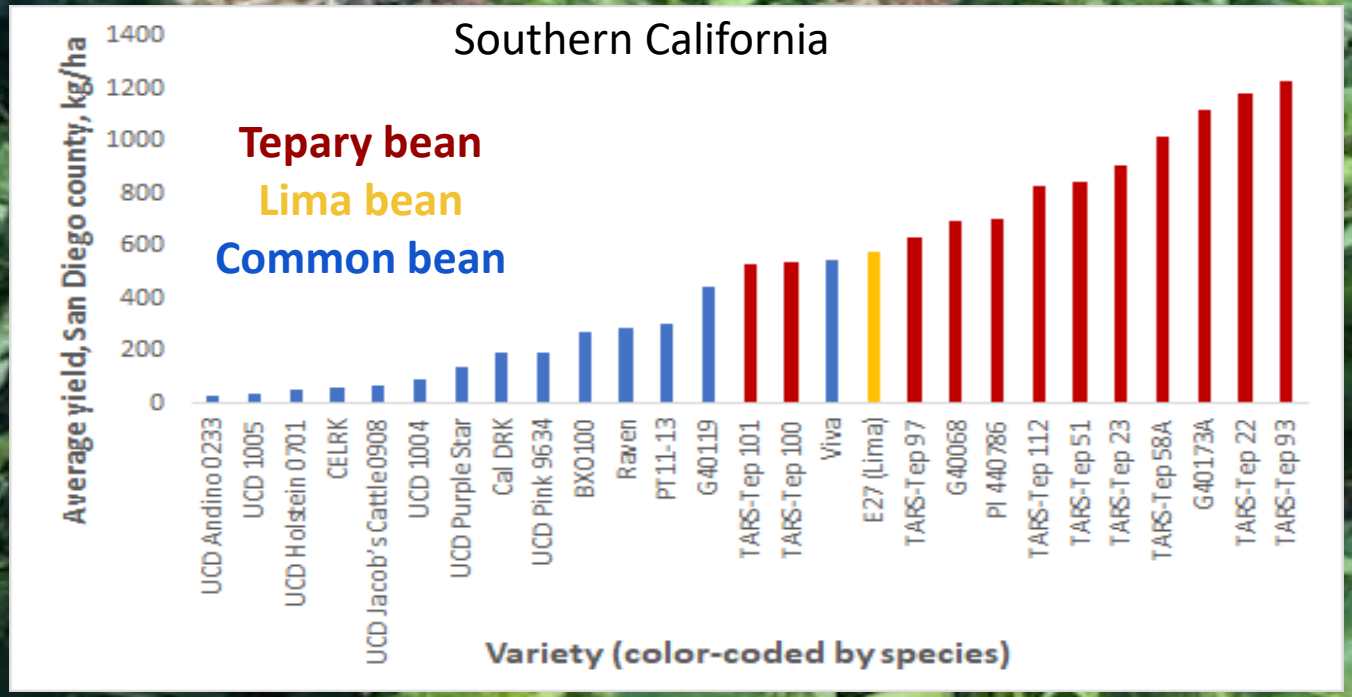
Accession	2021 seed source	Seed quantity
TARS-Tep 23	USDA-ARS PR	400 grams
PI 440786	UC Davis	400 grams
PI 310801	UC Davis	400 grams
G40068	UC Davis	400 grams
G40006A	UC Davis	400 grams
G40119	UC Davis	400 grams
G40200	UC Davis	400 grams
G40173A	UC Davis	400 grams
TARS-Tep 22	USDA-ARS PR	400 grams
TARS-Tep 93	USDA-ARS PR	400 grams
TARS-Tep 51	USDA-ARS PR	100 grams
TARS-Tep 58A	USDA-ARS PR	100 grams
TARS-Tep 97	USDA-ARS PR	100 grams
TARS-Tep 100	USDA-ARS PR	100 grams
TARS-Tep 101	USDA-ARS PR	100 grams
TARS-Tep 112	USDA-ARS PR	100 grams
TARS-Tep 32	UC Davis	<5 grams



*nine lines contributed by Dr. Tim Porch, USDA-ARS



Troy Williams
UC Davis



Mike Reeske,
Rio del Rey Farm

United States Department of Agriculture
National Institute of Food and Agriculture
USDA ARS
ORGANIC FARMING RESEARCH FOUNDATION

Dr. Santos Barrera Lemus
UC Davis, Feb. 2023

One UC DAVIS

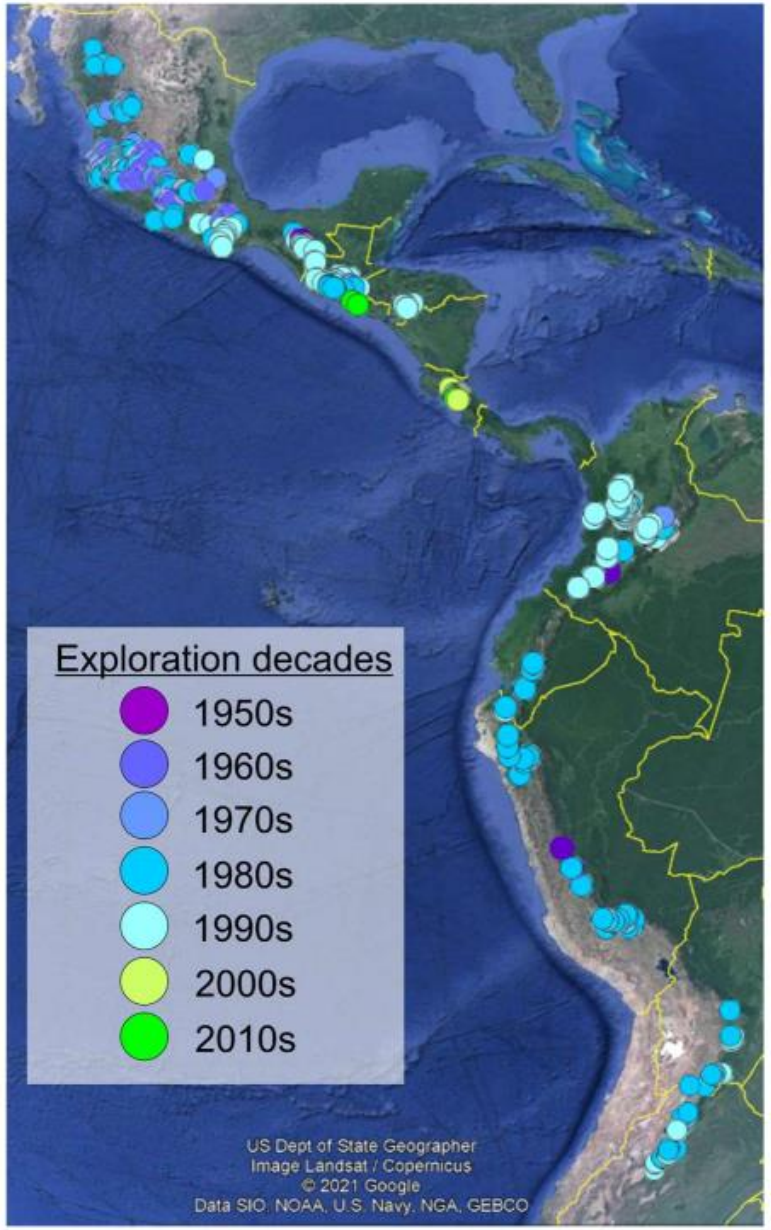
PLANT TRANSFORMATION FACILITY

The Ralph M. Parsons Foundation

Genetic Resources and Breeding Priorities in *Phaseolus* Beans: Vulnerability, Resilience, and Future Challenges

Travis A. Parker[1], Jorge Acosta Gallegos[2], James Beaver[3], Mark Brick[4], Judith K. Brown[5], Karen Cichy[6], Daniel G. Debouck[7], Alfonso Delgado-Salinas[8], Sarah Dohle[9], Emmalea Ernest[10], Consuelo Estevez de Jensen[3], Francisco Gomez[11], Barbara Hellier[12], Alexander V. Karasev[13], James D. Kelly[11], Phillip McClean[14], Phillip Miklas[15], James R. Myers[16], Juan M. Osorno[14], Julie S. Pasche[14], Timothy Porch[17], James R. Steadman[18], Carlos Urrea[19], Lyle Wallace[12], Christine H. Diepenbrock[1], Paul Gepts[1]*

***Plant Breeding Reviews*, I. Goldman, ed., in press**



Visiting researchers 2023!

- Celestina Jochua
- Mwiinga Molube


An exciting time for bean breeding…

Future directions?

Other new tech

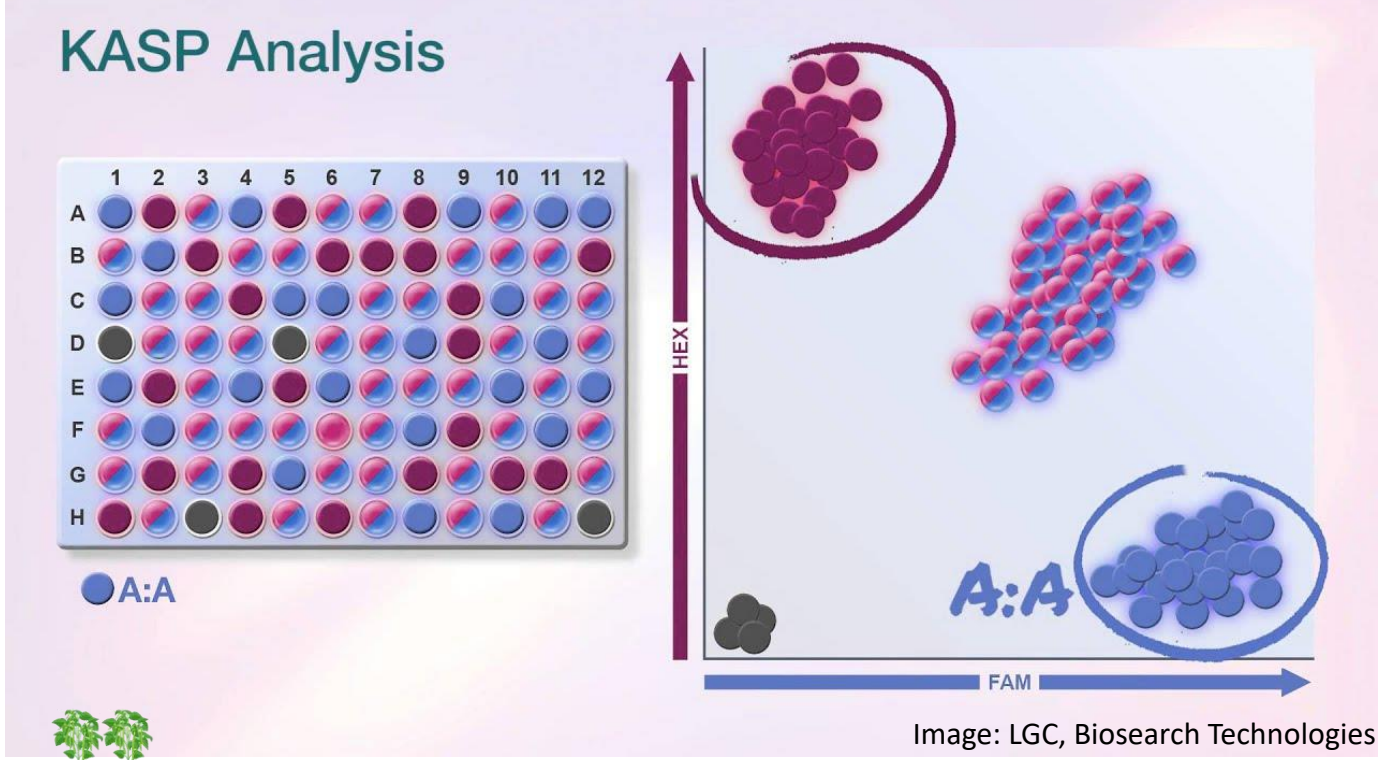
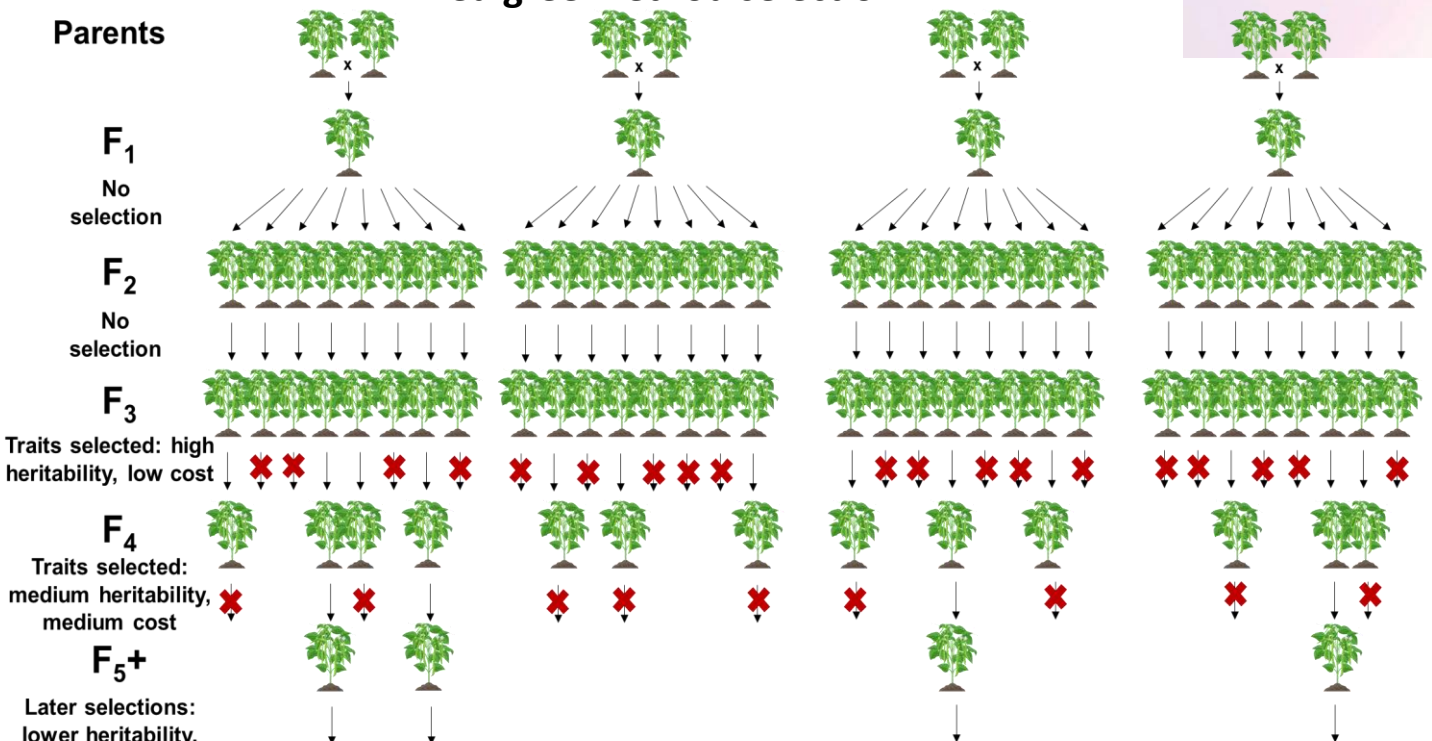
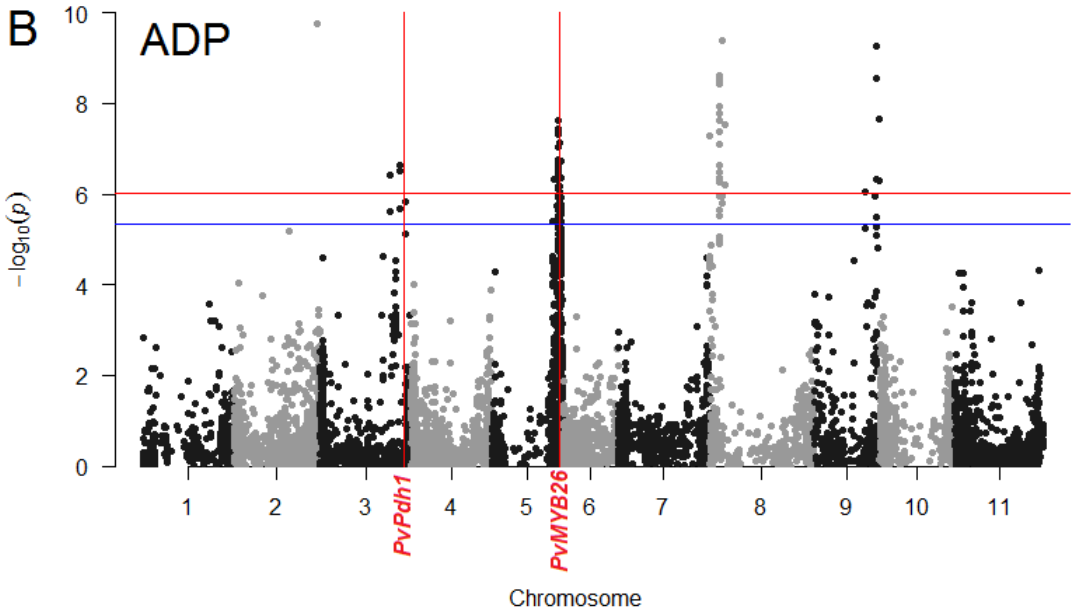


Image: LGC, Biosearch Technologies

Pedigree method selection





DAY 2	Monday, 27th February 2023: African Bean Consortium (ABC)					
ITEM	**Start Time**	**Duration**	**Presentation Title**	**Presenter**	**Institute/Organisation**	**Country**
Chair – Dr Travis Parker						
Session I						
	08:00	10 mins	**Meeting Opening by Vice Chancellor**	Professor Anne Sikwibele	UNZA	Zambia
	08:10	25 mins	**ABC Opening Remarks** **Title to be confirmed**	Dr Travis Parker (KT Consultant)	UC Davis	USA
	08:35	25 mins	**Genetic improvement of common bean in Zambia for multiple diseases resistance using marker-assisted and conventional breeding**	Dr Kelvin Kamfwa (KT PI)	UNZA	Zambia
	09:00	25 mins	**Genetic dissection of common bacterial blight resistance in the Andean gene pool of common bean**	Mr Mwiinga Mulube (KT PhD Scholar/Agricultural Officer {ZARI})	UNZA	Zambia
	09:25	25 mins	**Introgression and pyramiding into market class French beans of genes conferring resistance to multiple diseases**	Dr Esther Arunga (KT PI)	UoEm	Kenya
	09:50	25 mins	**Biofortification and Improvement of the Iron-to-Phytate Molar Ratio in two Yellow Common Bean (Phaseolus vulgaris L.) Varieties in Tanzania**	Dr Mashamba Philipo (KT PI)	NM-AIST	Tanzania
COFFEE	10:15	15 mins				
Session II						
	10:30	25 mins	**Leveraging system change in agricultural systems**	Dr. Barry Pittendrigh/Dr. John Medendorp	USAID-IL	USA
	10:55	25 mins	**Legume research in Cambridge and its implications for sustainable production**	Dr Sigrid Heuer / Professor Giles Olderoyd	NIAB/Cambridge CSC	UK
	11:20	25 mins	**Leveraging bean crop genetics and diversity for climate adaptation**	Dr Caspar Chater	Kew	UK
	11:45	25 mins	**Marker assisted pyramiding resistance genes against major disease into common bean (*Phaseolus vulgaris L*) varieties with food and market values for Ethiopia (Phase-III)**	Dr Yayis Rezene (KT PI)	SARI	Ethiopia
LUNCH	12:10	90 mins				
Session III						
	13:40	25 mins	**Genetic improvement of biofortified common bean varieties in Uganda for multiple disease resistances using marker assisted backcrossing**	Dr Stanley Nkalubo (KT PI)	NaCRRI	Uganda
END	14:05					
KT ONLY	14:20	60 mins	**NaCRRI Project Meeting**	Dr Stanley Nkalubo		
COFFEE	15:20	15 mins				
Session IV						
KT ONLY	15:35	60 mins	**UoEm Project Meeting**	Dr Esther Arunga		
KT ONLY	16:35	60 mins	**SARI Project Meeting**	Dr Yayis Rezene		
KT ONLY	17:35	60 mins	**NM-AIST Project Meeting**	Dr Mashamba Philipo		
END	18:35					