



Une initiative sur le riz dans un cadre international autour du GCRAI

JC Glaszmann, Cirad, Agap, Montpellier

IRRI

3000 Rice Genomes: The First Step to a Digital Rice Genebank

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IRRI



Rice
Science
for a Better
World



COLLEGE OF AGRICULTURE & LIFE SCIENCES
ARIZONA GENOMICS
INSTITUTE



De nouveaux regards sur la diversité du génome du riz (*Oryza sativa* L.)

Jean Christophe Glaszmann

Visite de l'Académie d'Agriculture de France

Mercredi 6 juin 2018 - Montpellier

« Des avancées sur les recherches en biologie et génétique
au service de la riziculture »

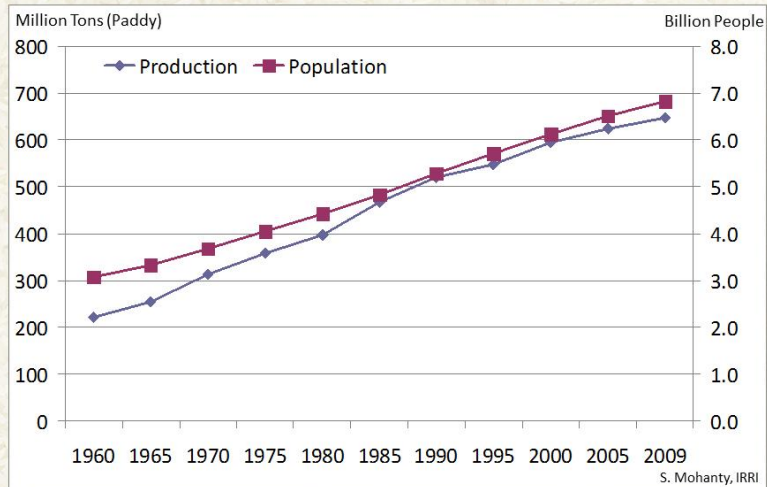


Genetic improvement and adaptation
of mediterranean and tropical plants





Global rice production vs. population



IRGC – the International Rice Genebank Collection

World's largest collection of rice germplasm held in trust for the world community and source countries



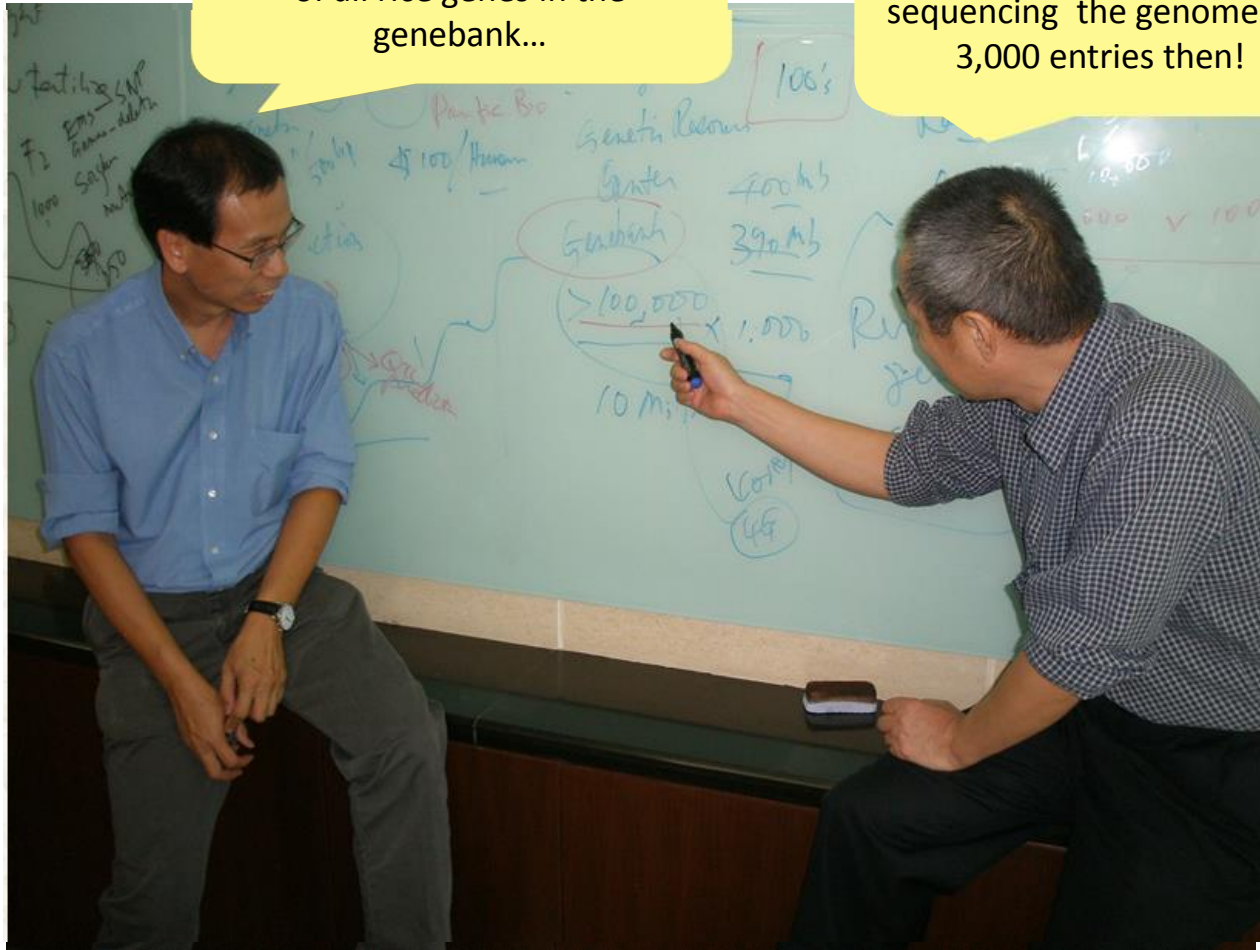
- Over 137,000 registered and incoming accessions from 117 source countries
- Two cultivated species
 - Oryza sativa*
 - Oryza glaberrima*
- 25 (or 26) wild species depending on the taxonomic treatment
- BUT, relatively few accessions (**5% of collection**) used to donate alleles to current, high-yielding varieties

<http://irri.org/our-work/seeds>

3000 Rice Genomes

We need to know the variation
of all rice genes in the
genebank...

Agreed! Let's start with sequencing the genomes of 3,000 entries then!



Hei Leung (IRRI) and Wang Jian (BGI) Shenzhen, October 2010

The rice 3K project is funded by the Bill & Melinda Gates Foundation through the Green Super Rice Phase 2 project, the Chinese Ministry of Science and Technology and the Shenzhen local government.

3K Rice genomes project: applying diversity



IRG Traditional Germplasm 100,000 cultivated accessions



3 to 10% sampling



Apply low-cost NGS technology (12-14X depth)



Reveal functional diversity

Phenotype
Phenotype
Phenotype

+

GWAS

Network analysis
Machine Learning



3000 Rice Genomes Consortium



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华大基因
BGI



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cirad
AGRICULTURAL RESEARCH FOR DEVELOPMENT



BILL & MELINDA GATES foundation



MOST: 科学技术部



Research Program on Rice
Global Rice Science Partnership



Donors:

Top

Abstract

Data description...

Availability and requirements

Discussion

Availability ...

The 3,000 rice...

Abbreviations

Competing interests

Authors' contributions

Acknowledgements

References

Data Note

Highly accessed

Open Access

The 3,000 rice genomes project

The 3,000 rice genomes project[†]

Correspondence: The 3,000 rice genomes project

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GigaScience 2014, 3:7 doi:10.1186/2047-217X-3-7

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Data note, Commentary and Dataset
Released on World Hunger Day (May 28, 2014)nature
International journal of science

Article | OPEN | Published: 25 April 2018

Genomic variation in 3,010 diverse accessions of Asian cultivated rice

Wensheng Wang, Ramil Mauleon, Zhiqiang Hu, Dmytro Chebotarov, Shuaishuai Tai, Zhichao Wu, Min Li, Tianqing Zheng, Roven Rommel Fuentes, Fan Zhang, Locedie Mansueto, Dario Copetti, Millicent Sanciangco, Kevin Christian Palis, Jianlong Xu, Chen Sun, Binying Fu, Hongliang Zhang, Yongming Gao, Xiuqin Zhao, Fei Shen, Xiao Cui, Hong Yu, Zichao Li, Miaolin Chen, Jeffrey Detras, Yongli Zhou, Xinyuan Zhang, Yue Zhao, Dave Kudrna, Chunchao Wang, Rui Li, Ben Jia, Jinyuan Lu, Xianchang He, Zhaotong Dong, Jiabao Xu, Yanhong Li, Miao Wang, Jianxin Shi, Jing Li, Dabing Zhang, Seunghee Lee, Wushu Hu, Alexander Poliakov, Inna Dubchak, Victor Jun Ulat, Frances Nikki Borja, John Robert Mendoza, Jauhar Ali, Jing Li, Qiang Gao, Yongchao Niu, Zhen Yue, Ma. Elizabeth B. Naredo, Jayson Talag, Xueqiang Wang, Jinjie Li, Xiaodong Fang, Ye Yin, Jean-Christophe Glaszmann, Jianwei Zhang, Jiayang Li, Ruairadh Sackville Hamilton, Rod A. Wing ✉, Jue Ruan ✉, Gengyun Zhang ✉, Chaochun Wei ✉, Nickolai Alexandrov ✉, Kenneth L. McNally ✉, Zhikang Li ✉ & Hei Leung ✉ - Show fewer authors

Nature 557, 43–49 (2018) | Download Citation ↓

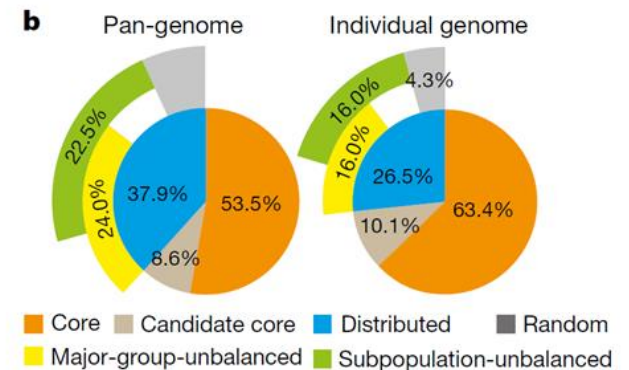
<https://doi.org/10.1038/s41586-018-0063-9> (Open)Indica → Xian ‘籼’
Japonica → Geng ‘粳’

Institute of Crop Sciences, CAAS;
International Rice Research Institute;
Life Sciences and Biotechnology,
Shanghai Jiao Tong University;
BGI Genomics, BGI-Shenzhen;
Agricultural Genomics Institute at
Shenzhen, CAAS;
Shenzhen Institute for Innovative
Breeding, CAAS;
Anhui Agricultural University;
Arizona Genomics Institute;
China Agricultural University, Beijing;
Institute of Genetics and
Developmental Biology, CAS;
DOE Joint Genome Institute;
Lawrence Berkeley National Laboratory
ASTI-DOST, Philippines;
Cirad, UMR Agap;
University of Montpellier, UMR Agap;
Shanghai Center for Bioinformation
Technology

Online on April 25, 2018
<DNA Day!>

Major Findings

- Identified 27 million single nucleotide polymorphisms (SNPs), 2.4 million small insertion-deletions, and 90,000 genomic structural variations (SVs) that all contribute to within and between population variation
- SNPs, SVs and gene presence-absence variations (PAVs) defined population structure and identified previously unreported subpopulations with clear geographic origins
- Nucleotide diversity was significantly reduced near agronomically important genes
- Pan-genome analysis revealed more than 10,000 novel full-length protein-coding genes
- Complex patterns of introgression at domestication genes are consistent with multiple modes of rice domestication



Sur les quelque 24000 familles de gènes connues chez le riz, seulement 60% sont communes à toutes les variétés; les autres sont présentes, ou absentes, selon les variétés

Activated, rapid-response genetic resources

- Reveal functional diversity of GeneBank genomes and their phenotypes
- Sequenced breeding populations with predictive power for genotype to phenotype (G2P) relationships
 - e.g., MAGICs, NAMs, RILs, BILs
- Elite gene pools that can be readily evaluated for new traits

Modernized Phenotyping: *Scope and scale*

- Multiple levels
 - molecular, cellular, tissue, whole-plant
- Developmental Stages
- Different environments and managements
 - Laboratory
 - Controlled conditions
 - Managed field
 - Farmer's field
- Capture phenotypes over time
- Non-destructive (if possible)
- High-throughput, automated

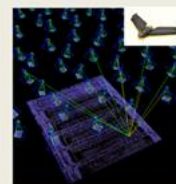
$G \times E_t \times D_t \times M_t$

HTP Field Phenotyping

Autonomous flight
5 min/ha at 1 cm pixel resolution
1-5 cm spatial accuracy
1 hour/ha processing time on desktop PC

Plot size: 1-4' m²
Entries: 100-1500
Area: 1-10 ha

TRAITS
canopy cover
canopy height
days to flowering/maturity
biomass
greenness/nitrogen
lodging
canopy temperature (drought, biomass)
temporal modeling (growth, biotic & abiotic stress)



3D Point Cloud



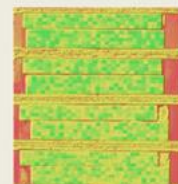
RGB



Hand launch



Thermal



Multispectral Reflectance

Automated image processing produces dense 3D model and high resolution geo-referenced ortho-mosaics used for plot level data analysis. Showing ortho images of 900 Magic Indica entries planted in augmented design with 1080 plots in 1 ha field.

Credit: Steve Klassen

International Rice Informatics Consortium



<http://iric.irri.org>



1. Organize available information about rice into a consistent and reliable source of knowledge
2. Provide user-friendly portal to browse, search and analyze the data
3. Support information sharing and facilitate collaborations

snp-seek.irri.org

Rice SNP-Seek Database

Home Search Browse My Lists Order Seeds Download Help

By using SNP-Seek, you abide by the data use license stated [here](#)

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 Genebank Collection Information System (IRGCIS). 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.



Genotypes
Query for SNPs from the 3000 genome project



Varieties
Query for Variety passport and phenotypes



JBrowse
Rice Genome Browser



GWAS
GWAS Results and tools



Help
Help and documentation

How to cite:

- Mansueto, et al. **Rice SNP-seek database update: new SNPs, indels, and queries.** *Nucl. Acids Res.* (2017) 45 (D1): D1075-D1081. doi: [10.1093/nar/gkw1135](https://doi.org/10.1093/nar/gkw1135) This paper describes new features and datasets added to SNP-Seek in 2015-2017 as well as software and database updates.

- [Other publications >>](#)

SNP-Seek is the largest plant SNP database

<http://snp-seek.irri.org>

Accessed >150,000 times by >12,000 users

Steps to a Digital Rice Genebank

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Digital Rice Genebank: Second Step

- Proposed by Prof. Sanwen Huang, DG of the Agricultural Genomics Institute at Shenzhen (AGIS)
- Sequence 10,000 more accessions of cultivated and wild rice
 - 6,000 from IRRI genebank
 - 4,000 from provincial collections
- Collaboration with AGIS, CAAS, IRRI-CAAS Joint Lab at AGIS, Jiangsu AAS, Guangdong AAS, Guangxi AAS, and Yunnan AAS
- ~1000 genomes completed or underway
- Seeking funds for remainder

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Digital Rice Genebank: Third Step

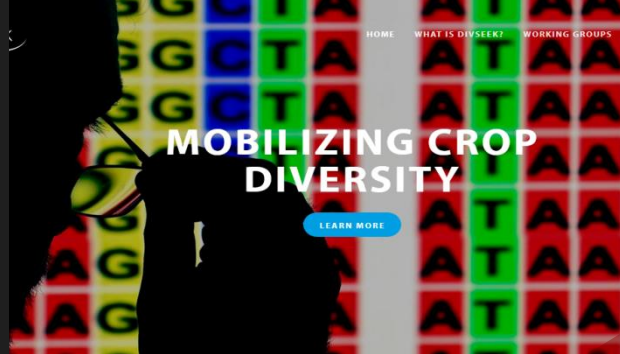
- 1) Generate PSRefSeqs that represent the 15 subpopulations of cultivate Asian rice
- 2) Resequence ~20,000 rice accessions at 20-40X coverage
- 3) Detect all SNP & Structural variation relative to all 15 PSRefSeqs to create a pan-haplotype map of cultivated Asian rice
- 4) Resequence remaining collection of ~100,000 accessions at <1X coverage
- 5) Impute SNP and Structural variation across IRRI's entire Genebank to create a *Digital Genebank for Cultivated Rice*
- 6) Generate omics datasets (transcriptomic, proteomic, metabolomic, ...) on PSrefSeqs and selected representatives with high-depth resequencing data
- 7) In parallel – Generate a 15-way Multi-parent Advanced Generation Intercrosses (MAGIC) and other populations
- 8) Phenotype populations using the *Global Rice Array*



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DivSeek is a community driven effort consisting of a diverse set of partner organizations that have voluntarily come together to unlock the potential of crop diversity so that it can be utilized to enhance the productivity, sustainability and resilience of crops and agricultural systems.

DivSeek will work with partners and other researchers and organizations to develop and share methodologies, open-sources software tools, and best practices to facilitate the generation, integration, and sharing of data and information related to plant genetic resources (PGR).

By creating a community of practice and making it possible to track and share information about PGR, DivSeek aims to empower gene bank managers, breeders, researchers and farmers to better characterize, disseminate and utilize plant genetic variation for accelerated crop improvement, strategic research, and sustainable production of food and agricultural products around the world.

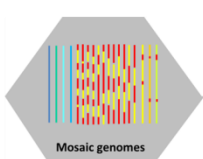
To help achieve its mission DivSeek has established a number of **working groups** to actively engage partners and assist them in addressing issues of importance to the DivSeek Community. The DivSeek Working Groups are proposed and established by DivSeek Partners and function as the key mechanism for DivSeek to advance its goals.

- 1 - Data Standards for Interoperable Tools
- 2 - Genebank Information Management System
- 3 - Genomics for Genebanks
- 4 - Phenotyping for Seed Diversity
- 5 - Semantics for Harmonizing Trait and Agronomic Data
- 6 - Translational Approaches for Minor and Underutilized Crops
- 7 - FAIR Data

DivSeek, une initiative de la recherche publique
68 membres (dont INRA et Cirad), un comité de pilotage
des groupes de travail
68 membres (dont INRA et Cirad) ... très très peu du Sud
→ intégrer des institutions de tous les pays
→ partager les capacités de valoriser les données

agropolis fondation

GenomeHarvest

Mobilizing biomathematics/bioinformatics and genomics/genetics to decipher genome organization and dynamics as pathways to crop improvement

Mobilisation de la recherche sur l'analyse de données

WP1 - Management - Federate the community around research actions

Methods to characterize genome architecture of crops derived from multiple founder (sub)species

→ mosaic genome structure within crops genome

WP2 → fine structure variations within crops genome

Methods to analyze the impact of genome architecture

→ on chromosome recombination/segregation

→ on allele (gene) expression

WP3

WP4 - Implement tools in platform - Capacity building/Training - Scientific event



CultiVar Training in plant breeding

agropolis fondation

INVESTISSEMENTS D'AVENIR

Les 3000 génomes du riz

Une introduction à la diversité génétique

JC Glaszmann, C Billot, G Droc, JP Jacquemoud-Collet, Cirad (agap), équipes COSE et ID




Formation des étudiants du Nord et du Sud

agap

Université de Montpellier

CultiVar Training in plant breeding

About CultiVar | CultiVar and you | Pedagogical material

Pedagogical material > Material list > Genome editing issues

Genome editing in agriculture: engaging in policy, legal and institutional issues

Genome editing tools allow direct modification of plant genomes more quickly, cheaply and accurately than ever before. It is a technological innovation with long term implications. The tools are changing the practices of using and exchanging biological material in plant science including the way breeding is conducted. The emergence of such a technology raises a series of social, institutional, legal and policy issues.

Whether you are a biologist or a geneticist, or a social scientist, this thematic session will help you better grasp the various social dimensions of genome editing.

- What are regulatory considerations for products derived from these technologies?
- What are the practical impacts on legal cooperation, such as intellectual property, access and benefit sharing?
- What are the implications of genome editing on sustainable agriculture?

It is organized in collaboration with the Secretariat of the International Treaty on Plant Genetic Resources for Food and Agriculture and the UNESCO Chair in World Food Systems.

Food and Agriculture Organization of the United Nations

The International Treaty on Plant Genetic Resources for Food and Agriculture

UNESCO Chair in World Food Systems

Formations et réflexions de recherche sur les technologies et les cadres d'utilisation



Innovation et amélioration variétale en Afrique de l'Ouest

Dispositif de recherche et d'enseignement en Partenariat

Dispositifs partenariaux impliquant la recherche, l'enseignement supérieur, les organisations paysannes du Sud

iaavao

Innovation et amélioration variétale en Afrique de l'Ouest

J.-F. Rami - CIRAD

Les 3000⁺ génomes de riz

... Chine et IRRI ...

Initiative emblématique en matière d'analyse de
diversité biologique et adaptative

- diversité: jeu de grands nombres
- biologique: jeu d'intégration
- adaptation: dimension comparative et évolutive

=> Valeur ajoutée maximale de la coopération

- mobilisation
- durabilité

... ssi égalité face aux opportunités