Genebank Impacts

Working Paper No. 3 | December 2019

The contribution of the International Rice Genebank (IRG) to varietal improvement and crop productivity in Eastern India

Donald Villanueva
International Rice Research Institute (IRRI), Philippines
d.villanueva@irri.org

Grace Lee Capilit
International Rice Research Institute (IRRI), Philippines
g.capilit@irri.org

Melinda Smale
Michigan State University, USA
msmale@msu.edu

Nelissa Jamora
Global Crop Diversity Trust (Crop Trust), Germany
nelissa.jamora@croptrust.org

Ruaraidh Sackville Hamilton
International Rice Research Institute (IRRI) Philippines
ruaraidh.sh@gmail.com

Abstract

This paper investigates the contribution of rice genetic resources through varietal improvement on the rice productivity of farmers in Eastern India. Pedigree analyses were conducted to construct indicators of the genetic contribution of ancestors maintained by the International Rice Genebank (IRG) to cultivated rice varieties. The countries of origin of the IRG progenitors were examined and three of the most popular IRG progenitors were characterized. Results show that 45 to77% of the genetic composition of improved rice varieties derived from the genes of IRG accessions. Employing data collected from almost 9000 farmers in Eastern India, we tested empirically the relationship of ancestry to productivity changes while controlling for the effects of other farm inputs and environmental factors. Coefficient estimates of the preferred translog model indicate that a 10% increase in the genetic contribution of IRG accessions in an improved rice variety is associated with a yield increase of 27%. The Coefficient of Parentage (COP) was computed to determine the level of diversity among the 10 most adopted improved rice varieties. The average COP of all pairwise combinations of the top 10 varieties is 0.0973, which implies high diversity. High diversity among these varieties is likely a result of crossing germplasm received from 19 countries of origin. The latent diversity measured by the COP may also translate into multiple, functional trait combinations in a released variety. Findings demonstrate the valuable contribution of IRG's genetic resources to the development of improved rice varieties.

Suggested citation

Villanueva, Donald, Grace Lee Capilit, Melinda Smale, Nelissa Jamora and Ruaraidh Sackville Hamilton. 2019. The contribution of the International Rice Genebank (IRG) to varietal improvement and farm productivity in Eastern India. Genebank Impacts Working Paper No. 3. CGIAR Genebank Platform, IRRI, and the Crop Trust.

Acknowledgement

Funding for this research was provided by the CGIAR Genebank Platform, IRRI, and the Crop Trust through the 2018 Genebank Impacts Fellowship. We would like to acknowledge the International Rice Genebank (IRG) and the Rice Monitoring Survey (RMS) team for sharing the data.

Acronyms

AIC	Akaike’s information criterion
BIC	Bayesian information criterion
BMGF	Bill and Melinda Gates Foundation
COP	Coefficient of parentage
DGWG	Dee Geo Woo Gen
GRIMS	Genetic Resources Information Management System
ICIS	International Crop Information System
INGER	International Network for the Genetic Evaluation of Rice
IRG	International Rice Genebank
IRGC	International Rice Germplasm Collection
IRIS	International Rice Information System
IRRI	International Rice Research Institute
RMS	Rice Monitoring Survey
TN-1	Taichung Native 1
VIF	Variance Inflation Factors

Contents

1 Introduction

Rice is the most important cereal crop and the staple food of more than half the world's population with Asia representing the largest producing and consuming region (FAO 2014). During the Green Revolution in 1960s, high-yielding rice varieties were introduced in response to the specter of famine as population densities rose and productivity stagnated. However, this remarkably successful advancement created an unintended consequence of crop diversity loss. Traditional varieties and the wild species of rice were rapidly replaced by new varieties. Genetic variation from traditional varieties and related wild species is needed in crop improvement to cope with the many biotic and abiotic stresses that challenge rice production around the world (IRRI n.d.).

To protect against the loss of rice diversity, the International Rice Research Institute (IRRI) initiated the collection of rice genetic resources in 1962 which eventually lead to the establishment of the International Rice Genebank (IRG) in 1971. IRG has the largest and most diverse collection of rice genetic resources in the world. As of June 2018, the collection includes 130,139 accessions, comprising accessions of 123,837 *Oryza sativa*, 1,655 of *O. glaberrima*, and 4,647 wild relatives and interspecific hybrids. Over the past decades, the rice genetic resources maintained by the IRG have been used effectively to increase the productivity of the rice crop particularly among smallholder farm families in lower income countries. Rice genetic improvement using IRG accessions was accomplished through IRRI's breeding program which produces improved cultivars both in the form of "varieties" that are ready for use in farmers' fields and in the form of "advanced lines" suited for use as parent material in national plant-breeding programs (Evenson and Gollin 1997, p. 471). However, other than the landmark studies by Evenson and Gollin (1997) and Gollin and Evenson (1998), we are not aware of analyses that have explicitly related productivity changes on farm to genebank accessions through varietal improvement.

Evenson and Gollin (1997) consulted the genealogies of 1,709 rice varieties released by national programs and IRRI from 1965 to 1990, correlating productivity changes with changes in IRRI programs in an econometric model. They estimated that adding 1,000 cataloged accessions was associated with the release of 5.8 additional varieties. Assuming a 10-year lag for variety development, and a 10% discount rate, they calculated that these new accessions generated a present value (in 1990 dollars) of $325 million. High payoffs provided an economic justification for the continued operation of the International Network for the Genetic Evaluation of Rice (INGER) and the IRG.

Another analysis by Gollin and Evenson (1998) examined impacts in India only. The authors conducted a pedigree analysis of the 306 rice varieties released for planting in India over the period 1965–1986. They applied two-staged regression analysis to the district-level time series data to estimate the relative contribution of varietal improvement to productivity growth in rice. Results showed that varietal change contributed more than one-third of the rice productivity gains realized over the post-Green Revolution period, 1972–1984. In addition, findings illustrated that the economic value of genetic resources in India exceeded the costs of maintaining them.

Two decades later, this analysis provides renewed, evidence-based documentation of the value of the IRG operation in raising productivity on farms in Eastern India. However, in comparison with the studies conducted earlier, we are able to draw on data collected in a large-scale farm survey to test the genetic contribution of IRG accessions. We are also able to benefit from a digitized pedigree information system to better characterize ancestry and measure latent genetic diversity. The unique feature of this study is that it uses a cross-sectional farm-level data and employs pedigree analysis on the released rice varieties cultivated by the farmers

Our main objective is to test the effect of IRG genetic ancestry on the rice productivity of farmers in Eastern India. We also used surveys to examine the country of origin of all IRG accessions in the ancestry of improved rice varieties grown and characterize the most widely used progenitors. Lastly, this study evaluates the genealogical (latent) diversity of the most popular improved rice varieties grown by farmers using Coefficients of Parentage (COP). Our findings demonstrate the benefits of investing in maintaining rice genetic resources in the IRG.

2 Data and methods

2.1 Data

India is the world's second largest producer of rice. More than half of India's population depends on rice as the staple food. IRG has been active in seed distribution to India. In fact, India ranks first among the top recipients of germplasm from IRG. Figure 1 shows that around 60% of the seeds distributed in India were used in research, evaluation and crop improvement while the other 40% were for seed restoration of the national genebanks. As shown in Figure 2, IRG annually distributed significant number of IRG accessions to India which purposely related to varietal improvement since 1976. Half (50%) of seed recipients have been India's local genebanks. A total of 45% are national centers, academic institutions, international organization and private companies, with a small percentage distributed to individuals and non-governmental users. National centers refer to the national agricultural research and extension systems (NARES) while non-governmental users include non-government organizations (NGO) which are involved in breeding and seed distribution.

Eastern India, comprising of the states of Assam, Bihar, Jharkhand, Chhattisgarh, Orissa, Eastern Uttar Pradesh and West Bengal, is the largest rice growing region of the country. This region accounts for approximately 60% of the total rice area of India and generates around 48% of the national rice production (Adhya et al. 2008, p. 1). In 2016, IRRI conducted a farm-level survey in four states of Eastern India (Eastern Uttar Pradesh, Bihar, Orissa and West Bengal) through a project called Rice Monitoring Survey (RMS), funded by the Bill and Melinda Gates Foundation (BMGF). This survey aims to gather information on the rice varieties cultivated by the farmers during the *kharif* or wet season of 2015 and examine diffusion of submergence as well as drought-tolerant rice varieties. A total of 720 villages were randomly selected from the rural villages defined in the 2011 Census of India and in each village, 12 households were randomly selected. The total number of households interviewed is 8,640 with the sample size in each state proportional to the rural population across states. Figure 4 shows the geographical location of the villages included in the survey. Table 1 shows the distribution of sample villages and household by state as well as the average rice area per household. The current study used cross-sectional, farm-level data from RMS to determine the name of improved or released rice varieties grown by the farmers during wet season of 2015 and construct variables to explain productivity.

In the econometric analysis, plot-level data was used since there is one variety planted per plot and most of the farmers have more than one plot. However, only those plots that were planted to the improved rice varieties identified by this study and with pedigree information were included in the analysis. Those observations with outlier values were dropped in the dataset and excluded in the analysis. The final sample size used for model estimation is 8,967 rice plots which correspond to 4,298 farmers.

In the pedigree analysis of the improved rice varieties, data were retrieved from existing databases such as the International Rice Information System (IRIS), Genetic Resources Information Management System (GRIMS) and Gateway to Genetic Resources (GENESYS). IRIS is the rice information management system of the International Crop Information System (ICIS). ICIS provides integrated management of global information on genetic resources and crop cultivars and is used to manage germplasm information of materials developed, received and maintained by IRRI. GRIMS is utilized to manage data from the different operations of the genebank, such as seed acquisition, multiplication, characterization, storage management and seed distribution. GENESYS is a gateway through which germplasm accessions from genebanks around the world can be easily found and ordered.

2.2 Methods

Descriptive analysis was conducted for all the improved rice varieties identified under the RMS project. Each improved rice variety was classified according to the breeding institution responsible for its development and the source of its direct parent(s). Breeding institutions were classified as IRRI or non-IRRI. The source of direct parent(s) was classified as IRRI or another research institution. Using the results of the area estimates from RMS, the improved rice varieties which covered 95% of the total area planted by improved rice varieties were identified and became the focus of the succeeding analysis. Each of the identified varieties was classified according to whether it has direct parent(s) acquired from IRG.

Pedigree analysis was employed to quantify the genetic contribution of each IRG accession to each improved rice variety. Mendelgram, the program of IRIS used for this analysis, commonly assumes that each parent contributed an equal amount to their progeny. Using an algorithm that is consistent with Mendelian genetics, the genetic contribution is calculated as the probability that an unselected allele comes from a progenitor with values ranging from 0 to 1.

In this study, the progenitor contribution of the IRG accessions was classified into four categories: definite contribution, possible contribution, no contribution, and unknown contribution. Definite contribution refers to identified progenitor contribution of the IRG accession in the ancestry of an improved rice variety. IRG accessions can be identified when the progenitor in the pedigree tree obtained in the BROWSE application of IRIS has an International Rice Germplasm Collection (IRGC) number opposite the variety name. This implies that the accession was obtained directly from IRG. Possible contribution refers to a progenitor that does not have an IRGC number opposite the variety name in the pedigree tree but it has a match by name somewhere in the IRG collection. In this case, it is possible that the progenitor came from IRG but due to human error in encoding or a random error in the program of the application/tool used in migrating and processing the data, the wrong name was recorded as the source. If a progenitor had no IRGC number opposite the variety name in the pedigree tree and had no match by name in the whole collection of the IRG, then it was classified as no contribution. Lastly, unknown contribution refers to the progenitor with unknown or confidential information.

Definite contribution was computed first during the aggregation of the progenitor contribution of IRG to each modern rice variety. In this process, the progenitors in the extracted pedigree tree with an IRGC number were identified and their ancestry levels were examined. If their pedigree lines are independent, then the progenitor contributions were added. However, in the case of recurrence of the IRGC accession in the same pedigree line, only the IRG accession with the lowest ancestry level was included in the aggregation. Afterwards, following the same procedure for aggregating the progenitor contribution, the remaining progenitors in the extracted pedigree tree with names matched in the IRG collection were identified and their contributions were aggregated. This type of contribution is classified as the possible contribution. Similar procedures were employed for the aggregation of no and unknown contributions. The percent area of the improved rice varieties adopted by farmers surveyed was used as a weight in computing the overall average progenitor contribution of IRG accessions by category.

A plot-level yield response function was estimated to test the effect of the genetic contribution of genebank accessions to productivity, while controlling for the influence of conventional inputs (fertilizer, labor, machinery, plant protection, irrigation), management (age, education, access to inputs, credit and extension advice), and environmental factors (submergence, salinity, drought). The values of continuous variables pertaining to production output and input were transformed into unit per hectare. In the initial exploratory analysis, both definite and possible contributions of IRG on the variety were included in the model. However, in the final model, we only used the index for definite contribution to measure the clear impact of IRG on productivity.

Similar methodology has been employed in a small number of studies in the past (e.g. Widawsky and Rozelle 1998; Smale et al. 1998; Smale et al. 2008; Di Falco and Chavas 2009), but these studies focused on the effects of variety diversity and genetic diversity on yield or yield risk and did not link their analyses directly to genebank accessions. Widawsky and Rozelle applied a generalized Cobb-Douglas yield model with a stochastic specification to test the effects of diversity on mean and variance of rice yield, using township data from Zhejiang and Jiangsu Provinces. Smale et al. (1998) used a Cobb-Douglas function with a Just and Pope (1979) specification to test the effects of wheat diversity on mean and variances of yields in the irrigated and rainfed districts of the Punjab of Pakistan from 1979 to 1985. In a different study, Smale et al. (2008) tested the effects of area-weighted variety age, the average coefficient of diversity and the interaction between them on partial productivity by applying a Cobb-Douglas yield model. Di Falco and Chavas (2009) used a moment-based approach of stochastic production function to capture the effects of crop genetic diversity on mean, variance and skewness of farm productivity and production risk in the highlands of Ethiopia.

While moment-based approaches might be tested in further analysis, the focus of the current study is on the effect of the genetic contribution of accessions from IRG on mean yields. Four functional forms were tested: linear, extended linear, Cobb-Douglas and translog. Below are the specifications of these models:

1. Linear:

$$y_i = \beta_0 + \sum_{i=1}^{n} \beta_i x_i + \sum_{i=1}^{n} \alpha_i z_i + \mu_i$$

2. Extended linear:

$$y_i = \beta_0 + \sum_{i=1}^{n} \beta_i x_i + \sum_{i=1}^{n} \sum_{j}^{n} \beta_{ij} x_i x_j + \sum_{j=1}^{n} \alpha_i z_i + \mu_i$$

3. Cobb-Douglas:

$$lny_i = \beta_0 + \sum_{i=1}^{n} \beta_i lnx_i + \sum_{i=1}^{n} \sum_{j}^{n} \beta_{ij} lnx_i lnx_j + \sum_{j=1}^{n} \alpha_i z_i + \mu_i$$

4. Translog:

$$lny_i = \beta_0 + \sum_{i=1}^{n} \beta_i lnx_i + \frac{1}{2} \sum_{i=1}^{n} \sum_{j}^{n} \beta_{ij} lnx_i lnx_j + \sum_{j=1}^{n} \alpha_i z_i + \mu_i$$

where y_i is yield of rice per hectare, x_i is the quantity of conventional production inputs per hectare, and z_i is the non-conventional input variables (management, environmental factors, and progenitor contribution).

In each functional form, two different models were generated. The first model did not control for location effects while the second model controlled for state effects. Initially, we tested a third model which controlled for the village effects. However, due to small sample sizes per village, we excluded this model in the final analysis. Model diagnostics were performed to determine whether the necessary model assumptions are valid. We used Variance Inflation Factors (VIF) to test multicollinearity among independent variables and Breusch-Pagan/Cook-Weisberg test for heteroscedasticity. To evaluate the economic performance of the functional specification for each model, both Akaike's information criterion (AIC) and Bayesian information criterion (BIC) were used. The most preferred model specification is the one with the minimum AIC and BIC value. Stata 14.2 was used to estimate the model and to perform other necessary tests discussed above.

The key variable of interest in all models is the variable measuring genetic (progenitor) contribution. The null hypothesis is that the genetic contribution of IRG accessions does not affect rice yield. If the coefficient of this variable is significantly different from zero, then the null hypothesis is rejected and the alternative hypothesis that the contribution of IRG accession affects the yield of the improved rice varieties is accepted.

This study also explored the origin of the IRG accessions found in the ancestry of the improved rice varieties identified in the survey. For each variety, the countries of origin of the progenitors with definite and possible contribution were identified and tabulated. In addition, a summary table was generated showing the country of origin for all progenitors without duplication.

Furthermore, the most popular IRG accessions in the ancestry of those adopted improved rice varieties were identified. Initially, the progenitors with definite and possible contribution were segregated according to the decade when the variety was released. From this list, the study selected the three most common IRG accessions across decades. The morphological characteristics of those IRG accessions were extracted from GRIMS and a table of varietal traits by IRG accession was constructed.

Lastly, 10 of the most adopted varieties by the farmers during the 2015 season according to area planted were selected for further analysis. Coefficients of parentage (COP) were computed for all pairwise combination among these 10 varieties to measure genetic diversity. The COP between two individuals is defined as the probability that a random allele at a random locus in one individual is identical by descent to a random allele at the same locus in the other individual (Cox et al. 1985, p. 529). The values of COP range between 0 (no common ancestor) to 1 (same individual or variety). The lower the value of the COP, the higher is the latent genetic diversity conferred by parentage among the varieties included.

3 Results and discussion

3.1 Description of improved rice varieties grown by the farmers

A total of 132 improved rice varieties (124 inbred and 8 hybrid) were cultivated by rice farmers in Eastern India during 2015 wet season (Table 2). Five percent of these varieties were developed by IRRI while the majority (80%) was developed by research institutions under the national breeding program in India and other private companies. Non-IRRI-developed varieties cover around 78% of the total cultivated area of released varieties. Only 2% of area was planted to IRRI-developed varieties. In terms of the identity of the first-degree progenitor or direct parents, 24% of the cultivated improved rice varieties have at least one IRRI parent (7% have both direct IRRI parents and 17% have only one direct IRRI parent). This result implies that rice research program in other research institutions in India received some elite lines from IRRI in the development of new rice varieties. The germplasm exchange between the breeders of IRRI and India, as well as among other countries, was speed up through INGER, a system of international nurseries through which advanced genetic materials are exchanged and evaluated. INGER is maintained and coordinated by IRRI.

Of the 132 improved rice varieties cultivated by farmers during 2015 wet season, 45 varieties covered 95% of the total cultivated area of improved rice varieties and are the focus of the succeeding analysis. Table 3 shows that 20% of these popular varieties have at least one direct parent which definitely came from the IRG. This comprises 43% of the total area. If possible IRG acquisition is included, which means that the direct parent has no IRGC number but has a name match with one of the IRG accessions, then 53% of the varieties have at least one direct IRG parent (corresponding to 71% of the total area).

3.2 Progenitor contribution of IRG

Table 4 shows the basic information about the varieties and the progenitor contribution of the IRG. A total of 45 released varieties (inbred and hybrid) were cultivated on about 10.78 million hectares. Fourteen of these varieties (six hybrid and eight inbred) do not have pedigree information from the IRIS database, and thus the progenitor contribution of IRG in these varieties is unknown.

Table 5 shows the summary of the progenitor contribution of IRG on most adopted rice varieties by farmers during 2015 wet season in Eastern India. In definite, possible and unknown progenitor contribution, the minimum and maximum contribution is 0 and 1, respectively while the no contribution has a minimum of 0 and maximum of 0.50. The unweighted mean shows that the average definite and possible progenitor contribution of IRG to a released variety is about 35% and 25%, respectively. Considering the estimated percent planted area as weights, the average definite and possible progenitor contribution of IRG to a released variety is about 45% and 32%, accordingly. These results mean that, on average, 45% of the genetic composition of a released rice varieties cultivated by farmers during 2015 wet season came from IRG accessions. The progenitor contribution increases up to 77% if the possible contribution is added. This value can still be higher if there are IRG accessions in the pedigree of the hybrid and inbred varieties with no information. These results serve as evidence of the significant contribution of IRG to the development of improved rice varieties in Eastern India.

3.3 Contribution of IRG genetic resources to productivity

Table 6 reports the definition and some basic descriptive statistics for the variables included in the yield response function. The average yield is around 2.5 tons per hectare (t/ha) with standard deviation of 1.7 t/ha. Farmers applied an average of 153 kg/ha of nitrogen (N), phosphorus (P) and potassium (K) fertilizer on aggregate. Labor, power cost and other material inputs has an average of 93 person-days/ha, Php5,521/ha and Php778/ha, respectively. About half of the total plots experienced drought based on the perception of the farmer. The average age and education of the farmers is about 48 and 6 years, respectively. Only a few of the respondents have access to input, credit and extension worker. The plot-level average of the definite contribution is 0.49 which means that about 49% of the genetic composition of the variety came from the genes of IRG accessions.

Appendices 1 to 4 show the estimated models in different functional forms. The results of VIF confirm that there is a moderate multicollinearity (mean VIF=1.55) among independent variables but it is not severe enough to warrant corrective measures (Table 7). On the other hand, the results of Breusch-

Pagan/Cook-Weisberg test for heteroscedasticity is significant which means that there is a problem of heteroscedasticity in the model (Table 8). To deal with this problem, robust standard errors were used in all models instead of the ordinary standard errors. AIC and BIC were computed to assess the most appropriate functional form in each model (Table 9). In all three models, results show that the translog has the lowest values of AIC and BIC among all the functional forms. This result implies that translog is the functional form that best fits the data.

Between the two models with translog functional form, Model 2 was selected as the final model because it controls for state effects and captures significant yield variation across observations. The final yield response model of this study is presented in Table 10.

The definite IRG contribution is the main variable of interest to us. The coefficient of the definite IRG contribution is positive and significant. This result means that higher value of the genetic contribution from IRG in an improved rice variety increases its yield. The magnitude of the increase in yield can be computed by obtaining the exponential value of the coefficient of variable pertaining to the definite IRG contribution using the formula exp (coefficient). Applying this formula, the result is 1.027. In terms of percent change, this result can be interpreted as a 1% increase in the definite IRG contribution on an improved rice variety can increase the yield by about 2.7%. Furthermore, a 10% increase in the definite IRG contribution can lead to a 27% yield increase. These findings imply that the germplasm acquired from IRG is associated with yield improvement of rice varieties on farms in Eastern India.

Other results show that, except for labor, the conventional production inputs have positive and significant effects on productivity, conforming to the economic theory of production. The negative sign of labor input may be attributed to measurement error as labor input was not adjusted with respect to the difference in quality between skilled and non-skilled farm workers. Person-days per ha are often overstated, with variable lengths of workday. These results are consistent when we explored different labor transformation and included it in the translog model. The sign of labor input remained negative while the signs of other variables are consistent in various models that we evaluated.

Transplanted rice has significantly higher yield compared to broadcasted or direct seeded rice. Plots with a higher percentage of irrigated area have higher yield. Even in the wet season, some areas in Eastern India experience erratic rains and farmers need supplementary sources of irrigation for their crops. The coefficients of submergence, salinity and drought are negative and significant. These abiotic stresses affect the growth of rice crop and decrease its productivity. In some parts of Eastern India, rice is cultivated in low-lying areas which are prone to submergence due to heavy rains and intrusion of river or sea water. On the other hand, salinity can be caused of rising ground water or the intrusion of sea water which brings salts to rice areas. Drought during the wet season can be caused by untimely or low amounts of rainfall and without other sources of water for irrigation, rice productivity will be affected.

Effects of management factors are weaker. The age and education of the farmers do not significantly affect the yield. Plots owned by farmers with access to credit have higher yield compared to those who do not have access. Credit can be in a form of farm input or cash which is used to provide the optimal needs in rice production.

3.4 Country of origin

The complete list of countries of origin of all ancestors by type of IRG contribution is shown in Table 11. The number in parenthesis beside the name of country is the number of unique progenitors originating in that country. The progenitors developed or bred by IRRI headquarter were separated from the progenitors originating in the provinces of the Philippines. Results show that Cottondora Sannalu (MTU 1010) and Pratikshya have the greatest number of unique countries of origin of progenitor with definite and possible IRG contribution with 12 countries followed by Swarna-Sub1 with 11 and Vijetha (MTU 1001) and IR64-Sub1 with 10. If we focus on progenitors with definite IRG contribution, Cottondora Sannalu (MTU 1010), Pratikshya and IR64-Sub1 have the greatest number of countries of origin with 10 countries followed by Swarna-Sub1 with nine. According to Ramirez et al. (2013, p. 44), the wide use of landraces from different countries as a source of desired traits has contributed to the increase in rice production in most rice-growing countries. The combined traits from these landraces conferred the necessary characteristics that allowed the different cultivars to cope with changing pest and disease pressures, various soil and nutrient conditions and particular regional climatic conditions (Sebastian et al. 1998).

Table 12 shows the summary of the distribution of progenitors by country of origin and by type of progenitor contribution of IRG. Values shown in this table represent the aggregated frequency of unique progenitors of all released varieties by their country of origin. Here, progenitors which appeared in the pedigree of more than one progeny have been counted only once to avoid double counting. Results show that there are 122 unique progenitors from 19 countries with definite and possible contribution of IRG on released varieties in Eastern India cultivated during 2015 wet season. Combining the results for definite and possible IRG contribution, the most popular country of origin is India with 30 progenitors, followed by IRRI-Philippines (28) then United States (15) and Taiwan (8). These results demonstrate the diversity of the progenitors in terms of their country of origin which can also translate into multiple trait combinations in a released variety. Analyses such as these can also be used to identify future potential sources of additional genetic accessions for varietal improvement.

3.5 Most popular progenitors

In Table 13, the progenitors that frequently appear in the pedigree of the released varieties in India during the 2015 wet season are enumerated by decade of varietal release. Peta, Dee Geo Woo Gen (DGWG), and Fortuna are the three most popular progenitors with definite IRG contribution. Cina, Latisail and Taichung Native 1 (TN-1) are the three most popular progenitors with possible IRG contribution. Below, we focus on popular progenitors with definite IRG contribution.

Peta and DGWG are the direct parents of IR8, the variety which revolutionized rice production in tropical Asia and has been called as the “miracle rice.” Figure 8 shows the standing crop of IR8, Peta, and DGWG in a field experiment in IRRI. The development of IR8 was the start of the green revolution in rice not only because of rapid increase in rice production but also because this variety is the most widely used parent in several crosses in tropical Asia. On the other hand, Fortuna is one of the ancestors of elite varieties such as IR24, IR36, IR64, Lalat, Pooja and Swarna-Sub1. The following section provides information about Peta, DGWG, and Fortuna. Table 14 describes the morphological and other special characteristics of these progenitors based on the field and screen house evaluation.

3.5.1 Peta (IRGC 35)

Peta, a tall and vigorous indica rice variety from Indonesia, was produced from a cross of Tjina and Latisail by H. Siregar. Tjina is synonymous with China while Latisail came from Bengal (Dalrymple 1986, p. 33). The first acquisition of this variety by IRG from Indonesia is in the early 1960s, however the exact date was not documented. IRG assigned an IRGC number of 35 for this acquisition. Other Peta seed samples were acquired by IRG in 1961, 1971, 1972 and 1976. However, we focus on IRGC 35 (DOI 10.18730/1PH8F) since it is the accession used by IRRI breeders to produce IR8.

Peta is a late-maturing variety (145 days) with medium length (28.6 cm) and semi-compact panicle at post-harvest stage. It has an intermediate size of leaf length and width. Its grain length and width are 9.3 mm and 2.9 mm, respectively, with grain weight per 100 grains of 2.9 gm. Based on the results of field evaluation on biotic stresses, Peta is resistant to tungro virus and moderately resistant to blast. However, this variety is susceptible to bacterial blight and moderately susceptible to sheath blight and ragged stunt virus. In terms of response to insects, this variety is susceptible to all destructive insects except zigzag leafhopper. For abiotic stresses, this variety is tolerant to saline condition. However, it is susceptible to drought, flood, and cold conditions.

To examine the immediate contribution of Peta in breeding, we searched the elite lines and varieties where Peta was one of the ancestors from first up to fourth degree of their pedigrees. Based on the available information in IRIS, there are 5,728 unique advanced lines and released varieties found. Most these identified released varieties were developed in the 1960s. The popularity of Peta in their ancestries is due to the crossing of IR8 with other varieties or landraces to produce more improved rice varieties. Aside from IR8, other most notable released varieties with Peta in their ancestries are IR36, IR42, IR64, IR72, Swarna, Pooja and Lalat. In the current study, 20 out of 31 popular varieties (65%) cultivated during 2015 wet season in Eastern India and with available pedigree data have Peta as one of their ancestors. These 20 varieties were planted in around 6.6 million hectares during that season which covered 58% of the total area of improved rice varieties. This result implies that IRG plays a significant role in the conservation and distribution of the seeds of Peta in producing improved rice varieties that are currently well-adopted by farmers.

3.5.2 Dee geo woo gen (*IRGC* 123)

Dee-geo-woo-gen (DGWG) is the earliest known semi-dwarf rice which was found in Taiwan and also known as "I-geo-woo-gen." The prefixes Dee-geo and I-geo mean dwarf (Dalrymple 1986, p. 17). The origins of DGWG are unclear. One account suggests that it may have been brought from Fujian several hundred years ago (Miu 1959, p. 67) while another suggests that it may have been a spontaneous mutant from another traditional variety named Woo-gen (Hu 1976, p. 566). DGWG soon became popular in Taiwan which was planted in 10,907 ha during the first cropping season in 1953.

Before the development of IR8 in early 1960s, DGWG was used in the first cross involving a semi-dwarf in Taiwan. DGWG was crossed with Tsai-yuan-chung, a tall disease-resistant local variety. A selection from this cross was named Taichung Native 1 (TN-1) in 1956. TN-1 was rapidly accepted by farmers due to its short-statured and high tillering characteristics. By 1965, 79,000 ha were planted with TN-1, making it the second most popular variety that year (Dalrymple 1986, p. 18).

In March 24, 1962, IRG acquired DGWG seeds from Taiwan and assigned 123 as its IRGC number (DOI 10.18730/1PKYV). Afterwards, this variety became the donor of dwarfism trait in IR8. Dr. Robert Chandler, former director general of IRRI, described DGWG as “a high-yielding, heavy-tillering, short-statured variety from Taiwan (Hangrove and Coffman 2006).”

DGWG is a medium maturing (111 days) variety and known for its short plant height. It has intermediate size of leaf in terms of length and width. Its grain has a length of 8.1 mm and width of 3.1 mm and its 100-grain weight is about 2.3 gm. It has a short and drooping panicle with length of 24 cm. DGWG was categorized as non-glutinous or non-waxy rice based on the starch in the endosperm, is moderately resistant to blast but very susceptible to tungro and ragged stunt virus; susceptible to pests such as brown planthopper, green leafhopper, whorl maggot, white-backed planthopper and striped stemborer; and susceptible to drought and cold conditions.

According to the available data in the database, DGWG with IRGC# 123 is present in the first up to fourth pedigree of 5,649 advanced lines and released varieties which shows its immediate contribution in developing improved rice varieties. From this list, some of the notable released varieties are IR6, IR8, CO 36 and Giza 180. Similar to Peta, the popularity of DGWG is due to the development of IR8 which was crossed with other varieties to produce new improved rice varieties. Some of the well-known released varieties which are progenies of DGWG are IR36, IR42, IR64, IR72, Swarna, Pooja and Lalat. Based on the analysis conducted here, DGWG was found in the ancestry of 15 out of 31 popular varieties (48%) with pedigree information. These varieties were cultivated on around 6.2 million hectares during the 2015 wet season in Eastern India, covering 55% of the total area of improved rice varieties. This result implies that IRG’s conservation and distribution of DGWG seeds creates a field-level impact in rice production by sharing DGWG germplasm with breeders who then develop improved rice varieties.

3.5.3 Fortuna (*IRGC* 139)

Fortuna is a landrace javanica rice which originated in Taiwan. It was acquired by IRG on July 7, 1978 and assigned 139 as its IRGC number (DOI 10.18730/1PME6). Fortuna is a late maturing variety (124 days) with intermediate plant height, with grain length (9.8mm), width (3.0) and 100-grain weight (3.1 gm) is similar to Peta. The variety has an intermediate size of leaf with long (32 cm) and spreading panicle (open). Based on its endosperm, Fortuna is classified as non-glutinous or non-waxy rice. This variety is susceptible to bacterial blight, sheath blight, tungro virus and ragged stunt virus as well as to all common destructive insects. In the early vegetative stage, it is resistant to drought but it becomes susceptible in the late vegetative stage. While it exhibits intermediate tolerance to salinity condition, it is susceptible to flooding and cold conditions.

Fortuna with IRGC 139 was found in the first up to fourth degree of the pedigree of 765 advanced lines and released varieties, illustrating its immediate genetic contribution to improved rice varieties. Some of the noteworthy varieties in this list are Blue Bonnet, Sigadis, Star bonnet and Sun bonnet. These varieties were then crossed with other improved rice varieties and elite lines to develop other improved rice varieties, including the popular varieties Milfor, IR64, Lebonnet, IR72, Lalat, Pooja and Swarna-Sub1. Among the 31 popular improved rice varieties with pedigree information, we found that 11 varieties (35%) have Fortuna in their ancestries. During the 2015 wet season, these varieties were cultivated on around 2.5 million hectares in Eastern India, amounting to 22% of the total area of improved rice varieties. This result illustrates the significance of IRG in storing and sharing Fortuna seeds with the breeders to develop new improved rice varieties.

3.6 Coefficient of parentage

The coefficient of parentage (COP) measures how two varieties are related based on the identical alleles they are share in their pedigrees. COP is an indicator of genealogical or latent genetic diversity. The lowest value of COP is 0 which means the two varieties have no common ancestors and the highest value is 1 which means that the two varieties have the same ancestors and are thus identical in Mendelian terms.

Table 15 shows the off-diagonal matrix of the COP of the pairwise combinations among the ten most adopted varieties by farmers with pedigree information during 2015 wet season in Eastern India. All values in the diagonal of the half matrix are 1 since the progenitors between a variety and itself are perfectly the same. Among the 45 pairwise combinations of these varieties, 34 of them (76%) have values of COP less than or equal to 0.10. Four varieties (Pooja, Lalat, Sarjoo 52 and Moti) have no identical progenitors with Mahsuri because the values of their COP are zero. On the other hand, the pairwise combination with the highest value of COP is between Swarna and Swarna-Sub1 (0.94) followed by the combination of Mahsuri and Sambha Mahsuri (0.50). Swarna-Sub1 is closely related to Swarna because Swarna-Sub1 is the improved version of Swarna after adding the *Sub1* gene which makes this variety tolerant to submergence. Samba Mahsuri is the progeny after crossing two Indian popular varieties, Sambha and Mahuri, that is why 50% of their progenitors are identical.

On average, the COP for all pairwise combinations among these varieties (excluding the COP of a variety to itself) is 0.0973. This means that two varieties have a mean of 9.73% identical progenitors in their pedigrees, suggesting a high degree of latent genetic diversity. High diversity among these varieties is likely the result of crossing germplasm from different countries of origin, as shown in the previous section. This ancestral diversity may also be reflected in diverse, multiple trait combinations that provide functional diversity.

4 Conclusion

This paper provides evidence of the impact of IRG's genetic resources on rice productivity among smallholder farms in Eastern India. Using data from the farm household survey conducted by IRRI in 2016 in Eastern India, pedigree analysis was conducted and the analysis related productivity changes in farmers' fields explicitly to genebank accessions through varietal improvement. We also examined the country of origins of the IRG progenitors and characterized three of the most popular IRG progenitors. Lastly, the COP for all pairwise combinations among the 10 most adopted improved rice varieties by farmers was computed.

We found that, on average, 45% of the genetic composition of an improved rice variety cultivated by farmers in Eastern India was definitely contributed by IRG accessions. If possible IRG contributions are included, the total progenitor contribution could increase up to 77%. To assess the farm-level impact, the index for the definite IRG contribution was included as one of the explanatory variables of the yield response function. The results of the translog model show that the definite IRG contribution has a positive and significant impact on yield. A 1% increase in the definite IRG contribution to an improved rice variety increases rice yield by about 2.7%, other factors held constant.

Based on the country of origin of the progenitors, there are 122 unique progenitors from 19 countries with definite and possible IRG contribution. This finding demonstrates the diversity of the IRG progenitors in terms of their country of origin, implying that the wide use of combined traits from the landraces originating in different countries conferred the necessary characteristics that allowed farmers to cope with biotic and abiotic conditions and raise their rice production.

The most popular IRG progenitors with definite contribution identified in this study are Peta, DGWG, and Fortuna. Each of these varieties was crossed with other varieties, landrace or elite lines and produced new improved rice varieties. Peta and DGWG were popular progenitors because they are the direct parents of IR8 and the development of IR8 is the start of the green revolution on rice. Twenty out of 31 popular varieties (65%) identified by this study have Peta, DGWG or Fortuna in their ancestry. These 20 varieties were planted on around 6.6 million hectares during the 2015 wet season, covering 58% of the total area of improved rice varieties in Eastern India.

At the same time, COP analysis indicates that the top 10 most adopted varieties have only 9.73% identical progenitors in their pedigrees, implying a high degree of diversity conferred by ancestry. High diversity among these varieties probably reflects the crossing of germplasm sources from different countries of origin, and may also imply functionally diverse, multiple trait combinations.

The findings of this study demonstrate the valuable contribution of IRG's conservation and distribution of genetic accessions to the development of improved rice varieties and rice production on farms in Eastern India. In future research, the total monetary contribution of IRG can be estimated for the whole of Eastern India, considering the estimated yield gain attributable to the progenitor IRG contribution in an improve rice variety. Due to the availability of RMS data in Bangladesh, a similar case study can also be conducted in this country to assess the farm-level impact of IRG. The results of another country study will show a different perspective and can add information about the impact of the IRG.

5 References

Adhya, T.K., O.N. Singh, P. Swain and A. Ghosh. 2008. “Rice in Eastern India: Causes for Low Productivity and Available Options.” *Journal of Rice Research* 2: 1-5.

Cox, T. S., Y. T. Kiang, M. B. Gorman, and D. M. Rodgers. 1985. “Relationship Between Coefficient of Parentage and Genetic Similarity Indices in the Soybean.” *Crop Science 25* (May-June): 529-532.

Dalrymple, D. 1986. “Development and Spread of High-Yielding Rice Varieties in Developing Countries.” *Bureau for Science and Technology* 33: 17-18.

Di Falco, S. and J.P. Chavas. 2009. “On Crop Biodiversity, Risk Exposure, and Food Security in the Highlands of Ethiopia.” *American Journal of Agricultural Economics* 91 (3): 599-611.

Evenson, R.E., Gollin, D., 1997. “Genetic Resources, International Organisations, and Improvement in Rice Varieties.” *Economic Development and Cultural Change* 45 (3): 471–500.

Hu, C.H. 1973. "Evaluation of Breeding Semi-Dwarf Rice by Induced Mutation and Hybridization," *Euphytica* (22):566.

International Rice Research Institute (IRRI). n.d. “The International Rice Genebank.” Accessed June 29, 2018. http://irri.org/our-work/research/genetic-diversity/international-rice-genebank.

Just, R.E. and R.D. Pope. 1979. “Production Function Estimation and Related Risk Considerations.” *American Journal of Agricultural Economics* 61: 276-284.

Evenson, R.E. and D. Gollin. 1997. “Genetic Resources, International Organizations, and Improvement in Rice Varieties.” *Economic Development and Cultural Change* 45: 471-500. http://dx.doi.org/10.1086/452288.

FAO. 2014. “Asia and the Pacific Food and Agriculture.” Food and Agriculture Organization of the United Nations Regional Office for Asia and the Pacific, Bangkok: 72.

Gollin, D. and R.E. Evenson. 1998. “An Application of Hedonic Pricing Methods to Value Rice Genetic Resources in India.” *Evenson, R. E. Gollin, D. and Santaniello, V. (ed.) Agricultural Values of Plant Genetic Resource*: 139–150. CAB International., Wallingford, U.K.

Hargrove, T. and W.R. Coffman. 2006. “Breeding History”. *Rice Today* 5, no. 4 (October-December): 35-38. International Rice Research Institute.

McLaren, G., I. DeLacy and J. Crossa. n.d. “Routine Computation and Visualization of Coefficients of Parentage Using the International Crop Information System.” Accessed 15 November 2018. https://cropforge.github.io/iciswiki/articles/t/d/m/TDM_COP2.htm

Miu, T.S. 1959. “A Photographic Monograph of Rice Varieties of Taiwan.” *Taiwan Agricultural Research Institute* (2): 67.

Ramirez M., Ortiz R., Taba S., Sebastian L., Peralta E., Williams D., Ebert A., Vezina A. 2013. “Demonstrating Interdependence on Plant Genetic Resources for Food and Agriculture.” In: *Crop Genetic Resources as a Global Commons: Challenges in International Law and Governance,* edited by Halewood M, Lopez Noriega I, Louafi S, 39-61. London, UK: Routledge.

Sebastian, L.S., L.R. Hipolito and J. Garcia. 1998. “Molecular Contribution of Landraces in the Development of Philippine-bred Modern Rice Varieties,” *SABRAO Journal of Plant Breeding and Genetics* 30(2): 73–82.

Smale, M., J. Hartell, P. Heisey, B. Senauer. 1998. “The Contribution of Genetic Resources and Diversity to Wheat Productivity and Stability in the Punjab of Pakistan.” *American Journal of Agricultural Economics* 80: 482–493.

Smale, M., J. Singh, S. Di Falco and P. Zambrano. 2008. "Wheat Breeding, Productivity and Slow Variety Change: Evidence from the Punjab of India after the Green Revolution." *Australian Journal of Agricultural and Resource Economics* 6 (52): 419-432.

Widawsky, D., and S. Rozelle. 1998. "Varietal Diversity and Yield Variability in Chinese Rice Production." In *M. Smale (ed.), Farmers, Gene Banks, and Crop Breeding.* Boston: Kluwer.

6 Tables

Table 1. Distribution of sample households in Eastern India, RMS 2016.

State	**Number of villages**	**Number of households**	**Average rice area (ha)**
Eastern Uttar Pradesh	151	1,812	0.61
Bihar	176	2,112	0.81
Orissa	225	2,699	0.74
West Bengal	168	2,016	0.38
Total	720	8,640	0.66

Source of data: Rice Monitoring Survey (RMS) 2016 in India

Table 2. Distribution of rice varieties cultivated during the wet season of 2015, Eastern India, according to the institution that developed the variety and source of parents.

Parameters	Count	Percent	Area (000 ha)	% Area
Varietal development				
IRRI	6	5	259	2
Non-IRRI	106	80	8,860	78
Unknown	20	15	2,221	20
Total	**132**	**100**	**11,340**	**100**
Having direct IRRI parents				
Both parents	9	7	345	3
One parent	23	17	723	6
None	62	47	8,772	77
Unknown	38	29	1,501	13
Total	**132**	**100**	**11,340**	**100**

Sources of data: Rice Monitoring Survey (RMS) 2016 in India
International Rice Information System (IRIS)

Table 3. Distribution of rice varieties adopted on 95% of area during the wet season of 2015, Eastern India, by IRG parentage.

Parameters	**Count**	**Percent**	**Area (000 ha)**	**% Area**
With direct IRG parents (with IRGC# only)				
Both parents	2	4	124	1
One parent	7	16	4,494	42
None	22	49	4,485	42
Unknown	14	31	1,677	16
Total	**45**	**100**	**10,780**	**100**
With direct IRG parents (with IRGC# and possible IRG acquisition)				
Both parents	8	18	623	6
One parent	16	36	7,034	65
None	7	16	1,447	13
Unknown	14	31	1,677	16
Total	**45**	**100**	**10,780**	**100**

Sources of data: Rice Monitoring Survey (RMS) 2016 in India
International Rice Information System (IRIS)

Table 4. Varietal information and the progenitor contribution of IRG to rice varieties adopted on 95% of area during wet season 2015, Eastern India.

Variety name	Released Year	Variety type	Cultivated area (000 ha)	% Area	Progenitor contribution			
					Definite	Possible	No	Unknown
Swarna	1979	Modern/ HYV	3,592.58	31.68	0.7500	0.2500	0.0000	0.0000
Mahsuri	1972	Modern/ HYV	1,254.79	11.07	0.0000	1.0000	0.0000	0.0000
Arize 6444	2001	Hybrid	840.56	7.41	0.0000	0.0000	0.0000	1.0000
Sarjoo 52	1980	Modern/ HYV	436.31	3.85	0.0000	0.6250	0.3750	0.0000
Pooja	1999	Modern/ HYV	712.84	6.29	0.8750	0.1250	0.0000	0.0000
Lalat	1988	Modern/ HYV	572.86	5.05	0.6172	0.0078	0.3750	0.0000
Moti	1988	Modern/ HYV	222.08	1.96	0.2813	0.4063	0.3125	0.0000
Moti gold	2010	Modern/ HYV	201.24	1.77	0.0000	0.0000	0.0000	1.0000
Samba Mahsuri	1986	Modern/ HYV	168.71	1.49	0.2500	0.7500	0.0000	0.0000
Vijetha (MTU 1001)	1995	Modern/ HYV	421.06	3.71	0.3936	0.3493	0.2572	0.0000
Sonam		Modern/ HYV	131.91	1.16	0.0000	0.0000	0.0000	1.0000
CR Dhan 501	2010	Modern/ HYV	79.13	0.70	0.5000	0.5000	0.0000	0.0000
Swarna Sub1	2009	Modern/ HYV	158.81	1.40	0.7452	0.2548	0.0000	0.0000
GK 5003	2008	Hybrid	90.15	0.79	0.0000	0.0000	0.0000	1.0000
Cottondora Sannalu (MTU 1010)	2000	Modern/ HYV	157.34	1.39	0.5165	0.1671	0.3164	0.0000
Pratikshya	2005	Modern/ HYV	151.55	1.34	0.8684	0.1277	0.0039	0.0000
Samba-Sub1	2003	Modern/ HYV	50.44	0.44	0.0000	0.0000	0.0000	1.0000
IR64-Sub1	2014	Modern/ HYV	137.37	1.21	0.8305	0.0533	0.1162	0.0000

Niranjan		Modern/ HYV	125.76	1.11	0.0000	0.0000	0.0000	1.0000
Sita	1972	Modern/ HYV	70.85	0.62	1.0000	0.0000	0.0000	0.0000
Annapoorna	1976	Modern/ HYV	74.52	0.66	0.5000	0.0000	0.5000	0.0000
Jaya	1968	Modern/ HYV	112.48	0.99	0.0000	1.0000	0.0000	0.0000
Khandagiri	1992	Modern/ HYV	86.38	0.76	0.6152	0.3848	0.0000	0.0000
Ranjeet	1994	Modern/ HYV	90.65	0.80	1.0000	0.0000	0.0000	0.0000
Geetanjali	2005	Modern/ HYV	87.80	0.77	0.0000	1.0000	0.0000	0.0000
Naveen	2005	Modern/ HYV	77.67	0.68	0.1250	0.6250	0.2500	0.0000
Udayagiri	1999	Modern/ HYV	74.29	0.66	0.4922	0.5078	0.0000	0.0000
Pioneer		Hybrid	44.56	0.39	0.0000	0.0000	0.0000	1.0000
Mehak		Modern/ HYV	22.43	0.20	0.0000	0.0000	0.0000	1.0000
Bhuban	1988	Modern/ HYV	53.03	0.47	0.5000	0.5000	0.0000	0.0000
Krishna	1970	Modern/ HYV	31.80	0.28	0.5000	0.5000	0.0000	0.0000
Super Shyamali		Modern/ HYV	55.84	0.49	0.0000	0.0000	0.0000	1.0000
Tulasi	1988	Modern/ HYV	49.04	0.43	0.1250	0.3750	0.5000	0.0000
Jamuna	1970	Modern/ HYV	44.22	0.39	0.0000	1.0000	0.0000	0.0000
Miniket		Modern/ HYV	33.45	0.29	0.0000	0.0000	0.0000	1.0000
Santosh	2001	Modern/ HYV	41.58	0.37	0.5000	0.0000	0.5000	0.0000
Gorakhnath 509	2011	Hybrid	14.50	0.13	0.0000	0.0000	0.0000	1.0000
IR 36	1981	Modern/ HYV	28.30	0.25	0.9688	0.0313	0.0000	0.0000
Arzel		Modern/	30.49	0.27	0.0000	0.0000	0.0000	1.0000

		HYV						
Pankaj	1969	Modern/ HYV	33.40	0.29	1.0000	0.0000	0.0000	0.0000
Kaveri 108 (Sampurna)		Hybrid	10.69	0.09	0.0000	0.0000	0.0000	1.0000
NK 5251	2009	Hybrid	24.53	0.22	0.0000	0.0000	0.0000	1.0000
Savithri	1983	Modern/ HYV	28.03	0.25	0.5000	0.5000	0.0000	0.0000
Annada	1987	Modern/ HYV	29.62	0.26	0.5000	0.0000	0.5000	0.0000
Sahbhagi Dhan	2009	Modern/ HYV	24.38	0.21	0.7809	0.1937	0.0254	0.0000

Sources of data: Rice Monitoring Survey (RMS) 2016 in India
International Rice Information System (IRIS)

Table 5. Summary of the progenitor contribution of IRG to rice varieties adopted on 95% of area during the 2015 wet season, Eastern India.

Type of contribution	Min	Max	Mean	
			Unweighted	Area-weighted
Definite	0.00	1.00	0.35	0.45
Possible	0.00	1.00	0.25	0.32
No	0.00	0.50	0.09	0.07
Unknown	0.00	1.00	0.31	0.16
Total			1.00	1.00

Sources of data: Rice Monitoring Survey (RMS) 2016 in India
International Rice Information System (IRIS)

Table 6. Definition of variables and some descriptive statistics.

Variable name	Variable label	Mean	SD
Yield	Yield (kg/ha)	2,464	1,718
Fertilizer	Fertilizer (NPK) quantity (kg/ha)	153	87
Labor	Total labor (person-days/ha)	93	55
Power_cost	Cost of power inputs (machine rental, animal rental, fuel and electricity) in Rs/ha	5,521	5,049
Other_inputs	Cost of other material inputs (herbicide, pesticide, and others) in Rs/ha	778	1,370
Irrigation_percent	Percent of plot with irrigation	49	49
Crop_establishment	Crop establishment method (1-transplating, 0-otherwise)	0.85	0.36
Submergence	Submergence condition of the plot (1-yes, 0-no)	0.05	0.23
Salinity	Salinity condition of the plot (1-yes, 0-no)	0.004	0.06
Drought	Drought condition of the plot (1-yes, 0-no)	0.52	0.50
Age	Age of the respondent (years)	48	13
Education	Education of the respondent (years)	6.0	4.5
Access_input	Access to material inputs (1-yes, 0-no)	0.12	0.32
Access_credit	Access to credit (1-yes, 0-no)	0.08	0.27
Access_extworker	Access to agricultural extension services (1-yes, 0-no)	0.07	0.26
Definite_contribution	Definite contribution of IRG on the variety (index)	0.49	0.35

Sources of data: Rice Monitoring Survey (RMS) 2016 in India
International Rice Information System (IRIS)

Table 7. Variance inflation factors (VIF) among independent variables.

Variable	VIF	1/VIF
Access_credit	3.47	0.2885
Access_input	2.63	0.3799
Access_extworker	2.51	0.3981
Irrigation_percent	1.73	0.5785
Power_cost	1.49	0.6730
Definite_contribution	1.33	0.7515
Drought	1.25	0.8016
Crop_establishment	1.23	0.8145
Education	1.12	0.8901
Other_inputs	1.12	0.8949
Fertilizer	1.11	0.9010
Labor	1.10	0.9064
Submergence	1.09	0.9158
Age	1.07	0.9372
Salinity	1.01	0.9931
Mean VIF	1.55	

Sources of data: Rice Monitoring Survey (RMS) 2016 in India
International Rice Information System (IRIS)

Table 8. Chi-squared value of Breusch-Pagan/Cook-Weisberg test for heteroscedasticity.

Functional form	Model 1	Model 2
Linear	55.30 **	62.72 **
Extended linear	57.75 **	67.70 **
Cobb-Douglas	2,721.90 **	3,021.21 **
Translog	2,638.71 **	2,927.56 **

** significant at 1%

Sources of data: Rice Monitoring Survey (RMS) 2016 in India
International Rice Information System (IRIS)

Table 9. Akaike information criterion (AIC) and Bayesian information criteria (BIC).

Functional form	**AIC**		**BIC**	
	Model 1	**Model 2**	**Model 1**	**Model 2**
Linear	154,670	154,283	154,784	154,418
Extended linear	154,424	154,073	154,623	154,293
Cobb-Douglas	38,609	38,358	38,723	38,493
Translog	38,472	38,202	38,670	38,422

Sources of data: Rice Monitoring Survey (RMS) 2016 in India
International Rice Information System (IRIS)

Table 10. Estimation results of the final yield response function, 2015 wet season, Eastern India.

Independent variables		Coef.	Std. Err.	t
ln_Fertilizer (lnFer)	α1	0.869	0.21	4.15**
ln_Labor (lnLab)	α2	-0.673	0.31	-2.19*
ln_Power_cost (lnPow)	α3	0.139	0.08	1.78
ln_Other_inputs (lnOth)	α4	0.206	0.07	2.89**
lnFer x lnFer	α11	-0.034	0.01	-2.52*
lnLab x lnLab	α22	0.236	0.03	7.80**
lnPow x lnPow	α33	-0.002	0.00	-0.48
lnOth x lnOth	α44	0.015	0.00	3.20**
lnFer x lnLab	α12	-0.088	0.04	-2.32*
lnFer x lnPow	α13	0.027	0.01	3.06**
lnFer x lnOth	α14	-0.040	0.01	-4.85**
lnLab x lnPow	α23	-0.055	0.01	-3.87**
lnLab x lnOth	α24	-0.034	0.01	-3.65**
lnPow x lnOth	α34	0.013	0.00	4.21**
ln_Irrigation_percent		0.127	0.01	10.41**
Crop_establishment		0.315	0.08	3.97**
Submergence		-2.469	0.16	-15.52**
Salinity		-1.279	0.51	-2.51*
Drought		-1.247	0.04	-29.66**
Age		-0.013	0.01	-1.35

Age x Age	0.000	0.00	1.11
Education	-0.017	0.01	-1.15
Education * Education	0.002	0.00	1.43
Access_input	-0.244	0.12	-2.04*
Access_credit	0.305	0.15	2.09*
Access_extworker	-0.128	0.12	-1.03
ln_Definite_contribution	0.027	0.01	4.33**
i.State		Included	
Constant	4.764	1.02	4.66**

No. of observations = 8,967

Dependent variable = yield (kg/ha)

** significant at 1%, *significant at 5%

Sources of data: Rice Monitoring Survey (RMS) 2016 in India
International Rice Information System (IRIS)

Table 11. Country of origin of progenitors with definite and possible IRG contribution by variety, 2015 wet season, Eastern India.

Variety name	Country of origin of progenitors		
	Definite contribution	**Possible contribution**	**All**
Swarna	Taiwan (1), Malaysia (1), Indonesia (1)	India (3), Japan (2), Taiwan (1), Indonesia (1), Malaysia (1), IRRI (1)	India (3), Taiwan (2), Indonesia (2), Japan (2), Malaysia (2), IRRI (1)
Mahsuri		Japan (2), Malaysia (1), Taiwan (1)	Japan (2), Malaysia (1), Taiwan (1)
Sarjoo 52		Taiwan (2), Ecuador (1)	Taiwan (2), Ecuador (1)
Pooja	Taiwan (2), Philippines (1), United States (1), Indonesia (1)	United States (3), India (2), Ecuador (1), Indonesia (1), IRRI (1)	United States (4), Taiwan (2), India (2), Indonesia (2), IRRI (1), Philippines (1), Ecuador (1)
Lalat	India (3), Indonesia (3), United States (3), Taiwan (2), IRRI (1), Philippines (1)	India (5), United States (3), IRRI (2), Philippines (1), Taiwan (1), Indonesia (1), Thailand (1)	India (8), United States (6), Indonesia (4), Taiwan (3), IRRI (3), Philippines (5), Thailand (1)
Moti	India (1), Peru (1)	United States (5), Taiwan (2), India (1), Indonesia (1), Philippines (1)	United States (5), Taiwan (2), India (2), Peru (1), Indonesia (1), Philippines (1)
Sambha Mahsuri	Gambia (1)	Taiwan (3), Japan (2), Malaysia (1)	Taiwan (3), Japan (2), Gambia (1), Malaysia (1)
Vijetha (MTU 1001)	India (4), United States (4), Taiwan (3), Indonesia (3), IRRI (1), Philippines (1), Thailand (1)	India (8), IRRI (4), United States (4), Indonesia (2), Japan (2), Malaysia (2), Philippines (1), Taiwan (1), Ecuador (1), Thailand (1)	India (12), United States (8), Taiwan (4), IRRI (5), Indonesia (5), Philippines (2), Japan (2), Malaysia (2), Thailand (2), Ecuador (1)
CR Dhan 501	Bangladesh (1), Indonesia (1), Malaysia (1), India (1)	India (3), Indonesia (2)	India (4), Indonesia (3), Bangladesh (1), Malaysia (1)
Swarna-Sub1	India (6), IRRI (5), Taiwan (3), Indonesia (3), United States (3), Malaysia (2), Philippines (2), Thailand (2), Vietnam (1)	IRRI (11), India (5), United States (3), Taiwan (2), Japan (2), Indonesia (1), Malaysia (1), Philippines (1), Vietnam (1)	IRRI (16), India (11), United States (6), Taiwan (5), Indonesia (4), Malaysia (3), Philippines (3), Japan (2), Thailand (2), Vietnam (2)
Cottondora Sannalu (MTU 1010)	United States (4), IRRI (3), Philippines (3), Taiwan (3), India (3), Indonesia (3), Thailand (2), South Korea (1), Malaysia (1), Vietnam (1)	IRRI (7), United States (5), India (4), Taiwan (2), Japan (2), Malaysia (2), Thailand (2), Philippines (1), Ecuador (1), Indonesia (1), Vietnam (1)	IRRI (10), United States (9), India (7), Taiwan (5), Philippines (4), Indonesia (4), Thailand (4), Malaysia (3), Japan, (2), Vietnam (2), Ecuador (1), South Korea (1)

Pratikshya	IRRI (3), Philipines (3), Taiwan (3), India (3), Indonesia (3), United States (3), Malaysia (2), Thailand (2), South Korea (1), Vietnam (1)	IRRI (7), India (5), United States (3), Taiwan (2), Japan (2), Thailand (2), Philippines (1), Indonesia (1), Malaysia (1), Vietnam (1)	IRRI (10), India (8), United States (6), Taiwan (5), Philippines (4), Indonesia (4), Thailand (4), Malaysia (3), Japan (2), Vietnam (2), South Korea (2)
IR64-Sub1	IRRI (4), India (5), Philippines (3), Taiwan (3), Indonesia (3), United States (3), Thailand (2), South Korea (1), Malaysia (1), Vietnam (1)	IRRI (10), India (3), United States (3), Thailand (2), Philippines (11), Taiwan (1), Indonesia (1), Vietnam (1)	IRRI (14), India (8), United States (6), Philippines (4), Taiwan (4), Indonesia (4), Thailand (4), Vietnam (2), South Korea (1), Malaysia (1)
Sita	Taiwan (2), IRRI (1), Vietnam (1), Indonesia (1)	IRRI (1), India (1), Indonesia (1)	Taiwan (2), IRRI (2), Indonesia (2), Vietnam (1), India (1)
Annapoorna	Taiwan (1), Indonesia (1)	Indonesia (1), IRRI (1), India (1)	Taiwan (1), Indonesia (2), IRRI (1)
Jaya		Taiwan (2), India (1)	Taiwan (2), India (1)
Khandagiri	Taiwan (3), India (3), Indonesia (3), United States (3), IRRI (1), Philippines (1), Thailand (1)	India (5), IRRI (4), United States (3), Philippines (1), Indonesia (1), Thailand (1)	India (8), United State (6), IRRI (5), Taiwan (3), Indonesia (4), Philippines (2), Thailand (2)
Ranjeet	Malaysia (2), Bangladesh (1), Indonesia (1)	Japan (2), Malaysia (1), Taiwan (1), India (1), Indonesia (1)	Malaysia (3), Japan (2), Indonesia (2) Taiwan (1), India (1), Bangladesh (2)
Geetanjali		Pakistan (1)	Pakistan (1)
Naveen	India (1)	Taiwan (2), India (2)	India (3), Taiwan (2)
Udayagari	Taiwan (3), India (3), Indonesia (2), United States (3), IRRI (2), Philippines (1), Thailand (1)	IRRI (5), India (3), United States (3), Indonesia (1), Ivory Coast (1), Philippines (1), Senegal (1), Thailand (1)	IRRI (7), India (6), United States (6), Indonesia (4), Taiwan (3), Philippines (2), Thailand (2), Ivory Coast (1), Senegal (1)
Bhuban	India (2), Taiwan (1), Indonesia (1), Thailand (1)	India (1), Taiwan (1)	India (3), Taiwan (2), Indonesia (1), Thailand (1)
Krishna	Gambia (1)	Taiwan (2)	Taiwan (2), Gambia (1)
Tulasi	India (1)	India (3), Taiwan (2), Indonesia (1)	India (4), Taiwan (2), Indonesia (1)
Jamuna		Taiwan (2), Pakistan (1)	Taiwan (2), Pakistan (1)
Santosh	Indonesia (1), Malaysia (1)	Indonesia (1), India (1), Bangladesh (1)	Indonesia (2), India (1), Bangladesh (1), Malaysia (1)

IR36	India (3), Indonesia (3), United States (3), Taiwan (2), IRRI (1), Philippines (1)	India (3), United States (3), IRRI (2), Philippines (1), Taiwan (1), Indonesia (1)	India (6), United States (6), Indonesia (4), Taiwan (3), IRRI (3), Philippines (2)
Pankaj	Indonesia (1), Malaysia (1)	Indonesia (1), India (1)	Indonesia (2), Malaysia (1), India (1)
Savithri	Bangladesh (1), Indonesia (1), Malaysia (1)	India (2), Indonesia (1)	India (2), Indonesia (2), Malaysia (1)
Annada	India (1)		India (1)
Sahbhagi Dhan	United States (5), Indonesia (3), Taiwan (2), India (1), Malaysia (1), Philipines (1)	IRRI (4), United States (5), India (4), Philippines (2), Indonesia (2), Taiwan (1), China (1)	United States (10), India (5), Indonesia (5), IRRI (4), Philippines (3), Taiwan (3), China (1), Malaysia (1)

Sources of data: Rice Monitoring Survey (RMS) 2016 in India
International Rice Information System (IRIS)

Table 12. Country of origin of progenitors with definite and possible IRG contribution, 2015 wet season, Eastern India.

Country of origin	**Type of contribution**		**All**
	Definite	**Possible**	
India	12	18	30
IRRI-Philippines	8	20	28
United States	6	9	15
Chinese Taipei (Taiwan)	4	4	8
Indonesia	3	4	7
Philippines	5	2	7
Malaysia	3	2	5
Thailand	4	3	7
Japan	0	2	2
Viet Nam	2	1	3
Bangladesh	1	1	2
Ecuador	0	1	1
Korea, Republic Of	1	0	1
Pakistan	0	1	1
Gambia	1	0	1
China	0	1	1
Ivory Coast (Côte D'Ivoire)	0	1	1
Peru	1	0	1
Senegal	0	1	1
Total	51	71	122

Sources of data: Rice Monitoring Survey (RMS) 2016 in India
International Rice Information System (IRIS)

Table 13. Most popular progenitors of popular improved varieties with definite and possible IRG contribution by decade of varietal release, 2015 wet season, Eastern India.

Year of release	Type of progenitor contribution		All
	Definite	Possible	
1968-1970	GEB 24, Peta, Tangkai Rotan	Dee Geo Woo Gen, Taichung Native 1, Cina, Latisail, T 141, Basmati 370	Dee Geo Woo Gen, Taichung Native 1, Cina, Latisail, T 141, Basmati 370, GEB 24, Peta, Tangkai Rotan
1971-1980	Dee Geo Woo Gen, Peta, I Geo Tze, IR 12-178-2-3, Mahsuri, Mong Chim Vang A	Cina, IR 8, Latisail, Kameji, Mayang Ebos 80, Shinkiri, Taichung 65	Dee Geo Woo Gen, Cina, IR 8, Latisail , Peta
1981-1990	Peta, Dee Geo Woo Gen, TKM 6, B 5580 A 1-15, Benong, Bluebonnet, Century Patna 231, CO 13, CR 94-13, Fortuna, IR 579-48-1-2 (Nilo 11), Sigadis, Tadukan, W 1543	Taichung Native 1, Dee Geo Woo Gen, Blue Rose Supreme, Cina, Latisail, Rexoro, Sinampaga, Texas Patna	Taichung Native 1, Dee Geo Woo Gen, Peta, Blue Rose Supreme, Cina, Latisail, Rexoro, Sinampaga, Texas Patna, Century Patna 231, TKM 6
1991-2000	Peta, Dee Geo Woo Gen, Fortuna, B 5580 A 1-15, Benong, Bluebonnet, Century Patna 231, Gam Pai 30-12-15, IR 579-48-1-2 (Nilo 11), Sigadis, Tadukan, Taichung Native 1, TKM 6, W 1543	Cina, Latisail, IR 8, Rexoro, Blue Rose Supreme, CO 18, Gam Pai, IR 24, IR 262-43-8-11, Sinampaga, SLO 17, Texas Patna	Cina, Latisail, Fortuna, Peta, IR 8, Rexoro, Dee Geo Woo Gen
2001-2014	Peta, B 5580 A 1-15, Benong, Bluebonnet, Century Patna 231, Dee Geo Woo Gen, Fortuna, Seraup Besar 15, Sigadis, W 1543	Cina, Latisail, Fortuna, Blue Rose Supreme, CO 18, IR 24, IR 8, Rexoro, Sinampaga, SLO 17, Texas Patna	Fortuna, Cina, Latisail, Peta, Dee Geo Woo Gen
ALL	Peta, Dee Geo Woo Gen, Fortuna, B 5580 A 1-15, Benong, Bluebonnet, Century Patna 231, Sigadis, TKM 6, W 1543	Cina, Latisail, IR 8, Rexoro, Taichung Native 1, Blue Rose Supreme, Sinampaga, Texas Patna, CO 18, IR 24, SLO 17	Dee Geo Woo Gen, Peta, Cina, Latisail, Taichung Native 1, Fortuna, IR 8, Rexoro

Sources of data: Rice Monitoring Survey (RMS) 2016 in India
International Rice Information System (IRIS)

Table 14. Morphological characteristics of popular IRG progenitors of improved rice varieties, 2015 wet season, Eastern India.

Characteristics	IRG Accessions		
	Peta	**Dee Geo Woo Gen (DGWG)**	**Fortuna**
Variety group	Indica	Indica	Javanica
Country of origin	Indonesia	Taiwan	Taiwan
Date of acquisition	-	24-Mar-1962	7-Jul-1978
Maturity (days)	145	111	124
Seedling height	Intermediate (30-59 cm)	Short (<30 cm)	Intermediate (30-59 cm)
Grain length (mm)	9.3	8.1	9.8
Grain Width (mm)	2.9	3.1	3.0
100-grain weight (gm) - cultivated	2.9	2.3	3.1
Leaf length - cultivated	Intermediate (41-60 cm)	Intermediate (41-60 cm)	Intermediate (41-60 cm)
Leaf width - cultivated	Intermediate (1-2 cm)	Intermediate (1-2 cm)	Intermediate (1-2 cm)
Panicle length (cm) at post-harvest	28.6	24	32
Panicle type	Semi-compact	Drooping	Spreading (open)
Endosperm type	-	Non-glutinous	Non-glutinous
Response on diseases			
Bacterial blight	Susceptible	-	Susceptible
Blast	Moderately resistant	Moderately resistant	Susceptible
Sheath blight	Moderately susceptible	-	-
Rice tungro virus (% infected)	34	92	89
Rice ragged stunt virus (% infected)	61	89	71
Response on insects			
Brown planthopper	Susceptible	Susceptible	Susceptible
Green leafhopper	Intermediate	Susceptible	Susceptible
Rice whorl maggot	Susceptible	Susceptible	Susceptible
White-backed planthopper	Susceptible	Susceptible	Susceptible

Zigzag leafhopper	Resistant	-	Susceptible
Rice leaf folder	Susceptible	-	Susceptible
Yellow stemborer	Susceptible	-	Susceptible
Striped stemborer	-	Susceptible	-
Drought tolerance			
Early vegetative stage	-	Intermediate	Resistant
Late vegetative stage	Intermediate	-	Intermediate
Reproductive stage	Susceptible	Susceptible	-
Flood tolerance	Susceptible	-	Susceptible
Salt tolerance	Tolerant	-	Intermediate
Cold tolerance	Susceptible	Susceptible	Susceptible

Sources of data: Rice Monitoring Survey (RMS) 2016 in India
International Rice Information System (IRIS)

Table 15. Coefficient of parentage of 10 most adopted varieties with pedigree information, 2015 wet season, Eastern India.

Variety name	Swarna	Mahsuri	Pooja	Lalat	Sarjoo 52	Vijetha (MTU 1001)	Moti	Sambha Mahsuri	Swarna Sub1	Cottondora Sannalu (MTU 1010)
Swarna	1.0000									
Mahsuri	0.3125	1.0000								
Pooja	0.0547	0.0000	1.0000							
Lalat	0.0513	0.0000	0.0521	1.0000						
Sarjoo 52	0.0313	0.0000	0.0391	0.0330	1.0000					
Vijetha (MTU 1001)	0.0833	0.1250	0.0934	0.0555	0.0869	1.0000				
Moti	0.0039	0.0000	0.0076	0.0050	0.0313	0.0119	1.0000			
Sambha Mahsuri	0.1719	0.5000	0.0156	0.0203	0.1250	0.1068	0.0156	1.0000		
Swarna Sub1	0.9415	0.2930	0.0556	0.0546	0.0320	0.0849	0.0041	0.1630	1.0000	
Cottondora Sannalu (MTU 1010)	0.0915	0.1250	0.1036	0.0558	0.0358	0.1207	0.0069	0.0852	0.0926	1.0000

Sources of data: Rice Monitoring Survey (RMS) 2016 in India
International Rice Information System (IRIS)

7 Figures

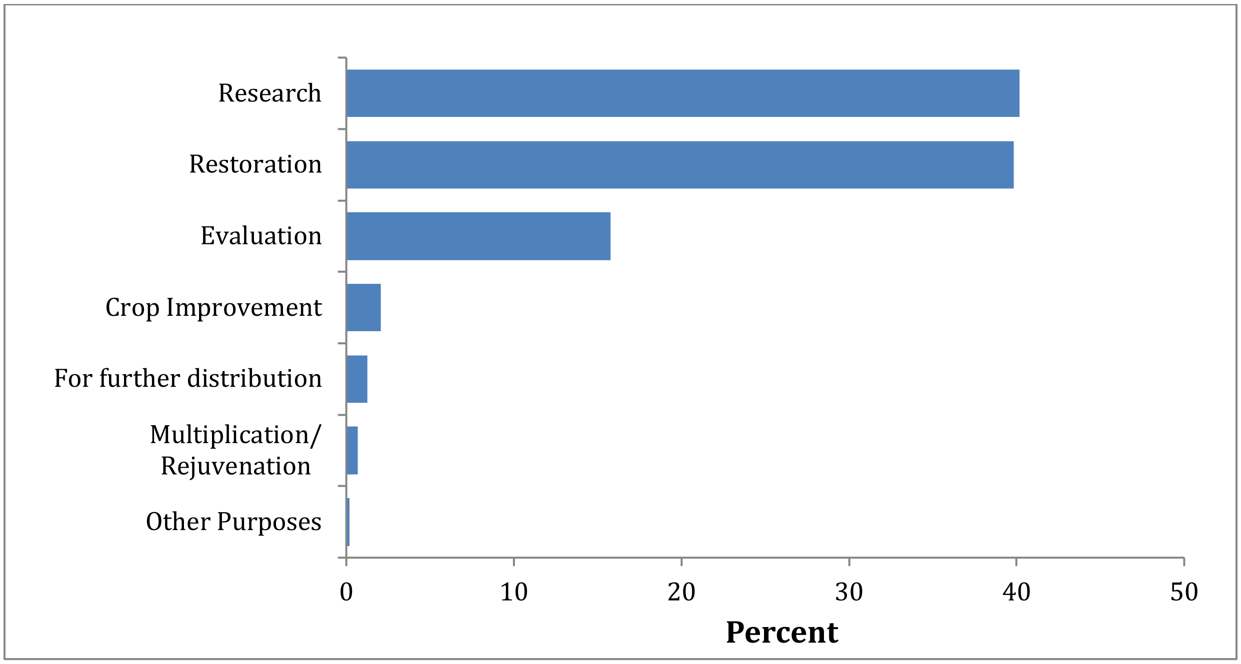

Figure 1. Seed distribution of IRG in India by purpose in percent (1976-2018).

Source: Genetic Resources Information Management System (GRIMS)

Note: Total number of accessions distributed between 1976 to 2018 is 81,703.

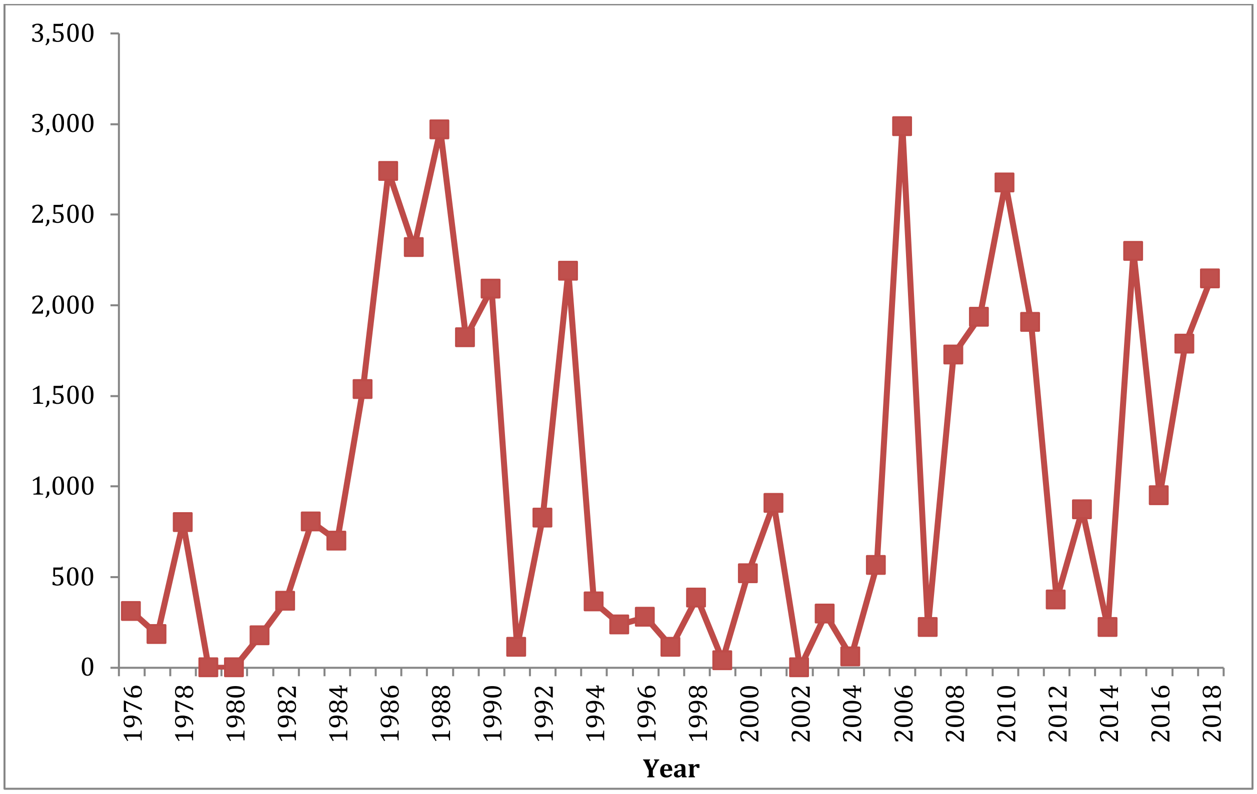

Figure 2. Annual number of accessions distributed by IRG in India (1976-2018)

Source: Genetic Resources Information Management System (GRIMS)

Note: The graph excludes accessions distributed for restoration purposes (n=32,548). Total number of accessions distributed between 1976 to 2018, excluding restoration, is 49,155.

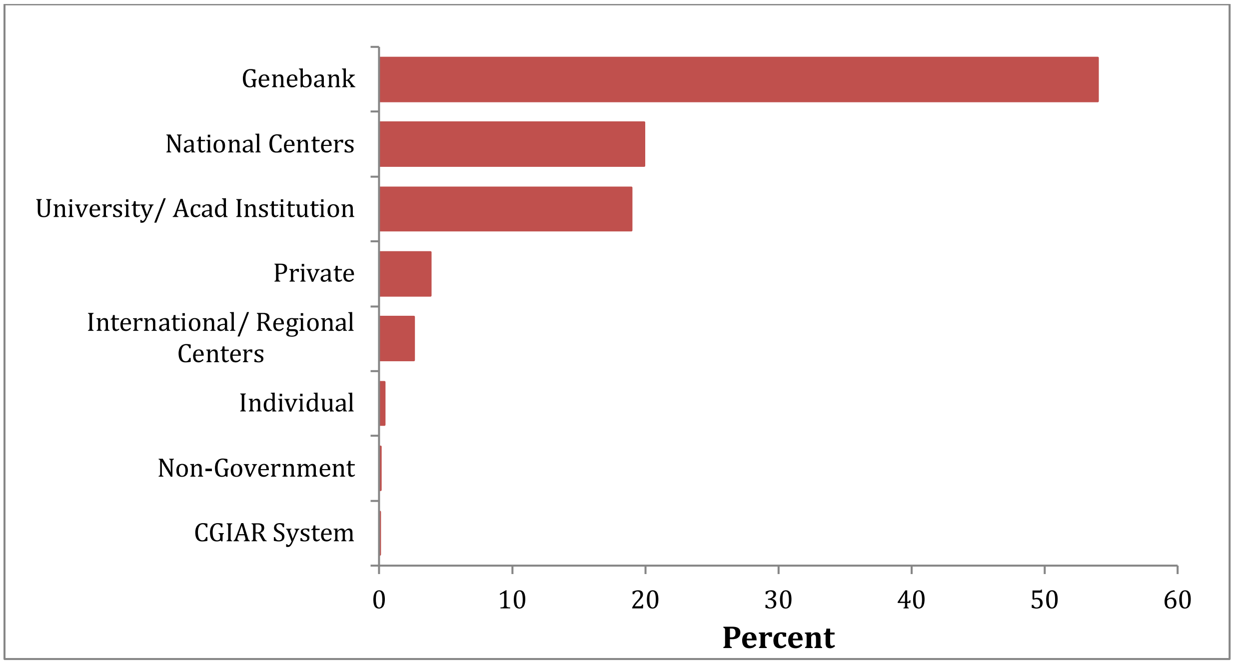

Figure 3. Seed distribution of IRG in India by type of recipient institution in percent (1976-2018).

Source: Genetic Resources Information Management System (GRIMS)

Note: Total number of accessions distributed is 81,703.

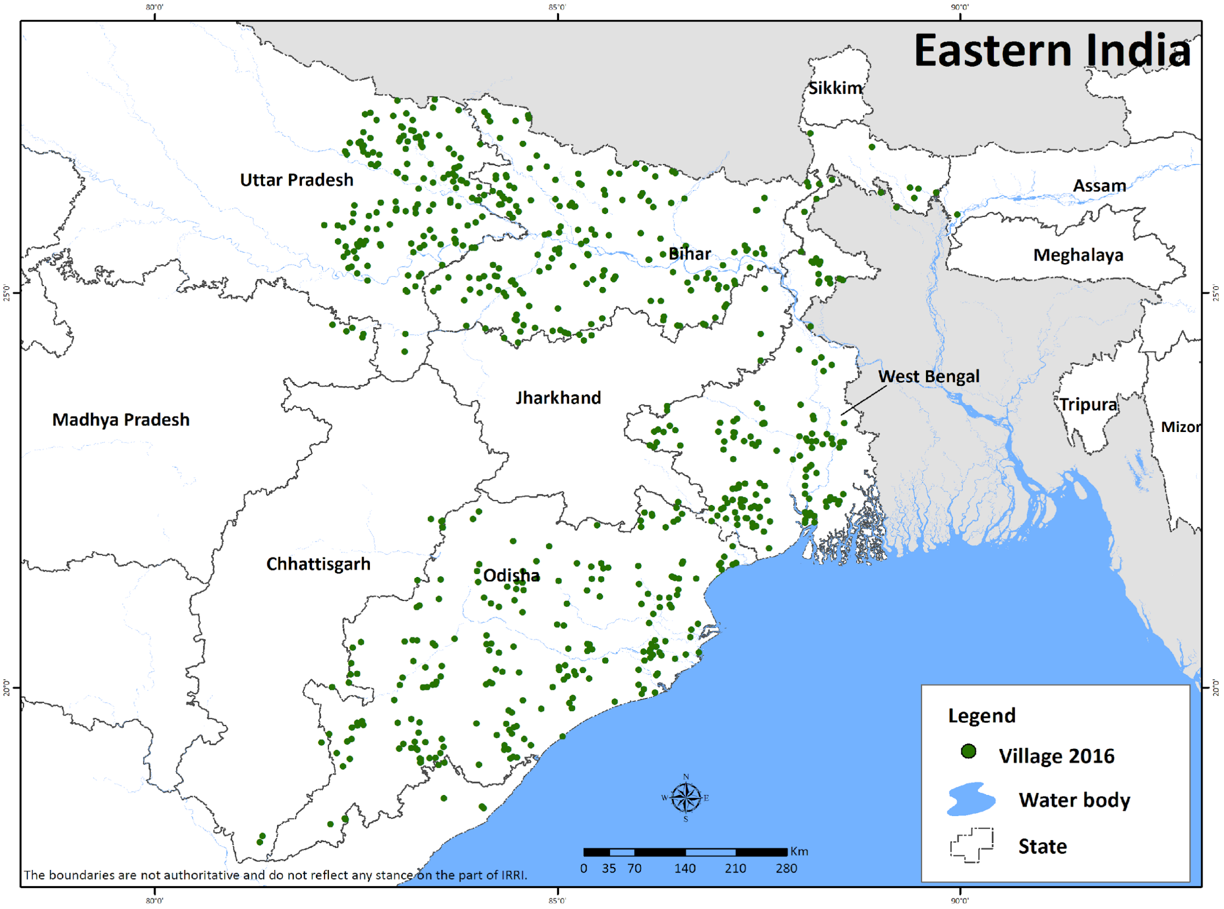

Figure 4. Geographical location of the sample villages of the Rice Monitoring Survey in 2016.

Source of data: Rice Monitoring Survey (RMS) 2016 in India

Figure 5. IR8 (left) and its parents: Peta (center) and Dee-geo-woo-gen (right).

Source: International Rice Research Institute

8 Appendices

Appendix 1. Estimation results of yield response function in linear form, 2015 wet season, Eastern India.

Variables		Model 1			Model 2		
		Coef.	**Std. Err.**	**t**	**Coef.**	**Std. Err.**	**t**
Fertilizer	α1	3.39	0.18	18.45**	4.20	0.18	23.11**
Labor	α2	4.16	0.28	14.7**	2.50	0.30	8.35**
Power_cost	α3	0.03	0.00	6.87**	0.03	0.00	8.48**
Other_inputs	α4	0.11	0.01	10.10**	0.09	0.01	7.39**
Irrigation_percent		3.44	0.39	8.79**	4.27	0.44	9.70**
Crop_establishment		206.92	37.98	5.45**	167.81	39.12	4.29**
Submergence		-1148.97	85.87	-13.38**	-1371.62	87.80	-15.62**
Salinity		-1314.78	211.39	-6.22**	-1052.95	207.56	-5.07**
Drought		-1529.92	32.12	-47.63**	-1413.88	32.28	-43.81**
Age		0.74	1.15	0.64	-0.06	1.11	-0.05
Education		7.02	3.39	2.07*	9.92	3.28	3.02**
Access_input		-659.91	70.18	-9.40**	-449.00	66.94	-6.71**
Access_credit		644.66	97.93	6.58**	544.78	94.18	5.78**
Access_extworker		246.54	92.16	2.68**	93.59	90.27	1.04
Definite_contribution		603.25	48.76	12.37**	316.35	54.08	5.85**
i.state							Included
Constant		1477.31	82.00	18.02**	1792.18	93.96	19.07**

No. of observations = 8,967
Dependent variable = yield (kg/ha)
** significant at 1%, *significant at 5%
Sources of data: Rice Monitoring Survey (RMS) 2016 in India
International Rice Information System (IRIS)

Appendix 2. Estimation results of yield response function in extended linear form, 2015 wet season, Eastern India.

Variables		Model 1			Model 2		
		Coef.	**Std. Err.**	**t**	**Coef.**	**Std. Err.**	**t**
Fertilizer (Fer)	α1	6.41	0.63	10.18**	7.97	0.62	12.86**
Labor (Lab)	α2	7.86	1.01	7.81**	5.70	1.01	5.63**
Power_cost (Pow)	α3	0.11	0.01	9.98**	0.10	0.01	9.35**
Other_inputs (Oth)	α4	0.26	0.04	6.82**	0.23	0.04	5.93**
Fer x Fer	α11	-0.01	0.00	-4.10**	-0.01	0.00	-5.38**
Lab x Lab	α22	-0.02	0.00	-3.75**	-0.01	0.00	-1.92
Pow x Pow	α33	0.00	0.00	-8.75**	0.00	0.00	-8.03**
Oth x Oth	α44	0.00	0.00	-5.12**	0.00	0.00	-5.14**
Fer x Lab	α12	0.00	0.00	0.61	0.00	0.00	-0.84
Fer x Pow	α13	0.00	0.00	-4.05**	0.00	0.00	-1.92
Fer x Oth	α14	0.00	0.00	-0.87	0.00	0.00	-0.7
Lab x Pow	α23	0.00	0.00	0.04	0.00	0.00	-1.16
Lab x Oth	α24	0.00	0.00	-2.23*	0.00	0.00	-1.97*
Pow x Lab	α34	0.00	0.00	3.04**	0.00	0.00	2.92**
Irrigation_percent		2.81	0.40	7.05**	3.62	0.44	8.2**
Crop_establishment		174.24	38.40	4.54**	136.93	39.72	3.45**
Submergence		-1180.37	84.95	-13.89**	-1370.53	86.78	-15.79**
Salinity		-1295.15	203.12	-6.38**	-1035.81	197.50	-5.24**

Drought	-1442.21	32.82	-43.94**	-1345.72	33.13	-40.62**
Age	-1.32	7.01	-0.19	0.21	6.79	0.03
Age x Age	0.01	0.07	0.18	-0.01	0.07	-0.15
Education	0.13	9.54	0.01	2.25	9.33	0.24
Education x Education	0.34	0.75	0.46	0.37	0.73	0.50
Access_input	-643.22	69.93	-9.20**	-439.77	66.55	-6.61**
Access_credit	581.46	99.22	5.86**	490.78	95.32	5.15**
Access_extworker	233.49	92.43	2.53*	86.37	90.31	0.96
Definite_contribution	551.07	48.86	11.28**	284.56	53.49	5.32**
i.State					Included	
Constant	1007.34	185.15	5.44**	1278.05	183.44	6.97**

No. of observations = 8,967
Dependent variable = yield (kg/ha)
** significant at 1%, *significant at 5%
Sources of data: Rice Monitoring Survey (RMS) 2016 in India
International Rice Information System (IRIS)

Appendix 3. Estimation results of yield response function in Cobb-Douglas form, 2015 wet season, Eastern India.

Independent variables	Model 1			Model 2		
	Coef.	**Std. Err.**	**t**	**Coef.**	**Std. Err.**	**t**
ln_Fertilizer	0.303	0.03	9.96**	0.340	0.03	11.06**
ln_Labor	0.390	0.03	12.76**	0.320	0.03	9.76**
ln_Power_cost)	0.021	0.01	2.25*	0.018	0.01	1.91
ln_Other_inputs	0.051	0.01	7.21**	0.077	0.01	9.94**
ln_Irrigation_percent	0.113	0.01	9.96**	0.134	0.01	10.92**
Crop_establishment	0.234	0.08	3.01**	0.366	0.08	4.65**
Submergence	-2.789	0.16	-17.00**	-2.607	0.16	-16.13**
Salinity	-1.728	0.53	-3.24**	-1.367	0.51	-2.70**
Drought	-1.421	0.04	-34.54**	-1.280	0.04	-30.88**
Age	-0.002	0.00	-1.08	-0.003	0.00	-1.78
Education	-0.002	0.01	-0.43	0.003	0.00	0.56
Access_input	-0.476	0.13	-3.77**	-0.273	0.12	-2.26*
Access_credit	0.437	0.15	2.87**	0.248	0.15	1.67
Access_extworker	-0.063	0.13	-0.50	-0.103	0.13	-0.82
ln(Definite_contribution)	0.027	0.00	5.53**	0.029	0.01	4.75**
i.State					Included	
Constant	4.109	0.22	18.96**	4.578	0.22	20.71**

No. of observations = 8,967

Dependent variable = yield (kg/ha)

** significant at 1%, *significant at 5%

Sources of data: Rice Monitoring Survey (RMS) 2016 in India
International Rice Information System (IRIS)

Appendix 4. Estimation results of yield response function in translog form, 2015 wet season, Eastern India.

Independent variables		**Model 1**			**Model 2**		
		Coef.	**Std. Err.**	**t**	**Coef.**	**Std. Err.**	**t**
ln_Fertilizer (lnFer)	α1	0.743	0.21	3.47**	0.869	0.21	4.15**
ln_Labor (lnLab)	α2	-1.127	0.32	-3.56**	-0.673	0.31	-2.19*
ln_Power_cost (lnPow)	α3	0.141	0.08	1.82	0.139	0.08	1.78
ln_Other_inputs (lnOth)	α4	0.210	0.07	2.96**	0.206	0.07	2.89**
lnFer x lnFer	α11	-0.057	0.01	-4.20**	-0.034	0.01	-2.52*
lnLab x lnLab	α22	0.253	0.03	8.32**	0.236	0.03	7.80**
lnPow x lnPow	α33	-0.004	0.00	-1.07	-0.002	0.00	-0.48
lnOth x lnOth	α44	0.012	0.00	2.62*	0.015	0.00	3.20**
lnFer x lnLab	α12	-0.021	0.04	-0.52	-0.088	0.04	-2.32*
lnFer x lnPow	α13	0.020	0.01	2.25*	0.027	0.01	3.06**
lnFer x lnOth	α14	-0.031	0.01	-3.73**	-0.040	0.01	-4.85**
lnLab x lnPow	α23	-0.042	0.01	-2.98**	-0.055	0.01	-3.87**
lnLab x lnOth	α24	-0.042	0.01	-4.42**	-0.034	0.01	-3.65**
lnPow x lnOth	α34	0.011	0.00	3.45**	0.013	0.00	4.21**
ln_Irrigation_percent		0.107	0.01	9.37**	0.127	0.01	10.41**
Crop_establishment		0.162	0.08	2.06*	0.315	0.08	3.97**
Submergence		-2.697	0.16	-16.69**	-2.469	0.16	-15.52**

Salinity	-1.654	0.54	-3.06**	-1.279	0.51	-2.51*
Drought	-1.379	0.04	-33.2**	-1.247	0.04	-29.66**
Age	-0.014	0.01	-1.39	-0.013	0.01	-1.35
Age x Age	0.000	0.00	1.28	0.000	0.00	1.11
Education	-0.022	0.02	-1.49	-0.017	0.01	-1.15
Education * Education	0.002	0.00	1.46	0.002	0.00	1.43
Access_input	-0.435	0.13	-3.46**	-0.244	0.12	-2.04*
Access_credit	0.506	0.15	3.38**	0.305	0.15	2.09*
Access_extworker	-0.102	0.13	-0.81	-0.128	0.12	-1.03
ln_Definite_contribution	0.024	0.00	4.92**	0.027	0.01	4.33**
i.State					Included	
Constant	5.880	1.05	5.59**	4.764	1.02	4.66**

No. of observations = 8,967
Dependent variable = yield (kg/ha)
** significant at 1%, *significant at 5%

Sources of data: Rice Monitoring Survey (RMS) 2016 in India
International Rice Information System (IRIS)