Bioinformatics and crop information systems in rice research

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About the cover: Researchers gather raw data from the field that would later be used, using bioinformatics tools, to develop information systems that would help solve current problems in rice research.

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Bioinformatics and crop information systems in rice research

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The triple revolution in biotechnology, computing science, and communication technology has stimulated informatics applications in rice research. This review specifically covers the impact of biology-focused informatics ("bioinformatics") in rice research on the discovery of genotype-phenotype relationships for priority traits, using diverse data sources.

Bioinformatics is a scientific discipline lying at the intersection of biology, mathematics, computing science, and information technology. Bioinformatics can be discussed within the following frameworks:

- Applications: What kind of research questions can be answered using bioinformatics?
- Databases: What data sources and applicable semantic standards (ontology[1]) are pertinent to answering these research questions?
- Protocols, algorithms, and tools: What analysis protocols, computing algorithms, and software tools can be applied to answer these research questions?

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[1] Ontology refers to the formal definition of a dictionary of concepts and their interrelationships. There are many international bioinformatics efforts in this area, such as Gene Ontology (www.geneontology.org) and Plant Ontology (www.plantontology.org), pertinent to crop research.

• Infrastructure: What hardware, software, and networking systems are required to support the above?

This review will focus primarily on germplasm-based crop research, although many of the same tools can be applied to current problems in soil microbiology, entomology, and other areas of crop research. Also, some of the design principles of bioinformatics information systems will be useful for other research fields, such as geographic and agronomic information systems.

Bioinformatics applications in crop research

The fundamental scientific question underlying germplasm research is, What is the causal relationship between genotype and phenotype? DNA is transcribed into RNA, which is either bioactive itself (as noncoding RNA gene products) or is translated into peptides that form part of protein gene products. Ultimately, these products act as structural elements, genetic regulatory control factors, or modulators of the biochemical fluxes within metabolic and physiological pathways, at the subcellular, tissue, organ, and whole organism level. This sum total of molecular expression integrates to give the overall structural and behavioral features of the plant—its "phenotype." The unfolding of this story also has an essential environmental context, including biotic (ecosystem) and abiotic (geophysical) factors modulating expression in a variety of ways via diverse sensory and regulatory mechanisms in the plant. Various classes of experimental data associated with this tapestry of germplasm function are summarized in Figure 1.

Germplasm

Proper management of germplasm information is essential for the elucidation of genotype-expression-phenotype associations. Management goals include systematic tracking of germplasm origin (passport and genealogy information), recording of alternate germplasm names, accurate linkage of experimental results to applicable genotypes, and proper material management of germplasm inventories.

An important aspect of any good germplasm information system is the separation of the management of nomenclature from identification. Users must be free to name germplasm as they like, and the system must make sure the names are bonded to the right germplasm. A key to effective management of such variable germplasm information is the assignment of a unique germplasm identifier (GID) to each distinct germplasm sample—seed package or clone—that needs to be tracked ("bar coded"). The acid test is to ask whether or not mixing two germplasm samples together will result in an unacceptable loss of biological or management information. If the answer to this question is "yes," then each sample should be assigned a distinct GID. The GID is the essential reference point for managing all meta-data about the germplasm, for accurately attributing all experimental observations made about that sample, and for cross-linking related germplasm samples with one another, for
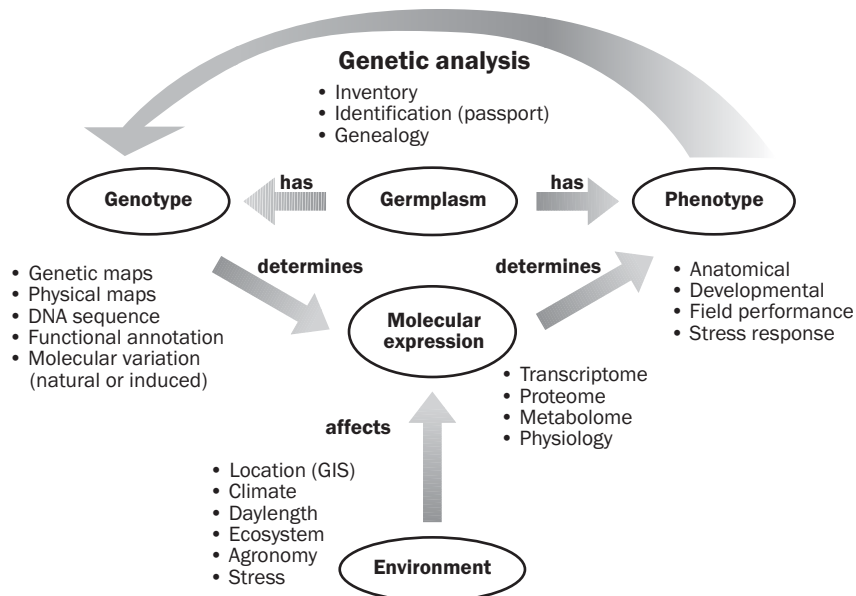

Fig. 1. Biological and information relationships in germplasm research.

example, the parents (sources) and progeny of the given sample, including membership of the sample in global "management neighborhoods.[2]"

Once assigned, a GID is never destroyed, but rather persists in the crop database long after the associated sample has become unavailable (after being fully consumed, nonviable, or otherwise lost). In this manner, historical information about germplasm may be efficiently integrated with information about extant descendants of that germplasm. Although a given GID is generally a database primary key defined locally to a given database, it should be convertible into a globally unique identifier within a community of germplasm databases. There are various protocols for achieving this, for example, the life science identifier (LSID) protocol.[3] This requirement is not unique to GID usage. In fact, most biological data to be shared by a distributed community should be assigned global identification in this manner.

Genotypes

Genotypes can be characterized at various levels of abstraction and resolution. In all instances, what is being measured and tracked across meiotic events, either directly or indirectly, is sequence variation ("alleles") in the DNA of organisms. Experimental systems conceived to make those measurements are designated "markers." Markers can be any scientific protocol used to observe a biological process causally coupled to the molecular variation of interest. This broad definition includes laboratory measurements of DNA (e.g., polymerase chain reactions or DNA-DNA hybridization events) and simple observations of visible phenotypes (e.g., classical visible genetic markers such as morphological variants). The molecular variation measured by genotyping can be neutral or biologically significant.

Neutral molecular variation generally involves markers that simply exhibit DNA structural polymorphism that is usefully applied to answer the following basic questions:

- To what extent are germplasm samples similar to or different from one another (i.e., "fingerprinting" experiments)?
- What is the chromosome location of a marker (i.e., "mapping" experiments)?

Answering such questions will often lead to deeper exploration of germplasm, such as evolutionary studies, practical management of plant crosses, and genetic resource management.

Molecular variation that is biologically significant is that postulated to be causally correlated with differences in structure (i.e., genome content or arrangement), biochemical function (resulting from critical functional changes in RNA bases or amino acid residues), or regulation of gene products (by affecting promoter or enhancer sequences).

Whatever the nature of genotype measurements, the primary task of bioinformatics is to completely capture and accurately codify the raw and derived genotype data. Bioinformatics also applies statistical algorithms to raw genotype measurements to make useful inferences such as locus assignments on genetic and physical maps, assessments of germplasm relatedness and biodiversity, or assays of the impact of molecular variation on the biological system. Bioinformatics methodology assists in all stages of genotyping experiments and in the interpretation of results: from raw data capture (e.g., gel image processing), documentation, and storage to semiautomated analysis of raw data into inferences (i.e., germplasm fingerprinting and mapping, alignments of DNA variation to RNA and protein structures to elucidate functional variance, etc.) through visualization and publication of the information.

A growing foundation for modern genotyping is, of course, the sequence-level structural characterization of plant genomic DNA, an activity within which bioinformatics has played an enormous technical role. The publication of the *Arabidopsis thaliana* genome in 2000 (AGI 2000) gave plant biologists a major information resource for indexing current and future understanding of plant genotypes. Since that time, a complete survey of the rice genome sequence has also become available (IRGSP 2005). Several other crop genome-sequencing projects are rapidly constructing a rich and diverse repository of public information about plant DNA sequence structure across many species, which will enable significant and fruitful future studies in comparative genomics.

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[2] A "management neighborhood" of germplasm is defined as the entire population of germplasm that essentially shares and is intended to conserve the distinct genetic composition of a specified founding germplasm sample. This concept finds utility in institutional decisions to conserve, describe, and globally share specified germplasm sets like mapping populations (e.g., Azucena/IR64), genomics stocks (e.g., mutants), parental breeding releases (e.g., cultivar releases like IR64), and accessions held in genetic resource collections.

[3] See http://lsid.sourceforge.net/.

Phenotypes

Bioinformatics management of phenotype data primarily focuses on cataloging simple phenotypes. Bioinformatics researchers, such as in the Open Biomedical Ontologies initiative (http://obo.sourceforge.net), are cataloging controlled vocabulary and ontology to formalize phenotype descriptions by cross-linking concepts of "observable," "attribute," and "value." A simple application of this paradigm is the following phenotype specification: leaf (observable) color (attribute) is red (value). Observables for plants can be codified using plant anatomy and developmental process terms being defined by the Plant Ontology Consortium (POC) (www.plantontology.org; POC 2002). IRRI scientists are collaborating with POC and others to systematically index descriptions for phenotypes of interest relating to agronomic traits such as yield, biotic and abiotic stress tolerance, and improved grain quality.

Molecular expression

Moving beyond the map characterization of genomic DNA highlighted above, the task of functional genomics (and other "-omics" fields such as proteomics and metabolomics) is to characterize the dynamic picture of molecular expression within the living organism at the level of RNA, protein, and metabolites. The rice genome contains thousands of predicted genes. The primary motivation of functional genomics research is to narrow down the list of candidate genes implicated in specified biological processes, for example, as contributors to specified agronomic traits of interest. The overall strategy is that of intersecting evidence from positional, functional, expression, selection, and crop modeling information sources (Fig. 2).

Databases

Computerized databases are a relatively recent innovation in biology, expanding dramatically in scope, usage, and online accessibility during the 1990s. At the cornerstone of modern biological research are the international public sequence databases, of which there are three major ones: Genbank at the National Center for Biotechnology Information (NCBI; www.ncbi.nlm.nih.gov), the European Molecular Biology Laboratory (EMBL) sequence database hosted at the European Bioinformatics Institute (EBI; www.ebi.ac.uk), and the DNA Data Bank of Japan (DDBJ; www.ddbj.nig.ac.jp). In fact, basic sequence data submitted to any of these three databases are automatically mirrored to the other two databases on a routine basis, so visiting any one of the databases usually suffices for basic data. Each site, however, has specialized information resources worth exploring independently.

Although Web user interfaces for these sequence databases are well developed, deployment of local copies of major public and semipublic databases pertinent to crop research permits higher efficiency for repetitive high-throughput searches that result from the processing of large experimental data sets.
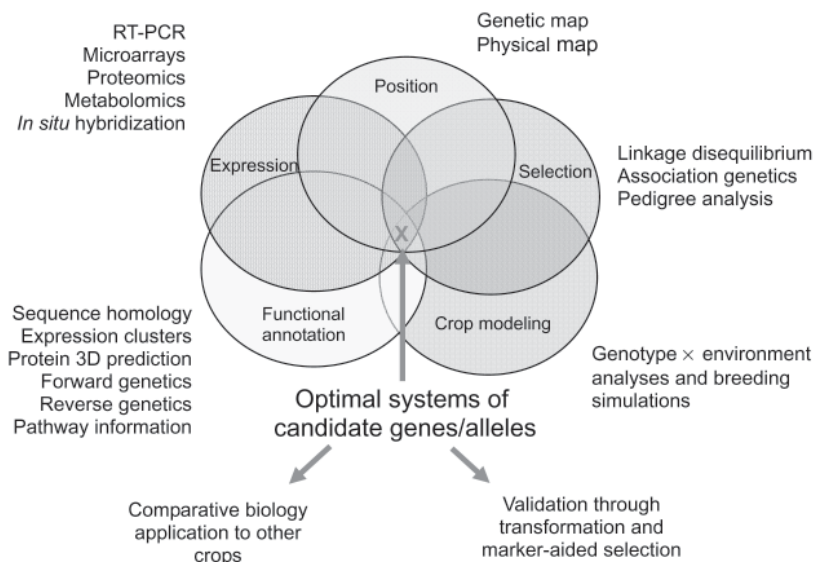

Fig. 2. Intersecting evidence for candidate genes.

The "BioMirror" project (www.bio-mirror.net/) provides valuable database mirroring facilities in this regard.

Beyond sequence data, the range of pertinent functional genomics experiments and associated data is too extensive to fully enumerate here, but several public sources of such crop-related bioinformatics data are listed in the table. The reader is also encouraged to consult various books and journal reviews providing surveys of available resources.[4] Some excellent online indices of data sources (and related software tools) exist, for example, the Expasy Life Sciences Directory (www.expasy.org/links.html).

The International Crop (Rice) Information System
The International Crop Information System (ICIS; www.icis.cgiar.org) is an "open-source" and "open-licensed" generic crop information system[5] under development since the early 1990s by the CGIAR, national agricultural research and extension systems, agricultural research institutes, and private-sector partners (McLaren et al 2005, Bruskiewich et al 2003, Fox and Skovmand 1996). Using the GID protocol previously discussed, ICIS is designed to fully document germplasm genealogies[6] with associated meta-data such as passport data and to accurately cross-link germplasm entries with associated experimental observations[7] from

Table 1. Partial inventory of online public rice/crop/plant bioinformatics databases.

Database	Description/organism	URL
Rice Genome Project/IRGSP	International Rice Genome Sequencing Project	http://rgp.dna.affrc.go.jp/IRGSP
RAP DB	"Rice Annotation Project" database	http://rapdb.lab.nig.ac.jp
TIGR Rice	TIGR rice genome database	www.tigr.org/tdb/e2k1/osa1/
BGI Rice Information System	(BGI) Indica (93-11) rice genome data	http://rise.gneomics.org/cn/rice/index2.jsp
Oryzabase	NIG Oryza genetics database	www.shigen.nig.ac.jp/rice/oryzabase
Gramene	Comparative grasses, anchored on rice	www.gramene.org
MOsDB	MIPS *Oryza sativa* database	http://mips.gsf.de/proj/plant/jsf/rice/index.jsp
IRIS	International Rice Information System	www.iris.irri.org
IRFGC	International Rice Functional Genomics Consortium Web site	www.iris.irri.org/IRFGC
OryzaSNP	IRFGC hosted rice single nucleotide polymorphism (SNP) survey	www.oryzasnp.org
OMAP	Comparative genome physical maps of *Oryza* wild relatives	www.omap.org
MPSS	Massive parallel signature sequencing gene expression data	http://mpss.udel.edu
RED	(NIAS) rice expression database	http://cdna02.dna.affrc.go.jp/RED
Rice Array Db	NSF-funded oligo rice gene expression array	www.ricearray.org
Yale Plant Genomics	Gene expression from tiling path arrays and rice tissues	http://plantgenomics.biology.yale.edu/
Rice Proteome Database	NIAS rice proteome database	http://gene64.dna.affrc.go.jp/RPD/main_en.html
Tos17 rice mutants	NIAS rice TOS 17 insertion mutants	http://tos.nias.affrc.go.jp
T-DNA Rice Insertion lines	(Gyn An) Korean T-DNA rice insertion mutants	www.postech.ac.kr/life/pfg
OryGenesDb	(CIRAD) Reverse genetics for rice	http://orygenesdb.cirad.fr/
KOME database	Knowledge-Based Oryza Molecular Biological Encyclopedia	http://cdna01.dna.affrc.go.jp/cDNA
RIKEN	*Arabidopsis* and rice functional genomics data	www.gsc.riken.go.jp/eng/output/topics/plant.html
Rice Blast	*Magnaporthe grisea* genomics	www.riceblast.org
Genevestigator	(Gruissem) Gene networks in *Arabidopsis* and rice	http://genevestigator.ethz.ch
MaizeGDB	Maize	www.maizegdb.org
PlexDB	Plant expression data	www.plexdb.org/
GRIN	Plant genetic resources	www.ars-grin.gov/
TAIR	The *Arabidopsis* Information Resource	www.arabidopsis.org
NASC	*Arabidopsis thaliana*	http://arabidopsis.info/
MATDB	*Arabidopsis thaliana*	http://mips.gsf.de/proj/thal/db/
PLACE db	Plant cis-acting regulatory DNA elements database	www.dna.affrc.go.jp/PLACE
PlantCare	Plant cis-acting regulatory DNA elements database	http://intra.psb.ugent.be:8080/PlantCARE/
NCBI Plant	Plant genomes central at NCBI	www.ncbi.nlm.nih.gov/genomes/PLANTS/PlantList.html
EXPASY	Index to other plant-specific databases	www.expasy.org/links.html

[4] *Nucleic Acids Research* has a "database edition" at the start of each calendar year with an online index (www3.oup.co.uk/nar/database/). See also *Plant Physiology*, May 2005, Vol. 138, wh ich recently published an extensive set of review papers on available plant databases.

[5] "Open source" refers to the accessibility of the computer source code of the system. "Open license" essentially means that anyone can freely use and modify the code for their use. "Generic" means that it is adaptable to any other crop (not just rice).

[6] The ICIS Genealogy Management System (GMS) efficiently tracks the extended network of GID relationships and the meta-data associated with each GID.

[7] The ICIS Data Management System (DMS) documents studies of germplasm using a biometric "study" model mildly reminiscent of a computer spreadsheet. In fact, some DMS input and display tools are based on Excel.

evaluations undertaken in the field, greenhouse, or laboratory.

ICIS meets the need for global identification of GID and other data objects (e.g., field studies) by maintaining globally unique information about the local database installation and user who created the entry, as the authority for the information assigned to a given ICIS object identifier. This entry may eventually be published in a central ICIS repository and receive a second new "public" identifier cross-linked to the original identifier. Such ICIS object identifiers (e.g., GIDs) like LSIDs are not names, and, although they do contain some information on domain and authority, no one will generally use them as names for germplasm.

In addition to specifying a common database schema, the ICIS community has collaboratively developed many freely available[8] specialized software analysis tools and interfaces for the system for efficiently documenting, analyzing, and retrieving information about germplasm samples and studies. These include practical tools (Fig. 3) to manage lists of germplasm for plant crosses, evaluative nurseries, and collections.[9]

The public rice implementation of ICIS is IRRI's flagship germplasm database, the International Rice Information System (IRIS; www.iris.irri.org). IRIS currently contains about two million germplasm (GID) entries with millions of associated data points in hundreds of experimental studies, including many phenotypic observations and a growing number of genotypic measurements. IRIS also publishes phenotype information for the Institute's IR64 rice mutant collection (Wu et al 2005). This latter information is searchable using a query interface permitting the specification of mutant phenotypes using the "observable," "attribute," and "value" model previously discussed. IRRI scientists have generated a number of high-throughput data sets, including genetic maps; transcript, protein, and metabolomic expression experiments; and genotypic measurements on a growing set of germplasm. Many of these data sets are now published in IRIS or in collaborating databases such as Gramene.

Protocols and tools

Bioinformatics analysis requires a very broad range of protocols and algorithms. Many freely available tools can be used to apply such protocols and algorithms to crop research problems. A few representative tools will be mentioned here.

The European Molecular Biology Open Software Suite (EMBOSS; www.emboss.org) is an open-source sequence-analysis package that provides more than 200 sequence analysis utilities, including wrappers for most publicly available algorithms such as pairwise and multiple sequence alignments, primer design, and sequence feature recognition algorithms. EMBOSS also reads and writes a wide variety of sequence and annotation formats. The Open-Bio community (www.open-bio.org) is host to a series of computer language-specific bioinformatics tool kits useful for bioinformatics data transformation scripts and Web site development. The Generic Model Organism Database project (GMOD; www.gmod.org) is a clearinghouse of many freely available, open-source software tools for managing and manipulating biological information in databases. Another good source of freely available, open-source tools is the TIGR software site (www.tigr.org/software), which has various software systems useful in particular experimental contexts. For proteomics tools, the Expasy Web site at the Swiss Institute of Bioinformatics (www.expasy.ch) is a valuable resource. For metabolomics tools, the Systems Biology Markup Language site (SBML; www.sbml.org) is a good starting point.

A principal limitation of many online databases is their dependence on regular Web server interfaces for data publication, interfaces solely searchable using standard Web browsers. Technologies such as semantic Web languages and Web services protocols are being explored as a means of creating frameworks for "computer program-friendly Web surfing," such that more powerful client software than Web browsers can be designed, implemented, and deployed on the biologist's desktop. One such protocol is BioCASE (www.biocase.org). Another notable protocol is the BioMOBY project (www.biomoby.org; Wilkinson et al 2005) that is striving to apply biological semantics in a formal manner to integrate bioinformatics data sources and computational services into complex workflows that can be managed and visualized by sophisticated clients, such as the Taverna workflow tool (http://taverna.sourceforge.net/).

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[8] Information and links to ICIS tools are available off the ICIS Web site at www.icis.cgiar.org.
[9] Including specialized tools for genetic resource collection management.
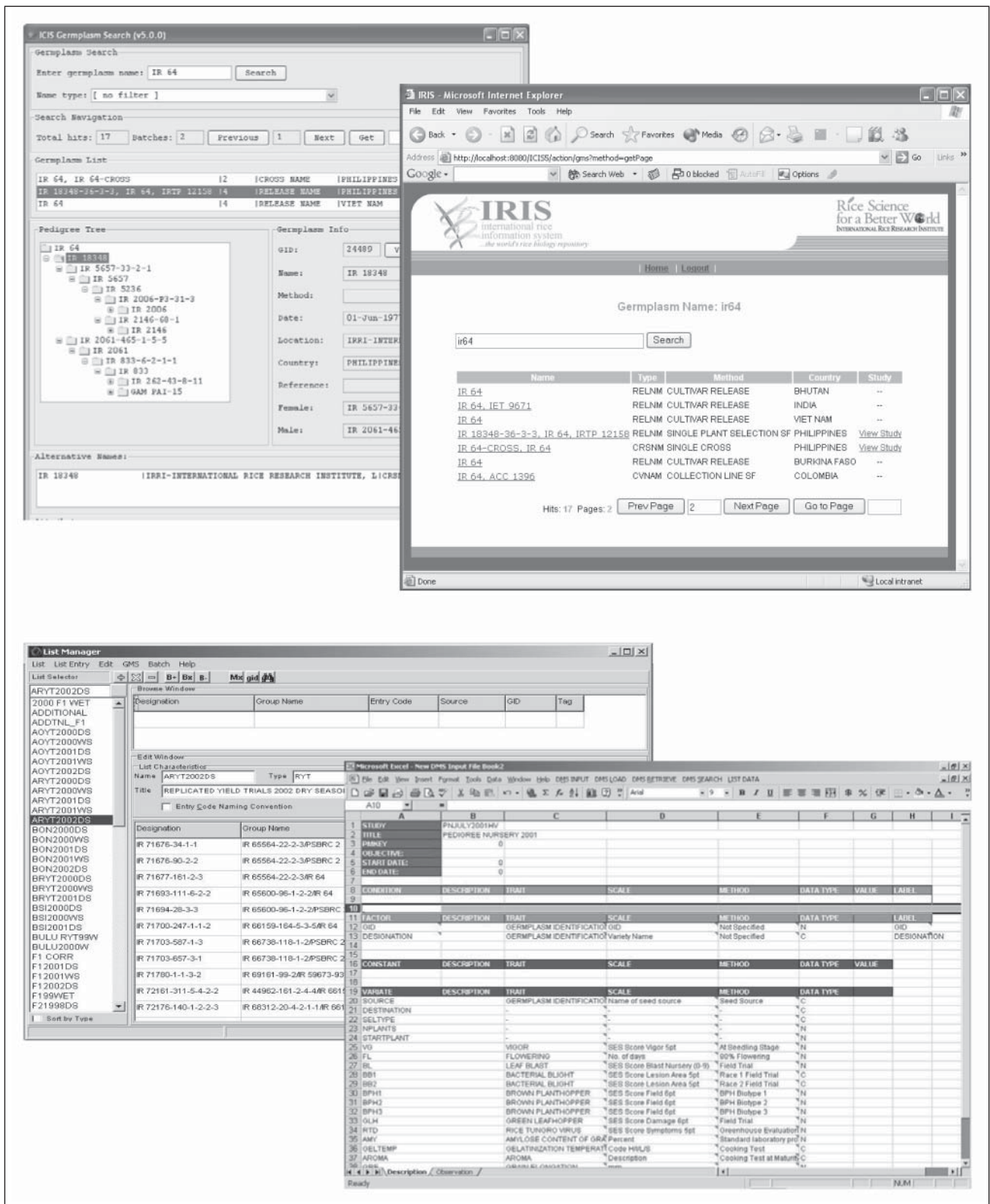
Fig. 3. Sample screen images of some ICIS software tools.

Future challenges

IRRI finds itself involved in various international research consortia and alliances, in particular, the International Rice Functional Genomics Consortium (IRFGC; www.iris.irri.org/IRFGC), the Generation Challenge Programme (GCP; www.generationcp.org) (Fig. 4), and a formal alliance with CIMMYT.[10] Such partnerships require much greater integration across data resources and research outputs, integration that will require the application of novel state-of-the-art bioinformatics methodology and technologies, developed as a team effort across many institutes. The GCP in particular has a formal subprogram for crop information platform and network development that is accelerating the pace of development of bioinformatics standards and tools for crop research. These tools will soon be freely downloadable from a Web site called "CropForge" (www.cropforge.org), which also now hosts the latest releases of ICIS software.

Summary

Bioinformatics is a rapidly expanding and evolving field. Like any such field, keeping up with new resources and methodology is a taxing quest. Many good introductory books are now available to help crop researchers apply bioinformatics to their own research problems (see Mount 2001, Gibas and Jambeck 2001, Lacroix and Critchlow 2003, Claverie and Notredame 2003, Baxevanis and Ouellette 2005). For rice researchers with a deeper interest in bioinformatics, there are a number of professional organizations to contact: globally, the International Society for Computational Biology (www.iscb.org) serves as a global community of practice in the field; the Asia Pacific Bioinformatics Network (www.apbionet.org) is a good regional source of bioinformatics information in Asia.

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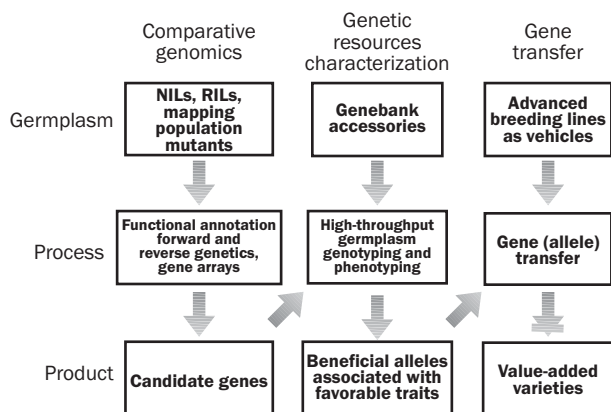
Fig. 4. Research agenda of the Generation Challenge Programme.

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[10]CIMMYT is the International Maize and Wheat Improvement Center located in Mexico. In January 2006, the biometrics, crop information, and bioinformatics teams across both institutes were merged into a single "Crop Research Informatics Laboratory" (CRIL) spanning crop information management and comparative biology research in rice, maize, and wheat.

Dhanrasi, a new lowland rice variety with *Oryza rufipogon* genes for improving yield potential and resistance to biotic stresses

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Rice production in the rainfed shallow lowlands in the eastern region and the favorable shallow lowlands in the southern region of India has, for a long time, remained stagnant. The potential of high-yielding varieties is not fully realized. Several breeding lines are being evaluated every year in these ecosystems in trials organized under the All India Coordinated Rice Improvement Program (AICRIP). When compared with national checks Salivahana and Pranava, none could qualify for release in favorable shallow lowlands in the southern region. However, in the rainfed shallow lowlands of the eastern region, CR1002 (1992) and Pooja (1999) were released for cultivation. This shows that yield improvement per se of varieties bred for these ecosystems, especially in favorable shallow lowlands, is limited, though improvement was considerable in quality and pest resistance as reflected by the release of several varieties at the state level.

Dhanrasi (C11-A-41) was released in 2002 for cultivation in the rainfed and favorable shallow lowlands in southern India, for the states of Andhra Pradesh, Tamil Nadu, Karnataka, and Maharashtra. It was developed by introgressing genes for yield components from one of the *Oryza rufipogon* accessions collected from the submerged areas in Moirang (Manipur, India). The *O. rufipogon* accession, which is resistant to blast and tungro and moderately resistant to bacterial blight, was crossed to high-yielding, medium-duration breeding line B32-Sel-4. The F_1 was crossed with another high-yielding, late-duration line, B127. In the F_2 population, 50 plants of B32-Sel-4/*O. rufipogon*//B127 with better agronomic traits were selected and intermated to develop 25 crosses. The selection against weedy traits was done in the F_1 and F_2 populations derived from intermating. Similarly, a second cycle of intermating in the resulting F_2 population was followed. Single-plant pedigree selection was followed after the second intermating cycle, considering plant height, number of tillers $plant^{-1}$, panicle length, number of grains $panicle^{-1}$, and grain yield $plant^{-1}$.

In the F_5 generation, 32 lines with better yield potential were evaluated along with their indica parents B32-Sel-4 and B127. They were screened for yield and for blast and bacterial blight resistance under natural and artificial infection. Eight lines were found to outyield both parents, by 10.2–21.4% in the preliminary yield trial. C11-A-41 yielded the highest (6.48 t ha^{-1}) and recorded a yield superiority of 38.2% and 21.4% over B32-Sel-4 and B127, respectively. The main agronomic characteristics of the parents and Dhanrasi are given in Table 1. The four lines with superior yield

Table 1. Important traits introgressed from *O. rufipogon* Griff into Dhanrasi (C11-A-41).

Trait	Parents			Dhanrasi
	B32-Sel-4	B127	*O. rufipogon*	
Yield trait				
Plant height (cm)	90–100	105–110	135–145	105–110
Days to 50% flowering	95 ± 5.2	100 ± 4.5	126 ± 6.5	117 ± 3.9
Panicles $plant^{-1}$ (no.)	10–12	8–12	20–27	12–14
Grains $panicle^{-1}$ (no.)	136 ± 12.3	145 ± 10.6	40 ± 15.2	210 ± 14.8
1,000-grain weight (g)	21.6	23.8	24.8	22.5
Grain type	Long slender	Short bold	Short bold	Short bold
Grain yield (t ha^{-1})	4.7	5.3	–	6.5
CD at 5% = 0.23				
Reaction to diseases and insect pests[a]				
Artificial screening				
Blast	S	S	Immune	R
Bacterial blight	S	S	MR	MR
Sheath blight	S	S	MR	MR
Rice tungro disease	S	S	R	MR
Natural field screening				
Stem borer	S	S	–	MR

[a]R = resistant, MR = moderately resistant, S = susceptible, – = not evaluated.

were evaluated under AICRIP auspices in 1996, 1997, 1998, and 1999. Yield comparisons were made, involving the newly bred high-yielding cultures, national checks (Salivahana and Pranava), the most popular variety Swarna, and the latest released Pooja, in four states of the southern region and two states in the eastern region. The same trial also screened for reaction to insect pests and diseases.

In multilocation testing under AICRIP in irrigated medium land, Dhanrasi (IET15358) yielded 5.28 t ha^{-1} in 1996, 13.3% and 2.5% higher than the yield national checks Pranava and Salivahana, respectively. It was superior to the highest yielding check by 7.8% in Tamil Nadu, 20.1% in Karnataka, and was on a par in Andhra Pradesh (Table 2). Dhanrasi was evaluated at seven locations in 1997, ranking first in overall yield (4.6 t ha^{-1}). This was 26.5% and 14.11% higher than the yield of Salivahana and Swarna, respectively. In Andhra Pradesh and Tamil Nadu, the yield superiority of Dhanrasi over Salivahana was 11.7% and 32.9% and 5.4% and 13.5% over Swarna, respectively. In 1998, this variety was evaluated at 10 locations, along with checks and other cultures, and it registered a mean yield of 4.4 t ha^{-1}, with 5.4% and 5.3% yield superiority over Salivahana and Pravana, respectively. It recorded the highest yield (7.3 t ha^{-1}) at Maruteru. In Andhra Pradesh and Karnataka, it showed 18.6% and 16.7% higher yield, respectively, than the best check Salivahana. In 1999, it had 8.7% higher yield than Salivahana, 6.2% higher yield than Swarna in Andhra Pradesh, and 11.7% and 19.7% over Salivahana and Swarna, respectively, in Karnataka (Table 2).

Dhanrasi was also evaluated with several newly bred cultures, national check Swarna, and newly released variety Pooja in the eastern and western regions of the country under rainfed shallow lowland conditions. It showed a yield superiority of 11.0% and 38.2% over Pooja and 4.3% and 8.8% over the highest yielding check in Orissa and Bihar, respectively. In Maharashtra, it outyielded check variety Salivahana and Swarna, by 3.8% and 22.5%, respectively.

In overall yield performance, Dhanrasi outyielded Salivahana by 7.4%, Pranava by 9.24%, Swarna by 10.36%, and Pooja by 24.6%. Maximum yield was 6.58 t ha^{-1} in 1996, 5.63 t ha^{-1} in 1997, 7.31 t ha^{-1} in 1998, and 6.10 t ha^{-1} in 1999. Besides its high yield potential, Dhanrasi has also introgressed genes from *O. rufipogon* for resistance to blast and moderate resistance to tungro and bacterial blight.

Considering its higher yield potential, disease and pest resistance, and very stable yield, Dhanrasi was released for cultivation in Andhra Pradesh, Tamil Nadu, Karnataka, and Maharashtra in 2002-03.

Table 2. Yield performance of Dhanrasi (C11-A-41) in rainfed and favorable shallow lowland ecosystems in different states under multilocation (AICRIP) testing.

| State | Year of testing | Locations (no.) | Grain yield (t ha^{-1}) | | | | Percent yield increase over | |
| | | | Dhanrasi (IET15358) | National check | | Swarna | Best check | Swarna |
				Salivahana	Pravana			
Favorable shallow lowland								
Andhra Pradesh	1996	2	6.2	6.1	6.2	–	0.8	–
	1997	3	4.5	4.0	–	4.2	11.9	5.4
	1998	2	5.8	4.9	4.8	–	18.6	–
	1999	1	5.1	4.7	–	3.2	8.7	62.0
Mean			5.4	5.0	5.5	3.7		
Tamil Nadu	1996	2	5.5	5.1	4.1	–	7.8	–
	1997	2	5.0	3.8	–	4.3	32.9	13.5
	1998	2	4.6	5.7	5.3	–	–18.9	–
	1999	2	5.1	5.0	–	4.9	1.8	9.3
Mean			5.1	4.9	4.7	4.6		
Karnataka	1996	3	4.5	3.8	3.5	–	20.1	–
	1998	3	4.3	3.3	3.7	3.6	16.1	21.3
	1999	2	5.0	4.5	–	4.2	11.7	19.7
Mean			4.6	3.9	3.6	3.9		
Rainfed shallow lowland								
Maharashtra	1998	3	3.5	3.2	3.5	–	0.3	–
	1999	3	3.6	3.5	–	2.9	3.8	22.5
Mean			3.5	3.3	3.5	2.9		
Orissa	1999	2	3.9	3.7	3.4	3.5 (Pooja)	4.3	11.0
Bihar	1999		4.8	4.4	4.0	3.5 (Pooja)	8.8	38.2
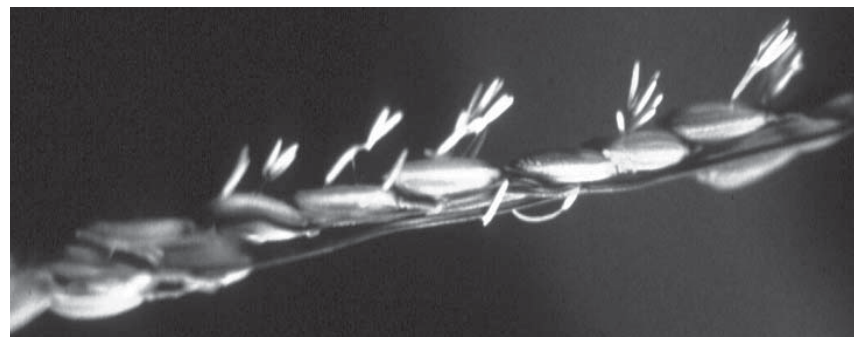
NDR2026: a new rice variety released for mid-early irrigated areas of Uttar Pradesh, India

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In irrigated areas in Uttar Pradesh, the rice-wheat and rice-potato cropping patterns are most common. Early-maturing (110–120 d) rice varieties are in great demand and so are those with high yield potential and resistance to prevalent pests and diseases. There are limited releases (Narendra 80 and Saket 4) of this mid-early irrigated group. These varieties are grown to increase the overall productivity of such areas. Released by the State Variety Release Committee of Uttar Pradesh in October 2004, NDR2026 (IET14998) is one of the new additions in the mid-early group.

This variety was developed through a three-way cross—SIPI 632-63/Chainung Sen yu 47// Taichung Sen 12. The breeding material came from IRRI under an institutional collaborative program. Single-plant selection to identify varieties with the desirable trait of mid-early maturity was made and the pedigree breeding method was applied in developing NDR2026. To as-sess the yield performance in local/station trials, the culture was nominated in the All-India Coordinated Rice Improvement Programme (AICRIP) during the 1995 wet season (WS). The performance of NDR2026 and other cultures during the 1995-97 WS is presented in Table 1. NDR2026 consistently outyielded check varieties for 3 y. It is 90–95 cm tall, produces 9–14 tillers plant^{-1} with semicompact panicle, is awnless, has 1,000-grain weight of 23 g, and matures in 110–115 d. It has high milling recovery (67%). Its long slender grains (6.71 mm length, 2.05 cm breadth, and L/B of 3.27) make it more attractive.

In the state adaptive trials during 1999-2000 WS, NDR2026 consistently outyielded check varieties in different regions (Table 2). The average yield of NDR2026 was 3.9 t ha^{-1}, higher than that of the highest yielding check variety, Narendra 80 (3.0 t ha^{-1}). The average yield advantage was about 22%. This variety is moderately resistant to brown spot, sheath

Table 1. Yields (t ha^{-1}) of NDR2026 and check varieties, advanced variety trial^a-irrigated mid-early, 1995-97 wet seasons.

Year	Locations (no.)	NDR2026	Checks		
			Ratha (national)	Vikas (national)	NDR80 (local)
1995 WS	7	3.6	2.6	2.7	3.2
1996 WS	10	4.3	3.8	3.7	4.0
1997 WS	11	4.0	3.8	3.0	3.6
Mean percentage yield advantage over checks	28	4.0	3.4	3.2	3.6
1995			+40.26	+30.70	+12.35
1996			+15.38	+19.14	+10.57
1997			+6.50	+32.38	+12.07
Percentage advantage over 3-y means			+18.34	+26.72	+11.74

^{a}Conducted in adaptability zone 2: Uttar Pradesh, Madhya Pradesh, and Assam.

Table 2. Comparative yield performance (t ha^{-1}) of NDR2026 in adaptive trials at the Regional Agriculture Testing and Demonstration Stations (RATDS), 1999-2000 wet seasons.^{a}

Culture	Eastern region			Western region			Central region	Bundel khand region (northern Uttar Pradesh)	Tarai region (southern Uttar Pradesh)	State mean
	Varanasi	Azamgarh	Barabanki	Meerut	Bareilly	Mathura	Hardoi	Jhansi	Haldwani	
NDR2026	4.3	3.5	4.9	5.4	2.9	4.3	1.9	3.4	3.8	3.9
HUR1006	–	2.8	3.8	3.3	3.0	–	–	2.6	3.2	3.1
Narendra 80 (check)	3.7	–	–	3.2	2.5	–	2.3	–	–	3.0
Saket 4	3.4	2.9	4.1	3.5	2.7	–	1.5	2.5	3.1	2.9

^{a}Source: RATDS combined report for 1999-2000 WS.

blight, and sheath rot under natural field conditions. It has some degree of tolerance for stem borer, whorl maggot, and leaffolder. To validate its yield performance, NDR2026 was extensively evaluated in farmers' fields in different districts of eastern Uttar Pradesh (Faizabad, Sultanpur, Barabanki, Gonda, and Ambedkarnagar) during 2000-01 WS (Table 3). It recorded a significantly stable yield advantage over check varieties Narendra 80 and Saket 4.

The results show that NDR2026 is well suited for irrigated conditions and may be best for use in rice-wheat and rice-potato cropping systems because of its consistent yield superiority, disease and pest resistance, and excellent grain quality. This variety will be a good replacement for Narendra 80, which was released in the early eighties.

Table 3. Yield performance of NDR2026 in farmers' fields in eastern Uttar Pradesh, 2000 and 2001 wet seasons.

District	Locations (no.)	Yield (t ha^{-1})		
		NDR2026	Narendra 80	Saket 4
Ambedkarnagar	5	5.4	4.7	4.4
Faizabad	6	5.4	4.8	4.5
Gonda	3	5.2	4.8	4.6
Sultanpur	5	4.9	4.5	4.6
Barabanki	3	5.1	4.8	4.3
Mean	22	5.2	4.7	4.5

CSR23: a new salt-tolerant rice variety for India

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A vast area of sodic soils in India lies in the provinces of Uttar Pradesh and Haryana, whereas coastal saline soils are spread throughout the coastline of India running through Maharasthra, Gujarat, Kerala, Tamil Nadu, West Bengal, and Pondicherry. Most of these areas lie barren or produce low yields. However, these same areas can be transformed into arable and highly productive land if suitable salt-tolerant crop varieties are available. The rice crop is the obvious choice in coastal and sodic areas as it can withstand standing water and also sustain salt stress.

The major problem in alkaline soils is the exchangeable sodium percentage (ESP) that raises soil pH from more than 8.5 to more than 10.0. This consequently exerts high sodicity stress throughout the crop's growth period and affects nutrient availability. However, in coastal saline areas, stress varies with crop growth as salinity regime is highly variable. High water depth submerges the crop during its growth and this ranges from a few days to a few weeks. Farmers need a high-yielding, salt-tolerant variety with strong culm and intermediate stature, which can enable it to survive water stagnation as well. Unfortunately, most of the varieties in such areas are traditional types with poor grain quality and low yielding ability due to salt sensitivity and susceptibility to lodging. These areas require a rice variety with intermediate stature and medium to fine grain qualities, and that is nonlodging, nonshattering, high-yielding, and fertilizer-responsive, and has high salt tolerance. In this regard, CSR23 is a good candidate.

CSR23 (IET13769) is a high-yielding, salt-tolerant variety with medium slender grains. It is derived from a three-way cross (IR64//IR4630-22-2-5-1-3/IR9764-45-2-2) made in the Plant Breeding, Genetics, and Biotechnology Division, IRRI, Philippines. The breeding materials in the form of advanced bulk populations (ABPs) were received in 1989 by the Central Soil Salinity Research Institute, Karnal, from IRRI under the ICAR–IRRI Collaborative Research Project on "Germplasm improvement for saline soils in rice." This included ABP no. 085 (IR52713-2B-8-2B), selection from which consequently resulted in the development of CSR23. All the ABPs were screened under artificially created stress environments in concrete microplots and natural hot spots.

Variety CSR23 was entered in the All-India Coordinated Rice Improvement Program through a national salinity trial. It was tested under the Saline Alkaline Tolerant Varietal Trial (SATVT) in 1994 as CSR-89IR-5 (IET13769) and evaluation was repeated in 1995, 1996, and 1997. Later, agro-

nomic comparison with standard checks was done to assess yielding ability under varying nitrogen regimes. Based on its superiority shown over the years, this variety was identified in 2003 and, upon recommendation of the Central Sub-Committee on Crop Standards, Notification, and Release of Varieties, was released in 2004 by the Ministry of Agriculture, Government of India, for alkaline soils of Uttar Pradesh and Haryana and the coastal saline soils of Maharasthra, Gujarat, Tamil Nadu, Kerala, and West Bengal. A sister line (IR52713-2B-8-2B-1-2), derived from the same cross, was also released in the Philippines as PSBRc 88 in 1999.

In the coordinated trials over the years, CSR23 has shown a consistent increase over all the checks and qualifying varieties throughout the years of testing for salt tolerance—1994 to 1997. It recorded a yield increase over all checks by as much as 125% over Usar 1, 90% over Vyttila 4, 104% over Jaya, 51% over Panvel 1, and 37% over CSR10. It was convincingly superior to all the checks (Fig. 1, see table).

CSR23 has intermediate plant stature (115–120 cm) with fully exserted panicles, is awnless, has purple stigma, and takes 100–105 days to 50% flowering. Its grain is the medium slender type with 5.8 mm length and a length-breadth ratio of 2.8. It is best-suited to meet most of the requirements in the problem areas. It can withstand the sodicity stress up to pH2 ~ 10.0 and salinity (ECe) up to 8 dS m^{-1}. It has high yield (even on nonstressed or moderately stressed soils) and a high degree of salt tolerance. Field screenings showed its moderate resistance to blast, neck blast, and brown spot. Besides having other desirable agronomic traits, it was found
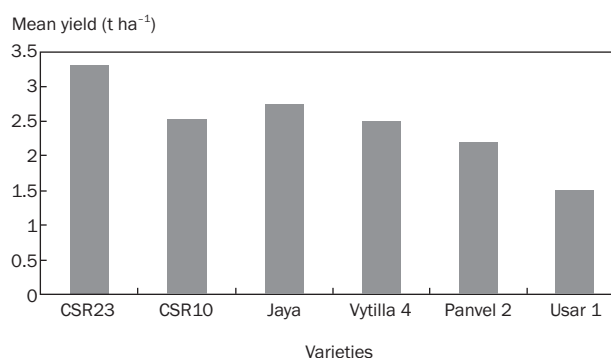
Fig. 1. Summary mean yield performance of CSR23 in comparison with check varieties (1994-97).

Grain yield evaluation of CSR23 under coordinated trials (1994-97).

	Year	Trials (no.)	CSR23	Salt-tolerant checks				High-yielding check
				CSR10	Vyttila 4	Panvel 2	Usar 1	Jaya
Mean yield	1994	11	3761	2,971	–	–	–	2,991
(kg ha^{-1})	1995	10	3027	2,398	2,748	–	–	3,302
across	1996	6	3342	2,428	1,758	2,203	1,493	1,638
locations	1997	10	2973	2,214	2,714	–	–	2,614
	Mean		3297	2,539	2,519	2,203	1,493	2,775
Yield	1994			+26.6	–	–	–	+25.7
advantage	1995			+26.2	+10.1	–	–	–8.3
over checks	1996			+37.6	+90.1	+51.7	+124.8	+104.0
(%)	1997			+34.3	+9.5	–	–	+13.8
	Mean			+29.9	+30.9	+49.7	+120.8	+18.8

Fig. 2. Salt-tolerant CSR23.

resistant to leaffolder and moderately resistant to gall midge biotype 5. CSR23 has intermediate tissue tolerance, better K^+ uptake, and Na^+ exclusion ability, desirable attributes of a salt-tolerant variety.

There is a great demand for this variety in Uttar Pradesh and other states. The Uttar Pradesh Land Development Corporation (UPLDC) in Lucknow conducted adaptive "on-farm" trials in salt-affected fields at 19 locations in Uttar Pradesh and got a 4.5 t ha^{-1} average yield (large-plot basis). The variety has become popular and there was a great demand for its seed from agencies such as UPLDC, which has targeted the reclamation of more than 140,000 ha of sodic land. The average grain yield of this variety, recorded in station trials in various years, was 6.5–7.0 t ha^{-1} under normal soil conditions. These results demonstrate the yield stability of the new variety for saline and nonsaline field conditions.

Rajendra Sweta, a new high-yielding quality rice variety for Bihar's irrigated ecosystem

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After the introduction of high-yielding rice varieties in the 1960s, breeding programs were started in India to develop high-yielding semidwarf lines. One decade later, research efforts focused on developing high-yielding quality rice. Both customers and farmers appreciate fine-grained quality rice as it fetches a high market price.

Rajendra Sweta (RAU710-99-22) was developed from the cross Sita/Pusa Basmati-1//Katarni, varieties with superior grain quality and high yield potential. The State Variety Release Committee of Bihar approved the release of Rajendra Sweta for the irrigated ecosystem in 2004.

Rajendra Sweta is a photoperiod-insensitive, medium-maturing, semidwarf variety with good grain quality (Table 1). The variety was tested in breeding trials in Bihar from 2000 to 2003. It gave a higher average yield (3.5 t ha^{-1}) than did the checks Pusa Basmati 1 (2.3 t ha^{-1}) and Sugandha (2.7 t ha^{-1}) (Table 2). In a nutrient-use efficiency trial, Rajendra Sweta gave the highest grain yield at 80-40-20 kg NPK ha^{-1} nutrient level (Table 3).

Rajendra Sweta was tested in 55 farmers' fields in Bihar from 2001 to 2003. It had an average yield of 4.7 t ha^{-1} and a 10% yield advantage over the local check varieties. In 18 front-line demonstrations, its average yield was 4.9 t ha^{-1}, while that of the check was 3.9 t ha^{-1}. Yield consistency and wide adaptability under varying agroclimatic conditions are some of the merits of this new variety.

Table 1. Morphological and grain quality characteristics of Rajendra Sweta and Pusa Basmati 1.

Characteristic	Rajendra Sweta	Pusa Basmati 1
Plant height (cm)	85–90	85–90
Duration (d)	135–140	130–135
Plant type	Erect, compact	Erect, compact
Tillers hill^{-1} (no.)	10–15	8–10
Panicle type	Compact	Compact
Panicle exsertion	Compact	Compact
Awn	Awnless	Awned
Hulling (%)	79.2	80.0
Milling (%)	70.0	69.6
Head rice recovery (%)	66.0	57.3
Kernel length (mm)	5.03	7.25
Kernel breadth (mm)	1.65	1.8
Length-breadth ratio	3.04	4.02
Grain type	Medium and slender	Long and slender
Grain chalkiness	Occasionally present	Occasionally present
Volume expansion ratio	4.8	5.4
Water uptake (mL)	250	375
Alkali spreading value	4.0	7.0
Amylose content (mm)	23.6	24.8
Gel consistency	63	63

Table 2. Performance of Rajendra Sweta in breeding trials at four sites in Bihar, India, 2000-03.

Entry	Av grain yield (t ha^{-1})					Increase over check (%)
	Patna	Bikramganj	Pusa	Sabour	Mean	
Rajendra Sweta	4.2	4.4	3.3	1.9	3.5	–
Pusa Basmati 1 (check)	2.4	3.1	2.0	1.8	2.3	52.2
Sugandha (check)	2.7	2.8	3.2	2.0	2.7	29.6

Table 3. Performance of Rajendra Sweta in nutrient-use efficiency trials in Bihar, India, 2002-03.

Entry	Av grain yield (t ha⁻¹)			Mean	Increase over check (%)
	N1 (40-40-20 kg NPK ha⁻¹)	N2 (80-40-20 kg NPK ha⁻¹)	N3 (120-40-20 kg NPK ha⁻¹)		
	Patna				
Rajendra Sweta	3.4	4.5	4.2	4.0	–
Pusa Basmati 1 (check)	2.5	3.2	2.9	2.9	38.0
	Bikramganj				
Rajendra Sweta	2.5	4.6	4.8	4.0	–
Pusa Basmati 1 (check)	2.5	3.8	3.9	3.3	21.2
	Pusa				
Rajendra Sweta	2.8	3.4	2.8	3.0	–
Pusa Basmati 1 (check)	2.3	2.3	2.2	2.3	30.4

Karjat 6, a new, superfine medium-duration rice variety in Maharashtra, India

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Rice is grown on 1.5 million ha in Maharashtra State, India. Of the total area under rice, about 56% is planted to fine and superfine varieties; the rest is under coarse-grained varieties. Early, medium-late, and late varieties, respectively, occupy about 40%, 40%, and 20% of the area in the state. Because fine-grained varieties are preferred, the Karjat rice research station developed Karjat 4, an early-maturing variety (115–120 d), and Karjat 6, a medium-duration (130–135 d) line suitable to the varied agroecological conditions in the state.

Karjat 6 (KJT-12-6-25-9-13-50-13) was developed through the pedigree method. It involved a cross of Heera and Karjat 4. Recommended for commercial cultivation in Maharashtra in 2005, Karjat 6 is a semidwarf (95–100 cm) variety having short, slender grains, 1,000-kernel weight of 13.30 g, and average grain yield of 3.5–4.0 t ha⁻¹. The variety has 68.1% milling and 65% head rice recovery. Its other grain characteristics are given in Table 1.

Karjat 6 recorded an 8.6% and 5.3% yield advantage over check Mahsuri in initial and advanced station trials conducted in 2000 and 2001 kharif, respectively (Table 2). It has given a 10.3% and 33.3% increase in grain yield over the check in the state coordinated trials in 2002 and 2003 kharif, respectively, at nine locations in the state.

The variety recorded a 5.7% increase in yield over the check in the All India Coordinated trial conducted at 22 locations in the country during 2004 kharif. A yield increase of 23.7% was observed in 19 adaptive trials conducted in farmers' fields at the same time (Table 2). Karjat 6 gave a 28.9% increase in grain yield with the application of 100 kg N ha⁻¹ over the 50-kg treatment in 2004 kharif. It has recorded

Table 1. Grain characteristics of Karjat 6 compared with Samba Mahsuri.

Characteristic	Karjat 6	Samba Mahsuri (BPT5204)
Milling (%)	68.1	70.1
Head rice recovery (%)	65.0	67.5
Kernel length (mm)	5.51	4.99
Kernel breadth (mm)	1.80	1.79
Length-breadth ratio	3.06	2.78
Volume expansion ratio	5.5	4.7
Water uptake (mL)	210	170
Kernel length after cooking (mm)	8.1	9.2
Elongation ratio	1.70	1.84
Alkali spreading value	4.5	5.0
Amylose content (%)	25.43	25.25
Gel consistency (mm)	43	43
Grain type	Short, slender	Medium, slender
Grain chalkiness	Absent	Absent

a 10.5% increase in grain yield over check Karjat 4 in front-line demonstrations during the 2004-05 rabi season. Screening trials showed that it is resistant to leaffolder, stem borer, and neck blast. Karjat 6 will become popular in the state in view of its superior grain type, high yield potential, and good quality traits.

Table 2. Yield performance of Karjat 6 in different trials and demonstrations conducted at different locations.

Trial	Av grain yield (t ha⁻¹)		Increase over check (%)
	Karjat 6	Check	
Initial variety trial (station), 2000	3.8	3.5	8.6
Advanced variety trial (station), 2001	4.0	3.8	5.3
State-coordinated trial (initial) (9 locations), 2002	3.2	2.9	10.3
State-coordinated trial (advanced) (9 locations), 2003	3.6	2.7	33.3
AICRIP trial-SG (22 locations), 2004	3.7	3.5	5.7
Adaptive trial (19 locations), 2004	4.9	3.8	23.7
Agronomic trial, 2004	4.0	3.2	28.9
Field demonstration, 2004-05	6.3	5.7	10.5
Av	4.18	3.63	15.2

Sahyadri 2, an early rice hybrid for Maharashtra State in India

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In India, rice is predominantly grown on 1.4 million ha of traditional and 0.9 million ha of nontraditional areas in the state of Maharashtra. Average productivity is 1.7 t ha⁻¹. A total of 53 high-yielding rice varieties (HYVs) have been released for commercial cultivation in the state for various agroecological conditions. The productivity of rice nevertheless remained stagnant during the last decade. The adoption of rice hybrids, along with proper crop management practices, is certainly an alternative for increasing productivity in the state. The RARS in Karjat, District Raigad, has identified and released the first rice hybrid, Sahyadri, for commercial cultivation. It has medium-late growth duration and a high yield potential, (6.5–7.5 t ha⁻¹). The area under hybrid rice is increasing gradually in the state, but nearly 60% is planted to early-duration rice varieties. Efforts were therefore made to develop suitable early-duration rice hybrids with desirable characteristics to increase rice productivity.

Karjat rice hybrid 3 (KJTRH 3) was developed at RARS and was released as Sahyadri 2 for commercial cultivation in Maharashtra in 2004. Seed production of Sahyadri 2 was easier because of less staggered flowering between parental female and male lines of the hybrid. Therefore, ample seed production is possible on a large scale in suitable areas to meet demand for seed.

The new hybrid meets farmers' requirements in both state and country and its adoption may contribute to higher rice production and productivity (Tables 1–3).

Table 1. Morphological and grain quality characteristics of Sahyadri 2.

Characteristic	
Duration (d)	115–120
Plant height (cm)	114–119
Yield (t ha⁻¹)	6.0–6.5 (potential, 12.1)
Tillers hill⁻¹ (no.)	15–20
Grains panicle⁻¹ (no.)	175–200
Panicle length (cm)	25.5
1,000-grain weight (g)	23.5
Milling (%)	70.2
Head rice recovery (%)	56.0
Kernel length (mm)	6.63
Kernel breadth (mm)	2.18
Length-breadth ratio	3.04
Grain type	Long and slender
Alkali value	6.0
Amylose content (%)	20.89
Grain chalkiness	Occasionally present
Reaction to diseases/insect pests	
False smut	Highly resistant
Bacterial blight	Resistant
Blast	Resistant
Sheath rot	Moderately resistant
Brown spot	Moderately resistant
Rice tungro virus	Moderately resistant
Stem borer	Moderately resistant
Brown planthopper	Moderately resistant

Table 2. Yield performance of Sahyadri 2 in the All India Coordinated Trials, by region, 2001-02.

Season/year	Av yields (t ha⁻¹) in different regions[a]					% mean yield advantage over different checks[b]		
	RM2	RM3	RM4	RM5	Overall mean	National check[b]	Regional check[c]	Local check[d]
2001 kharif	6.6	4.3	6.0	6.5	5.8	21.6	22.4	8.3
2002 kharif	6.1	3.1	6.2	5.1	5.0	27.2	28.8	8.9
Av	6.3	4.1	6.1	5.8	5.4	24.4	25.6	8.6

[a]RM2: Delhi, Uttaranchal, Punjab, Haryana, Jammu plains, and Rajasthan; RM3: Orissa, Bihar, Jharkand, West Bengal, Uttar Pradesh, Chhattisgarh, Madhya Pradesh, Tripura, Manipur, Meghalaya, and Assam; RM4: Maharashtra and Gujarat; RM5: Andaman, Nicomar, Andhra Pradesh, Tamil Nadu, Kerala, Karnataka, and Pondicherry. [b]Annada (2001) and Govinda (2002). [c]Tulsi. [d]Karjat 3.

Table 3. Yield performance of Sahyadri 2 under different trials and demonstrations in Maharashtra State.

Type of trial	Season and year	Av yield (t ha⁻¹)		Advantage over Ratna (%)
		Sahyadri 2	Ratna (check)	
Observational yield trial	Kharif, 2001	5.6	4.1	37.1
Station trial	Kharif, 2001	5.6	4.1	35.5
State-coordinated trials	Kharif, 2001	4.7	4.3	11.9
State-coordinated trials	Kharif, 2003	5.5	4.5	20.1
State-coordinated trials	Kharif, 2004	5.8	4.3	36.6
Adaptive trials in farmers' fields (21 sites)	Kharif, 2003-04	7.8	6.1	27.1
Demonstration	Kharif, 2003-04	8.4	6.2	34.7
Agronomic trial	Kharif, 2004	5.3	3.8	36.6
Adaptive trials in farmers' fields (40 sites)	Kharif, 2004	6.4	4.1	35.2
Av		6.1	4.6	30.5

Analysis of *Pyricularia grisea* populations from three different blast epidemics

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In spite of a great deal of research on the blast pathogen (*Pyricularia grisea* (Cooke) Sacc., an anamorph of *Magnaporthe grisea* (T.T. Hebert) Yaegashi & Udegawa) of rice and the disease itself, blast remains a serious constraint to rice production in areas with conducive environments and where susceptible cultivars are grown. There has been no effort to analyze the pathogen populations that occurred during the blast epidemics in India. Three of these epidemics occurred in the state of Orissa in the past decade. The first epidemic was in Banki, Cuttack District, in the 1997 wet season, during which traditional rice cultivars Laghubhutia and Golabondi were heavily infected by neck blast. The second epidemic, in the wet season of 2000 in Dhenkanal, Dhenkanal District, involved traditional cultivar Latamohu and high-yielding semidwarf Dhala Heera. They got severely infected by leaf blast. During the third epidemic (2002 wet season, Ganjam District), high-yielding variety Swarna grown in farmers' fields was severely infected by leaf blast.
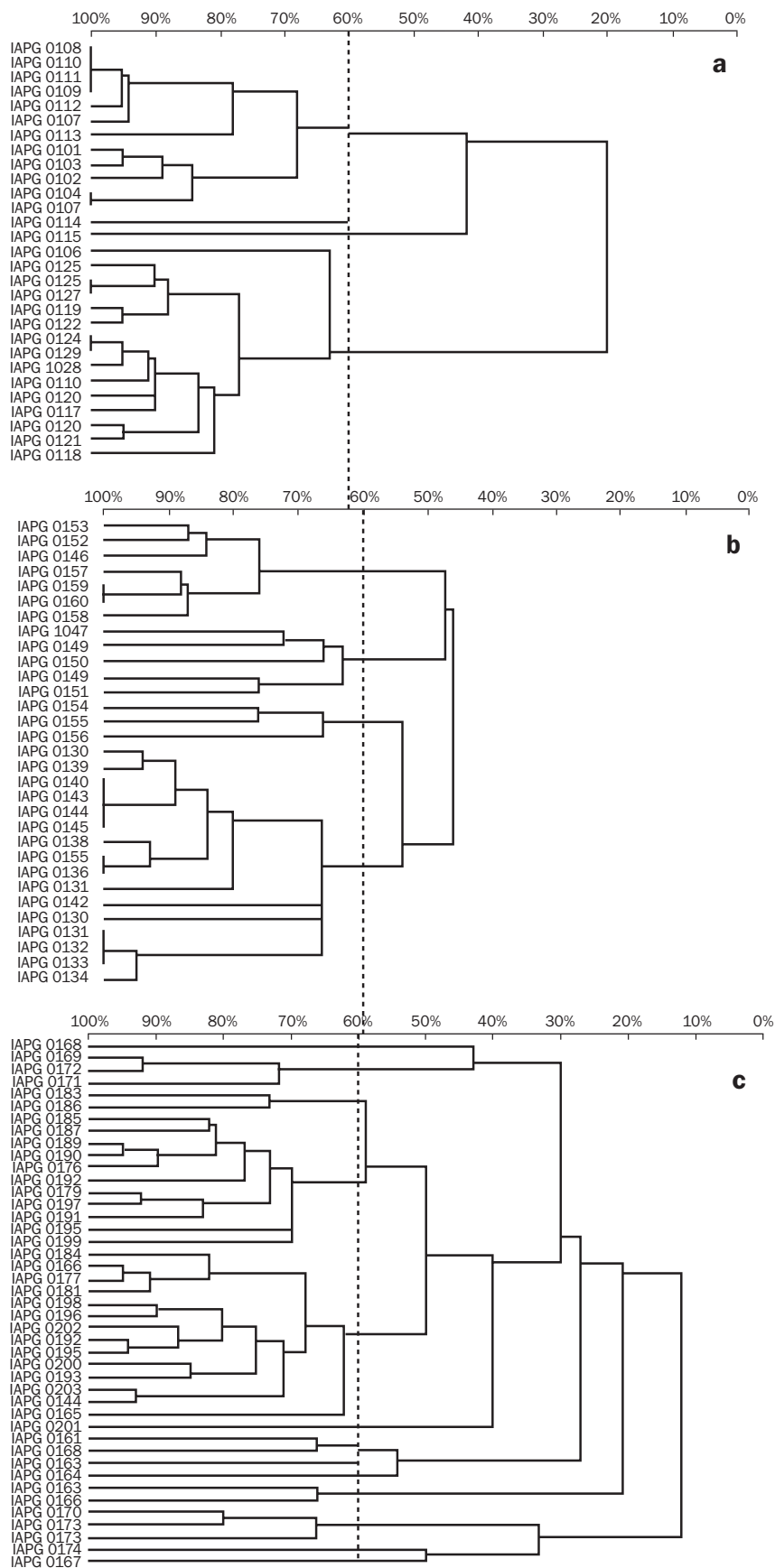
A repetitive element-based polymerase chain reaction (rep-PCR), with primer sequences from Pot2 (an element found in approximately 100 copies in the *P. grisea* genome), provides an efficient way to monitor the population dynamics of the blast pathogen. This method is compa-

rable with that determined with MGR586 restriction fragment length polymorphism lineages (George et al 1998). Our analysis clearly brought out the population structure of the pathogen in the three blast epidemics and showed the difference between traditional and modern rice cultivars.

Three sets of monoconidial isolates of the pathogen *P. grisea* were obtained from infected leaf/neck blast samples collected from farmers' fields during the epidemics. Totaling 103, these were stored on filter paper bits at –20 °C and were used for DNA fingerprinting (Table 1). Genomic DNA was extracted following the procedure of Murray and Thompson (1980) for plant DNA with modifications for mini-scale preparation as described by Scott et al (1993). Polymerase chain reaction with primers Pot2-1 (5' CGGAAGCCCTAAAGCTGTTT 3') and Pot2-2 (5' CCCTCATTC-GTCACACGTTC 3') and visualization of the DNA fragments were as described previously (George et al 1998). The gel images were photographed using a gel documentation system equipped with Bio-Capt software (Vilber Lourmat, France). The structure of the pathogen population was analyzed using the Bio-1D++ software (Vilber Lourmat, France). For each band position between 400 bp and 23 kb, the presence or absence of the band

was indicated by this software in a computer for each isolate. The binary matrix indicating presence or absence of the bands was used to construct a matrix of similarities between all pairs of isolates based on Dice's coefficient (F = 2Nxy + Ny), where Nxy is the total number of bands observed for that pair of isolates.

Fingerprint patterns of *P. grisea* subpopulations from Banki (29 isolates), Dhenkanal (31 isolates), and Berhampur (43 isolates) revealed the presence of 23, 24, and 43 haplotypes, respectively. The Banki population was differentiated into three lineages of the pathogen at 60% similarity (Fig. 1a). Two of the lineages detected were obtained from a single cultivar, Golabondi, whereas the third lineage was obtained from the other cultivar, Laghubhutia. However, one of the isolates obtained from the former cultivar belonged to the third lineage. The Dhenkanal population obtained from two rice cultivars (Dhala Heera and Latamohu) was grouped into four lineages of the blast pathogen (Fig. 1b). All the isolates belonging to the first three lineages were obtained from Dhala Heera, which is a modern semidwarf variety, while the isolates of the fourth lineage were obtained from Latamohu, which is a traditional rice cultivar. The subpopulation of the pathogen isolates obtained from the blast epidemic in Berhampur was dif-

ferentiated into 12 lineages (Fig. 1c). Interestingly, all the isolates of the subpopulation of the pathogen were obtained from a single modern rice cultivar, Swarna, which was the predominant variety in farmers' fields in this location. In general, traditional rice varieties were infected by a single predominant lineage of the pathogen during epidemics, whereas modern rice cultivars were infected by multiple lineages of the blast pathogen (Fig. 2).

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Fig. 1. Dendrogram constructed with UPGMA on the basis of Pot2 repetitive element-based polymerase chain reaction fingerprint data of *Pyricularia grisea* **for a collection of 29 isolates from two rice cultivars: Golabondi (isolates: IAPG 0101–IAPG 0115) and Laghubhutia (isolates: IAPG 0116–IAPG 0129) grown in Banki (a); 31 isolates from two rice cultivars: Latamohu (isolates: IAPG 0130–IAPG 0145) and Dhala Heera (isolates: IAPG 0146–IAPG 0160) grown in Dhenkanal (b); and 43 isolates from a single rice cultivar Swarna (isolates: IAPG 0161–IAPG 0203) grown in Berhampur (c). Homology level of 60% is marked with broken lines vertically.**
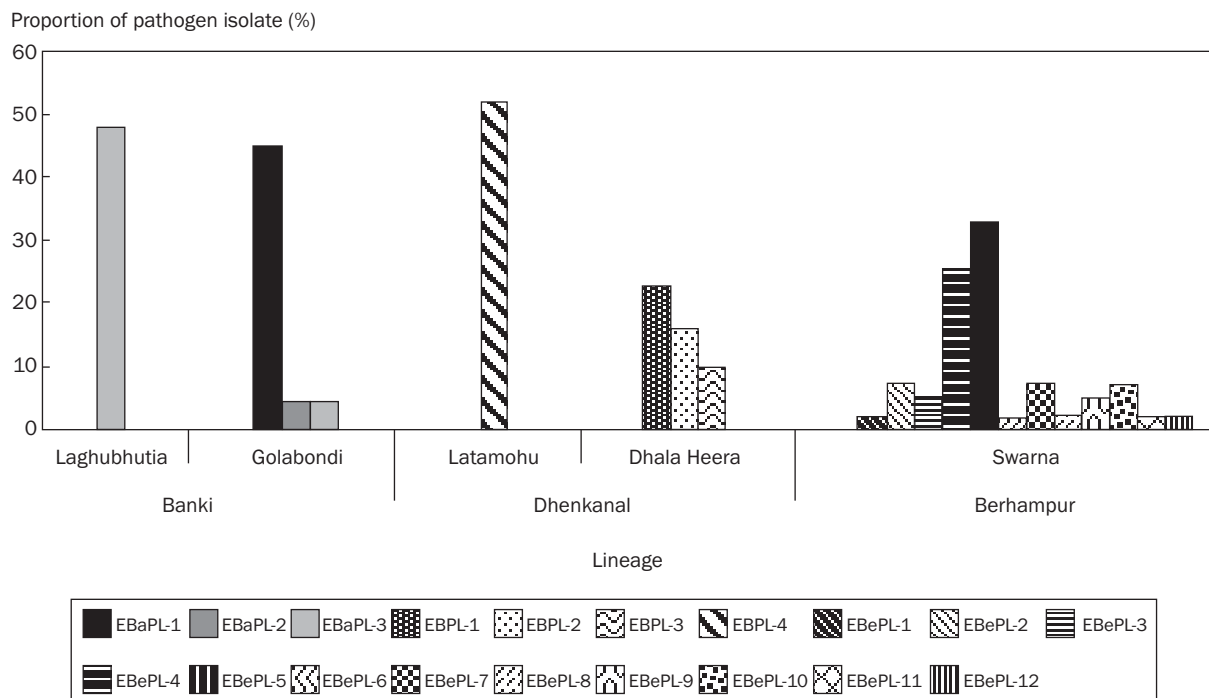
Fig. 2. Occurrence of different blast pathogen lineages in three different blast epidemic outbreaks at Banki, Dhenkanal, and Berhampur in the state of Orissa.

Isolates of *Pyricularia grisea* collected from farmers' fields in epidemic regions for comparative study.

Site	District in Orissa	Ecosystem	Season[a]	Rice genotypes	No. of isolates		
					Tissue		
					Leaf	Neck	Total
Banki	Cuttack	Rainfed upland	1997 WS	Laghubhutia and Golabondi	–	29	29
Dhenkanal	Dhenkanal	Rainfed upland	2000 WS	Latamohu and Dhala Heera	31	–	31
Berhampur	Ganjam	Rainfed upland	2002 WS	Swarna	43	–	43
Total					74	29	103

[a]WS = wet season.

Record of a hyperparasitoid on *Pseudogonatopus nudus* Perkins (Dryinidae: Chrysidoidea) parasitizing *Nilaparvata lugens* (Stål) from Asia

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Plant- and leafhoppers of rice are well-recognized noxious pests and severe populations have often caused serious rice yield losses. Many natural enemies are reported on these hoppers in rice. Among the parasitoids, mymarids and trichogrammatids are the most common. The rest of the parasitoids, dryinids, pipunculids, strepsipterans, and vellids, are unstable but still contribute to the biological management of hoppers.

In a routine attempt to collect dryinids, parasitized brown planthopper (BPH) and green leafhopper (GLH) nymphs and adults showing the larval sac protrusion symptom were collected during the 2004 Kuruvai crop (July-Sep). They were transferred to potted plants under greenhouse conditions and reared till

the matured dryinid larvae came out and pupated on the surface of the culm region. Surprisingly, from a few pupae of dryinids, instead of dryinid adults emerging, other parasitoids came out. Later, these parasitoids were identified as *Cheiloneurus exitiosus* (Perkins) [*Echthrogonatopus nigricornis* (Hayat) is a synonym] belonging to the family Encyrtidae. It is a larval-pupal parasitoid. This hyperparasitoid on dryinid (*Pseudogonatopus nudus*) Perkins, seems to be the first record from Asia.

This encyrtid hyperparasitoid was reared in the laboratory on 50% honey solution and its oviposition behavior and host preference were studied and photographed (Nikon Coolpix 5400 using macro-close-up option) on *P. nudus* (see figure). The mated female preferred to oviposit in later instars of *P. nudus* larva through the larval sac. One day after parasitization, the matured dryinid larva came out of the larval sac and pupated. From a single dryinid pupa, four encyrtid parasitoids emerged.

The total life cycle took about 14 d, starting from egg laying through the larval sac until adult emergence. The hyperparasitoid spent nearly 2 d in the larval stage of dryinid and the remaining period in the pupal stage. The adult took totally 1 min and 55 s from insertion of the ovipositor to withdrawal after egg laying. This process was repeated three times by the same adult in the same host but at different locations of the larval sac. The timings in the subsequent ovipositions were 1 min 10 s, 55 s, and 20 s, respectively. However, it is yet to be confirmed whether the encyrtid laid all four eggs during the first insertion or laid one egg during each insertion at different locations of the larval sac. The male and female adult parasitoids survived for 10 and 14 d, respectively. The sex ratio observed was either 1:3 or 2:2.

The type species of *Echthrogonatopus*, *E. exitiosus* Perkins, has been recorded from a dryinid (*Gonatopus* sp.) from Australia (Perkins 1906). In India, *E. nigricornis* (Hayat) was originally described by Hayat (1980) in the genus *Metapterencyrtus*, but in the same paper, Hayat (1980 : p.645) transferred this species and parvus to *Echthrogonatopus*. However, no host was recorded until 2002. Behera et al (2002) have reported *E. nigricornis* as a hyperparasitoid of *Goniozus* sp. (Bethylidae: Hymenoptera) parasitizing rice leaffolder *Cnaphalocrocis medinalis* (Guenée) from India. Guerrieri and Viggiani (2004), in their review of the encyrtid parasitoids of Dryinidae, have reported the genera *Cheiloneurus* and *Helegonatopus* and 31 species as hyperparasitoids, and further synonymized *Echthrogonatopus* with *Cheiloneurus*, and *E. nigricornis* with *exitiosus*.

This hyperparasitoid may be responsible for the reduced effectiveness of dryinids, thereby allowing the hopper population to flare up and sporadically cause hopperburn.

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Hyperparasitoid, *Echthrogonatopus nigricornis* (Hayat) parasitizing through the larval sac of *Pseudogonatopus nudus* Perkins on *Nilaparvata lugens* (Stål).

Endo- and ectoparasites of the Philippine rice field rat, *Rattus tanezumi* Temminck, on PhilRice farms

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The Philippine rice field rat, *Rattus tanezumi* Temminck, is one of the principal pre- and postharvest pests of rice and other agricultural crops. This species usually thrives in lowland and upland rice fields but can also be found in or near places of human habitation. They damage agricultural crops and also serve as reservoir hosts for diseases of certain human and domestic animals caused by helminths, protozoans, and microbes.

Many endoparasites infecting the different viscera of *R. tanezumi* belong to taxonomic groups Nematoda (roundworms), Cestoda (tapeworms), and Trematoda (flukes). The more important ones are those that are transmissible to humans. In contrast, there have been few reports on the ectoparasites that infest these rats. These are the mites, ticks, and fleas, some of which may serve as vectors of microbial infections to humans and domestic animals.

Rattus tanezumi is an alternative meat source for the rural folk. Rat meat is a favorite accompaniment to alcoholic beverages during drinking sprees. Unknowingly, some zoonotic infections can be transmitted to humans through improperly cooked rat meat and viscera, accidental wound contamination with rat urine, or rat bites during handling and precooking preparations.

When rats frequent human abodes, they can contaminate objects such as clothing and dishes with their ectoparasites. Though they have low host specificity, these arthropods can infect humans and domestic animals—their bites may result in microbial infections or hypersensitive reactions.

In this study, we identified, according to viscera, the endoparasites and ectoparasites affecting *R. tanezumi* and described their mode of transmission to humans. The monthly prevalence of infected *R. tanezumi*, by sex and endo- and ectoparasite species, was also determined.

Rattus tanezumi collected from PhilRice rice fields, irrigation systems, and rat burrows were brought to the laboratory for identification. They were sorted according to sex, weight, and sexual maturity. The weight of male and female rats ranged from 80 to 150 g and from 100 to 150 g, respectively. The ectoparasites were collected immediately after killing the rat. Chloroform was used to kill the ectoparasites on the dead rats. The parasites were combined from the rat into a white, enameled pan. The rat's internal organs were removed and dissected for microscopic examination of endoparasites. Parasite specimens were transferred into 1.5-mL microtubes containing 95% ethanol for storage and for permanent mounting after identification. The monthly prevalence of infected *R. tanezumi* was calculated.

Six species of endoparasites and three species of ectoparasites infected *R. tanezumi* on PhilRice farms (Table 1). (Voucher specimens, accession numbers 2006-30 to 37, are deposited in the Parasite Collection, College of Veterinary Medicine, University of the Philippines Los Baños, Philippines.) The endoparasites were found in the liver, lungs, pulmonary arteries, duodenum, and small intestines. The ectoparasites, on the other hand, were detected in the skin and, in a few cases, in the small intestines because of accidental ingestion. A majority of the parasites identified were zoonotic to humans. The mode of transmission varied between parasites.

Nematode infections between rat sexes were similar, except for *Angiostrongylus cantonensis* (Table 2). In August, *A. cantonensis* emerged. The incidence of *Nippostrongylus muris* was observed to be higher throughout the study period. *Rodentolepis* spp. (=*Hymenolepis* spp.), *Raillietina garrisoni*, and *Taenia taeniaeformis* (=*Strobilocercus fasciolaris*) infections were much lower than other endoparasitic infections. *Euparyphium* spp. infections were higher than those of cestodes. The kind of food sources consumed at a particular time is probably related to infections of endoparasites. All *R. tanezumi* samples were infected with *Liponyssus bacoti* (=*Ornithonyssus bacoti*), but few animals had the

two species of rat louse (*Polyplax* spp. and *Hoplopleura* spp.).

A majority of the parasites observed in this study are zoonotic to human beings and infect domestic animals. The best protection is to maintain environmental sanitation and to discriminate in the cooking and consumption of rat meat. Hand washing, good hygiene with food preparation, and insect management are equally important in preventing parasite transmission cycles.

Table 1. Endo- and ectoparasite(s) observed in the organs of *R. tanezumi* and their mode of transmission to humans, PhilRice, Nueva Ecija, Philippines, June-December 2005.

Parasite identified	Common name	Organ of origin	Zoonotic to humans	Mode of transmission to humans
Taenia taeniaeformis (=*Strobilocercus fasciolaris*)	Tapeworm	Liver	?	Ingestion of raw liver containing viable larvae
Rodentolepis (=*Hymenolepis* spp.) (=*Vampirolepis* spp.)	Tapeworm	Duodenum	Yes	Accidental ingestion of intermediate host— beetles infected with parasite eggs (*H. diminuta*) or direct ingestion of parasite eggs from infected humans (*H. nana*)
Raillietina garrisoni	Tapeworm	Small intestines	Yes	Accidental ingestion of intermediate host—beetles infected with parasite eggs
Angiostrongylus cantonensis	Rat lungworm (nematode)	Lungs, pulmonary arteries	Yes	Ingestion of improperly cooked land snail/ golden apple snail (*Pomacea canaliculata*) carrying the larvae of the parasite
Nippostrongylus muris	Roundworm	Small intestines	No	–
Euparyphium spp.	Fluke	Small intestines	Yes	Ingestion of infected land snails containing cercariae
Liponyssus bacoti (=*Ornithonyssus bacoti*)	Tropical mite	Skin	Yes	Ingestion can transmit *Pasteurella tularensis*
Polyplax spp.	Rat louse	Skin	No	–
Hoplopleura spp.	Rat louse	Skin	No	–

Table 2. Monthly prevalence (%) of infected *R. tanezumi*, by endo- and ectoparasitic preference, PhilRice, Nueva Ecija, Philippines, June-December 2005.

Sex	Month	Endoparasites[a]						Ectoparasites	
		Nematoda		Cestoda			Trematoda	Tropical mite	Rat louse
		A[b]	B	C	D	E	F		
Male	June (24)[c]	0	91.7	8.3	4.2	8.3	29.2	100	–
	July (45)	0	100	8.9	0	2.2	68.9	100	–
	August (7)	14.3	100	28.6	14.3	14.3	57.1	100	–
	September (7)	0	100	28.6	14.3	28.6	71.4	100	–
	October (6)	0	100	0	0	0	33.3	100	–
	November (11)[3][d]	0	100	9.1	0	0	54.6	100	0
	December (8)[4]	0	100	0	0	0	87.5	100	25.0
Female	June (23)	0	100	4.3	0	26.1	60.9	100	–
	July (43)	0	97.7	16.3	2.3	7.0	67.4	100	–
	August (9)	22.2	100	11.1	0	11.1	44.4	100	–
	September (11)	27.3	90.9	18.2	9.1	45.5	81.8	100	–
	October (14)	7.1	92.9	14.3	14.3	21.4	71.4	100	–
	November (9)[3]	22.2	100	0	0	0	88.9	100	33.3
	December (8)[4]	0	100	0	0	0	100	100	0
Juvenile with hair	November [6]	–	-	–	–	–	–	100	83.3
	December [5]	–	-	–	–	–	–	100	40.0

[a]A = *Angiostrongylus cantonensis*, B = *Nippostrongylus muris*, C = *Hymenolepis* spp., D = *Raillietina garrisoni*, E = *Taenia taeniaeformis*, F = *Euparyphium* spp. [b]The sex bias of infection of A. cantonensis was for female rats. [c]Total number of rats examined. [d]Total number of rats examined for two species of ectoparasitic rat louse.

Effects of cultivating a rice crop under aerobic conditions with film mulching on soil microbial activity

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Cultivated rice is a heavy consumer of fresh water. Approximately 50% of the fresh water used in Asian agriculture goes to rice production. Traditional lowland rice with continuous flooding has relatively high water inputs and its sustainability is now being threatened with increasing water shortage. Water savings and "producing more rice with less water" are crucial to food security in China. Plastic film mulching cultivation of dryland rice has been reported to use only 40% of the amount of water usually needed to grow rice in submerged conditions. Grain yields remained at 90% of those of high-yielding submerged systems (Peng et al 1999). A recent study of film mulching on upland cultivated rice focused on the changes in plant morphology and yield, cultivation techniques, water-saving effects, and nutrient use (Liang et al 1999, Cheng et al 2003). The aim of this study was to examine the effects of film mulching on soil microbial amount and enzyme activities.

Rice cultivar Yue-Xiang-Zhan was used in the experiment conducted in the early and late season of 2002. It was laid out using a random complete block design with three replications in Guangzhou. Three treatments were used: T1 = rice cultivated under aerobic conditions; T2 = rice cultivated under aerobic conditions, covered by plastic film; and T3 (check) = traditional rice production. All 32-m^2 plots were enclosed by dams 50 cm wide and 15 cm high to ensure independent hydrological conditions. Except for traditional rice production, for the T2 and T3 treatments, the field was not irrigated only at transplanting time (1 wk after transplanting); the remaining growth stages completely depended on rainfall.

For all treatments, N fertilizer (180 kg N ha^{-1} as urea) was split into three doses: 40% as basal fertilizer, 30% topdressed at the beginning of tillering, and 30% at booting. P and K were given at 75 kg P ha^{-1} and 150 kg K ha^{-1} at the start of the experiment. Thirty-day-old seedlings were transplanted at 20×33.3-cm spacing at two seedlings hill^{-1}. Soil samples were collected at different times to measure soil microbial amount and activity. The amount of soil bacteria, fungi, and actinomycetes and the activity of soil enzymes such as catalase, sucrase, and urease were determined using standard protocols (Xu and Zhang 1986).

Compared with T3, film mulching (T2) and no mulching (T1) under aerobic conditions increased the amount of soil bacteria by 71.48% and 98.47% at tillering (Table 1). It was two or three times more at ripening stage, but the effect was adverse during heading. Soil fungi at tillering and ripening stages and soil actinomycetes at heading and ripening showed trends similar to that of bacteria.

The effects of film mulching on soil sucrase, urease, and catalase activity are shown in Table 1. Film mulching (T2) increased soil catalase activity by 33.8% over that of the check at ripening stage. There was no significant difference at tillering and heading stages. Sucrase activity reflects carbon transformation and soil respiration. Compared with the control, film mulching increased soil sucrase activity by 42.82%, 28.8%, and 69.9% at tillering, heading, and ripening stages, respectively. There was no difference in soil urease activity among the different treatments at tillering. But, at heading, T2 and T3 had increased soil urease activity by 57.58% and 63.64% over that of T1. Compared with the control, no mulching (T1) and film mulching (T2) under aerobic conditions also increased soil urease activity by 16.16% and 6.06%, respectively, at the ripening stage.

In conclusion, film mulching under aerobic conditions could increase the amount of soil bacteria, fungi, and actinomycetes and the activity of soil enzymes catalase, sucrase, and urease, especially at the ripening stage. This would enhance nutrient uptake of the root system. But, a reduction in soil nutrient content at the late growth stage, the result of an increase in nutrient uptake, is a problem to be considered (Liu et al 2003, Cheng et al 2003, Ai et al 2004).

Effects of film mulching on the amount of soil microorganisms and soil enzyme activity.[a]

Treatment[a]	Bacteria (no. × 10⁶)	Fungi (no. × 10⁴)	Actinomycetes (no. × 10⁴)	Catalase (× 10⁻² mL g⁻¹)	Sucrase (mg g⁻¹)	Urease (mg g⁻¹)
Tillering						
T1	5.22±1.09 a	2.55±0.07 a	1.50±0.27 b	5.35±0.45 a	7.55±1.57 a	1.03±0.07 a
T2	4.51±1.10 a	1.25±0.07 b	2.00±0.20 a	4.50±0.28 b	5.97±1.74 ab	0.95±0.15 a
T3	2.63±0.29 b	1.23±0.51 b	1.97±0.57 a	4.70±0.30 b	4.18±0.21 b	1.09±0.18 a
Heading						
T1	2.78±0.65 c	2.37±0.45 b	3.27±0.40 a	4.17±0.75 a	7.99±1.32 a	0.66±0.11 b
T2	4.91±0.47 b	2.30±0.61 b	3.78±1.72 a	3.95±0.85 a	6.53±0.44 ab	1.04±0.17 a
T3	6.85±0.26 a	3.10±0.26 a	1.70±0.28 b	2.30±0.87 a	5.07±0.90 b	1.08±0.11 a
Ripening						
T1	11.8±1.67 a	6.81±0.54 a	4.44±0.47 a	5.48±0.84 ab	6.85±0.14 a	1.15±0.11 a
T2	12.5±1.98 a	5.18±1.21 a	4.70±0.82 a	6.25±0.48 a	6.90±0.41 a	1.05±0.27 a
T3	4.5±0.95 b	1.27±0.35 b	1.63±0.57 b	4.67±0.21 b	4.21±0.32 b	0.99±0.22 b

[a]In a column, means followed by the same letter are not significantly different at the 5% level by DMRT. [b]T1 = rice cultivated under aerobic conditions. T2 = rice cultivated under aerobic conditions, covered by plastic film. T3 = traditional paddy production (check).

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The nature of humic substances under long-term manuring and fertilization in a rice-wheat system

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Humic substances (HS) are the most abundant organic constituents present in soil and aquatic environments. These substances result from a humification process that involves microbial and chemical transformation of organic debris. On the basis of varying solubility in acid and alkali media, the HS are divided into three fractions: (i) humic acid (HA)—alkali soluble but acid insoluble, (ii) fulvic acid (FA)—soluble in both alkali and acid, and (iii) humin—insoluble in both alkali and acid. Information on the nature of HS synthesized in a fixed cropping sequence is lacking. This study was conducted during the 28th year of a long-term fertilizer experiment established in 1971 with a rice-wheat-cowpea sequence on virgin land classified as Mollisol at Pantnagar (29° N, 79° 3′ E) in northern India. The initial soil characteristics were pH 7.3, EC of –0.35 dS m⁻¹, and –1.48% organic C (Nand Ram 1995).

The details of the selected long-term nutrient input treatments quadruplicated in a randomized block design in the permanent field experiment are shown in Table 1. These nutrient inputs were regularly applied only to rice and wheat, while cowpea has been grown as a fodder crop without any nutrient input. In rice-wheat, annual rates of optimal N, P, and K addition were 240, 52, and 70 kg ha⁻¹, respectively. In NPK + FYM, farmyard

Table 1. Quantity of organic carbon, total N, and humic substances in soil under different long-term treatments.

Treatment	Details of treatment	Soil pH	Organic C (%)	Soil N (%)	Humic substances (g kg⁻¹ soil)	
					HA	FA
Fallow	No crop, no use of fertilizers or manure	7.6	1.36	0.126	3.4	11.8
Control	Cropping without fertilizers or manure	7.7	0.47	0.107	1.8	3.7
NPK	Cropping with optimal NPK fertilizers	7.7	0.81	0.145	2.5	7.7
NPK+FYM	Cropping with optimal NPK and FYM	7.6	1.54	0.157	3.5	17.6
CD (5%)	NS[a]	0.04	0.008	0.010	0.057	

[a]NS = nonsignificant.

Table 2. Elemental ratios and E4/E6 of HA and FA under different long-term treatments.

Treatment	Elemental ratio			E4/E6
	C/H	C/N	O/H	
Humic acid				
Fallow	10.42	13.02	7.78	8.34
Control	12.75	14.57	10.37	7.74
NPK	11.41	11.93	8.36	8.20
NPK+FYM	10.29	11.82	6.35	8.55
CD (5%)	0.744	2.203	0.697	0.148
Fulvic acid				
Fallow	9.20	12.92	11.31	10.57
Control	10.26	13.92	14.32	9.51
NPK	9.64	11.12	10.71	10.21
NPK+FYM	8.88	10.32	9.26	10.90
CD (5%)	0.940	1.414	0.286	0.283

manure (FYM) was incorporated at 15 t ha⁻¹ y⁻¹ before wheat sowing, along with optimal NPK. Composite surface soil samples were collected at 0–15-cm depth to diagnose the nature of HA and FA synthesized under the different long-term treatments.

Humic substances were extracted after initial decalcification of soil samples by repeated treatment with 0.1 N NaOH. These were then fractionated into HA and FA by acidifying the alkaline extract. HA was purified by redissoving in 0.1 N NaOH, followed by centrifuging, treatment with HF + HCl, dialyzing against distilled water, and finally drying. FA was purified by adsorbing on activated charcoal, washing with 1 N H_2SO_4 until free of Fe^{2+}, eluting with 1 N NH_4OH, and finally drying (Nand Ram and Raman 1984).

The nature of HA and FA synthesized under different long-term treatments was evaluated in terms of elemental ratios and E_4–E_6 ratio. In both HA and FA, the percentage of C, H, and N was determined using a CHN analyzer and O was computed by difference. E_4/E_6 was estimated by dissolving 2.5 mg HA or 5 mg FA in 10 mL 0.5 N NaOH and measuring the absorbance of HS at 465 (E_4) and 665 nm wavelengths (E_6) (Schnitzer and Vendette 1975).

The quantity of HA and FA isolated from the different treatments ranged from 1.8 to 3.5 and 3.7 to 17.6 g kg⁻¹ soil, respectively (Table 1). In general, the FA fraction dominated about 2–5 times over HA, possibly due to biochemical transformations of open-chain compounds of plant residues into soil humus. Compared with fallow, the amounts of HA and FA in the control were reduced to about half and one-third, respectively, owing to the decay of organic matter by intensive cultivation (Skjemstad et al 1986). Even the use of optimal NPK fertilizers could not prevent the decline in HS. However, integrated nutrient management (NPK+FYM) not only restored the status of HA but also enhanced that of FA considerably (Sen et al 1994).

The elemental ratios of C/H, C/N, and O/H (Table 2) ranged from 10.29 to 12.75, 11.82 to 14.57, and 6.35 to 10.37 in HA; and from 8.88 to 10.26, 10.32 to 13.92, and 9.26 to 14.32 in FA, respectively. The HA showed comparatively wider C/H and C/N but narrower O/H than FA isolated from the same treatment. This may be attributed to the stronger aromatization of HA in comparison with FA (Rautela and Nand Ram 2000).

As compared with fallow, the elemental ratios of the HS were larger in the control but smaller under the NPK+FYM treatment. The HS synthesized under the control appears to be highly mature due to the dominance of hydrophobic properties with low mobility. With continuous manuring and fertilizers in rice and wheat, the HS seemed to be younger and more labile, having hydrophilic properties under NPK+FYM (Olk et al 2000).

Absorbance of HS measured at 465 (E_4) and 665 nm (E_6) varied from 0.719 to 0.968 and 0.084 to 0.125 for HA; and from 0.109 to 0.352 and 0.010 to 0.037 for FA, respectively, revealing that HA absorbed more light than FA owing to the large proportion of C in the nuclear matrix of the former. The higher absorbance at shorter wavelength is attributed to accelerated mobility of electrons over unsaturated structures conjugated with HS nuclei.

The E_4/E_6 is independent of the concentration of HS but varies with source of origin. It ranged from 7.74 to 8.85 and 9.51 to 10.90 for HA and FA, respectively (Table 2), indicating a more humified HA. As compared with fallow, the lower magnitude of E_4/E_6 in the control indicated

more maturity of HS. Long-term manuring and fertilizer use in rice and wheat resulted in higher E_4/E_6 under NPK+FYM, inferring the presence of large proportions of aliphatic structures during the synthesis of HS. Consequently, HA and FA were least humified (Chen et al 1977). These results showed great resemblance with C/H and C/N, whose lower magnitude reflected weak aromatization of HS.

Continuous cropping of rice-wheat without any nutrient input (control) results in decreased synthesis of HS, which could not be restored even by long-term use of optimal NPK fertilizers. The joint use of optimal NPK fertilizers and FYM not only maintained the level of HA but also enhanced that of FA, being less humified and having poorer aromatization than those under fallow.

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Impact analysis of Technology Assessment and Refinement through Institution-Village Linkage Program

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The Indian Council of Agricultural Research has developed a new approach, the Technology Assessment and Refinement through Institution-Village Linkage Program (TAR-IVLP), that emphasizes the participatory approach in technology selection, testing, evaluation, refinement, and adoption. The TAR-IVLP has been implemented in the village Hodawade of Vengurle tahsil in Sindhudurga District, Maharashtra, India, since 1996, providing an ideal platform through which appropriate technology is disseminated to stakeholders.

Agricultural data (e.g., area under different crops) before the project (1995-96, period I) and after the 5-y implementation (2000-01, period II) were collected using participatory rural appraisal (PRA) and consultations with the land revenue office in the village (Table 1).

During period I, the total area planted to different crops was 352.68 ha. Of this, 25.32% was occupied by local kharif-season rice varieties, followed by mango (21.60%), kharif high-yielding varieties (HYVs) (16.88%), coconut (10.25%), cashew nut (9.82%), rabi hot-weather rice (7.91%), rabi hot-weather groundnut (5.53%), rabi fingermillet (1.16%), vegetables (0.86%), and kharif groundnut (0.67%).

During period II, the area under cultivation increased by 103.14 ha because the area under each crop expanded, except for rabi rice, which totally disappeared, and local rice varieties (kharif), under which 60.72% of the area was reduced with the simultaneous increase in area (201.24%) under HYVs in the same season. The area devoted to rabi rice was used to grow other seasonal, more remunerative crops with less water requirements—e.g., rabi groundnut, vegetables, and fingermillet. Moreover, the available water was diverted to maintain the newly planted cashew nut, coconut, and mango orchards, which exhibited area expansion of 39.67%, 28.63%, and 28.08%, respectively.

Rice and fingermillet have traditionally been the favorite food crops among the local people. More of the newly introduced HYVs (R-24, Palghar 1, Sahyadri, R-3) were grown because of their higher productivity in response to balanced fertilizer use, suitability in different topographical situations, and grain type and taste that local consumers preferred. Similarly, fingermillet variety HR 374 and rabi groundnut became more popular because of their high productivity and the introduction of HYVs Konkan Gaurav and TG 26. The kharif groundnut varieties introduced

Table 1. Impact of IVLP on area under different crops and income of farm families.[a]

Crop grown	Farmers growing this crop (no.)			Area (ha)		
	Period I	Period II	Difference (no.)	Period I	Period II	Difference (%)
Kharif rice	372	156	-216	89.29	35.52	–60.22
Local varieties	(74.85)	(24.68)		(25.32)	(7.79)	
HYVs	123	473	+350	59.52	170.30	201.24
	(24.75)	(74.85)		(16.88)	(39.34)	
Rabi rice	153	–	–	27.90	–[b]	–
	(30.78)			(7.91)		
Ragi (finger millet)	31	56	+25	4.10	8.60	+109.76
	(6.24)	(8.86)		(1.16)	(1.89)	
Kharif groundnut	16	68	+52	2.35	5.45	+131.91
	(3.22)	(10.76)		(0.67)	(1.20)	
Rabi groundnut	185	45	−140	19.51	27.25	+39.67
	(37.22)	(7.12)		(5.53)	(5.98)	
Mango	305	428	+123	76.20	97.60	+28.08
	(61.37)	(67.72)		(21.60)	(21.41)	
Cashew nut	245	379	+134	34.62	48.25	+39.37
	(49.30)	(59.97)		(9.82)	(10.59)	
Coconut	99	142	+43	36.15	46.50	+28.63
	(19.92)	(22.47)		(10.25)	(10.20)	
Vegetables	50	128	+78	3.04	7.35	+141.78
	(10.06)	(20.25)		(0.86)	(1.61)	
Total	497	632	135	352.68	455.82	+29.24
	(100.00)	(100.00)		(100.00)	(100.00)	

[a]Numbers in parentheses are percentages of total. [b]Production of rabi hot-weather groundnut and vegetables decreased in 1999-2000 (period II) as farmers failed to construct a temporary dam.

were Konkan Guarav and Phule Pragati. The package of balanced fertilizer use, timely weed control, and intercropping motivated farmers to expand the area under groundnut.

Mango (variety Alphonso) and coconut (variety West Coast tall) have traditionally been grown. Verification trials and on-farm trials on the use of growth inducers and insecticides encouraged farmers to cultivate mango. The use of manure and balanced fertilization for both mango and coconut increased yield and enabled many farmers to grow these in additional areas.

The area under cashew nut increased because of the introduction of varieties such as Vengurle 4 and Vengurle 7, which have bold nut size. The high yield potential of these varieties was observed in the large-scale coppice grafting program established for local cashew trees. As in IVLP activities, the increase in area under horticultural crops was brought about by giving farmers access to facilities under an employment guarantee scheme.

Noteworthy is the number of farmers taking agriculture as a profession—it increased from 497 to 632. Many of them showed interest in cultivating HYVs of rice, mango, cashew nut, and veg-etables such as chili, particularly the local variety that gets a price premium for its color and taste.

Rice productivity increased from 2.30 t ha^{-1} (period I) to 4.52 t ha^{-1} (period II), an increase of 96.5% (Table 2). This increase with respect to the important

Table 2. Increase in productivity of different crops five years after inception of IVLP implementation.

Crop	Period I	Period II	District[a] average
Rice (t ha^{-1})	2.30	4.52	1.91
Mango (t ha^{-1})	1.59	4.05	2.00
Cashew (t ha^{-1})	0.82	0.99	0.91
Coconut (nuts palm^{-1})	45,600	96,280	47,000
Vegetable—lady finger (t ha^{-1})	6.00	7.30	–

[a]Non-IVLP area.

crops such as mango, cashew nut, coconut, and lady's finger was 155%, 20.5%, 11%, and 21.67%, respectively. Compared with the whole Sindhudurga District, which is a non-IVLP area, the increase in productivity of rice, mango, cashew nut, and coconut in Hodawade was 136.6%, 102.5%, 8.8%, and 104.85%, respectively, signifying the impact of TAR-IVLP. Also, between the two periods, the number of pump sets in the village increased by 20.83%, drinking water wells by 54%, cows by 417%, buffaloes by 816%, and poultry by 141%. The increase in number of farm families in the higher, medium, and lower income group was 32,

58, and 45, respectively. The corresponding increase in income was Rs 25,000, Rs 25,000, and Rs 8,000 from period I to period II (Table 3).

Thus, because of the IVLP activities in Hodawade, there was a significant increase in the area under different crops, indicating an increased level of adoption. Similarly, crop productivity improved, leading to favorable changes in the socioeconomic status of the villagers. This is gleaned from the change in asset position of the farmers and the increase in their annual income.

Table 3. Change in number of farm families and their annual income.

Group	Period I	Period II	Difference (no.)
	Number of farm families		
	Annual income (Rs)		
Higher income	12	44	+32
	125,000	150,000	+25,000
Medium income	180	238	+58
	30,000	55,000	+25,000
Lower income	305	350	+45
	10,000	18,000	+8,000
Landless	34	34	0
	6,000	9,000	+3,000

A preliminary forecast of the intensification of global and regional rice production

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Rice is the staple food that feeds nearly half of the world population (Way and Heong 1994). In the past 3 decades, the steadily increasing rice production has reduced the food shortage in Asia and the world (IRRI 2003). However, the increased use of land and pesticides aggravates the deterioration of environmental quality and human health (Altieri 1994, Heong and Escalada 1998, Tilman et al 2001). A perspective on future rice production is essential for estimating the biological and

environmental impacts caused by intensive rice production and for taking appropriate measures to avoid these side effects without threatening overall food security. In this paper, seven variables related to intensive rice production were fitted with data in the past 3 decades and a forecast for the years 2005-25 was made.

The historical data for this forecasting exercise were downloaded from *World rice statistics* (www.irri.org/science/ricestat/index.asp). Seven variables representing rice production, and biological and environmental impacts—e.g., rough rice area (1961-2002), rough rice production (1961-2002), rough rice yield (1961-2002), rice insecticide sales (1980-96), rice fungicide sales (1980-96), rice herbicide sales (1980-96), and rice pesticide sales (1980-96)—were included for the world, Asia, South America, North and Central America, Africa, Europe, and Oceania (IRRI 2003). Missing data were reasonably interpolated or extrapolated by linear interpolation and linear trend at point (SPSS for Windows 11.0.0, 2001). The temporal trend of each variable was a linear function of time. We thus use univariate linear regression (SPSS for Windows 11.0.0, 2001) to fit and forecast global and regional trends for each of the variables (see table). The adjusted R^2 of the regression was tested with levels of significance P. The forecasting involved estimates of rice production trajectories of the past 3 decades. These trajectories included impacts of past technological developments, changes in consumer choices, and policy factors. Like other agricultural forecasts, ours assume similar technological, environmental, and behavioral changes in the future (Tilman et al 2001).

Each variable, except for rough rice area of South America, was a linear and strong function of time (see table). With an estimated growth rate of 748,240 ha y^{-1}, the global rough rice area would have an increase of 17.47% by 2025 compared with 2002. Asia ranks first in the growth rate of land use (589,630 ha y^{-1}) and to-

Univariate linear regressions and forecasts for years 2005 and 2025, based on trends observed in the past 3 decades and their time dependence.

		World	Asia	South America	North & Central America	Africa	Europe	Oceania
	Annual growth rate	748.24	589.63	17.71	15.68	119.8	7.22	3.36
	Adjusted R^2	0.853**	0.857**	0.020	0.527**	0.964**	0.685**	0.853**
Forecasts of	2005	157,883	140,312	6,417	2,081	8,064	606	178
rough rice	2010	161,624	143,260	6,505	2,159	8,663	642	195
area	2015	165,366	146,208	6,594	2,237	9,262	678	211
(000 ha)	2020	169,107	149,157	6,682	2,316	9,861	714	228
	2025	172,848	152,105	6,771	2,394	10,459	750	245
	Annual growth rate	9790.95	8926.58	314.59	188.24	307.31	44.96	31.07
	Adjusted R^2	0.989**	0.987**	0.910**	0.902**	0.915**	0.824**	0.908**
Forecasts of	2005	649,279	593,278	21,001	12,332	17,419	3,215	1,401
rough rice	2010	698,234	637,911	22,574	13,273	18,956	3,440	1,557
production	2015	747,189	682,544	24,147	14,214	20,492	3,664	1,712
(000 t)	2020	796,144	727,177	25,719	15,155	22,029	3,889	1,868
	2025	845,099	771,809	27,293	16,097	23,566	4,115	2,023
	Annual growth rate	0.055	0.057	0.051	0.072	0.014	0.022	0.091
	Adjusted R^2	0.984**	0.983**	0.805**	0.964**	0.662**	0.310**	0.690**
Forecasts of	2005	4.22	4.26	3.58	6.21	2.26	5.49	8.52
rough rice	2010	4.49	4.55	3.84	6.57	2.33	5.59	8.97
yield	2015	4.77	4.83	4.09	6.93	2.4	5.7	9.43
(t ha^{-1})	2020	5.04	5.12	4.35	7.28	2.47	5.81	9.88
	2025	5.32	5.41	4.59	7.64	2.54	5.92	10.34
		Insecticide	Fungicide	Herbicide	Pesticide			
	Annual growth rate	47.29	41.43	59.57	163.52			
	Adjusted R^2	0.801**	0.944**	0.949**	0.949**			
Forecasts of	2005	1,818	1,346	1,895	5,306			
rough rice	2010	2,054	1,553	2,193	6,124			
pesticide	2015	2,291	1,761	2,491	6,942			
sales ($ million)	2020	2,527	1,968	2,789	7,759			
	2025	2,764	2,175	3,086	8,577			

ᵃLevels of significance: ** = P < 0.0001; * = P < 0.01.

tal area, whereas South America and Africa rank second and third, respectively (see table). Of the six regions, Oceania has the smallest growth rate of land use and total area. If past patterns continue, global rough rice production would increase with an annual rate of 9,790,950 t, largely driven by Asia's growth rate (8,926,580 t y^{-1}) and prevailing production. South America and Africa would share similar annual growth rates and production expectations in rough rice production (see table), while Oceania would hold the least annual growth rate and proportion of rough rice production. With values of 9.88 t ha^{-1} and 0.091 t ha^{-1} y^{-1}, Oceania has the largest yield expectation and annual growth rate in the six regions, followed by North and Central America. With its predominant proportion in rice production, Asia would yield a similar production forecast in 2025 (5.41 t ha^{-1}) and annual growth rate (0.057 t ha^{-1} y^{-1}) with the world (5.32 t ha^{-1} and 0.055 t ha^{-1} y^{-1}, respectively). Global annual pesticide sales would continually increase at the annual growth rate of $163.52 million (see table). The global increase in annual herbicide sales ($59.57

million y^{-1}) is the fastest compared with sales of insecticide ($47.29 million y^{-1}) and fungicide ($41.43 million). By 2025, global rice pesticide sales would reach $8,577 million.

If past patterns continue, area, production, yield, and pesticides of rough rice for the world, Asia, America, Europe, Africa, and Oceania would increase at constant annual growth rates. Asia is the rice production center in the world and this continent would determine the future trend of global rice production. South America and Africa would remain second and third in production, yield, and annual growth rate of rough rice. Oceania would continue to hold the highest yield in the next 20 years. The global need for rice herbicide was larger than that for insecticide and fungicide and this trend would remain in the future. Habitat destruction and pesticide use in rice production cause environmental degradation or affect human health (Altieri 1994, Heong and Escalada 1998, Tilman et al 2001). Advances in rice science and technology and sound policy decisions are needed to avoid these outcomes.

With advances in technology and in societies, however, these

patterns could change and future intensification of rice production could deviate from what is predicted. Further forecasts may be conducted with more dependent and independent variables taken into consideration.

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Farmer participatory learning on integrated crop management of lowland rice in Mali

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The African rice gall midge (AfRGM) *Orseolia oryzivora* Harris and Gagné and rice yellow mottle virus (RYMV) are principal biotic constraints to the sustainable intensification of rainfed and irrigated lowland rice, posing the most serious challenge to human endeavors in West Africa (Nwilene et al 2002). Considerable progress has been made to control both stresses through integrated pest management (IPM) components. But, there has been no focus on farmers' needs, knowledge, and capacity for learning ways of managing pest and disease problems under

locally observed conditions (Defoer et al 2004). Often, farmers are handicapped because they lack a basic understanding of pest and disease symptoms, ecology, natural enemies, development patterns of crops and pests, appropriate control measures, soil condition and its effect on the crop, and the effect of weather conditions on pest populations and disease incidence. They do not understand pest resurgence and the reasons for not using insecticides indiscriminately. There is a growing realization that future agricultural growth hinges on smallholder farmers, who must be knowledgeable and exposed to a learning process that involves continuous observation and feedback from the local environment and that enhances decision-making capacity. This paper reports efforts made to train lowland rice farmers on crop management practices and IPM options to enable them to carry out their own experiments on their own farms.

Studies were carried out in two rice-cropping systems of Mali—the rainfed lowland rice system in Sikasso and the irrigated rice system in Niono. Fifty farmers (31 men and 19 women) participated in the learning and training activities (30 farmers from three villages in Sikasso and 20 farmers from two villages in Niono). A number of criteria were used to select the farmer participants: residence in one of the selected villages, experience in rice cultivation, gender (number of active males and females), availability to participate in training sessions, and possession of an easily accessible field. A training manual, prepared in the local language (*Bambara*), was given to participating farmers. A questionnaire was developed to elicit

information on production constraints and farmers' perceptions, local knowledge, and practices. Before the training exercise, all constraints listed by the farmers were summarized and elucidated on, giving technical explanations and practical advice for a better understanding of each problem. Some key indicators to assess farmers' performance were used before and after the training as well as to compare trained (participating) with untrained (nonparticipating) farmers.

The following constraints were identified in Sikasso: low soil fertility, high price of mineral fertilizers, iron toxicity, late weeding, low rice yields, noncompliance with cultural calendar, pest problems (stem borers, AfRGM, termites), disease problems (RYMV, neck blast), unavailability of good seed, lack of seed conservation methods, and lack of local names for improved varieties, leading to confusion in their use and dissemination.

In Niono, the constraints identified were low soil fertility, high price of mineral fertilizers, users' inadequate knowledge of chemical pesticide effects, no proper seed conservation method, problems on water management, lack of agricultural equipment, not following the cultural calendar, iron toxicity, and problems of pests (caseworms, AfRGM, stem borers) and diseases (RYMV).

Before the training, a majority of the farmers in Sikasso did not follow the cultural calendar (synchronous planting, crop rotation) and did not know any improved rice varieties and techniques (plowing, seedbed preparation, planting). After the training, a great number of farmers began using improved varieties, plant-based pesticides, mineral fertilizers, and improved techniques.

A striking observation at Sikasso was the greater participation of national agricultural research and extension systems and extension agents; they were seen interacting more frequently with farmers.

In Niono, the scenario was different. Many farmers already had regular contact with extension agents before and after the training. They knew improved rice varieties and had applied improved techniques and mineral fertilizers even before the training. The training only added to what they knew. However, the training afforded them the opportunity to appreciate the value of following a cultural calendar, using chemical pesticides judiciously, rotating nursery places, using organic fertilizers in addition to mineral ones, and using plant-based pesticides.

For the first time in both locations, farmers started putting down observations in their own field books (Fig. 1).

The crop yields of the trained farmers were higher than those of the untrained ones (Fig. 2). Rice yield increased by 2.0 t ha^{-1} (36% increase) in the irrigated system and by 1.3 t ha^{-1} in the rainfed lowland (93% increase). In the latter system, pest and disease problems decreased from 80% and 75%, respectively, before the training, to 16.6% and 36.6% after the training. In the irrigated system, these problems decreased from 60% and 80% before the training to 10% and 20% after.

In conclusion, these studies showed that farmers' pest management practices in Sikasso and Niono had undergone significant changes. Farmers have become so knowledgeable that they can now challenge agrochemical salesmen to prove the harmlessness of their products to target and nontarget organisms. It was suggested that
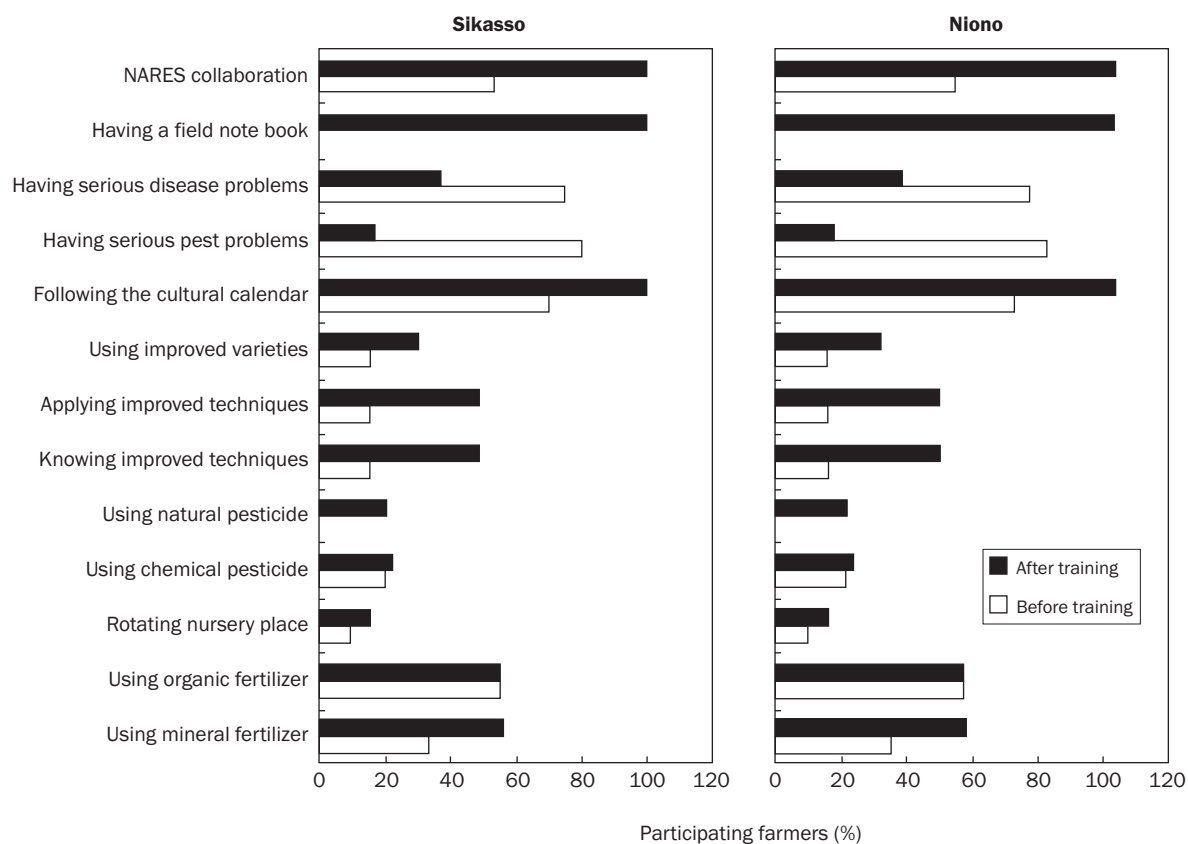
Fig. 1. Indicators to assess farmers' knowledge before and after training, Sikasso and Niono, Mali, 2004 wet season.
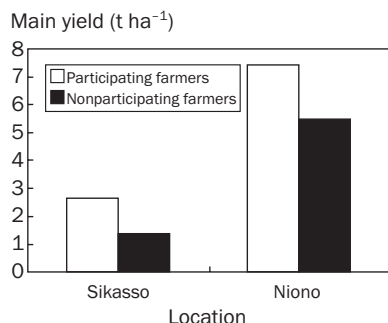

Fig. 2. Mean yields of participating and nonparticipating farmers, Sikasso and Niono, Mali, 2004 wet season.

this training has the potential to complement the extension delivery systems in Mali and therefore should be scaled up to cover larger groups of farmers.

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TAR-IVLP: an effective institutional mechanism for assessing the appropriateness of rice varieties

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Rice is cultivated under different types of production systems by farmers living in varied socio-economic and agroecological conditions. Farmers' participation in technology assessment is essential in generating technologies suitable to their needs. The Technology Assessment and Refinement through Institution-Village Linkage Program (TAR-IVLP), promoted by the Indian Council

of Agricultural Research (ICAR), adopts a holistic approach with the village as an operational unit. The use of farmers' participatory research was the main component in the technology assessment. The CTCRI under ICAR implemented the TAR-IVLP in Chenkal village in Thiruvananthapuram District, Kerala State, southern India. Here, rice is cultivated as a transplanted crop under canal-irrigated conditions. Average productivity in this lowland production system is 1.9 t ha^{-1}; the district average is 2.2 t ha^{-1}. Conway et al (1987) revealed that not using high-yielding varieties suited to local farming conditions contributed to the low productivity of this rice-based production system.

Initially, farmers cultivated local varieties such as Thulunadan, Kochuvithu, and Thavalakkannan in addition to improved variety H4 (Anantharaman et al 2001). These varieties were preferred because of their high straw yield and good cooking quality. To identify suitable high-yielding rice varieties, farmer participatory on-farm trials were conducted during kharif (Jun-Sep) and rabi (Oct-Jan) seasons. Invited to participate were 200 farmers from the village. The IVLP aimed to compare the performance of more than 20 high-yielding rice varieties—Kanchana, Matta Triveni, Bhagya, Gowri and Harsha (short duration), Sabari, Kanakom, ASD16, IR64, Athira, Aiswarya, Uma, Remya, Karishma and Bhadra (medium duration), Ponmani, Dhanya, Karuna, Sagara, Makaram and Kumbham (long duration)—with those of local varieties. All agronomic practices were followed under farmers' management.

The farmers rejected the short- and long-duration varieties, owing to the low straw yield of the former and the susceptibility to lodging and late maturity of the latter. The farmers preferred the medium-duration varieties because of their high grain yield (>4 t ha^{-1}) and high straw yield (>5 t ha^{-1}). Of the 20 odd varieties tested, farmers preferred Uma, Athira, Aiswarya, and Remya. The matrix ranking conducted with 50 farmers showed Uma and Athira to be the most preferred because they had high grain yield (5 t ha^{-1}), high straw yield (up to 6 t ha^{-1}), tolerance for pests and diseases, good cooking quality, high volume of cooked rice, threshability, good grain and straw quality, and high marketability. There was an increase in net returns of 25–30% (see table).

The performance evaluation of these high-yielding varieties revealed their suitability for cultivation in both seasons and qualities comparable with those of local types. Currently, these high-yielding varieties occupy a considerable area in the village— 52% under Uma, 25% under Athira, 4% each under Aiswarya and Remya, and the rest (15%) under local varieties (see figure). Through a farmer-to-farmer seed-exchange program, these
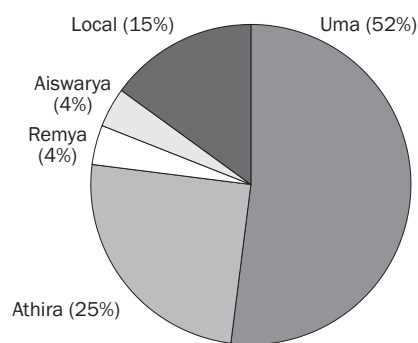
Varietal coverage of rice under IVLP.

varieties have saturated the entire rice-growing area in the village in both seasons, gradually replacing the traditional varieties in the neighboring villages. In helping identify appropriate rice varieties in the adopted village, the TAR-IVLP has established itself as a model technology evaluation mechanism.

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Matrix ranking[a] of rice varieties based on preferred characters.

Character	Kochuvithu	Thulunadan	Uma	Athira	Aiswarya	Remya
Grain yield (>4 t ha^{-1})	1	2	5	4	4	4
Straw yield (>5 t ha^{-1})	2	3	4	5	3	3
Pest and disease tolerance	1	1	4	4	4	3
Good cooking quality	3	3	4	5	4	3
Threshability	2	2	4	4	4	4
Quality of grain	2	4	4	5	4	3
Quality of straw	3	4	4	5	4	3
Marketability	3	4	5	4	4	3
Net returns	1	3	5	4	5	4

[a]1 = least/minimum, 5 = maximum/highest/most/best.

Rice yellow mottle virus disease, a new disease of rice in Zamfara, Nigeria

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Following a report to IAR of a disease outbreak in Zamfara, an important rice-growing state in northwestern Nigeria, an extensive survey was carried out to assess the situation. The disease symptoms observed were stunting, reduced tillering, mottling, yellowing, empty seeds, poor panicle development, distorted spikelets, and sterility. On the basis of these observations, it appeared that the plants were infected with rice yellow mottle virus (RYMV).

Samples were collected and analyzed by ELISA with the antibody for the virus. The absorbance values for virus-free samples were, in most cases, similar to those of the extraction buffer control, indicating a clear background. The average ELISA readings (absorbance value) from the diseased samples were within the 1.89–1.95 range, while those of the healthy and infected controls were 0.24 and 1.96, respectively. The pathogen was therefore identified as RYMV.

The total area surveyed was about 80 ha. The varieties planted, under lowland conditions, were 'ex-China' and ITA150. The fields were badly affected, showing a scale of damage not previously seen in Nigeria. Farmers could not harvest any rice; others had to abandon their fields. The same incidents were reported in some wards in Tanzania (Luzi-Kihupi et al 2000), a country where isolates are highly diverse (Banwo et al 2004). Visual observations indicated the presence of *Trichispa sericea* and *Conocephalus longipennis*, which are known vectors of RYMV.

Recent surveys showed that the disease has spread to other states such as Kaduna, Katsina, and Sokoto (all in northwestern Nigeria). Even within these states, the disease has become increasingly important. Rice yellow mottle disease was not known to occur in this part of the country. Insect pests and iron toxicity are the major biophysical constraints observed in other parts of the country.

RYMV disease was first noticed in 1966 in Kenya. It is now known to occur in most countries of eastern, western, southern, and Central Africa where rice is grown. Very recently, the first report of its occurrence in Europe was made (Köklü and Yilmaz 2004). Early infection of susceptible varieties can cause death of plants and yield loss estimates can range from 20% to 100% in several countries.

In view of the increasing incidence and importance of RYMV in African rice production, additional work is needed in Nigeria, which is one of the main rice producers in Africa.

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International Rice Research Notes

IRRN@30   1976 - 2006

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Designation of IRRI breeding lines

IRRI has decided to change the system for designation of its elite lines and fixed breeding lines. The new policies were outlined in a DG memo on 26 January 2006. The following are new policies regarding the designation of IRRI germplasm.

Designation of IRRI crosses

1. All IRRI-developed breeding materials should have an "IR" designation used as an official name. This applies to improved breeding lines, genetic stocks, mapping populations, and transgenic materials. All these materials should be entered into the IRIS database and have a GID number assigned.
2. All crosses made at IRRI should have an "IR" cross number designation assigned by the database administrator of PBGB. The hybridization unit of PBGB can assist any researcher with making crosses and numbering them.
3. Segregating generations resulting from IRRI crosses should be numbered by generation using the SetGen module of IRIS. Plant numbers are followed by a dash with the first number being the F_2 plant (F_3 row) (e.g., IR88888-21-2-2-2 is an F_6 line harvested from an F_5 plant). If a segregating line is planted in a place other than IRRI (e.g. Shuttle Breeding Program, nurseries in other sites), the resulting derivative should have a 3-letter code for the site and a space before the plant number (e.g IR88888-21-2-UBN 2-2) to indicate that the F_5 generation was grown in Ubon, Thailand. Also, to avoid duplication, this letter will differentiate segregating generations planted in different locations (for example, IRRI farm and Ajuy, Iloilo). Generations after the location code are selected from that location unless another code is encountered. Letter codes that designate breeding methods other than plant selection are as follows: -B for bulk, -R for rapid generation advance or single seed descent, and -AC for anther culture.
4. Mapping populations will receive an IR cross designation from the database administrator of PBGB. Fixed lines from a mapping population can be assigned a shorter designation using the IR cross number followed by the plant number and 'MP' (e.g. IR72746-1 MP, -2 MP, etc.)

Designation of IRRI fixed lines

1. Fixed lines are those that have reached uniformity and are harvested in bulk from an advanced generation row (or are the F_1 cross of two fixed lines, in the case of hybrid rice). These lines are usually entered into observational or yield trials. Fixed lines receive a shortened "IR" designation with the following format: IRYYX###
   where
   - 'YY' is the year the line was bulk-harvested for advanced evaluation
   - 'X' is a letter designation representing the source breeding program (see Table 1)
   - '###' is a serial number assigned by the developer, usually beginning with 101
   - Example: IR05U121 is an upland line (no. 121) bulk-harvested in 2005

Table 1. Letters assigned to each breeding program/ecosystem.

Letter	Ecosystem
N, A, M	Irrigated rice
	N= NPT
	A= Indica favorable lowland
	M= Micronutrients
L	Rainfed lowland and aerobic rice
T	Salinity
U	Upland
K	KSMP and GUVA
W	Wide hybridization
H	Hybrid
F	Anaerobic/submergence
J	JIRCAS-IRRI collaboration
G	GML
E	Africa

2. For hybrid rice, the letter codes will continue to be placed after the line designation: H for the hybrid, R for the restorer lines, A for the CMS line, B for the maintainer line, and S for a TGMS or PGMS parent.

Examples:
- IR06H101 is a fixed breeding line developed in the hybrid breeding program.
- IR06H105H is an F_1 hybrid.
- IR06N232A is an A line derived from the irrigated breeding program (N). The corresponding B line would be IR06N232B.
- IR06H203S is a TGMS line.

3. The database administrator of PBGB will coordinate the designation of fixed lines to avoid any duplication.

Designation of IRRI elite lines

1. IRRI elite lines are those that combine multiple superior characteristics such as high yield, good eating quality, and resistance to insects, diseases, or abiotic stresses. IRRI-developed germplasm released as cultivars by national programs or germplasm that performed well in at least 2 years of multilocation yield trials can be designated as IRRI elite lines. The initial set of elite lines includes the varieties released in national programs. The IRRI elite lines will be given a three-digit number that follows the name "IRRI", beginning with IRRI 101 (see Table 2).

2. Future decisions on naming IRRI elite lines will be made by the Standing Committee on Naming Elite Germplasm. The committee will follow a two-track system for naming elite lines. Those lines released as cultivars in the Philippines or another country will be named upon submission of a summary of the performance in the national testing program. Those not released by a national program will be considered on an annual basis upon submission of appropriate data (at least 2 years of multilocation trials and supporting screening data).

3. IRRI scientists using fixed or elite lines from the IRRI breeding program should use the new names as the primary designation for these lines and can use other popular names as an additional descriptor when needed. For example: "IRRI 105 (PSBRc 18)"; "IRRI 132 (Apo)", etc.

4. For distribution of seed from IRRI, scientists should use the IRRI name in preference to any local names. However, national programs are allowed and encouraged to rename IRRI lines in a manner compatible with their own naming system, as long as the source of the material is acknowledged.

5. For IRRI scientists conducting field experiments using a variety released in that country, the country name can be used as the first designation, with the IRRI name following in parentheses, for field signs or reports.

Table 2. IRRI elite lines.

Elite name	Designation	Cross	Released name (Philippines)
IR5	IR5-47	PETA/TANGKAI ROTAN	
IR8	IR8-288	PETA/DEE GEO WOO GEN	
IR20	IR532-E576	IR262-24-3/TKM 6	
IR22	IR579-160-2	IR8/TADUKAN	
IR24	IR661-1-140	IR8/IR 127-2-2	
IR26	IR1541-102	IR24/TKM 6	
IR28	IR2061-214-3-8	IR833-6-2-1-1//IR 1561-149-1/IR 1737	
IR29	IR2061-464-4-14	IR833-6-2-1-1//IR 1561-149-1/IR 1737	
IR30	IR2153-159-1	IR24/TKM 6//IR 20*4/O NIVARA	
IR32	IR2070-747-6-3	IR20*2/O NIVARA//CR 94-13	
IR34	IR2061-213-2	IR833-6-2-1-1//IR 1561-149-1/IR 1737	
IR36	IR2071-625-1	IR1561-228-1-2/IR 1737//CR 94-13	
IR38	IR2070-423-2-5	IR20*2/O NIVARA//CR 94-13	
IR40	IR2070-414-3	IR20*2/O NIVARA//CR 94-13	
IR42	IR2071-586-5-6	IR1561-228-1-2/IR 1737//CR 94-13	
IR43	IR1529-430-3	IR305-3-17-1-3/IR 24	
IR44	IR2863-38-1	IR1529-680-3/CR 94-13//IR 480-5-9-3	
IR45	IR2035-242	IR1416-128-5/IR 1364-37-3-1//IR 1824-1	
IR46	IR2058-78-1-3	IR1416-131-5/IR 1364-37-3-1//IR 1366-120-3-1/IR 1539-111	
IR48	IR4570-83-3-3	IR1702-74-3-2/IR 1721-11-6-8-3-2//IR 2055-481-2	
IR50	IR9224-117-2-3-3	IR2153-14-1-6-2/IR 28//IR 36	
IR52	IR5853-118	NAM SA GUI 19/IR 2071-88//IR 2061-214-3-6-20	
IR54	IR5853-162-1-2	NAM SA GUI 19/IR 2071-88//IR 2061-214-3-6-20	
IR56	IR13429-109-2-2	IR4432-53-33/PTB 33//IR 36	
IR58	IR9752-71-3	IR28/KWANG CHANG AI//IR 36	
IR60	IR13429-299-2-1	IR4432-53-33/PTB 33//IR 36	
IR62	IR13525-43-2-3-1-3	ARIKARAI///IR 24/TKM 6//IR 20*4/O NIVARA/4/IR 1561-228-1-2/IR 1737//CR 94-13	
IR64	IR18348-36-3	IR5657-33-2-1/IR 2061-465-1-5-5	
IR65	IR21015-196-3-1	BATATAIS/IR 36//IR 52	
IR66	IR32307-107-3-2	IR13240-108-2-2-3/IR 9129-209-2-2-2-1	
IR68	IR28224-3-2-3	IR19660-73-4/IR 2415-90-4-3-2//IR 54	
IR70	IR28228-12-3-1-1	IR19660-73-4/IR 54//IR 9828-36-3	
IR72	IR35366-90-3-2-1	IR19661-9-2-3-3/IR 15795-199-3-3//IR 9129-209-2-2-2-1	
IR74	IR32453-20-3-2	IR19661-131-1-2/IR 15795-199-3-3	
IRRI 101	IR10147-113-5-1-1-5	KN-1B-361-1-8-6/IR 1750-F5 B-3//BPI 76*9/DAWN	PSBRc 1
IRRI 102	IR32809-26-3-3	IR4215-301-2-2-6/BG 90-2//IR 19661-131-1-2	PSBRc 2
IRRI 103	IR41985-111-3-2-2	IR4547-4-1-2/IR 1905-81-3-1//IR 25621-94-3-2	PSBRc 4
IRRI 104	IR50404-57-2-2-3	IR33021-39-2-2/IR 32429-47-3-2-2	PSBRc 10
IRRI 105	IR51672-62-2-1-1-2-3	IR24594-204-1-3-2-6-2/IR 28222-9-2-2-2-2	PSBRc 18
IRRI 106	IR57301-195-3-3	IR35293-125-3-2-3/IR 32429-47-3-2-2//IR 41985-111-3-2-2	PSBRc 20
IRRI 107	IR64616 H	IR62829 A/IR 29723-143-3-2-1R	PSBRc 26 H
IRRI 108	IR56381-139-2-2	IR28239-94-2-3-6-2/IR 64	PSBRc 28
IRRI 109	IR58099-41-2-3	IR72/IR 24632-34-2	PSBRc 30
IRRI 110	IR59469-B-B-3-2	IR9202-5-2-2-2//KN-1B-361-1-8-6/IR 15889-32-1	PSBRc 44
IRRI 111	IR25976-12-2-2-2-1-1	JUMALI/IR 9129-159-3//KN-1B-361-1-8-6-9	PSBRc 46
IRRI 112	IR9884-54-3-1	NONA BOKRA/IR 2070-414-3-9-6//IR 34	PSBRc 48
IRRI 113	IR51500-AC 11-1	IR5657-33-2/IR 4630-22-2-5-1-3	PSBRc 50
IRRI 114	IR47686-30-3-2	IRAT 104/PALAWAN	PSBRc 5
IRRI 115	IR59682-132-1-1-2	IR48613-54-3-3-1/IR 28239-94-2-3-6-2	PSBRc 52
IRRI 116	IR60819-34-2-1	IR72/IR 48525-100-1-2	PSBRc 54
IRRI 117	IR41431-68-1-2-3	IR8234-OT-9-2/IR 19661-131-1-2	PSBRc 60
IRRI 118	IR59552-21-3-2-2	PSBRC 2/IR 39292-142-3-2-3	PSBRc 64
IRRI 119	IR57515-PMI 8-1-1-SRN 1-1	IR43581-57-3-3-6/IR 26940-20-3-3-3-1//KHAO DAWK MALI 105	PSBRc 68
IRRI 120	IR60267-11-2-2-1	RD 15/IR 43485-22-2-2//IR 68	PSBRc 70
IRRI 121	IR68284 H	IR58025 A/IR 34686-179-1-2-1 R	PSBRc 72 H
IRRI 122	IR62141-114-3-2-2-2	IR50401-77-2-1-3/IR 42068-22-3-3-1-3	PSBRc 80
IRRI 123	IR64683-87-2-2-3-3	IR47761-27-1-3-6/PSB RC 28	PSBRc 82
IRRI 124	IR65185-3B-8-3-2	CSR 10/TCCP 266-B-B-B-10-3-1	PSBRc 84
IRRI 125	IR65195-3B-13-2-3	IR10198-66-2/TCCP 266-B-B-B-10-3-1	PSBRc 86
IRRI 126	IR52713-2B-8-2B-1-2	IR64//IR 4630-22-2-5-1-3/IR 9764-45-2-2	PSBRc 88
IRRI 127	IR69726-29-1-2-2-2	IR52256-84-2-3/IR 72//IR 1561-228-3*2/UTRI MERAH	MATATAG 2
IRRI 128	IR61920-3B-22-2-1	IR32429-47-3-2/WAGWAG	NSIC Rc 106
IRRI 129	IR9202-25-1-3	IR2053-521-1-1-1/K 116//KN-1B-361-1-8-6-9-1	PSBRc 92
IRRI 130	IR61336-4B-14-3-2	IR44535-22-3-3-3/IR 8866-30-3-1-4-2	PSBRc 94
IRRI 131	IR61608-3B-20-2-2-1-1	IR32429-47-3-2-2//DOBONGBYEO/MOROBEREKAN	PSBRc 96
IRRI 132	IR55423-1	UPL RI 5/IR 12979-24-1 (BROWN)	NSIC Rc 9
IRRI 133	IR54068-B-60-1-3-3	DHULA/IR 28878-R-R-27-3-1//IR 31802-48-2-2-2	PSBRc 102
IRRI 134	IR73885-1-4-3-2-1-6	IR64*2/O RUFIPOGON (IRGC 105908)	MATATAG 9
IRRI 135	IR71606-1-1-4-2-3-1-2	IR1561*3/HABIGANJ DW 8//5*IR 64	NSIC Rc 110
IRRI 136	IR72102-4-159-1-3-3-3	IR1561*2/O BARTHII//4*IR 64	NSIC Rc 112
IRRI 137	IR75207 H	IR68888 A/IR 62161-184-3-1-3-2 R	NSIC Rc 114 H
IRRI 138	IR75217 H	IR68897 A/IR 60819-34-2 R	NSIC Rc 116 H
IRRI 139	IR68144-2B-2-2-3	IR72/ZAWA BONDAY	MS 13
IRRI 140	IR68305-18-1-1	BALIMAU PUTIH/4*IR 64	NSIC Rc 118
IRRI 141	IR61979-138-1-3-2-3	IR44625-139-2-2-3/IR 32822-94-3-3-2-2	NSIC Rc 122
IRRI 142	IR68333-R-R-B-22	JINMIBYEO/CHEOLWEON 46	MS 11

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Apply these rules, as appropriate, to all research notes:

Methodology
- Include an internationally known check or control treatment in all experiments.
- Report grain yield at 14% moisture content.
- Quantify survey data, such as infection percentage, degree of severity, and sampling base.
- When evaluating susceptibility, resistance, and tolerance, report the actual quantification of damage due to stress, which was used to assess level or incidence. Specify the measurements used.
- Provide the genetic background for new varieties or breeding lines.
- Specify the rice production systems as irrigated, rainfed lowland, upland, and flood-prone (deepwater and tidal wetlands).
- Indicate the type of rice culture (transplanted, wet seeded, dryseeded).

Terminology
- If local terms for seasons are used, define them by characteristic weather (dry season, wet season, monsoon) and by months.
- Use standard, internationally recognized terms to describe rice plant parts, growth stages, and management practices. Do not use local names.
- Provide scientific names for diseases, insects, weeds, and crop plants. Do not use local names alone.
- Do not use local monetary units. Express all economic data in terms of the US$, and include the exchange rate used.
- Use generic names, not trade names, for all chemicals.
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Mini reviews
Mini reviews should address topics of current interest to a broad selection of rice researchers, and highlight new developments that are shaping current work in the field. Authors should contact the appropriate editorial board member before submitting a mini review to verify that the subject is appropriate and that no similar reviews are already in preparation. (A list of the editors and their areas of responsibility appears on the inside front cover of each IRRN issue.) Because only 1-2 mini reviews can be published per issue, IRRN will require high quality standards for manuscripts accepted for publication. The reviews should be 2000-3000 words long, including references. Refer to the guidelines for research notes for other aspects of writing and content.

Notes from the field
Notes from the field should address important new observations or trends in rice-growing areas, such as pest outbreaks or new pest introductions, or the adoption or spread of new crop management practices. These observations, while not the result of experiments, must be carefully described and documented. Notes should be approximately 250 words in length. Refer to the guidelines for research notes for other aspects of writing and content.

Review of manuscripts
The IRRN managing editor will send an acknowledgment card or an email message when a note is received. An IRRI scientist, selected by the editorial board, reviews each note. Depending on the reviewer's report, a note will be accepted for publication, rejected, or returned to the author(s) for revision.

Submission of manuscripts
Submit the original manuscript and a duplicate, each with a clear copy of all tables and figures, to IRRN. Retain a copy of the note and of all tables and figures.
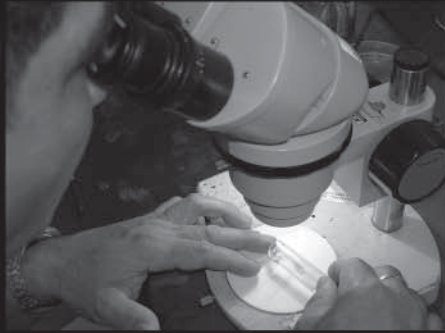
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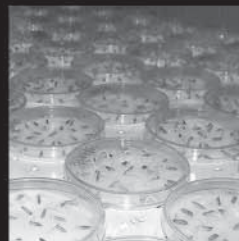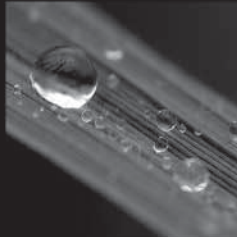
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Call for entries
IRRN Best Article Awards

To celebrate its 30th year, the International Rice Research Notes (IRRN) is now accepting entries for the 2006 IRRN Best Article Award. The Best Article Award reaps the contributions of rice researchers from national agricultural research and extension systems (NARES) in developing countries toward the advancement and exchange of rice-related knowledge and technology.

There will be six winning papers from the six sections of IRRN: plant breeding (includes papers on molecular biology and biotechnology); genetic resources; pest science and management; soil, nutrient, and water management/environment; crop management and physiology; and socioeconomics/agricultural engineering.

Mechanics of the Best Article Award:
- Competition is open to all NARES rice researchers.
- Research must have been conducted in a developing country.
- Manuscripts that have been accepted from 1 August 2005 to 30 June 2006 will be evaluated for the award.
- Authors who are requested to revise their manuscripts must send the final version within three weeks after the receipt of the reviewer's comments.
- The deadline for submission of articles is on 30 June 2006.
- Winners will be chosen by the IRRN Editorial Board and invited reviewers. The winning entries will be selected on the basis of scientific content, originality, relevance, and organization.
- The Award will be given to the first author of each paper. Additional authors may come from any organization.
- Each winner will receive a plaque and a US$500 cash prize.
- The awarding ceremony will be held during the International Rice Research Conference in India in October 2006.
- The winning entries will be announced in the October 2006 of Rice Today and the winning articles will be published in the December 2006 issue of IRRN.

For details, contact the IRRN Managing Editor, IRRI, DAPO Box 7777 Metro Manila, Philippines
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International Rice Congress 2006 is jointly organized by the Government of India (Ministry of Agriculture, Food Technology, and Cooperation through the Department of Agricultural Research and Education and Indian Council of Agricultural Research [ICAR]) and the International Rice Research Institute (IRRI).

For more information:
www.icar.org.in/irc2006
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