

**Feed the Future Global Hunger and Food Security Research
Strategy: Climate Resilience, Nutrition, and Policy
Program Area: High-Yielding, Climate Resilient Legumes**

(1) Advancing the Productivity Frontier

This theme focuses on improving food availability. While better management practices can reduce the prevailing yield gaps in many developing countries, productivity gains necessary to meet future food demand under limited resources and with potentially adverse impacts from climate change require developing new seeds To enable such improvements, the FTF research strategy has a focal theme on breeding and genetics for major crops and This is expected to increase the yield potential and provide solutions for major production constraints. To more effectively integrate the use of these technologies among poor farmers, research under this theme includes socio-behavioral and economic factors for male and female farmers.

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(b) Research Implementation

The *Feed the Future Research Strategy* used spatial analysis to identify four major production zones where high rates of poverty and malnutrition overlaid areas with high production potential: the Indo-Gangetic plains of South Asia, the Sudano-Sahelian region of West Africa, the maize-based, mixed systems of East and Southern Africa, and the Ethiopian Highlands; these same four systems are the subject of the Sustainable Intensification research programs. Outputs from all of these research programs are intended to support USAID Mission and other agriculture, nutrition and food security investments in Feed the Future focus countries (<http://www.feedthefuture.gov/countries>) and beyond.

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USAID Feed the Future Innovation Lab for Climate Resilient Cowpea

12 Sept 2013 - 11 Sept 2018

Timothy J. Close
Athens, Greece
14 May 2014

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United States Agency for International Development (USAID)
Feed the Future Program Area: High Yielding, Climate-Resilient Legumes

Project Title: Innovation Lab for Climate Resilient Cowpea

Lead Institution: University of California, Riverside

Dr. Timothy Close (PD); Professor of Genetics & Geneticist
Dr. Philip Roberts (Co-PD); Professor and Chair, Department of Nematology
Dr. Stefano Lonardi (Co-PD); Professor, Department of Computer Sciences

Sub-Awards: Institut Senegalais Recherches Agricole (ISRA)
Dr. Ndiaga Cisse, Cowpea Breeder & Director CERAAS

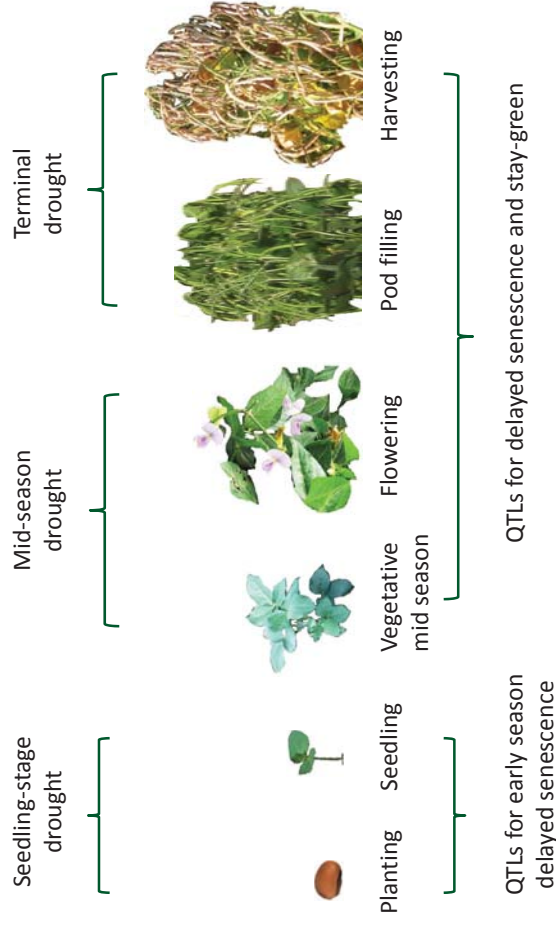
Institut de l'Environnement et de Recherches Agricoles (INERA)
Dr. Issa Drabo, Cowpea Breeder
Dr. Jean-Baptiste De La Salle Tignegre, Cowpea Breeder

Council for Scientific & Industrial Research - Savanna Agricultural Research
Institute (CSIR-SARI)
Dr. Ibrahim Atokple, Breeder

International Institute of Tropical Agriculture (IITA)
Dr. Boukar Ousmane, Cowpea Breeder

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Drought events across cowpea growing stages



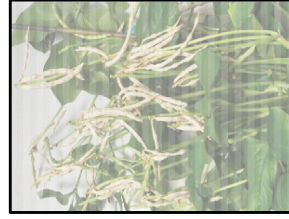
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Other Abiotic Stress-Related Target Traits



Heat sensitivity: heat-induced abortion of pollen development resulting in reduced pod set. Have evidence of tolerance QTLs.

***Macrophomina phaseolina* (ashy stem blight or charcoal rot): drought-stressed plant are prone to infection and disease from this pathogen. Have evidence of resistance QTLs.**



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The Cowpea Team Locations

Four host country locations in the Sudano-Sahelian region of West Africa. Spanning the main cowpea production agroecologies in this sub-Saharan zone.



Location of the UC Riverside Coachella Valley Agricultural Research Station. August planting provides rain-free conditions for drought and heat tolerance phenotyping.



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Objective 1: Foundation Development: high-density SNP genotyping, marker development and phenotyping for yield, biotic and abiotic stress tolerance and other traits relevant to sub-Saharan Africa

- 20x sequencing of 37 breeding accessions (Jan/Feb 2014)
- SNP discovery & 60k iSelect design (Mar/Apr 2014)
- 60k iSelect available (by Jul/Aug 2014; to be used for LIL also)
- New map from ~1000 biparental & 300 MAGIC RILs (from TL1)
- Genotypes of 200+ germplasm accessions previously phenotyped (in TL1)
- Baseline genotypes of breeders' favorites (intersects LIL interests)
- Emphasizing *Macrophomina* resistance, drought tolerance (flowering, terminal), heat tolerance (reproductive), seed quality & yield

Objective 2: Training: Workshops and support of West African breeders in the use of markers to accelerate breeding

- Annual workshop (Mar 2014 at UC Riverside)
- Continuous support of breeders (years 1-5)
- Student training (years 1-5)

Objective 3: Implementation: Deploy new marker knowledge for production of improved cowpea seed for farmer evaluation in sub-Saharan Africa

- Throughout the life of the project

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Cowpea MAGIC Parents – yield, diversity, traits

Genotype	Source	High Yielding Under Drought in:				Key Traits
		Diversity Group	Senegal	Burkina Faso	Mozambique	
CB27	UCR	A			Yes	Heat tolerance
IT00K-1263	IITA	F			Yes	Striga (races 1,2,3,4,5) resistance
IT82E-18	IITA	B			Yes	Broadly adapted, high yield
IT84S-2049	IITA	C	Yes			Aphid, bacterial blight, CABMV Root-knot nematode resistance
IT84S-2246	IITA	G	Yes		Yes	Aphid, bacterial blight, CABMV Root-knot nematode resistance
IT89KD-288	IITA	D	Yes		Yes	Yield, grain quality
IT93K-503-1	IITA	H	Yes			Drought tolerance, Macrophomina, Striga (races 1,3,4) resistances
SuVita 2	INERA	E	Yes	Yes	Yes	Striga (races 1,2,4) resistant, drought tolerance, high yield

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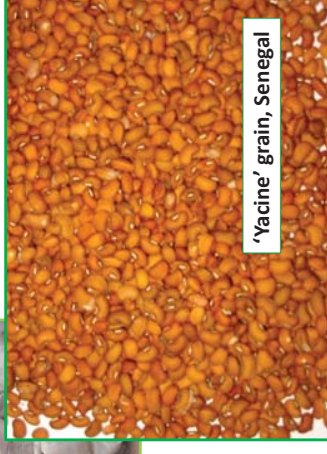
Cowpea in sub-Saharan Africa



A Cowpea Forage Vendor

Kano, Northern Nigeria

Grain vitally important in human diet



'Yacine' grain, Senegal

Forage is highly valued for livestock feed

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60k iSelect Infinium Assay



April 2014

Breeding Climate-Resilient Cowpea for Improved Food Security in West Africa

ILLUMINA high-density genotyping expected to accelerate marker-assisted breeding.



Recognizing that its technology could play a critical role in alleviating global hunger, malnutrition, and poverty, Illumina created the Agricultural Genes Initiative. Each year, Illumina awards Greater Good grants to agricultural research organizations that are focused

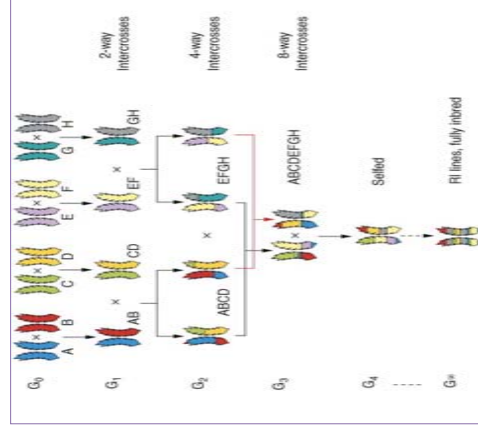
on identifying and breeding plants and animals that will increase the sustainability, productivity, and nutritional density of crop and livestock species. Under the grants, Illumina sequencing and genotyping reagents are provided free of charge.



2014 Illumina Greater Good Initiative Award Winner

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MAGIC Population Design



Cavanaugh et al. 2008. From mutations to MAGIC: resources for gene discovery, validation and delivery in crop plants. *Curr Opin Plant Biol* 11:215-221.



Cowpea MAGIC

G2-G3: ~330 pair crosses made, Spring & Fall 2011 (TL1)

G4 and beyond: Single seed descent of F2s 2012-2014 (TL1)

- Most now at F8 seed
- Planting May 2014 to advance stragglers to F6, F7, F8 and carry F8 to F9.

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Cowpea-Common Bean Synteny

Cowpea Genetic Map

- 11 RIL populations
- 1117 individuals
- 1091 EST-derived SNPs
- 11 linkage groups

Common Bean Genome

- Phytozome *P. vulgaris* v1.0
- 11 pseudomolecules

Relationships

- Best BLAST *P. vulgaris* gene model for each *V. unguiculata* SNP source sequence
- Illustrated using Circos
- 6 of 11 LGs have complete synteny

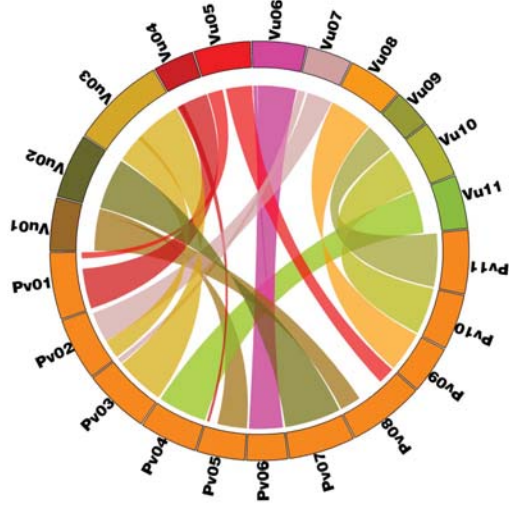


Image from Mitch Lucas, UC Riverside, 2012

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Phylogeny of African Cowpea Landraces

305 landraces (from IITA)

SNP genotyping

SNPs MAF >0.1

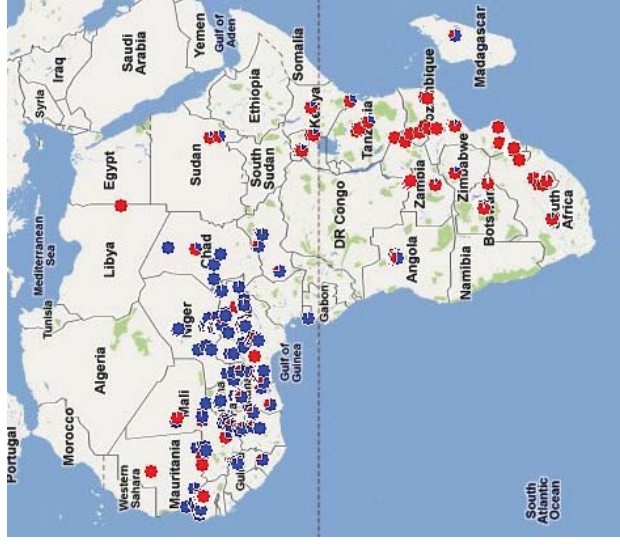
STRUCTURE:

Two predominant genetic groups:

Southeastern Africa:

Kenya, Tanzania, Mozambique, Zimbabwe, Botswana, South Africa

Western Africa: Senegal, Cameroon, Burkina Faso, Niger, Mali, Chad, Ivory Coast, Ghana, Benin



Huynh et al. (2013) The Plant Genome 6: doi:10.3835/plantgenome2013.03.0005

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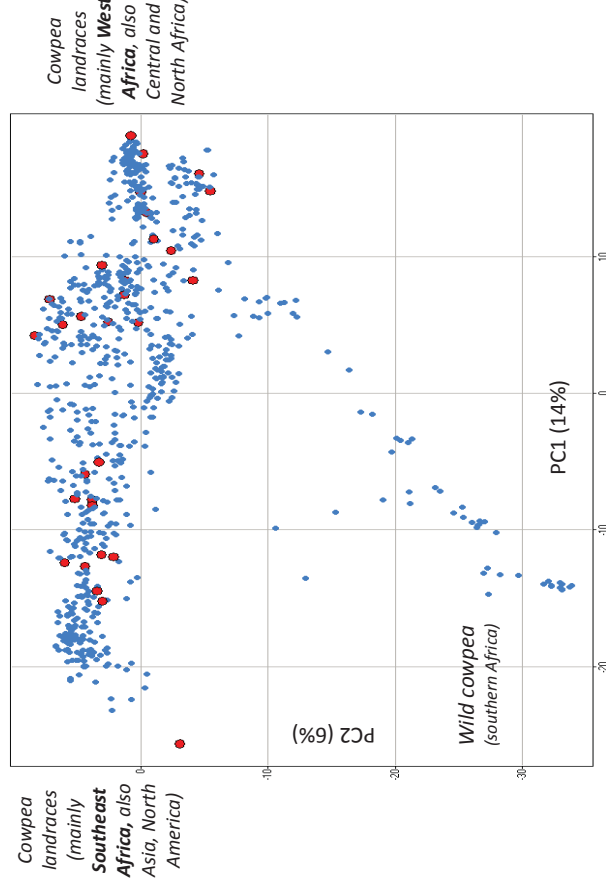
SNP design summary

- 56,719 SNPs in design of 60,000 BeadAssays
- ~39,500 target cowpea sequences matching 20,788 *P. vulgaris* gene models
- ~19,300 target other cowpea sequences genome-wide
- 1163 are recycled from GoldenGate Assay (all genic)
- 60 target plastid or mitochondrial genome

Intended Genotyping Workflow

- Tissue sent to UCR in ziplock bags with desiccant
- DNA extracted at UCR, sent to local genotyping provider
- SNP data transferred by FTP to UCR
- SNP data imported into GenomeStudio, exported as Excel files:
 - Flapjack for visualization
 - ICI Mapping for QTLs
 - OPTIMAS to guide crosses for QTL pyramiding (foreground)
 - Backcross Selector also to guide parent and progeny selection (background)

SNP Ascertainment



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By end of 2014, we expect to have the following:

Genotype-informed view of breeder's favorites

- Initial 48 tissue samples sent from each host country partner to UCR in March 2014, more are possible
 - Will clarify extent of variability within lines
 - Will confirm or correct pedigree information
- Increased seed from favorite individuals sampled for genotyping
- New phenotype data from breeders' favorites

Each partner has an allocation of 192 "favorites" for genotyping and 800 other samples to support breeding objectives during the life of the project

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Materials Needed for Tissue Collection for SNP Genotyping



2 Silica gel packs



Plastic zip lock bag with cowpea variety name and the date collected

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U California, Riverside

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Bao Lam Huynh Stefano Lonardi
Mitchell Lucas Steve Wanamaker
Yi-Ning Guo Arsenio Ndeve*
Jose Rodriguez Savanah St. Clair
Jasmine Dixon Sassoum Lo*
Seyed Mirebrahim* Maria Muñoz-Amatriain

African Breeding Partners

ISRA, Senegal
Ndiaga Cisse, Mohammadou Moussa Diangar
INERA, Burkina Faso
Issa Drabo, Jean-Baptiste Tignegre, Joseph Batiemo

IITA, Nigeria
Ousman Boukar, Christian Fatokun

CSIR-SARI, Ghana
Ibrahim Atokple, Francis Kusi



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Drying and Shipping the leaves

- Package in the zip lock bag with 2 silica gel packs
- Make sure to seal the bag
- Leaf tissue will dry within a few days before or during shipment



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