Welcome!

Kirkhouse Trust Annual Meeting 17-20 June 2024 Arusha, Tanzania



Review

The Kirkhouse Trust: Successes and Challenges in Twenty Years of Supporting Independent, Contemporary Grain Legume Breeding Projects in India and African Countries

<u>Claudia Canales Holzeis</u>^{*}, <u>Paul Gepts</u>, <u>Robert Koebner</u>, Prem N Mathur, Sonia Morgan, <u>María Muñoz Amatriaín</u>, <u>Travis Parker</u>, Edwin M Southern, <u>Michael P Timko</u>

Posted Date: 23 April 2024

doi: 10.20944/preprints202404.1462.v1

Keywords: legumes; crop breeding; Africa; cowpea; common bean; dolichos; Bambara groundnut; marker assisted selection



he University of Zambia in Collaboration with the Kirkhouse Trust Hosts a Scientific Meeting in Bean and Cowpea Improvement In Africa

OBJECTIVE: TO SHARE KNOWLEDGE GAINED IN BEAN AND COWPEA IMPROVEMENT ON THE AFRICAN CONTINENT DATE : MONDAY 27TH FEBRUARY TO THURSDAY 2ND MARCH 2023

Last meeting: Livingstone Zambia, 2023



Southern Agricultural Research Institute (SARI), Hawassa, Ethiopia



Yayis Rezene



Releas e Date	Variety	Outstanding Characteristics	Program/Developer	Yield potenti al
2023	Key-Wolaita	Small dark red; Tolerant to ALS, CBB and BSM	Yayis Rezene, SARI	1700- 3100 kg/ha
2023	Key-Burre	Large red mottled; Tolerant to ALS, CBB and BSM	Yayis Rezene, SARI	1800- 2400 kg/ha



National Crops Resources Research Institute (NaCRRI), Kampala, Uganda





Stanley Nkalubo

Releas e Date	Variety	Outstanding Characteristics	Program/Developer	Yield potential
2024	NABE 12CR	Large cream with purple speckles; Resistant to root rot; Tolerant to ALS, CBB and ANTH, Susceptible to BSM and Rust.	Stanley Nkalubo and Annet Namayanja	2200-3800 kg/ha
2024	NABE 14R	Medium red; Resistant to ANTH; Tolerant to ALS, CBB and Root rot, Susceptible to BSM and Rust.	Stanley Nkalubo and Annet Namayanja	1500-2700 kg/ha

Legum P	LOS	ONE			Check for upd	lates
l ori Eva R			RESEA	Vol. 16(2), pp. 27-35, April-June 2024 DOI: 10.5897/JPBCS2024.1033 Article Number: CAA38DA72036 ISSN 2006-9758 Copyright ©2024 Author(s) retain the copyright of this article http://www.academicjournals.org/JPBCS	iyoba Sansala Plant Disease	
Bri Kel ¹ De Agr		5 UF			mon Bean	au
Cor Rec RESEARC Fui Key Gen (Pho high r Saul Eric t Publishe	ACCESS E HARTICLE ACCESS ACCES	PEER-REVIEWED differentia s acutifolio sity DArTs Hussein Shimelis, er 14, 2023 • https	ation of a sou us A Gray) ge seq SNP mar Wilfred Abincha, Wilson NI	Full Length Research Paper Evaluation of yellow common bean (<i>Phaseolus</i> <i>vulgsaris</i> L.) genotypes for resistance to anthracnose Kelvin Kamfwa	Parker²,	,
t Article ✓ ✓ Cav	vara iso	Authors	Metrics te mvesugaçao Ag	Anthracnose, caused by the fungus <i>Colletotrichum lindemuthianum</i> , is a significant disease affecting common bean (<i>Phaseolus vulgaris L.</i>). The identification of sources of anthracnose resistance within the yellow market class is crucial for developing yellow bean varieties resistant to anthracnose. The objective of this study was to assess a set of yellow common bean genotypes for resistance to eight races of <i>C. lindemuthianum</i> . A total of 30 vellow-seeded bean genotypes were evaluated for their resistance to races	California 1	
Equ To	uipmer link to	⁴ Departmen ⁵ National C	nt of Biological ar Center for Genome	5, 19, 38, 39, 51, 183, 1050 and 1105. Among these genotypes, Y1612-04 demonstrated exceptional performance as it exhibited resistance to seven of the eight races used in this study. This genotype holds potential as a source of resistance to enhance the Manteca yellow bean market class, which is popular in East and Southern Africa.		
		*Correspon	nding author. Ema	Key words: Anthracnose, Colletotrichum lindemuthianum, Common bean, races, yellow beans.		



The genetic architecture of pod and seed traits in common bean

Travis Parker 17/06/2024 Arusha, Tanzania

Pod traits







"Two smaller experiments with *Phaseolus* species have been completed and may be mentioned here...

The green color of the pod, the <u>curved</u> <u>shape of the pod</u> and the high axis were, as with *Pisum*, dominant features..."

-Gregor Mendel, Versuche über Pflanzen-Hybriden, 1865



Pod shape+fiber spontaneously and heritably reverts!







Travis Parker



Jorge Duitama





Esther Arunga

Pod shape



Chromosome

QTL Mapping for Pod Quality and Yield Traits in Snap Bean (*Phaseolus vulgaris* L.)

Serah Nyawira Njau^{1,2†}, Travis A. Parker^{2†}, Jorge Duitama³, Paul Gepts², Edith Esther Arunga^{1*}

¹Department of Water and Agricultural Resource Management, University of Embu, Kenya

²Department of Plant Sciences, University of California, Davis, USA

³Department of Systems and Computing Engineering, University de los Andes, Bogotá, Colombia

*Correspondence: Edith Esther Arunga arunga.esther@embuni.ac.ke

[†]These authors contributed equally to this work









Bar locus in Drosophila



Explanation for reversion!





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, Alfredo Herrera-Estrella, Paul Gepts X... See fewer authors

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



Epilogue... Second independent in mutation in the same gene

Duplication + partial deletion

Resistant to reversion?





Postdoctoral scholar Dr. Burcu Celebioglu



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Fig. 8: Model for the concurrent regulation of Chl biosynthesis and catabolism by BCMs.

Closest Arabidopsis homolog

During early leaf development (encompassing leaf initiation, growth, and maturation), optimized Chl biosynthesis ensures efficient photosynthesis, while Chl breakdown is largely suppressed. BCM1 promotes Chl biosynthesis by stimulating MgCh through GUN4 action, and in addition interacts with and destabilizes SGR1 to prevent Chl degradation. Upon the onset of leaf senescence, although BCM1 is greatly suppressed, *BCM2* and *SGR1* are both up-regulated. BCM2 is therefore able to contribute to the inhibition of Chl breakdown. However, the strong accumulation of SGR1 eventually allows plants to initiate Chl breakdown. Figure and caption from Wang et al. 2020

Pod summary:

- I. Pod shape/wall fiber variation appear to be caused by multiple reversible duplications
- II. Yellow pods may be due to "failed brakes" on chlorophyll degradation



Seed color



"We need varieties with high culinary quality and that visually stand out in the market"



Black Nightfall



Which genes?



Phbw affects seed color







P^{hbw}; Bassett 1996, 2003

Black Nightfall

Orca seed pattern



(Bassett 2000)





QTL mapping of seed color



WGS

12x, 150 bp paired-end

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Seven independent loss of function alleles in *T* among 22 with partly-colored seeds!

Score		Expect	Method			Identities	(Positives		Gap	s	
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Sbjct	421	KKTLFKV	PFMHRSYFSRKS	QKESDRMQ	WTSKFD	NADDGFM	GKAFSD	KKGEIKNF	QVVKS	L 4	180	• •

One non-synonymous SNP between wild type vs. mutants.

Highly conserved residue: 98/100 of the most similar proteins in the NCBI reference database have a C (two exceptions: probable bioinformatic error in one gene model)

Alignment of *P. vulgaris* Phvul.007G171333.1 transcript with other legumes

Site of 612 bp deletion in partial-LOF line Black Nightfall

Sections \lor

Articles Research Topics

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Volume 9 - 2018 | https://doi.org/10.3389/fgene.2018.00672

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Introns as Gene Regulators: A Brick on the Accelerator

Alan B. Rose*

Department of Molecular and Cellular Biology, University of California, Davis, Davis, CA, United States

A picture is beginning to emerge from a variety of organisms that for a subset of genes, the most important sequences that regulate expression are situated not in the promoter but rather are located within introns in the first kilobase of transcribed sequences. The

actual sequences involved are difficult to identify either by sequence comparisons or by deletion analysis because they are dispersed, additive, and poorly conserved. However, expression-controlling introns can be identified computationally in species with relatively small introns, based on genome-wide differences in oligomer composition between promoter-proximal and distal introns. The genes regulated by introns are often expressed in most tissues and are among the most highly expressed in the genome. The ability of some introns to strongly stimulate mRNA accumulation from several hundred nucleotides downstream of the transcription start site, even when the promoter has been deleted, reveals that our understanding of gene expression remains incomplete. It is unlikely that any diseases are caused by point mutations or small.

19.5-fold reduction in *P* expression!!

RT-qPCR

Co-dominant tests developed for all three genes

Tests co-developed and run by Mwiinga Mulube and Celestina Jochua, UC Davis 2023

Part II. Environmental effects

Southwest

Summary

- Color pattern genes encode proteins that combine as regulatory complexes.
- Mutations were identified in each gene, sometimes strongly parallel.
- Seed color signal propagation is unstable and temperature-dependent.
- Mechanism?

THE PREPRINT SERVER FOR BIOLOGY

New Results

A Follow this preprint

Sequence characterization of *T*, *Bip*, and *Phbw* demonstrates the role of **MYB**bHLH-WD40 complexes and temperature in common bean seed color pattern formation

Travis Parker,
 Tayah Bolt,
 Troy Williams,
 R.Varma Penmetsa, Mwiinga Mulube, Antonia Palkovic, Celestina Nhagupana Jochua,
 Maria del Mar Rubio Wilhelmi,
 Sassoum Lo,
 Gail Bornhorst,
 Li Tian,
 Kelvin Kamfwa, Sam Hokin, Andrew Farmer,
 Christine Diepenbrock,
 Paul Gepts

doi: https://doi.org/10.1101/2023.09.23.559151

This article is a preprint and has not been certified by peer review [what does this mean?].

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Abstract Full Text

Info/History Metrics

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Abstract

Seed colors and color patterns are critical for the survival of wild plants and the consumer appeal of crops. In common bean, a major global staple, these patterns are also critical for determining market classes, yet the genetic and environmental control of many pigmentation patterns remains unresolved. In this study, we genetically mapped variation for three important seed pattern loci, *T*, *Bip*, and *p^{hbw}*, which co-

Thanks!

UC Davis

Burcu Celebioglu Tayah Bolt Troy Williams R. Varma Penmetsa Antonia Palkovic Maria del Mar Rubio Wilhelmi Sassoum Lo Gail Bornhorst Li Tian Christine Diepenbrock Paul Gepts

University of Zambia

Mwiinga Mulube Kelvin Kamfwa

National Center for Genome Resources Andrew Farmer

Instituto de Investigação Agrária, Mozambique

Celestina Nhagupana Jochua

