



Biotech and innovative breeding for the new Agri-Food System CGIAR Research Programs (CRPs)

10th Asia-Pacific Biotech Congress, Bangkok Thailand

P. Ellul, Senior Officer
CGIAR System Organization
25-27 July 2016

Yield increase and the Green Revolution



- Pilot program (1940s-50s) for developing semi-dwarf, high-yield and disease-resistant varieties
- Mexico self-sufficient in wheat in the 1950s
- Varieties imported by India and Pakistan => Green Revolution

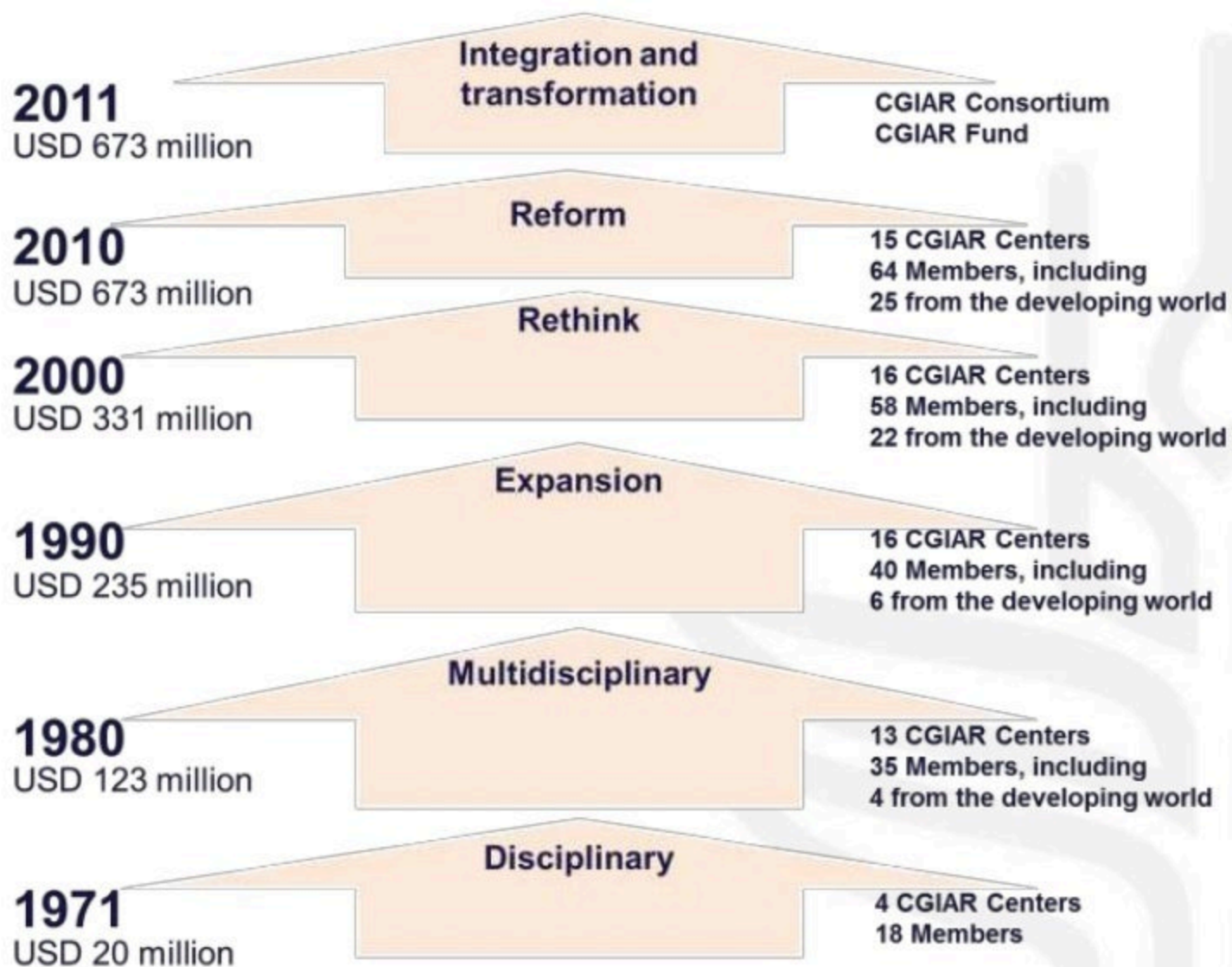


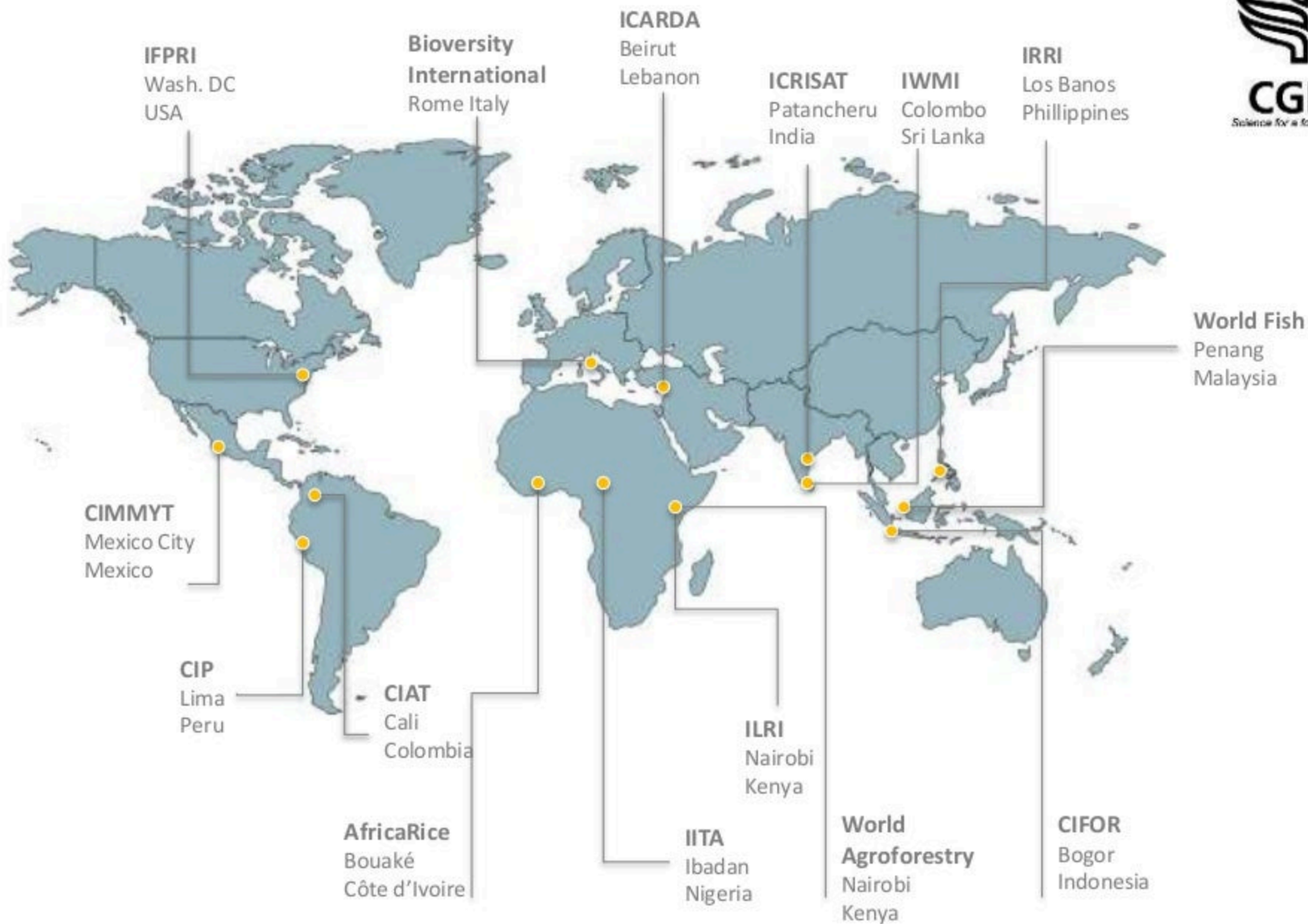
Norman Borlaug
1970 Nobel Peace Prize



- CIMMYT created in 1966 (Rockefeller and Ford Foundations, and the Mexican Government)

CGIAR from 1971 to 2011





1st Strategic Research Framework (2008)

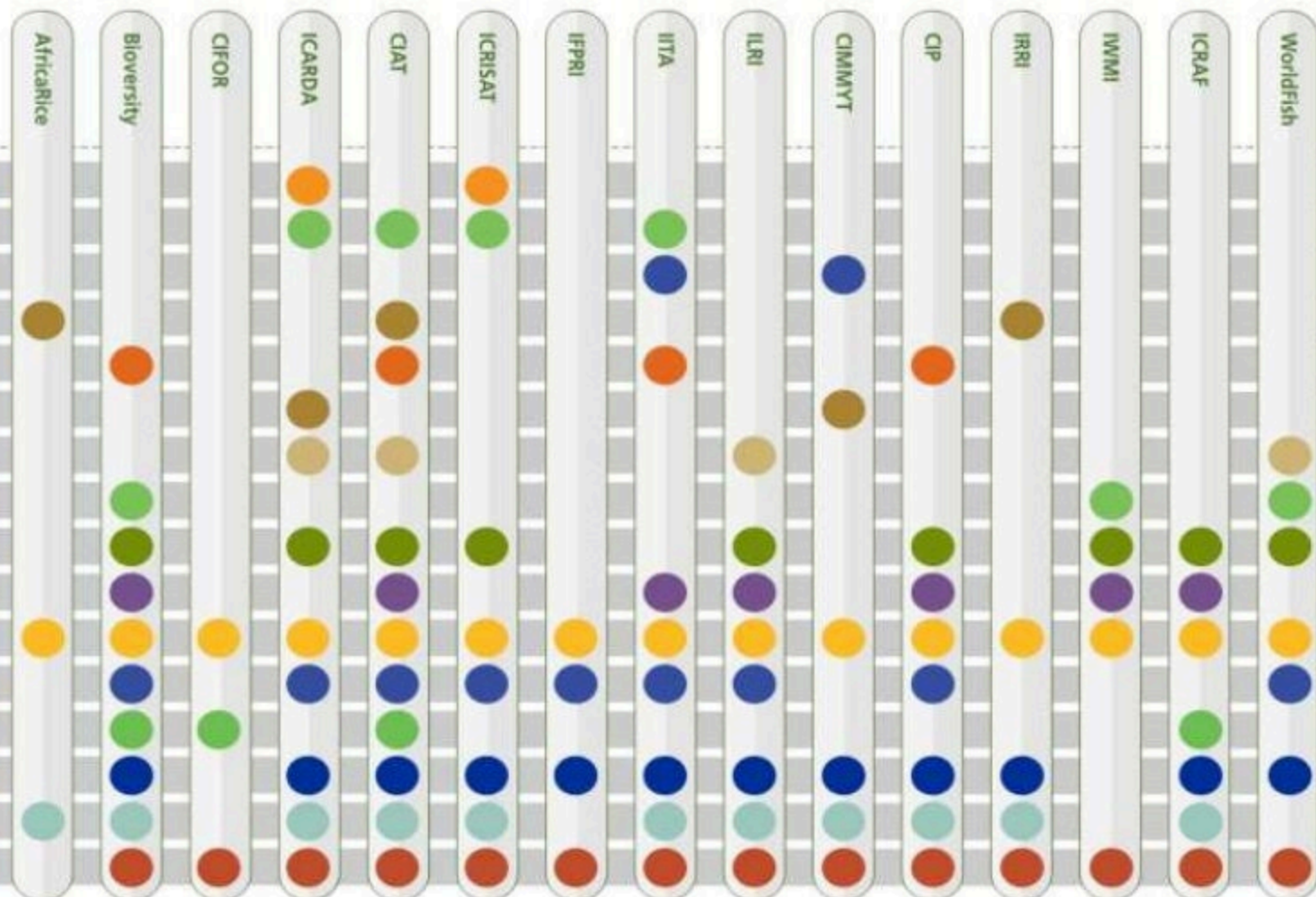


- Donors united in CGIAR Fund
- 15 Centers collaborating in transversal cross-cutting CGIAR Research Programs (CRPs)
- 1st Portfolio of 16 CRPs
- 80% part of CGIAR's work, through CRPs
- Focused on delivering + development outcomes
- CGIAR funding average growth ... from \$0.7B USD (2011) to \$1B USD in 2014

16 CGIAR Research Programs (CRPs)



Research Programs



16 CGIAR Research Programs (CRPs)



- **MAIZE**
- **WHEAT**
- **GRiSP** (Global Rice Science Partnership)
- **Roots, Tubers & Bananas**
- **Dryland Cereals**
- **Grain Legumes**
- **Livestock & Fish**
- **CRP for Managing & Sustaining Crop Collections**
- **Policies, Institutions & Market**
- **Agriculture for Nutrition & Health**
- **Humid Tropics**
- **Aquatic Agricultural Systems**
- **Dryland Systems**
- **Climate Change, Agriculture and Food Security (CCAFS)**
- **Forests, Trees and Agroforestry (FTA)**
- **Water, Land and Ecosystems (WLE)**

2nd CGIAR's Strategy and Results Framework (SRF) 2017–2030 is ambitious. It defines our aspirations and strategic actions to deliver on our mission.

Our vision: A world free of poverty, hunger and environmental degradation.

Our Mission: To advance agri-food science and innovation to enable poor people, especially poor women, to increase agricultural productivity and resilience, share in economic growth, feed themselves and their families better, and conserve natural resources in the face of climate change and other threats.

New SRF and the second generation of CRPs



New SRF guides the development and implementation of an ambitious portfolio of “second-generation” CGIAR Research Programs ([CRPs](#))

Focuses on selected grand challenges, and is articulated in 3 strategic goals, or System Level Outcomes (SLOs), which by 2030 will contribute significantly to the achievement of key Sustainable Development Goals ([SDGs](#))

REDUCE
POVERTY

IMPROVE
FOOD AND
NUTRITION
SECURITY

IMPROVE
NATURAL
RESOURCES AND
ECOSYSTEM
SERVICES

System Level Outcome (SLO) 1

Reduced Poverty



Targets for 2030



- 350 million more farm households should have adopted improved varieties, breeds or trees, and/or improved management practices
- 100 million people, of which 50% are women, assisted to exit poverty



1 NO POVERTY



2 ZERO HUNGER



3 GOOD HEALTH AND WELL-BEING



5 GENDER EQUALITY



8 DECENT WORK AND ECONOMIC GROWTH



10 REDUCED INEQUALITIES



17 PARTNERSHIPS FOR THE GOALS



System level Outcome (SLO) 2

Improved Food & Nutrition Security for Health



Targets for 2030



- Yield increase rate of major food staples from current <math><2.0</math> to 2.5%/yr.
- 150 million more people, of which 50% are women, meeting minimum dietary energy requirements
- 500 million more people, of which 50% are women, without deficiencies of one or more of the essential micronutrients
- 33% reduction of women in reproductive age who are consuming less than the adequate number of food groups



1 NO POVERTY



2 ZERO HUNGER



3 GOOD HEALTH AND WELL-BEING



5 GENDER EQUALITY



6 CLEAN WATER AND SANITATION



10 REDUCED INEQUALITIES



12 RESPONSIBLE CONSUMPTION AND PRODUCTION



17 PARTNERSHIPS FOR THE GOALS



System level Outcome (SLO) 3 Improved Natural Resource Systems & Ecosystem Services



Targets for 2030



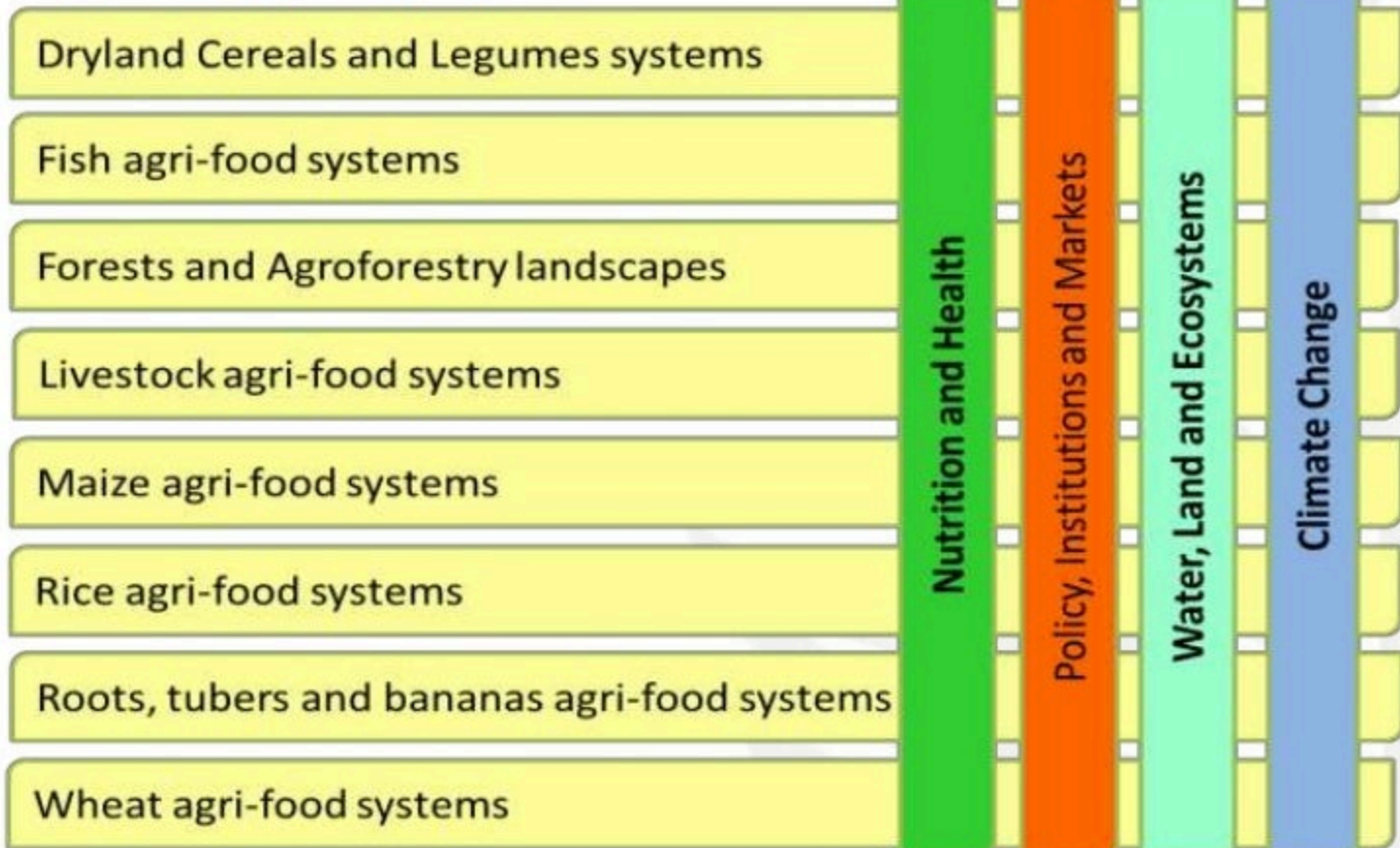
- 20% increase in water and nutrient (inorganic, biological) use efficiency in agro-ecosystems, including through recycling and reuse
- Reduce agriculturally-related greenhouse gas emissions by 0.8 Gt CO₂-e yr⁻¹ (15%) compared with a business as usual scenario in 2030
- 190 million hectares (ha) degraded land restored
- 7.5 million ha of forest saved from deforestation



The 2nd generation of CRPs (2017-22)



8 Agri-Food System programs



4 Global Integrating Programs

3 Platforms



CGIAR Genebanks (CRP / Platform)

25 food crops and 740,000 accessions



		Accessions
AfricaRice	Rice	20,000
Bioversity	Banana, Plantain	1,298
CIAT	Beans, Cassava, Tropical forages	65,635
CIMMYT	Maize, Wheat	155,129
CIP	Potato, Sweet potato, Andean Roots & Tubers	16,495
ICARDA	Grain legumes, Wheat, Barley, Forage & range crops	135,406
ICRAF	Trees	5,144
ICRISAT	Dryland cereals, Grain cereals	156,313
IITA	Banana, Plantain, Maize, Cowpea, Cassava, Yam	28,286
ILRI	Tropical forages	18,291
IRRI	Rice	116,817
	Total	712,568

Agri-Food System's workflow & biotech



Genetic Diversity

- PGR managers
- Researchers
- (Pre-breeders)

- Genebanks & passport data
- Genotyping/genomic data (GbS, Reseq.)
- Phenotypic data
- Geo-location data

Trait Discovery

- Pre-breeders
- Researchers
- Breeders

- Mapping lines
- QTL discovery
- Gene discovery
- SNP discovery
- Doubled Haploids
- Mutagenesis
- Genetic engineering
- Reverse breeding
- Trait performance

Variety Improvement

- Breeders
- Implementers/technicians

- ✓ SNP validation
- ✓ Gene pyramiding
- ✓ MAS
- ✓ Genomic Selection
- ✓ Genome editing
- ✓ Genetic engineering
- ✓ Multi-location field trials

Seed Systems

- Seed Researchers
- Implementers, developers

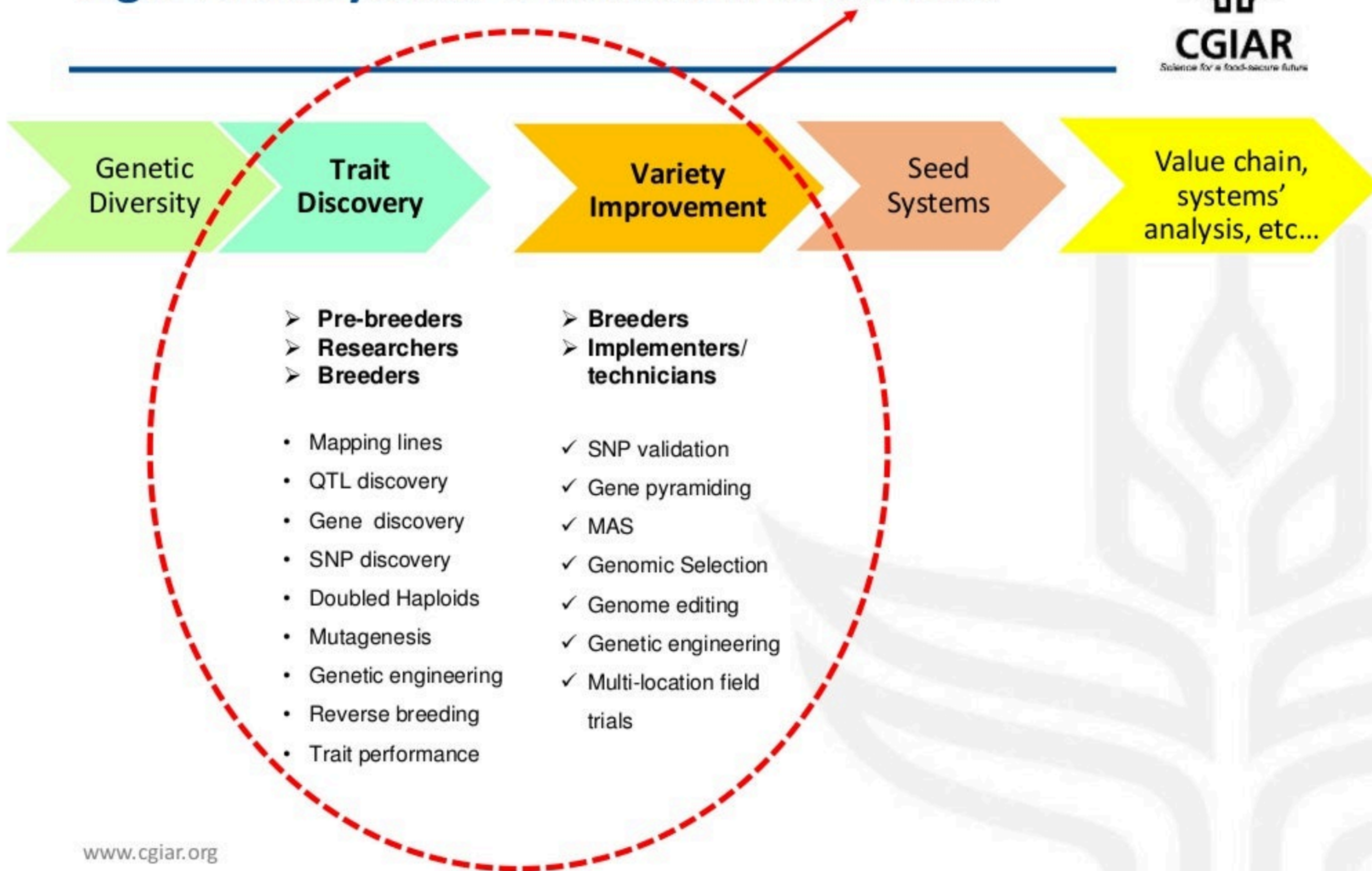
- Seed multiplication
- Seed Quality Control
- Seed storage
- Seed dissemination

Value chain, systems' analysis, etc...

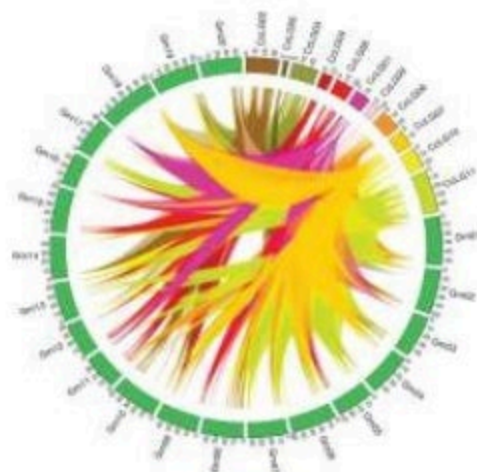
- Multidisc. Res. (ecology, social sciences,...)

- ❖ Foresight
- ❖ Cropping systems
- ❖ Value chain
- ❖ Scaling out
- ❖ Post harvesting technologies
- ❖ Capacity building
- ❖ Other SAI approaches

Agri-Food System's workflow & biotech

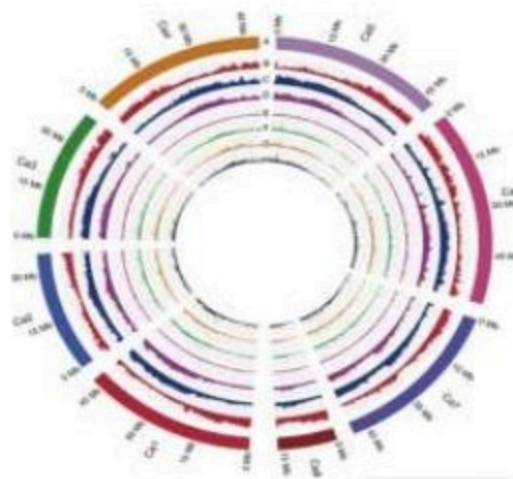


Leading international sequencing consortia ICRISAT / Grain Legumes & Dryland Cereals CRPs



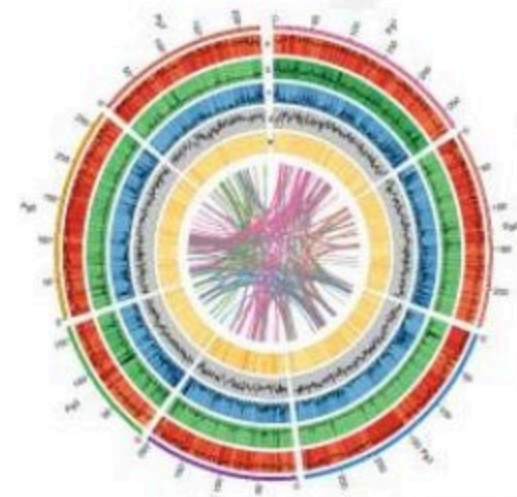
Pigeonpea

(Nature Biotechnology- 2012)



Chickpea

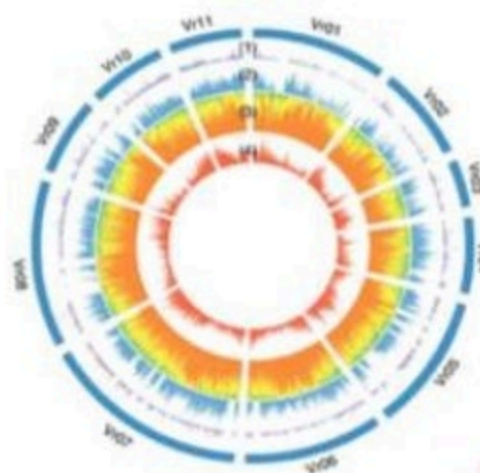
(Nature Biotechnology- 2013)



Pearl millet- 2016

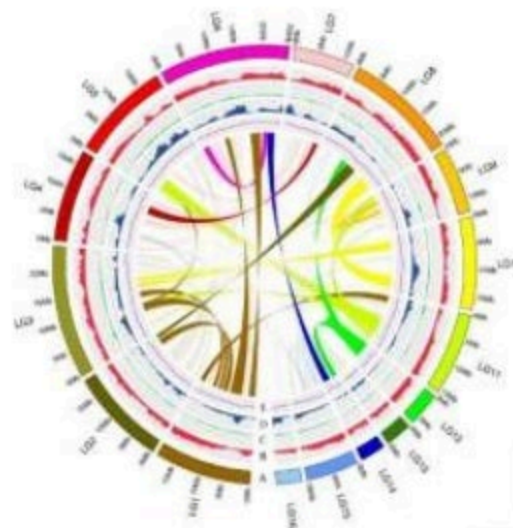
Kindly provided by Dr Rajeev Varshney (ICRISAT/ Grain Legumes and Dryland Cereals)

Co-leading international sequencing consortia ICRISAT / Grain Legumes & Dryland Cereals CRPs



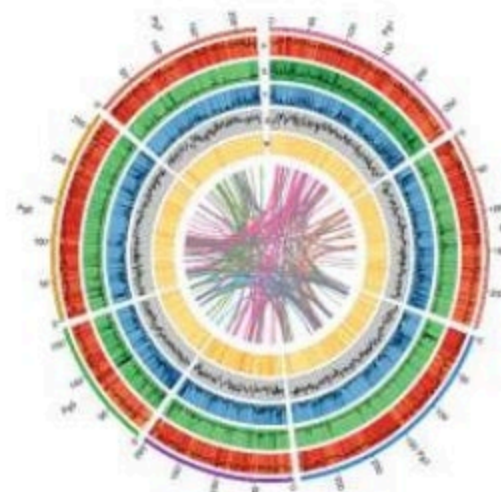
Mungbean

(Nature Communication- 2014)



Sesame

(Genome Biology 2014)



Pearl millet- 2016
(in revision)

Kindly provided by Dr Rajeev Varshney (ICRISAT/ Grain Legumes and Dryland Cereals)

From re-sequencing 300 chickpea accessions... to the 3K genome initiative

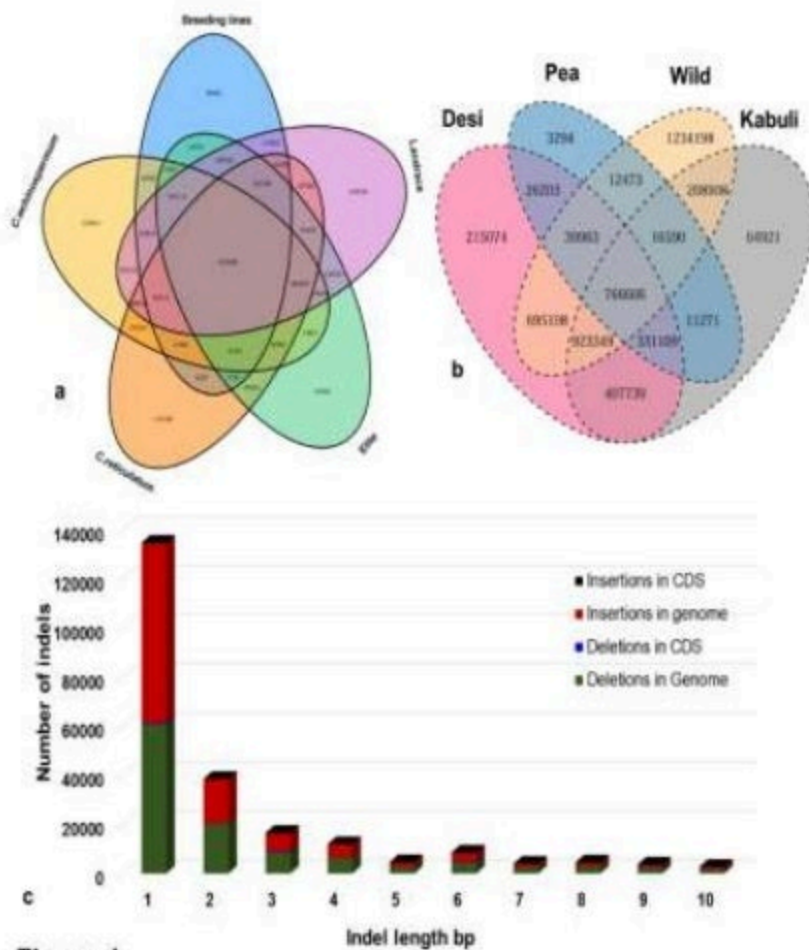


Figure 1

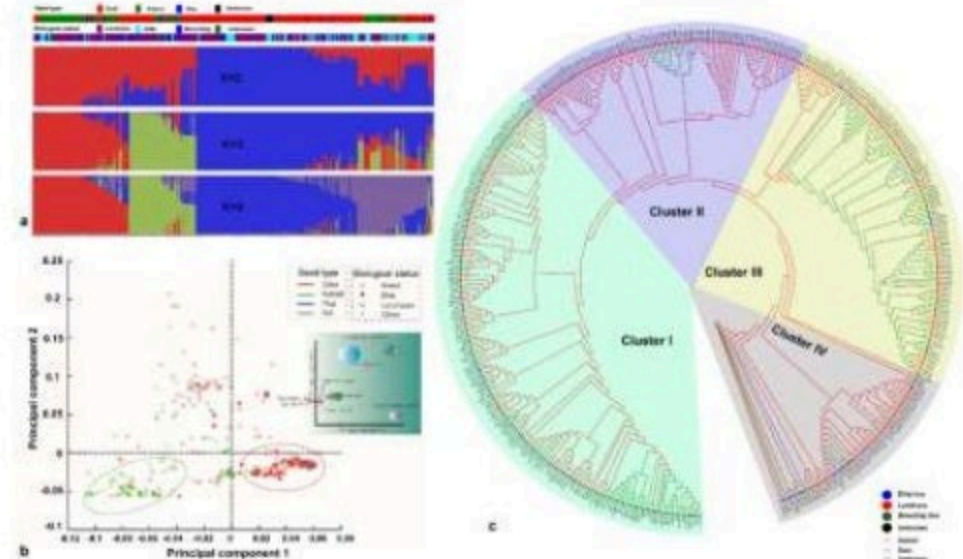


Figure 2

- 4.9 Million SNPs
- 596,000 indels
- 512,000 CNVs

Kindly provided by Dr Rajeev Varshney (ICRISAT/ Grain Legumes and Dryland Cereals)

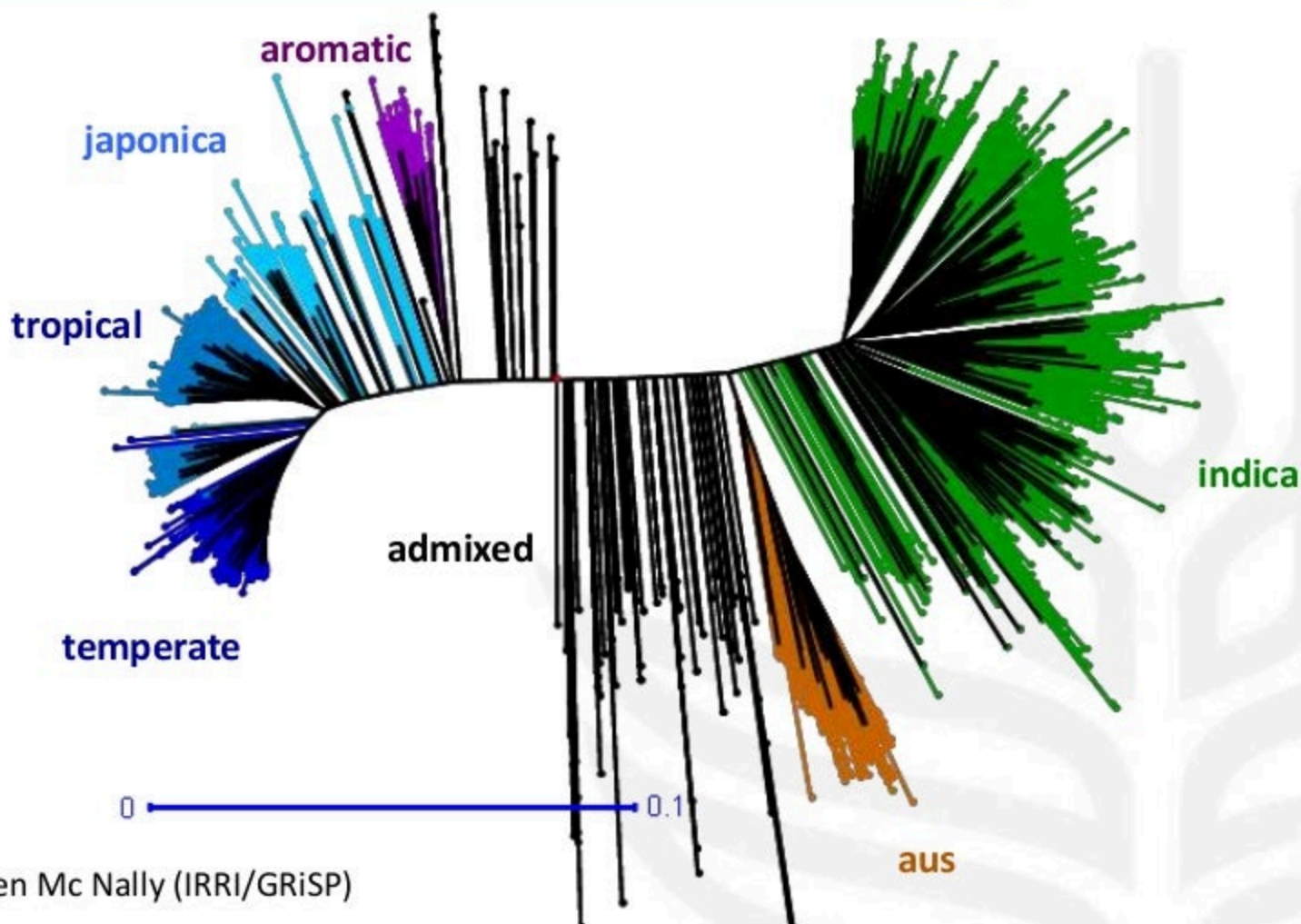
Sequencing 3,000 rice accessions



华大基因
BGI



GRiSP



Kindly provided by Dr. Ken Mc Nally (IRRI/GRiSP)

From Alexandrov, et al. SNP-Seek database of SNPs derived from 3000 rice genomes. Nucl. Acids Res. 2015;43(D1):D1023-D1027

Rice SNP-Seek database / 20 Million SNPs



Rice SNP-Seek Database

Home Search Browse My Lists Download Help

This site provides Genotype, Phenotype, and Variety Information for rice (*Oryza sativa* L.). SNP genotyping data (called against [Nipponbare reference: Os-Nipponbare-Reference-IRGSP-1.0](#)) came from [3,000 Rice Genomes Project](#). Phenotype and passport data for the 3,000 rice varieties came from the [International Rice Information System \(IRIS\)](#). We are a part of an ongoing effort by the [International Rice Informatics Consortium \(IRIC\)](#) to centralize information access to rice research data and provide computational tools to facilitate rice improvement via discovery of new gene-trait associations and accelerated breeding.

To cite this resource: [Alexandrov, et al. SNP-Seek database of SNPs derived from 3000 rice genomes. Nucl. Acids Res. 2015;43\(D1\):D1023-D1027](#)



Genotypes

Query for SNPs from the 3000 genome project



Varieties

Query for Variety passport and phenotypes



JBrowse

Rice Genome Browser



Help

Help and documentation

From Alexandrov, et al. SNP-Seek database of SNPs derived from 3000 rice genomes. Nucl. Acids Res. 2015;43(D1):D1023-D1027

High density genotyping: Seed of Discovery

<http://seedsofdiscovery.org>



The screenshot shows the website interface for 'Seeds of Discovery'. At the top, the title 'Seeds of Discovery' is followed by the tagline 'Unlocking the genetic potential of maize and wheat'. The MasAgro logo is in the top right. A navigation menu includes 'about SeedD', 'how we work', 'maize', and 'wheat'. A sidebar on the left has green buttons for 'ABOUT SEEDD', 'HOW WE WORK', 'MAIZE', and 'WHEAT', along with a search bar. The main content area is titled 'FOOD SECURITY AND GENETIC RESOURCES' and features a list of links under 'About SeedD', including 'Food security and genetic resources', 'Philosophy of our approach', 'Research portfolio', and 'Genotyping platform'. A central image shows a person holding ears of maize, with a caption: 'Zona maize from the Huasteca state of Mexico. ©2012 CIMMYT'. To the right, a text block discusses the impact of climate change on agriculture and the need for yield acceleration. Logos for SAGARPA and CIMMYT are visible in the bottom left. A small photo of a group of people is in the bottom right.

Seeds of Discovery

Unlocking the genetic potential of maize and wheat

about SeedD / how we work / maize / wheat

SeedD / About SeedD / Food security and genetic resources

FOOD SECURITY AND GENETIC RESOURCES

- About SeedD
 - Food security and genetic resources
 - Philosophy of our approach
 - Research portfolio
 - Genotyping platform

Climate change, land degradation, and a declining agricultural resource base (water, soil, nutrients, energy), are threatening our ability to sustainably grow sufficient food for rising and increasingly urban populations. The Food and Agriculture Organization (FAO) estimates that cereal crop outputs will need to increase by 70% by 2050, which will require a considerable **acceleration of the rates** at which global crop yields have been increasing in the past. This is a formidable challenge given that changing environments are increasingly affecting agriculture through eroding soils, greater heat stress, new diseases and pests, and more frequent droughts and other extreme weather events.

Mexico, alongside countries like India, may be one of the countries **most severely affected by climate change**. Mexico's food self-sufficiency is at risk—a risk that is exacerbated by the fact that maize and wheat prices are set on a global scale and could rise.

SAGARPA
SECRETARÍA DE AGRICULTURA, GANADERÍA Y PESQUERÍA

CIMMYT
CENTRO INTERNACIONAL DE INVESTIGACIÓN EN MAÍZ Y TRIGO

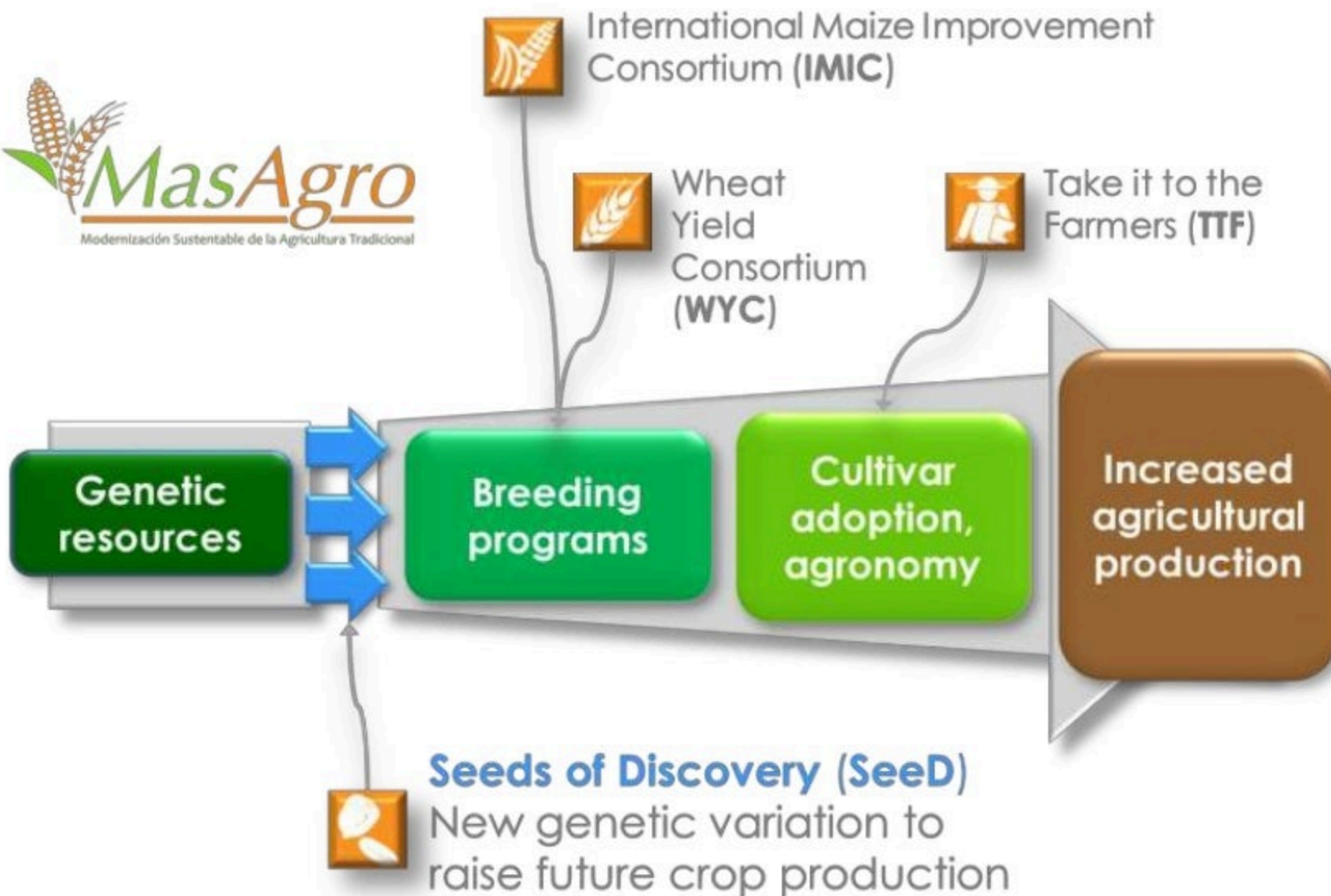
High density genotyping: Seed of Discovery



- **Maize:** ~27,000 accessions in CIMMYT's genebank
 - Developed new GbS method for **composite DNA samples** (30 plants per accession); the method simultaneously
 - ▶ Quantifies **allele frequencies** within accessions (SNP), and
 - ▶ Estimates **genetic distances** among accessions
 - Completed the sequencing of **20,000 accessions** → diversity analysis in progress
- **Wheat:** ~140,000 accessions in CIMMYT's genebank
 - Completed sequencing of **42,000 accessions**
 - Data being used to assemble AM panels

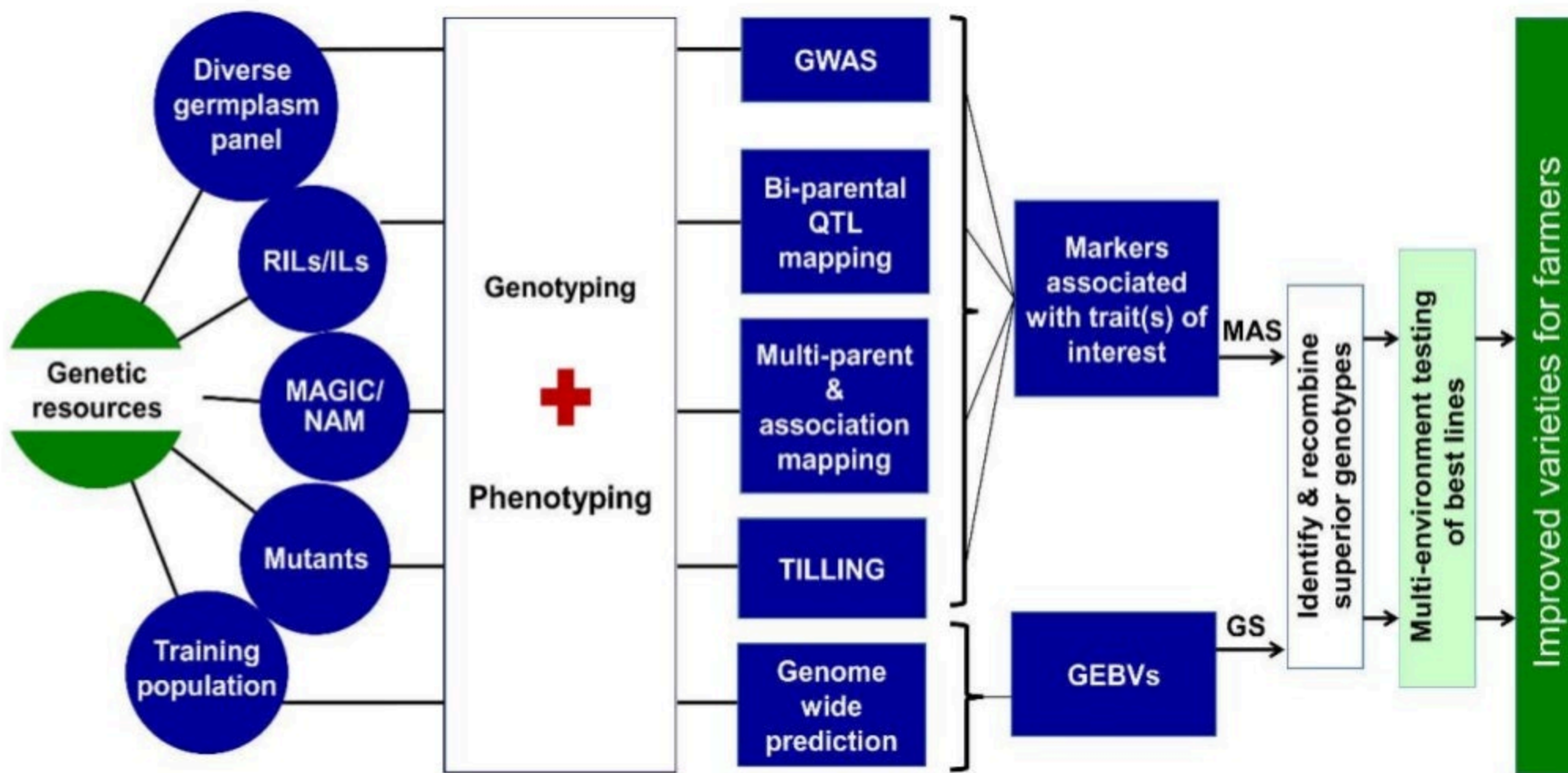
Kindly provided by Dr. Peter Wenzl, ex-SeeD Project leader at CIMMYT; currently Genebank Manager at CIAT

High density genotyping: Seed of Discovery



Translational genomics for agriculture

From Varshney et al., PLOS Biology 2014



SCIENTIFIC REPORTS

OPEN

Biofortified indica rice attains iron and zinc nutrition dietary targets in the field

Received: 11 September 2015

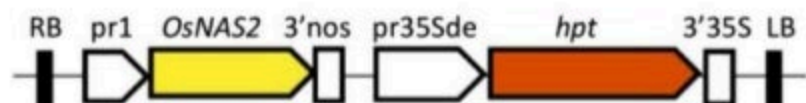
Accepted: 07 December 2015

Published: 25 January 2016

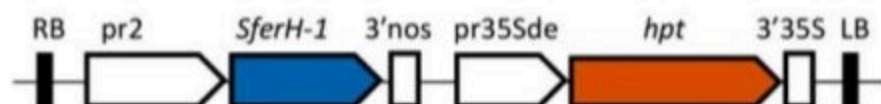
Kurniawan R. Trijatmiko^{1,10}, Conrado Dueñas¹, Nikolaos Tsakirpaloglou¹, Lina Torrizo¹, Felichi Mae Arines¹, Cheryl Adeva¹, Jeanette Balindong¹, Norman Oliva¹, Maria V. Sapasap¹, Jaime Borrero², Jessica Rey¹, Perigio Francisco¹, Andy Nelson^{3,4}, Hiromi Nakanishi⁵, Enzo Lombi⁶, Elad Tako⁷, Raymond P. Glahn⁷, James Stangoulis⁸, Prabhjit Chadha-Mohanty¹, Alexander A. T. Johnson⁹, Joe Tohme², Gerard Barry¹ & Inez H. Slamet-Loedin^{1,11}

More than two billion people are micronutrient deficient. Polished grains of popular rice varieties have concentration of approximately $2 \mu\text{g g}^{-1}$ iron (Fe) and $16 \mu\text{g g}^{-1}$ zinc (Zn). The HarvestPlus breeding programs for biofortified rice target $13 \mu\text{g g}^{-1}$ Fe and $28 \mu\text{g g}^{-1}$ Zn to reach approximately 30% of the estimated average requirement (EAR). Reports on engineering Fe content in rice have shown an increase up to $18 \mu\text{g g}^{-1}$ in glasshouse settings; in contrast, under field conditions, $4 \mu\text{g g}^{-1}$ was the highest reported concentration. Here, we report on selected transgenic events, field evaluated in two countries, showing $15 \mu\text{g g}^{-1}$ Fe and $45.7 \mu\text{g g}^{-1}$ Zn in polished grain. Rigorous selection was applied to 1,689 IR64 transgenic events for insert cleanliness and, trait and agronomic performances. Event NASFer-274 containing rice nicotianamine synthase (*OsNAS2*) and soybean ferritin (*SferH-1*) genes showed a single locus insertion without a yield penalty or altered grain quality. Endosperm Fe and Zn enrichment was visualized by X-ray fluorescence imaging. The Caco-2 cell assay indicated that Fe is bioavailable. No harmful heavy metals were detected in the grain. The trait remained stable in different genotype backgrounds.

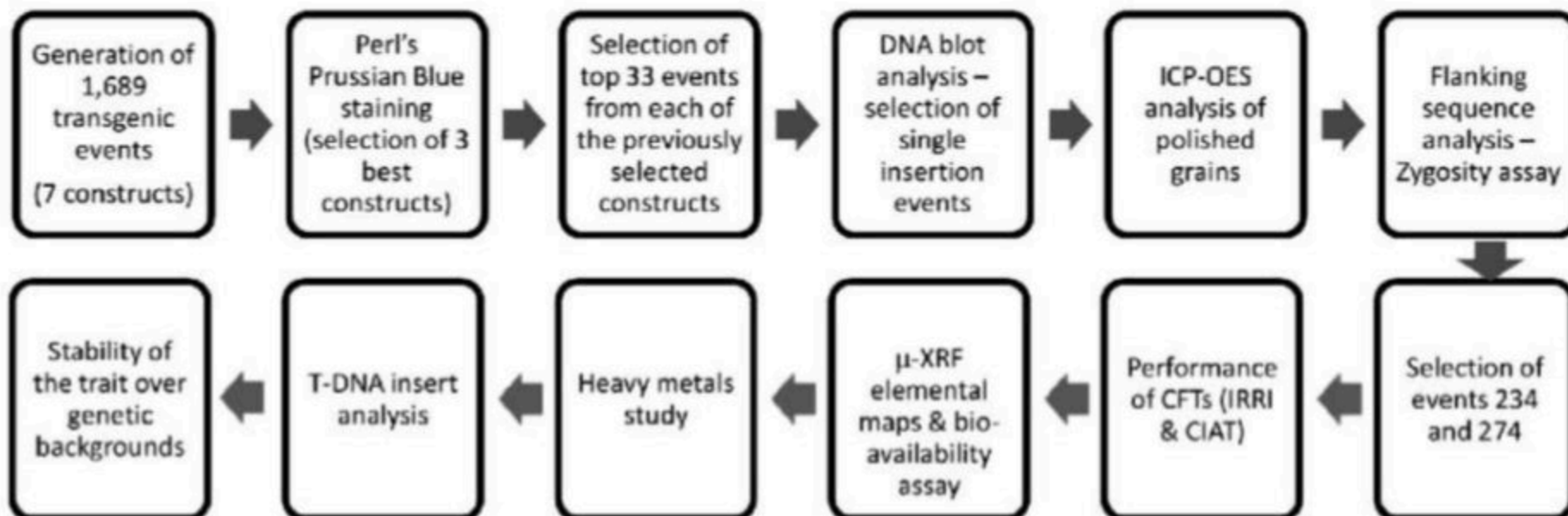
Engineering biofortified rice varieties



OsNAS2 = rice nicotianamine synthase

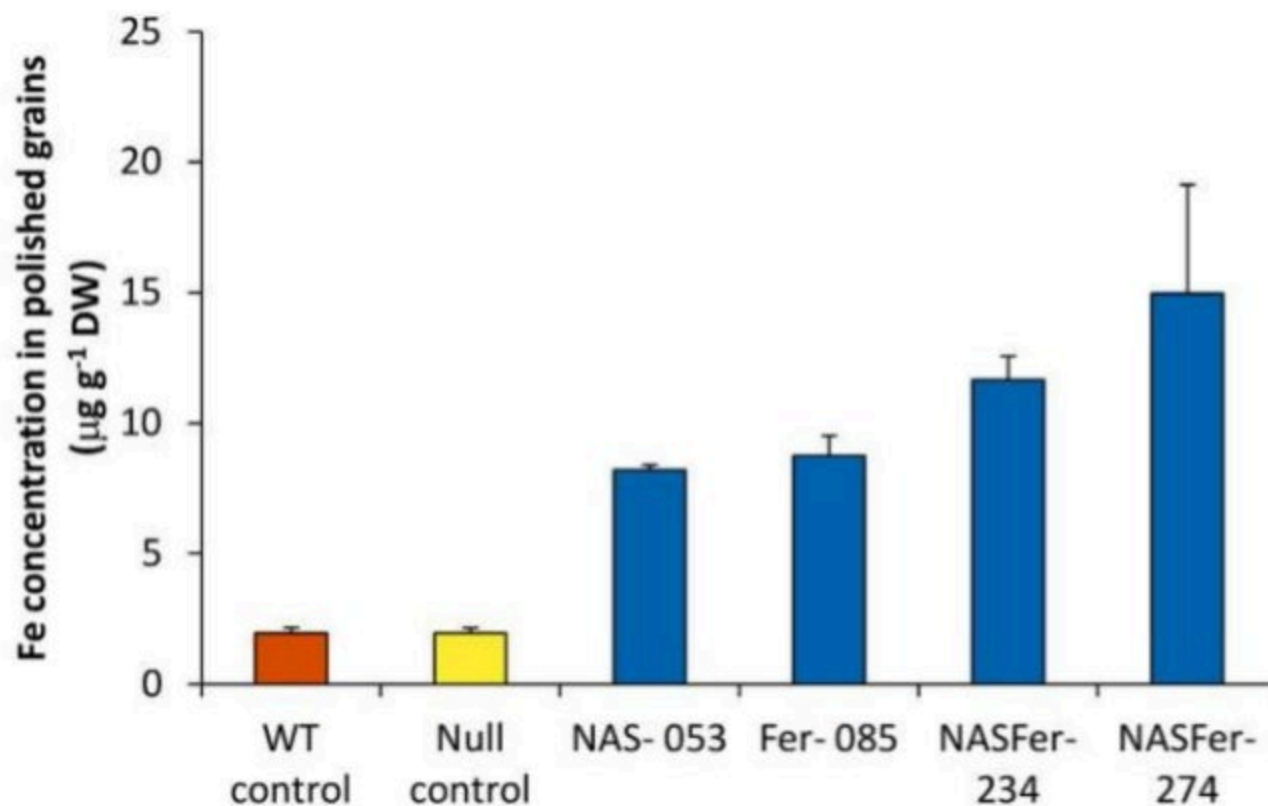


SferH-1 = soybean ferritin gene

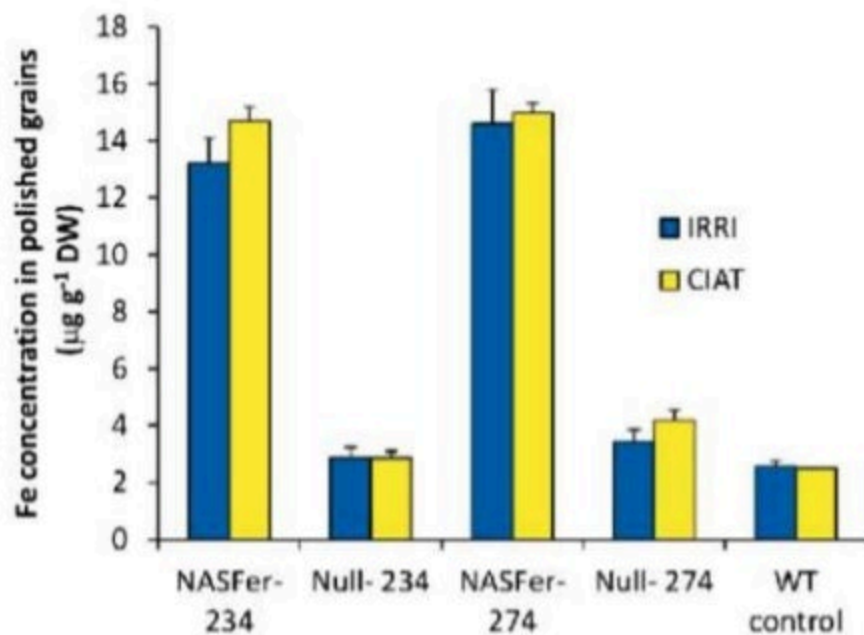


Engineering biofortified rice varieties

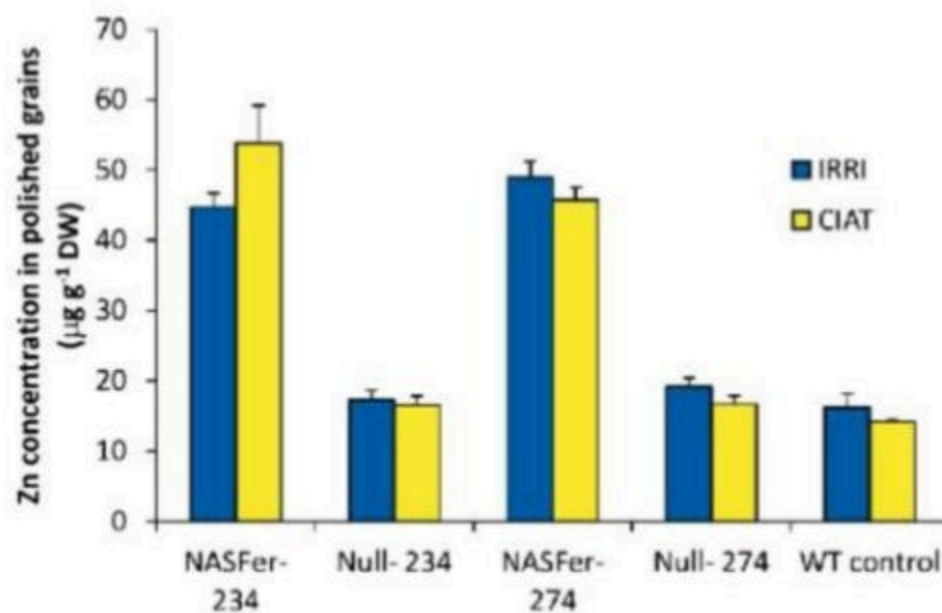
Fe concentration ($\mu\text{g g}^{-1}$ DW) of **polished seeds** harvested from T1 homozygous plants of representative NAS, Fer, and NASFer events, null segregant, and non-transformed rice under greenhouse conditions.



Engineering biofortified rice varieties



Proof of concept = attaining Fe/Zn nutritional targets under flooded field conditions to fulfil 30% of EAR (Estimated Average Requirement) in the human diet



Impacting research for development => multi-institutional + multi-disciplinary



1. Plant Breeding, Genetics, and Biotechnology Division, International Rice Research Institute (**IRRI**), Manila, Philippines.
2. Centro Internacional de Agricultura Tropical (**CIAT**), Cali, Colombia.
3. Social Sciences Division, **IRRI**, Manila, Philippines
4. Faculty of Geo-Information and Earth Observation (ITC), University of Twente, The Netherlands.
5. Graduate School of Agricultural and Life Sciences, The University of Tokyo, Japan.
6. Centre for Environmental Risk Assessment and Remediation, University of South Australia, Australia.
7. United States Department of Agriculture-Agricultural Research Service, Cornell University, USA.
8. School of Biological Sciences, Flinders University of South Australia, Adelaide, Australia.
9. School of Botany, The University of Melbourne, Victoria 3010, Australia.
10. Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development, Bogor, Indonesia.
11. Research Center for Biotechnology, Indonesian Institute of Sciences, Cibinong, Indonesia.

Sweet potato : a naturally transgenic crop ?

Root, Tubers and Bananas CRP



PNAS

Proceedings of the National Academy of Sciences of the United States of America

CURRENT ISSUE // ARCHIVE // NEWS & MULTIMEDIA // AUTHORS // ABOUT // COLLECTED ARTICLES // BROWSE BY TOPIC // EARLY EDITION // FRONT MATTER

Current Issue > vol. 112 no. 18 > Tina Kyndt, 5844–5849, doi: 10.1073/pnas.1419685112



The genome of cultivated sweet potato contains *Agrobacterium* T-DNAs with expressed genes: An example of a naturally transgenic food crop

Tina Kyndt^{a,1}, Dora Quispe^{a,b,1}, Hong Zhai^c, Robert Jarret^d, Marc Ghislain^b, Qingchang Liu^e, Godelieve Gheysen^a, and Jan F. Kreuze^{b,2}

Author Affiliations *

Edited by Eugene W. Nester, University of Washington, Seattle, WA, and approved March 16, 2015 (received for review October 13, 2014)

Abstract Full Text Authors & Info Figures SI Metrics Related Content PDF PDF + SI

Significance

We communicate the rather remarkable observation that among 291 tested accessions of cultivated sweet potato, all contain one or more transfer DNA (T-DNA) sequences. These sequences, which are shown to be expressed in a cultivated sweet potato clone ("Huachano") that was analyzed in detail, suggest that an *Agrobacterium* infection occurred in evolutionary times. One of the T-DNAs is apparently present in all cultivated sweet potato clones, but not in the crop's closely related wild relatives, suggesting the T-DNA provided a trait or traits that were selected for during domestication. This finding draws attention to the importance of plant–microbe interactions, and given that this crop has been eaten for millennia, it may change the paradigm governing the "unnatural" status of transgenic crops.

This Issue



May 5, 2015
vol. 112 no. 18
Masthead (PDF)
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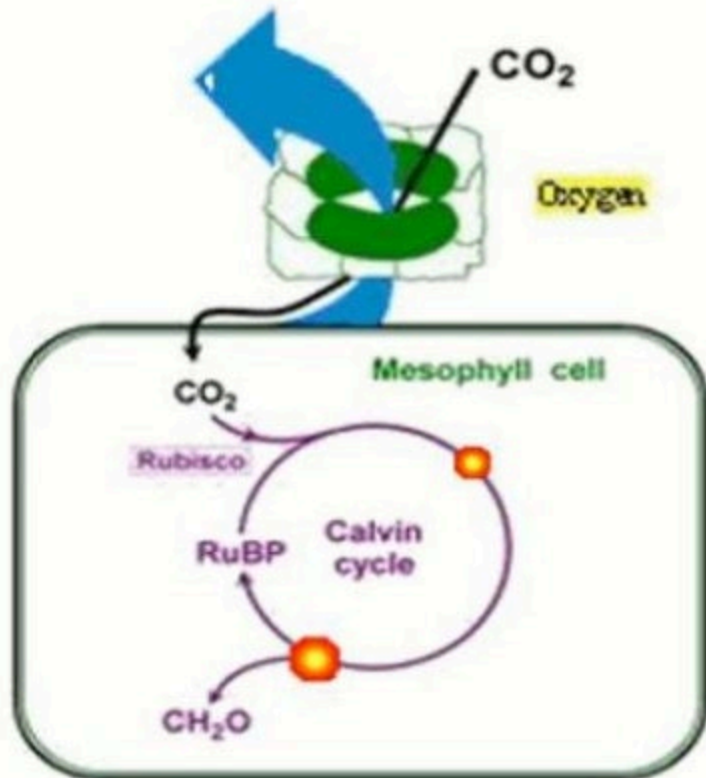


Published online before print
April 20, 2015, doi:

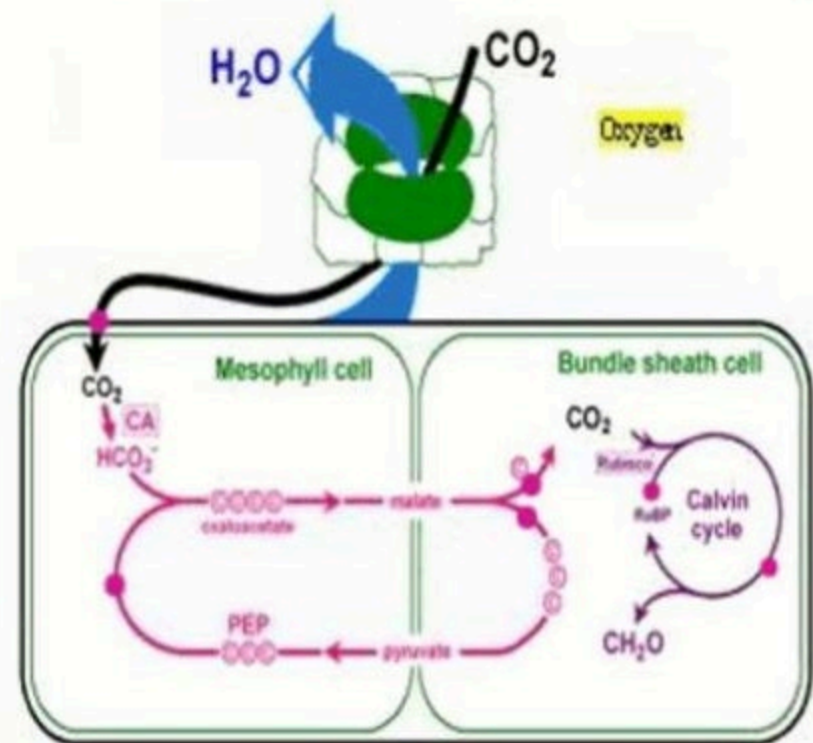
Blue sky biotech research: the C4 rice project



C₃ Photosynthesis: Rubisco



C₄ Photosynthesis: PEP Carboxylase then Rubisco



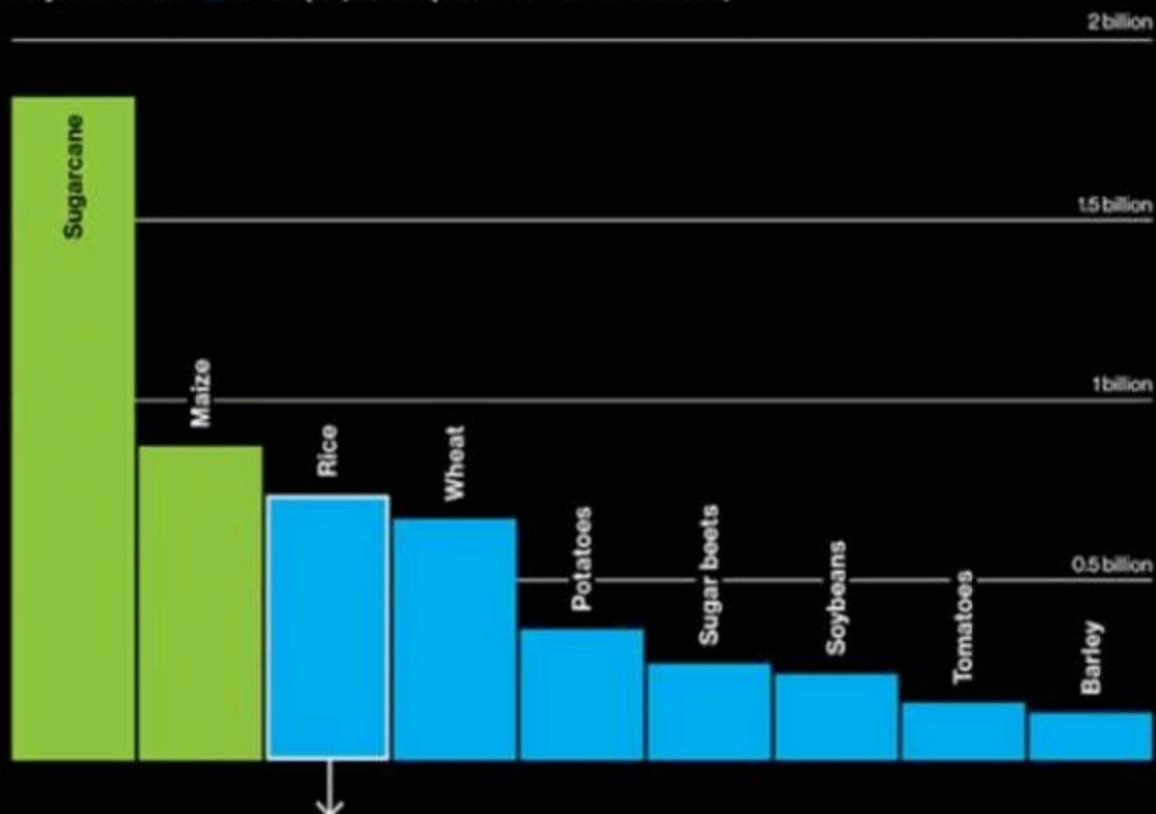
www.c4rice.irri.org

Challenge: Kranz (C4) anatomy into C3 plants

Photosynthesis Boost

The world's highest-production crops use a super-efficient form of photosynthesis. It's known as C4 photosynthesis because the first step is the formation of a four-carbon molecule. C3 photosynthesis, found in most plant species, starts with a three-carbon molecule.

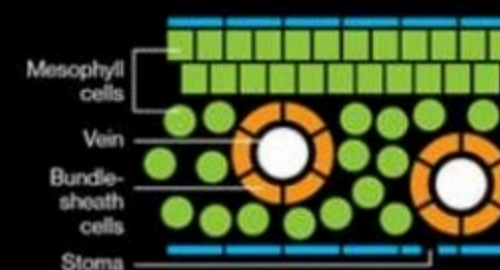
Major ■ C4 and ■ C3 crops (annual production in metric tons)



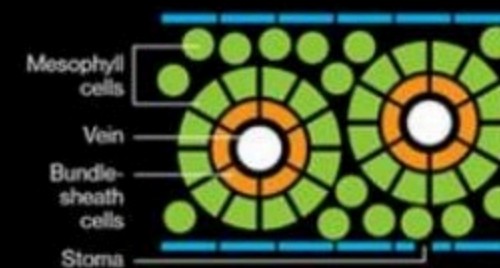
Carbon Concentrators

In C4 plants, a wreathlike arrangement of cells (lower image) helps concentrate carbon dioxide. A ring of mesophyll cells (green) captures the carbon dioxide, which is conveyed to an inner ring of bundle-sheath cells (orange). The arrangement is known as the Kranz anatomy, after the German word for wreath.

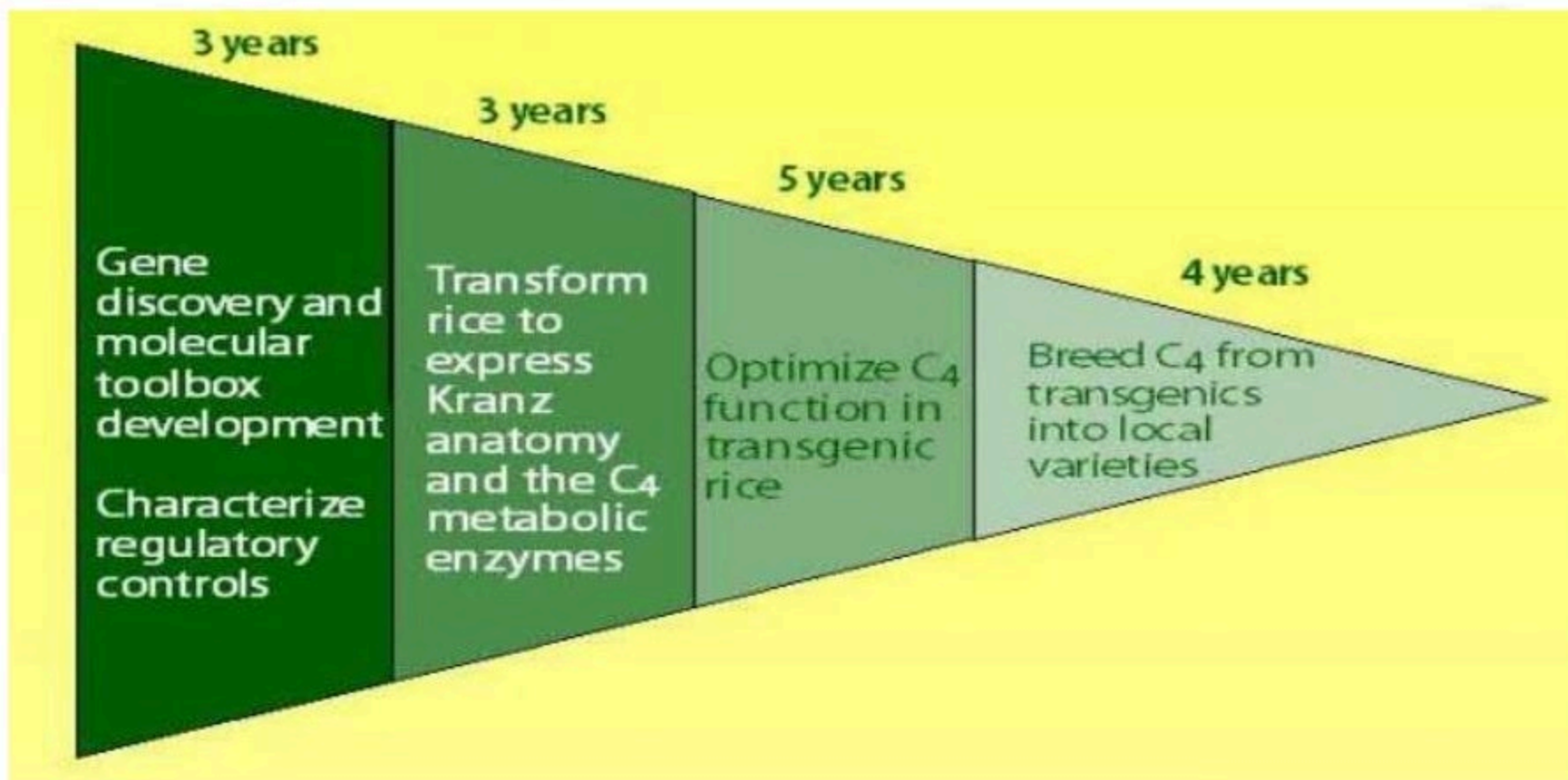
C3



C4



Roadmap of the C4 rice project



www.c4rice.irri.org

C4 rice principal investigators



An, Gynheung	Kyung Hee University , Republic of Korea
Brutnell, Thomas	Danforth Institute, USA
Burnell, James	James Cook University, Australia
Cousins, Asaph	Washington State University, USA
Edwards, Gerry	Washington State University, USA
Furbank, Robert	ARC Centre of Excellence for Translational Photosynthesis / CSIRO , Australia
Hibberd, Julian	University of Cambridge, UK
Hsing, Caroline	Academia Sinica, Taiwan
Kelly, Steven	University of Oxford, UK
Langdale , Jane	University of Oxford, UK
Leegood, Richard	University of Sheffield, UK
Murchie, Erik	University of Nottingham, UK
Myers, Chris	Cornell University, USA
Quick, William Paul	International Rice Research Institute, Philippines
Sage, Rowan	University of Toronto, Canada
Sage, Tammy	University of Toronto, Canada
Sheehy, John	International Rice Research Institute, Philippines
von Caemmerer, Susanne	The Australian National University, Canberra Australia
Voytas, Dan	University of Minnesota, USA
Westhoff, Peter	Heinrich Heine University, Dusseldorf, Germany
Yu, Su May	National Taiwan University, Taiwan
Zhu, Xinguang	PICB, Shanghai China

Disruptive technology: Genome Editing (GE)

GE is the process of precise genome modification using engineered endonucleases



Nucleotides can be

- added
- deleted
- replaced

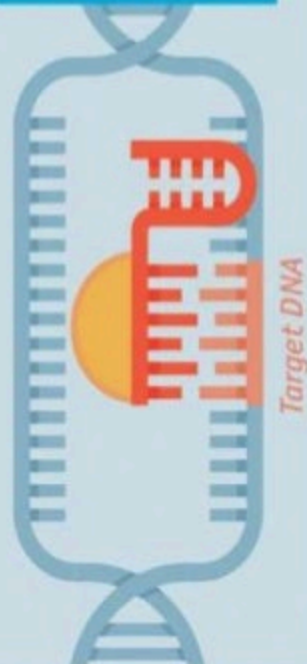
Disruptive technologies: Genome Editing

Using CRISPR

The tools



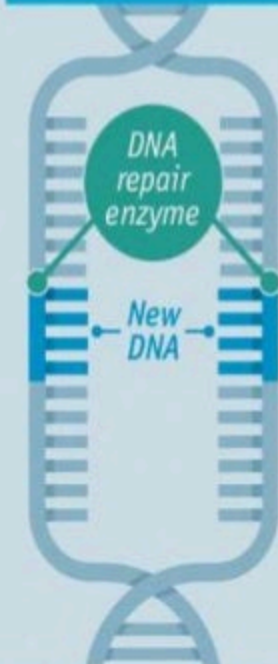
STEP 1 Guide RNA finds target DNA in cell



STEP 2 Cas9 protein cuts DNA strands



STEP 3 Replacement DNA inserted



Source: *The Economist*

Pigs edited to protect them against African Swine Fever (Roselyn Institute, University Edinburgh)



MENU ▾

SCIENTIFIC REPORTS



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Mammalian interspecies substitution of immune modulatory alleles by genome editing

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Scientific Reports **6**, Article number: 21645
(2016)

[doi:10.1038/srep21645](https://doi.org/10.1038/srep21645)

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[Genetic engineering](#)

Received: 20 October 2015

Accepted: 27 January 2016

Published online: 22 February 2016

GE => Interspecies allele introgression in one generation

- RELA (transcription factor) is one of the pig genes associated with ASFV infection.
- RELA gene causes the immune system to overreact with devastating effects
- Warthogs and bush pigs – both more resilient to ASFV - carry a different allelic version of the RELA gene



=> by changing 'only' 5 nucleotides in the pig RELA gene, it is converted into the resistant-gene that is found in the warthog.

From Science Daily, 23 February 2016.

www.sciencedaily.com/releases/2016/02/160223132535.htm

Genetic engineering or Genome editing ?

From “Root, Tubers and Bananas” CRP full proposal



Cassava:

- Cassava starch composition by switching on/off genes of the starch synthesis pathway using genome editing.
- Modifying alleles for herbicide tolerance or carotenoid production (editing ALS and PSY genes).
- Cassava virus replication can be altered by modifying host protein required for their replication and movement. Proof-of-concept work at Danforth Center and ETH, Switzerland, and the National Agricultural Crops Resources Research Institute (NaCRRI), Uganda, has demonstrated efficacy of transgenic approaches.
- Bacterial effectors of *Xanthomonas* pathogens affecting cassava have been recently identified, together with some of their cognate genes in the host.

Potato:

- Cisgenes for LB, virus Y, and leafroll exist; transgenes for bacterial wilt disease appear promising.
- Bacterial effectors of *Ralstonia*, pathogens, have been recently identified together with some of their cognate genes in the host. This opens the way to edit susceptibility genes as well as adding executor genes (Kyndt et al. 2015; Nyabonga et al. 2014).
- Gene editing to alter day-length sensitivity, early tuberization, and heat tolerance in potato.
- Potatoes with 3R genes from wild relatives have been able to withstand LB disease in the absence of any fungicide protections in the Netherlands, Belgium, and Uganda. NARS partners are now engaged in event selection and soon in multilocational trials.

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- Sweetpotato:* • Bt and RNAi technology for weevils and virus disease resistance.
- Yam:* • RNAi and transgenes are under the concept phase for nematode resistance.
- Banana and plantain:* • Transgenes and RNAi for control of Banana bunchy top virus (BBTV) and aphids; resistance to nematodes using cystatins, synthetic peptides, and targeting the expression of genes to roots only.
- Gene editing to inactivate integrated Banana streak virus copies so they cannot re-constitute infections after tissue culture or other stresses.
- Transgenic bananas with resistance to *Xanthomonas* wilt have passed successfully the proof-of-concept stage using constitutive expression of sweetpotato genes conferring disease resistance. National partners are now in the first stages of multilocational trials.

<http://www.cgiar.org/our-strategy/second-call-for-cgiar-research-programs/cgiar-research-programs-platforms-full-proposals-for-review/>

Genome Editing (GE) & Freedom To Operate?



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Conclusions



- ⇒ CGIAR Portfolio 2017-22 addresses the [3 SLOs + n SDGs]
- ⇒ 8 Agri-Food System (AFS), 4 Global Integrating CRPs and 3 platforms (Excellence in breeding, Genebank, Big data)
- ⇒ Genomic characterization (sequencing and re-sequencing)
- ⇒ High throughput genotyping and phenotyping
- ⇒ Translational genomics and pre-breeding: Molecular Assisted Selection (MAS), Genomic Selection (GS), Genome Wide Association Studies (GWAS), etc...
- ⇒ Genetic engineering for specific traits
- ⇒ Genome editing for specific traits

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Thank you

