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YALE UNIVERSITY

P.O. Box 208269
27 Hillhouse Avenue
New Haven, Connecticut 06520-8269

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GENETIC RESOURCES, INTERNATIONAL ORGANIZATIONS, AND RICE VARIETAL IMPROVEMENT

Robert E. Evenson
Yale University

Douglas Gollin
University of Minnesota

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Abstract

This paper examines the economic role of three programs of the International Rice Research Institute designed to achieve genetic improvement in rice. These programs are the international genetic resource collection (IRGC), the international plant breeding program (IRPB), and the international network for the genetic evaluation of rice (INGER a system of "nurseries" in which varieties and advanced lines are tested in national programs. All of these programs are designed to contribute to rice genetic improvement by collaborating with counterpart national rice research programs.

A genealogical analysis of 1709 rice varieties, constituting more than 90 percent of all improved rice varieties from the 1965 - 1991 period in tropical and subtropical countries, was undertaken. All ancestors of these varieties were traced back to the original "landrace" genetic resources on which they were based. This analysis showed a very high degree of international exchange of genetic materials. Fewer than 8 percent of these improved varieties were developed entirely from national genetic resources. More than two-thirds utilized genetic resources made available by the IRPB and IRGC programs. Most of these were transferred through INGER.

A statistical analysis of varietal production showed that the IRGC and IRPB programs stimulated increased national use of the INGER nurseries. (National decisions regarding the number of national nurseries were treated as endogenous choices.) The IRPB and the INGER programs, as well as national plant breeding programs, contributed to varietal production. Coefficient estimates indicated that the INGER system facilitated a 20 to 25 percent expansion of varietal production by making genetic materials readily available to large numbers of national plant breeding programs through the 900 to 1000 nurseries managed by INGER each year. The implied economic value of additional accessions to the genetic resource collections (IRGC and national collections) was high and a strong economic justification for further collection, cataloging and preservation of these genetic resources was implied.

KEY WORDS: Genetic Resources, Rice, Technology Research, Agriculture

GENETIC RESOURCES, INTERNATIONAL ORGANIZATIONS, AND RICE VARIETAL IMPROVEMENT

R. E. Evenson
Yale University

and

D. Gollin
University of Minnesota

Rice varietal improvement is an important component of productivity gains in rice production. Genetic resources from the two cultivated species of rice (*Oryza sativa* and *Oryza glaberrima*), 20 wild species of rice and related relatives of rice in the genus Oryza constitute the germplasm from which improved rice cultivars have been developed. Until the development of the modern agricultural experiment stations in the middle of the 19th century, farmers themselves created improved rice cultivars in the form of distinct subspecies types or "landraces" of rice. Modern plant breeders in National Agricultural Research (NAR) programs have been systematically developing improved rice cultivars in many countries for the past century. Since 1959, the International Rice Research Institute (IRRI) located in the Philippines has ben providing international leadership and support to rice genetic improvement.

IRRI has three programs to facilitate rice genetic improvement. It has its own plant breeding (IRPB) program designed to produce both improved cultivars, "varieties" and "advanced lines" suited to use as parent material in National Plant Breeding (PNB) programs. It maintains an international collection of genetic resources (IRGC) design to provide genetic resources to both international and national plant breeders and to provide complementary support to national germplasm collection (NGCs). In addition it maintains and coordinates a system of international nurseries, where advanced genetic materials are exchanged and evaluated. This is the International Network for the Genetic Evaluation of Rice (INGER).

In this paper we analyze the economic role of the international programs (IRPB, IRGC and INGER) and estimate their economic contributions as collected in improved rice cultivars. We conduct a genealogical analysis of released rice varieties from national rice breeding programs and IRRI since 1965, when the first modern high-yielding rice varieties were released. We trace the "routes" by which rice germplasm is incorporated into improved varieties. A statistical analysis is undertaken to estimate the impacts of the IRPB, IRGC and INGER programs on the number of improved varieties developed over the 1965–1990 period. Economic calculations based on these estimates provide estimates of economic value.[1]

In Part I of the paper a brief discussion of rice breeding methods and the role of genetic resources is presented. Part II discusses data bases and reports basic tabulations of genetic resource characteristics of released rice varieties. Part III reports an analysis of "routes" taken by varieties from origin to release. Part IV reports on econometric analysis designed to test the impacts of IRRI's IRGC, IRPB, and INGER programs on the number and characteristics of released rice varieties. The final section summarizes economic implications.

I. RICE BREEDING AND GENETIC RESOURCES

Rice is a "self-pollinated" crop. Because of this, genetically segregated lines as progeny remain genetically stable from generation to generation. Genetic changes occur mostly through deliberate "crossing" — or hybridizating of parental cultivars — and pureline selection of the resultant offspring.[2]

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[1]The genealogy of a released rice variety contains a wealth of information about the process of rice breeding and about the dissemination and flow of rice genetic materials. The usefulness of rice genealogies as a tool for analyzing research programs was first noted by Hargrove, Cabanilla, and Coffman in a series of papers. Gollin and Evenson (1990) first attempted to use genealogical analysis in the economic evaluation of agricultural research and (1991) in the setting of agricultural research priorities.

[2]See De Datta (1981), p. 3.

This technique of varietal improvement, known as "pedigree breeding" (De Datta, 1981), is not widely practiced with other cereal grains.[3]

Varietal improvement efforts in rice, as in all other domesticated crops, date back to the origins of domestication. The very processes of harvesting and planting tend to select for such traits as non-shattering, uniform maturation, high germination, and adaptation to local growing conditions. Harvesting for consumption will also tend to imply selection for high palatability and nutritional value. Farmer selection over many centuries has produced today's "landraces" of rice.

Cultivated rice falls into two species, *Oryza sativa* and *Oryza glaberrima*. The former is the common Asian cultigen, while the latter accounts for a small fraction of African rice production. In addition to these two cultigens, the genus *Oryza* includes about 20 wild species, although some scholarly disagreement remains on the exact number (Chang, 1985). Dr. T. T. Chang, former director of the rice germplasm collection at the IRRI, has estimated that about 140,000 cultivars of rice exist in the world today. These include cultivated varieties, landraces and wild species.

Organized breeding efforts probably date back to before 1000 A.D. in China, with the development of the Champa varieties of early ripening, drought-resistant rices. Modern efforts, however, can be traced to the late 19th century in several parts of Asia. In temperate East Asia, the first significant advances were made by Japanese farmers and scientists in developing relatively short-statured and fertilizer-responsive varieties called the *rono* varieties. These varieties, which included the popular Shinriki, belonged to the *japonica* class of rices, and were widely cultivated in Japan as early as the 1890s.[4]

In the following 30 years, Japanese scientists sought to create similar varieties that were adapted to Taiwan, which the Japanese then occupied. The main thrust of this research was to create *japonica* rices

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[3]The term "pedigree breeding" is used by De Datta (1981). With wheat and sorghum, for instance, methods of bulk breeding are generally preferred. For our purposes, these methods make it more difficult to trace flows of specific genetic material.

[4]See Chang (1985), pp. 441–443.

that were adapted to the more tropical conditions of Taiwan; the result was a group of varieties refereed to as *ponlai* rices.[5] At the same time researchers in tropical Asia were busy seeking more productive varieties of rice from the other two main classes or races: the so-called *indica* and *javanica* rices.

Among the most important goals of rice breeding historically has been the development of fertilizer-responsive varieties that are widely adaptable to regions of different day length and intensity of sunlight. More recently, breeders have also sought to incorporate multiple disease and pest resistance as well as tolerance of certain environmental stresses, such as soil salinity, iron toxicity, drought or flooding.[6]

This process has inherently involved the exchange and use of foreign germplasm. As early as the 19th century, scientists were transporting rice varieties across national borders in an effort to bring in new and advantageous genetic materials. This effort attained new levels in the post-World War II period with the initiation of a program by the United Nations Food and Agricultural Organization (FAO) to cross *indica* rice with *japonicas*. Because the *japonica* rices tended to yield better than the *indicas*, this was seen as a possible means of increasing yield of rice in South Asia — and hence as a means of averting hunger.[7]

In 1950 the *japonica–indica* crossing program was started at India's Central Rice Research Institute in Cuttack. The FAO program developed several varieties that proved enormously successful including Mahsuri, which remains one of the most widely grown varieties in the world. Perhaps more importantly, the FAO program served as a model or a more intensive project initiated in 1960 by the Ford and Rockefeller Foundations along with other donor agencies. The new research center was the International Rice Research Institute (IRRI), located in Los Banos, the Philippines.

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[5]See Dalrymple (1986). See also Barker, Herdt, and Rose (1985), pp. 54–55.

[6]Recent technological advances require us to broaden our understanding of germplasm, however. Through tissue culture of various kinds, a number of types of plant tissue can be used to regenerate plants. In addition, some species have traditionally been regenerated from stems, shoots, tubers and cuttings, rather than from seed. Germplasm in its broadest sense is thus any genetic material that can be used to reproduce adult plants.

[7]See Dalrymple (1986). See also Barker, Herdt, and Rose (1985), pp. 54–55.

Many authors have recounted the development of the earliest high-yielding rice varieties at IRRI. Hargrove (1981) has pointed out that the first scientists at IRRI had a deliberate blueprint to create a semi-dwarf, fertilizer-responsive rice variety that would grow well under a wide range of conditions. The eighth cross made at IRRI in fact turned out to be a near-immediate success; IR-8, as it was designated, was a cross between the Indonesian *indica*, Peta, and the Chinese semi-dwarf variety, Dee-Geo-Woo-Gen (DGWG). An earlier Taiwanese cross of DGWG with the tall variety Tsai-Yuan-Chung had led to a similar plant, known as Taichung Native 1 (TN 1). The two new varieties quickly achieved enormous popularity among farmers and scientists around Asia, and a large-scale internationalization of breeding efforts resulted.[8]

Plant breeders rely on *ex situ* collections of genetic resources for "raw materials." About 85,000 landraces and wild species are currently stored in a long-term *ex situ* facility at IRRI (IRGC). A subset of these cultivars are catalogued according to agronomic and genetic characteristics, and they are stored under conditions of low temperature and humidity.

The germplasm bank serves two related functions. One is as a repository for genetic materials. By keeping little-used or uncommon varieties of rice in a long-term storage facility, the bank serves as a protective facility to prevent the loss of potentially valuable gene sources.

The second function of the germplasm bank is as a "lending library" of genetic resources for use by plant breeders. Breeders request materials from the bank — either by name or by some set of characteristics — and incorporate the materials into their programs of evaluation and breeding.

Unimproved materials from the collection are used by breeders at IRRI and are also sent out freely to scientists around the globe. In addition, genetic materials are also incorporated in the genealogies of improved lines that are sent out from IRRI through the International Network for the Genetic Evaluation of Rice (INGER).

Other germplasm collections are maintained by various national programs (as in India). Most local

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[8]See Barker, Herdt and Rose (1985), pp. 56–57.

stations also have short-term storage facilities or keeping seeks of some advanced lines. Breeding activities at the local, regional, and national levels recombine genetic materials. We can thus see a complex and involved interchange of germplasm throughout the international system of rice research establishments.

II. RICE VARIETIES AND CHARACTERISTICS

The role of IRRI is to improve rice productivity in the rice-producing countries of the world. IRRI's main program emphasis has been on the development of new rice varieties that have desirable characteristics.

The breeding sequence entails a series of events. First, a cross is made (based on a strategy). This cross may be a cross between landraces (or wild species), advanced lines or released cultivars. The progeny from this cross are then evaluated over several self-pollinated generations. Selection of plants for uniformity is undertaken. This produces uniformity of the selected plants. Promising selections (cultivars or advanced lines) are field tested. Release as a variety is subject to careful evaluation and only a small proportion of crosses are ultimately released as a variety (less than one percent for most programs). Most released varieties are planted by farmers although there is considerable variation in the degree of success in the field.

From 1965 to 1974, IRRI's breeding program released several important varieties directly as IRRI varieties (IR–8 to IR–36). National programs were responsible for most varietal release prior to 1974 and for all releases after 1974. Some IRRI crosses have been released as national varieties (sometimes with IR names) often after selection in the releasing countries. Similarly crosses originating in a national program may ultimately be released as a variety in another national program.

A. The Varietal Data Base

For this study we have compiled a data base for 1,709 modern rice varieties released since the early 1960s.[9] For each of these released varieties a complete genealogy was compiled. This included the date and origin of the cross on which the variety was based, as well as the data and origin of all parents, grandparents and other ancestors. Thus ancestry was traced back to original landraces or wild species. In addition we were able to determine whether the cross or any ancestors appeared in the INGER nurseries and whether they were selected from these nurseries for crossing.[10]

Of the 1,709 modern varieties and elite (advanced) lines, 33 were released prior to 1965 (and thus prior to the release of any IRRI materials).[11] Table 1 gives the frequency of release by country and by time period. For some varieties, release dates were not available; in such cases, approximate dates were estimated based on available information.

The data set includes materials from numerous countries, but it is relatively more complete for rice-producing countries of South and Southeast Asia than for those from other regions. India, in particular, is represented in the data set at a level that appears to be disproportionately large, with 643 varieties. Although India's breeding programs have a long and productive history, the data set probably reflects a

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[9]The study drew heavily on a number of data sets available through IRRI. The first of these was a list of elite lines and released varieties from more than 40 countries. This data set, collected by V. L. Cabanilla and T. R. Hargrove for the International Rice Genealogy Database provides information on the parentage and release dates of most Indica rice varieties since 1968. An accompanying data set, containing more than 6,500 entries, contains breeding records that make it possible to trace complete or partial genealogies for all the elite lines and released varieties in the first data set. This data set is also based on work by Cabanilla and Hargrove, although much expansion and modification was carried out for this study. These alterations transformed the two data sets into a united, self-contained, self-referencing data set.

[10]It was also possible to combine the varietal data with additional data sets from INGER. Two INGER data sets, from IRRI, were used. The first was a list of entries in INGER since its inception; the second was a list of the nurseries in which these entries were tested. By matching the names of varieties to the list of INGER entries, it was possible to infer the inclusion of varieties and ancestors in INGER.

[11]These 32 varieties were generally regarded to be early "modern" varieties.

bias towards India based on the extensive and available data.[12] Other countries represented by large numbers of varieties in the data set include Korea, with 106 varieties, and the combined countries of Latin America (239 varieties) and Africa (101 varieties). Japanese varieties were not included in this analysis since limited ancestral information was available.

The data indicates that numbers of released varieties rose steadily during the 1970s but have stabilized over the past 15 years. In some countries and regions, however, such as Latin America, varietal release totals have climbed markedly in the most recent period.

B. International Flows of Genetic Resources

Table 2 reports measures of international flows of genetic resources associated with the released varieties and the parents of the released varieties. Of the 1,709 released varieties, 390 (23 percent) were the result of a cross made outside the releasing country. IRRI was the source for 294 (17 percent) of these varieties. Other national programs were the source for 96 releases. (Appendix Table 1 provides country detail for varieties.)

After IRRI, India was the next largest "exporter" of varieties, with 28 Indian varieties released elsewhere. India was also a larger importer of varieties; 70 of its 643 varieties originated elsewhere, with 53 from IRRI. Sri Lankan varieties were released 11 times in other countries. Twelve Thai varieties were released in Myanmar (Burma). Myanmar was one of the largest importers of rice varieties; 43 of its 76 releases were imported varieties, including varieties from Bangladesh, China, India, Indonesia, IRRI, the Philippines, Sri Lanka, Thailand, and Vietnam.

In addition to IRRI's direct role as a source of exported varieties, IRRI has served as a conduit through which elite lines have moved from country to country. Even before the establishment of INGER in 1975, IRRI scientists helped test and disseminate elite lines of rice around the world. This function

[12]Most released varieties have been planted on significant acreage. In India, the Indian Council of Agricultural Research reports yields of two leading rice varieties in a number of districts. More than 150 varieties have been noted as important varieties in farmers' trials over the 1977 to 1989 period.

was formalized with the inauguration of INGER. Through INGER's activities, elite lines and released varieties from national research programs have been made available for international testing and evaluation. Participating countries have gained access to promising varieties, and in some cases, they have been able to import them directly from the INGER nurseries.

INGER itself keeps a complete and accurate set of data on varietal importing that has occurred through its programs. INGER has documented more than 300 instances of varieties imported after appearing in INGER trials (Sehsu, pers. comm., 1992). Our study lacks complete data on varietal releases in INGER participant countries, especially in Africa and Latin America. Nonetheless, this study was able to identify nearly 200 instances in which varieties could have been imported through INGER.[13] INGER has played a significant role in disseminating IRRI lines. About half of imported IRRI varieties came through INGER, all of them in the period, 1976–91.

Since 1976, INGER has also become the primary channel through which nationally-developed varieties have been imported. Since 1976, 37 national program varieties have been imported through INGER. During the same period, the number of national program varieties imported through other avenues has diminished from 13 in 1976–80 to 6 in 1986–91. INGER has played an important role in facilitating the transfer of varieties across geographic zones; for instance, both of two Sri Lankan varieties released in Africa came through INGER, and both of two Indian varieties released in Latin America came through INGER.

Perhaps more remarkable than the direct international flows of varieties has been the international flows of parents of the varieties. Nearly three-quarters of the varieties in the data set (1,263) have at least one imported parent. Including imported varieties, 810 releases (47%) have at least one parent from

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[13]The criterion used was whether varieties developed in one country were released in another country two or more years following their appearance in INGER. (Given the omission in our data set of many countries in Africa and Latin America, which have imported actively from INGER, the figures appear to be consistent with the data maintained by INGER.) Since typography and nomenclature also make it difficult to match named varieties with INGER entries, it is likely that imports through INGER have been undercounted, rather than overcounted, in our study.

IRRI, and 619 (36%) have at least one parent from another national program (Table 2). Excluding imported varieties, more than 500 varieties have at least one parent from IRRI. Excluding both imported varieties and those with IRRI parents, more than 350 released varieties have at least one parent from another national program. This indicates that parental importing is taking place across national programs on a large scale. (Appendix Table 2 reports country details for parents.)[14]

The extent of international exchange — both of varieties and of parents — implies that a large majority of the varieties in the data set were developed using breeding lines from outside the country of release. In fact, only 145 varieties out of 1,709 (8.5%) were developed entirely from own-country parents, grandparents and other ancestors. Most of these were simple varieties with fewer than 4 landraces in their pedigree. The extent of this international flow of germplasm is extraordinary. No country in the data set has failed to take advantage of unimproved or improved germplasm from other countries.

C. Genealogical Complexity

One outcome of the increased flows of varieties across national borders has been the increasing complexity of the genealogies of rice varieties. In a sense, the complexity of these pedigree measures breeding inputs in the development of new varieties. Pedigree complexity can most easily be measured as the number of landraces, pureline selections, and mutants that are ultimate ancestors of a released variety. For released varieties containing more than one such ancestor, at least one cross must have been made by breeders corresponding to every two ultimate ancestors. Thus, varieties with large number of ancestors — and hence complex pedigrees — are the product of intensive breeding efforts.

The pedigree complexity of released varieties has clearly increased over time (Table 3). Varieties released before 1970 averaged 3.78 landrace and pureline ancestors; those released since 1980 averaged

[14]As many as 422 of the varieties based on internationally exchanged parents may have been developed from materials chosen out of INGER, in the sense that the parent first appeared in INGER trials four years or more prior to the release of the variety. About half of the INGER parents were IRRI materials, and half were varieties from national programs other than the one of eventual release. Parents chosen out of INGER have steadily grown to account for larger proportions of borrowing. By 1986–91, as many as 80 percent of parental selection may have taken place via INGER.

almost twice as many ancestors, with 7.36 for each released variety. Of the 33 varieties in the data set released before 1965, only 3 contained more than 4 ultimate ancestors. In contrast, of 400 varieties released between 1986 and 1991, 222 could be traced to 5 or more ancestors, and 72 had more than 15 ultimate ancestors.

This change mirrors the expansion of national breeding programs as well as the lengthening history of modern rice research. Breeders now cross advanced lines that, in themselves, represent crosses between advanced lines.

The relative roles of national and international breeding programs can be observed by calculating the number of ancestors in released varieties when all IRRI lines are filtered out of their genealogies. This corresponds to the number of landraces brought into genealogies by national breeding programs (as well as by the early efforts of FAO's relatively short-lived *indica-japonica* crossing program). In general, national programs are the source of about 30 percent of the ancestors embodied in the typical released variety. The remaining 70 percent of the ultimate ancestors arrive in the pedigrees through IRRI lines.

Moreover, the share of ancestors delivered through IRRI lines has increased over time. For varieties released in 1965–74, IRRI provided 54 percent of ancestors. For varieties released in 1981–90, IRRI delivered 72 percent of ancestors. Thus, the usefulness of IRRI's breeding lines has not diminished following the early release of semi-dwarf rices. Instead, IRRI continues to offer national breeding programs highly useful packages of genetic material. These packages form the nucleus of contemporary breeding programs in most countries.

National rice improvement programs have depended on differing extents on IRRI lines as sources of genetic materials (Table 4). Some countries have borrowed many of their released varieties or parent lines from IRRI, while others have used IRRI materials in conjunction with local varieties or other internationally available breeding lines. For example, Vietnam and Pakistan have based their modern varieties almost completely on IRRI lines, but Sri Lanka used a large pool of other breeding lines as sources of germplasm.

D. Landrace Pools

Released varieties with IRRI ancestry have significantly more landraces than varieties with no IRRI ancestry. The 1,709 varieties in the data set trace to a total of 11,592 ancestors. Of these, 8,208 have come through IRRI lines and 3,384 have been acquired independently of IRRI lines.[15] In fact however there are only 838 distinct ancestors. Most ancestors occur repeatedly in the genealogies of released varieties. Dee Geo Woo Gen, for example, is an ancestor for 1,105 varieties in the data set; Cina and Latisail each appear in more than 1,000 varieties. These three landrace selections are the parents and grandparents of IR-8, and thus have appeared jointly as ancestors to nearly 700 varieties in the data set.

In addition to DGWG, Cina, and Latisail, 14 other varieties have appeared as ancestors of more than 100 varieties (Table 5). These 17 varieties together account for 8,439 of the 11,592 accumulated ancestors. The frequency with which these varieties appear as ultimate ancestors of releases indicates the enormous value of the genes they contain.

Although a relatively small number of landraces accounts for such a large amount of the genetic material embodied in the released varieties, it would be incorrect to assume that this figure implies genetic uniformity. In many cases, these ancestors appear far back in the genealogies of released varieties, so that they may be contributing only small amounts of genetic material, or even single genes.

For example, DGWG probably contributes little more to most varieties than the semi-dwarfing gene *sdl*. Similarly, *Oryza nivara*, which appears as an ancestor of 244 varieties, is represented only by the *Gsv* gene for resistance to grassy stunt virus, biotype 1 (see Chang and Li, 1991). The Indian varieties Ptb 21 and Ptb 18, each of which is an ancestor to more than 100 varieties, are both known to have

[15]Note, however, that the total number of ancestors includes ancestors that have been replicated many times, not only in the total set of varieties, but even in a single variety.

resistance to brown planthoppers, tungro, and green leafhoppers (Swaminathan, 1984, cited in Plucknett et al., 1987).

By and large, national program breeders have sought to incorporate the useful genes from these varieties (and others like them) into local varieties, which are well adapted to environmental stresses and ecologies, and which satisfy local tastes and preferences. In some countries, breeders have worked directly with these landraces and pureline selections. More often, however, national programs have taken advantage of work performed by IRRI breeders in "packaging" these useful traits in improved lines. This continues to be true even in recent years, despite expanded international access to the original unimproved varieties.

Evidence for the role of IRRI in packaging advantageous germplasm can be found in the frequency with which IRRI has been the source of the most commonly used ancestors (see Table 5). The 17 most commonly used ancestors have appeared independent of IRRI lines in fewer than 15 percent of their accumulated occurrences. For example, *Oryza nivara* has appeared in the genealogies of released varieties exclusively via IRRI lines. Similarly, the Thai variety Gam Pai 15 appears as an ancestor for 139 varieties, but only 2 varieties (both Thai) have obtained Gam Pai 15 independent of IRRI. A variety from Andhra Pradesh, India, occurs in the genealogies of 379 released varieties, but only 5 releases have made direct use of the ancestor.

Thus, IRRI has played a major role in identifying sources of advantageous genes, and in packaging these genes in forms that can be readily used by national programs. IRRI continues to function in the same role today, working extensively with unimproved materials. Curiously, however, relatively few additional materials have entered the ancestor pool through IRRI's efforts since the mid-1970s.

For each of the 838 ancestors of our released varieties, our study has identified all of its released progeny, and has noted the earliest release date for these progeny. Table 6 summarizes the growth in landrace pools over time.

The data indicates that only 80 ancestors appeared for the first time through IRRI materials. An additional 47 appeared in released national varieties before 1965, and were thus part of the international varietal pool before IRRI was established. Since 1970, however, 687 ancestors have been added to the ancestral pool — but only 41 have been added through IRRI lines.

This suggests that national programs have continued to make use of IRRI lines that package material already used in released varieties. In some cases, these IRRI lines may be re-packaging IRRI's own old materials; in other cases, IRRI is re-packaging lines used in one country in a form suitable for another country. However, it must be noted that IRRI's narrow focus on the semi-dwarf plant type has limited its success in providing a broader landrace base for modern rice varieties.[16]

Many of the ancestors introduced by national programs are landraces that are locally adapted to certain micro-environments. Of the 606 landraces introduced by national programs since 1970, 414 have appeared in the pedigrees of a just one released variety. In effect, then, national programs have been using IRRI packages of germplasm to upgrade the quality of local and traditional varieties.

The total pool of ancestors incorporated in released varieties appears to have grown by 25 to 50 landrace and pureline ancestors in almost every year since 1970. This suggests that as the available stock of improved varieties expands, farmers have more choices, and can choose locally adapted high-yielding varieties. The improvements of the original high-yielding varieties are no longer limited to favorable agro-ecological zones in major rice producing countries; instead, an increasing number of released varieties is available for widely varying production environments.

Some have suggested that germplasm collection need not be exhaustive, since a relatively small sample of rice varieties will contain, statistically, almost all the alleles in the rice genome. It is clear that "core" collections offer a useful approach to the management and handling of germplasm collections

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[16]In fact we regard IRRI's poor performance in contributing to the landrace pool to be a disappointing part of a program that otherwise has made great contributions. IRRI has introduced a new plant type in recent years and this may ultimately allow a broader base for landrace contributions by IRRI. It would appear, in retrospect, that IRRI was slow in moving to other plant types and less concerned than it should have been with broadening the landrace pool.

(Hodgkin 1991). However, most experts appear to believe that comprehensive collection serves an important purpose (Chang 1989a).

Although it is true that a relatively small sample of the total population of rice landraces would contain virtually all the genes in the species, it is equally true that genes for specific traits are often found only in minuscule numbers of landraces. This is true because cultivated rices are self-pollinated, with relatively low genetic variability within most localities. However, rice is grown across enough environments that significant genetic differentiation can be found across landrace populations of *Oryza sativa* (Oka, 1991a). Upland rices are even more polymorphic genetically than are lowland rices, and wild species are far more polymorphic than either upland or lowland varieties of *Oryza sativa* (Oka, 1991a).

Empirical data suggest that wild species, isolated landraces, and other such "fringe" materials are important sources of resistance to diseases and pests of cultivated rice. For example, Oka notes that Chang (1989a) reported finding resistance to white-backed planthoppers in only 0.8% of the 48,544 varieties of *Oryza sativa* screened at IRRI, whereas 45.4% of the 681 varieties of *Oryza glaberrima* displayed resistance, as well as 46.2% of the 437 wild *Oryza* species tested. Oka concludes that in rice, "wild relatives and primitive landraces are important objectives in germplasm collecting and conservation because they are expected to be treasure-houses of useful genes."

Vaughn (1991) reports that more than 40,000 accessions in the International Rice Germplasm Collection have been screened for resistance to blast, with comparable numbers for bacterial blight, green leafhopper, and brown planthopper. Vaughan notes that for blast and green leafhopper, resistance is evenly distributed across the germplasm collection. For brown planthopper and bacterial blight, however, resistance is concentrated in materials from given geographic regions and strata of the collection. Some sources of resistance have come from unlikely landraces; for example, Vaughan cites the discovery of cold tolerance genes in an Indonesian variety (Silewah) from 1,200 m elevation in Sumatra. Similarly, a variety from the dry zone of Sri Lanka has been used as a source of genes for flood tolerance.

Saxena (1991) notes that researchers first identified resistance to brown planthopper in the 1960s, with IR26 in 1973 the first semi-dwarf variety to show resistance. The single gene responsible for resistance, *Bph-1*, suppressed the original biotype of brown planthoppers. Evolution of new planthopper biotypes forced researchers to seek a succession of new resistance genes, however. To date, seven resistance genes have been identified, and resistance has been transferred to *O. officinalis* to *O. satuva*.

Similarly, Ikeda (1991) reports that resistance to six strains of bacterial blight has been found in varying levels in rice varieties from Asian countries. The frequency of resistance to different races of bacterial blight was different across countries; for example, varieties with the *Xa-3* resistance gene were found in almost all countries, but with a frequency of 17.2 percent in Indonesia and only 0.3 percent in India.

All of these examples suggest that large germplasm collections are important economically as sources of desirable genes. Evidence to support the importance of large germplasm collections can be found in the genealogy data analysis of released varieties. Some landrace and ancestor materials are used for very specific traits. They may have been identified through special searches of the germplasm collection, or they may be widely recognized for possessing particular characteristics. These varieties are desirable only for one attribute; they may possess other undesirable attributes. These landraces or wild species may occur in the pedigrees of numerous varieties, but they are used only infrequently as parents. *O. nivara*, for example, has been used solely as a source of resistance to grassy stunt. Its other characteristics make it an undesirable parent. Thus, *O. nivara* has appeared seven times as a parent in our data set, but it appears in the genealogies of 244 released varieties. The resulting ratio, 244:7, provides an index of its "rare trait" characteristics. Table 6 reports this rare trait index for the most widely used ancestors — most of which have high rare trait indexes.

III. ROUTES (PATHWAYS) FROM ORIGIN TO RELEASE

In order to analyze more formally the impacts of IRGC, IRPB, and INGER, it is useful to trace the routes by which varieties were released. Table 7 provides a tabular summary of released varieties by pathway or route. These routes are defined to be mutually exclusive categories, so that each variety in the data set falls into exactly one of the following categories:

Borrowed Varieties

1. IRRI line, borrowed through INGER (IRRI/INGER)
2. IRRI line, borrowed independent of INGER, (IRRI/NO INGER)
3. Variety from another national program, borrowed through INGER (OTHER NATL/INGER)
4. Variety from another national program, borrowed independent of INGER (OTHER NATL/NO INGER)

Nationally Developed Varieties, Borrowed Parents

5. At least one parent from IRRI, borrowed through INGER (IRRI PARENT/INGER)
6. At least one parent from IRRI, borrowed independent of INGER (IRRI PARENT/NO INGER)
7. No IRRI parents, but at least one parent borrowed from another national program via INGER (OTHER NATL PARENT/INGER)
8. No IRRI parents, but a least one parent borrowed from another national program independent of INGER (OTHER NATL PARENT/NO INGER)

Nationally Developed Varieties and Parents, Borrowed Grandparents

9. At least one grandparent from IRRI, borrowed through INGER(IRRI/GPARENT/INGER)
10. At least one grandparent from IRRI, borrowed independent of INGER (IRRI/GPARENT/NO INGER)
11. No IRRI grandparent, but at least one grandparent borrowed from another national program via INGER (OTHER GPARENT/INGER)
12. No IRRI grandparents, but at least one grandparent borrowed from another national program independent of INGER (OTHER GPARENT/NO INGER)

Nationally Developed Varieties, Parents, Grandparents

13. All parents and grandparents from country of release (PURE NATIONAL)

In practice, virtually no varieties fell into categories 9 or 11, since INGER has not been in existence long enough to provide many grandparent materials. Moreover, many varieties with borrowed grandparents also have borrowed parents — or even are borrowed varieties. Thus, in some of the tables that follow, routes 9–12 are collapsed into a single category labeled "OTHER."

Table 7 indicates the enormous importance of international genetic exchange. Since 1970, only 7.8 percent of new varieties have been of "pure" national development. The most significant channels of release have been the use of IRRI parents. Before 1975, IRRI parents were obviously not channeled through INGER, but in recent years, the largest single pathway for developing new varieties has been to use IRRI parents taken from INGER.

The importance of INGER can be seen by looking at the time trends on borrowing through INGER. Since 1981, more than half of released varieties (440 out of 797) have either been borrowed through INGER or were bred from parents borrowed through INGER.[17]

Table 8 reports numbers of landraces and proportions of rare traits by route and by region. This table shows that IRRI material has been the conveyor of high landrace content and high rare trait content. Data on area planted are also reported.

IV. IRGC, IRPB, AND INGER IMPACTS ON NUMBERS OF RELEASED VARIETIES

The data for routes suggest a substantial impact for IRRI programs. A considerable number of borrowed varieties, parents, grandparents and ancestors from IRRI attests to the impact of the IRPB program, through not to its recent contribution. Flows through INGER also attest to its impact, although at least some of the INGER flows are diversions from other flows. IRGC has contributed to the flows through IRPB and through sending material directly to IRPBs. Some of this material flows through INGER as well.

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[17]Note that grandparent varieties will have had a shorter period to have been influenced by INGER because of the time lag between appearance in INGER and their ultimate appearance as a grandparent. INGER, however, may have had a large impact on these flows, even if they were NO INGER flows because it stimulated more international searching for genetic resources. Similarly the IRRI landrace pool may also stimulate these flows by inducing national program efforts to complement IRRI materials. (See Gollin and Evenson 1991.)

In order to statistically address the question of impact a model that takes national choices into account is required. Variables measuring the impacts on investments in IRGC, IRPB, and INGER are required.

Table 9 provides a summary of the variables defined for this analysis. These are defined for 15 countries (or groups of countries) for the 1965–1990 period. The key endogenous variables to be "explained" are R1–R9, the annual varietal releases by route. This set of varieties by route is "jointly" determined by a set of explanatory variables. In addition the number of landraces and the number of international and national rare trait materials are also endogenous variables.

The explanatory variables include variables measuring IRGC, IRPB, and INGER activities, national demand and national plant breeding activities.

Of these, the most complicated is the measure of INGER activities, NING, the number of nurseries in a country. Since this is chosen by the country, it cannot be treated as an exogenous or predetermined variable. It must be modeled as simultaneously determined along with the other endogenous variables.

The variables measuring IRGC and IRPB, on the other hand, can be considered to be predetermined and thus exogenous to the national level variables. IRGC, the cumulated number of catalogued IRGC accessions (with passport data), can be considered to be a determinant of NING, and the rare trait contents. It can also be considered to contribute to the index of IRPB activities, which is measured by the cumulative size of the internationally contributed landrace pool, POOLRI and to the size of the total landrace pool, POOLR.

Other exogenous variables include the cumulated landraces both international and national, CNLR, and CILR, which are measures of national plant breeding activity. In addition the area planted to rice in a country (AREA) should be governing genetic resource flows because it reflects demand.

Table 10 reports coefficient estimates and "t" values from the third stage of a 3SLS estimate of the system of ten equations. The intercept and country dummy and time dummy variables coefficients are not reported since they do not generally enter into the policy implications of the results.

The first equation is the equation determining the number of INGER nurseries that the host country chooses (NING). The nurseries have expanded over time and the time dummies reflect this expansion. The rice area variable (AREA) also explains why countries add more INGER nurseries. We also find that countries respond positively to their neighbors' decisions to conduct INGER nurseries (OING) and, most importantly, that as the catalogued accessions in IRGC expands, the number of INGER nurseries expands. INGER nurseries do not respond to the number of materials placed in trials by IRRI and have actually declined as the total landrace pool has expanded, given the response to IRGC. Thus we find a number of factors influencing the number of INGER nurseries placed in different countries. The 3SLS model treats this number as endogenously determined in the nine route or pathway equations.

As noted earlier, the "model" underlying the Table 10 estimates is one in which the "flow" of varietal releases through each route or pathway responds to four governing variables in addition to rice area, and country and time effects. Two of these variables measure international plant breeding activities (CILR and POOLRI), one measures national plant breeding activities (CNLR), and the fourth, NING, is the outcome of both international (IRGC) and national activities. We expect each of these activities to have different impacts on each flow. In particular, the introduction of INGER is expected to direct flows away from NO INGER flows to INGER flows. We are, however, interested in the total impact, i.e., the sum of the flow impacts because this tells us whether the activity caused an expansion in the total number of varieties released.

We note first that the AREA variable, while a strong determinant of NING, is not a significant determinant of flows. This is consistent with the interpretation that plant breeding activities govern releases, not simply the size of the country.

Now consider the impact of the variables indexing national and international plant breeding activities. National plant breeding programs effort is indexed by the cumulated stock of landraces placed in varietal release by each national program (CNLR). This variable has generally positive impacts on most routes and a positive and statistically significant total impact. Not surprisingly, successful national breeding programs cause more varietal releases.

The two variables measuring the IRRI plant breeding program, CILR and POOLRI, clearly indicate that it is the size of the IRRI origin landrace pool that is important and not the cumulative stock. In other words, what seems to be important is the introduction of new landrace material into the pool, not the replication of those landraces which are largely the contribution of national programs. Each landrace added to the pool by IRRI contributes .045 varieties annually in each country as indicated by the statistically significant sum of the coefficients.

Now consider the INGER impact. The expansion of INGER diverted varietal flows away from NO INGER routes (R2 and R4) to INGER routes (though this diversion was not highly significant). For parental materials INGER has a positive impact on all routes including stimulus of NO INGER routes (R6 and R8). This suggests that the INGER nurseries stimulated more international search for genetic resources. It also reflects the fact that INGER nurseries actually include parent and grandparent cultivars that were not initially introduced through INGER.

F tests tell us that NING has a significant positive impact on the total flow of released varieties. The coefficient .0295 indicates that one additional INGER nursery is associated with or causes .0295 additional released varieties. Thus the addition of 34 nurseries (a nursery is counted in each location in each year) adds 1 released variety. The implication for stopping INGER (i.e., stopping the 900 to 1000 nurseries each year in recent years) is that this would reduce the recent annual flow of released varieties from 80 per year to around 60 per year. This indicates that INGER has added to the production of released varieties by roughly 25 percent. This is a large impact.

Each landrace added from IRRI sources causes approximately .68 added varieties to be released in each future year. (This coefficient is based on replication in 15 countries.)

IRGC also has an impact on released varieties because it induces added INGER nurseries. The addition of one accession to IRGC causes (.000875 × 15) .0013 INGER nurseries. This, in turn, means that (.0295 × .0013 × 15) = .0058 more varieties are produced. Thus adding 1,000 accessions to IRGC causes 5.8 added released varieties in each future year.

V. ECONOMIC IMPLICATIONS

The economic implication of these estimates are quite important. We estimate that the IRGC, IRPB (through POOLRI), and INGER programs have caused a larger number of varietal releases than would otherwise have occurred. We show that the varieties produced in this expansion are probably not qualitatively different in terms of characteristics than all other varieties (Gollin and Evenson, 1991). In order to develop estimates of the value of these varieties we require an estimate of the average value of modern rice varieties in farmer fields.

Evenson and David (1993) report estimates of modern variety impacts for India, Pakistan, Bangladesh, Philippines, Thailand, Indonesia and Brazil. These range from a relatively high value for India to lower values for other countries. The approximate value of modern varieties in 1990 (in US dollars) in Indica rice regions was 3.5 billion dollars. If we consider this to be the cumulated contribution of the first 1400 modern varieties, we obtain an average value of a released variety of 2.5 million dollars per year and this annual value continues into perpetuity because we are considering varietal improvements to be additive.

Now we can compute the economic effects of INGER, of one added IRRI landrace and of added accessions to IRGC.

First consider the consequences of ending the INGER program. We estimate that this would reduce the flow of released varieties by 20 varieties per year. There is a time lag between appearance in INGER and production. Suppose this to be 5 years. Then further suppose that the INGER effect lasted only 10 years, i.e., INGER chiefly speeded up the release of varieties that would have been released an average of 10 years later. The present value of the 20 varieties over the 6th to 15th years discounted at 10 percent is 1.9 billion dollars. This is an estimate of the loss if INGER nurseries were to be eliminated.[18]

We can also compute the value of adding 1,000 catalogued accessions to IRGC. According to our estimate, this will generate 5.8 added released varieties. This will generate an annual 145 million dollar income stream with a delay of, say, 10 years. The present value of this stream at a 10 percent discount rate is 325 million dollars.[19]

The value of an added landrace introduced by IRRI also is high. The coefficients indicated that after an IRRI landrace is added, variety releases expand by .68 varieties in the first year, 2 × .68 in the second year, etc. Assuming this process begins after 5 years and then continues for 10 more years, we can compute the present value of an IRRI-added landrace to be 50 million dollars discounted at 10 percent.[20]

There is thus little question that the continued operation of INGER, the operations of IRGC and the completion of accessions to IRGC are economically justified. These are high payoff activities. In addition, the expansion of the landrace pool by IRRI also has a high payoff.

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[18]If a 5 percent discount rate is used, this value is 6 billion dollars.

[19]At 5 percent it is 1,450 million dollars.

[20]158 million when discounted at 5 percent.

TABLE 1

Numbers of Varieties Included in the Data Set,
by Country of Release and by Time Period of Release

Country/Region	Pre–1965	1966–70	1971–75	1976–80	1981–85	1986–91	Total
Africa	3	7	8	17	26	42	101
Bangladesh	1	7	8	11	4	33	34
Burma	0	4	6	21	37	8	76
China	0	1	8	30	31	12	82
India	10	67	136	139	125	166	643
Indonesia	1	2	5	21	10	9	48
Korea	0	5	11	35	40	15	106
Latin America	7	9	48	32	43	100	239
Nepal	0	0	1	10	4	2	17
Oceania	0	1	4	1	0	0	6
Pakistan	0	4	2	3	3	0	12
Philippines	3	4	13	23	8	2	53
Sri Lanka	3	14	4	8	21	3	53
Taiwan	0	3	0	3	0	0	6
Thailand	1	2	4	8	5	3	23
USA	2	5	18	17	3	6	51
Vietnam	0	16	6	16	16	5	59
Other S.E. Asia	2	1	8	7	6	5	29
Other	0	7	15	15	15	19	71
Total	32	150	284	394	377	378	1,709

TABLE 2

International Genetic Resource flows by Time Period

	Pre–1965	1966–70	1971–75	1976–80	1981–85	1986–91	Total
I. Released Varieties, percent based on							
IRRI Cross	3	25	19	22	18	12	17
Other NAR Cross	16	7	6	6	6	5	6
Own NAR Cross	81	68	75	72	76	83	77
II. Parents of Released Varieties, percent with one or more parents							
IRRI Cross	0	24	29	33	23	19	24
Other NAR Cross	27	25	21	15	18	20	18
Own NAR Cross	73	51	50	52	59	61	58

TABLE 3

Number of Varieties with Given Numbers of Landrace, Pureline, and Mutant Ancestors, by Time Period

	Pre-1965	1966–70	1971–75	1976–80	1981–85	1986–91	Total
1–3	22	31	43	70	97	120	383
3–4	8	78	116	67	55	58	382
5–6	2	42	68	72	73	53	310
7–8	1	3	35	46	38	42	166
9–10	0	3	14	22	15	21	75
11–12	0	1	11	35	35	17	99
13–14	0	0	6	19	15	17	57
15–20	0	1	9	79	60	64	213
20+	0	0	0	7	9	8	24
Total	33	159	303	417	397	400	1,709
Average per Released Variety	2.55	4.01	5.29	8.15	7.49	7.23	
Percent obtained through IRRI	3	53	59	79	74	70	

TABLE 4

Proportion of Ancestors Obtained Through IRRI Lines,
by Date, Selected Countries

Country	Average Number of Ancestors	Average Number Obtained Independent of IRRI	Percent Obtained Through IRRI
Bangladesh	6.85	1.26	81.6
Burma	5.36	1.37	74.4
India	5.94	2.08	65.0
Indonesia	9.65	2.04	78.9
Korea	10.36	2.53	75.6
Nepal	8.35	1.65	80.2
Pakistan	5.67	0.67	88.2
Philippines	9.55	1.74	81.8
Sri Lanka	7.28	4.25	41.6
U.S.A.	6.32	5.46	13.6
Vietnam	8.76	0.17	98.1

TABLE 5

Widely Used Ancestors, by Date of First Appearance
in Released Varieties, Frequency of Use
Independent of IRRI Lines, and Total Occurrences
in Genealogies of Released Varieties

Variety	Origin	Date of First Appearance	Frequency of Use Independent of IRRI	Total Occurrences	Rare Trait Index
Benong	Indonesia	1968	37	412	412
CI 5094	USA	1931	31	411	411
Cina	China	1964	152	1,053	62
CO 18	India	1967	70	399	100
DGWG	China	1965	184	1,105	48
Fortuna	USA	1921	107	538	30
Gam Pai 15	Thailand	1969	2	139	46
GEB 24	India	1965	120	564	21
Latisail	India	1964	145	1,043	58
O. Nivara	India	1969	0	244	35
Ptb 18	India	1970	24	164	27
Ptb 21	India	1972	12	140	< 20
Rexoro	India	1931	73	505	< 20
Sup. Blue Rose	USA	1931	31	411	205
Tadukan	Japan	1969	9	295	< 20
Tsai-Yuan-Chon	China	1965	170	637	637
Unk. (A.P.)	India	5	379	< 20	

TABLE 6

Landrace Pools, by Avenue of Introduction

Year	Landraces Introduced by IRRI	Landrace Introduced by Other Sources	Total Landrace Pool
1921	0	2	2
1931	0	4	4
1934	0	2	2
1939	0	2	2
1959	0	4	4
1962	0	1	1
1964	0	6	6
1965	0	27	27
1966	0	2	2
1967	1	11	12
1968	1	12	13
1969	11	47	58
1970	3	15	18
1971	3	21	24
1972	3	26	34
1973	1	24	25
1974	2	23	25
1975	5	32	37
1976	5	31	36
1977	2	20	22
1978	1	27	28
1979	8	41	49
1980	5	27	32
1981	1	47	48
1982	3	38	41
1983	4	19	23
1984	2	23	25
1985	1	44	45
1986	1	34	35
1987	1	31	32
1988	9	39	48
1989	0	58	58
1990	1	12	13
1991	1	6	7
	80	758	838
Old core (pre-1966)			48
Introduced by IRRI			80
Introduced by NARS (post-1966)			710
Total			838

TABLE 7

Number of Varieties Released by Route, by Date

	Pre–1965	1966–70	1971–75	1976–80	1981–85	1986–91	Total
IRRI/INGER	0	0	5	50	52	39	146
IRRI/NO INGER	1	37	50	38	16	6	148
OTHER NATIONAL/INGER	0	0	0	10	15	12	37
OTHER NATIONAL/NO INGER	5	10	16	13	9	6	59
IRRI PARENT/INGER	0	0	0	46	89	79	214
IRRI PARENT/NO INGER	0	52	110	117	15	19	313
OTHER NATIONAL PARENT/INGER	3	2	15	34	69	85	208
OTHER NATIONAL PARENT/NO INGER	9	30	50	22	13	27	151
OTHER	7	10	33	63	90	85	288
PURE NATIONAL	8	18	24	24	29	42	145
Total	33	159	303	417	397	400	1,709

TABLE 8

Routes of Varietal Release: Descriptive Statistics

Route	Number of Varieties	Percent of Varieties	Total Area	Percent of Area	Average Number of Landraces		Average Number of Landraces Independent of IRRI		Average Number of Landraces with Rare Trait Index > 5.0
					Pre–1976	Post–1976	Pre–1976	Post–1976	
IRRI/INGER	146	8.5	5,177	13.3%	n.a.	13.2	n.a.	0.0	12.55
IRRI/NO INGER	148	8.7	3,959	10.2%	5.4	12.4	0.0	0.0	7.66
OTHER/INGER	37	2.2	411	1.1%	n.a.	4.2	n.a.	2.1	3.35
OTHER/NO INGER	59	3.5	2,954	7.6%	4.4	5.2	2.5	1.6	4.14
IRRI PARENT/INGER	214	12.5	6,570	16.9%	n.a.	10.4	n.a.	1.2	9.55
IRRI PARENT/NO INGER	313	18.3	5,589	14.4%	5.6	9.5	1.7	1.4	6.53
OTHER PARENT/INGER	208	12.2	4,283	11.0%	n.a.	2.9	n.a.	2.5	1.52
OTHER PARENT/NO INGER	151	8.8	3,228	8.3%	3.4	4.8	3.4	3.8	2.68
IRRI GPARENT/INGER	14	0.8	670	1.7%	0.0	7.2	0.0	3.0	6.00
IRRI GPARENT/NO INGER	94	5.5	1,436	3.7%	7.4	10.7	4.6	3.6	8.93
OTHER GPARENT/INGER	0	0.0	0	0.0%	0.0	0.0	0.0	0.0	0.00
OTHER GPARENT/NO INGER	180	10.5	1,482	3.8%	4.4	4.1	4.3	3.8	2.04
PURE NATIONAL	145	8.5	3,121	8.0%	3.2	2.6	2.7	2.2	1.10

TABLE 9

Variables: IRGC, IRPB, INGER Impacts
on Flows of Genetic Resources

I. Endogenous Variables Measured at the National Level	
NING	The number of INGER nurseries in the country in each year
R1–R9	Flows of released varieties by year by route
II. Predetermined Variables: IRRI	
POOLR	Size of total landrace pool
POOLRI	Size of IRRI origin landrace pool
ENTRIES	The number of IRRI materials placed in INGER
III. Predetermined Variables: National Level	
CNLR	Cumulated landraces of national origin in released varieties
CILR	Cumulated landraces of IRRI origin in released varieties by year
IV. Exogenous Variables: International Level	
IRGC	Cumulated Number of IRGC occasions catalogued with identifiers by year
V. Exogenous Variables: National Level	
OING	Number of INGER nurseries in other countries
AREA	Land area planted to rice
Country Dummy Variables	
Time Dummies	(1975–80), (1981–85), (1986–90)

TABLE 10

Estimates of INGER, IRGC, IRPB and NPB Impacts
3SLS Estimates of Ten Equation System

	Independent Variables								
Dependent Variable	OING	IRGC	ENTRIES	POOLR	NING	CNLR	CILR	POOLRI	AREA
NING	.0588 (7.85)	.000875 (2.17)	-.00007 (.04)	-.0999 (2.60)					.0319 (16.59)
R1 IRRI/INGER					.00037 (.16)	-.0034 (2.57)	.0021 (4.42)	.00013 (.05)	.0001 (1.09)
R2 IRRI/NO INGER					-.0078 (3.16)	.0013 (1.00)	-.0008 (1.70)	.00628 (2.38)	.0002 (2.38)
R3 OTHER/INGER					.0010 (.74)	.0002 (.30)	.0006 (.57)	.00036 (.24)	-.00003 (.93)
R4 OTHER/NO INGER					-.0002 (.13)	-.0001 (.09)	.0001 (.20)	.00389 (2.89)	-.00007 (1.44)
R5 IRRI PARENT/INGER					.0036 (1.05)	.0054 (2.89)	.0010 (1.47)	-.00416 (1.10)	-.00004 (.58)
R6 IRRI PARENT/NO INGER					.0053 (.89)	.0036 (1.13)	-.0032 (2.69)	.0254 (3.86)	-.00000 (.00)
R7 OTHER PARENT/INGER					.0087 (1.72)	.0040 (1.43)	-.0002 (.22)	.00062 (.11)	-.0004 (1.82)
R8 OTHER PARENT/NO INGER					.0121 (3.56)	-.00068 (.35)	-.0005 (.92)	.0124 (3.42)	-.00051 (3.86)
R9 NATIONAL					.0065 (1.25)	.0068 (2.38)	.0010 (1.00)	.00015 (.03)	-.00006 (2.21)
Sum of Coefficients					.0295	.0173	-.0003	.0451	
F Test on Sum					4.75	5.26	.014	8.35	
Prob > F					.037	.021	.903	.004	
System R^2 = .54									

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APPENDIX TABLE 1

Matrix of Varietal Borrowing
(Numbers in parentheses represent borrowings through INGER)

	Other	Latin America	Oceania	Bangladesh	Africa	Burma	USA	China	India	Indonesia	IRRI	Korea	S.E. Asia	Nepal	Pakistan	Philippines	Sri Lanka	Taiwan	Thailand	Vietnam	Total
Other	9	7	0	0	0	1	0	5 (2)	16	3 (2)	18 (9)	6	5	0	0	0	0	1	0	0	71 (13)
Latin America	3 (1)	185 (2)	0	0	1 (1)	0	5	0	2 (2)	0	39 (15)	1	0	0	0	2	1 (1)	0	0	0	239 (22)
Oceania	0	0	1	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0	0	0	6 (0)
Bangladesh	0	0	0	17	0	0	0	1	4 (1)	0	11 (3)	0	1	0	0	0	0	0	0	0	34 (4)
Africa	1	1 (1)	0	0	69 (1)	0	0	0	1 (1)	0	26 (12)	0	0	0	0	1	2 (2)	0	0	0	101 (17)
Burma	2	0	0	1 (1)	0	33	0	1 (1)	1	1 (1)	18 (5)	0	2 (1)	0	0	1	2 (2)	0	12 (6)	2 (2)	76 (19)
USA	0	1	0	0	0	0	48	0	0	0	2 (2)	0	0	0	0	0	0	0	0	0	51 (2)
China	0	0	0	0	0	0	0	66	1	0	13 (8)	1	0	0	0	0	1 (1)	0	0	0	82 (9)
India	5	0	0	0	1	0	0	0	573	0	53 (33)	0	1	0	1	1	4 (3)	2	1 (1)	1	643 (37)
Indonesia	0	0	0	0	0	0	0	0	0	29	18 (13)	0	0	0	0	1	0	0	0	0	48 (13)
SE Asia	0	0	0	0	0	0	0	0	1	0	7 (2)	0	21	0	0	0	0	0	0	0	29 (2)
Korea	0	0	0	0	0	0	0	0	0	0	1	105	0	0	0	0	0	0	0	0	106 (0)
Nepal	0	0	0	0	0	0	0	0	0	0	5 (2)	0	1	8	0	0	1 (1)	0	0	0	17 (3)
Pakistan	0	0	0	0	0	0	0	0	0	0	7	0	0	0	5	0	0	0	0	0	12 (0)
Philippines	0	0	0	0	0	0	0	0	0	0	25 (15)	0	0	0	0	26	0	0	0	1	53 (15)
Sri Lanka	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	51	0	0	0	53 (0)
Taiwan	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0	0	6 (0)
Thailand	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	23	0	23 (0)
Vietnam	0	0	0	0	0	0	0	0	0	0	44 (27)	0	0	0	0	0	0	0	0	15	59 (27)
Total	20	194	1	18 (1)	71 (2)	34 (0)	53 (0)	73 (3)	601 (4)	34 (3)	294 (146)	113 (0)	31 (1)	8 (0)	6 (0)	32 (0)	62 (10)	9 (0)	36 (7)	19 (2)	1,709 (183)

APPENDIX TABLE 2

Matrix of Parental Borrowing
(Numbers in parentheses represent borrowings through INGER)

	Other	Latin America	Oceania	Bangladesh	Africa	Burma	USA	China	India	Indonesia	IRRI	Korea	S.E. Asia	Nepal	Pakistan	Philippines	Sri Lanka	Taiwan	Thailand	Vietnam	Total
Other	28 (2)	2	0	0	0	1	1	0	42 (23)	4	48 (13)	1	7	0	0	4 (3)	0	2 (1)	2	0	142 (42)
Latin America	116 (26)	73 (20)	0	0	4 (3)	0	22 (3)	0	62 (58)	3 (5)	161 (68)	4	0	0	0	8	6 (3)	5 (2)	10 (3)	4 (3)	478 (198)
Oceania	0	0	0	0	2	0	2	0	5	0	0	0	0	0	0	0	0	1	2	0	0 (0)
Bangladesh	4 (1)	0	0	1 (1)	0	0	2	1	18 (11)	2	34 (9)	0	2	0	0	2	0	1 (1)	0	1 (1)	68 (24)
Africa	33 (20)	3 (2)	0	0	34 (13)	0	0	2 (2)	57 (51)	6 (4)	42 (24)	0	6 (3)	0	0	3	3 (3)	5 (1)	5	3 (3)	202 (126)
Burma	26 (15)	0	0	0	0	1	0	1	68 (68)	5 (1)	38 (29)	0	1	0	0	7 (5)	0	2	0	3 (4)	152 (122)
USA	28	2	0	0	0	0	47 (1)	0	15 (15)	0	6 (4)	0	0	0	0	0	1	1	2 (4)	0	102 (24)
China	42 (13)	0	0	0	0	0	0	20 (7)	27 (29)	1 (2)	72 (52)	0	0	0	0	0	1	1	0	0	164 (103)
India	150 (32)	1	0	3 (2)	4 (4)	0	2 (1)	10 (3)	637 (101)	14 (7)	351 (174)	0	23 (13)	0	0	15 (6)	10 (4)	57 (14)	7 (4)	0	1,284 (365)
Indonesia	11 (3)	0	0	0	0	0	0	1	22 (12)	22 (1)	35 (14)	0	1	0	0	2	0	0	2	0	96 (32)
SE Asia	0	0	0	0	0	0	0	1	9 (5)	3	17 (7)	0	9 (1)	0	0	3 (2)	0	2	2	0	58 (20)
Korea	0	0	0	0	0	0	0	0	3 (3)	0	49 (15)	74 (8)	0	0	0	0	0	0	0	0	201 (29)
Nepal	9	0	0	1	1	0	0	0	7 (4)	1	10 (4)	0	2	0	0	1	2 (2)	0	0	0	34 (14)
Pakistan	1	0	0	0	0	0	0	2	6 (3)	0	12 (4)	0	0	0	0	1	0	0	2	0	24 (8)
Philippines	20	0	0	0	0	0	4	0	11 (2)	5 (1)	45 (13)	0	2	0	0	18 (2)	0	0	0	0	105 (18)
Sri Lanka	24 (3)	0	0	0	0	0	1 (1)	1 (1)	4 (3)	3 (1)	22 (4)	0	0	0	0	0	50 (5)	1	0	0	106 (18)
Taiwan	2	0	0	0	0	0	0	0	3 (2)	0	5	0	0	0	0	0	0	2	0	0	12 (2)
Thailand	12 (5)	0	0	0	0	0	0	0	12 (11)	2	7 (5)	0	0	0	0	1	0	1	11 (1)	0	46 (22)
Vietnam	11 (1)	0	0	0	0	0	0	3	34 (22)	3	63 (23)	0	1	0	0	1	0	0	0	2	118 (46)
Total	603 (132)	81 (22)	0	5 (5)	43 (20)	2	81 (6)	43 (13)	1,039 (423)	74 (22)	1,022 (462)	79 (8)	54 (17)	0	0	66 (22)	72 (17)	81 (19)	45 (14)	13 (11)	3,404 (000)