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The impact of the international rice genebank (IRG) on rice farming in Bangladesh

Donald Villanueva^{1*} , Yuji Enriquez¹ and Grace Lee Capilit²

Abstract

Background: The International Rice Genebank (IRG) currently safeguards the largest and most diverse collection of rice genetic resources in the world. Over the past decades, genetic resources from the IRG have been used effectively to increase smallholder farmers' rice productivity in developing economies. Bangladesh is one of the direct and indirect recipients of IRG germplasm for rice genetic improvement. This study aimed to map the impact pathways of IRG germplasm transfers to Bangladesh, evaluate the genetic contribution of IRG germplasms to rice productivity of farmers, and compute the equivalent economic benefit.

Methods: Impact pathway analysis was conducted to map the IRG's germplasm transfer for varietal improvement and seed dissemination of improved rice varieties in Bangladesh using the information collected from key informant interviews. Using data from the farm household survey conducted by the International Rice Research Institute (IRRI) in 2016 in five divisions in Bangladesh, a pedigree analysis was conducted that related the productivity changes in farmers' fields explicitly to genebank accessions through varietal improvement. Afterward, we evaluated the economic benefit of IRG contribution in rice varietal improvement in Bangladesh using the computed marginal increases in productivity, average paddy price, and estimated total rice area.

Results: IRG's impact pathway on germplasm transfer in Bangladesh showed that impacts for farmers were achieved through joint efforts with IRRI and the National Agricultural Research and Extension System's research-for-development programs. On average, 52% of the improved rice varieties' genetic composition, cultivated by farmers in Bangladesh, definitely came from IRG accessions. This contribution factor could increase up to 67% if possible contributions were taken into account. The results of the Cobb–Douglas model implied that for every 1% increase in the definite IRG contribution to an improved rice variety, there was an increase in rice yield of about 0.99%, holding other factors constant. This yield increase can be translated into an additional US\$ 8,576,973 aggregated net benefit of farmers during the wet season in Bangladesh. The enhanced yield can be associated with the added important agronomic traits contributed by the accession provided by the IRG in the genetic background of the rice varieties developed for farmers in Bangladesh.

Conclusions: The findings of the study demonstrate that IRG accession forms a significant part of the ancestry of improved rice varieties which is associated with improved yield. The study highlights the valuable contribution of IRG's conservation and distribution of genetic accessions to the research and development of improved rice varieties and rice production on farms in Bangladesh.

Keywords: Rice, Genetic resources, Progenitor contribution, Productivity, Economic benefit, Impact pathway

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Introduction

Rice is not only an important crop and food staple for more than half of the world's diet, of which the majority are Asian countries (FAO Statistical Yearbook 2014),



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but it is also crucial to the food, nutrition, and economic growth of rural communities. In Bangladesh, rice is the staple food for approximately 135 million people across the country, and the rice sector contributes to half of the country's agricultural gross domestic product and one-sixth of Bangladesh's national income (Wright and Countries 2020).

Since the 1960s, Bangladesh has experienced significant rice productivity gains, achieved through yield improvements. The country's ten-year average rice production (1961–1970 and 2010–2019) increased by 229% from 15.8 to 52 million metric tons, respectively. This was attained without significant increases in corresponding averages for area harvested, which only increased by 22% or 9.37 to 11.42 million ha, respectively. To date, Bangladesh is the world's fourth-largest rice producer (GRiSP Global Rice Science Partnership 2013).

Bangladesh's story was one of the successes of international agriculture research that spurred the Green Revolution in the 1960s, which helped avert food security challenges driven by population growth and stagnant productivity. However, the Green Revolution also increased the cultivation of rice varieties with similar genetic backgrounds, raising concerns for an impending crop diversity loss. Increasing the genetic uniformity of cultivated modern rice varieties poses threats to the existence of traditional varieties and wild species that, in turn, reduces the available global genetic resources. These traditional varieties and wild species are important sources of genetic variation needed in crop improvement to cope with the many biotic and abiotic stresses that challenge rice production around the world (International Rice Research Institute IRRI, n.d; Bailey-Serres et al. 2010; Gilliam et al. 2017).

The International Rice Genebank (IRG) was set up in 1971 by the International Rice Research Institute (IRRI) after initiating the first wide-scale collection of rice genetic resources in 1962. IRG currently safeguards the largest and most diverse collection of rice genetic resources globally. Many of these genetic resources have benefitted international rice research programs and the National Agricultural Research and Extension System (NARES) that aim to advance work on crop improvement. Over the past decades, genetic resources from the IRG have been used effectively to increase smallholder farmers' rice productivity in developing economies (Evenson and Gollin 1997; Gollin and Evenson 1998; Hossain et al. 2003; Villanueva et al. 2020).

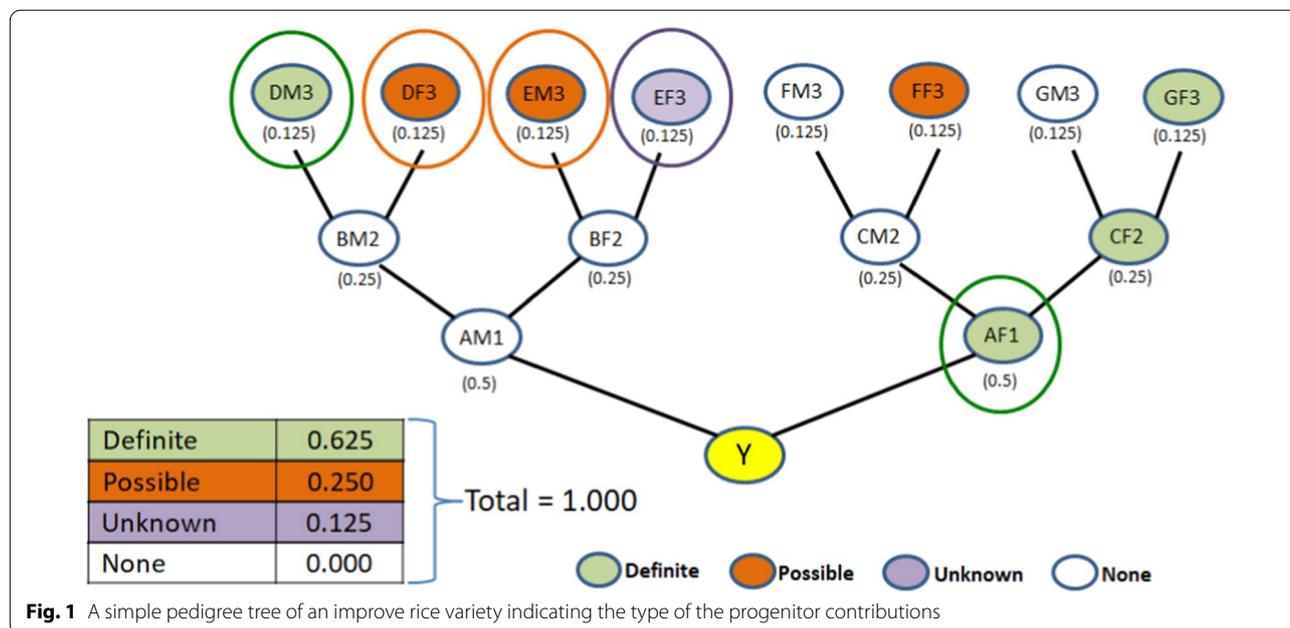
Bangladesh is one of the direct and indirect recipients of IRG germplasm for rice genetic improvement. It currently ranks fifteenth among the top recipients of germplasm from IRG. Since 1987, the country has received an average of 134 accessions per year (see Additional file 1:

Fig. S1). Almost 75% of these accessions were used in research, evaluation, and crop improvement (see Additional file 1: Fig. S2), and three-fourths (74%) of the recipients of seeds were national centers that conduct rice breeding programs, and some of them are managing Bangladesh's local genebanks (see Additional file 1: Fig. S3). Accession is a set of samples managed and conserved by a genebank as a single genetic entity, derived from, and intended to be genetically the same as a single sample acquired by the genebank from elsewhere with documented provenance and representing a cultivar, breeding line, or a population. Samples of the same cultivar acquired by the genebank on different occasions are different accessions (Guzman and Hamilton, 2019).

IRG accessions are foundational in IRRI's rice genetic improvement programs. The IRG allows the breeding programs to tap into the diverse genetic resource pool from around the world and use them in their breeding programs to produce 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). The accessions provided by the IRG in the genetic background of the improved rice varieties added important agronomic traits that enhance farm yields (Bailey-Serres et al. 2010; Ismail and Atlin 2019; Cobb et al. 2019a, b). However, we only note a few studies that have explicitly related, in quantitative terms, the on-farm productivity changes to genebank accessions through varietal improvements, such as the landmark studies by Evenson and Gollin (1997) and Gollin and Evenson (1998), and the most recent study by Villanueva et al. (2020).

In addition, there has been no attempt made yet to map the impact pathways of IRG's contribution to farmer incomes and wellbeing through its genetic contribution. This study looked at the various processes in IRG impact pathways, from upstream to downstream, and the key causal pathways that ultimately make a difference to farmers' income and wellbeing as well as environmental sustainability. This analysis not only strengthens IRG's impact contribution claims to developing countries but scrutinizes the causal chain for process and performance improvement.

This study applied a similar methodology to that found in Villanueva et al. (2020) but with additional components. First, we mapped out impact pathways of IRG germplasm transfers to Bangladesh, including the seed dissemination of improved rice varieties. Second, we evaluated the genetic contributions of IRG germplasms to rice productivity of farmers in Bangladesh by analyzing the IRG germplasm's progenitor contribution to the improved rice varieties. Lastly, using the analysis of



progenitor contribution, we computed the economic benefit of IRG contribution in rice varietal improvement in Bangladesh.

Methods and data

Methods

To address the first objective, we drew from the impact pathway evaluation approach. First used in international agricultural research by (Doutwaite et al. 2003), impact pathway evaluation is a theory-driven approach that enables explicit mapping of how research activities and outputs induce behavioral outcomes that contribute to an impact. Emphasis is given on how interactions of networks and actors co-produce and transform knowledge over time to achieve development outcomes and impacts (Matt et al., 2017). We adopted this framework first to describe the complex landscape of interventions and actors that govern the rice breeding and seed systems in Bangladesh. Second, to map the pathways through which IRG germplasms, together with IRRI research-for-development programs, interact across various stages of innovation, piloting, and scaling to impact farmers.

To evaluate the quantitative impact contribution of IRG accessions to yield benefits of improved rice varieties, we first identified the improved rice varieties cultivated by the farmers in Bangladesh during the 2015 wet season in the RMS dataset. Then, pedigree analysis was employed to measure the progenitor contribution of IRG accessions to each improved rice variety. Progenitor contribution is the probability that an unselected allele comes from that progenitor with values ranging from 0 to 1. This analysis

used the Mendelgram, a program of the International Rice Information System (IRIS), to calculate the progenitor contribution. The program assumes that each parent contributed an equal amount to their progeny based on Mendelian genetics.

Figure 1 shows a simple illustration of the pedigree tree of a rice variety Y that follows Mendelian genetics with three hierarchical levels of ancestors or progenitors.¹ In this pedigree tree, the first level contains the direct parents of Y, which are AM1 and AF1 that have a progenitor contribution (values in parenthesis) of 0.5 each. The second level includes the grandparents of Y, which are BM2 and BF2 (parents of AM1), and CM2 and CF2 (parents of AF1). The progenitor contribution of each grandparent is half of the parent’s progenitor contribution; therefore, all grandparents in this pedigree tree receive 0.25 progenitor contributions. The third level contains the great grandparents of variety Y, and each of them has 0.125 progenitor contributions, half of the progenitor contribution of the grandparents.

Following the definition and methodology of Villanueva et al. (2020), we classified the ancestors found in each varietal pedigree tree into four categories of progenitor contribution: (1) definite contribution, (2) possible contribution, (3) no contribution, and (4) unknown contribution. Definite contribution refers to a progenitor whose name is tagged with an International Rice Germplasm

¹ For simplicity, the figure is presented with three hierarchies, however, pedigree trees of varieties analyzed can contain more than three hierarchies.

Collection (IRGC) number in the IRIS records. Having an IRGC number in the variety name means that accessions were obtained directly from the IRG. There are progenitors in the pedigree tree that did not have an IRGC number but have a matching name in the IRG collection. For this kind of progenitors, we classified them as possible contributions. This means that there is a possibility that the ancestors came from the IRG, but there was no documented proof of accessing them. If a progenitor had no IRGC number in its variety name and had no match by name in the whole IRG collection, these were classified as no contribution. Lastly, unknown contribution refers to the progenitor with unknown or confidential information (e.g., hybrid varieties). In Fig. 1, we color-coded these various categories of progenitor contribution as green, orange, purple, and white, respectively.

After categorizing the progenitor contributions, we computed for total progenitor contribution of IRG accessions for each variety following a rule-based summing protocol. This method ensures proper computation of the progenitor contribution and eliminates double-counting as adopted from Villanueva et al. (2020). The first rule is that the summing procedure gives the highest priority to progenitors with definite contribution, followed by possible contribution, then unknown and lastly no contribution. This means that if both an immediate parent with definite contributions and a grandparent with possible contributions are present in one pedigree line, only the immediate parent will be considered in the computation to avoid double-counting. The second rule is that progenitors with the same classification can only be added if they come from independent pedigree lines. Lastly, if there is a recurrence of the progenitors with the same classification in the same pedigree line, only the progenitor located in the lowest ancestry level or the most immediate parent is included in the computation to avoid double-counting.

To illustrate the procedure using Fig. 1, first, the progenitors with definite contribution (green) were identified and examined for their location and independence in the pedigree tree. Since DM3 is independent of any other progenitor with definite contributions in one pedigree line, it is then included in the computation. For the case of AF1, CF2, and GF3, since they belong to the same pedigree line, only AF1 was included in the calculation since it is the most immediate parent. Thus, the computed definite progenitor contribution for variety Y is the sum of the contributions of DM3 (0.125) and AF1 (0.5), which is equal to 0.625.

The next step was examining the progenitors with possible contributions (orange). Only the progenitor contributions of DF3 (0.125) and EM3 (0.125) were considered in the computation since they satisfy the priority and

independence rules and do not have similar progenitors with the same classification in the same pedigree line. FF3 was not considered because it is under the pedigree line of AF1, which is already considered in the computation of the definite contributions. Hence, the total possible progenitor contribution for variety Y is 0.250.

Since EF3 was the only progenitor with unknown contributions (purple) and is independent with other progenitors with possible and definite classifications, its total progenitor contribution is 0.125. However, the progenitors with no IRG progenitor contributions (white) were in the same pedigree line of the progenitors included in the computation of definite, possible, and unknown contributions. Thus, the contribution of unknown progenitors is zero. Following this rule-based summing procedure, the total progenitor contribution for variety Y is the sum of the definite (0.625), possible (0.250), unknown (0.125), and no (0.000) progenitor contributions, which is equal to 1.

The analysis of the pedigree tree of a variety will be more complex and the computation will become more complicated if it has many progenitors and breeding crosses and has multiple appearances of the same progenitor in the different levels, which is the case of this study. For further illustration, (see Additional file 1: Figures S4 and S5) show the screenshot of the pedigree tree and the Mendelgram generated by IRIS for BR11, respectively. A detailed discussion on this computer-generated output can be found in Additional file 1. BR11 was one of the inbred varieties included in the analysis of this study. The pedigree tree and the Mendelgram of other varieties included in the analysis were not shown in this document because they will occupy many pages for a journal article.

The overall average progenitor contribution of IRG to an improved rice variety by category was computed in two ways. The first method was by using the simple average, and the second method was by using the percent area of the improved rice varieties adopted by farmers surveyed as weight.

To test the effect of the genetic contribution of genbank accessions to productivity, a plot-level yield response function was estimated. The estimation was done while controlling for the influence of conventional inputs (fertilizer, labor, machinery, plant protection, irrigation), age of variety, management (age and education), geographical location (the distance to the nearest input dealer and the division where the residence of the household was located), and environmental factor (submergence). To standardize the values of continuous variables pertaining to production output and input, they were transformed into units per hectare (ha). In the initial exploratory analysis, the sum of the definite and possible contributions of IRG on the variety was included in

the model. However, in the final model, only the index for definite contribution was used to measure the clear impact of IRG on productivity.

To examine the effect of the genetic contribution of accessions from IRG on mean yields, four functional forms were tested: (1) linear, (1) extended linear, (3) Cobb–Douglas, and (4) translog. Below are the specifications of these models.

Linear:

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

Extended linear:

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

Cobb–Douglas:

$$\ln y_i = \beta_0 + \sum_{i=1}^n \beta_i \ln x_i + \sum_{i=1}^n \sum_j \beta_{ij} \ln x_i \ln x_j + \sum_{j=1}^n \alpha_j z_j + \mu_i$$

Translog:

$$\ln y_i = \beta_0 + \sum_{i=1}^n \beta_i \ln x_i + \frac{1}{2} \sum_{i=1}^n \sum_j \beta_{ij} \ln x_i \ln x_j + \sum_{j=1}^n \alpha_j z_j + \mu_i$$

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

The validity of the necessary model assumptions was determined by performing model diagnostics. In this study, variance inflation factors (VIF) and Breusch-Pagan/Cook-Weisberg were used in testing the multicollinearity among independent samples and the presence of heteroscedasticity in the model, respectively. 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 model with the lowest AIC and BIC values was the most preferred model specification. Model estimations and necessary diagnostic tests were performed using Stata 16.1.

To account for the yield contribution of IRG accessions, we measured and incorporated genetic (progenitor) contributions in our model. A statistically significant coefficient means that IRG accessions affected rice yield, while a statistically insignificant coefficient means it did not make any detectable effect on yields. A positive coefficient sign relates IRG accessions to increases in yields and negative to decreases in yield.

To evaluate the economic benefit of IRG contribution in rice varietal improvement in Bangladesh, this study focused on estimating the marginal effect of the IRG genetic contribution for the whole of Bangladesh. From the results of the yield response function model, the marginal effect of IRG progenitor contribution was computed in terms of kg/ha. Then, the marginal effect on the net income of Bangladesh Taka (Tk)/ha was calculated after considering the changes in the farm gate price of paddy and in the total input cost brought by the yield changes. Afterward, this estimated change in net income was multiplied by the estimated total rice area cultivated by modern rice varieties during the wet season of 2015 in the five divisions of Bangladesh included in the survey. The result was the estimated marginal effect on the economic (monetary) benefit (Tk) of the genetic contribution of the IRG in 2015. Additional computations were performed to convert this monetary benefit into a real value of 2020 US\$. All the above computations were summarized in the formula below.

$$Q = (((((A * ((\exp(B) - 1) * 100)/100)) * (E - (E * F/100))) - ((A * (((\exp(B) - 1) * 100)/100)) * I)) * L * 1000)/N) * (P/100)$$

where: Q—estimated marginal change in net income in Bangladesh due to a 1% change in IRG contribution in 2015 (2020 Tk). A—average yield of modern varieties (kg/ha). B—coefficient of $\ln_Definite_contribution$ in the Cobb–Douglas model. E—average paddy price of modern varieties during Aman 2015 (Tk/kg). F—estimated increase in paddy price due to the increase in production (%) computed from the IRRI Global Rice Model (IGRM)². I—estimated total input cost/kg of paddy during 2015 wet season (Tk/kg). L—estimated area cultivated by modern varieties during 2015 wet season (000 ha). N—exchange rate of 1 US\$ to Tk (2015) (Tk). P—consumer price index in 2020 (base=2015) (Tk).

Data

Key informant interviews were conducted to characterize the impact pathway on IRG’s germplasm transfer to Bangladesh and the dissemination of improved rice varieties to farmers. The interview respondents were purposely selected based on their knowledge and involvement with IRG germplasm. Particularly, the target respondents were involved either in the germplasm transfer from IRRI to Bangladesh, the development of improved rice varieties

² IGRM is a dynamic partial equilibrium framework developed by IRRI where each country model includes equations representing supply, demand, trade, and price relationships. The model covers the global rice market in 31 countries and regions that represent about 90% of the worlds’ rice consumption and production (Hoang and Meyers, 2015).

using IRG germplasm, the process of the varietal release, or the dissemination of improved rice varieties in Bangladesh. A total of 11 respondents were successfully interviewed. Eight of the respondents were IRRI staff, where three of them were working directly in the IRG. Two respondents were from the NARES partners and one was from a private seed company in Bangladesh. Due to the COVID-19 pandemic, the interviews were conducted via Google Hangouts using a semi-structured survey questionnaire. The guide questions mainly focused on the roles and responsibilities of respondents in germplasm transfer, varietal improvement, or seed dissemination of improved rice varieties. Other questions were about the institutional arrangements or protocol on germplasm transfer from IRG to Bangladesh. There were also questions on the various pathways from accessing an IRG germplasm to breeding new rice varieties and from new rice varieties to release, dissemination, and farmer adoption in Bangladesh.

To assess the genetic contribution of IRG accessions on rice productivity and to evaluate its economic benefit, this study used cross-sectional farm-level data from the Rice Monitoring Survey (RMS) of Bangladesh, which was funded by the Bill and Melinda Gates Foundation. The survey was conducted in five divisions of Bangladesh, namely Barisal, Chittagong, Dhaka, Khulna, and Rajshahi, in 2016. This survey aimed to monitor rice system that captures varietal turnovers over time and to examine the diffusion of stress-tolerant rice varieties in Bangladesh. A total of 150 villages were randomly selected from the rural villages defined in the 2013 village census, and in each village, 10 households were randomly selected. The total number of households interviewed was 1500, with the sample size in each division proportional to the rural population across divisions. To be able to correct the potential biases due to the sampling design and to make our data representative of the target population, we used weights that are equal (or proportional) to the inverse of the probability of being sampled. Although the data was not yet published in any data repository, the scientist-in-charge allowed us to use the data for the purpose of this study. Figure 2 shows the geographical location of the villages included in the survey, while Table 1 shows the distribution of sample villages and households by division as well as the average rice area per household. The farm-level data of RMS were used to determine the name of improved or released rice varieties grown by the farmers during the wet season of 2015. In the econometric analysis, plot-level data were used since some farmers had more than one rice plot. Only those plots that were planted by improved rice varieties with pedigree information were included in the analysis. The final sample size used for the model was 763 rice plots, which corresponded to 743 farmers.

The data used in the pedigree analysis of the improved rice varieties were retrieved from IRIS. IRIS is the rice information management system of the International Crop Information System, which is a database system that provides integrated management of global information on genetic resources and crop cultivars. This system is used to manage germplasm information of materials developed, received, and maintained by IRRI.

Results and discussions

Impact pathway

The main feature of the IRG's impact pathway on germplasm transfer in Bangladesh is that farmer impacts are achieved through joint efforts with IRRI and NARES's research-for-development programs. The IRG is an important source of rice germplasm for crop improvement, and Bangladesh is one of the recipients of plant genetic materials from IRG. IRG lines, such as the IR8 and the IR64, which drove the Green Revolution, are germplasms that are conserved within the bank and have been made available to many developing countries and breeding programs since the late 1960s and mid-1980s, respectively.

While we found that majority of the accessions requested from IRG were for the development of advanced breeding lines facilitated by IRRI, these are also open to other institutions and individuals. National genebanks and research institutions are also significant groups that request or access germplasms. Also, farmers, non-governmental organizations (NGOs), and private sectors can request germplasms as well.

Figure 3 illustrates the impact pathway of IRRI and IRG in the breeding and seed systems in Bangladesh. IRRI's research activities involve capacity development, both on upgrading partner NARES technical capacity and facility upgrading, knowledge sharing, joint research, social science, consumer and market, and monitoring and evaluation research with a development focus (IRRI experts, interview by the authors, 05 November 2020). This interdisciplinary approach recognizes the multifaceted nature of bringing about impacts on farmers and achieving food security. In IRRI's breeding work, IRG plays a foundational role in providing access to diverse collections of rice genetic resources. IRG also performs a supporting role in facilitating the international exchange of germplasms through its Seed Health Unit.

Another mechanism supporting national breeding and release systems is the International Network for Genetic Evaluation of Rice (INGER). INGER is a network between IRRI and its NARES partner organizations. It is a platform where national research partners can evaluate advanced pre-variety breeding lines of their interest, test in different environments and countries, and access traits

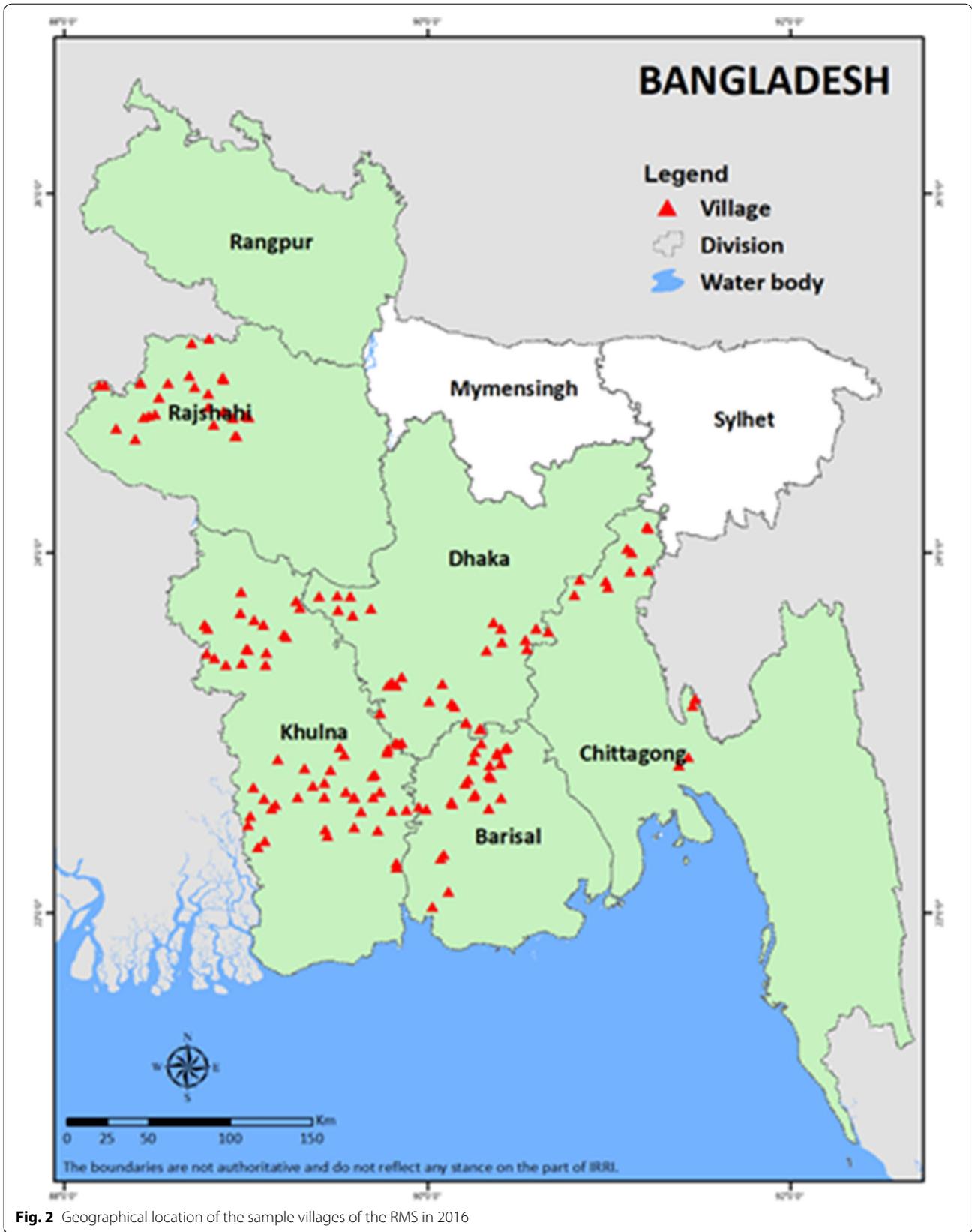


Fig. 2 Geographical location of the sample villages of the RMS in 2016

Table 1 Distribution of sample households in Bangladesh from RMS 2016

State	Number of villages	Number of households	Average land area (ha)	Average rice area (ha)
Barisal	28	280	0.58	0.52
Chittagong	14	140	0.91	0.58
Dhaka	28	280	0.67	0.48
Khulna	54	540	0.65	0.57
Rajshahi	26	260	1.13	0.91
Total	150	1,500	0.75	0.60

information for their breeding research. Doing these activities without INGER would incur NARES partners' significant expenses.

In the past 5 to 10 years, significant improvements have been achieved by IRRI on improving the breeding's pathways to impact. There are three areas in which the breeding and seed dissemination systems in Bangladesh continuously evolve: (1) product fast-tracked breeding coupled with improved capacities of NARES partners, (2) linking market and farmer preferences to breeding, seed system dissemination, and (3) national and private partnerships.

Fast-tracked or rapid cycle breeding provides a way for increasing the rate of genetic gains without significantly increasing the program costs (Cobb et al. 2019a, b). Genetic gains are important for increasing crop productivity. Under this strategy, genetic gains are achieved through continuous optimization and improvement of breeding processes, such as molecular marker-assisted breeding (MAB) and rapid generation advance (RGA). These technologies increase the selection differential and accuracy and shorten the breeding cycles. RGA can be done by reducing the fixed-line development so that field and multi-location trials can be performed earlier to complete one cycle. Earlier development and release of improved varieties, in turn, would allow earlier adoption and benefits to farmers.

IRRI mainstreamed these modern approaches in plant breeding and practices in the private sector to improve program performance. This also includes building the local capacity of NARES partners, including Bangladesh. Collaboration in transferring MAB and RGA technology with the Bangladesh Rice Research Institute (BRRI) in 2014 became fully functional in 2015. Through this process, improvement from the traditional time of 14–15 years to develop one variety using a one-season pedigree method has been shortened to 5–6 years (BRRI and IRRI experts, interview by the authors, 05 November

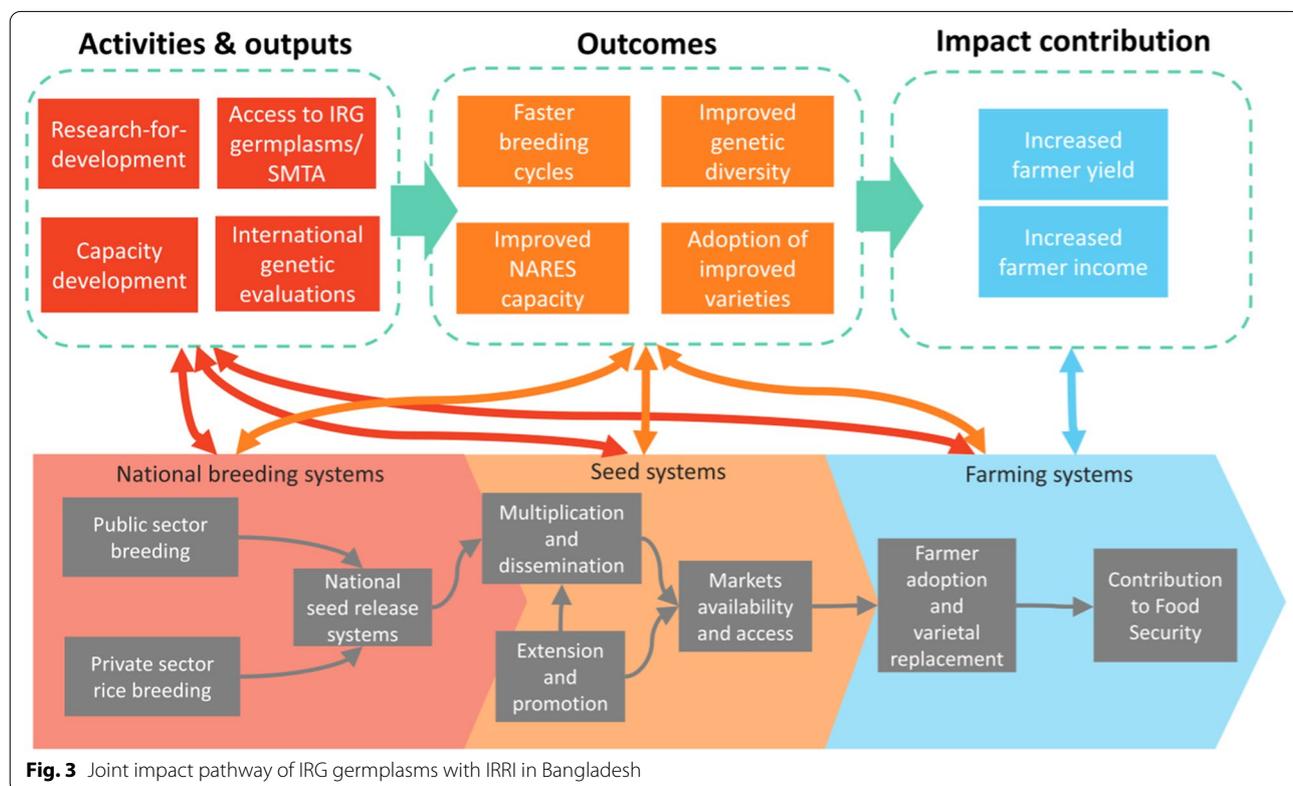


Fig. 3 Joint impact pathway of IRG germplasms with IRRI in Bangladesh

2020). This also resulted in improving the probability of getting a higher yield by five to ten folds. MAB, together with improvements in shortening the breeding process enables more accurate and efficient targeting of traits for forward breeding, while backcrossing good traits to popular varieties can be achieved within 3–4 years.

Another development is enhancing the relevance of varietal products to market and consumer preferences through the formulation of product profiles. Product profiles are a compilation of trait packages required for effectively penetrating a market segment that informs breeding programs at the early stage (Ragot et al. 2018). This set of information introduces evidence-based manners of targeting trait developments that have a higher probability of value creation. Product profile typically covers information on the varietal preferences and gathers feedback on the existing variety from all actors in the value chain apart from the farmers (Cobb et al. 2019a, b).

Before a breeding pipeline can be designed or optimized, it must have plausible objectives with respect to the type of product it will produce. Many breeding programs refer to this as the product profile. The product profile describes the trait package needed to replace a specific reference or target variety. A product profile, as defined by Ragot et al. (2018), is “a set of targeted attributes that a new plant variety is expected to meet in order to be successfully released onto a market segment.” Rather than an imaginative venture to design the perfect variety, a product profile attempts to focus breeding efforts on the key traits that drive incremental value creation. Based on this profile, IRRI and its NARES partners can make transparent advancement decisions using the profile as criteria for advancing certain varieties for national trials and release. Product profiles also allow harmonization of interest and priorities between breeding programs and value chain actors, facilitating the more effective matching of investment priorities that yield better targeting and employment of resources.

IRRI, together with NARES partners, has facilitated the production and distribution of about 230,000 tons (t) of stress-tolerant rice seeds in 2017, which were used in 2018 (Baltazar and Samantaray 2018). These are roughly estimated to reach 8 million farmers through various dissemination mechanisms, such as head-to-head trials, participatory varietal selection, and crop cafeteria (ibid). Bangladesh share in this total is roughly estimated at 80,000t or 2.9 million farmers. Recently, IRRI and national public and private partners are using the information from product profiles to inform what varieties to scale in the seed systems.

Table 2 Summary of the progenitor contribution of IRG on the adopted rice varieties by farmers during the 2015 wet season, Bangladesh

Type of contribution	Min	Max	Mean	
			Unweighted	Area-weighted
Definite	0.00	1.00	0.52	0.67
Possible	0.00	1.00	0.15	0.18
No	0.00	1.00	0.14	0.12
Unknown	0.00	1.00	0.19	0.03
Total			1.00	1.00

Progenitor contribution of IRG

In (see Additional file 1: Table S1) shows the basic information about the varieties and the progenitor contribution of the IRG. A total of 53 improved rice varieties (43 inbred and 10 hybrids) were cultivated on about 2 million ha. Additional file 1: Table S2 (see Additional file 1) shows that out of the 43 inbred varieties, 38 (88%) have at least one progenitor in the pedigree tree that definitely came from the IRG. If possible contributions were included, the number of inbred varieties with at least one progenitor that came from the IRG would be 41 (95%). The average number of IRG progenitors with definite and possible contributions in an inbred variety is 25, with a minimum of 1 and a maximum of 60. All hybrid varieties do not have pedigree information from the IRIS database, and thus, the progenitor contribution of IRG in these varieties is unknown.

Table 2 shows the summary of the computed progenitor contribution of IRG to each of the adopted improved rice varieties by farmers during the 2015 wet season in Bangladesh. In all types of IRG contributions, the minimum and maximum progenitor contributions were 0 and 1, respectively. The unweighted mean shows that the average definite and possible progenitor contribution of IRG to an improved rice variety was about 52 and 15%, respectively. Using the estimated percent planted area as weights, the average definite and possible progenitor contribution of IRG to an improved rice variety was about 67 and 18%, respectively. On average, 67% of the genetic composition of an improved rice variety cultivated by farmers during the 2015 wet season came from IRG accessions. The progenitor contribution can increase by up to 85% when the possible contribution is added. If there are IRG accessions in the pedigree of the hybrid varieties with no information, the progenitor contribution can still be higher. These findings reveal that IRG accessions form a significant

Table 3 Definition of variables and some descriptive statistics

Variable name	Variable label	Mean	SD
Yield	Yield (kg/ha)	4,964	1,443
Fertilizer	Fertilizer (NPK) quantity (kg/ha)	171	92
Labor	Total labor (person-days/ha)	116	35
Power_cost	Cost of power inputs (machine rental, animal rental, fuel, and electricity) in Tk/ha	12,923	5,991
Other_inputs	Cost of other material inputs (herbicide, pesticide, and others) in Tk/ha	1,394	1,795
Variety_age	Age of variety (years)	26	12
Irrigated	Use a supplemental source of water for irrigation (1=yes, 0=no)	0.46	0.50
Submergence	Submergence condition of the plot (1=yes, 0=no)	0.03	0.17
Distance_dealer	The distance of the house from the nearest input dealer (km)	2.03	1.96
Age	Age of the household head (years)	46	13
Education	Education of the household head (years)	5.6	4.5
Definite_contribution	Definite contribution of IRG on the variety (index)	0.68	0.25
Barisal	Plot's location is in Barisal (1=yes, 0=no)	0.12	0.32
Chittagong	Plot's location is in Chittagong (1=yes, 0=no)	0.12	0.33
Dhaka	Plot's location is in Dhaka (1=yes, 0=no)	0.12	0.32
Khulna	Plot's location is in Khulna (1=yes, 0=no)	0.42	0.49
Rajshahi	Plot's location is in Rajshahi (1=yes, 0=no)	0.22	0.42

SD = standard deviation

part of the genetic composition of improved rice varieties in Bangladesh.

Genetic contribution of IRG to productivity³

Table 3 reports the definition and some basic descriptive statistics for the variables included in the yield response function. The average yield was about 4.96 t/ha, with a standard deviation of 1.44 t/ha. Farmers applied an average of 171 kg/ha of nitrogen (N), phosphorus (P), and potassium (K) fertilizer on aggregate. Labor input had an average of 116 days/ha, while the cost of power and other material inputs had an average of Tk 12,923 and Tk 1394, respectively. The average age of the variety from the time of its official release up to the survey year was around 26 years, with a standard deviation of 12 years. Forty-six percent of the plots used supplemental water irrigation sources, while only 3% experienced submergence conditions. On average, the distance of the respondent's house from the nearest input dealer was about 2.03 km, with a standard deviation of 1.96 km. The average age and education of the farmers were about 46 and 6 years, respectively. The plot-level average of the definite contribution was 0.68, which means that about 68% of the genetic composition of the variety came from the genes of IRG accessions. The shares of the plots cultivated by modern rice varieties that are located in Barisal, Chittagong, and Dhaka were 12% each, while 42% and 22% of the total plots were located in Khulna and Rajshahi, respectively.

In this study, there were four estimated models in different functional forms (see Additional file 1: Tables S3–S6). To arrive at these estimates, the basic diagnostic tests for linear regression were conducted, and the results were evaluated. The results of VIF confirmed that there was moderate multicollinearity (mean VIF = 1.85) among independent variables, but it was not severe enough to warrant corrective measures (see Additional file 1: Table S7). On the other hand, the results of the Breusch-Pagan/Cook-Weisberg test for heteroscedasticity were significant, which meant that there was a problem of heteroscedasticity in all models (see Additional file 1: Table S8). To deal with this problem, heteroskedastic linear regression was used in all models instead of the ordinary least square regression. This study employed the `-hetregress-` function of Stata 16.1, which fits a multiplicative heteroskedastic linear regression by modeling the variance as an exponential function of the specified variables using either maximum likelihood or Harvey's two-step generalized least-squares method. Only the results of the primary model of the heteroskedastic linear regression were presented in the tables since that was the focus of the analysis of this study. The AIC and BIC were computed to assess the most appropriate functional form in each model (see Additional file 1: Table S9). Among the three models, results showed that the Cobb–Douglas had the lowest values of AIC and BIC. This result implied that Cobb–Douglas was the functional form that best fit the data.

³ Hybrids have unknown progenitor contributions in the dataset and were excluded in the subsequent analysis.

Table 4 Estimation results of the final yield response function, 2015 wet season, Bangladesh

Independent variables	Coef	Std. err	z	p-value
ln_fertilizer (lnFer)	0.044	0.01	2.96	0.003
ln_labor (lnLab)	0.196	0.03	6.37	0.000
ln_power_cost (lnPow)	0.102	0.02	4.14	0.000
ln_OTHER_inputs (lnOth)	-0.001	0.00	-0.41	0.679
Variety_age	-0.002	0.00	-2.09	0.037
Irrigated	0.010	0.02	0.45	0.655
Submergence	-3.506	0.85	-4.12	0.000
Distance_dealer	-0.016	0.01	-2.70	0.007
Age	0.001	0.00	1.02	0.307
Education	0.003	0.00	1.61	0.107
ln_definite_contribution	0.010	0.00	2.95	0.003
Division				
Chittagong	0.211	0.04	4.83	0.000
Dhaka	0.462	0.06	8.05	0.000
Khulna	0.353	0.04	9.12	0.000
Rajshahi	0.436	0.04	9.99	0.000
Constant	6.123	0.25	24.75	0.000

No. of observations = 763

Dependent variable = lnyield (kg/ha)

The final yield response model of this study is presented in Table 4. Results showed that, except for other material inputs, the conventional production inputs were positive and significant, which conformed to the production theory. The negative sign and insignificant effect of other material inputs in yield can be attributed to the dependence of the cost of herbicides and pesticides applied to the occurrence of weeds and pests, respectively. Plots planted with recently released modern rice varieties had a higher yield. The use of a supplemental source of water for irrigation did not significantly affect the yield. This result can be associated with the adequate supply of water brought by rain during the wet season. The coefficient of submergence was negative and significant. This abiotic stress affected the growth of the rice crop and decreased its productivity. In some parts of Bangladesh, rice is cultivated in low-lying areas that are prone to submergence due to heavy rains and water intrusion from rivers or seas. The distance of the house from the nearest input dealer negatively affected the yield. Farmers who lived farther from the shop of the input dealer had a lower yield. Based on this result, lower yield can be attributed to the insufficient amount and untimely application of farm inputs due to their high cost caused by additional logistic costs and the difficulty in traveling to the input dealer's shop. The age and education of the farmers did not significantly affect the yield.

In this study, the main variable of interest was the definite IRG contribution. The model results showed that the coefficient of the definite IRG contribution was positive and significant. This result means that as the size of the genetic contribution of progenitors from the IRG in an improved rice variety increased, its yield also increased. The magnitude of the increase in yield was computed by obtaining the exponential value of the coefficient of variable pertaining to the definite IRG contribution. The result of the computation was 1.0099. In terms of percent change, this result was interpreted to mean that a 1% increase in the definite IRG contribution on an improved rice variety can increase the yield by about 0.99%. Furthermore, a 10% increase in the definite IRG contribution can lead to a 9.9% yield increase. These results imply that the germplasm acquired from IRG contributed to the yield improvement of rice varieties. The enhanced yield can be associated with the added important agronomic traits contributed by the accession provided by the IRG in the genetic background of the rice varieties developed for farmers in Bangladesh.

Economic benefit of the IRG contribution

The economic benefit of IRG contribution was estimated from the resulting income and yield increases that can be attributed to the marginal increase in progenitor contribution. Table 5 shows the step-by-step procedure used to calculate the marginal increase in net income in Bangladesh due to a 1% increase in IRG contribution. Results showed that a 1% increase in the definite IRG contribution (variable B in Table 5) leads to a 0.99% yield increase (C). This is equivalent to 49.36 kg/ha (D), calculated at the mean yield of modern rice varieties of 4964 kg/ha (A).

Following the law of supply and demand in economics, the increase in production of a particular commodity shifts the supply curve to the right and results in a lower price of that commodity. Using the IGRM model, the increase in rice production in Bangladesh by 0.99% decreased the price by 1.89%/kg (F).

On the other hand, the increase in productivity can also incur additional costs of labor and material inputs. Using the plot-level data of the RMS, the average input cost of producing 1 kg of paddy was about Tk 10.00. Considering the corresponding decrease in price and increase in the production costs, the results showed that the estimated marginal increase in net income due to a 1% increase in IRG contribution was about 261.38 Tk/ha (K).

Given that Bangladesh had an estimated rice area cultivated by modern varieties during the 2015 wet season of 1.946 million hectares (L), the total increase in net income for the whole country was about Tk 508,620,707 (M). The US\$ equivalent of this estimate for 2020 was around US\$ 8,576,973 (Q). Although this study was

Table 5 Step-by-step computation of the economic benefit of IRG contribution

Variable name	Variable description	Unit	Formula	Value
A	The average yield of modern rice varieties during the 2015 wet season	kg/ha	–	4964
B	Coefficient of ln_Definite_contribution in the Cobb–Douglas model	–	–	0.01
C	The marginal increase in yield due to a 1% increase in IRG contribution	%/ha	$(\exp(B)-1) * 100$	0.99
D	The marginal increase in yield due to a 1% increase in IRG contribution	kg/ha	$A * (C/100)$	49.36
E	Average paddy price of modern varieties during the 2015 wet season	Tk/kg	–	16.60
F	The estimated increase in paddy price due to the increase in production	%	$I\text{GRM}^a$	1.89
G	The estimated paddy price due to the increase in production during the 2015 wet season	Tk/kg	$E-(E * F/100)$	16.28
H	The estimated marginal increase in gross income due to a 1% increase in IRG contribution	Tk/ha	$D * G$	803.81
I	The estimated total input cost/kg of paddy during the 2015 wet season	Tk/kg	Cost and return ^b	10.99
J	The estimated total input cost for 49.36 kg of paddy during the 2015 wet season	Tk/ha	$D * I$	542.43
K	The estimated marginal increase in net income due to a 1% increase in IRG contribution	Tk/ha	$H-J$	261.38
L	The estimated area cultivated by modern varieties during the 2015 wet season	000 ha	–	1946
M	The estimated marginal increase in net income (local currency) in Bangladesh due to a 1% increase in IRG contribution in 2015	Tk	$K * L * 1000$	508,620,707
N	The exchange rate of 1 US\$ to Tk (2015)	Tk	–	77.87
O	The estimated marginal increase in net income in Bangladesh due to a 1% increase in IRG contribution in 2015	US\$	M / N	6,531,455
P	Consumer price index in 2020 (base = 2015)	index	–	131.32
Q	The estimated marginal increase in net income in Bangladesh due to a 1% increase in IRG contribution in 2020	US\$	$O * (P/100)$	8,576,973

^a IRRI Global Rice Model

^b The total input cost/kg was computed using the cost and return data of RMS

limited in looking at the economic benefit for one season only, the farm-level contribution of IRG in Bangladesh has most likely happened in multiple years. The results demonstrate the significant contribution of IRG in the rice economy of Bangladesh.

Conclusions

This paper provides evidence of the impact of IRG's genetic resources on rice productivity among smallholder farms in Bangladesh. Using data from the farm household survey conducted by IRRI in 2016 in five divisions in Bangladesh, a pedigree analysis was conducted and related the productivity changes in farmers' fields explicitly to genebank accessions through varietal improvement. Afterward, we evaluated the economic benefit of IRG contribution in rice varietal improvement in Bangladesh using the computed marginal increase in productivity, average paddy price, and estimated total rice area. We also mapped out the impact pathways of IRG in germplasm transfer for varietal improvement and seed dissemination of improved rice varieties in Bangladesh using the information collected from key informant interviews.

IRG's impact pathway on germplasm transfer in Bangladesh shows that farmer's impacts are achieved through joint efforts with IRRI and NARES's

research-for-development programs. The interdisciplinary research and development efforts of IRRI, where IRG also performs a necessary role, recognize the multifaceted nature of bringing about the impacts on farmers and achieving food security.

The study found that, on average, 52% of the improved rice varieties' genetic composition, cultivated by farmers during the 2015 wet season in Bangladesh, definitely came from IRG accessions. This contribution factor can increase up to 67% if possible contributions are taken into account. Using the yield response, this study assessed the farm-level impact of the IRG on productivity by including the index for the definite IRG contribution as one of the explanatory variables. The results of the Cobb–Douglas model showed that the definite IRG contribution had a positive and significant impact on yield. For every 1% increase in the definite IRG contribution to an improved rice variety there was an increase in rice yield of about 0.99%, holding other factors constant. This yield increase can be translated into an additional US\$ 8,576,973 aggregated net benefit for farmers in 2015 wet season in Bangladesh.

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 Bangladesh. The

results can also be used to justify the continuity of collecting accessions and identify future potential sources of additional genetic acquisitions for varietal improvement. Most importantly, this case study illustrates the benefits of maintaining rice genetic resources, which can be used as evidence to attract funding from donors for the continuous support of IRG.

For future research, a combined analysis to assess the farm-level impact of IRG in eastern India and Bangladesh could also be conducted due to the availability of similar data. Another potential study could be performing a surplus analysis to estimate the overall net economic benefit of the IRG after the deduction of its research and operational costs. The results of these studies can then strengthen the evidence and can add value to the aggregated impact of IRG on farmers' productivity and income.

Abbreviations

AIC: Akaike's information criterion; BIC: Bayesian information criterion; BRRI: Bangladesh rice research institute; 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; MAB: Marker-assisted breeding; NARES: National agricultural research and extension system; NGOs: Non-government organizations; RGA: Rapid generation advance; RMS: Rice monitoring survey; SMTA: Standard material transfer agreement; Tk: Bangladesh taka; VIF: Variance inflation factors.

Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s43170-022-00113-7>.

Additional file 1: Figure S1 Seed distribution of the International Rice Genebank (IRG) in Bangladesh by year (1987–2019). **Figure S2** Seed distribution of IRG in Bangladesh by purpose in percent (1987–2019). **Figure S3** Seed distribution of IRG in Bangladesh by type of recipient institution in percent (1987–2019). NGO = non-government organization. **Figure S4** Pedigree tree of BR11 generated by IRS. **Figure S5** Mendelgram for BR11 generated by IRIS. **Table S1** Varietal information and the progenitor contribution of IRG on improved rice varieties cultivated by farmers, wet season 2015, Bangladesh. **Table S2** Number of ancestors in the pedigree tree with definite and possible progenitor contributions of IRG on inbred varieties cultivated by farmers, wet season 2015, Bangladesh. **Table S3** Estimation results of yield response function in linear form, 2015 wet season, Bangladesh. **Table S4** Estimation results of yield response function in extended linear form, 2015 wet season, Bangladesh. **Table S5** Estimation results of yield response function in Cobb-Douglas form, 2015 wet season, Bangladesh. **Table S6** Estimation results of yield response function in Translog form, 2015 wet season, Bangladesh. **Table S7** Variance inflation factors (VIF) among independent variables. **Table S8** Chi-squared value of Breusch-Pagan/Cook-Weisberg test for heteroscedasticity. **Table S9** Comparison of Akaike's information criterion (AIC) and Bayesian information criterion (BIC).

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Author contributions

The first author (DV) wrote the manuscript, conceptualized the research, designed the methodological approach, conducted the data gathering, constructed analytical models, and performed the analysis. YE contributed to the research conceptualization, data gathering, analysis, writing, and editing, particularly in the impact pathway analysis section. GLC contributed to the research conceptualization and extracted the pedigree data of the identified improved rice varieties by this study from the IRG database. All authors read and approved the final manuscript.

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Availability of data and materials

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Declarations

Ethics approval and consent to participate

Survey instruments and the conduct of key informant interviews (including securing prior informed consent) undergone ethics review and approval of the International Rice Research Institute Research Ethics Committee.

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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