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The role of CGIAR Germplasm Health Units in averting endemic crop diseases: the example of rice blast in Bangladesh

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Abstract

Background: One of the less known benefits of the CGIAR is the facilitation of international agricultural research for crop improvement by providing a continuous supply of breeding materials for the development of disease resistant varieties. The Germplasm Health Units (GHUs) of the CGIAR are phytosanitary mechanisms put in place to help ensure safe (from pests and diseases) and efficient international transfer of germplasm among genebanks and breeding programs around the world. To date, there is no systematic documentation of the pathways and extent to which GHUs contribute to economic impact in recipient countries.

Methods: We conducted interviews with key experts and reviewed secondary literature and data to trace the pathways through which the GHU of the International Rice Research Institute (IRRI) contributes to the impact of breeding for rice blast. We applied an ex ante economic surplus framework to the case of rice blast in Bangladesh, considering productivity maintenance and time saving factors from GHU facilitation. Data were drawn from a national panel dataset of farm households (from 2013 to 2016 with about 4490 households) and field surveys of blast incidence and severity (from 2011 to 2012 in 10 agroecological zones). We augmented our model with Monte Carlo sampling to simulate distributions of parameters.

Results: Our model predicts that, in the most probable scenario (modal values), the IRRI GHU contributed about US$ 5.9 million of the total US$ 295 million net benefits over a 20-year time frame of continuous blast resistance breeding and deployment. In the most optimistic conditions (maximum), the IRRI GHU contributed as much as US$ 62 million of the US$ 1.46 billion benefits. The modal benefit–cost ratio of the GHU in this breeding program alone was estimated at 112. The results are sensitive to the rate of yield savings, which is contingent on yield levels, timing of deployment, effectiveness of resistance, and lifespan of resistance to blast.

Conclusions: The study reinforces the important, and often overlooked, role of the GHUs in the international agricultural research that aims to enhance genetic gains in crops through efficient and timely access to clean and healthy germplasm.

Keywords: Rice, Germplasm health units, Germplasm, Genebanks, Rice blast, Yield savings, Time savings, Bangladesh

Introduction

CGIAR GHUs and interdependence of plant genetic resource

The historic success of global agriculture research for crop improvement is built on the strong scientific partnership between the CGIAR centers and the national agricultural research systems (NARS). Since 2004, this

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has been further enabled by the International Treaty for Plant Genetic Resources for Food and Agriculture (or the Plant Treaty) of the Food and Agriculture Organization (FAO) and its Multilateral System for access and benefit sharing (MLS), which allows for unrestricted flow of plant genetic resources (Johnson et al. 2003; Visser et al. 2000; Vernooy and Clancy 2017). The MLS is a breakthrough achievement of the Plant Treaty, to which all Contracting Parties adhere. The CGIAR is officially recognized as a supporting component to the Treaty (cfr. Art. 15 of the Treaty).

Since 2004, the contracting countries of the Plant Treaty have agreed to participate in the MLS in creating an international collection of genetic resources for 64 crops and forages, stored in a decentralized way in all participating genebanks around the world, listed in the Plant Treaty (Galluzzi et al. 2016). National food systems have benefited from this partnership, especially in countries where diets and agricultural production systems largely rely on genetic diversity traceable to foreign origins (Khoury et al. 2015). However, seed-borne pathogens are often barriers to seed movement. Seed destination countries need assurance that the plant germplasm that enter their borders are free from any pathogen or pest of quarantine importance. The unintended introduction of diseases and pests is often irreversible and could spell significant crop losses.

The increased risk of transboundary transfer of diseases and pests would likely discourage access to and sharing of benefits from global use of germplasm and, worse, might lead to the tightening of national quarantine and administrative regulations. All these factors could slow down the international exchange of plant genetic resources. In this regard, seed health testing and phytosanitary clearances are mandatory for collection holders or any other person who is involved in seed/germplasm exchange. Processes are regulated under the International Plant Protection Convention and respective policies of the national plant protection organizations (NPPOs) of all involved countries (i.e., the country hosting the collection/donor germplasm and the country requesting to import) (Kumar et al. 2021).

The CGIAR has an important role in the Plant Treaty. CGIAR centers agreed under the convention that the ex-situ collections under the CGIAR genebanks are made available and accessible through the MLS. Since the 1970s, CGIAR centers have established phytosanitary protection measures and protocols to ensure a pest-free international exchange of germplasm (see Kulkarni 2019 for measures and protocols). The Germplasm Health Units (GHUs) were formalized in the 1990s to serve as a single gateway for international germplasm exchange through the recommendations of the Sixth International Plant Protection Congress in 1993 in Montreal. Some CGIAR centers, like the International Rice Research Institute (IRRI), name their GHUs as Seed Health Units (SHUs)[1] because they deal mostly with seed crops.

The GHUs are institutional phytosanitary units of the CGIAR designed to facilitate bioresource transfer for their breeding programs and their genebanks. They work in close partnership with NPPOs to help perform their national mandates through awareness raising, capacity development, and partnership arrangements for phytosanitary regulation. At IRRI, for example, the functions and services for incoming and outgoing rice seeds for post-entry clearance and phytosanitary certification include the following: dry seed inspection; routine seed health testing, which screens for *Tilletia arclayana* and nematodes; blotter testing; bacterial testing; field or greenhouse inspection for newly introduced germplasms, wild rice varieties; seed treatment; and packaging.

In addition, GHUs maintain networks and relationships with country users and regulatory organizations[2]; provide phytosanitary and regulatory information; disease surveillance; and generate and build capacity of NARS partners on seed health, seed movement, and transboundary pest and disease. By providing crucial safeguards for the safe and efficient transfer of germplasm to crop improvement and genetic resource programs around the world, GHUs are instrumental for effective development of international public goods. The CGIAR GHUs are also making efforts to institutionalize a GreenPass System: a certification scheme for germplasm exchange. Apart from its processes, the GHUs also put in place networks and institutional arrangements that create value that support both CGIAR and NARS partners.

Despite the almost two decades of CGIAR GHU existence, the causal pathway linking them to farmer welfare and the magnitude of economic benefits is largely unknown. This is perhaps because GHUs are perceived as service support units within the MLS that are related indirectly to the impacts of agricultural research on farms. But recent developments in modern breeding approaches have underscored the importance of timing in raising the rate of genetic gain (through rapid-cycle breeding) (Cobb et al. 2019a, 2019b; Hellin et al. 2020)

[1] For consistency and easier readability, this paper does not distinguish between GHU and SHU and will use the term IRRI GHU consistently to refer to the IRRI SHU.

[2] It is important to note that the CGIAR GHUs are not the only institutions that perform the plant quarantine and regulation. In countries where there are no physical presence of CGIAR, the NPPOs, under their international and national mandate, perform this function. But unlike the CGIAR GHUs, which focus on their specific crop of interest, NPPOs also cover all other imported and exported crops for research and trade.

and in the dynamics of attaining durable protection from evolutionary capabilities of pathogens (Dossa et al. 2015; Meng et al. 2020; Ning et al. 2020).

In this context, one of the CGIAR's unknown success stories is the contribution of GHUs to reducing the risk of transboundary spread of pest and disease and the transfer delays that could have impaired time-sensitive progress in plant breeding. To date, there is no existing evidence that documents and quantifies the economic benefits and saved opportunity costs derived from the facilitation by CGIAR GHUs of safe and efficient international transfers of germplasm. We address this gap by documenting the specific case of improving the durability of cultivated rice varieties to blast in Bangladesh. This enables us to demonstrate the pathway linking GHUs to impacts on farms. We apply impact pathways analysis and an augmented ex ante surplus model that simulates the impact on farm yields of blast R variety deployment over a 20-year period. Data sources included interviews with key experts, a national panel dataset collected from farm households, and field surveys of blast incidence and severity. Next, we present literature about rice blast and the breeding approaches that address this disease.

Combating rice blast in Bangladesh

Rice is a significant income source for farmers in Bangladesh. Reardon et al. (2013) estimate that about 60% of the urban retail price is earned by rice farmers. Pest and diseases, particularly blast, are key threats to farmers' productivity and income. While fungicide can be an effective treatment, it adds substantial cost to farmers. But when they are needed the most during the cultivation season, most farmers find it difficult to access pesticides (Quddus and Kropp 2020).

Rice blast is a serious fungal disease caused by *Pyricularia oryzae* Cavara (sexual morph *Magnaporthe oryzae*). Blast disease can infect the aboveground tissue of rice plants and all their organs at any developmental stage, which could cause total crop failure (Ou 1985; Le et al. 2010; Asibi et al. 2019). Blast outbreaks are recurrent and known for their destructiveness across ecosystems and seasons (Ou 1985; Marchetti et al. 1976; Bonman 1992; Mekwatanakarn et al. 1999; Khan et al. 2017).

With a long history of rice cultivation and a dependence on rice for staple food security, Bangladesh confronts a severe threat from rice blast disease, with the potential to upturn its historical productivity gains. Estimates from various countries show that rice blast can result to 10–30% yield loss annually. Without preventive measures, in conditions most favorable to blast disease, it can also result in 100% losses in just a matter of 15–20 days of infection (Asibi et al. 2019). In Bangladesh, Hossain et al. (2017) found that computed yield losses from rice blast in ten representative agro-ecological zones (AEZ) could cause as high as 34.7% and 16.4% losses, a median of 16.85% and 11.35% and lowest at 11.9% and 6.4% in an AEZ in irrigated area (Boro) and rainfed area (Aman), respectively.

The most popular rice varieties, including aromatic varieties, are susceptible to blast in wet (Aman) and dry (Boro) seasons and in rainfed and irrigated areas (Hossain et al. 2017). These include popular varieties like the Bangladesh Rice Research Institute (BRRI) dhan 29 and BRRI dhan 28 (ibid). Bangladesh Bureau of Statistics (2016a, b) estimates in 2015–2016 that local rice varieties accounts for 1,440,635 ha with yield between 1.19 and 1.67 mt yield per ha and 47,300 ha with 1.89 mt yield per ha, in Aman and Boro respectively. The Bureaa estimates that high yielding varieties cover 4,149,705 ha with yield at 2.71 mt per ha and 4,043,531 ha with yield at 3.86 mt per ha, in Aman and Boro respectively. In the 2016 data of the Rice Monitoring Survey (RMS), the number of types of local varieties cultivated is estimated at 67 in Aman and 18 in Boro, while modern or high yielding varieties number 31 in Aman and 21 in Boro (IRRI 2016). Since the 1980s, Bangladesh has struggled with several blast disease outbreaks (Shahjahan 1994). Further, climate change has brought early rainfall and temperature and humidity changes, making environmental conditions more favorable for blast pathogens to thrive and infect early maturing varieties.

Modern approaches to breeding blast R rice varieties

Breeding resistance to blast disease in rice varieties is an environmentally friendly and economical solution compared to alternatives, such as the use of pesticides (Khan et al. 2016; Meng et al. 2020). However, conventional breeding for the development of rice blast resistant (R) varieties, which is based on crossing and selection using pedigrees and recombination, has proved challenging. Many new rice varieties have shown high levels of blast susceptibility, and those that are blast R often lose their resistance within 3–5 years (Shahjahan 1994; Xiao et al. 2017, 2019; Meng et al. 2020; Ning et al. 2020). The diversity of the blast population structure and the continuous development of its pathogenic race across time and space are key factors driving the demand for breeding new R varieties. In Bangladesh, Khan et al. (2016) found 331 representative blast isolates across various ecosystems, which were classified into 267 blast races. Such diversity indicates a high likelihood that a blast pathogen will break the resistance of blast R varieties.

The researchers from BRRI accessed 25 differential varieties (DVs) stored in IRG that represented monogenic lines for 23 blast R genes. These DVs were products of the international research program "Differential System for

Blast Resistance for a Stable Rice Production Environment" in the mid-2000s. By subjecting these DVs with the blast isolates collected from Bangladesh and comparing them with a susceptible control, Lijiangxintuanheigu, BRRI identified the most promising genes (Pish, Pi9, Pita-2, and Pita) across ecosystems in the country (Khan et al. 2014, 2016, 2017). Experts from BRRI estimated that this process significantly reduced time and resources needed through providing access to the DVs, which could take about 5–6 years each in development (BRRI experts, interview by the author, 12 December 2020).

Modern rice breeding solutions to blast have emphasized the importance of customized deployment of resistance genes as the most influential factor for durable disease protection (Dossa et al. 2015; IRRI expert, interview by the author, 02 December 2020). This involves the use of site-specific pathogen population information and forecasting in determining which blast R gene is most effective to deploy in target varieties (Dossa et al. 2015). Breeding programs also employ gene pyramiding, or the combining of two or more genes in a variety, to reduce the probability for blast pathogen to adapt and overcome a variety's resistance. Because of this, pyramiding of genes can improve or lengthen the resistance of varieties to blast (Xiao et al. 2019; Ning et al. 2020).

Customized deployment of resistant genes is made possible through advances in Marker Assisted Selection (MAS) which uses DNA markers for indirectly selecting agricultural traits for crossing or breeding, and rapid generation acceleration (RGA) which increases the number of crop generations per year. The transformation of the breeding processes, through RGA, at IRRI has fast tracked the breeding cycle from hybridization (including pyramiding of genes) to population advancement in 2–3 years to generate elite lines in as few as 1.5 years, shortening the time to release of varieties to 6 years. The modern breeding system integrates MAS and RGA to leverage genetic diversity for use in forward breeding and in-line augmentation (see Additional file 1).

Customized deployment applies these approaches to promote the shuffling of resistance mechanisms of rice varieties, through gene rotation or mixture in a single genetic background, to prevent dynamic pathogen populations rapidly adapting to single-gene virulence. Gene rotation involves the introduction of new R varieties, with new or more effective gene, to replace existing varieties currently cultivated by farmers which are already ineffective to new virulent race (Mundt 2014). The original R gene can still be used in the future after the new virulent race has declined or different race has taken over (ibid).

These approaches are not possible through conventional methods for public rice breeding, which takes 10 to 14 years to release a variety, or without access to important pre-breeding materials such as differential varieties or lines that contain the single R gene. These help public breeding institutions in their local selection and introgression of R genes effective to local virulent races. This is because the time it takes to develop even a single-gene R variety is lengthy and development cannot keep pace with the speed of local pathogen evolution. Blast races can break down varietal resistance within three to five years (IRRI expert, interview by the author, 02 December 2020; BRRI experts, interview by the author, 12 and 20 December 2020). Customized deployment underpinned by advancements in rapid-cycle and precision breeding and efficient access to safe and healthy germplasm materials provides the most promising solution to address blast (Dossa et al. 2015).

Analytical frameworks, methods, and data

Analytical approach

We combined analytical approaches to measure the IRRI GHU's economic contribution to averting yield losses from rice blast in Bangladesh. We applied (1) impact pathway analysis; (2) time-savings benefits in breeding programs (Brennan and Martin 2007; Lenaerts et al. 2018); (3) a yield-savings model for rice blast; (4) the economic surplus approach adapted to maintenance research (Marasas et al. 2003), which is a partial equilibrium method; and (5) the IRRI Global Rice Model (IGRM) to incorporate market-clearing effects on price of local and international rice markets. Additional details on construction of scenarios, parameters, and values can be found in Additional file 1.

Impact pathway analysis

Impact pathway analysis (Douthwaite et al. 2003) enabled us to trace the causal links of the IRRI GHU to breeding program activities, outcomes, and impacts derived from adopting improved crop varieties. Since facilitated exchanges are the primary means by which GHUs contribute to the impacts of crop improvement research, we considered both the germplasm collections of the IRRI genebank and IRRI breeding programs, which are headquartered in the Philippines. Impact pathway analysis helped estimate time saved for breeding in the scenarios we considered, which then fed into the economic surplus model for productivity maintenance. We used key informant interviews with breeders and staff of the IRRI GHU, IRRI, BRRI, and Bureau of Plant Industry (BPI) (the NPPO of the Philippines responsible for enforcing plant quarantine legislations). We complemented interviews with desk analyses of secondary literature and documents from breeding programs and GHUs.

Speeding up breeding

Brennan (1989) and Brennan and Martin (2007) demonstrated that shortening the time to development and release of new varieties generates greater benefits because society places a higher value on money earned today than tomorrow. This method was used by Lenaerts et al. (2018) to estimate the global impact of rapid generation acceleration or the rapid generation advance method on rice breeding programs. Benefits were attained by shortening the period of the breeding process (which may involve pre-breeding, germplasm transfer, and multi-environment trials), resulting in early time to release and adoption of varieties. We apply this framework to value the benefits from the IRRI GHU arising from an earlier release and earlier adoption of the new varieties brought about specifically by safe and efficient germplasm transfer.

We estimated the difference in the time of breeding process by exploring a counterfactual scenario where the international exchange of germplasm happens without the CGIAR GHUs. IRRI GHU applies stringent screening protocols and phytosanitary standards for incoming and outgoing rice seeds. Under the MLS, IRRI GHU facilitates the Standard Material Transfer Agreement (SMTA). The SMTA is a mandatory mechanism for countries that intend to provide and access germplasm material under the MLS. As part of this arrangement, signatory parties can freely share access to one another's plant genetic resources for breeding, research, and training under a benefit-sharing agreement to use germplasm materials for commercial purposes. However, transferring pest- or disease-ridden germplasm can result into rejection of entry of imported or outflow of exported germplasm materials and will cause substantial delays in transfer due to lost time from initial shipment and in restarting the whole processes again. And in worst case scenario, accidental introduction of exotic pests or diseases could result in major delays caused by tightening of entries of germplasm and quarantine protocols in the receiving country.

The main difference between the two scenarios is the time of the release and adoption of the varieties. The counterfactual is the scenario where IRRI GHU does not facilitate the transfer of germplasm. We confirmed the time aspect by conducting key informant interviews and reviewing secondary information on importation and exportation records.

Lenaerts et al. (2018) showed that time-saving benefits could be conveniently turned into a multiplier to derive the portion of benefit share of time saved for any benefit estimation of breeding impact. The calculation of the incremental benefits from time saving is shown in Eq. 1 below, where $\Delta\beta_{Time-saving}$ is the time-saving incremental benefits that can be linked with the GHUs. This was computed by deriving the benefits from breeding $\beta_{Breeding}$ and computing for the r, which is the time saved with the existing discount rate used for the breeding benefits $(1+i)^r$.

$$\Delta\beta_{Time-saving} = \beta_{Time-saving} \cdot \beta_{Breeding} = \left[(1+i)^r - 1\right] \cdot \beta_{Breeding} \tag{1}$$

To complete this time-saving estimation, the $\beta_{Breeding}$ blast resistance programs still needed to be derived. Here, we used the following frameworks to produce this information.

Benefits of yield savings

We adapted the partial equilibrium, economic surplus framework that Marasas et al. (2003) applied to wheat rusts (Byerlee and Traxler 1995). The useful feature of the approach is its construction of the counterfactual in terms of yield savings from losses averted. Under this framework, the counterfactual is the scenario where supply curve does not have the benefit of enhancement research from blast R varieties. The 'without scenario' is where yield is lost because of the disease. The counterfactual is represented by a leftward or upward shift in the supply curve as compared to an outward shift in productivity (Collins 1995). Our benefit scenario 'with yield savings from customized deployment of R genes' is the supply curve where the modeled yield-savings are applied.

This framework recognizes that pest resistance of varieties is not static. Pathogens can adapt to varietal resistance over time, and when that happens, the yield advantages of the improved crop decline. Thus, there is value in research to maintain yield or, in our study's case, the potential aversion of production losses by the steady flow of new varieties with higher resistance to blast pathogen.

Performing this analysis involved comparing with and without scenarios, where the without scenario is a situation where research benefits on yield maintenance were absent. The economic surplus thus generated can be represented as:

$$NPV = \sum_{t=1}^{n} \frac{1}{(1+i)^t}[(p_t \lambda y_t a_t) - C_t] \tag{2}$$

Table 1 Distribution of sample households in Bangladesh, RMS 2013–2016 cropping years (from RMS dataset)

Division	RMS 2013		RMS 2014		RMS 2015		RMS 2016	
	VIL	HHLD	VIL	HHLD	VIL	HHLD	VIL	HHLD
Barisal	44	440	–	–	28	280	44	440
Chittagong	20	200	32	320	14	140	20	200
Dhaka	18	180	38	380	28	280	18	180
Khulna	18	180	28	280	54	540	18	180
Rajshahi	29	290	28	280	26	260	29	290
Rangpur	20	200	24	240	–	–	20	200
Total	149	1490	150	1500	150	1500	149	1490

RMS 2013 and 2016 are panel datasets; VIL: number of villages; HHLD: number of households

Calculation of the net present value (NPV) (Eq. 2) requires the following information:

λ = the average annual farm-level percentage yield savings by growing varieties resistant to blast pathogens; a = the area to which yield savings apply; y = the average annual farm-level rice yield; p = price of rice; t = year; C = costs incurred by breeding program and IRRI GHU.

In addition to yield savings, planting R rice varieties would enable farmers to forego applying Tricyclazole group fungicides. We incorporated the cost-savings benefits accrued from avoiding the use fungicides in both seasons, computed as the product of (1) the average cost of fungicide per hectare (ha), (2) the proportion of rice area applicable for cost-savings, and (3) the area to which yield savings apply. Average cost represents the expenditure of farmers for treating blast in their field, converted into US$ per ha. The area applicable for cost savings is the product of the proportion of farmers that use pesticides and the proportion of pesticide users who use fungicide to treat rice blast.

Durable R varieties may offer better protection than pesticides. Pesticides pose health and environmental hazards, and their effectiveness can be limited given the inadequacy of current knowledge on proper use of fungicides to address blast (Rahaman et al. 2018; Asibi et al. 2019). However, given data limitations, we did not consider the health and environmental benefits of preventing the use of fungicide in our framework.

Next, we used the IGRM to estimate the partial equilibrium effects of the changes in supply of rice on the price per division in Bangladesh. The IGRM is a partial equilibrium statistical simulation and econometric model of the world rice economy (Hoang and Meyers 2015). Here, the Bangladesh country model was linked with other rice economies through net trade, which analyzed its independence with other countries. This model was used to analyze and estimate the effects of various policies and programs. We run our bio-economic model in a 20-year timeframe to sufficiently simulate the benefits of improved durability overtime (see Additional file 1 for detailed model specification).

For cost parameters, we used two variables derived from the breeding program and the IRRI GHU to estimate the NPV of breeding and the net incremental benefits accrued by GHUs. Details of the costs are discussed in the Additional file 1. Lastly, we computed for benefit–cost ratios (BCRs).

Stochastic simulation

Economic surplus modeling studies have applied stochastic simulation methods to incorporate risk and uncertainty by exploiting the probability distribution of values (Horna et al. 2008, Kergna et al. 2017; Ahmed and Sallam 2020). Risk analysis provides more robust results compared with the use of deterministic values, allowing for better sensitivity analysis of the results. We applied the basic version of ModelRisk application of the Vos Software (www.vosesoftware.com), which is a Microsoft

Table 2 Locations of blast incidence survey (from Hossain et al. 2017)

AEZ	Districts
AEZ 1	Panchagarh, Thakurgaon and north-western parts of Dinajpur districts
AEZ 2	The region occupies narrow belts, within and adjoining the channels, rivers in Nilphamari, Rangpur and Gaibhandha districts
AEZ 9	Sherpur, Jamalpur and Mymensingh districts
AEZ 11	Rajshahi, Shatkhira and minor areas in Noagaon districts
AEZ 12	North-eastern parts of Khulna and Bagerhat districts
AEZ 13	Barisal, Jhalokathi and Pirojpur districts
AEZ 19	Comilla, Chadpur and Noakhali districts
AEZ 20	Sylhet, Hobiganj and Moulovibazar districts
AEZ 23	Chittagong and Feni districts
AEZ 28	Gazipur and Tangail districts

$$Disease\ incidence\ (\%) = \frac{Total\ \ no.\ of\ \ infected\ panicle\ in\ hill}{Total\ no.\ of\ \ panicle\ in\ hill} \cdot 100 \tag{3}$$

Excel-based plug-in that employs Monte Carlo simulations based on repeated random sampling.

We used the full distribution of the dataset in stochastic simulation whenever possible, such as for our data on disease incidence, yield, and area. For others, we used a triangular distribution (minimum, maximum, and modal values). Studies commonly use triangular distribution in decision-making tools for risk and uncertainty analysis when the data are sparse (Hardaker et al. 2004). We used 50,000 sample iterations for our Monte Carlo simulation.

Disease incidence is accompanied by severity measurement based on scale symptoms[3] of the IRRI Standard Evaluation System for rice (2002). Disease severity is measured by computing the number of blasted panicles based on the severity scale, and then weights are applied to the proportions (see Eq. 4). The scale uses a score of 0 to 9 (excludes even numbers in the numerical scaling) where N1–N9 are the number of panicles with a score from 1 to 9.

$$Panicle\ blast\ severity \frac{(10 \times N1)(20 \times N3)(40 \times N5)(70 \times N7)(100 \times N9)}{Total\ no.\ of\ panicles} \tag{4}$$

Data

We used three main datasets and key informant interviews to set up our economic surplus model. First, we used the dataset from the Rice Monitoring Survey (RMS) funded by the Bill and Melinda Gates Foundation and conducted at the farm level in Bangladesh for crop years 2013–2016, inclusive. The surveys were designed to be representative of rice production areas of the country, collecting information on rice varieties cultivated by the farmers in two main seasons, Aman and Boro (Table 1). RMS 2013 and 2016 are the panel dataset, while RMS 2014 and 2015 are independent and are cross-sectional data. The data in Table 1 is disaggregated by division, which is the first-level administrative partition in Bangladesh. The second-level administrative boundary inside a division is the district (see Table 2).

Second, we used blast incidence and yield loss data from field surveys of Hossain et al. (2017). Hossain et al. (2017) surveyed disease incidence and severity during the Boro season of 2010–2011 and Aman season of 2011 in various districts representing ten agroecological zones (AEZs). The survey technicians performed a zigzag sampling pattern for 27 field locations in each AEZ and each season, following Savary et al. (1996). The survey collected information during the post-flowering stage of the rice crop to observe the panicle blast.

The survey used the following Eq. 3 to measure disease incidence (Hossain et al. 2017):

Third, we consulted import and export records from 2016 to 2020, annual reports from 2018 to 2020, and full cost recovery cost information from the IRRI GHU for descriptive analysis of its operations and cost estimation.

We also gathered primary data through interviews with 14 individuals who worked or undertook research in IRRI GHU and BPI, blast resistance, breeding programs in the IRRI and the BRRI, as well as other IRRI scientists, for additional context and technical clarifications. We conducted group interviews whenever possible. A validation exercise with key informants was undertaken after production of the initial results, which were used to refine the model parameters and technical basis of the findings. In compliance with the IRRI Research Ethics Committee, personal information was redacted and only accessible to the first author.

Results

Impact contribution pathway

Figure 1 shows the IRRI GHU contribution pathway to genebanks and breeding programs. Because of the nature of GHU operations, the IRRI GHU's causal link to the

[3] Panicle blast severity scale based on symptoms scale, which uses numbers 0 and the odd numbers from 1 to 9. The definitions of each scale are as follows: 0—No visible lesion or observed lesions on only a few pedicels; 1—Lesions on several pedicels or secondary branches; 3—Lesions on a few primary branches or the middle part of panicle axis; 5—Lesion partially around the base (node) or the uppermost internode or the lower part of panicle axis near the base; 7—Lesion completely around panicle base or uppermost internode or panicle axis near base with more than 30% of filled grains; and 9—Lesion completely around panicle base or uppermost internode or the panicle axis near the base with less than 30% of filled grains (IRRI 2002).

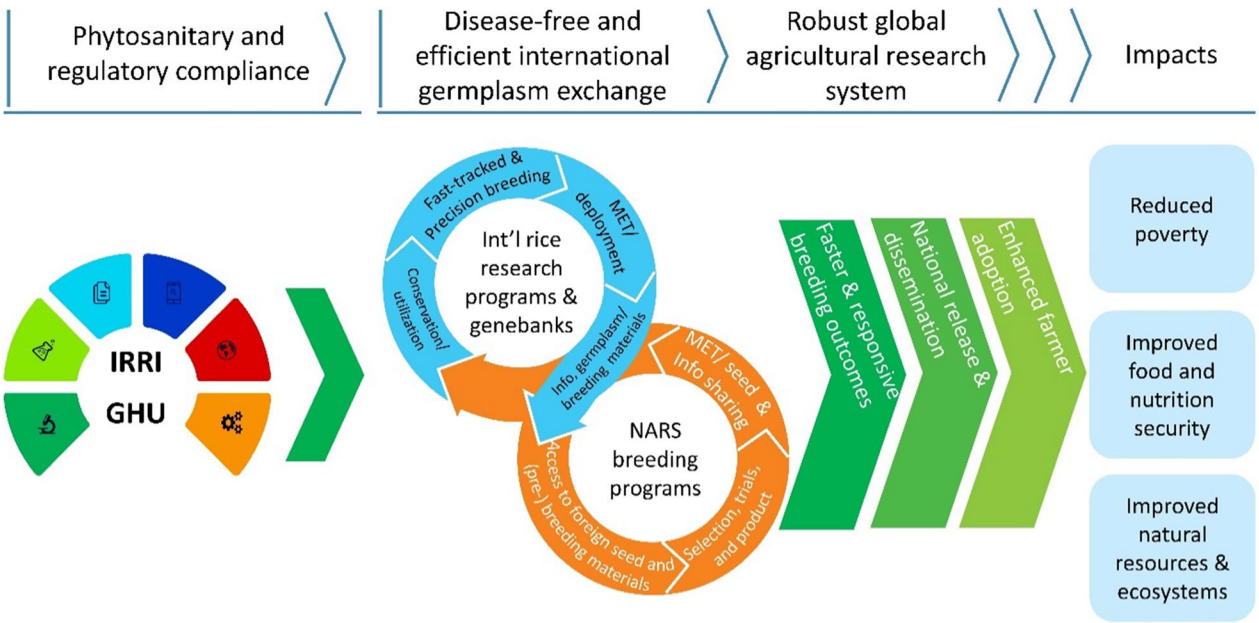

Fig. 1 The IRRI GHU contribution pathway to breeding impacts. MET: Multi-environment trials

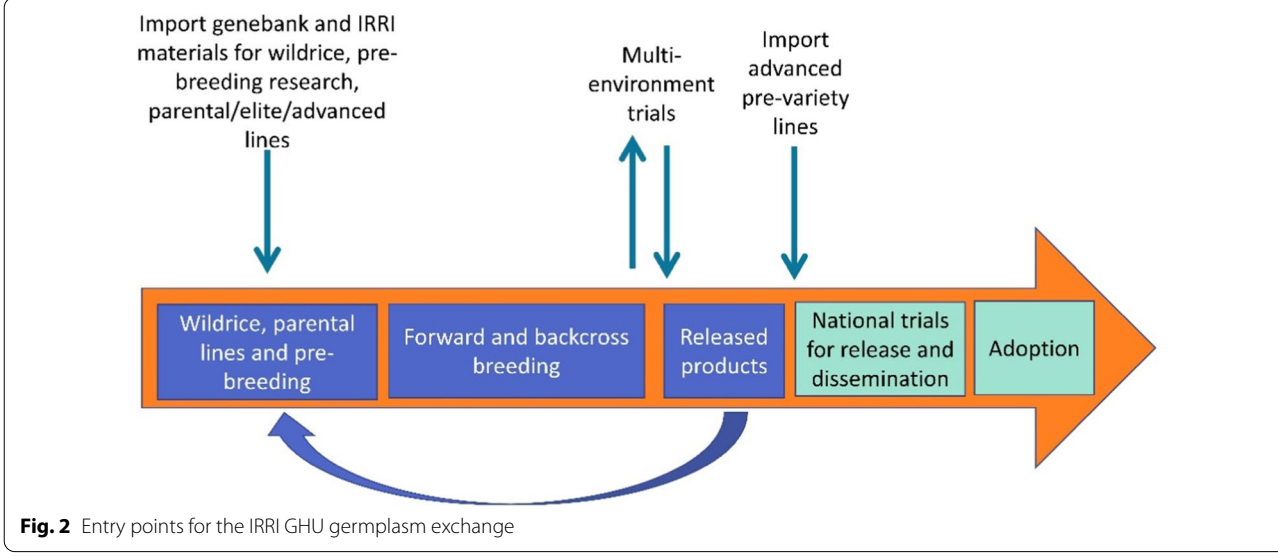

Fig. 2 Entry points for the IRRI GHU germplasm exchange

benefits earned by farmers who adopted improved crop varieties is indirect but essential to the success of crop improvement research. There are two distinct yield-savings impact pathways for GHUs. First is saving yield through prevention of transboundary spread of pests and diseases that otherwise could have disastrous implications on a country's agricultural productivity. The second is the contribution to the productivity impacts of crop improvement research on farms. Through the facilitation of efficient germplasm use and exchange, public breeding programs can efficiently access and evaluate valuable genetic materials, such as landraces, wild relatives, pre-bred materials, pathogen samples, elite and advance pre-variety lines such as DVs, from the IRRI Rice Genebank (IRG) and other participating research programs for their own use such as through participatory farmer field trials. This also applies for international or multi-environment evaluation initiatives. This second pathway pertains to this study. Figure 2 identifies the several entry points for germplasm exchange.

Table 3 Summary statistics of simulation results for customized deployment breeding program

	Gross benefits (in million US$)		NPV (in million US$)	BCR
	Aman	Boro		
Maximum	314	1223	1461	73
Minimum	− 86	− 7	− 94	5
Mode	54	254	295	24
Mean	62	315	362	26
Standard deviation	41	135	169	9

Table 4 Summary statistics of simulation results for the IRRI GHU time-saving benefits

	NPV (in million US$)	BCR
Maximum	62	3666
Minimum	0.29	3.8
Mode	5.9	112
Mean	12.6	305.8
Standard deviation	8.5	283

The primary mechanisms for enabling these outcomes are the IRRI GHU's phytosanitary actions and the utilization of the SMTA elaborated by contracting parties in the context of the MLS of the Plant Treaty.

Coordination of the legal and administrative requirements for germplasm exchange and shipment is an essential source of delay. The delays can increase due to non-compliance to requirements, which sometimes may require restarting/revisiting the SMTA process and an increase in the volume of requests during peak seasons. Lack of information is also a source of compliance failures. If the requesting actor does not have adequate knowledge of the phytosanitary regulations and administrative requirements of the receiving countries, shipments may fail to pass through borders, causing major delays until a proper compliant process is conducted.

Because of the memorandum of agreement between IRRI and the Philippine BPI, legal and administrative coordination between importing and exporting parties, phytosanitary testing, and clearance have been streamlined. This minimizes the delays and ensures adequate information and efficient import and exportation process of germplasm, especially in seasons where there are large volumes of shipments. On the other hand, BPI saves significant time and resources, which allows it to reallocate its attention to administration of other crops' phytosanitary regulations.

From 2018 to 2020, most of the germplasm exports were for research and breeding programs and for the International Network for Germplasm Evaluation Research (INGER) combined: 57.8% in 2018, 69.9% in 2019, and 80.5% in 2020 (data on IRRI GHU import and exportation records are in Additional file 2). INGER is a global network among IRRI and NARS for evaluation of advanced pre-variety breeding lines and multi-environment trials.

Results of economic surplus analysis

Tables 3 and 4 summarize the findings of the simulations, including multiple scenarios that depict the most optimistic (maximum), most likely (mode), and most pessimistic (minimum) outcomes. Probability and cumulative density functions and sensitivity analysis are discussed in Additional file 3.

We found that the NPV from the simulated customized deployment of blast R varieties, within a 20-year timeframe (to sufficiently reflect enough deployment cycles of blast R genes), ranged from US$ –94 million to US$ 1.461 billion, with a most probable outcome scenario of US$ 295 million NPV (mean value NPV at US$ 365 million). The BCR ranged from 5 to 73, with a mode of 24 to 1. Our mode is only slightly more modest than the BCR reported by Marasas et al. (2003) of 27 to 1, where their finding referred to ex post assessments of leaf rust R spring wheat varieties in the developing world.

Simulation results showed higher gross benefit streams in the Boro season ranging from a minimum of US$ –7 million, a modal value of US$ 254 million, and a maximum of US$ 1223 million. In the Aman season, benefits started from a minimum of US$ –86 million and reached a maximum value of US$ 314 million, with a most likely return of US$ 54 million. Seasonal differences can be explained by the fact that there was a higher adoption rate of modern varieties in Boro than in Aman.

In terms of benefits contribution from IRRI's GHU, simulation results revealed an NPV range from US$ 290,000 to US$ 62 million, with a modal estimate of US$ 5.9 million (with mean NPV at US$ 12.6 million). While the results appeared small in magnitude, relative to the range in the benefits of the breeding program, the BCR results indicated that return on investments in the GHU were high. The BCR of the GHU NPV minimum and maximum ranged from 3.7 to 3665, with a most likely BCR of 112 to 1. The simulation results were influenced mainly by the rate of benefits gained from yield savings (this parameter incorporated yield, disease incidence and severity, and resistance of effective blast R genes), followed by the discount rate (see Fig. 3).

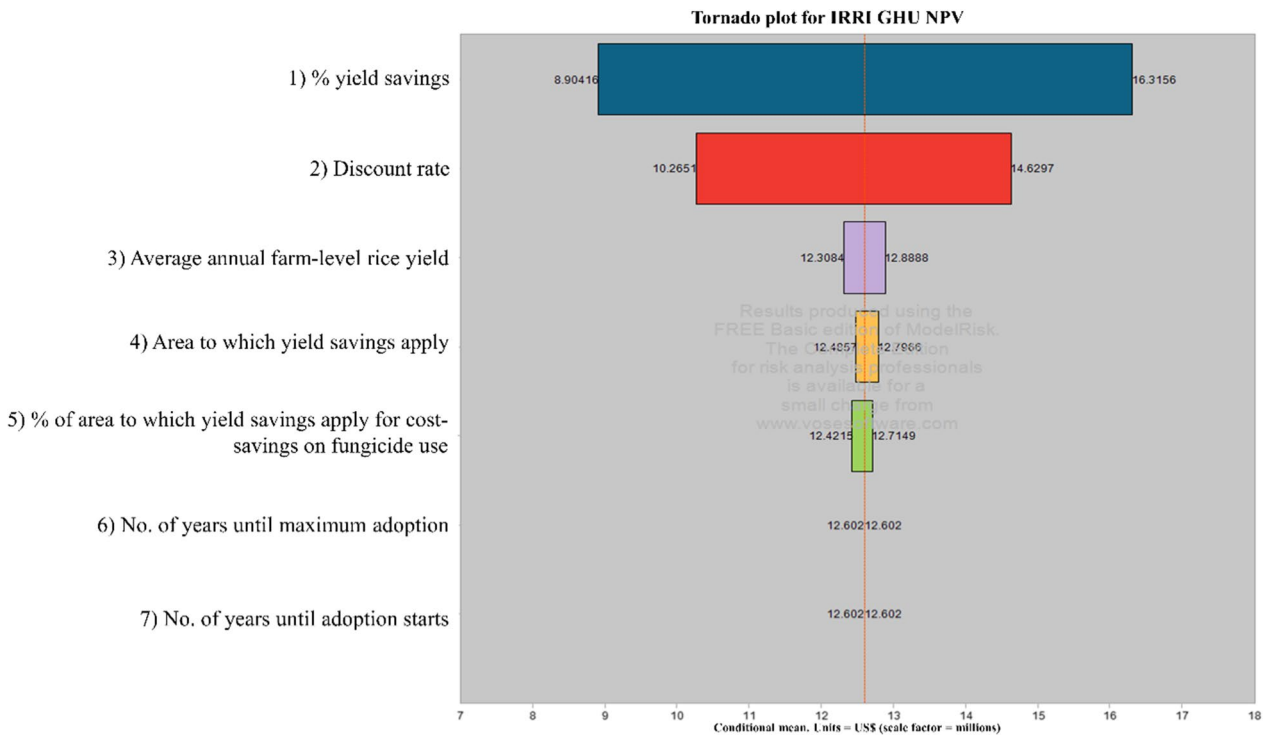

Fig. 3 Sensitivity analysis of parameters that influence the IRRI GHU NPV results

Our ex ante Monte Carlo simulation results showed that, in a most optimistic scenario, Bangladesh's economy can gain as much as US$ 1.461 billion from the customized deployment of blast R varieties, where IRRI GHU's contributes US$ 62 million of the total benefits. In its most likely scenario, benefits were still substantial, with total benefits from breeding blast R varieties at US$ 295 million, of which US$ 5.9 million is associated with IRRI's GHU. Further, the investments in IRRI's GHU can likely bring returns 112 times greater than the costs it spent to facilitate international germplasm access.

Model merits and limitations

This study demonstrates a novel approach for measuring a particular benefit stream of IRRI GHU that has an indirect but necessary role in averting rice blast disease in Bangladesh. This methodology has promising applications for revealing the value contributions of mechanisms and processes that are often difficult to quantify with the existing approaches.

Implementing the study also brought to light key contextual and design considerations. First, applying the time-saving framework only captured the partial economic value of IRRI's GHU. Our study examined one breeding program for one rice disease in one country. The IRRI GHU covers worldwide pests and diseases on rice and supports not just IRG and IRRI breeding programs all over the world, but also facilitates the work of NARS and other international rice research institutions through clean and healthy germplasm materials, disease testing and surveillance.

Second, the design of the valuation approach largely relied on the impact pathway of the mechanism we studied. For instance, the IRRIs GHU also has other work that supports NARS and NPPOs, such as capacity development, plant health matters, and disease monitoring and surveillance. Moreover, the CGIAR GHUs have critical roles in preventing the spread of pests across borders, which is perhaps the most impactful outcome of work by GHUs. However, the impact pathway of prevention of transboundary spread of diseases was not appropriate for our case study, as rice blast has been endemic in Bangladesh since 1980 (Khan et al. 2016). There are also multiple channels through which rice blast have entered Bangladesh, which makes

isolating the links of the IRRI GHU on preventing the arrival of rice blast in Bangladesh significantly difficult.

Conclusions

Our study sheds light on the impact of the CGIAR GHUs by valuing the contributions of the IRRI GHU to the potential impact of breeding blast R rice varieties in Bangladesh. We did this by first looking through which pathways the IRRI GHU contributes to breeding impacts. We then conducted an economic surplus analysis for maintenance research to estimate the potential economic benefits of breeding resistance to blast. We designed our surplus analysis parameter assumptions following the customized deployment strategy and linked the time-saving benefits of the IRRI GHU. We used Monte Carlo simulation to address sparse data challenges and to produce results augmented with risk analysis. We applied a partial equilibrium model to incorporate market-clearing price effects of local and international markets.

Our findings revealed that the IRRI GHU plays an indispensable role in ensuring robust international agricultural research, particularly time-sensitive breakthroughs to address highly adaptive virulent like blast, through safe and efficient access to diverse genetic resources and breeding technology. This is achieved through combined diagnostics expertise and partnerships. Our findings indicated that the IRRI GHU has a modest likely benefits contribution of US$ 5.9 million, a mean of US$ 12.6 million, and a best-case scenario of US$ 62 million, out of the total benefits of blast-resistance breeding of US$ 295 million, US$ 362 million and US$ 1.461 billion, respectively. The IRRI GHU's BCR results indicated that return on investments in the GHU were high. It had a BCR of 112 for the most likely benefits, 305.8 for mean benefits, and 3666 for the best-case scenario estimate.

Our model simulation revealed that the extent of yield savings from resistance and discount rate (time value of money) most influence the resulting NPV of the IRRI GHU. The sensitivity of results to the rate of yield savings, which is contingent on timing of deployment, yield performance, disease vulnerability, effectiveness of varietal resistance, and lifespan of varietal resistance to blast, reinforced the importance of, and economic returns to, investing in robust international research. Putting it another way, slowing down of the international germplasm movement could take a toll on the future economic gains from agricultural research. Despite this, we note that the total benefits estimated by our study for the IRRI GHU are understated. Time saving, while measuring an important contribution, captures partial or incremental benefits at best.

Abbreviations

BCR: Benefit–cost ratio; BPI: Bureau of Plant Industry; BRRI: Bangladesh Rice Research Institute; DV: Differential variety; GHU: Germplasm Health Unit; INGER: International Network for Germplasm Evaluation Research; IRG: International Rice Genebank; IRRI: International Rice Research Institute; MLS: Multilateral system for access and benefit sharing; NARS: National agricultural research system; NPPO: National plant protection organization; NPV: Net present value; QTL: Qualitative trait loci; R: Resistant; SHU: Seed Health Unit; SMTA: Standard Material Transfer Agreement.

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s43170-022-00084-9.

Additional file 1. Construction of scenarios, parameter settings, and values.

Additional file 2. The IRRI GHU germplasm import and export records 2018–2020.

Additional file 3. Simulation results on probability and cumulative density functions, and sensitivity analysis.

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Authors' contributions

The first author (YE) wrote the manuscript, contributed to research conceptualization, designed the methodological approach, gathered data, constructed analytical models and performed the analysis. MS and NJ contributed to research conceptualization, design and editing. MH contributed data on blast disease incidence and severity survey in Bangladesh. LK contributed to research conceptualization and editing. 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

Instruments and the conduct of interviews and validation workshops (including securing prior informed consent) gone through 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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