Rice Genome Research

中研院植物所
邢禹依

Academia Sinica Plant Genome Center
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<th>CC</th>
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栽培稻

亚洲型

Oryza sativa

非洲型

Oryza glaberrima

印度型 (秈稻, 在來稻)
Subsp. indica

日本型 (粳稻, 蓬萊稻)
Subsp. japonica
The importance of rice as a crop

- Rice is the world's most consumed staple food grain, i.e. more than 153 million Ha (1999) in 89 countries around the world - or about 10% of the world's arable land.
- Rice is one of the cheapest and most plentiful sources of food energy and protein.
- Rice feeds more people than wheat does.
Rice Production, by Country
(millions of tonnes)
1999

Source: UN Food & Agriculture Organization

Rice Production, by Region of the World
(millions of tonnes - 1999)

Source: UN Food & Agriculture Organization
Projected Rice Demand in Selected Countries – 2000 and 2025

(millions of tonnes)

Source: UN Food & Agriculture Organization
The importance of rice for genetic study

- 3267 genetic markers (RFLP) and 6483 EST markers (PCR based)
- Many insertion mutagenesis projects, e.g. Ac/Ds, T-DNA, Tos17
- Substitution lines available
- Many breeding programs, good germplasm collections
- Genome sequencing data available
## Summary by Organism - February 15, 2002

**Number of public entries: 10,373,216**

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<td>Glycine max (soybean)</td>
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<td>Xenopus laevis (African clawed frog)</td>
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<td>Caenorhabditis elegans (nematode)</td>
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RGP is a joint project of the National Institute of Agrobiological Sciences (NIAS) and the Institute of the Society for Techno-innovation of Agriculture, Forestry and Fisheries (STAFF) and a part of the Japanese Ministry of Agriculture, Forestry and Fisheries (MAFF) Genome Research Program.
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Clemson University Genomics Institute

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  - Physical Mapping | Functional Genomics | Wing Lab |

- Projects
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- Sequencing
  - Rice Genome Sequencing Project |
  - STCs: Rice | Tomato | Cotton | Maize |
  - ESTs: Cotton | Barley |

- Physical Mapping
  - FPCC | Rice | Rice Blast | Sorghum | Maize |

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  South Carolina, USA.
  Tel: (864) 656-4292
  Fax: (864) 656-4293
  Email: cugi@genome.clemson.edu

NEWS

- # Genomic Libraries: 72
- # EST Libraries: 47
- # Plants: 18,115
- # Clones: 6,917,280

August 2001
A Marker-Dense Physical Map of the
Bacillus subtilis Strain Genome
Tomkins et al.
Genome Research 11(6):1434-1440

July 2001
Sequence and Analysis of the
Tomato JOINTLESS Locus
Moo et al.
Plant Physiology 126:1331-1340

May 07, 2001
WebPep for Rice
Also see Maize and Sorghum

February 15, 2001
A Physical Map of the Human Genome
The International Human Genome
Mapping Consortium
Nature 405: 910-913

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Item(s) 1 - 48 of 48

**AM Ba-Library**

_Apis Mellifera_

This honey bee BAC library has an average insert size of 113 Kbp (Genome size: 180Mb) covering 23 genome equivalents. It was constructed in pCUGBAC1 and contains 36,864 clones (96 plates)

**AN_FBa-Library**

*A. nidulans* cv. FGSC04

The A. nidulans BAC library has an average insert size of 90 Kbp (Genome size: 40Mb) covering 30 genome equivalents. It was constructed in pBACWICH and contains 11,504 clones (31 plates)
OSIIBa-Library

Oryza sativa indica cv. IR8
This indica rice BAC library has an average insert size of 120 Kb (Genome size: 430 Mb) covering 17 genome equivalents. It was constructed at CUGI (Wang et al. unpublished). It was constructed in the HindIII site of pIndigoBac536 and contains 55,296 clones (144 plates).

OSIIBb-Library

Oryza sativa indica cv. IR64
This indica rice BAC library has an average insert size of 107 Kb (Genome size: 430 Mb) covering 46 genome equivalents. It was constructed by G. Khush. It was constructed in the HindIII site of pBeloBAC11 and contains 18,432 clones (48 plates).

OSIMBa-Library

Oryza sativa indica cv. Milyang 23
This indica rice BAC library has an average insert size of 115 Kb (Genome size: 430 Mb) covering 14 genome equivalents. It was constructed at CUGI (Kim et al. unpublished). It was constructed in the HindIII site of pIndigoBac536 and contains 55,296 clones (144 plates).

OSIMBb-Library

Oryza sativa indica cv. Milyang 23
This indica rice BAC library has an average insert size of 122 Kb (Genome size: 430 Mb) covering 17 genome equivalents. It was constructed at CUGI (Kim et al. unpublished). It was constructed in the HindIII site of pBACWICH and contains 55,296 clones (144 plates).

OSJIBa-Library

Oryza sativa japonica cv. Azucena
This japonica rice BAC library has an average insert size of 80 Kb (Genome size: 430 Mb) covering 7 genome equivalents. It was constructed at CUGI (Lagoda et al. unpublished). It was constructed in the HindIII site of pBACWICH and contains 38,784 clones (101 plates).

OSJIBb-Library

Oryza sativa japonica cv. Azucena
This japonica rice BAC library has an average insert size of 80 Kb (Genome size: 430 Mb) covering 7 genome equivalents. It was constructed at CUGI (Lagoda et al. unpublished). It was constructed in the HindIII site of pBACWICH and contains 38,784 clones (101 plates).

OSJLBa-Library

Oryza sativa japonica cv. Lemont
This japonica rice BAC library has an average insert size of 150 Kb (Genome size: 430 Mb) covering 2.5 genome equivalents. It was constructed by R. Wing. It was constructed in the HindIII site of pBeloBAC11 and contains 7,296 clones (19 plates).

OSJLBb-Library

Oryza sativa japonica cv. Lemont
This japonica rice BAC library has an average insert size of 150 Kb (Genome size: 430 Mb) covering 2.5 genome equivalents. It was constructed by R. Wing. It was constructed in the HindIII site of pBeloBAC11 and contains 7,296 clones (19 plates).

OSJNBa-Library

Oryza sativa japonica cv. nipponbare
This japonica rice BAC library has an average insert size of 130 Kb (Genome size: 430 Mb) covering 11 genome equivalents. It was constructed at CUGI (Budiman et al. unpublished) and is one of the most widely used libraries for the International Rice Genome Sequencing Project. It was constructed in the HindIII site of pBeloBAC11 and contains 36,854 clones (96 plates).

OSJNBb-Library

Oryza sativa japonica cv. nipponbare
This japonica rice BAC library has an average insert size of 130 Kb (Genome size: 430 Mb) covering 11 genome equivalents. It was constructed at CUGI (Budiman et al. unpublished) and is one of the most widely used libraries for the International Rice Genome Sequencing Project. It was constructed in the HindIII site of pBeloBAC11 and contains 36,854 clones (96 plates).
## WebFPC

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### Search for Contig

- **Search By Marker**: 
- **Search By Clone**: 

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Physical mapping of the most distal BAC clones 46L02 and 56G17 in an indica rice variety Zhongxian 3037
Chromosomal arm-specific bacterial artificial chromosome (BAC) markers and rice chromosome identification.
Karyotyping of rice pachytene chromosomes and mapping of euchromatin and heterochromatin in the rice genome.
Gramene: A Comparative Mapping Resource for Grains

Gramene was recently funded by the USDA IFAFS programme to create a curated, open-source, Web-accessible data resource for comparative genome analysis in the grasses. Data formerly in RiceGenes is now integrated in Gramene. Our goal is to facilitate the study of cross-species homology relationships using information derived from public projects involved in genomic and EST sequencing, protein structure and function analysis, genetic and physical mapping, interpretation of biochemical pathways, gene and QTL localization and descriptions of phenotypic characters and mutations.

The name is a play on the name of the Grameen Bank which specializes in small loans to the poor (mostly women) in emerging economies.

Gramene is a joint project shared between the laboratories and computer resources of Dr. Lincoln Stein, Cold Spring Harbor; Dr. Samuel Carthiour, USDA Center for Agricultural Bioinformatics, Cornell University (sc167@cornell.edu) and Dr. Susan McCouch, Cornell University.

Quick Search

Search for:

Search

Rice Genome View

[Graph showing rice genome view with bars indicating chromosomes 1 to 12]
ESTs and YAC contigs have been used for the genetic and molecular analysis of genes controlling traits that are of economic or biological interest. Currently, isolation of photoperiod sensitivity genes, disease resistance genes, genes involved in plant growth as well as genes controlling seed shattering, is done by a map-based cloning strategy. Research activities with direct relevance for rice breeding have focused on the identification of RFLP markers tightly linked to genes of economic interest. All these research activities have been progressing in collaboration with the STAFF Institute.
Rice gibberellin-insensitive dwarf mutant gene *Dwarf 1* encodes the α-subunit of GTP-binding protein
M. Ashikari et al., 1999. PNAS 98: 10284
Nipponbare × Kasalath

$\text{FL2}(d1) \times \text{SL18}$

13000 $F_2$

3185 ($d1$ homozygous) plants $\rightarrow$ 637 pools

Southern hybridization & linkage analysis

13 RELP markers (C309~~~G1458)

chromosome 5

37(V147) + 71(G5004) pools

37 + 71 plants: for fine mapping
High-resolution RFLP linkage map and physical map of the $d1$ locus. Genetic distances between adjacent markers are shown in parentheses.
A transgenic $d1$ mutant with GTP-binding protein gene restored the normal phenotype. Thus, the rice $Dwarf 1$ gene encodes GTP-binding protein and that the protein plays an important role in plant growth and development. Because the $d1$ mutant is classified as gibberellin-insensitive, we suggest that the GTP-binding protein might be associated with gibberellin signal transduction.
Quantitative trait loci (QTLs) for several agronomically and economically important traits have been detected by genetic analysis using DNA markers. Integration of this genetic information into rice breeding programs will be necessary for the development of new superior varieties. Marker-assisted selection (MAS) is mainly based on the production of nearly isogenic lines of target genes or QTLs, so we have started to develop a series of QTL-NILs for heading date. We are also trying to combine, or pyramiding, QTLs to make a wide variation of heading date. QTL analysis of heading date has been carried out by using BC1F3 190 plants derived from a cross between Koshihikari as recurrent parent and Kasalath as donor parent. Four QTLs on chromosomes 3, 4, 6 and chromosome 8 have been detected. To ensure minimal introgression of target chromosomal segment, we have developed CAPS (Cleave Amplified Polymorphic Sequence) markers which were tightly linked to target QTLs. PCR-based CAPS markers enabled us to select appropriate plants for backcrossing during transplanting and heading. Candidate plants for QTL-NILs were successively selected by the aid of genotype data for RFLP and CAPS markers from the advanced backcross progeny. Candidate individuals of QTL-NILs for 3 QTLs have been selected.
QTL analysis of rice heading date (Hd) genes – Hd1-Hd13

- *Hd1*, a Major Photoperiod Sensitivity Quantitative Trait Locus in Rice, Is Closely Related to the *Arabidopsis* Flowering Time Gene *CONSTANS*. *Plant Cell* 12:2473
- *Hd6*, a protein kinase CK2α
- *Hd3a* similar to *Arabidopsis* floral inducer FT (FLOWERING LOCUS T) gene
MAPMAKER/QTLMAPMAKER/QTL

QTL定位皆採用

MAPMAKER/QTLMAPMAKER/QTL，

此軟體是一套標準的

QTL定位軟體，考慮

單一QTL的區間定位

統計模式。

MAPMAKER/QTLMAPMAKER/QTL的

統計方法雖然不是很

精緻，但是他們有一

套很好的染色體置換

系統可以用來固定目

標QTL之外的QTL效

應，進而提高QTL定

位的精確度。
Graphical genotype of plant $\text{BC}_4 \text{F}_1$-37-7. Black and white regions represent segments of the chromosomes derived from Kasalath and Nipponbare, respectively. Triangles indicate three additional QTL detected in a BC1F5 population.
QTL analysis of rice heading date (Hd) genes – Hd1-Hd13

- \textit{Hd1}, a Major Photoperiod Sensitivity Quantitative Trait Locus in Rice, Is Closely Related to the \textit{Arabidopsis} Flowering Time Gene \textit{CONSTANS}. Plant Cell 12:2473
- \textit{Hd6}, a protein kinase CK2\textsubscript{\alpha}
- \textit{Hd3a} similar to \textit{Arabidopsis} floral inducer FT (FLOWERING LOCUS T) gene
Frequency distribution of days-to-heading for selfed progenis of transgenic plants

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http://shigen.lab.nig.ac.jp/rice/oryzabase/
## Symbol Detail

### GeneDictionary (CLMap symbol)

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<tr>
<td><strong>ClassName</strong></td>
<td>Level1: Reproductive organ</td>
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<tr>
<td></td>
<td>Level2: Pollination, fertilization, fertility, sterility</td>
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<td></td>
<td>Level3: Male sterility</td>
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<td><strong>Link map</strong></td>
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<td><strong>Explanation</strong></td>
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<td>Iwata et al. 1981</td>
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<td>Iwata &amp; Omura 1984</td>
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### Mutant image

- Photo from A. Yoshimura

- Mutant image: op4 vs Normal
Two yield-related genes in chromosome 5

nl-1  Normal  110 cM

nl-2  Normal  6 cM
Rice insertion mutant database (Experimental)

This page is an in silico rice mutant screening page by BLAST search against flanking sequences from our mutant lines induced by rice retrotransposon Tos17. You can request seeds of the mutant line identified by the screening up to 20 seeds/line. To search our mutant lines, your registration is required.

Mutant Search by BLAST
Your BLAST search results
Status of your request
Qualification (Your signature is required, when you request our seeds. Request and assurance forms will appear when you click links following your search result.)
Registration
Example of hit

If your browser shows 'Not Acceptable', select 'en' and/or 'ja' language in your configuration of the browser.

Functional Genomics Laboratory, National Institute of Agrobiological Sciences, Japan.
If you have a question, please mail to Hirohiko Hirochika or Ako Miyao.
http://pc7080.abr.affrc.go.jp/~miyao/pub/tos17/index.html.en

- >30,000 insertion mutants now
- May BLAST the sequence of your interested with the flanking sequence database
- Will send 20 seeds
## NE8542

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<td>2000-04-01</td>
<td>myao</td>
<td>Callus induction (MS + 2 mg/l 2,4-D + 0.3% gellan gum). Oct 13 1998, Transfer to Liquid medium (N6 + 1 mg/l 2,4-D). Nov 15 1998, Transfer to Pre-regeneration medium (N6 + 0.3% casein acid + 0.1% proline + 1 mg/l 2,4-D). Feb 27 1999, Regeneration (N6 + 0.1 mg/l BA + 0.01 mg/l NAA + 1% agarose). Mar 9 1999, Transfer to field. May 26 1999, Flash name: N25</td>
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<td>2000-08-15</td>
<td>murata</td>
<td>fine Dwarf</td>
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<td>myao</td>
<td>Zebra</td>
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<td>8</td>
<td>2000-08-15</td>
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Some examples for *Tos17*

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<td>ABA level decrease</td>
<td><em>OsABA2</em></td>
<td>zeaxanthin epoxidase</td>
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<td>Yellow-green mature leaves</td>
<td><em>CAO</em></td>
<td>Chlorophyll a oxygenase</td>
<td>10L</td>
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<td>Brittle culm</td>
<td><em>OsCesA7</em></td>
<td>Cellulose synthase</td>
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Welcome to the Rice Microarray Opening Site for Rice Microarray Project

This site is administered by National Institute of Agrobiological Sciences

No.12760

What's new?
- General Information
- Outline of Microarray
- Microarray is ...
The importance of rice as a material for genome sequencing

- Rice is an important crop in the world
- the genome size of rice is 430 Mb, the smallest one among crops
The importance of rice as a material for genome sequencing

• Linkage maps and physical maps of rice have been established and more than 70,000 rice EST sequences have been registered

• the transgenic rice technology has been established
The importance of rice as a material for genome sequencing

- Rice shares a co-linear gene organization with other cereal grasses, thus rice is a key to knowledge of the genomic organization of the other grasses.
'Green revolution' genes encode mutant gibberellin response modulators

Nature 400, 256 - 261 (1999)
World wheat grain yields increased substantially in
the 1960s and 1970s because farmers rapidly
adopted the new varieties and cultivation methods
of the so-called 'green revolution'. The new
varieties are shorter, increase grain yield at the
expense of straw biomass, and are more resistant to
damage by wind and rain. These wheats are short
because they respond abnormally to the plant
growth hormone gibberellin. This reduced
response to gibberellin is conferred by mutant
dwarfing alleles at one of two Reduced height-1
(Rht-\textit{B1} and Rht-\textit{D1}) loci.
the *Arabidopsis gai* (dwarf) sequence

a rice expressed-sequence tag (EST; D39460)

wheat cDNA C15-1

Chromosome 4A, 4B, 4D, wheat Rht-1 alleles also in these chromosomes

Cereal genomes show substantial conservation in gene order (colinearity):
Wheat chromosome 4
Rice chromosome 3
Maize chromosome 1 (*d8*)
GRASS GENOMES

Oats
Triticeae
Maize
Sorghum
Sugar cane
Foxtail millet
Rice
International Rice Genome Sequencing Project (IRGSP)
Why chromosome 5?

- Less repetitive sequences
- High YAC contig coverage
- Many interesting genes, e.g. $xa_5$, $xa_{13}$, dwarf, sterile, erect growth habit
Our team:
定序分析流程

一．国际合作部份

水稻基因組
～約430,000千鹼基

基因庫
～由美國、日本製備

二．我們的工作

含第五條染色體的載體
～約150千鹼基

以亂槍法製作次基因庫
～約2千鹼基

定序反應
～使用自動DNA定序儀

組合為完整序列
～生物資訊

解讀
～生物資訊
Sequencing Strategy

- pCYPAC2
- Rice genomic DNA inserts

Base-calling and assembly using Phred-Phrap

- PAC clone purification by CsCl gradients centrifugation
- Quality control by TaqMan PCR

Construction of Shotgun libraries (2kb and 5kb inserts / pUC 18)

- 2kb library
  - culture-direct PCR
  - Non-amplified clones
  - Plasmid DNA

- 5kb library
  - PCR product
  - Non-amplified clones
  - Plasmid DNA

- Sequencing using dye-terminator

Gap filling and finishing

Annotation
解讀水稻基因組序列 -- 生物資訊工作流程

以自動定序儀讀出水稻的DNA序列片段

電腦組合成完整的DNA序列

與公共資料庫比較

計算基因的位置

預測基因產物
-- 蛋白質

蛋白質
結構預測

蛋白質
功能預測

註冊到公共資料庫
http://genome.sinica.edu.tw/index.htm
Current Rice Genome Sequencing Status

ASPGC has submitted a total of 13,801,705 bps of DNA to GenBank.

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Annotation of P0574H01

- Annotation results with Rice-GAAS
- Marker: AU032791 / C22663 / C98076 / AU032646
- Overlapped clone: North: / South: P0016H04
- Miropeats result
- Detail
- Quality
- Low quality Information
Annotation of P0036D10

- Annotation results with RiceGAAS: Rice Genome Automated Annotation System (by RGP)
- Annotation results with Whole Rice Genome Automated Annotation Database (by TIGR)
- Marker: D25486
- Overlapped clone: North: / South: P0668H12
- Miropeats result
- Detail
- Quality
Miropeats result of P0001A07 (Threshold score = 100)
### Quality of P0036D10

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VLRFPLRRLLSDEVKGPLPPKETILKGMSEMQKQYYALLQDKLFLEVMAAGGKRKL
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GLGINLATAVIYSDWPQVLQPRORADHRIGQKEVQVFRCETYITEEKEVIER
AYKKLALDALVIQGRLEQKAVNKDELQMVRFQAEVFQSSKIDTEDIDRIIAK
GERATAQLDAMKMTEDAIKFDMDGAELYDFFDDMKCCILEDWSDFVIEETLFFKLD
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FQQNFQRQHNLSEYKEVYLYQANQKDITVDEGGDDDEQLEPLTVTEEQEKEQLEEGF
STWTTRDFNFTIRACEKYGRNDIKNISSEMEKETTEEVQRYAKVFQERYKELNDYDRV
IKNIEKERALYRDEIMKAIGKLDRAKYNPWELLKIQGYQNGKGLNEECDFMLCM
VHKLGYGNWDELKAAFRMSPFARFDFWFVKSRTTQLARRCTLIRLVEKENQYEDERE
RLARKDKNMSPAKRSSRSLDTPQSSSSKRRQQSYTANEAGSSRRRGR"
P-TYPE ATPase DATABASE

Maintained by Kristian B. Axelsen, axe@biobase.dk

P-type ATPases present in  P-type ATPase subfamilies  Additional information
**TEOS1** (Transposable element of *Orysa sativa* 1) 
~100 in the current rice genome sequence data  
7kb, similar LTR and spacer sequences

PBS: primer binding site, PPT: polypurine tract
EST Project

ASPGC is now initiating rice EST projects using developing panicles and seeds. This project is supported by the Theme Project of Academia Sinica.

SAGE Project

ASPGC is now initiating rice SAGE projects using developing seeds. This project is in collaborative with Dr. W. Crosby, PBI, Canada (http://bioinfo.pbi.org.cn/).

Insertional Mutant Project

A rice insertional mutagenesis population based on T-DNAs will be established through a team effort. The agronomic traits and flanking sequence of insertion sites will be collected in this database.

The rice insertional mutant team are:

- Generation of mutants:
  - Su-may Yu, Institute Molecular Biology, Academia Sinica.
- Flanking sequence and database:
  - Yu-ile Hsing, ASPGC
  - Teh-yuan Chow, ASPGC
- Phenotype recording and seed propagation:
  - Chih-Kuang Chen, Taiwan Agriculture Research Institute
EST (Expressed Sequence tags) Projects
Seeds and Panicles
<table>
<thead>
<tr>
<th>Query ID</th>
<th>Annotation</th>
<th>Source</th>
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<tr>
<td>5mmPR-A1A01S</td>
<td>GTP-binding protein</td>
<td>Cicer arietinum</td>
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<tr>
<td>5mmPR-A1A03S</td>
<td>MAP kinase homolog</td>
<td>Oryza sativa</td>
</tr>
<tr>
<td>5mmPR-A1A06S</td>
<td>elicitor-responsive gene 3 [imported]</td>
<td>Oryza sativa</td>
</tr>
<tr>
<td>5mmPR-A1A08S</td>
<td>superoxide dismutase [CU-ZN]</td>
<td>Oryza sativa</td>
</tr>
<tr>
<td>5mmPR-A1A10S</td>
<td>gibberellin-stimulated transcript 1 like protein</td>
<td>Arabidopsis thaliana</td>
</tr>
<tr>
<td>5mmPR-A1A11S</td>
<td>putative small nuclear ribonuculeoprotein G</td>
<td>Oryza sativa</td>
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<tr>
<td>5mmPR-A1B01S</td>
<td>hypothetical protein</td>
<td>Arabidopsis thaliana</td>
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<tr>
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<td>Oryza sativa</td>
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<tr>
<td>5mmPR-A1B05S</td>
<td>metallothionein-like protein type 2</td>
<td>Oryza sativa</td>
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<tr>
<td>5mmPR-A1B06S</td>
<td>probable protease inhibitor P322 precursor</td>
<td>Oryza sativa</td>
</tr>
<tr>
<td>5mmPR-A1B07S</td>
<td>Putative 40S Ribosomal protein</td>
<td>Oryza sativa</td>
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<tr>
<td>5mmPR-A1B10S</td>
<td>putative protein</td>
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<td>5mmPR-A1B12S</td>
<td>Histone H4</td>
<td>Triticum aestivum</td>
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<td>CG9248 gene product</td>
<td>Drosophila melanogaster</td>
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<td>Lycopersicon esculentum</td>
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<td>5mmPR-A1C09S</td>
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<tr>
<td>5mmPR-A1D02S</td>
<td>mitochondrial phosphate transporter</td>
<td>Oryza sativa</td>
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</table>
Overview of SAGE Technique (I)

1. Anchoring Enzyme
2. Isolate SAGE tags
3. Link tags together
4. Sequence linked tags
5. Quantitate tags and determine patterns of gene expression
This project is supported by grants from

Academia Sinica, Taiwan

Institute of Botany, Academia Sinica, Taiwan

National Science Council, Taiwan

Council of Agriculture, Taiwan

And in cooperated with

RGP
Rice Genome Research Program

Clemson University Genomics Institute

Monsanto Company, USA
Our collaborators with this project are:

Institute of Biotechnology, National Cheng Kung University

VGH-YMU Human Genome Sequencing Program

Vita Genomics, Inc.
Status of the International Rice Genome Sequencing Project

Total Number of BACs/PACs in Genbank: 1953
With A Total Number of bp: 262,620,239
Approximately 60.9% of the rice genome

Chromosome Distribution of Released Rice Genome Sequences in GenBank

1  2  3  4  4*  5  6  7  8  9  10  11  12
51.4 43.8 47.3 36.6 36.6 33.8 35.4 33.1 33.6 27.2 23.7 33.6 31.2 Mb
>100% 51.9% 49.2% 92.4% 7.5% 39.2% 83.2% 79.8% 78.7% 11.1% >100% 7.8% 4.0% **

* Oryza sativa spp. indica.
• Rice BAC/PAC Sequences Anchored to Rice Genetic Markers

To integrate the genetic maps with genomic sequences of rice, we downloaded all rice BAC/PAC sequences and searched these sequences against 13,995 marker sequences obtained from the Cornell RiceGenes Database (649 marker sequences) and the Japanese Rice Genome Program (13,246 marker sequences). The polyA/polyT and Ns at the ends of marker sequences were then trimmed. Using a high stringency cutoff of greater than 97% identity with the marker sequence over a minimum of 74 bases, we parsed out only the BAC and PAC clones that contained markers. We have tabulated the results of the search. The searches were performed separately with the RGP markers and the Cornell markers. The chromosome location, cM position, locus, marker accession number, BAC/PAC HTGS accession number, and the alignment of the marker sequence with the BAC/PAC are listed in the tables with links to Genbank, RGP, and/or Cornell. The searches are updated on a weekly basis.
At least 1 million children, weakened by vitamin-A deficiency, die every year and an additional 350,000 go blind. … but protesters believe such GMO are bad for us and our planet.
Golden rice: Solving Vitamin A deficiency?
Vitamin A supply where rice is a staple

adult's average daily requirement = 500 µg retinol

- Daily supply before "golden rice"
- Expected boost after "golden rice"
Vitamin A

Retinol metabolism in animals

Beta-Carotene → Terpenoid biosynthesis

Carotenoids biosynthesis → all-trans Dehydroretinal → 11-cis Dehydroretinal

11-cis Retinal → all-trans Retinal → 11-cis Retinol → 11-cis Retinyl palmitate

5.2.1.7 all-trans Retinol (Vitamin A) → 3.1.1.63

2.3.1.76 all-trans Retinyl ester → 2.3.1.76

3.1.1.64

1.2.1.36

1.1.1.105

1.1.1.105

11-cis Retinal → 5.2.1.11

1.2.3.11

Porphyropsin

β-Glucuronide → Starch and sucrose metabolism

Rhodopsin → Iodopsin → Bathorhodopsin → Luminorhodopsin → Metarhodopsin

hv
Introduced enzyme (source)

- Tocopherols (Vitamin E)
- Gibberellins
- Chlorophyll

**IPP**

- GGPP

**Phytoene synthase (psy)** (daffodil)

**Phytoene desaturase (crtl)** (bacteria)

**Lycopene**

- Lycopene β-cyclase (lcy) (daffodil)

**α-Carotene**

- β-Carotene

- Lutein

- Zeaxanthin
Put 3 enzymes that produce beta-carotene: two of the genes were from daffodil, and one from the bacterium *Erwina*. 
水稻白葉枯病 (bacterial blight, *Xanthomonas oryzae*) 與水稻稻熱病 (rice blast, *Magnaporthe grisea*) 是水稻最嚴重的病害之一.
抗水稻白葉枯病基因

目前已有近30個抗病基因被定位出來，其中的Xa1與Xa21兩基因亦被找出。而xa5與xa13則位於第五條染色體。
抗稻熱病基因中的*Pi-ta* 亦被找到。
Rice genome sequencing work:

Besides IRGSP
Rice Genome Sequencing
- the Science, the International Effort, and the Chinese Contribution

If a single plant species is crowned by popular vote, it would be rice (Oryza sativa L.): a model genome, an experimental model plant, a model crop, and above all, it is the most important crop for human consumption, providing staple food for more than half of the world population. The rice genome holds fundamental information in its biological "power", including physiology, development, genetics, and molecular evolution. This justifies the timely delivery of its basic genomic information, the genomic sequence, to the perhaps the largest agriculture-related research community around the globe. It, together with another model plant whose genome has been sequenced to completion, Arabidopsis thaliana, has opened new avenue for the plant genome research.

The estimated rice genome size is about 430 Mb, the smallest among all the cereal crops. It is about one seventh of human and 3.5 times of...
中国科学院基因组信息学中心

3月6日

您是第5999位访问者

人类基因组计划
1993年9月1日，我中心代表中国参加了人类基因组计划，承担了1M项目。

水稻基因组计划
启动以水稻为模式的遗传研究。

加入我们

中心介绍

SNP研究
单核苷酸多态性（又称SNP），是广泛分布于人类全基因组中稳定的多态位点。

蛋白质组学研究
蛋白质研究室承担着蛋白质组学、基因克隆与表达、蛋白质分离纯化等研究工作。

大规模测序
北京华大基因研究中心测序服务中心（BSS）提供全天候的DNA测序服务。

DNA文库构建
DNA是指以mRNA为模板，在反转录酶的作用下形成的互补DNA（cDNA）。

基因组文库的构建
本中心拥有超声仪、Genemachines公司的HydroShear、电转仪、等先进的仪器，有一批优...

战胜高性能的计算机服务
我们拥有目前国内最先进的高性能计算机，曙光3000，曙光2000，sun10000等先进的......

中国科学院基因组信息学中心

华大基因研究中心

北京空港工业区B-6

邮编：101300
中国杂交水稻基因组计划简介：

水稻是世界上最主要的粮食作物之一，是半数世界人口赖以生存的主要食物，也是有7000年种植水稻历史的中国经济、文化、传统和历史的一个重要组成部分。年总产值达千亿美元以上的大米是关系到我国国计民生的最主要的粮食。袁隆平院士的杂交水稻在我国水稻育种和东南亚各国有着广泛的影响。"中国杂交水稻基因组计划"这个项目着眼于中国粮食的主要物种水稻和以水稻为遗传背景的杂交水稻，它在农业上的意义可与人类基因组计划在人类健康中的意义相媲美。

通过对水稻全基因组序列分析，可以获得大量与水稻生育性、丰产、优质、抗病、耐逆、成熟期等有关的遗传信息和功能基因；可以促进水稻的品种改良，培育更好的优质高产品种；还有助于了解小麦、玉米等其它重要农作物基因组中的相关基因，从而带动整个粮食作物的基础与应用研究，还可以专利的方式，将优良的种质资源转化为信息资源进行保护，以利于农业的可持续发展。

众所周知袁隆平院士是我国水稻雄性不育系的最主要的发明和奠基人，有水稻之父和绿色革命先锋的全球美誉。选择这一水稻种作为切入点进行测序分析在政治、科学和经济上都有着积极的意义。开展超级杂交水稻基因组研究，在产业上，是密切联系生产实践的；在科学上，是对国际水稻基因组研究的补充与发展；在国家任务上，将促进和帮助我国正在进行的水稻四号染色体基因组序列图的完成。
Welcome to the Monsanto rice-research.org web site. This site provides access for academic and non-profit researchers to the Monsanto Rice Genome Sequence Database. In order to access the data, please read the New User Registration page and complete a one-time Database Registration Agreement.

Note: You might not be able to run BLAST searches on this site using the Netscape 6 web browser.
Syngenta

To view this site's dynamic homepage download the latest version of Macromedia Flash.
• **BAC-by-BAC strategy:**
  IRGSP
  Monsanto

• **Whole genome shotgun:**
  Syngenta
  Super hybrid rice
Some examples

- Decrease granule-bound starch synthase – sticky rice
- Increase granule-bound starch synthase – good for rice noodles, fast foods, etc.
- Decrease glutelin (major storage protein) – good for patients with kidney disease
- Decrease 16 kDa albumin (minor storage protein, an allergen) – good for people allergic to rice
- Giant embryos – good for hypertension patients
- Also golden rice, purple rice, etc.
水稻基因组研究在作物改良之应用

- 半矮株，直立型
- 多粒，高产，富营养
- 抗病，抗虫
- 耐旱，耐寒，耐热，耐盐，耐淹水
- 生产抗体，药品，及其他高价值产品
- 等等
Thank you
Any question?