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The economic contribution of CGIAR germplasm health units
to international agricultural research: the example of
rice blast disease in Bangladesh

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Abstract

This study measures the economic contribution of International Rice Research Institute's (IRRI) Germplasm Health Unit (GHU) to a breeding program that aims to avert yield losses from rice blast disease (*Pyricularia oryzae* Cavara) in Bangladesh. We first conceptualize the general pathways through which SHU contributes to the impact of international agricultural research. Then we use a farm-level panel dataset collected between 2013 to 2016 and data on blast incidence collected from field surveys in 2011 to 2012 to conduct an *ex-ante* economic surplus analysis in a productivity maintenance framework. We then apportion the incremental benefit contributions of the SHU by discounting and applying a time-saving multiplier. To address uncertainties in our estimates, we augment our model with Monte Carlo sampling to simulate distributions of model parameters. Simulating for the most probable outcome, our model estimates about USD 295 million net benefits over a 20-year time frame of continuous blast resistance breeding and deployment. About USD 5.9 million of the net benefits from the development of blast resistant rice varieties in Bangladesh could be attributed to the contribution of the IRRI GHU. The benefit-cost ratio of GHU on this breeding program alone is 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. The study reinforces the important, and often overlooked, role of the SHU in the international scientific partnership that aims to enhance genetic gains in rice through efficient and timely access to clean and healthy germplasm.

Suggested citation

Acknowledgement

Acronyms

BCR	Benefit Cost Ratio
BPI	Bureau of Plant Industry
BRRI	Bangladesh Rice Research Institute
DV	Differential Variety
GHU	Germplasm Health Unit
IITA	International Institute of Tropical Agriculture
INGER	International Network for Germplasm Evaluation Research
IPCC	International Plant Protection Convention
IRG	International Rice Genebank
IRRI	International Rice Research Institute
ITPGRFA	International Treaty for Plant Genetic Resources for Food and Agriculture or The Plant Treaty
JIRCAS	Japan International Research Centre for Agricultural Sciences
LTH	*Lijiangxintuanheigu*
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

Contents

1. Introduction and motivation

The historic success of global agriculture research in crop production and improvement is built on the firm foundation of scientific partnership between CGIAR centers and the national agricultural research systems (NARS). 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. 2016). To sustain this success, crop research and improvement must be a continuous long-term activity.

Crop improvement is an essential pathway for increasing resilience towards climate-induced biotic and abiotic stresses (Galluzzi et al. 2020). Because of that, the CGIAR and their genebanks established international mechanisms to ensure that genetic materials are safely conserved and readily accessible to stakeholders who need them when they need them (Vernooy and Clancy 2017; Johnson et al. 2003; Byerlee and Traxler 1995). This unrestricted flow of plant genetic resources gave rise to agri-food system innovations and productivity growth, which is perhaps one of the most significant impacts of international agriculture research (Johnson, Pachico and Voysest 2003; Vernooy and Clancy 2017; Visser et al. 2000).

The CGIAR has an important role in the implementation of the International Treaty for Plant Genetic Resources for Food and Agriculture (ITPGRFA, the Plant Treaty). CGIAR centers signed the Plant Treaty for which the *ex situ* collections under the CGIAR genebanks are made available and accessible through the CGIAR multilateral system for access and benefit-sharing (MLS).

As important mechanisms to prevent the spread of pest under the MLS, CGIAR centers since the 1970s have established phytosanitary protection measures and protocols to ensure a pest-free international exchange of germplasm. 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 Unit (SHU)[1] as they mostly deal with seed crops.

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

Seed-borne pathogens are often barriers to seed movement. Seed health testing and phytosanitary clearances are mandatory and regulated processes under the International Plant Protection Convention's (IPCC) conventions and respective policies of the national plant protection organizations (NPPOs) (Kumar et al. 2021). Seed-importing countries need assurance that plant germplasm that enters 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.

Further, the increased risk of transboundary transfer of diseases and pests would likely discourage access and benefit sharing of germplasm and, worse, might lead to the tightening of national quarantine and administrative requirements thereby slowing the international exchange of plant genetic resources. For this reason, the IPCC and NPPOs craft standards and policies to prevent these adverse events. The IPPC is the intergovernmental treaty that issues international standards for phytosanitary measures, and NPPOs, which participates as members in the IPPC, commits to these standards by reflecting and enforcing them in their respective country phytosanitary regulatory systems, policies, and procedures.

The GHUs serve as institutional phytosanitary unit of the CGIAR designed to facilitate bioresource transfer for their breeding programs and the genebanks. They do not exist in parallel or asynchronously act with the NPPOs of the countries. Instead, GHUs work in close partnership with NPPOs to help perform their national mandates through awareness-raising, capacity development, and partnership arrangements for phytosanitary regulation. The NPPOs may delegate certain phytosanitary actions with other private and public organizations, like CGIAR GHUs. Examples of these measures are inspections, treatments, surveillance, testing and sampling.

That said, GHUs possess interdisciplinary capabilities, not just for diagnostics, seed health testing, facilitation of regulatory compliance, and capacity building but also cover on-demand needs from NPPOs and CGIAR breeding programs on plant health matters and disease monitoring and surveillance (Kumar et al. 2021).

By providing crucial safeguards for the safe and efficient transfer of germplasms, GHUs are instrumental for effective and efficient public goods delivery of international crop improvement and genetic resources programs. As rapid-cycle breeding has been a promising strategy pathway to achieving positive impacts on farmers' welfare, which hinge on reliable germplasm exchange mechanisms, barriers to germplasm access can spell significant opportunity cost (Cobb et al. 2019;

Hellin et al. 2020; Cobb, Biswas, and Platten 2019). However, the contributions of GHUs to ensuring that this does not happen is perceived as one of the CGIAR's unknown success stories. To date, there is no existing evidence that documents and attributes the economic contributions of GHU's to impacts achieved through the global scientific partnership of the CGIAR.

2. Background and research objectives

2.1 Study objectives

We explore the case of the IRRI GHU to demonstrate the economic contribution of GHUs to the impacts of rice breeding programs. We focus on the rice blast disease threats because of its economic importance for all rice-producing countries worldwide and it being a threat to global food security (Wang and Valent 2017; Asibi, Chai, and Coulter 2019). Particularly, we investigated the case of Bangladesh being one of the countries highly threatened by the disease and because the preponderance of data is enough to meet our analytical demands.

We do this by first conceptualizing the pathways through which IRRI GHU contributes to international breeding strategies on development and deployment of blast resistant varieties. Second, we estimate the economic benefits of IRRI's breeding program that applies a combination of rapid-breeding cycles with modern plant breeding technologies to averting yield losses. We then apportion the net benefits of GHU, through a time-saving model, in the development of improved rice varieties. By and large, this case study illuminates the significance of IRRI GHU's contribution to breeding programs developing countries.

2.2 Rice blast in Bangladesh

Rice (*Oryza sativa* L.*)* is an essential food crop for most developing countries and a staple food for almost half of the global population (Fairhurst et al. 2002; Ricepedia.org). Bangladesh is among these and has a long tradition of rice cultivation. The agriculture sector, which is predominantly rice-based, employs about 47.5% of its total workforce and contributes to 19.3% of its GDP (Shelley, Takahashi-nosaka, and Kano-nakata 2016). The country faces the challenge of sustaining its surplus rice production as it experiences multiple drivers of rising population growth, land-use conversion, and climate change (Kabir et al. 2015; Shelley, Takahashi-nosaka, and Kano-nakata 2016). Consequently, increasing rice productivity still rings synonymous with staple food security in the nation.

On top of that, Bangladesh confronts a severe threat from rice blast disease, with a potential to upturn its historical productivity gains. Rice blast is a serious fungal disease caused by *Pyricularia oryzae*

Cavara (sexual morph *Magnaporthe oryzae*). Blast disease can infect the rice plants' aboveground tissues and all its organs at all developmental stages, which could cause total crop failure (Asibi, Chai, and Coulter 2019; Le, Arie, and Teraoka 2010; Ou 1985). Blast outbreaks are recurrent and known for their destructiveness across ecosystems and seasons (Khan et al. 2017; Bonman, 1992; Marchetti et al. 1976; Mekwatanakarn et al. 1999; Ou 1985).

In Bangladesh, 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 (Mohammad Ashik Iqbal Khan et al. 2014; Hossain, Ali, and Hossain 2017). These include popular varieties like BRRI dhan 29 and BRRi dhan 28 (Hossain et al. 2017). Since the 1980s, Bangladesh has struggled with several blast disease outbreaks (Ahmed et al. 1985; Shahjahan, 1994). Further, climate change has brought early drizzling and temperature and humidity changes, making environmental conditions more favorable for blast pathogens to thrive and infect early maturing varieties.

2.3 Modern approaches in rice blast-resistance breeding

Success in the face of constantly evolving natural and human-made challenges will depend on sustained advances in the rate of genetic gains by research partners. Currently, the most promising advances in increasing the rate of genetic gain is a combination of rapid-breeding cycles with modern plant breeding technologies (Cobb et al. 2019). To tackle challenges, strategic global partnerships will allow scientists to use genebank accessions and other germplasm collections for rapid gene discovery and gene deployment.

Breeding resistance to blast disease in rice varieties is an environmentally friendly and economical solution compared to alternatives such as use of pesticides (Khan et al. 2016; Meng et al. 2019). However, conventional breeding for the development of rice blast resistant varieties in Bangladesh is very challenging. Many new rice varieties have shown high levels of blast susceptibility, and those that are blast-resistant often lose their resistance within 3 to 5 years (Meng et al. 2020; Ning et al. 2020; N. Xiao et al. 2017; W. Xiao et al. 2019; Ahmed et al. 1985; Shahjahan 1994). 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 replacement of resistant varieties that can tolerate the emergent pathogen strains that overcome resistance. In Bangladesh, Khan et al. (2016) found 331 representative blast isolates across various ecosystems, classified into 267 blast races. Such diversity indicates a high likelihood that a blast pathogen will break the resistance of blast resistant (R) varieties.

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 (IRRI expert, interview by the author, 02 December 2020; Dossa et al. 2015). 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 (Ning, Yunyu, and Aihong 2020; W. Xiao et al. 2019).

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 adapt to single-gene virulence. But these are not possible through conventional methods for public rice breeding and without access to international agricultural research system and diverse genetic resources. This is because the time it takes to develop even a single-gene resistant variety is lengthy and cannot catch-up with the speed of local pathogen evolution. There is a high likelihood that a resistant variety developed through conventional means would be ineffective by the time it is cultivated in farmers' fields (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).

3. Data and Methods

3.1 Analytical approach

There is a void in terms of documented evidence of GHU impacts in the progress of international agricultural research. Existing valuation studies has focused on measuring breeding program benefits, agrobiodiversity conservation benefits, or MLS arrangements where the contribution of GHUs is subsumed. The methodological challenge is how to unbundle GHUs benefits.

We combine analytical approaches to measure the contribution of GHUs with the benefits arising from the breeding programs. Drucker and Caracciolo (2013) provides a useful entry-point for disentangling GHUs benefits from the MLS and the Plant Treaty (see Table 1). Using a total economic value framework, they map out the various benefit streams of the Plant Treaty, the MLS, and related mechanisms. As indicated in Table 1, the CGIAR GHUs, as part of the MLS service

mechanism, indirectly contribute to the monetary and non-monetary benefits. This link is possible by reducing transaction costs, which results in greater germplasm exchange that ultimately benefit the farmers.

Our valuation approach measures the indirect value of the GHUs to the impact of CGIAR breeding programs, using IRRI and rice blast in Bangladesh as an example. We combined several the following frameworks to conduct an ex ante valuation of GHU benefits: (i) impact pathway analysis; (ii) time-saving benefits of GHUs on breeding programs (Brennan and Martin 2007; Lenaerts, de Mey, and Demont 2018); (iii) rice blast yield savings model; (iv) general economic surplus approach adapted to maintenance research (Marasas, Smale, and Singh 2003); (iv) IRRI Global Rice Model to incorporate the price effects.

3.2 Impact pathway analysis

Impact pathway analysis enables us to trace the causal links of IRRI GHU to breeding program activities, outcomes, and impacts derived from adopting improved crop varieties. Douthwaite et al. (2003) first introduced its use in international agricultural research.

The focus of the analysis is to determine how GHUs enable sharing germplasm materials and how it contributes to achieving better impacts for the farmers. Since the facilitated exchanges are our study's primary variable for measuring GHUs' link and contribution to impacts, we consider both the germplasm collections from the genebank and breeding programs. This is useful in tracing indirect benefits and contributions of interventions in complex systems.

Impact pathway analysis helps estimate time-saved for breeding for the scenarios considered, which feeds into the economic surplus model for productivity maintenance (Marasas, Smale, and Singh 2003). For this approach, we use key informant interviews with breeders, staff of IRRI GHU, IRRI, Bangladesh Rice Research Institute (BRRI) and Bureau of Plant Industry (BPI), the NPPO of the Philippines responsible for enforcing plant quarantine legislation (Table 2). We complement this with desk analysis of secondary literature and documents from breeding programs and GHU.

3.3 Estimating IRRI GHU benefits through contributions to speeding up breeding

Our core theoretical approach for valuing the benefits of GHUs is through estimating their additionality to breeding impacts through the time-saving framework. Brennan (1989) and Brennan and Martin (2007) appear to have been the first to demonstrate 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. Figure 2 illustrates the fundamentals of the framework. Benefits are attained by shortening the time period of the breeding process, resulting in early time to release and adopt varieties. This study also adopts the framework's assumption that the research benefits from the customized deployment with or without the facilitation of IRRI GHU would be the same, with the only difference that benefits from IRRI GHU arises from an earlier release and earlier adoption of the new varieties through safe and efficient germplasm transfer.

In measuring the counterfactual for which to base the time-saving benefit of the GHUs, we estimate the difference in the time of breeding process by exploring a scenario where the international exchange of germplasms happens without the GHUs. The main difference between the two scenarios is the time of the release and adoption of the varieties. 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 in equation 1 below – where $\Delta\beta_{Time-saving}$ is the time-saving incremental benefits that can be linked with the GHUs. This is 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 $(1 + i)^r$.

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

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

3.4 Estimating the yield savings benefits breeding programs on preventing yield loss

To estimate the potential economic benefits of blast resistance breeding, we adapt 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 represented by a leftward or upward shift in the supply curve as compared to an outward shift in productivity (see Figure 3) (Collin 1995).

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.

The surplus framework depicts S0 as the supply with maintenance without enhancement research, S2 as the supply without maintenance or enhancement research, and S1 as the supply with maintenance and enhancement research. Our study refers to using S0 as our 'with the yield savings scenario from breeding' and S2 as our 'without scenario' where yield losses from blast persist.

Performing this analysis involves comparing with and without scenarios, where the without scenario is a situation that research benefits on yield maintenance are absent. The economic surplus thus generated is shown as the shaded area in Figure 1.

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

To perform this method, it 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
- C = costs incurred by breeding program and IRRI GHU

We explain the derivation of these parameters in the succeeding sections.

Additional to yield benefit, planting resistant rice varieties would also enable farmers to do away with need to apply Tricyclazole group fungicides in their field. Durable resistant varieties may offer better protection than pesticides as they pose health and environmental hazards and their effectiveness can be limited given the existing inadequate knowledge on proper use of fungicides for blast (Rahaman, Islam, and Jahan 2018; Asibi, Chai, and Coulter 2019).

We also incorporate the corresponding cost-savings benefits accrued from avoiding the need to use fungicides in farmers field to control rice blast in both seasons. The cost-savings benefit is computed using a product of three variables, namely, average cost of fungicide per hectare (ha), proportion of rice area applicable for cost-savings, and area to which yield savings apply.

Average cost represents the expenditure of farmers for treating blast in their field, converted into USD per ha. The area applicable for cost-savings is a product of two parameters. First is the proportion of farmers that use pesticides, sourced from the same farmer household dataset of RMS. Second parameter is the proportion of pesticide users that use fungicide to treat rice blast. Since the second variable is not available from the RMS dataset, we refer to available statistics available from literature in Bangladesh. We, however, note that the corresponding health and environmental benefits of preventing the use of fungicide is not considered in this valuation framework.

For modelling price effects, we use the IRRI Global Rice Model (IGRM) to estimate the partial equilibrium effects of the changes 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 (see Figure 4) (Hoang and Meyers 2015). Here the Bangladesh country model is linked with other rice economies through net trade, which analyzes its independence with other countries. This model has been used to analyze and estimate the effects of various policies and programs.

For cost parameters, we use two variables derived from the breeding program and GHU of IRRI to estimate the net present value of breeding and the net incremental benefits accrued by GHUs. Details of the costs are discussed in section 3.5. Lastly, we compute for benefit-cost ratios.

3.5 Stochastic simulation

Economic surplus modeling studies have increasingly applied stochastic simulation methods to take advantage of the probability of distribution values (Kergna et al. 2017; O. Ahmed and Sallam 2020; Horna et al. 2008). We apply the basic version of ModelRisk application of the Vos Software

(www.vosesoftware.com), which is an Microsoft Excel-based plug-in that allows for simulation and risk analysis using the Monte Carlo method. Monte Carlo simulations perform a repeated random sampling of the distributions and generate summary statistics, density functions, cumulative distributions, and other statistics for each summary measure.

Risk analysis provides more robust results as compared with the use of deterministic values. It also allows for better sensitivity analysis of the results from data parameters (Kergna et al. 2017; Hareau, Mills, and Norton 2006; Horna et al. 2008). We use 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 triangular distribution, using 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.

3.6 Data

We use three main datasets and key informant interviews to set up our economic surplus model. First, we use the Rice Monitoring Survey (RMS) funded by the Bill and Melinda Gates Foundation. The RMS project administered a farm-level survey in Bangladesh for crop years 2013, 2014, 2015, and 2016. 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 3). RMS 2013 and 2016 are the panel dataset, while RMS 2014 and 2015 are independent and cross-section data.

We also use blast incidence and yield loss data from Hossain et al. (2017). This dataset surveyed disease incidence and severity covering cropping years 2010-2011 Boro season and 2011 Aman for various districts representing ten agroecological zones (AEZs) (Table 4). The survey technicians performed a zigzag sampling pattern for 27 field locations in each AEZ and each season, following Savary, Elazegui, and Teng (1996). The survey collected information during the rice crop's post-flowering stage to observe the panicle blast.

The survey used the following formula for measuring disease incidence (Hossain, Ali, and Hossain 2017):

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

Disease severity was assessed based on 0-9 scale symptoms using the IRRI Standard Evaluation System (2002).

Third, we access 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, respectively.

We also conducted primary data gathering through interviews with 14 individuals who work or undertake research in IRRI GHU and BPI, blast resistance, breeding programs in IRRI and BRRI, and other IRRI scientists for additional context and technical clarifications. We did 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 is redacted and only accessible to the first author.

3.7 Construction of scenarios, parameter setting and values

We set up a model to represent the customized deployment breeding approach for this study. The aim is to introduce the blast R gene every five years. Pathogen monitoring and hotspot surveillance system inform the customized development of the resistant gene to overcome the highly virulent and adaptive blast pathogen population structure in Bangladesh. This model simulates four deployment cycles that produce and disseminate at least two resistant varieties in each season over a 20-year timeframe.

Figure 1 describes the strategy aimed at the fast-paced and customized deployment of resistant genes, through gene rotation or mixture in a single genetic background, targeted for evolving or dynamic pathogen populations (Dossa et al. 2015). This strategy pyramids genes and promotes shuffling of resistance mechanisms displayed in the field to prevent rapid pathogen adaptation. This approach's critical component is the systematic monitoring of blast hotspots that incorporates (ibid). It also includes assessing effective R-genes in specific target areas and understanding the blast pathogen population's evolutionary potential.

Developments made in rapid generation advance and marker-assisted selection (MAS) and the international network for germplasm sharing enable this strategy. IRRI institutionalized a unified breeding system, where data-driven processes, use of genotypic information and coordinated

workstreams are its central feature (IRRI expert, interview by the author, 10 February 2021; Cobb et al. 2019). This breeding system integrates MAS with modern breeding approaches to leverage traditional genetic diversity from the International Rice Genebank (IRG) to achieve better reliability and efficiency in breeding outcomes.

The international system for germplasm exchange supported by IRRI GHU makes these technologies and germplasm materials accessible to partner NARS. Here the elite donors produced by upstream pre-breeding processes and QTL deployment, i.e., where resistant traits are identified and deployed, are used in forward breeding and in line-augmentation to increase frequency of new genes (Cobb et al. 2019). For more information refer to Cobb et al. (2019).

Through this model, breeding programs can rapidly and efficiently use the resistant genes and other useful traits like grain quality and stress-tolerance. There are long-term efficiency benefits of this open-ended system. Especially for the case of blast, where population structure may change rapidly, breeding programs can forecast in blast hotspots, and use elite donors containing resistant genes and other traits, to periodically reshuffle resistance mechanisms that are targeted to specific blast population structure, without sacrificing the potential for genetic gain (IRRI expert, interview by the author, 02 December 2020).

The transformation of the breeding processes 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 six years.

Adoption rate and adoption curve

The adoption rate is expressed in percent of the total area planted with modern varieties. We use the area planted with modern varieties from the RMS household survey as the maximum possible adoption rate for resistant varieties. To determine this ceiling, we estimate the mean area in Aman and Boro seasons using the pooled RMS dataset from 2013 to 2016. We use a maximum possible adoption rate of 25.6% in Aman and 48.6% in Boro.

We formulate the adoption curve or distribution to reflect the adoption trend of the modeled scenario. We draw from the study of Kabir et al. (2015), which uses secondary data from government-owned statistics and research institutes like BRRI to model the adoption lag of varieties from 1970 to 2015. Their model indicates that it takes 16 years on average, from the time of release, to attain the maximum adoption rate. We assume a triangular distribution to estimate the yearly incremental

increase in adoption. The yearly increase is calculated by dividing the maximum adoption rate for both seasons by 16 years.

Based on expert interviews, the timeframe for breeding or introgression of the resistant gene to popular varieties can be realistically achieved within 3–4 years, through advancements in breeding approaches such as marker-assisted selection and rapid generation acceleration (IRRI experts, interview by the author, December 2020). With an additional time of 2–3 years for the time it takes to release the varieties, deployment and the first adoption of the varieties can be expected within six years. We assume each deployment can start its first adoption every six years.

Since varietal resistance to blast eventually breaks down, we have incorporated this factor in our adoption curve. We do this by setting the lifespan of the yield benefits generated by variety adoption. With the application of pyramiding and customized deployment of resistant genes a resistant variety could last in farmers' fields as-long-as seven to 10 years. We assume a seven-year lifespan of benefits accrued from yield savings for each blast resistant variety adopted by farmers. Figure 5 and Figure 6 illustrate the adoption curve over 20 years.

We calculate a maximum adoption for the modelled scenario of 11.2% for Aman and 21.3% for Boro from the above. Refer to Figure 5 and Figure 6 for the illustration. In calculating the benefits, we consider discounting by adding six years before starting the first deployment.

Yield savings

Yield savings is a product of three variables (i) incidence of severe panicle blast (%) per division per season, (ii) % equivalent yield loss per disease incidence, and (iii) resistance of effective blast R genes.

We generate the first variable using two datasets, the blast incidence dataset (Hossain, Ali, and Hossain 2017) and the RMS dataset 2013-2016. We merged the two datasets by AEZ by district, by season, ecosystem, and variety type. From the merged output, we derived the incidence of panicle blast severity for division and season.

We then calculate the incidence of panicle blast severity by weighting the blast disease incidence, estimated using equation 3 by Hossain, Ali, and Hossain (2017) with the disease severity scale (Table 5). The disease severity scale uses a score of 1 to 9, which draw from the IRRI Standard Evaluation System, where N1-N9 are the number of panicles with a score of 1–9 (IRRI 2002). Using this formula, we weighted the disease incidence with a score of 1, 3, 5, 6, 9 with 10%, 20%, 40%, 70%,

and 100%, respectively. After checking for goodness-of-fit of the dataset's full distribution, we assumed a normal distribution and generated the mean and standard deviation per division per season to input in the Monte Carlo simulation (Annex 1).

$$Panicle\ Blast\ Severity\ \frac{(10\ x\ N1)\ (20\ x\ N3)\ (40\ x\ N5)(70\ x\ N7)(100x\ N9)}{Total\ no.\ of\ panicles} \qquad (4)$$

The second variable, % equivalent yield loss per disease incidence, is available from the literature. Several studies produced around the 1990s or earlier have found a significant linear relationship between panicle blast incidence and yield loss. A study in India found that susceptible varieties incur yield loss of 98% of the total % neck blast incidence (Padmanabhan, 1965 as cited in IRRI, 1990). To illustrate, a 100% incidence of severe panicle blast is equivalent to 98% yield loss and a 50% incidence would result in 49% yield loss. For our model, we used a triangular distribution for the statistic % equivalent yield loss per disease incidence with a min, mode, and max of 46%, 69%, 98%, respectively (Table 6).

The third variable is needed to estimate the % yield savings from blast-resistant varieties. This estimate derives from data on resistance or protection from blast R genes. Since new blast-resistant varieties are still in the process of national yield trials and release, there are still no data available on actual yield advantage or yield savings from the new blast resistance gene.

This study uses the data generated by (Khan et al. 2016) and an unpublished study by Hossain (n.d.). The study of Khan et al. (2016) tested 23 differential varieties (DV), which came from IRRI, each harboring single blast resistance gene and a control variety *Lijiangxintuanheigu (LTH)* (which is 100% susceptible to blast pathogens) to 331 blast isolates that are collected across Bangladesh. Hossain (n.d.), on the other hand, tested 26 DV targeting 23 resistant genes with 139 isolates collected in 8 AEZs in the country (AEZ1, AEZ2, AEZ9, AEZ11, AEZ13, AEZ19, AEZ23, and AEZ28).

Both studies found four genes to possess high resistance frequencies from tested blast isolates, namely, Pish, Pi9, Pita-2, and Pita. We use the data on R genes' resistance frequency to estimate for triangular distribution with a min of 79%, max of 93% and a mode of 87% (Table 7). We multiply these three variables to produce potential % yield savings by division, by season (Table 8).

Cost-savings on fungicide use

This is an additional benefit added to the benefit streams of the economic surplus analysis. We use the average cost estimates of Rashid et al. (2019) which amounts to 4,448 taka per ha[2] or 53.38[3] USD per ha for both Aman and Boro seasons. The variable proportion of area applicable for cost-savings is computed using the percentage of farmers using pesticide input, 28.6%, and the assumption on the proportion of pesticide users that use fungicide for treating blast, 23% from Quddus and Kropp (2020) (Table 9).

These variables are multiplied to the area to which yield savings apply to derive the potential cost-saving benefit from avoiding the use of fungicides for controlling rice blast in the field. This is simulated using Monte Carlo using normal distribution of the parameters.

Area to which yield savings apply

Area to which savings apply represents the area planted with modern varieties. We use the pooled RMS 2013-2016 dataset to estimate for this parameter per division per season (Table 10). We assume a normal distribution where we plug-in the mean and standard deviation for the simulation.

Average farm yield by season

This parameter is estimated using the pooled RMS 2013-2016 dataset (Table 11). After checking for goodness-of-fit on the dataset, we assumed a normal distribution for the simulation (see Annex 1).

Discount rate

Studies on rates of return to crop improvement research by publicly-funded programs have generally used 5% as the minimum social discount rate (Brennan and Martin 2007; Raitzer et al. 2015). Several international agricultural research institutions such as the ACIAR use the 5% standard discount rate for impact assessments. A higher discount rate would reduce the present value of future costs and increase the current value of previous costs and benefits. To test the robustness of results, we assume a triangular distribution of discount rate, 5%, 10% and 15% for a min, mode and max, respectively.

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[2] 4,448 taka per ha is derived from an estimate of costs for application of Tricyclazole group fungicides of average 600 taka/bigha (33 decimal).

[3] Conversion rate 1 taka = 0.012 USD

Time-saving benefits of IRRI GHU

We estimate the time-saving benefits, we used IRRI GHU records in 2019 and 2020, and supplemented these with key informant interviews to derive a triangular distribution for the time-saving parameters. We use exportation records as this represents most of the flow of germplasm and there are significantly fewer volumes of importation compared with exportation. Exportation records also has consistent measurement across years. From the dataset, we filtered for transactions that require a Standard Material Transfer Agreement (SMTA). This indicates that the transfer is for exportation and for purposes of scientific research and breeding.

We derive a triangular distribution of the time it takes to facilitate germplasm exportation request. the turnover ranges from as fast as just 6 days to the longest recorded time of 421 days, with the most likely duration of 48 days. The range estimates for minimum and mode, except for maximum, elicited from interviews are close, i.e., seven days minimum, usual duration of 1.5 months and maximum of 3.5 months. We use the measurements from the records and proportioned these in a year by dividing by 365 days. We then derive a min, mode and max of 0.02, 0.13 and 1.16, respectively.

Quantifying the time-saving advantage is difficult. While different interviews affirmed that SHU contributes to safer and much efficient germplasm exchange, as discussed in section 4.1, we were not able to probe for quantified estimates of time-saving advantages. Based on the knowledge where SHU provides better exchange mechanism and arrangements, we assume a triangular distribution time-saving ratio of 0.75, 1 and 1.25. The final parameter for use in the model is the product of the two measurements.

Price

We used the IGRM model to project the nominal farmgate price of rice from 2020–2039. This considers the market clearing effect of % change in the supply of rice per year in each region simulated in Bangladesh. The % change in the supply of rice is derived by calculating the effect of the average annual farm-level yield loss (in tons) from planting blast resistant rice per year per region to corresponding regional supply of rice.

Cost

We account for two cost streams, including both the breeding program and GHU of IRRI.

The information on breeding costs comes from the IRRI project data and interviews. We estimate an upper bound yearly cost of USD 1.5 million for six years for 2-4 varieties before deployment. The

estimate considers expenses related to establishing and running pathotype and biotype surveillance system, a pyramiding of blast R genes/QTLs into at least two popular rice varieties in both seasons, capacity development of NARS partners on scientific breeding, pest surveillance, and resistance evaluation targeting. We further add a cost of USD 170,000 for two years after release of the variety to catalyze dissemination and promote the new variety. Since the scenario constructed has four deployment cycles, we repeat these costs throughout the simulated timeline.

For the costs of IRRI GHU facilitation of germplasm exchanges, we used the SHU import and export records for germplasm exchange. We used the data on yearly average volume (in terms of seed lots) of export and importation of germplasms facilitated by SMTA for BRRI from 2016 to 2020. From this data, we derived a triangular distribution for the number of seed lots imported and exported between IRRI and BRRI. We used a costing table from IRRI GHU to monetize the volume of germplasm shipments or events. This approximation also captures other international transfers between IRRI and BRRI that might not be relevant for the modeled scenario. Teasing this out is challenging as cooperation can involve exchanging pre-breeding materials, elite lines, multi-environment trials, and pathogen samples. To make the estimates more representative, we assume arbitrarily that 25% of the cost would represent the costs associated with the modeled scenario. We use a min, mode and max distribution of USD 6,6145 USD 20,828 USD 34,093 respectively. We note that this cost estimate is also an upper bound.

4. Results and discussion

4.1 Analysis of IRRI GHU's impact contribution pathway

The IRRI GHU is one of the 11 GHUs of the CGIAR. As early as the 1960s, IRRI has been performing its seed health testing for seed certification. In 1982, IRRI and the Philippines' BPI the country's NPPO, agreed to establish and authorize the SHU to conduct major rice seed health testing phytosanitary certification and post-entry clearance. Issuance of the import clearance and export certification is performed under the mandate of the BPI (Kulkarni 2019). IRRI GHU became the designated gateway for all rice seeds going in and out from IRRI in 2002, and the coverage expanded to non-seed biological materials and soil samples in 2005 (ibid).

Like other GHUs, the IRRI GHU is co-located with the IRG and breeding programs, which mainly drive the demand for SHU's operations. 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*, nematodes, blotter test;

and bacterial testing; field or greenhouse inspection for newly introduced germplasms, wild rice varieties; seed treatment and packaging. But SHU's role is not just about phytosanitary actions. Critical to its function includes generating the appropriate SMTA, maintaining a network and relationship with country users and regulatory organizations, provisioning of phytosanitary and regulatory information and generation and capacity building of NARS partners on seed health, seed movement and transboundary pest and disease.

The SMTA is a mandatory mechanism for countries that intend to provide and access germplasm material under the multilateral system. Since 2004, the participating countries to the Plant Treaty agreed to participate in the MLS in creating an international collection of genetic resources for 64 crops and forages, listed in the Plant Treaty under (Galluzzi et al. 2016). 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.

From 2018 to 2020, IRRI GHU has been facilitating international germplasm transfers from genebanks and breeding programs (Figure 7). The SHU assisted 535 events in 2018, 447 in 2019 and 224 in 2020. There is a notable decrease across these years and the steep decline in 2020 is mainly due to the restrictions caused by COVID-19 pandemic and lockdowns. In all these years, majority of these events were from breeding programs, 409, 353 and 173 events, respectively.

These events where largely comprised by germplasm exports. From 2018 to 2020, the yearly seed samples processed for export were 28,871, 38,577, and 8,956, respectively. The majority of these exports are for the breeding programs and the International Network for Germplasm Evaluation Research (INGER), 57.8% in 2018, 69.9% in 2019, and 80.5% in 2020 (Figure 8). INGER is a global network among IRRI and NARS for sharing and evaluation of advanced pre-variety breeding lines. Seed samples processed for importing germplasms are in much lower frequency at 289 in 2018, 259 in 2019, and 5 in 2020 (Figure 9).

Table 12 shows that there is higher rate of samples rejected by the SHU for exportation and importation for genebank than for breeding research purposes. Same records show that 5.28%, 6.61%, and 2.8% of exports from genebank were rejected from 2018 to 2020, respectively, and 2.74% of imports in 2019 only. With regards to import and export requests from breeding and INGER, rejection rate from exports is smaller at 1.08% in 2018, 0.36% in 2019, and 2.8% in 2020. Imports are only

0.36% in 2019 only. There were no registered rejections for imports in 2018 and 2020 from both sources.

Figure 10 shows IRRI GHU's contribution pathway to genebanks and breeding programs. Because of the nature of GHUs operations, the IRRI GHU's causal link to the farmers is indirect. But their work is instrumental in enabling the partnership of international research programs and NARS partners to succeed. Through the SHU's activities, NARS partners have safer and more timely access to the diverse germplasm held in the IRRI genebank and breeding programs. Particularly to study's context, the primary causal links of IRRI GHU's phytosanitary actions is not on preventing the introduction of rice blast in the country as it is already endemic but on enabling efficient science partnership for improving the resistance of rice to blast.

Accessing useful pre-breeding, elite or advanced pre-variety lines enables public breeding programs to benefit from the more diverse genetic resources from the genebank and IRRI. NARS partners' public programs benefit from state-of-the-art breeding approaches and technologies, and valuable plant genetic resources. This includes sharing and transfer of technology and capacity requirements. NARS partners can access wild rice, pre-breeding materials, elite lines or parental lines for forward breeding, and advanced lines for direct yield trials and release (Figure 11 and Figure 12). On the other hand, IRRI breeding programs can access germplasm from NARS partners, such as BRRI, in their programs.

Apart from giving NARS partners better access to genetic resources and breeding materials that benefit from advanced technologies and approaches, IRRI GHU also has facilitated rice blast research. International research partnership on blast resistance dates from the mid-2000s with the "Differential System for Blast Resistance for a Stable Rice Production Environment." This scientific effort involves the Japan International Research Centre for Agricultural Sciences (JIRCAS), IRRI and Africa Rice Centre, and NARS partners such as the BRRI.

The network studied the pathogenicity of blast isolates from different countries to identify the most effective genes. The DVs from IRRI play an essential role. International and national partners got access to 25 DVs that represent monogenic lines for 23 blast resistant genes. By subjecting these DVs with the blast isolates collected from Bangladesh and comparing them with a susceptible control *LTH*, BRRI was able to identify the most promising genes Pish, Pi9, Pita-2, and Pita across ecosystems in the country (Ashik and Khan 2020; Khan et al. 2016). Experts from BRRI estimate that this have significantly saved time and resources through access to the developed differential varieties, which

could take about 5–6 years for each to develop (BRRI experts, interview by the author, 12 December 2020).

NARS partners, like BRRI, also benefit from participation from INGER. It is a global network between IRRI and its NARS partners. Participating organizations nominate and test advanced pre-variety breeding lines, facilitating their access to diverse genetic resources. This mechanism enables IRRI and partners to do multi-environment trials in targeted local environments to see their performance. Doing this without INGER would incur NARS partner considerable resources and time. The IRRI GHU supports these international evaluations as part of its import and exportation phytosanitary and regulatory compliance.

Importantly, IRRI GHU's serve as a mechanism to prevent the unintended transboundary spread of exotic disease and pests. Since the risk pathway is also through the genebanks and breeding programs, their respective operations are immediately affected. It is important to note that CGIAR GHUs are not the only institutions that perform the plant quarantine and regulation. In countries where there is 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.

The memorandum of agreement between IRRI and the Philippines' BPI has been beneficial in that aspect. In this arrangement, IRRI GHU performs all legal, administrative coordination between importing and exporting parties and phytosanitary testing and clearance. The BPI then makes the final assessment of the results and issues the permit. IRRI GHU also maintains a 12-hectare post-entry quarantine area for the initial planting of imported rice seeds, the Genetic Resource Center nursery area for wild races, and the Phytotron for transgenic materials. It makes crop health monitoring, treatment, and isolation of the imported germplasm more efficient and safer.

Coordination of the legal and administrative requirements is an essential source of delay. The delays can increase due to non-compliance to requirements, which sometimes may require restarting/revisiting of the SMTA process and increase in the volume of requests during peak seasons. Lack of information is also a source of misses in compliance. Without adequate knowledge of the phytosanitary regulations of receiving countries, shipments may fail to pass through borders causing major delays until a proper compliant process is conducted.

Because of the partnership arrangement, IRRI benefits by minimizing the delays, adequate information and ensure an efficient and safe import and exportation process given the large annual

germplasm exchange volume. It also waives some of IRRI's regulatory fees for imports except for the phytosanitary certification fee. On the other hand, BPI saves significant time and resources that benefit the administration of other crops' phytosanitary regulations. IRRI GHU also provides periodical training to the staff of BPI concerning rice seed quarantine and regulations.

The CGIAR GHUs are also making efforts to institutionalize a Green Pass System, a certification scheme for germplasm exchange. Overall, there are several entry-points where IRRI GHU contributes to better facilitation of germplasm exchange. Apart from its processes, the SHU also put in place networks and institutional arrangements that create value that support both CGIAR and NARS partners.

4.2 Results of economic surplus analysis

Table 13, Table 14, Figure 13 and Figure 14 summarize the simulation findings. The economic model simulates multiple scenarios, namely, most optimistic (maximum), most likely (mode), most pessimistic (minimum), and average of all scenarios (mean).

We estimate that the net present value (NPV) from the simulated customized deployment of blast resistance varieties, within a 20-year timeframe, ranges between USD -94 million to USD 1.461 billion, with a most probable outcome scenario of USD 295 million NPV. The mean estimate of NPV is at USD 365 million with a standard deviation of USD 169 million. The benefit-cost ratio (BCR), respectively, ranges between -5 and 73, with a mode of 24. Comparing this ratio with that of Marasas et al. (2003), and Byerlee and Traxler (1995), with an BCR of 41 and more than 50, respectively, indicates more modest but well supported estimates of our study.

Figure 15 indicates that the discount rate is the main parameter, followed by % area for which cost-savings apply and % yield savings (this parameter incorporates yield, disease incidence and severity and resistance of effective blast R genes). These parameters influence the model's results for the breeding program.

In terms of seasonality, simulation results show higher gross benefit streams in the Boro season ranging from a minimum of USD -7 million, a modal value of USD 254 million, and a maximum of USD 1,223 million. In Aman season, benefits start from a minimum of USD -86 million to a maximum value of USD 314 million, with a most likely return of USD 54 million. This finding could be explained by the fact that there is a higher adoption rate of modern varieties in Boro than in Aman.

In terms of benefits contribution from IRRI's SHU, simulation results reveal an NPV range of USD 290,000 to USD 62 million, with a modal estimate of USD 5.9 million. Mean NPV registers at USD 12.6 million with a standard deviation of USD 8.4 million. While the results may appear small relative to the range in the benefits of the breeding program, the BCR results indicate that return on investments in the GHU are high. The BCR of the GHU NPV min and max ranges from 3.7 to 3,665, with a most likely BCR of 112. The mean BCR is at 305.8 with a standard deviation of 283. The simulation results are influenced mainly by the rate of benefits gained from yield savings, followed by the discount rate (see Figure 16).

Results of Monte Carlo simulations that account for risk are shown in the probability density functions of Figure 13 and Figure 14. The density function of the breeding program illustrates that about 95% of the comparable values are within the positive range and equal or below the amount of USD 680.08 million. On the other hand, IRRI GHU has positive values within 95% of its density under USD 29.25 million. Results of the cumulative distribution function for their respective NPV show similar results at 95% of USD 680.08 million and USD 29.25 million, respectively (Figure 19 and Figure 20).

Our *ex-ante* Monte Carlo simulation results show that in a most optimistic scenario, Bangladesh's economy can gain as much as USD 1.461 billion from the customized deployment of blast resistant varieties, where IRRI GHU's contributes USD 62 million of the total benefits. In its most likely scenario, benefits are still substantial with total benefits from breeding blast R varieties at USD 295 million, of which USD 5.9 million is associated with IRRI's GHU. Further, the investments in IRRI's GHU can likely bring returns 112 times.

4.3 Reflections on the merits and limitations of the approach

This study demonstrates a novel approach for measuring a particular benefit stream of IRRI GHU that have 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.

This study also identifies limitations that brought to light key contextual and design considerations. First, applying the time-saving framework does not capture the total but only the partial economic value of IRRI's GHU. Our study only looks at one breeding program for one rice disease in one country. IRRI GHU supports not just IRG and IRRI's breeding programs all over the world, but also

facilitates the work of NARS and other international rice research institutions. IRRI GHU covers worldwide pests and diseases on rice.

Second, the design of the valuation approach largely relies on the impact pathway of the studied mechanisms. For instance, IRRI's GHU also has other work which supports NARS and NPPOs, such as capacity development, plant health matters, and disease monitoring and surveillance. Moreover, CGIAR GHUs have critical role for preventing the spread of pests across borders, which is perhaps the most impactful outcome of work by GHUs.

But the impact pathway of prevention of transboundary spread of diseases is 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 IRRI GHU on preventing the arrival of rice blast in Bangladesh significantly difficult.

Still, we find the time-saving framework appropriate to the context of the case study for evaluating the benefits of IRRI GHU. The work to be done on rice blast in Bangladesh is not to prevent the introduction of the disease in the country anymore but to eliminate the losses from rice blast through crop improvement. Also, through this study, we bring to light a routine but crucial role GHU's that is often taken for granted.

5. Conclusions

Our study sheds light on the impact of CGIAR GHUs by valuing the IRRI GHU contributions of IRRI's SHU to the potential impact of breeding blast-resistant rice varieties in Bangladesh. We did this by first looking through which pathways 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 IRRI's SHU. We used Monte Carlo simulation to address sparse data challenges and to produce results augmented with risk analysis.

Findings reveal that IRRI's SHU plays an indispensable role in ensuring robust international agricultural research through safe and efficient access to diverse genetic resources and breeding technology. This is achieved through combined diagnostics expertise and partnerships. Our findings indicate that IRRI's GHU has a modest likely benefits contribution of USD 5.9 million, a mean of USD 12.6 million, and a best-case scenario of USD 62 million, out of the total benefits of blast resistance breeding of USD 295 million, USD 362 million and USD 1.461 billion, respectively. While

the economic contribution of IRRI's GHU to the breeding program is relatively not large, the GHU's BCR results indicate that return on investments in the GHU are high. It has a BCR of 112 for the most likely benefits, 305.8 for mean benefits, and 3,666 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 IRRI's SHU. 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, reinforces the importance of and economic returns to investing in robust international research. Putting it other way around, slowing down of 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 IRRI GHU are understated. Time saving, while measuring an important contribution, captures partial or incremental benefits at best.

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7. Tables

Table 1. Mapping of the total economic value of the Treaty, MLS and its mechanisms

Type of benefit	Benefits generated by the Treaty as a whole	Benefits generated under the MLS	Mechanisms through which benefits are shared	Type of economic value
Monetary	Payments; Activities undertaken by third parties within the funding strategy framework	Generation of monetary benefits paid to the benefit-sharing fund	Projects funded by BSF of the Plant Treaty Activities of Crop Trust and Svalbard	Use and non-use values
Indirect monetary and non-monetary (broadly defined)	Food, livelihood security improvement, econ & env sust. dev't (not just arising from SMTA)	Reduced transaction costs through facilitated access to Annex 1 crops under SMTA; Food, livelihood security improvement, econ & env sust. dev't (arising from SMTA)	Access at reduced transaction costs resulting automatically in higher levels of germplasm exchange and use	Use and non-use values, options
Non-monetary benefits (MLS, narrowly defined)		Exchange of information to and transfer of tech and capdev (arising from SMTA materials	Benefit-sharing mechanisms/activities under the Plant Treaty	Use values

Source: Drucker and Caracciolo 2013. The economic value of PGR for food and agriculture, Chapter 1 p.20 (in Moeller and Stannard 2013)

Table 2. List of key informant interviews

No.	Institution	Department/discipline/ area of work	Focus of interview
1	IRRI	Seed Health Unit	Background and operations of the SHU
2	IRRI	Research and Regulatory Compliance	History and governance of the phytosanitary compliance Partnership with the Philippines BPI
3	IRRI	Material Transfer Agreements Controller	SMTA requirements and process, Import and exportation protocols, data management
4	IRRI	Routine Seed Health Testing	Phytosanitary clearance and processes and protocols for seed health tests and treatments
5	IRRI	Plant Pathology and Host Plant Resistance	Knowledge on blast resistance and breeding strategies, disease profile
6	IRRI	Plant Pathology and Host Plant Resistance	Marker-assisted breeding and pyramiding, resistance genes and disease profile
7	IRRI	Breeding Innovations	Advanced approaches to breeding, breeding resistance
8	IRRI	Research Support	INGER, breeding activities and history of work
9	IRRI	Epidemiology	History of IRRI's work on disease and insect pest management
10	BRRI	Plant Pathology	History of research on blast resistance breeding and IRRI partnership Research on rice blast disease
11	BRRI	Plant Pathology	Research and challenges of rice blast disease
12	BRRI	Plant Pathology	Research and challenges of rice blast disease
13	BRRI	Plant Pathology	Research and challenges of rice blast disease
14	BPI	Plant Quarantine Services	IRRI and BPI partnership and benefits

Source: Authors

Table 3. Distribution of sample households in Bangladesh, RMS 2013-2016 cropping years

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	1,490	150	1,500	150	1,500	149	1,490

VIL – number of villages
HHLD – number of households
Source: RMS dataset

Table 4. Locations of blast incidence survey

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

Source: Hossain, Ali, and Hossain (2017)

Table 5. Panicle blast severity (%) in modern varieties by division, by season

Division	Aman		Boro	
	Mean	SD	Mean	SD
Barisal	17.67	4.84	6.14	0.57
Chittagong	6.31	2.42	6.48	2.95
Dhaka	7.41	2.06	17.06	9.21
Khulna	1.67	0.65	7.96	2.04
Rajshahi	14.20	0.00	13.07	0.00
Rangpur	17.08	6.06	17.02	7.80

*note that values are Monte Carlo simulated
Source: Authors

Table 6. % yield loss of modern varieties by division, by season

Division	Aman		Boro	
	Mean	SD	Mean	SD
Barisal	10.63	2.91	3.69	0.34
Chittagong	3.80	1.46	3.90	1.77
Dhaka	4.46	1.24	10.27	5.54
Khulna	1.00	0.39	4.79	1.23
Rajshahi	8.54	0.00	7.87	0.00
Rangpur	10.28	3.65	10.24	4.69

*note that values are Monte Carlo simulated
Source: Authors

Table 7. Resistance frequencies of blast R genes identified in Bangladesh

IRBLs/ Differential Varieties	Target R Genes	Resistance (%)	Source
IRBLsh-B	Pish	88.81	Khan et al. (2020)
IRBLsh-B	Pish	90.00	Hossain (Unpublished manuscript, no date)
IRBL9-W	Pi9	87.65	Khan et al. (2020)
IRBL9-W	Pi9	92.00	Hossain (Unpublished manuscript, no date)
IRBL ta2-Re	Pita2	92.54	Khan et al. (2020)
IRBL ta2-Re	Pita2	87.00	Hossain (Unpublished manuscript, no date)
IRBLta2-Pi[LT]	Pita2	90.44	Khan et al. (2020)
IRBLta2-Pi[LT]	Pita2	87.00	Hossain (Unpublished manuscript, no date)
IRBLta-K1	Pita	79.25	Khan et al. (2020)
IRBLta-K1	Pita	88.00	Hossain (Unpublished manuscript, no date)

Source: Extracted by authors from Khan et al. (2020) and Hossain (Unpublished manuscript, no date)

Table 8. % yield savings in modern varieties by division by season

Division	Aman		Boro	
	Mean	SD	Mean	SD
Barisal	8.41	2.30	2.92	0.27
Chittagong	3.00	1.15	3.09	1.40
Dhaka	3.53	0.98	8.13	4.39
Khulna	0.79	0.31	3.79	0.97
Rajshahi	6.76	0.00	6.23	0.00
Rangpur	8.13	2.88	8.10	3.72

*note that values are Monte Carlo simulated
Source: Authors

Table 9. Parameters for deriving cost-savings on fungicide use

	Mean percentage	Standard deviation	Source
Proportion of farmers that use pesticide inputs (including fungicide, molluscicide, rodenticide, etc.) in rice area planted with modern varieties	28.60%	45.20%	RMS 2016 database
Proportion of pesticide users that use fungicide	23.00%	No data	Quddus & Kropp 2020

Source: RMS 2016 dataset and Quddus and Kropp (2020)

Table 10. Total area planted (000 ha) with modern varieties by division by season

Division	Aman		Boro	
	Mean	SD	Mean	SD
Barisal	216.26	39.14	67.04	53.27
Chittagong	224.43	110.24	364.88	205.97
Dhaka	183.17	109.68	843.68	631.34
Khulna	295.17	103.46	295.54	123.40
Rajshahi	170.16	90.30	332.07	281.73
Rangpur	151.73	76.21	360.44	320.94

*note that values are Monte Carlo simulated
Source: Author

Table 11. Average annual farm-level yield (kg/ha) in modern varieties by division by season

Division	Aman		Boro	
	Mean	SD	Mean	SD
Barisal	3,992	1,401	5,516	1,844
Chittagong	3,735	1,400	4,666	1,751
Dhaka	5,017	1,836	6,119	1,286
Khulna	4,791	1,326	6,094	1,390
Rajshahi	4,965	1,390	6,501	1,219
Rangpur	3,634	1,678	6,736	1,489

*note that values are Monte Carlo simulated
Source: Authors

Table 12. Percent of rejected samples from genebank and breeding, by export and import, by year

Institution	2018		2019		2020	
	Import	Export	Import	Export	Import	Export
Genebank		5.28	2.74	6.61	0	2.80
Breeding and INGER		1.08	0.36	0.36	0	0.21

Source: IRRI GHU annual reports

Table 13. Summary statistics of simulation results for customized deployment breeding program

	Gross Benefits (in Million USD)		Net Present Value (in Million USD)	BCR
	Aman	**Boro**		
Maximum	314	1,223	1,461	73
Minimum	-86	-7	-94	-5
Mode	54	254	295	24
Mean	62	315	362	26
Standard deviation	41	135	169	9

Source: Authors

Table 14. Summary statistics of simulation results for IRRI GHU time-saving benefits

	NPV (in Million USD)	BCR
Maximum	62	3,666
Minimum	0.29	3.8
Mode	5.9	112
Mean	12.6	305.8
Standard deviation	8.5	283

Source: Authors

8. Figures
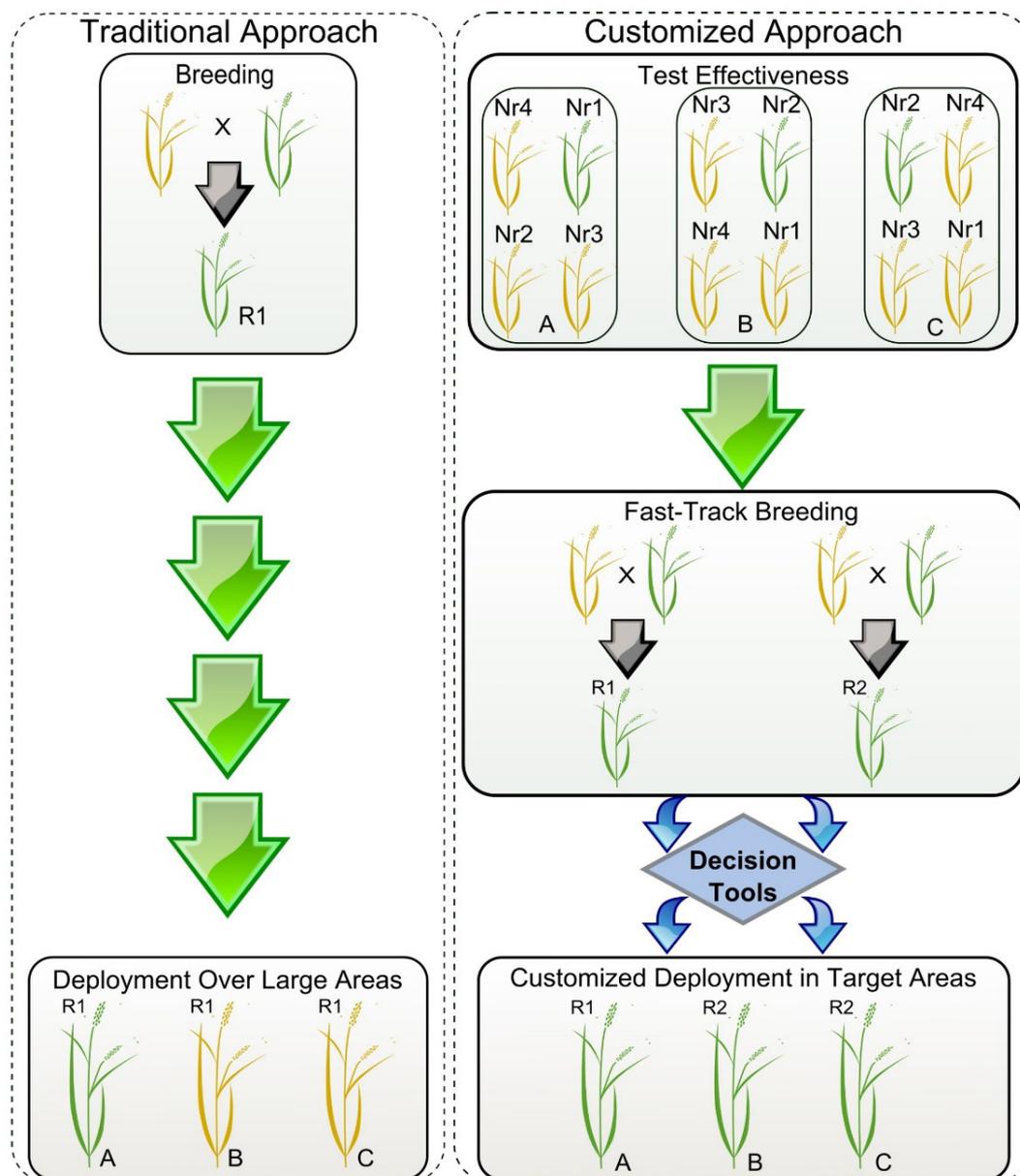
Figure 1. Simplified scheme showing the deployment of resistant varieties using traditional versus customized approaches. R1 and R2 represent resistant elite varieties carrying hypothetical genes 1 and 2. Yellow and green plants represent susceptible and resistant phenotypes, respectively. Locations A, B, and C represent cropping regions that do not share boundaries. Nr1, Nr2, Nr3, and Nr4 are near-isogenic lines (NILs) for each of the available resistance genes 1, 2, 3, and 4. During traditional deployment, variety R1 is bred and released in large areas but is effective only in particular locations. During customized deployment, the effectiveness of the resistance genes and pathogen population structures are monitored using disease hotspots, seasonal collections, and pathogenicity tests done in a confined setting. Using a decision tool, breeding programs can rapidly customize the elite varieties to be deployed in targeted locations based on variety profiles. (Source: Dossa et al. 2015)
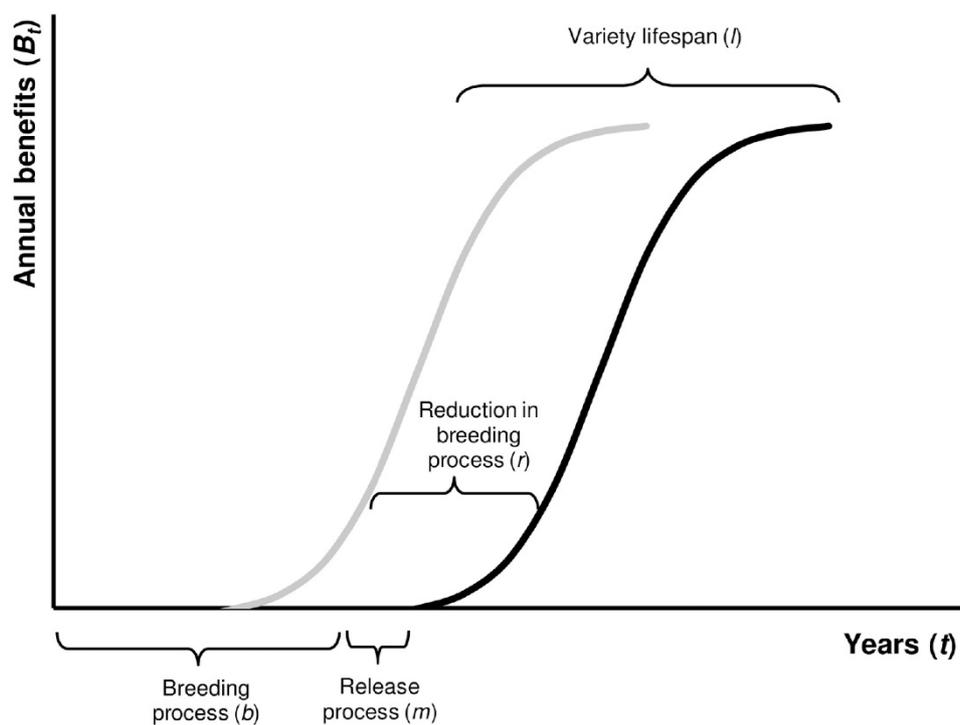
Figure 2. Time dimension of a breeding and illustration of time-saving on breeding process (Source: Lenaerts, de Mey, and Demont 2018)
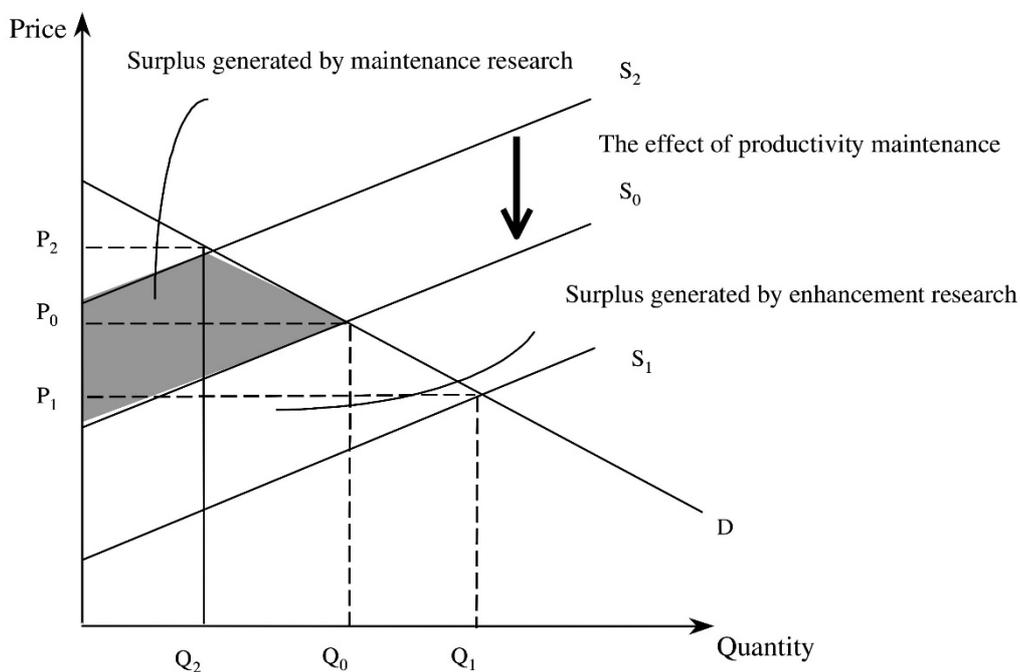
Figure 3. Economic surplus framework for maintenance research (Source: Marasas et al. 2003)
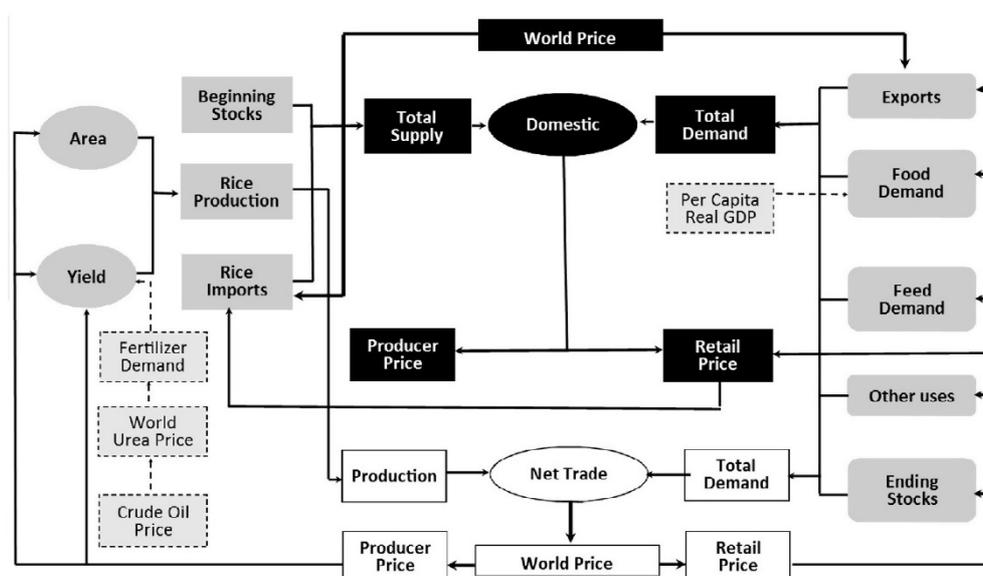
Figure 4. IGRM model structure (Source: Hoang and Meyers 2015*)*
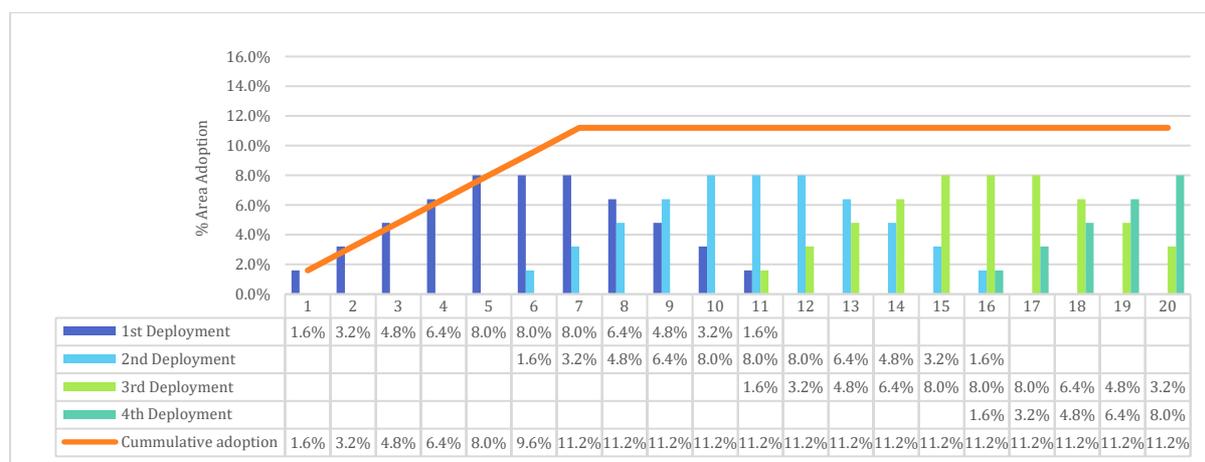
Figure 5. Adoption curve in Aman season (Source: Authors)

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
■ 1st Deployment	3.0%	6.1%	9.1%	12.2%	15.2%	15.2%	15.2%	12.2%	9.1%	6.1%	3.0%									
■ 2nd Deployment						3.0%	6.1%	9.1%	12.2%	15.2%	15.2%	15.2%	12.2%	9.1%	6.1%	3.0%				
■ 3rd Deployment											3.0%	6.1%	9.1%	12.2%	15.2%	15.2%	15.2%	12.2%	9.1%	6.1%
■ 4th Deployment																3.0%	6.1%	9.1%	12.2%	15.2%
▬ Cummulative adoption	3.0%	6.1%	9.1%	12.2%	15.2%	18.2%	21.3%	21.3%	21.3%	21.3%	21.3%	21.3%	21.3%	21.3%	21.3%	21.3%	21.3%	21.3%	21.3%	21.3%
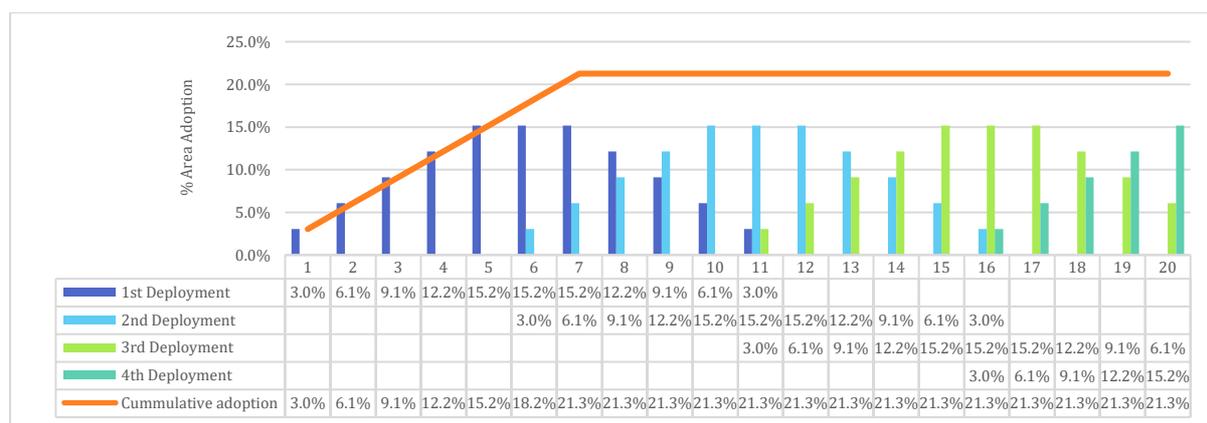
Figure 6. Adoption curve Boro Season (Source: Authors)
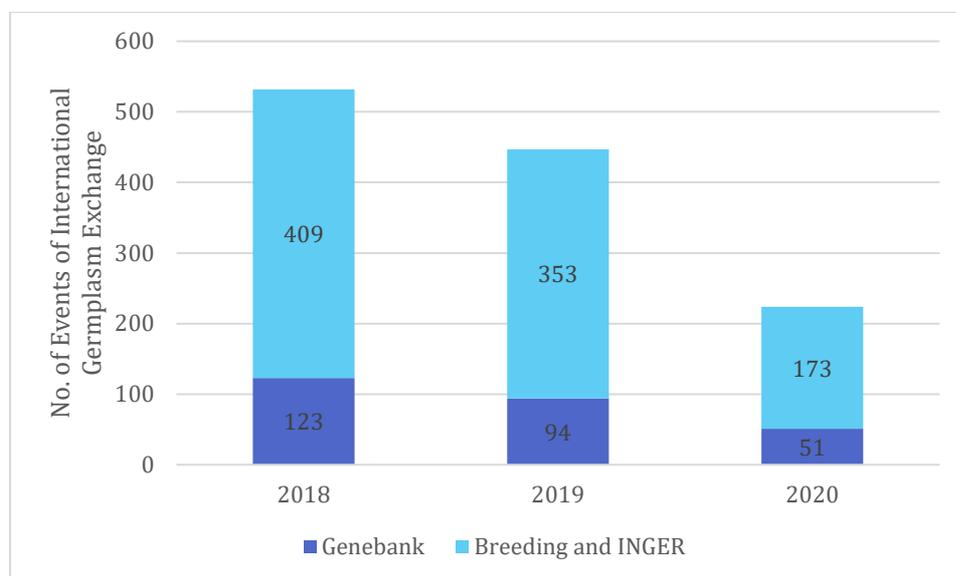
Figure 7. Number of events of international germplasm transfers by institution, by year (Source: IRRI GHU Annual Reports)
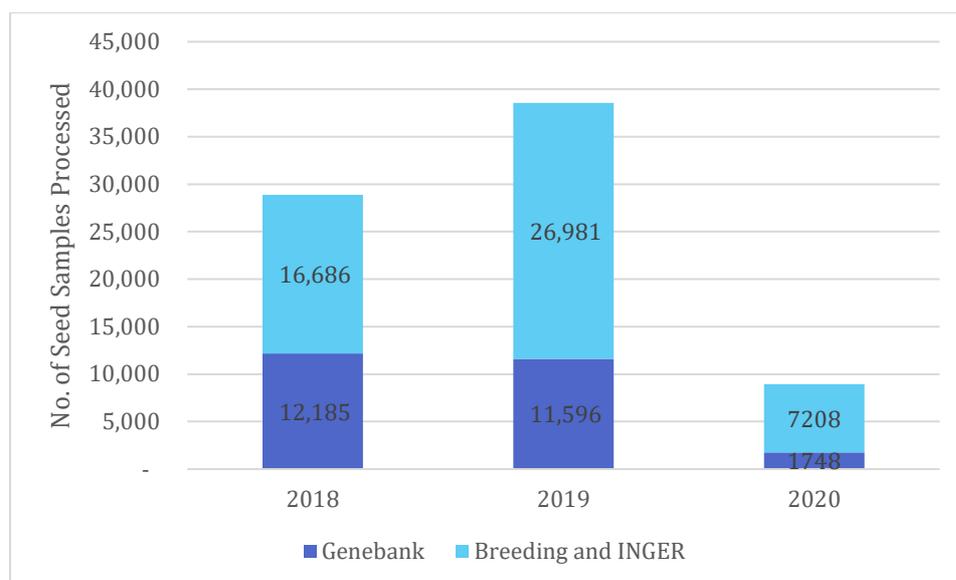
Figure 8. No. of seed samples processed for export by institution, by year (Source: IRRI GHU Annual Reports)
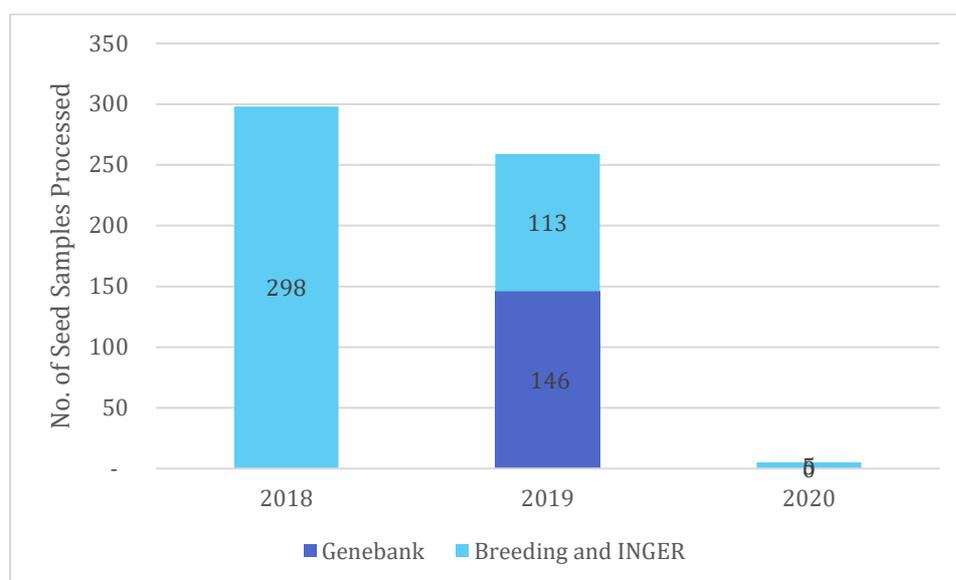
Figure 9. Number of seed samples processed for import by institution, by year (Source: IRRI GHU Annual Reports)
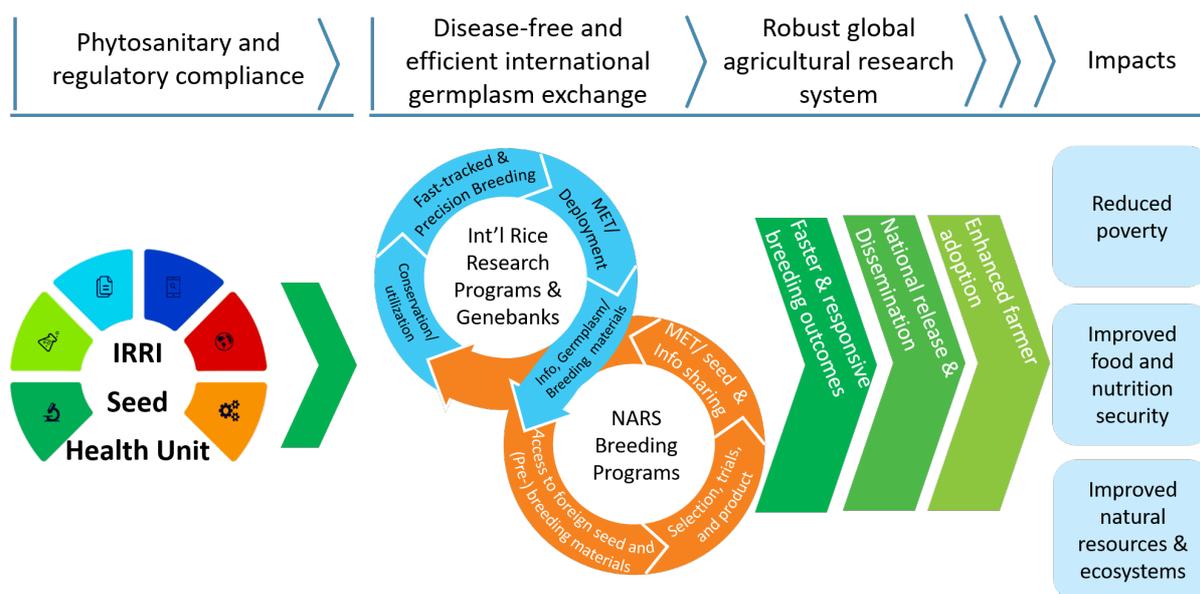
Figure 10. IRRI Seed Health Unit's contribution pathway to breeding impacts (Source: Authors)
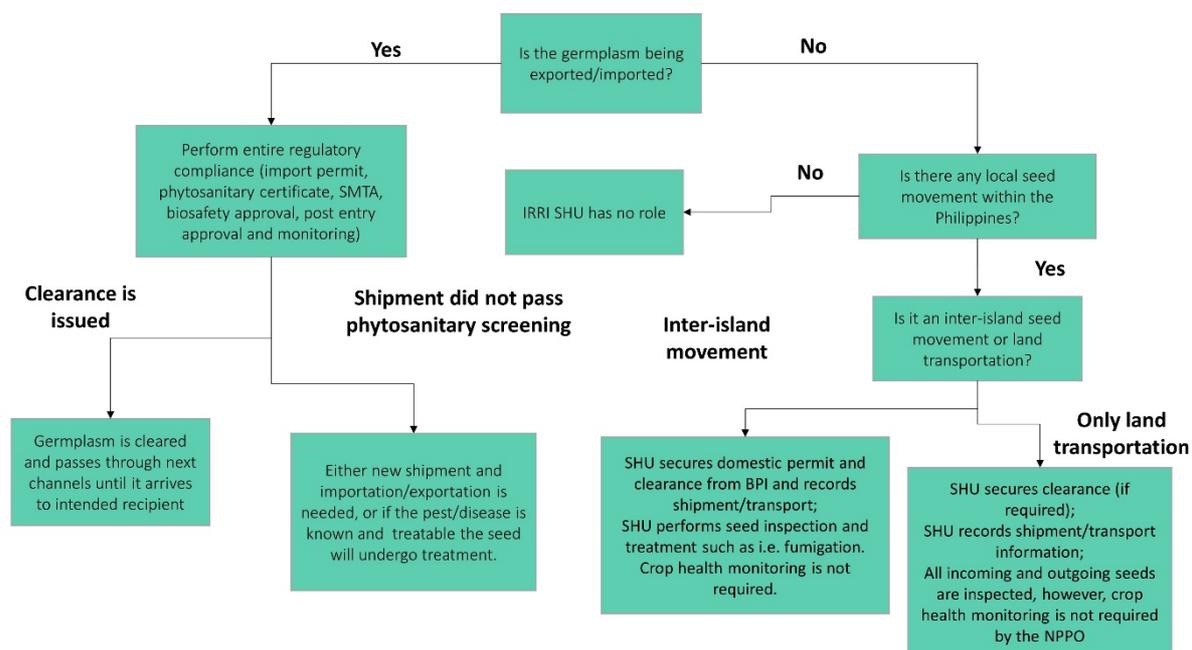
Figure 11. Decision Tree for IRRI GHU (Source: interviews; Kulkarni 2019)
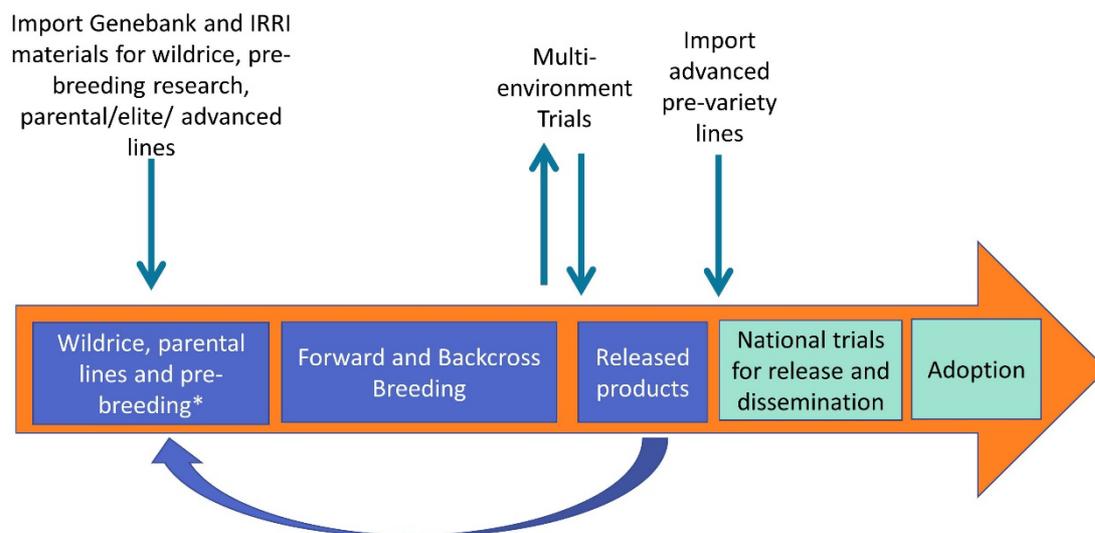
Figure 12. Entry-points for IRRI GHU germplasm exchange (Source: interviews)
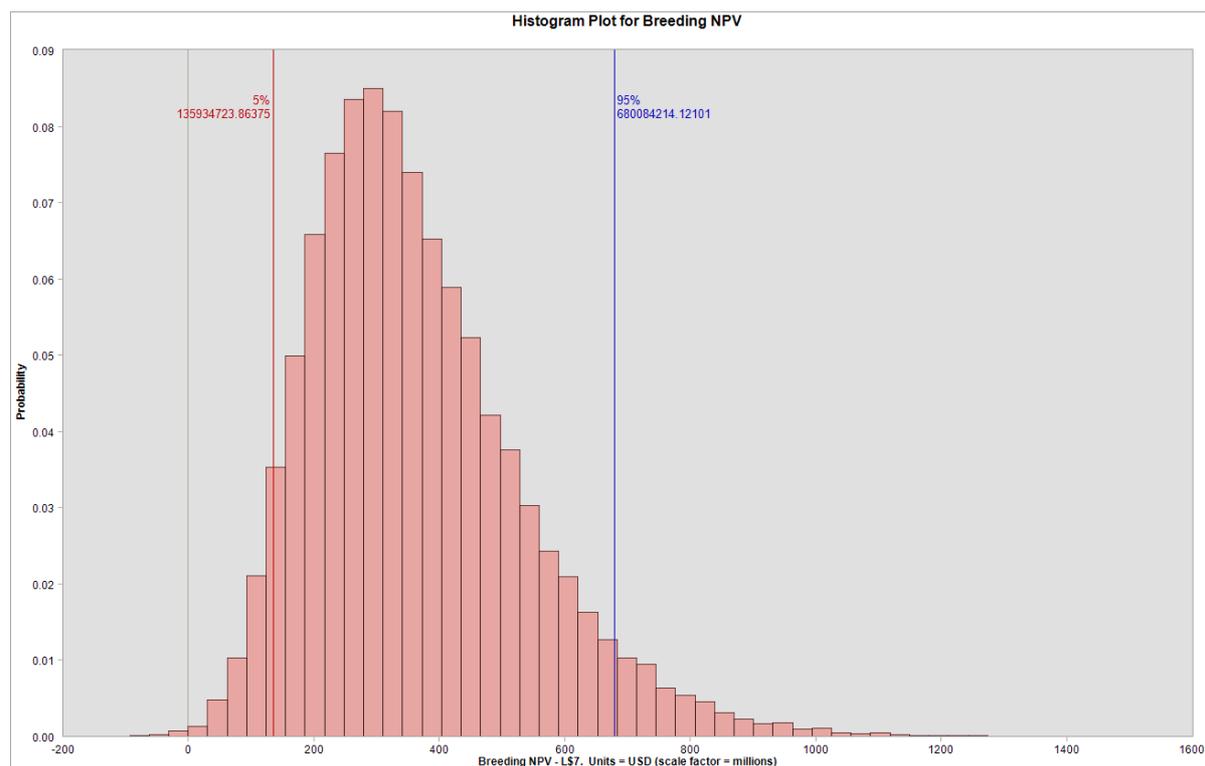
Figure 13. Probability distribution of Breeding NPV (Source: Authors)
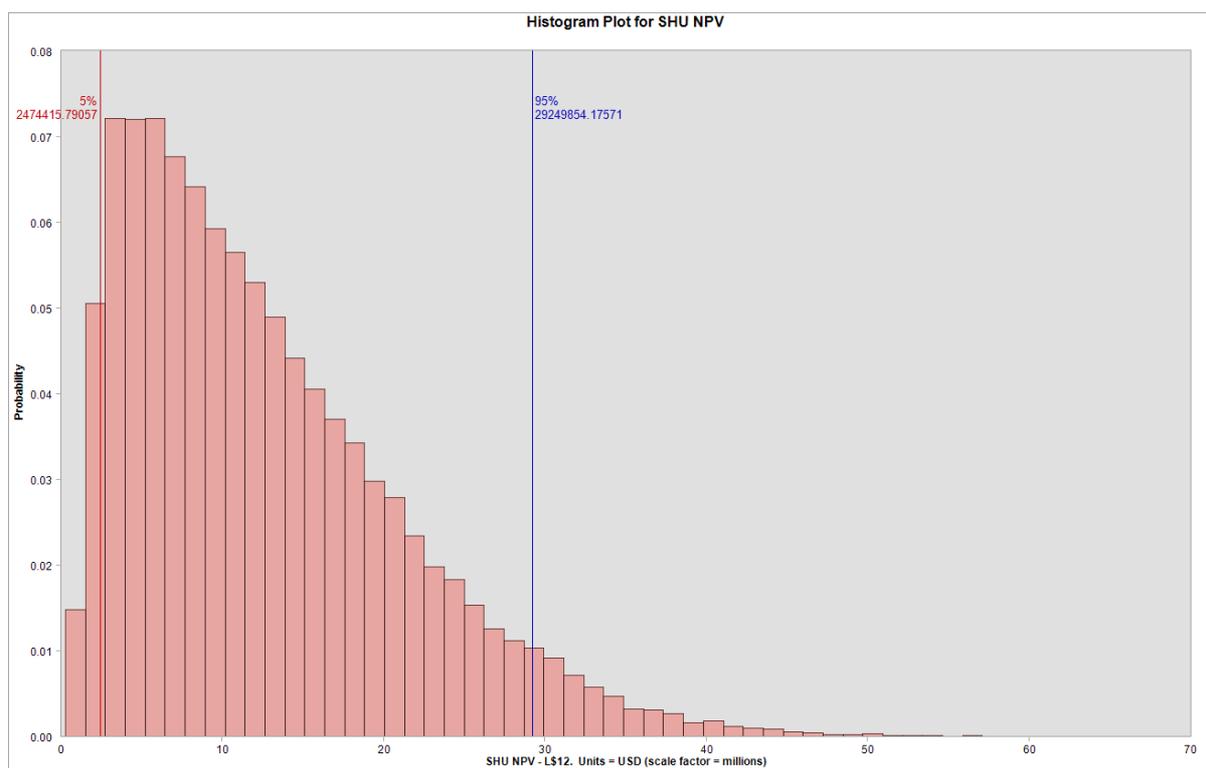
Figure 14. Probability distribution of IRRI GHU NPV (Source: Authors)
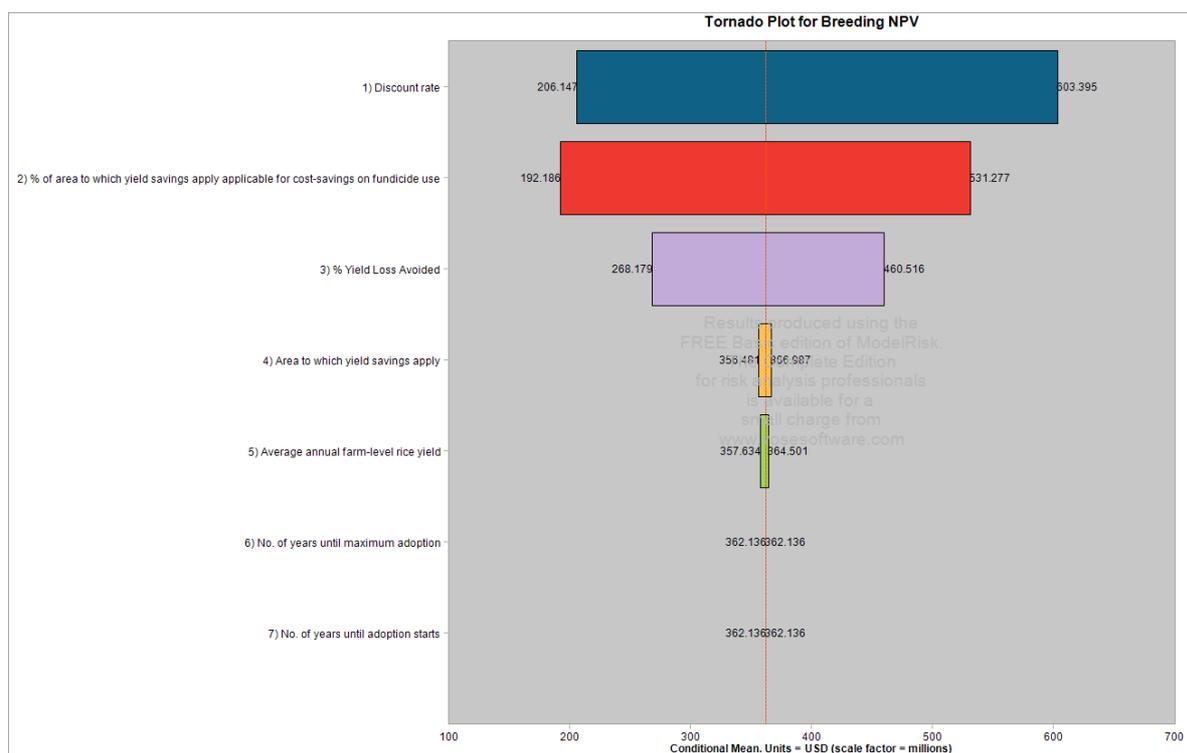
Figure 15. Sensitivity analysis of parameters that influence Breeding NPV results (Source: Authors)
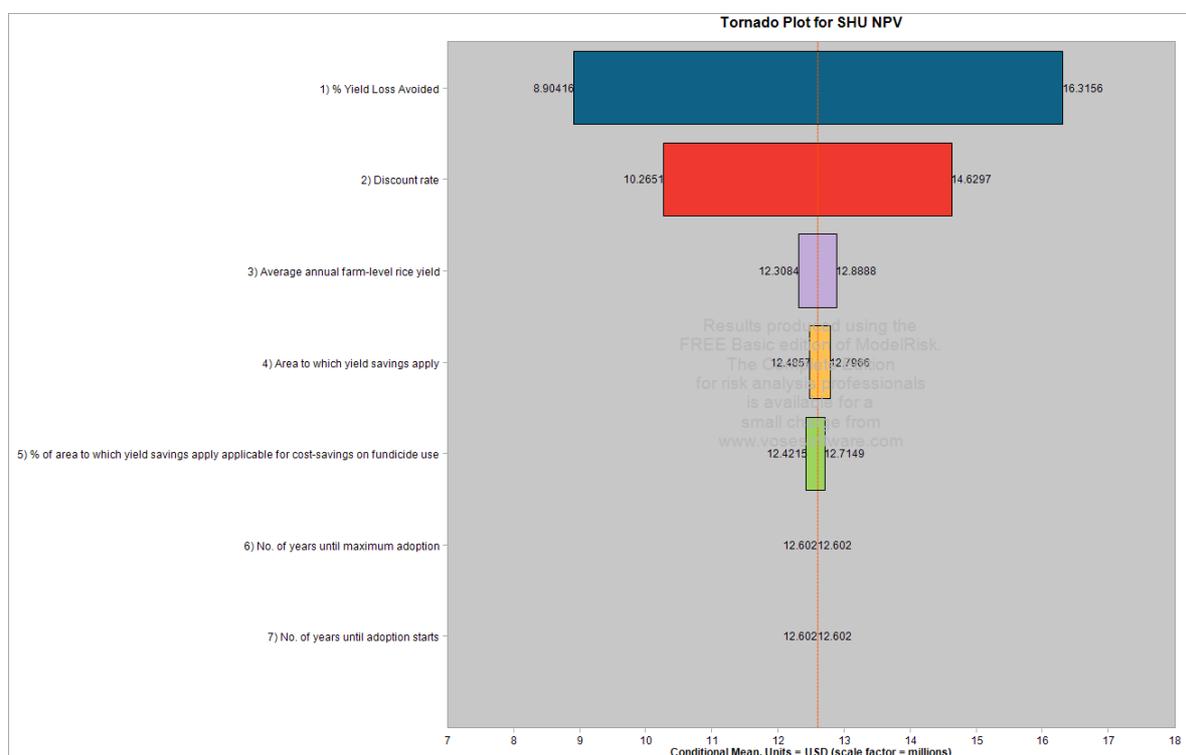
Figure 16. Sensitivity analysis of parameters that influence IRRI GHU NPV results (Source: Authors)
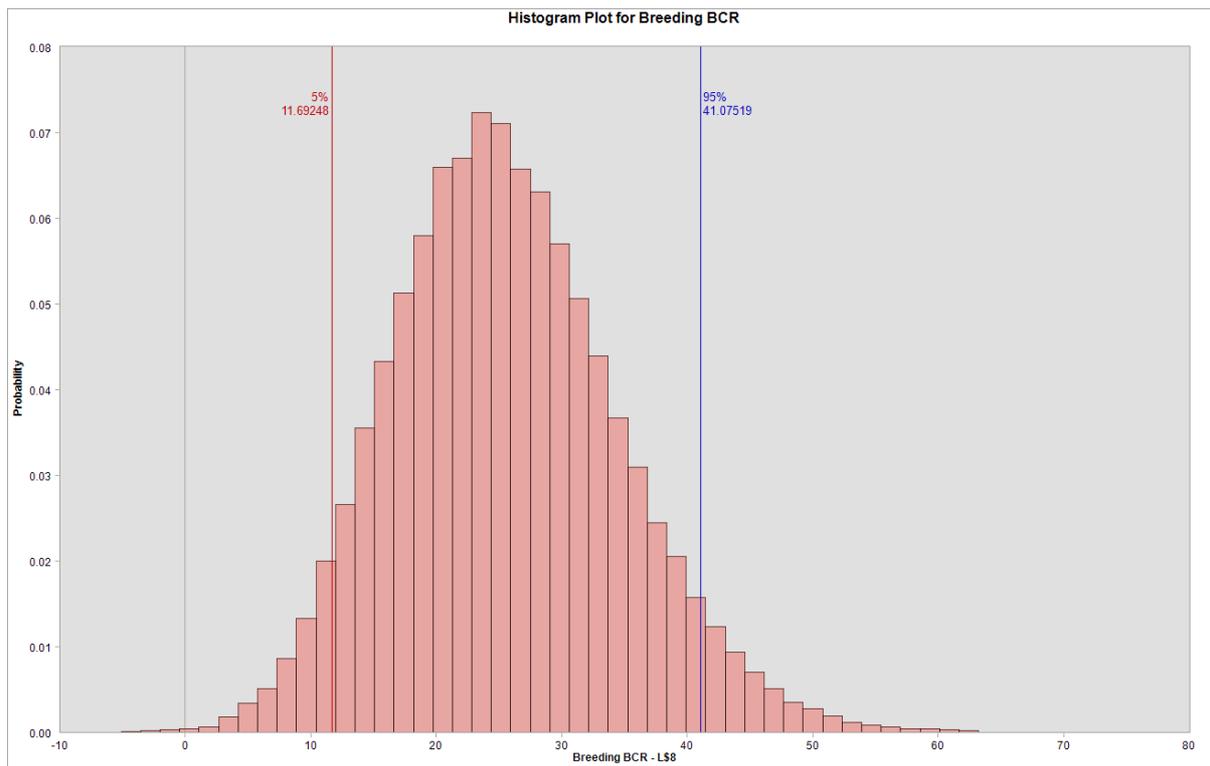
Figure 17. Probability distribution of Breeding BCR (Source: Authors)
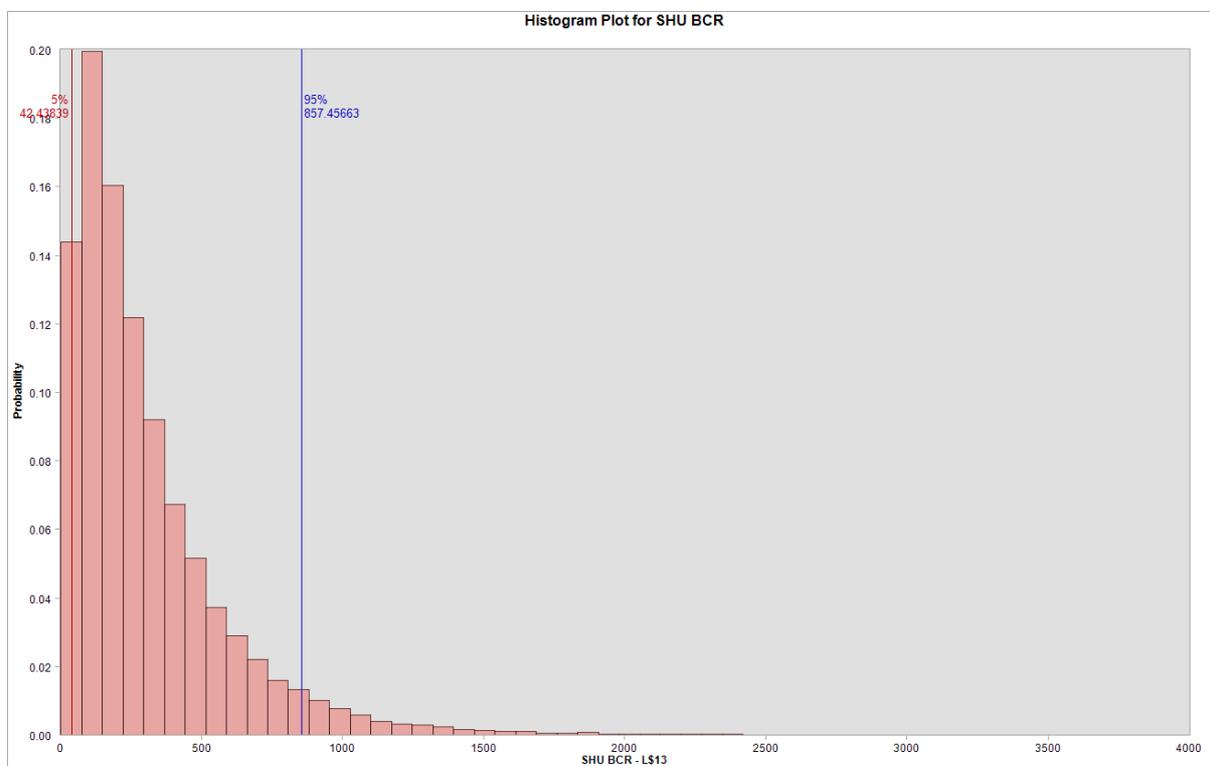
Figure 18. Probability distribution of IRRI GHU BCR (Source: Authors)
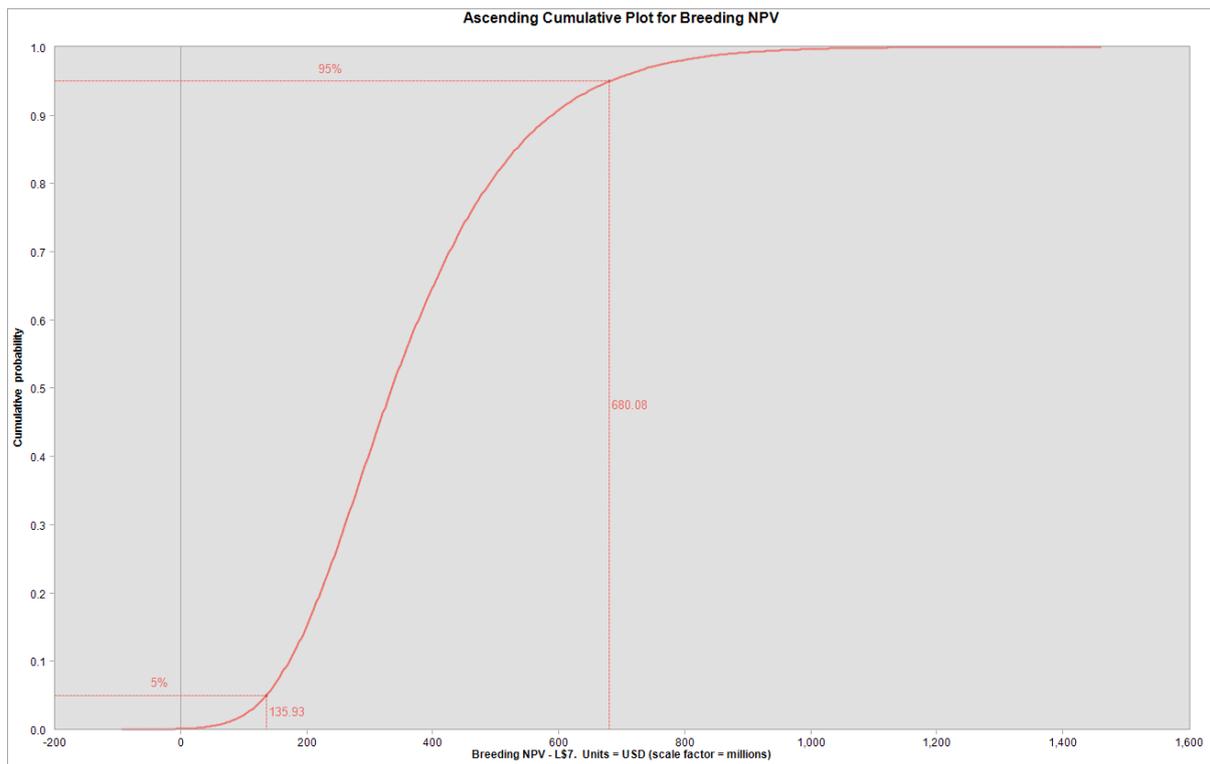
Figure 19. Cumulative distribution of Breeding NPV (Source: Authors)
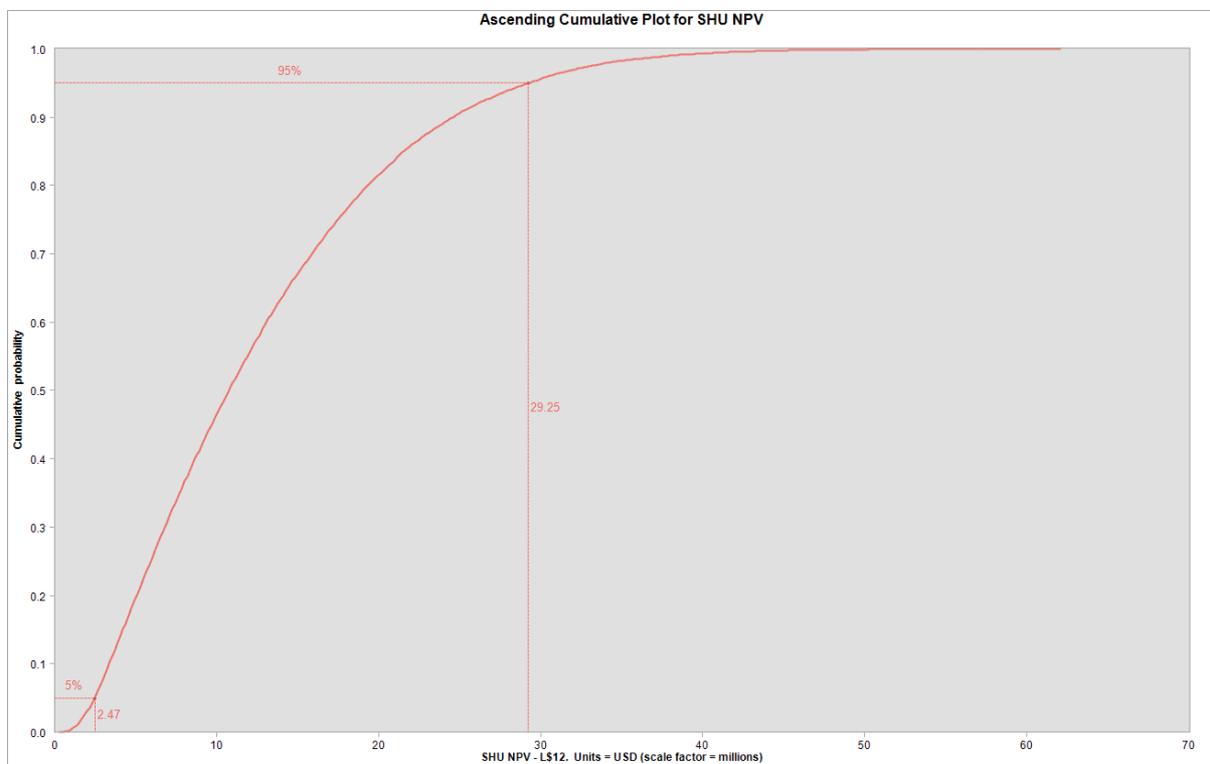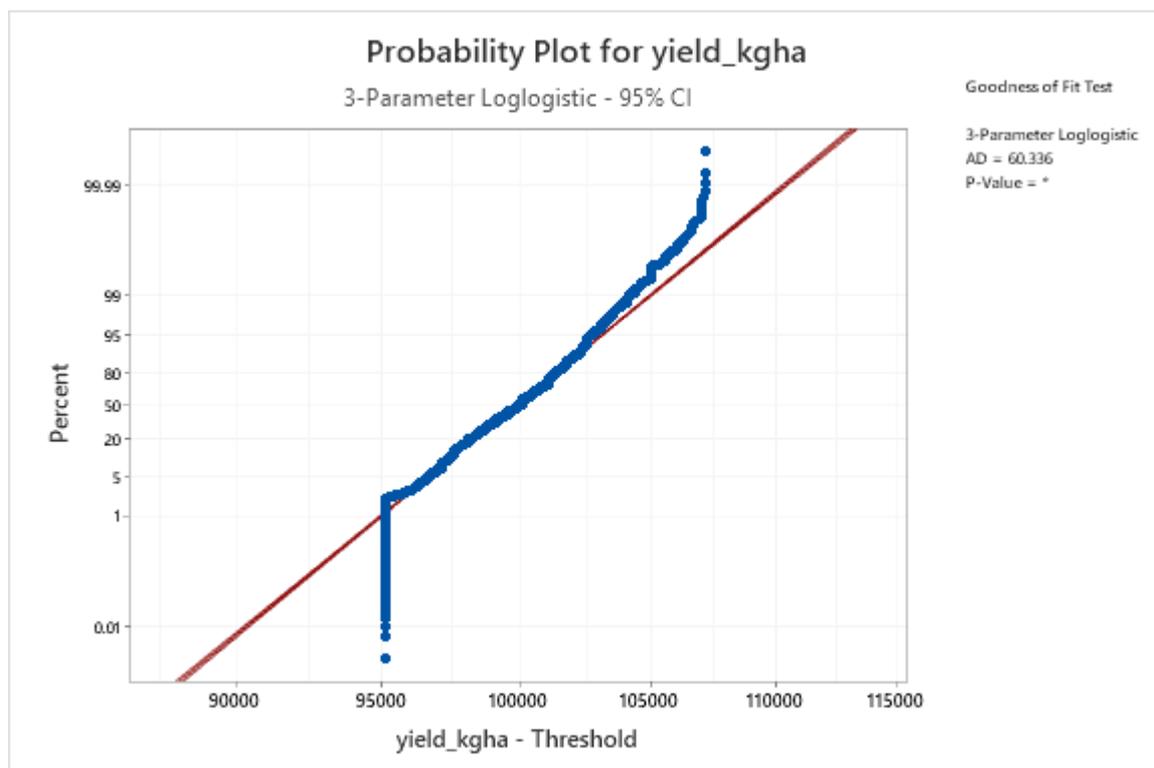

Figure 20. Cumulative distribution of IRRI GHU NPV (Source: Authors)

9. Annex

Figures on the Good-of-fitness Tests for Yield (Source: Authors)
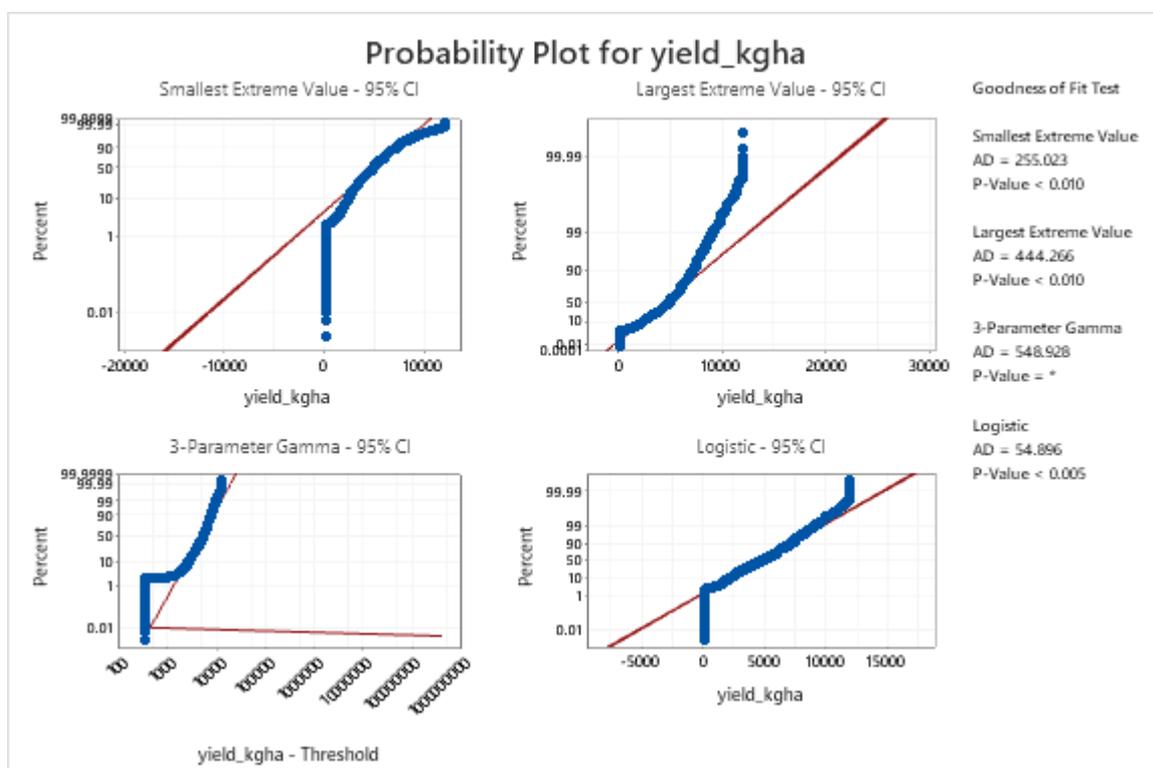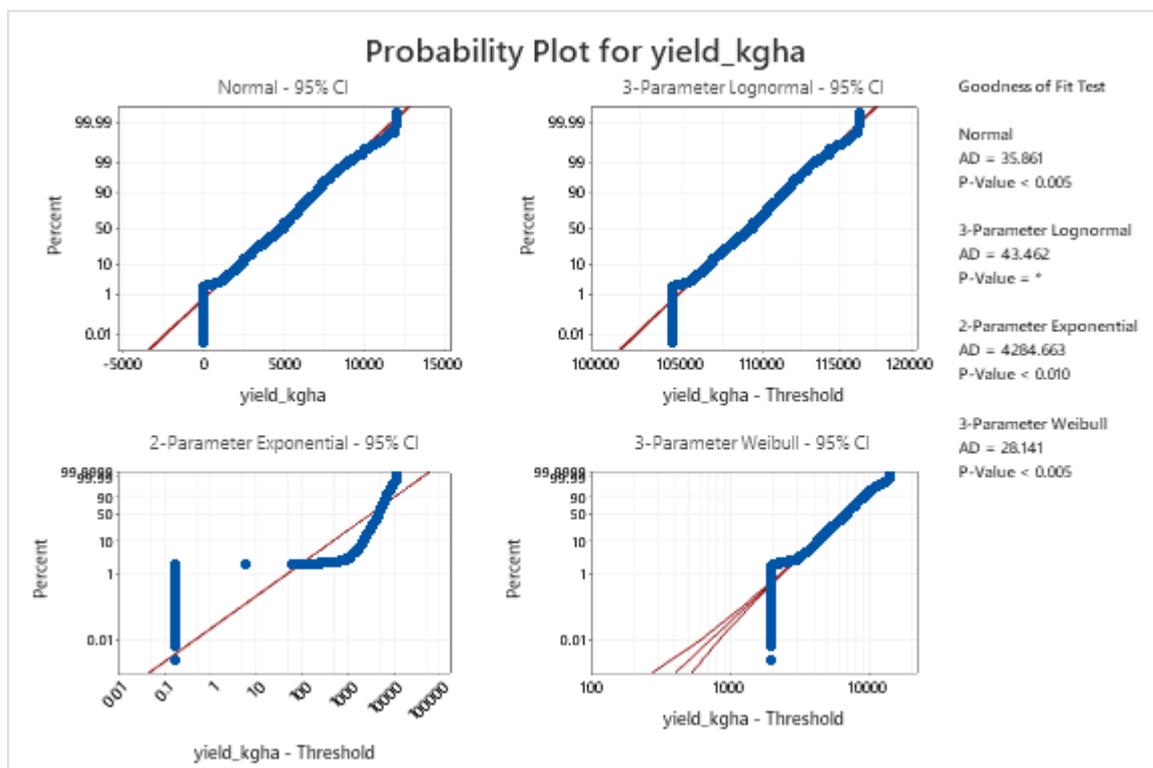
Goodness of Fit Test

Distribution	AD	P
Normal	35.861	<0.005
3-Parameter Lognormal	43.462	*
2-Parameter Exponential	4284.663	<0.010
3-Parameter Weibull	28.141	<0.005
Smallest Extreme Value	255.023	<0.010
Largest Extreme Value	444.266	<0.010
3-Parameter Gamma	548.928	*
Logistic	54.896	<0.005
3-Parameter Loglogistic	60.336	*

Figures on the Good-of-fitness Tests for Blast disease incidence (Source: Authors)
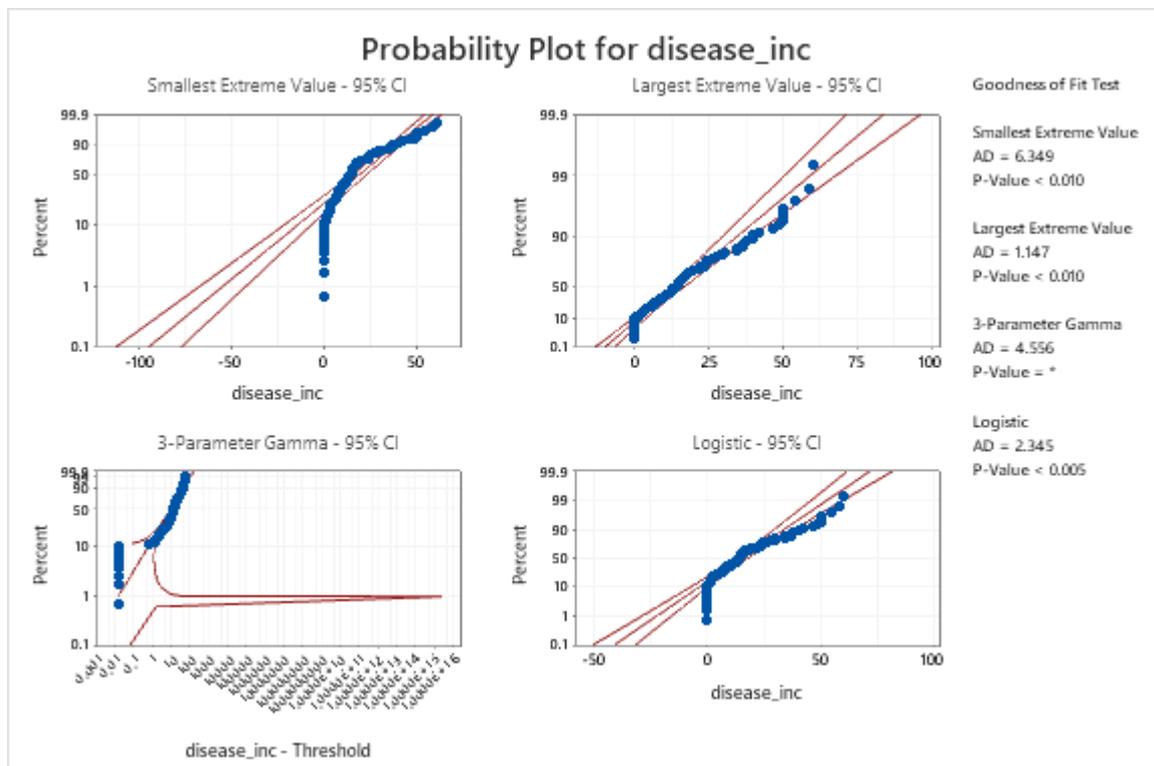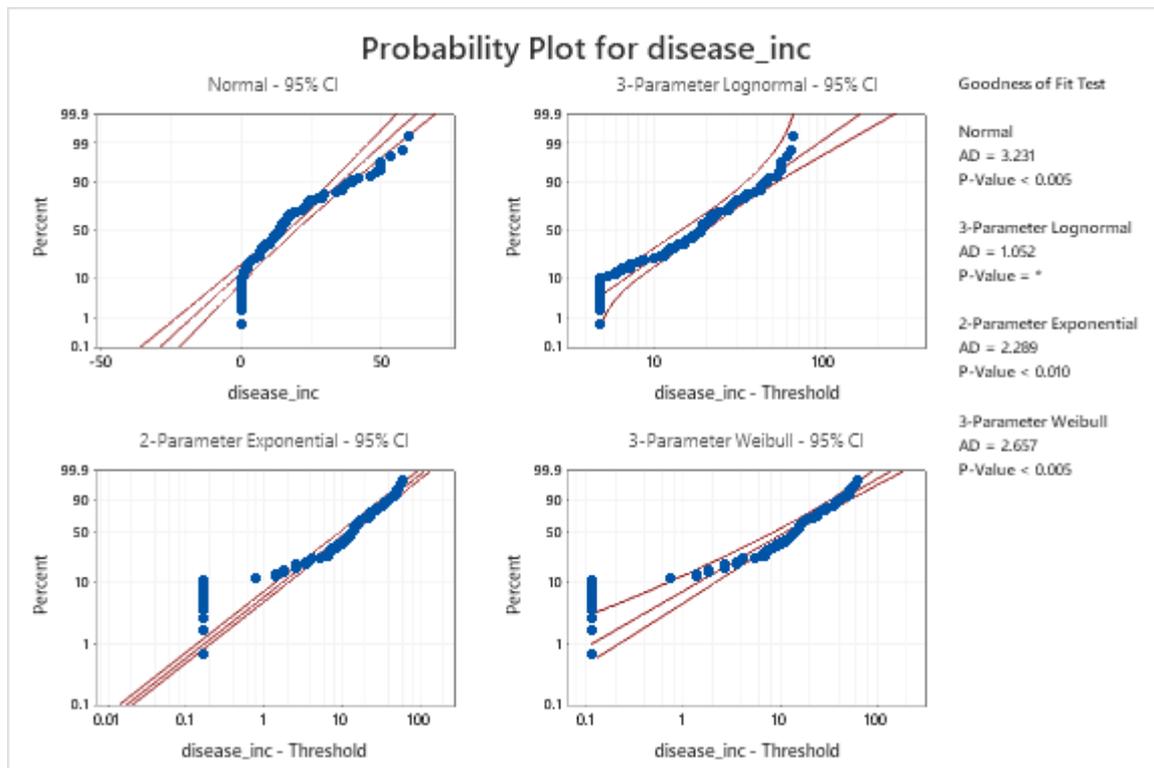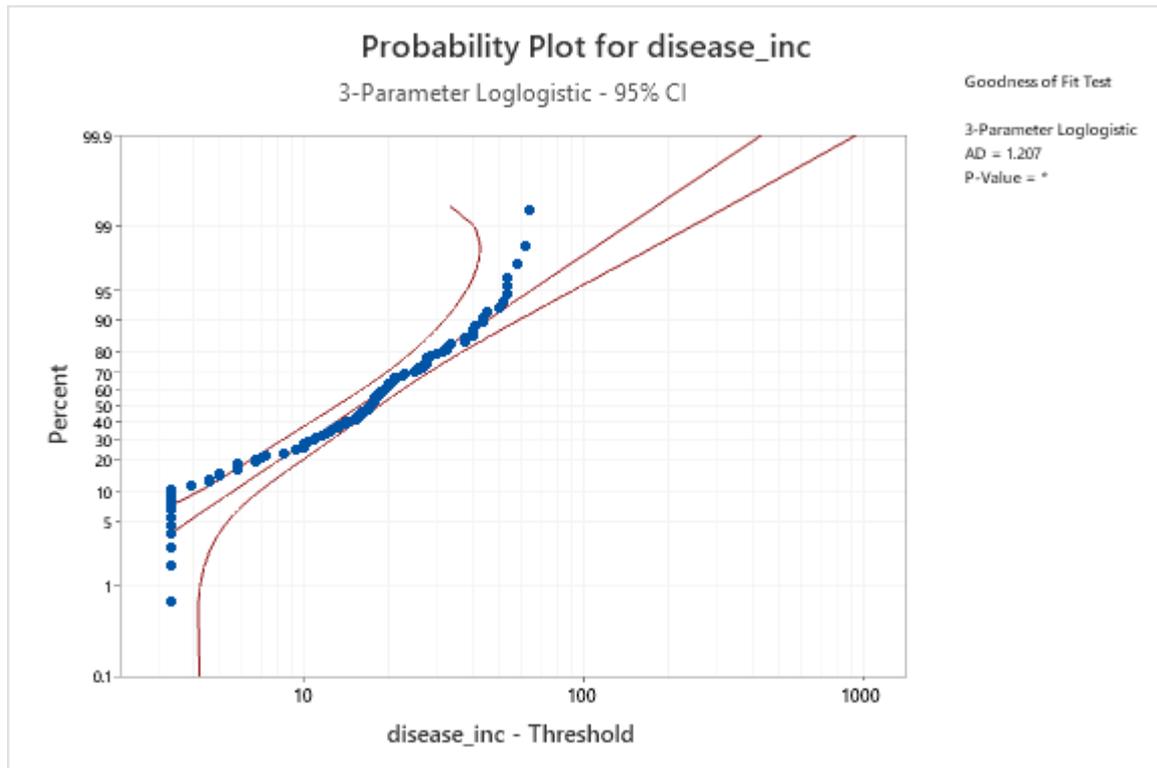
Goodness of Fit Test

Distribution	AD	P
Normal	3.231	<0.005
3-Parameter Lognormal	1.052	*
2-Parameter Exponential	2.289	<0.010
3-Parameter Weibull	2.657	<0.005
Smallest Extreme Value	6.349	<0.010
Largest Extreme Value	1.147	<0.010
3-Parameter Gamma	4.556	*
Logistic	2.345	<0.005
3-Parameter Loglogistic	1.207	*