

International co-operation to harness genetic diversity as a tool to face the challenge of enhancing the productivity, sustainability and resilience of crops and agricultural systems

Frank Ordon

Where are we now ?



- World hunger rising for first time this century
- 815 million chronically undernourished – up by 38 million
- 489 million located in countries affected by conflicts
- Today more people are hungry than entire population of South Asia at beginning of Green Revolution (1970)
- Public in high income countries against new technologies (GMO, CRISPR/Cas)

https://www.theguardian.com/global-development/2017/sep/15/alarm-bells-we-cannot-ignore-world-hunger-rising-for-first-time-this-century?CMP=Share_AndroidApp_Outlook

Challenges



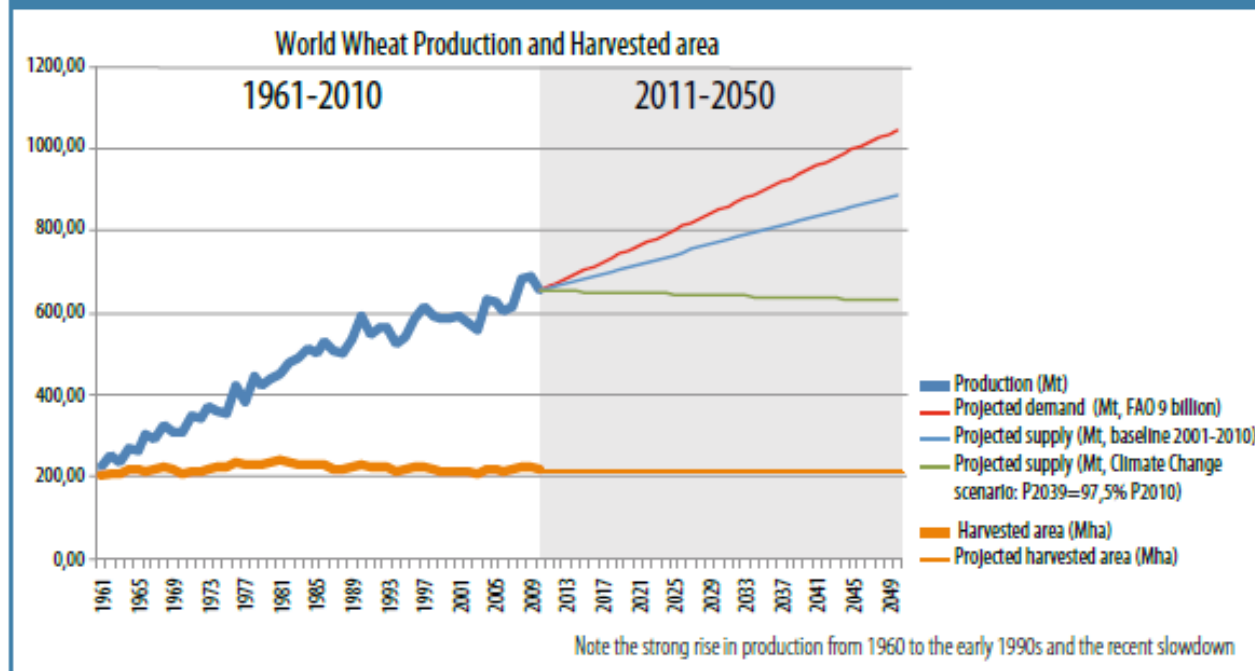
Financing for Development Office
Department of Economic and Social Affairs
United Nations

World population projected to reach 9.8 billion in 2050, and 11.2 billion in 2100

21 June 2017, New York

The current world population of 7.6 billion is expected to reach 8.6 billion in 2030, 9.8 billion in 2050 and 11.2 billion in 2100, according to a new United Nations report being launched today. With roughly 83 million.

Figure 1. Total wheat production and area harvested since 1960 (FAOSTAT 2012) and 2010-2050 projections.



Wheat Initiative (Vision paper)

Drought

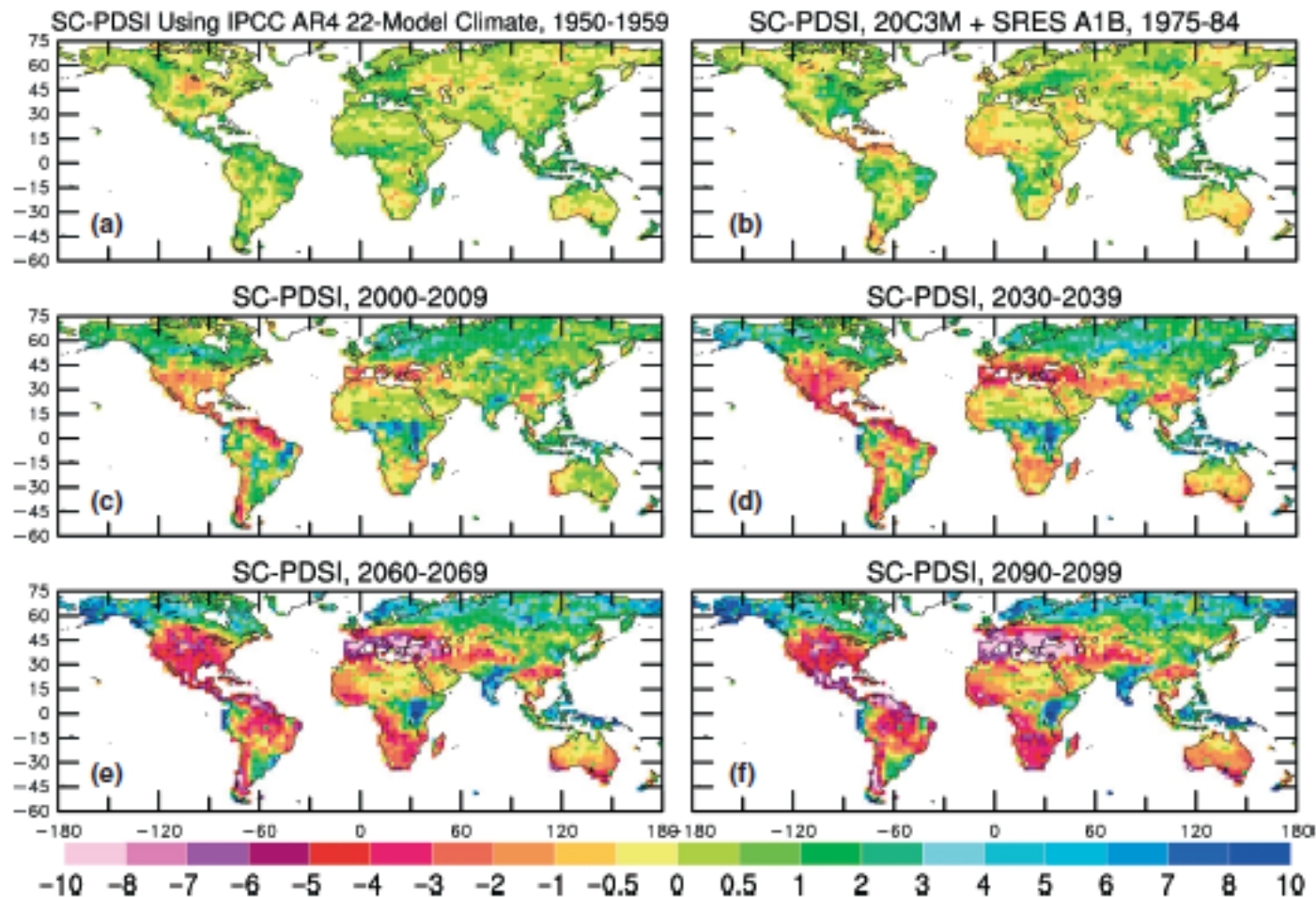
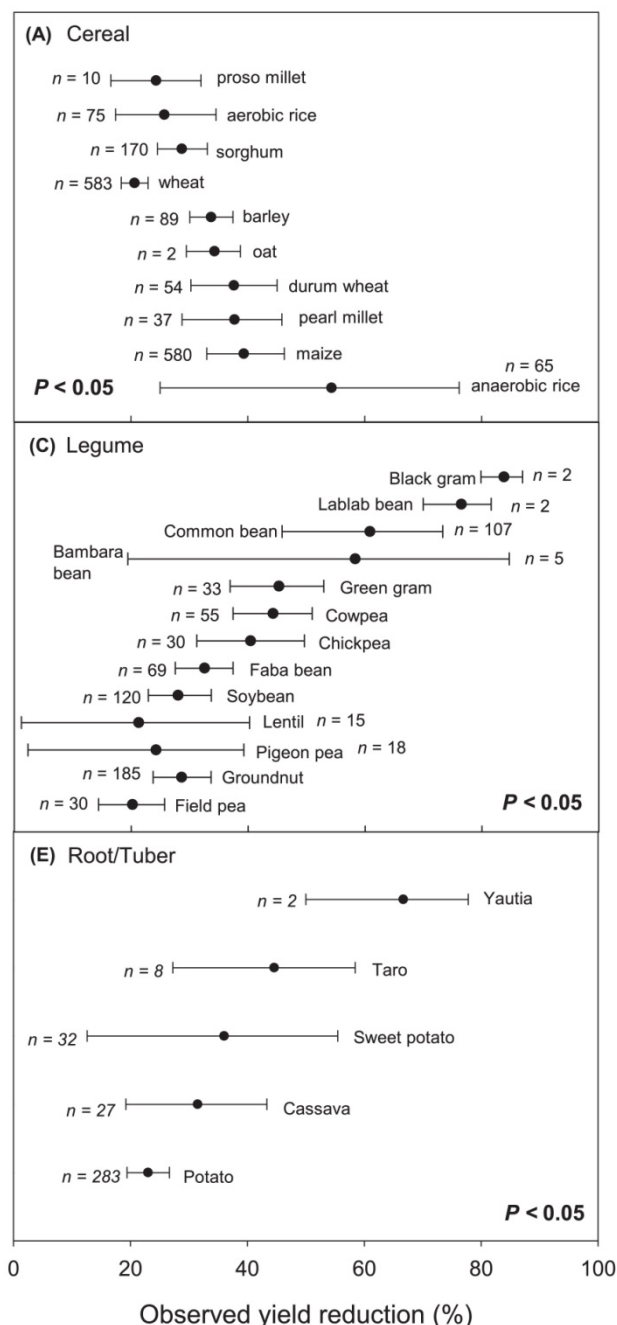


FIGURE 11 | (Corrected version) Mean annual sc-PDSI pm for years (a) 1950–1959, (b) 1975–1984, (c) 2000–2009, (d) 2030–2039, (e) 2060–2069, and (f) 2090–2099 calculated using the 22-model ensemble-mean surface air temperature, precipitation, humidity, net radiation, and wind speed used in the IPCC AR4 from the 20th century and SRES A1B 21st century simulations. Red to pink areas are extremely dry (severe drought) conditions while blue colors indicate wet areas relative to the 1950–1979 mean.

Dai, A. (2010) Drought under global warming: a review. Wiley Advanced Review 2, 45-66

Global yield reduction due to drought



Institute for Resistance Research and Stress Tolerance

Agricultural Water Management 179 (2017) 18–33



Contents lists available at ScienceDirect
Agricultural Water Management
 journal homepage: www.elsevier.com/locate/agwat



Global synthesis of drought effects on cereal, legume, tuber and root crops production: A review

Stefani Daryanto, Lixin Wang*, Pierre-André Jacinthe

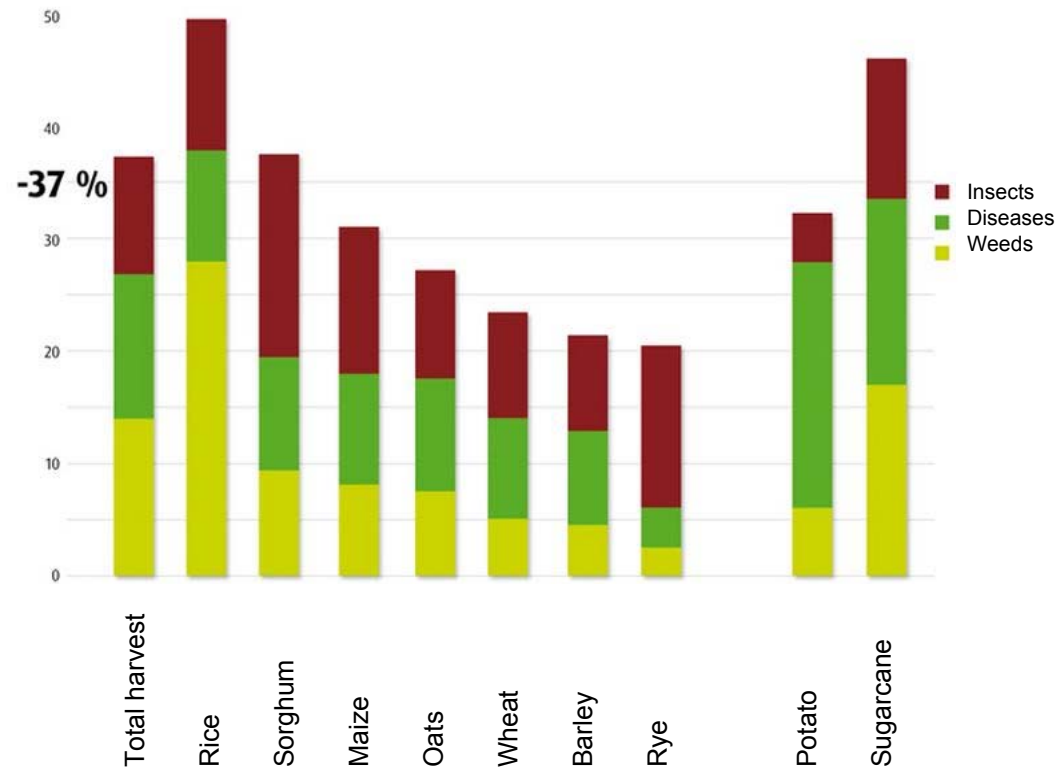
Department of Earth Sciences, Indiana University-Purdue University Indianapolis (IUPUI), Indianapolis, IN 46202, USA



Database for this study:

- peer-reviewed journal articles from 1980 to 2015
 - field conditions, drought ~40% water deficit
- 1674 data points from 228 studies worldwide

Average yield losses due to biotic stress



Wheat (2012)
~140 million t
~\$ 35 billion

FAOSTAT 2014

<http://www.transgen.de/pflanzenforschung/pflanzengesundheit/>

Challenges



Harnessing genetic diversity as a prerequisite for breeding for resistance to biotic stress and abiotic stress is of prime importance to:

- avoid yield losses
- to ensure a consumer and environmental friendly production
- to cope with the loss of insecticides and fungicides due to regulations
- to feed the earth's growing population



Reaping the benefits

Science and the sustainable intensification
of global agriculture

October 2009



The Royal Society

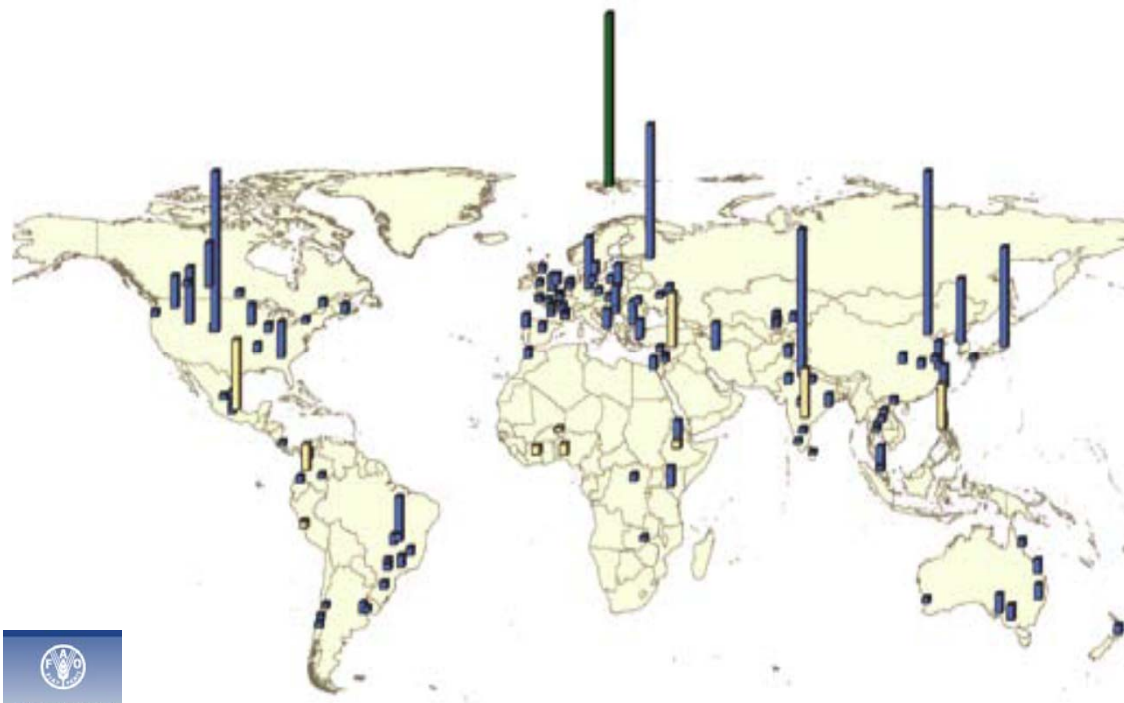
2. UK research funders should support public sector crop breeding and genomics programmes to understand, preserve and enhance the germplasm of priority crops and train the next generation of plant breeders. International programmes in collaboration with Consultative Group on International Agricultural Research (CGIAR) centres and others in Africa and India should include millet, sorghum and rice. The top UK priority should be wheat, followed by barley, oil seed rape, potato, vegetable brassicas and other horticultural crops. Public sector support for breeding needs to emphasise longer term strategic approaches than can be expected from the private sector and develop traits from public sector research.
3. RCUK should increase support for ecosystem-based approaches, agronomy and the related sciences that underpin improved crop and soil management.
4. RCUK, and BBSRC in particular, should support long-term high-risk approaches to high-return targets in genetic improvement of crops. These targets include GM crops with improved photosynthetic efficiency or nitrogen fixation. High risk approaches might also produce GM or conventionally bred crops with reduced environmental impact because they need lower fertiliser input or could be grown as perennials. Research into conventional breeding and GM approaches to increased yield and resistance to stress and disease should also continue to be funded.

Genetic Resources

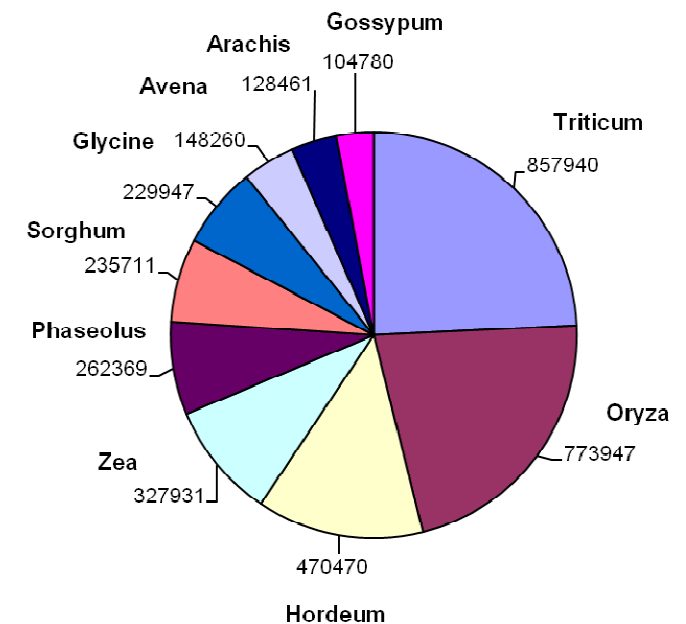


1.750 genbanks worldwide, 7.4 million accessions

130 genbanks hosting more than 10.000 accessions



Institute for Resistance Research and Stress Tolerance



**10 species = 3,540,000 accessions
~ 50% of the ex situ resources**

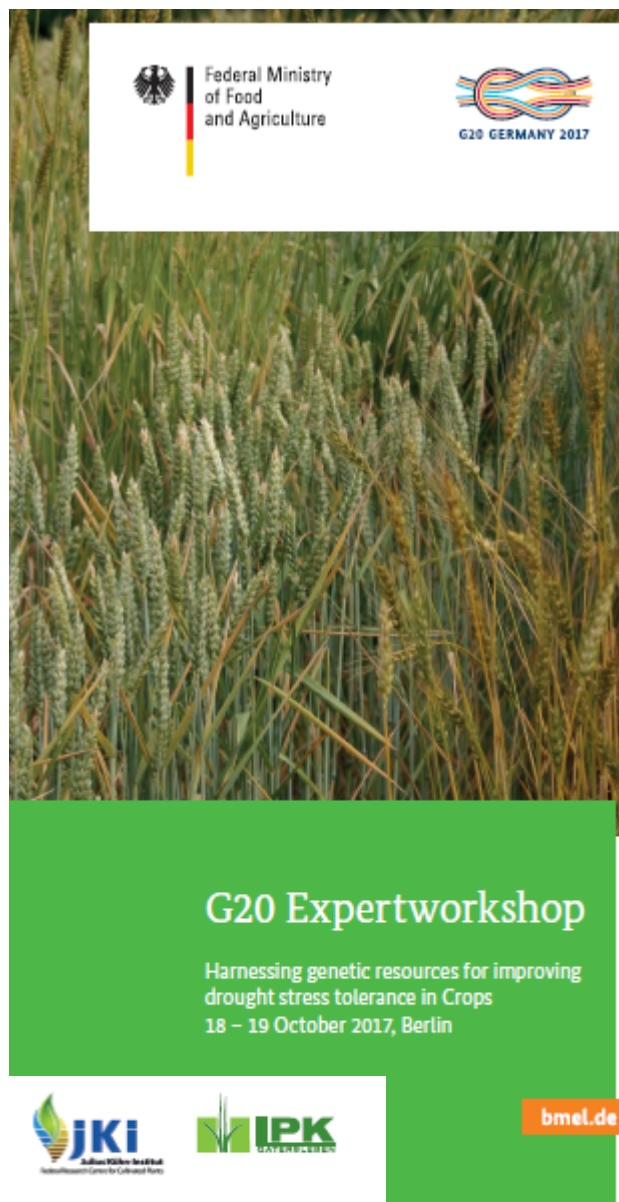
A. Graner


Informed access to genetic resources




Phenotypic Information

Genotypic Information




 Federal Ministry
of Food
and Agriculture


G20 GERMANY 2017

G20 Expertworkshop

Harnessing genetic resources for improving
drought stress tolerance in Crops
18 – 19 October 2017, Berlin

 **JKI**
Julius Kühn-Institut
Bundesforschungszentrum für Ernährung, Landwirtschaft und Umwelt

 **IPK**
GATENSHAGEN

 bmel.de



Questions to be answered:

- What is the current state of the genome analysis of gene bank collections regarding the main crops, what will happen in future in this regard?
- What protocols and platforms for a reliable assessment of agronomical important traits exist or need to be developed, and what are the requirements these must fulfill?
- How can an effective preliminary selection of gene bank accessions for phenotyping be made?
- How should the resulting data be stored and made accessible for science and breeding?
- What structures are necessary to achieve this objective?



HeDWIC Heat and Drought
Wheat Improvement
A Funding Proposal Consortium

Genomic prediction contributing to a promising global strategy to turbocharge gene banks

Xiaoping Yu, Xianran Li, Tingting Guo, Chengsong Zhu, Yuyue Wu, Sharon E. Mitchell, Kraig L. Rozeboom, Donghai Wang, Ming Li Wang, Gary A. Pederson, Tesfaye T. Tesse, Patrick S. Schnable, Rex Bernardo & Jianming Yu

Journal of Integrative Bioinformatics, 4(1):88, 2007

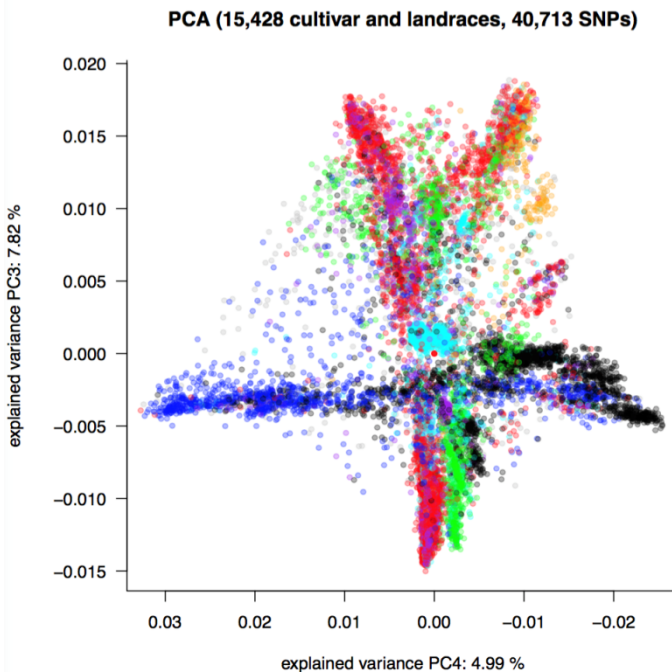
<http://journal.imbio.de>

Using Data Warehouse Technology in Crop Plant Bioinformatics

Christian Kuenne, Ivo Grosse, Inge Matthies, Uwe Scholz, Tatjana Sretenovic-Rajcic, Nils Stein, Andreas Stephanik, Burkhard Steuernagel and Stephan Weise*



Genotyping



N. Stein

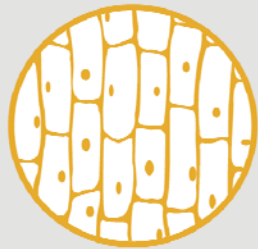
Genotyping by sequencing Chip technologies Imputation



- Genotyping/sequencing of gene bank collections and breeding populations is technically, economically and politically feasible
- Sequencing has begun, but efforts are sporadic, species-specific and lack coordination
- A well-coordinated, international effort would enhance efficiency, quality, & increase potential for data integration and biological insight, document plant /microbial biodiversity, and help address the grand global challenges we face

S. McCouch (Divseek chair)

Phenotyping



CELL

Microphenomics

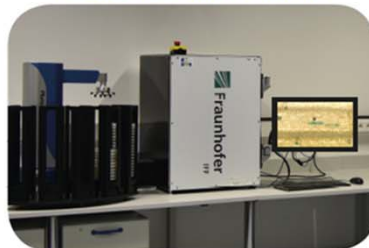


Phenobot



ORGAN

Macrophenomics

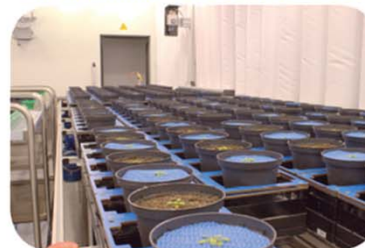


TD-NMR



ORGANISM

Phytochamber & Greenhouse



Plant Cultivation Hall

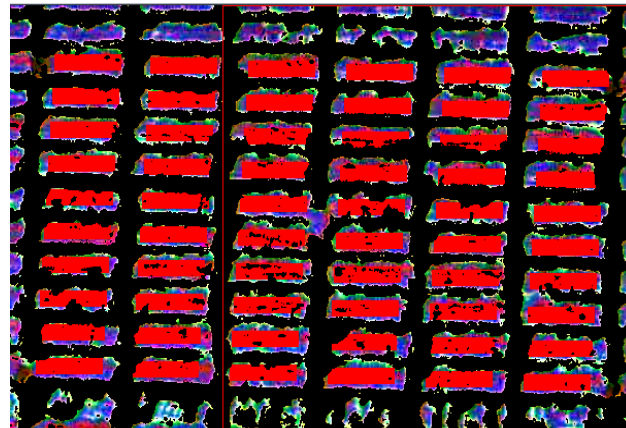


POPULATION

Field



Phenotyping for drought tolerance



M. Reynolds

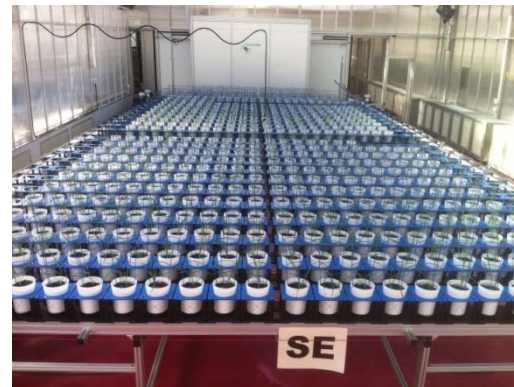
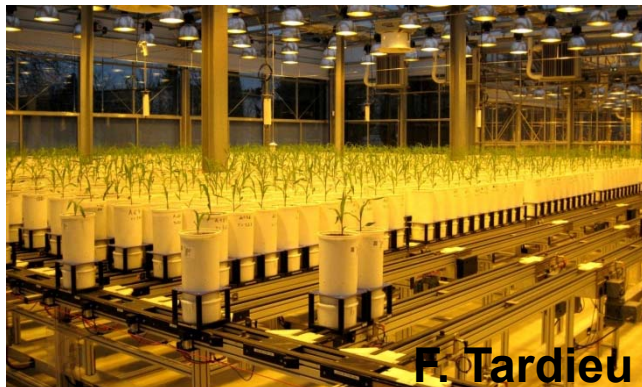
Tattaris M, Reynolds MP, Chapman SC, 2016. A direct comparison of remote sensing approaches for high-throughput phenotyping in plant breeding. *Front. Plant Sci.* 7: 1131.

Genomic prediction + quantitative relationships with environment.

$$\text{Yield}_{ij} = \text{geno}_i + \sum (\alpha_j \text{light}_i + \beta_j T_i + \delta_j \Psi_{\text{soil } i}) + \varepsilon_{ij}$$



F. Tardieu

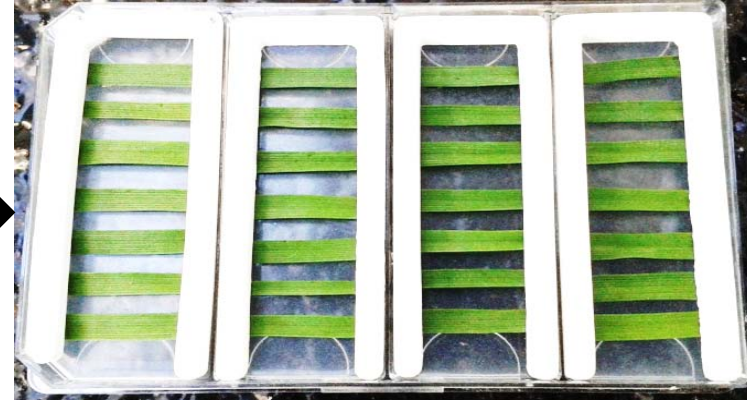


M. Tester

Phenotyping using highthroughput technologies: Macrobot



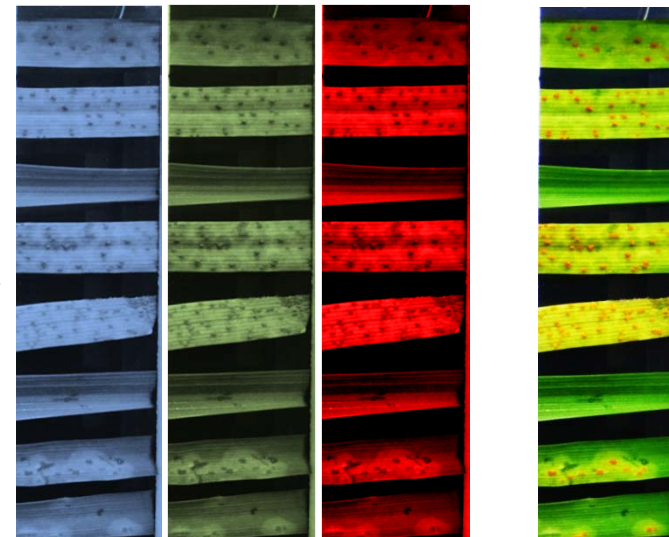
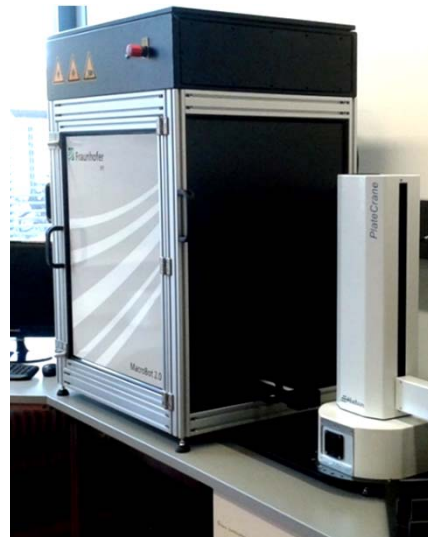
Preparation of seedlings



Detached leaves inoculated by settling tower



Highthroughput analysis of of 3200 detached leaves per day

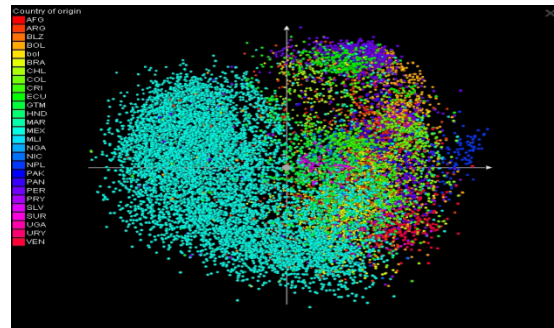


Infected area per leaf detected automatically

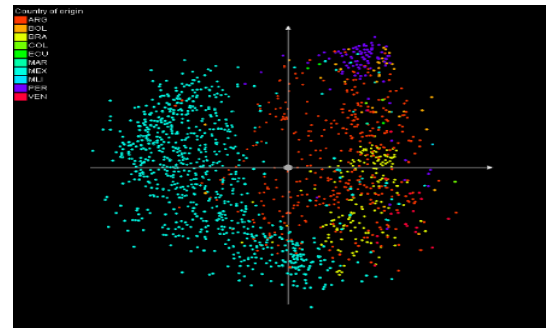
Infected leaf area (%)

7%
18.5%
0%
20%
25%
0%
5%
3%
0%

Pre-selection of accessions for phenotyping



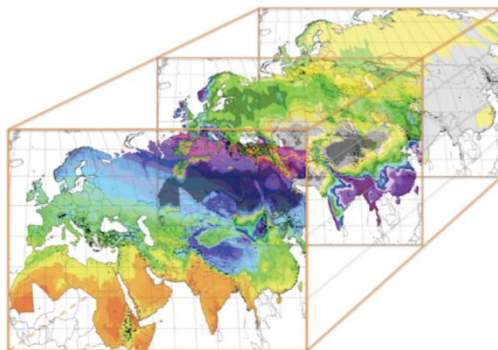
15,384 landraces



1,549 landraces from
drought prone
environments

H. Braun

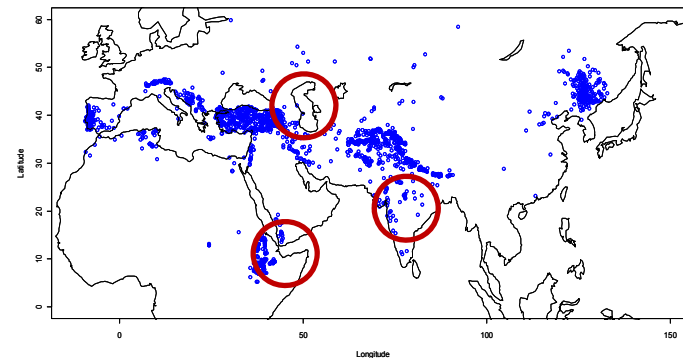
Focused Identification of Germplasm Strategy (FIGS)



Environnement



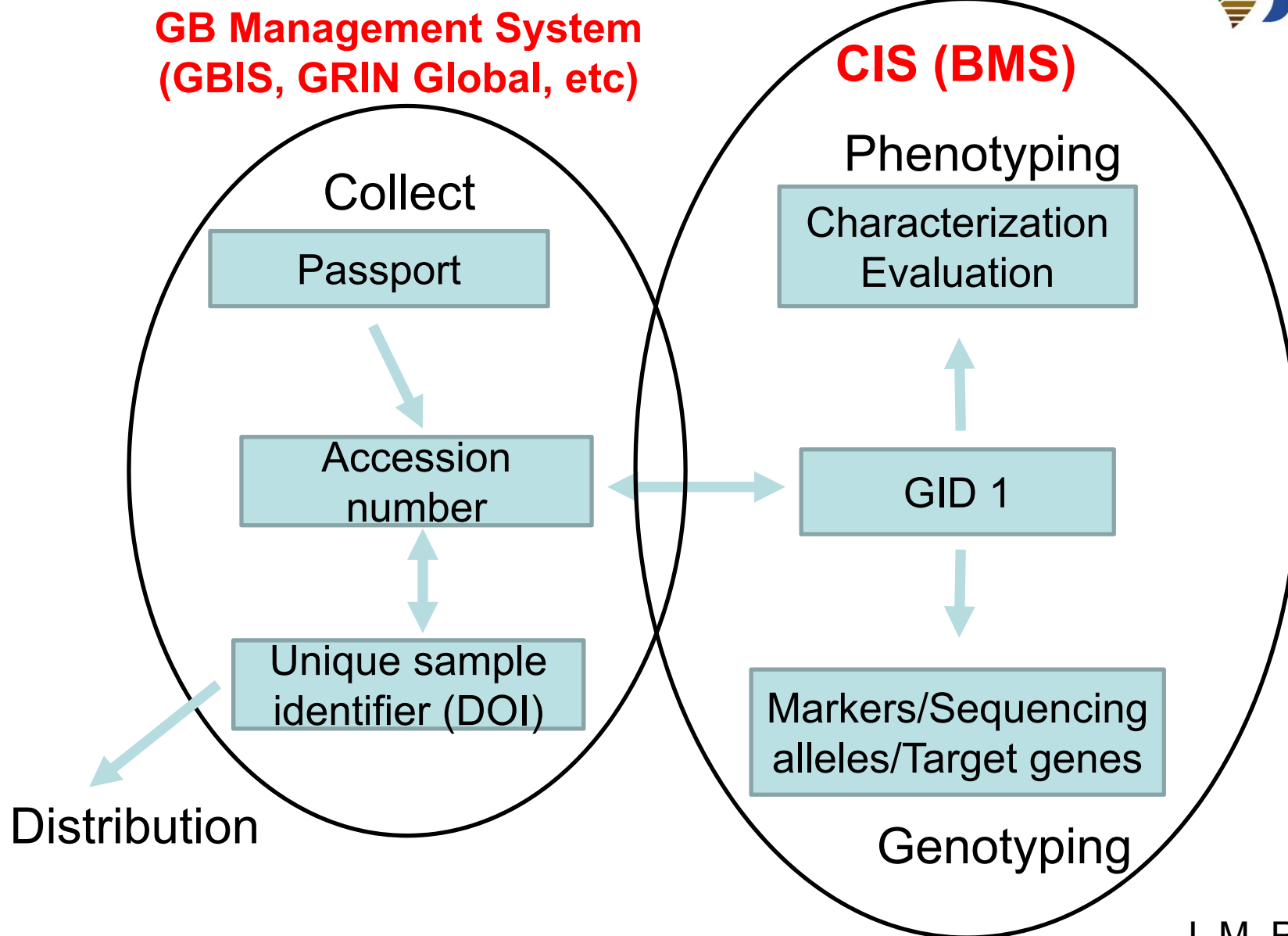
www.icarda.org/
Trait (disease score)



FIGS subset

M. Baum

Data storage and management



Example



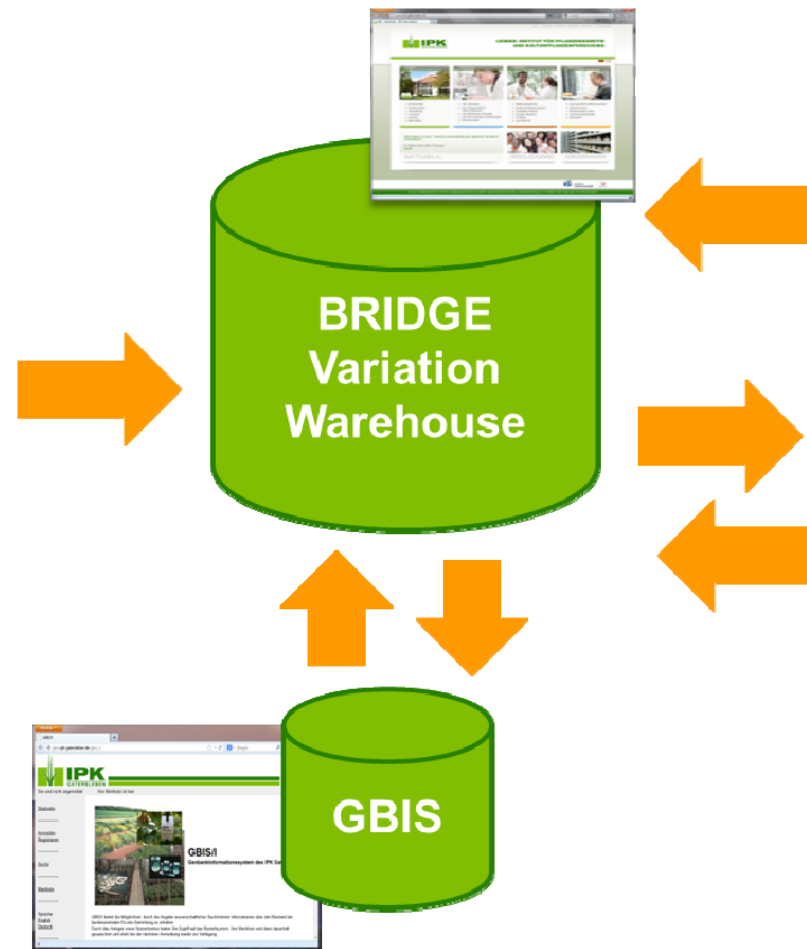
BRIDGE: Biodiversity infoRmatics to close the gap from genome Information to educated utilization of Diversity hosted in GEnebanks

Primary data analysis



Field based phenotyping

BRIDGE Web Portal



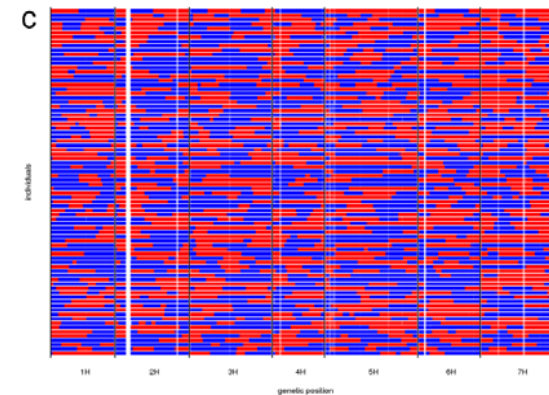
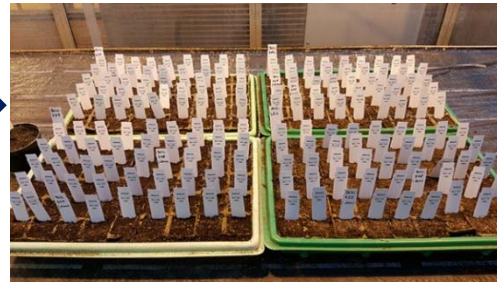
- Interactive haplotype browser
- Comparison to existing marker data to guide pre-breeding

Interfaces to other systems

- EURISCO
- EDBD
- transPLANT
- de.NBI
- SeedSeq
- Digital Seed Bank
- GENESYS

Example

BRIDGE project: GBS of >20,000 barley accs.



- + WGS / exome capture of selected accessions
- + historic evaluation data (morphologic and agronomic)
- + passport and geo-reference information
- + ear- and seed phenotyping at harvest

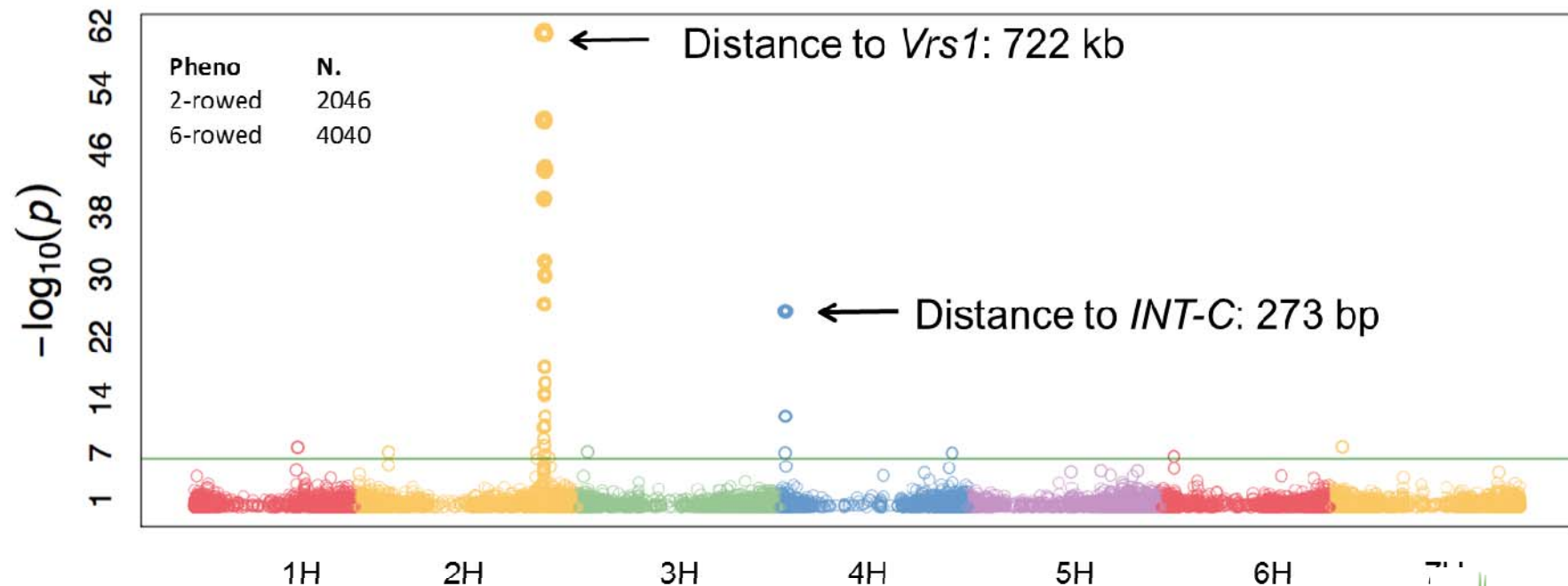
Example



GWAS for row-type

Genotypes: SNPs with a MAF $\geq 1\%$ (19,507 SNPs).

Software: GAPIT R package (Lipka et al. 2012), using a mixed linear model, kinship, PC1/2 as covariants



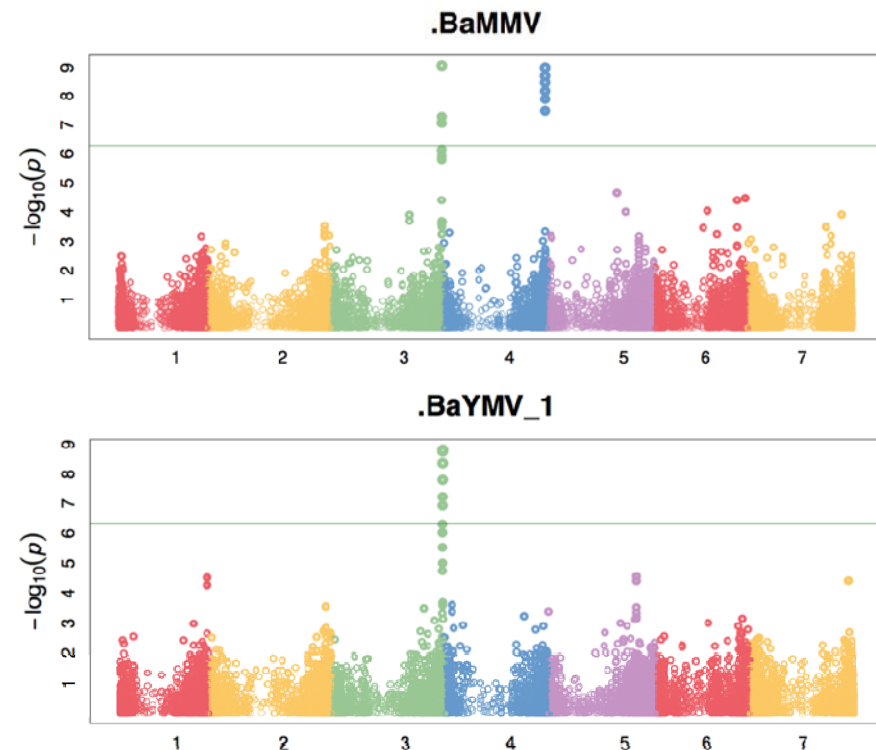
Example



GWAS for soil-borne virus resistance



1894 accessions tested
unpubl. data, collaboration with JKI QLB, Ordon+Habekuss



Harnessing of genetic diversity



BRIDGE
Genebank 2.0



Seeds of discovery



Canada: International hub
U.K.: National hub

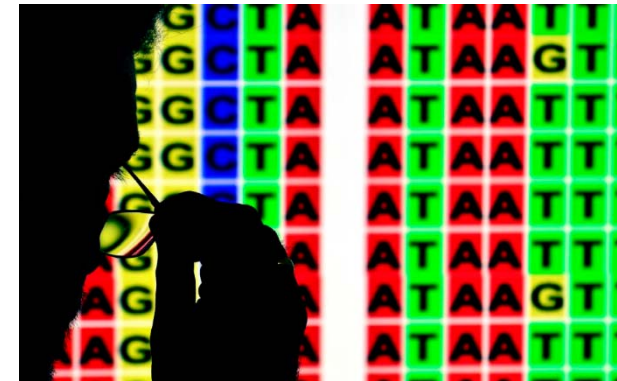
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68 partners (<http://www.divseek.org/partners/>)

Institute for Resistance Research and Stress Tolerance

Diversity Seek (DivSeek)

- A global, **community-driven** initiative to harness the genetic potential of crop diversity using science and technology
- Facilitate **networking** of like-minded, independent projects
- **Add value** to individual efforts around the globe



Global Challenges Require Global Solutions

- Sequencing efforts are underway, but they are fragmented, largely community-specific and lack coordination
- A well-coordinated, international effort would enhance efficiency, quality, & potential for data integration and biological insight
- Need to raise awareness of current policy issues related to PGR (e.g. framework for access and benefit sharing), promote inclusion of **scientific evidence** into **policy discussions** at the global level
- Big data approaches => characterize and model biodiversity (genotypic, phenotypic, environmental) - - key to sustainably intensifying food production
- Standards needed to facilitate data generation, management, annotation/ curation, sharing, integration
- Critically important to link digital information about genotype and phenotype (morphological, physiological, molecular- 'omics') to seed stocks and genetic resources

Knowledge Sharing

DivSeek has established Working Groups to actively engage DivSeek Partners in addressing issues of common interest:

1. Data Standards for Interoperable Tools, FAIR Data
2. Genbank Information Management System(s) linking Digital Sequence Information to physical Plant Genetic Resources (PGR)
3. Phenotyping to characterize diversity of PGR
4. Genotyping to characterize diversity of PGR
5. Semantics for Harmonizing Trait and Agronomic Data
6. Translational Approaches for Minor and Underutilized Crops

Recent developments /Next Steps

- Prof Susan Mc Couch, Cornell University, re-elected as Chair
- Global Institute for Food Security approves funding for International Network Co-ordination centre in Saskatoon, Canada
- Discussions initiated by national research bodies in US, Canada, Germany and UK- others welcome
- Establish a network to link national nodes of expertise and exemplar projects.

How can MACS help?

- Promote awareness of the huge unrealized potential of global gene banks to help tackle grand challenges e.g. climate change, food and nutritional security.
- Encourage and support national community efforts to establish country nodes to fully characterise collections-starting in areas of strength and interest
- Support the concept of a network to link national nodes and encourage co design, sharing of best practice, development of new tools
- Consider the establishment of a MACS Global Research Collaboration Priority – more detailed proposal in 2019

The Wheat Initiative

History

- Created in 2011 following endorsement by G20 Agriculture Ministries to improve food security
- Launched on the 15th September 2011 in Paris



16 Countries, 7 Breeding companies, 2 international Centres



Conclusions



- Genotyping of large gene bank collections is technically feasible
- Genotypic data, in combination with geographic and other information, can be used to pre-select genotypes for detailed phenotypic analysis
- Phenotypic analysis for simple and complex traits is feasible
- Data storage and information systems are available
- Consequently, it is now practicable to efficiently harness genetic resources for breeding crops suited to face the challenges of the future

But international collaboration and co-ordination is now needed to achieve these goals

A first step in this direction is Divseek

Institute for Resistance Research and Stress Tolerance