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REVIEW

Special Section: Enhancing Food Security through Innovative Agricultural Management

Onerice breeding framework: An end-to-end system to develop better varieties faster

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Abstract

Breeding in the Consultative Group on International Agricultural Research (CGIAR) system is an intricate process that integrates the contributions of market research, pre-breeding, breeding, breeding operations, and seed systems. Therefore, a well-defined framework is critical for the effective and efficient operation of a breeding program. The OneRice Breeding Framework developed at the International Rice Research Institute (IRRI) integrates these components, from initial market research to establish breeding goals, creating breeding strategies for improved product design and development, and swiftly testing and replacing products through effective seed systems. The framework represents a cutting-edge breeding approach that offers

Abbreviations: BLUP, best linear unbiased predictions; GEBV, genomic estimated breeding value; GS, genomic selection; MAS, marker-assisted selection; MET, multi-environment trial; NARES, National Agricultural Research and Extension System; OFT, on-farm trials; QTL, quantitative trait loci; RBI, Rice Breeding Innovations;; RGA, rapid generation advance; RYMV, rice yellow mottle virus; SSD, single seed descent; TPE, target population of environment.

comprehensive guidance on harnessing modern tools and technologies, including genomic selection, speed breeding, sparse testing, and so on. Additionally, the framework outlines strategies for systematically integrating novel genetic variation into elite breeding programs through pre-breeding efforts. It is adaptable across different crops and is dynamic, allowing adjustments in the breeding program based on target objectives, resource availability, and tools. The OneRice Breeding Framework is a comprehensive end-to-end framework that integrates all the components to enhance genetic gains and develop and disseminate better products faster to address food, nutrition, and income security. Consequently, the OneRice Breeding Framework is the fundamental blueprint for modern rice (*Oryza sativa*) crop breeding.

Plain Language Summary

The subject is related to global agriculture and how plant breeding plays an important role in addressing food security and feeding the growing population. Developing crop varieties in the international institutes is a very intricate process involving multiple components. This work is an effort to tackle the complexity by meaningfully integrating all the components to make the entire breeding process more effective and efficient. We have successfully developed and implemented an end-to-end framework to develop better crop varieties in short time. The framework leverages strong scientific principles and cutting-edge technologies to achieve this. The framework enabled the rice breeding program to breed rapidly and replace the old varieties in farmers' fields. It also serves as a blueprint for other crop breeding programs.

1 | INTRODUCTION

The global population is increasing, estimated to reach 9 billion by 2050, while the land available for agriculture is decreasing. This poses a challenge for feeding everyone on this planet. Increasing the yield potential of rice (*Oryza sativa*) and other cereals through plant breeding is a critical component of global food security (Cassman, 1999; Khush & Virk, 2005). High-yielding varieties developed during the Green Revolution in the 1960s were immensely successful in addressing the food shortages experienced at the time (Evenson & Gollin, 2003), which has enabled unparalleled economic development in developing countries. However, public-sector breeding programs have subsequently struggled, with yield of newly developed varieties plateauing, and facing difficulties in replacing old popular varieties that are being cultivated in the farmers' field. Increasing the yields of high-yielding varieties needs a disciplined breeding approach, the adoption of modern tools, and an effective way to integrate product development, delivery, and placement to increase genetic gains in farmers' fields.

The rice breeding program at the International Rice Research Institute (IRRI) has been active since 1960 and has produced numerous rice varieties that have resulted in immense benefits globally (Khush & Virk, 2005). The nutrient-responsive semi-dwarf rice variety IR8, bred at IRRI, played an instrumental role in the Green Revolution (Peng et al., 2010). This was followed by numerous famous varieties such as IR36, IR64, and IR74 that improved grain quality and disease resistance, and more recently, varieties incorporating the *Sub1* gene for tolerance to complete submergence. Many of these varieties are still growing in farmers' fields or are being used as parents and donors in rice breeding programs across South Asia, Southeast Asia, and East and Southern Africa (ESA). In addition to the high-yielding breeding lines for favorable environments, IRRI has bred varieties for challenging environments that are affected by drought, flood, heat, salinity, and so on (Khush & Virk, 2005).

Over the last six decades, IRRI's breeding strategies have changed constantly based on breeding objectives and goals as new tools, technologies, and funding opportunities became available. Breeders have responded to these changes by altering the breeding methodologies, such as breeding targets, choice of parents, mating designs, number and size of families, and selection tools (visual, phenotypic, or genotypic). Plant breeders at IRRI have historically prioritized product development over parent identification for new crosses, focusing on improving genotypes and identifying rare, once-off superstar lines rather than enhancing overall population performance through population improvement breeding schemes. As such, they lacked a systematic approach to recycling the best genetics for accelerated genetic gains through a closed population improvement-based breeding strategy. Besides a population improvement-based breeding strategy, the absence of a systematic best-by-best (elite-by-elite) crossing strategy and longer breeding cycles limited the genetic gains in IRRI's breeding programs.

The success of a public breeding program is measured by its ability to reach and impact millions of farmers and consumers and contribute to impact areas, such as (i) nutrition, health, and food security; (ii) poverty reduction, livelihoods, and jobs; (iii) gender equality, youth, and social inclusion; (iv) climate adaptation and mitigation; and (v) environmental health and biodiversity. In a world shaped by several megatrends (Independent Science for Development Council [ISDC], 2023), this means that breeding programs need to consistently increase the rate of genetic gain. Rates of genetic gain are typically described by the breeder's equation, defined as $\Delta G = (\sigma a) \times (i) \times (r)/L$ as defined by Eberhart (1970) and Lush (1937) where ΔG is the rate of genetic gain per breeding cycle, σa is the genetic standard deviation of the population, i is the selection intensity, r is the selection accuracy, and L is the cycle length. The breeder's equation is an excellent guiding framework where all the parameters can be manipulated to increase the rate of genetic gain but with varying return of investment. Many also consider a fifth parameter, cost per breeding cycle, which impacts the four key parameters. Most, or almost all, the breeding programs operate with finite resources; therefore, cost is a major driver forcing the breeding program to appropriately prioritize the efforts.

Despite the development and release of numerous varieties, the genetic gain in IRRI's breeding programs has been very low (Juma et al., 2021; Khanna et al., 2022). The lower rate of genetic gain is attributed to breeders making crosses with non-elite germplasm (Juma et al., 2021). A major challenge in global rice breeding in the 21st century is overcoming this yield stagnation and enhancing the genetic gains above 1.5% to meet increasing food demand amidst a changing climate and extreme weather events. The Consultative Group on International Agricultural Research (CGIAR) institutes and donors emphasize the importance of accelerating genetic gain rates in publicly and philanthropically funded breeding programs (von der Osten-Sacken, 1992). To ensure food security and achieve the desired genetic gains in rice breeding, modernization of the rice breeding programs by leveraging modern tools and technologies, data-driven approaches, and quantitative genetics is essential.

In response to these challenges, IRRI's rice breeding has embarked on a transformative journey in the past 10 years. Rice breeding programs at IRRI were previously classified into irrigated, rainfed, direct-seeded rice, upland, hybrid, and other stress-tolerance breeding programs. Each program had different breeding strategies and approaches to breed and develop the germplasm for the specific ecologies. Although IRRI has progressively been modernizing its breeding setup, there was an absence of a comprehensive and unified breeding strategy and end-to-end framework across the IRRI's breeding program. Implementing such a framework is paramount, offering a range of benefits that include establishing unified breeding philosophies and terminology, standardizing operations in rice breeding that could be emulated by similar crop programs, creating a structure for resource allocation and management, setting clear indicators for monitoring progress, and estimating the return on investment (RoI) and impact of the breeding program.

Core Ideas

- An end-to-end breeding framework is critical for the effective and efficient operation of a breeding program.
- Standardizes best practices and vocabulary for breeding rice and could serve as a model for other crops.
- Minimal breeding unit for a breeding pipeline is termed as "1X" where numbers at all the breeding steps are defined.
- The framework is a blueprint to increase genetic gain and address food, nutrition, and income security.

1.1 | Breeding program definition and management

In the past, the vocabulary and terminologies used by breeding programs varied within and across institutions. This has led to reduced collaboration and communication, variable priorities and redundant activities across teams, uneven application of new technologies, and widely variable rates of expected genetic gain. Creating a common language and metrics will ease the measure of success of breeding programs, which is encouraged by program reviewers and donors.

Key concepts in describing a breeding program include:

1. *Market Segment* is a group of farmers or end-users with a relatively homogeneous demand for a given crop variety (Friedmann et al., 2024) considering the maturity of the crop (early, medium, or late), establishment method (transplanted, direct-seeded), grain size and shape (long slender, short bold, etc.), and agro-ecological zones (lowland, upland) (Donovan et al., 2022; Lindqvist-Kreuze et al., 2024).

2. *Product Concept* (also known as target product profile or TPP in the CGIAR; see Donovan et al., 2022) is a document describing the breeding targets necessary to meet the product needs of the market segments of interest to a Breeding Network.
3. *Target Population of Environments (TPEs)* are a geographic region within which genotype-by-environment (G × E) interactions are minimized (to maximize prediction accuracy). As patterns of G × E are better understood, existing testing regions can be reviewed and refined. While a testing region should be defined by genetic correlations, it can be modified to meet local administrative needs.
4. *Breeding Program* is a program of work funded by one or more sources, governed by a breeding team, and managing a number of prioritized breeding pipelines of varying sizes.
5. *Breeding Pipeline* is defined by a set of crosses and selections made for a product concept that is mapped to a market segment involving a breeding network.
6. *Breeding cycle* is the duration between making the crosses and when the best progenies of the crosses are recycled back again as the parents.
7. *Breeding Network* is a group of National Agricultural Research and Extension System (NARES) partners and other collaborators working together with the CGIAR institutions to target a number of product concepts in the specific testing regions of interest.

It is critical to differentiate between the breeding framework and the breeding scheme. The former describes the overall strategy on how the entire breeding program and its associated components are integrated and managed for an effective product development process. The latter denotes the actual breeding process that is being followed, which is dynamic and is a subcomponent of the overall framework. The framework is like the hardware for any breeding program and changes very little despite the change in targets, germplasm, or even crops, whereas the breeding scheme acts like the software that evolves and undergoes periodical updates over time through breeding cycles.

2 | OVERVIEW OF ONERICE BREEDING FRAMEWORK

The OneRice Framework, conceptualized and developed at IRRI, integrates the key components of market demand, prebreeding, breeding, breeding operations, and seed system components of breeding programs together under a single set of operating principles (Figure 1). This promotes the use of best practices across the breeding programs by creating a unified language, usage of common shared standard operating procedure (SOP), and common performance and advancement criteria. The use of common operating procedures enables the IRRI shared services platform, creating significant economies of scale and further promoting standardization of workflows. The OneRice Breeding Framework, from start to end, covers the design, creation, testing, and advancement, and delivery of breeding products. Thus, both parent recycling and product extraction breeding objectives can be accomplished in an optimal way.

This overview is a reflection of IRRI's recent breeding modernization efforts, which are integrated into the OneRice Breeding Framework. It is a comprehensive blueprint of modern crop breeding, aiming to develop rice varieties more effectively, efficiently, and rapidly. It encompasses all aspects of the breeding process, from fine-tuning breeding goals through market research to optimizing product design, development, and efficient seed system dissemination. By embracing cutting-edge tools such as genomic selection (GS), speed breeding, and data-driven approaches in advancing the products, the OneRice Breeding Framework is a pioneering prototype in modern crop breeding. It is highly dynamic and adaptable across different self-pollinated crops based on the availability of resources and breeding objectives. The following sections delve into the product design, product creation, pre-breeding, product delivery, centralized breeding operations, and partner network management aspects adopted currently by the IRRI breeding programs.

3 | PRODUCT DESIGN

3.1 | Market intelligence: Trait preferences and feedback

A clear breeding target is the first and foremost requirement for success in the breeding process (Figure 2). Market research and intelligence define market segments that require a list of required traits for TPEs to serve the requirements of farmers, processors, and consumers (Figure 2) (Custodio et al., 2023; Donovan et al., 2022; Ynion et al., 2024) and capture impact opportunities (which can be estimated through the Global Market Intelligence Platform [GloMIP]; https://glomip.cgiar.org/impact-opportunities). Product creation requires an in-depth understanding of the trait requirements for a given market segment or the TPE (Ynion et al., 2024). These traits help define and distinguish a variety from existing products in a given market segment. The foundation of this understanding is the market demand and feedback, which is captured into a well-defined product concept. This product concept becomes the compass that guides the breeding process and decision-making process, underscoring its crucial role in any breeding program. Based on the product concept, breeders need to make the right decisions about choosing appropriate germplasm for the development of new varieties and, during the selection process, what traits the genotypes should possess to qualify for selection to the next stage and varietal release.

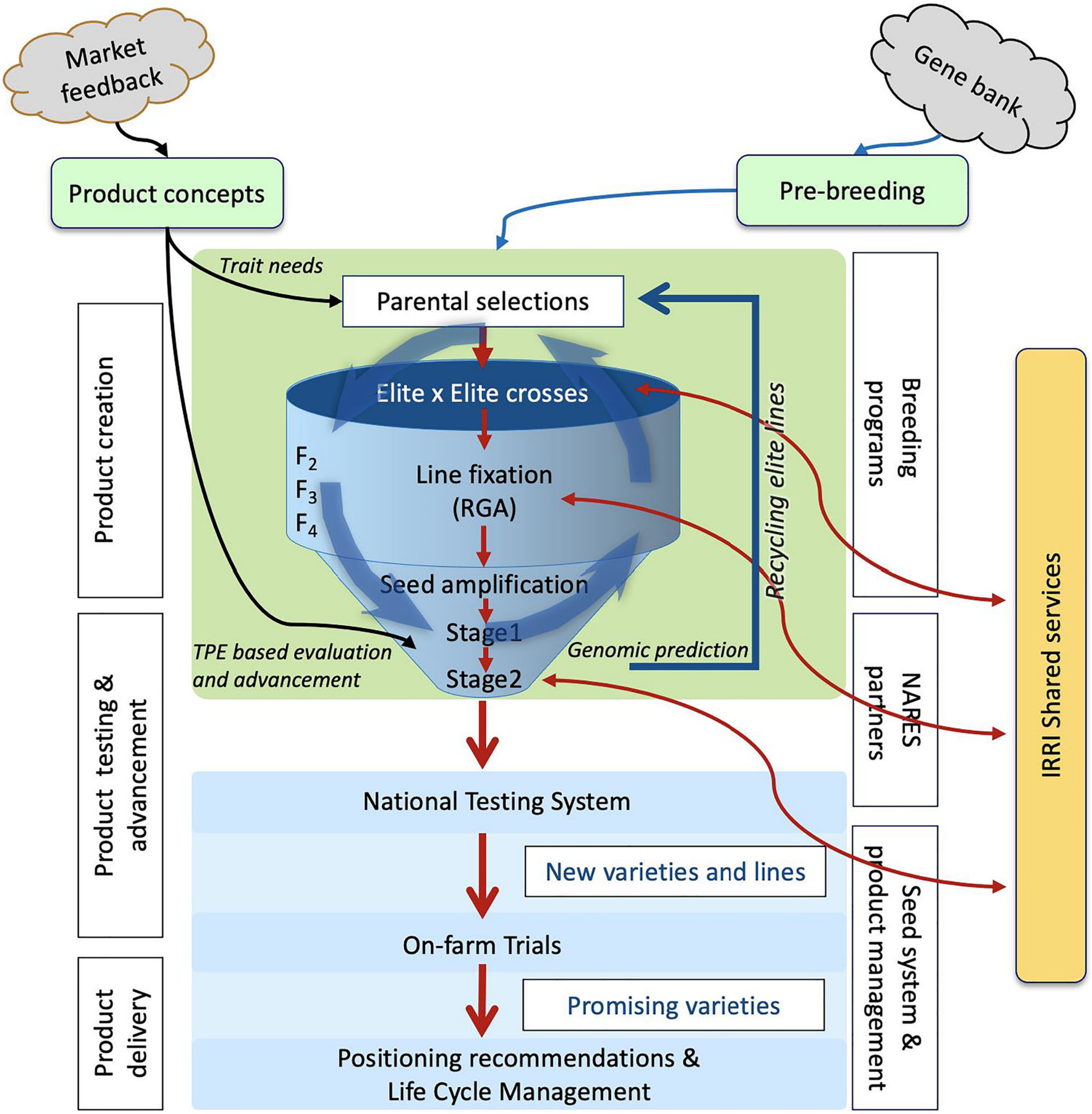
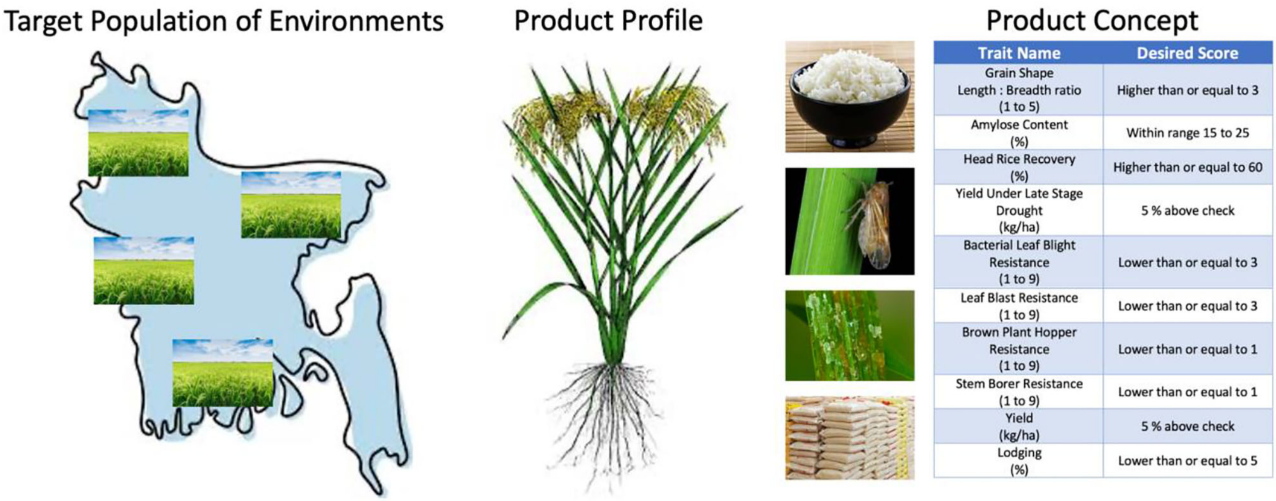


FIGURE 1 Schematic representation of the OneRice Breeding Framework and its interconnected components. On the upper left part, market research capturing the demand and feedback to define and update product concepts is shown. On the upper right part, the discovery breeding strategy is shown to imply the connection with the regular breeding program to deploy new alleles and haplotypes. The green section in the middle captures the population improvement-based breeding approach and the breeding scheme with activities that predominantly take place at International Rice Research Institute Headquarters (IRRI-HQ). The blue section at the bottom denotes the advanced product testing in the regions and the seed system activities. The far right IRRI Shared Service section in orange captures the breeding operations shared services unit that enables smooth functioning of all breeding activities. The left vertical panel of white boxes denotes the key stages of product development: product creation, product testing and advancement, and product delivery. The right vertical panel of white boxes denotes the major actors involved in the product development steps. NARES, National Agricultural Research and Extension System; RGA, rapid generation advance; TPE, target population of environment.

The OneRice Breeding Framework provides a clear guideline on what to breed for and how to engineer the development of new varieties based on precise product concepts. In the OneRice Breeding Framework, the trait preferences are formalized through product concepts to guide parental selections and the product creation process in the breeding programs, and the breeding and decision-making are guided by clear breeding objectives and priorities defined by the market segmentation and product profiles.



Trait Name	Desired Score
Grain Shape Length : Breadth ratio (1 to 5)	Higher than or equal to 3
Amylose Content (%)	Within range 15 to 25
Head Rice Recovery (%)	Higher than or equal to 60
Yield Under Late Stage Drought (kg/ha)	5 % above check
Bacterial Leaf Blight Resistance (1 to 9)	Lower than or equal to 3
Leaf Blast Resistance (1 to 9)	Lower than or equal to 3
Brown Plant Hopper Resistance (1 to 9)	Lower than or equal to 1
Stem Borer Resistance (1 to 9)	Lower than or equal to 1
Yield (kg/ha)	5 % above check
Lodging (%)	Lower than or equal to 5

FIGURE 2 Market research identifies a number of market segments in which specific rice products/varieties are preferred. The characteristics of the existing products are termed as product profiles and the regions where they are grown are termed as target population of environments (TPEs). Using the product profiles, product concepts are developed, which serve as breeding targets. The product concept is essentially a list of traits that need to be improved to effectively replace the benchmark varieties.

In 2019, IRRI initiated an effort to develop market segments and product concepts based on a global survey. These market segments and product concepts (TPPs) can be consulted publicly in the GloMIP. Market segmentation allows grouping geographies with similar breeding targets and assigning breeding pipelines to each target segment. Further, through the help of market intelligence and research, the product concepts for each market segment are defined, which contain the list of traits and the thresholds to determine the population development and advancement criteria for each market segment. Benchmark varieties for each segment are determined, which can be used as a replacement target. Further, released varieties are mapped to each segment for accurate placement in the seed systems. Global market survey data allowed the definition of 24 market segments, and among which 11 are currently covered by active IRRI breeding pipelines targeting multiple South Asian, South-east Asian and East and Southern African countries (Table S1).

4 | PRODUCT CREATION

4.1 | Breeding methodology

Recurrent selection is widely considered as the most effective way to breed for quantitative traits that are controlled by numerous alleles (Allard, 1999; Bernardo, 2002). Recycling (selecting and intermating the best individuals) is a cyclical process to continually improve the mean performance of the population, resulting in incremental genetic gains or improvement over time. Recurrent selection schemes focused on recycling the best genetics in a closed breeding system have been demonstrated to produce high rates of genetic gain (Breseghello et al., 2009; Shelton & Tracy, 2015), and some of the most successful plant breeding programs in the private sector currently manage their genetic diversity in this way (Smith et al., 2015).

Population improvement through recurrent selection is the chosen breeding strategy under the OneRice Breeding Framework. The selection of elite (best) individuals is based on their genomic estimated breeding value (GEBV) computed using genome-wide markers (Meuwissen et al., 2001). Depletion of genetic variability could pose a concern when adopting a closed recurrent selection and starting the crosses from fewer elite lines. In the past, breeders combated this through the introduction of diverse non-elite genetic materials. However, the OneRice Breeding Framework emphasizes systematic efforts such as optimized mating designs (Akdemir et al., 2019; Akdemir & Sánchez, 2016) and pre-breeding efforts to slow down the depletion of variation without direct introduction of diverse materials, which limits the genetic gains (Allier et al., 2020). All of the breeding programs at IRRI have been strictly aligned to a recurrent selection scheme involving an elite (best) × elite (best) crossing strategy to sustain the genetic gains and also to maintain the genetic variance (Allier et al., 2019; Breseghello et al., 2009; Cobb, Juma, et al., 2019; Dreisigacker et al., 2023; Morais Júnior et al., 2017).

4.2 | Breeding scheme

The objective of the breeding scheme is to generate and identify the best segregants for the target trait(s). Thus, a breeding scheme forms the core element of all breeding programs

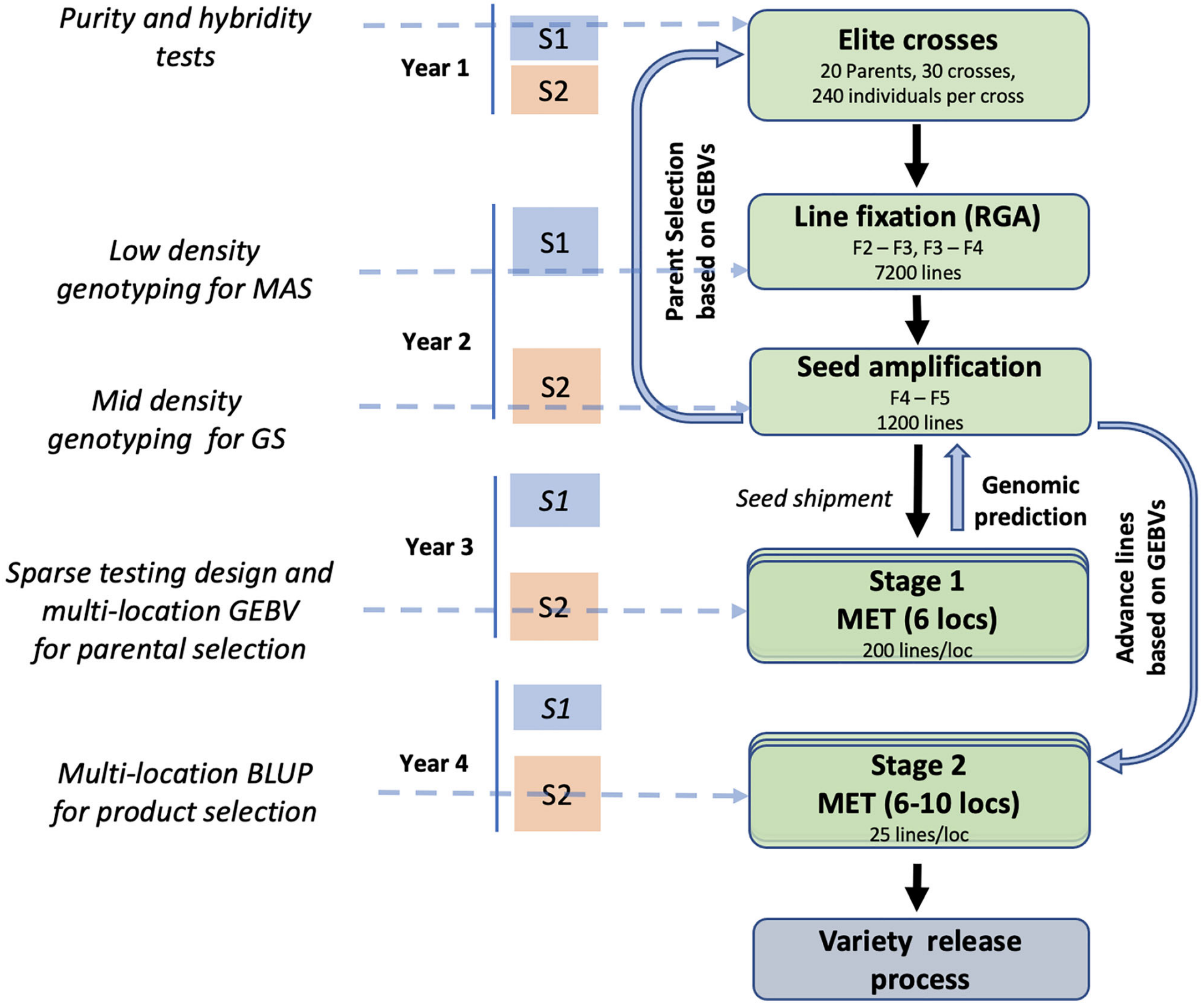


FIGURE 3 Flowchart of the 1X breeding scheme. Schematic representation of the breeding scheme followed in the OneRice Breeding Framework using population improvement through recurrent selection. Every rectangular box denotes the breeding activity steps with recommended numbers. The displayed scheme is a 3-year breeding cycle where parents are recycled based on their predicted genomic estimated breeding value (GEBV) in the seed amplification stage using multi-environment trial (MET) data as a training population. Each dotted arrow refers to the required genotyping or phenotyping activity for different stages of the breeding scheme. The low-density genotyping step screen for 10–20 trait-specific markers for marker-assisted selection (MAS), and the mid-density genotyping uses ∼1000 genome-wide markers used for genomic prediction. BLUP, best linear unbiased predictions; GS, genomic selection; RGA, rapid generation advance.

involving four key activities, namely, crossing, generation advance, evaluation, and selection steps (Rutkoski, 2019). Breeding is a numbers game, and therefore defining the size of the breeding program is critical to forecast and manage the resources of the program effectively. Further optimization of breeding schemes can happen only when the numbers at all the steps are clearly defined.

Under the OneRice Breeding Framework, the minimal breeding unit for a breeding pipeline is designated as “1X” (Figure 3). This 1X breeding pipeline size defines the number of parents selected, number of crosses made, number of progenies generated for each cross during generation advance, size of each cross after marker-assisted selection (MAS), number of lines tested in the early-stage testing, number of lines advanced to late-stage testing, and finally the number of lines nominated for national varietal testing systems. Defining the program size in this manner allows for the estimation of breeding program costs, and from there, appropriate scaling of investment between breeding programs and pipelines. These numbers are carefully defined by principles of Mendelian genetics, breeding simulation studies, operational capacity of the breeding program, and constraints in testing segregants. The breeding scheme, which acts as the software of the OneRice Breeding Framework, will undergo optimization through breeding simulation exercises (e.g., Seck et al., 2024) and be periodically updated.

Every step of the breeding scheme is important, time-consuming, and requires phenotyping and genotyping activities to successfully complete (Figure 3). It is also essential for a breeding pipeline to sketch and formalize the breeding scheme (Covarrubias-Pazaran et al., 2022) before it can be optimized. Therefore, under the OneRice Breeding Framework, every step of the breeding scheme is outlined and defined in the following sections.

4.3 | Elite parental pool

Elite breeding lines are defined through rigorous testing and selection processes that possess a high mean performance or breeding value for yield along with important traits for yield protection and grain quality. The elite breeding pool (referred to as the base population in recurrent selection) is a set of founder parental lines that serves as the source of genetic variation for the traits listed in a given product concept. A breeding line is termed “elite” only when it has a high breeding value and not just through its field performance at a single location or the beneficial traits it possesses. To strictly focus on recurrent selection breeding schemes, the presence of appropriately characterized elite lines with higher breeding values for grain yield and possessing the key alleles for Mendelian traits is required in the elite base population. Usually, the merit of the breeding lines as a good parent is measured through a metric called “breeding value,” which is calculated through a combination of an individual’s phenotypic value and genotypic profile. This is because the phenotypic data consist of both heritable and non-heritable variation. This explains the phenomenon where a phenotypically superior breeding line is not always necessarily considered to be good parent material. Therefore, to identify good parents for a breeding program, it is best to use breeding values.

In very few cases do breeding programs start from scratch; the majority of crop breeding programs have been operating and developing products over many years. These breeding programs may not be all optimized, but the breeding machinery would already be in place. Therefore, the generation step, where the identification of a set of elite lines that form the base population, is performed differently depending on the breeding program’s status. In Scenario 1, where a breeding program has been actively operating for many years, the data on the performance of the breeding materials over multiple years are available and it can be used to identify the best elite pool as a base population without pausing the breeding program. As an example, IRRI’s former irrigated program had been running for the last six decades and used its repository of multi-year advanced yield trial data to identify a base population based on their breeding value (Juma et al., 2021). A similar approach was also carried out in the former rainfed breeding program at IRRI later (Khanna et al., 2022). In Scenario 2, on the other hand, for a nascent program or for a breeding pipeline where there have been limited breeding efforts, it is critical to consolidate a set of breeding lines to be evaluated and selected before they are actively recombined. Thus, identifying the high-performing lines based on the breeding values for grain yield or any primary trait of interest that represents the overall diversity of the whole breeding collection is the key to success in future recurrent selection breeding strategies and enhancing genetic gains.

Genetic variation is a parameter in the breeder’s equation that serves as fuel to any breeding program and it should be accounted for when the base population is defined. Whether the genetic base is narrow or broad, the breeding program can achieve genetic gains for short-term or long-term, respectively, before the genetic variation starts to decline. Effective population size (N_e) is a metric used to measure the rate of inbreeding in a population and estimate the genetic diversity of a group of individuals (Crow & Kimura, 1970; Wright, 1931). The effective population size is indirectly proportional to the rate of inbreeding, and therefore breeders should be cautious while defining their base population depending on their breeding time horizon. Although larger N_e delays inbreeding and aids long-term selection, reports suggest that even relatively smaller N_e can sustain decades of breeding (Bernardo et al., 2006; Guzman, 1998). In the former irrigated breeding pipeline of IRRI, the N_e value was reported to be 22, which would sustain the gains for at least 22 cycles, allowing progress for approximately 80 years assuming a cycle length of 4 years (Juma et al., 2021).

4.4 | Crossing strategy

The core of breeding is the mating of desired breeding lines to generate new segregants and create new variation for the target traits. In previous breeding efforts at IRRI, the primary focus has been on crossing non-elite (donor/landrace) varieties with high-yielding elite breeding lines to develop improved, high-yielding lines (Juma et al., 2021; Khanna et al., 2024). Breeders have employed crossing strategies, including single, complex, double, and backcrosses, to create new breeding lines (Juma et al., 2021). To enhance genetic diversity and develop climate-resilient varieties, diverse materials such as landraces and donors have been extensively utilized. However, this strategy of diversifying the elite gene pool with a limited focus on recurrent selection has not been sufficient to maintain the higher genetic gains over time, and as a consequence, very low genetic gains for grain yield were observed (Juma et al., 2021). In the OneRice Breeding Framework, one of the major interventions was to strictly focus on population improvement breeding approach using elite lines as parents, wherein the parents of each breeding cycle are selected based on high GEBV for the grain yield or any other trait of interest.

The OneRice Breeding Framework strictly focuses on recurrent selection using the elite × elite crossing process as one of the main approaches to steadily increase genetic gain and eventually break the yield ceiling of already high-yielding lines. The elite × elite crossing scheme is advantageous because the average mean performance of the elite × elite cross is always higher than that of elite × non-elite crosses involving landraces or genebank resources as one of the parents. Although elite × non-elite crosses will bring more variation and diversify the breeding pool, the increased variance and diversification do not counterbalance the loss in mean performance or breeding value of the elite pool, which is crucial to driving the genetic gains in the breeding programs.

Besides the elite genotypes in a crossing scheme, it is also important to choose the appropriate number of parents and crosses to sustain the genetic gains and maintain the variance in the breeding program. The number of parents and crosses depends upon the program size, objectives, short-term and long-term genetic gains, and resources available to drive the breeding program. Each individual breeding program can be optimized to derive the appropriate number of parents needed in the crossing block and decide the number of cross combinations to make.

Under the OneRice Breeding Framework, for a breeding pipeline of 1X, which is the minimum breedable unit, we recommend starting with 20 new elite parents. The choice of 20 parents is based on the simulation exercises done in rice and other crops (https://excellenceinbreeding.org/toolbox/tools/optimal-program-sizes). It is also reported that excessive use of parents, such as more than 30, could result in lower genetic gains (Covarrubias-Pazaran et al., 2022).

More crosses with a given set of parents generally increase genetic gain. With 20 parents, a total of 195 (20 × (20 − 1)/2) unique cross combinations are possible using the half-diallel method. However, attempting all of them results in diminishing returns, and the optimum number should be less than all the total combinations. The total number of crosses for a 1X pipeline were finalized based on the cost per cross, capacity of breeding operations to perform crosses, and the constraint of total number of individuals to be evaluated in the yield trial. The proposed number of individuals tested in the earliest yield trial is determined as 1200 after MAS (Figure 3; discussed in the later sections). A simulation study in self-pollinated crops recommended 29 crosses for a moderately heritable trait with a testing capacity of 1000 individuals (Huehn, 2006). Therefore, based on the evidence and considering the practical limitations, we recommend a minimum of at least 30 crosses using the 20 parents for a 1X breeding pipeline (Figure 3). At the beginning of IRRI's breeding modernization, the crosses were finalized through the following steps: derive all the half-diallel combinations, eliminate the crosses between highly similar individuals using the coefficient of parentage, and restrict a parent to use in 10% of the total number of crosses. Currently, this is done using a single-step algorithm approach through optimal contribution by parents, which allows breeders to balance the genetic gain and genetic variance (Kinghorn, 2011).

4.5 | Generation advancement

Once crossing using parental material is completed, the next step is to advance the progenies so that breeders can test and select the best genetics for recycling and product identification. Compared to other parameters in the breeder's equation, cycle time has the highest RoI as it shows a reciprocal relationship with the rate of genetic gain (Cobb, Juma, et al., 2019); this means that genetic gains can be disproportionately improved through modest reductions in the breeding cycle time, resulting in significant economic benefits to society (Lenaerts et al., 2018). Since generation advance directly impacts the cycle time, shortening it enhances genetic gain.

The rapid generation advance (RGA) system, through which the generation time at the line fixation stage is reduced by early harvest, was originally proposed by Goulden (1939) and later modified by Grafius (1965). A major effort to reduce cycle time at IRRI through RGA coupled with single seed descent (SSD) was initiated in 2015 under the Transforming the Rice Breeding project, primarily utilizing very high-density planting and restricted root zones to induce earlier flowering and maturity (Collard et al., 2019). This system allows growth of 3.5–4 generations per year and essentially reduces what used to be 3–4 years of visual pedigree evaluation to 1 year of SSD in a greenhouse. Under the OneRice Breeding Framework, all of the IRRI breeding pipelines have adopted the SSD method using the RGA system for advancing generations. The pipelines uniformly exit the RGA at the same filial generation. The genotypes are advanced from F_1 to F_4 in the RGA without any selection except MAS for the major traits.

The RGA protocols have been further optimized to achieve more generations per year. A new "field RGA" protocol was developed that is relatively slower (fewer generations per year), but significantly cheaper (Collard et al., 2017) and is a viable option for breeding programs with a lower budget and infrastructure, especially certain NARES partners. Moving forward, the RGA system will be further improved at IRRI to achieve shorter generation length under a state-of-the-art speed breeding facility in house (Kabade et al., 2024).

Under the OneRice Breeding Framework, the number of individuals (or full-sibs) at the F_2 and F_3 generations under RGA are set at 240 individuals per cross. This is calculated to allow selection of 40 lines that are positive for major quantitative trait loci (QTL[+]) for two to three Mendelian traits, with a failure probability of less than 5% at the F_4 generation (Figure 3; Cobb, Biswas, et al., 2019). MAS is performed on the F_3 plants and the number of full-sib individuals advanced to the F_4 generation is brought down to a total of 1200, approximately 40 individuals per cross. All 1200 F_4 plants are subjected to a seed amplification (seed increase) step in the field condition to increase the seed quantity for the multi-location testing. Mid-density genotyping of all the 1200 lines is performed at the F_4 generation, which is later used to perform GS.

4.6 | Marker-assisted selection

MAS is a proven and an effective tool for selecting qualitative traits controlled by major effect loci in crop plants (Cobb, Juma, et al., 2019). Rice has a wealth of major genes contributing significant value to a wide range of traits on the product concepts (Supporting Information 1). Besides its contribution to improving specific traits, MAS has the benefit that it can be easily applied during line fixation (RGA), allowing selection for these traits at stages of the breeding cycle that are otherwise not amenable to selection and partially decoupling improvement in these traits from selection tradeoffs with yield. The breeding program at IRRI uses MAS to select for qualitative traits through low-density genotyping (Figure 3) at Intertek, a third-party genotyping service provider. The low-density genotyping entails screening of breeding materials from all of the crosses in the breeding pipeline using a predesigned marker panel with 10 trait markers. It costs around $4 a sample and enables breeders to select for QTL[+] lines in each cross, ensuring that only the most valuable progenies for these traits are advanced to the expensive stages of field evaluation. This process reduces the size of each cross/family from 240 to approximately 40 individuals that are positive for –two to three major genes (Cobb, Juma, et al., 2019). In the OneRice Breeding Framework, low-density genotyping is routinely used at the F_3 stage in RGA to select for key qualitative traits mentioned in the product concepts. The MAS step is also carried out at the F_2 generation in certain commercial breeding programs (Tiwari et al., 2022).

5 | PRE-BREEDING

Decades of genetic research in rice have identified dozens of major genes contributing to most of the traits needed to address the product concepts. The product concepts for rice require improvement in over 40 traits, including 13 abiotic stress traits, 16 diseases and pests, eight grain quality parameters, and three traits related to agronomic performance (Supporting Information 1). Many of these traits in rice are influenced by major genes, which can supply all or a large portion of the required improvement. This includes traits such as disease resistance (blast, bacterial blight, rice yellow mottle virus (RYMV), tungro virus, root knot nematode, etc.), abiotic stress tolerance (submergence, salinity, drought, heat), grain quality, and many others. Thus, selecting appropriate traits for improvement from among them is a gargantuan task. A summary of MAS opportunities is given in Supporting Information 1.

However, not all the genes needed for a product concept are found in the elite material or may be present at a very low frequency. Approximately 50% of useful trait genes or loci needed for IRRI's breeding pipelines are absent entirely in the elite breeding materials, and a further 20% are present but rare, with frequencies below 15% (Cobb, Biswas, et al., 2019). These include the majority of the most useful disease-resistance genes, including *Pi9*, *Pikh*, *Pi35*, *rymv1*, *rymv2*, *RYMV3*, *xa13*, *Xa21*, and *Xa23*. This is not just an issue with IRRI germplasm, as surveys of elite and breeding material from a wide variety of other rice breeding programs from India, Bangladesh, AfricaRice, and other African partners, CIAT, and South-east Asia have shown the same situation (IRRI data unpublished).

The lack of elite donor lines severely limits opportunities for selecting these genes in mainstream breeding. Available donor materials inevitably contain large quantities of undesirable background genome, presenting breeders with a compromise since utilizing these genes results in very poor performance of resulting populations due to the undesirable, non-elite donor background. In some cases there is also linkage drag associated with the target gene of interest. Consequently, the introduction of these genes is desirable, but this needs to be done in such a way as to avoid introducing substantial yield penalties.

5.1 | Deployment

To eliminate this compromise, the value of these genes is delivered to the breeding programs through the native trait deployment pipeline (Figure 4; Cobb, Biswas, et al., 2019). This process aims to make valuable genes available to elite breeding programs as high-quality introgressions into elite backgrounds through marker-assisted backcrossing, without the penalties of the source genomic background and linkage drag associated with the original donor lines. Native trait deployment employs strict quality control targets, including high recovery of elite genomic background (>95%) and very tight recombinant selection <1 cM on either side of target genes to reduce the risk of linkage drag. In later stages of deployment, value-added genetic products such as development of coupling-phase linkages and pyramids are also targeted. To date, over 50 major genes have been made available, mostly in the elite IRRI 154 background, along with complete

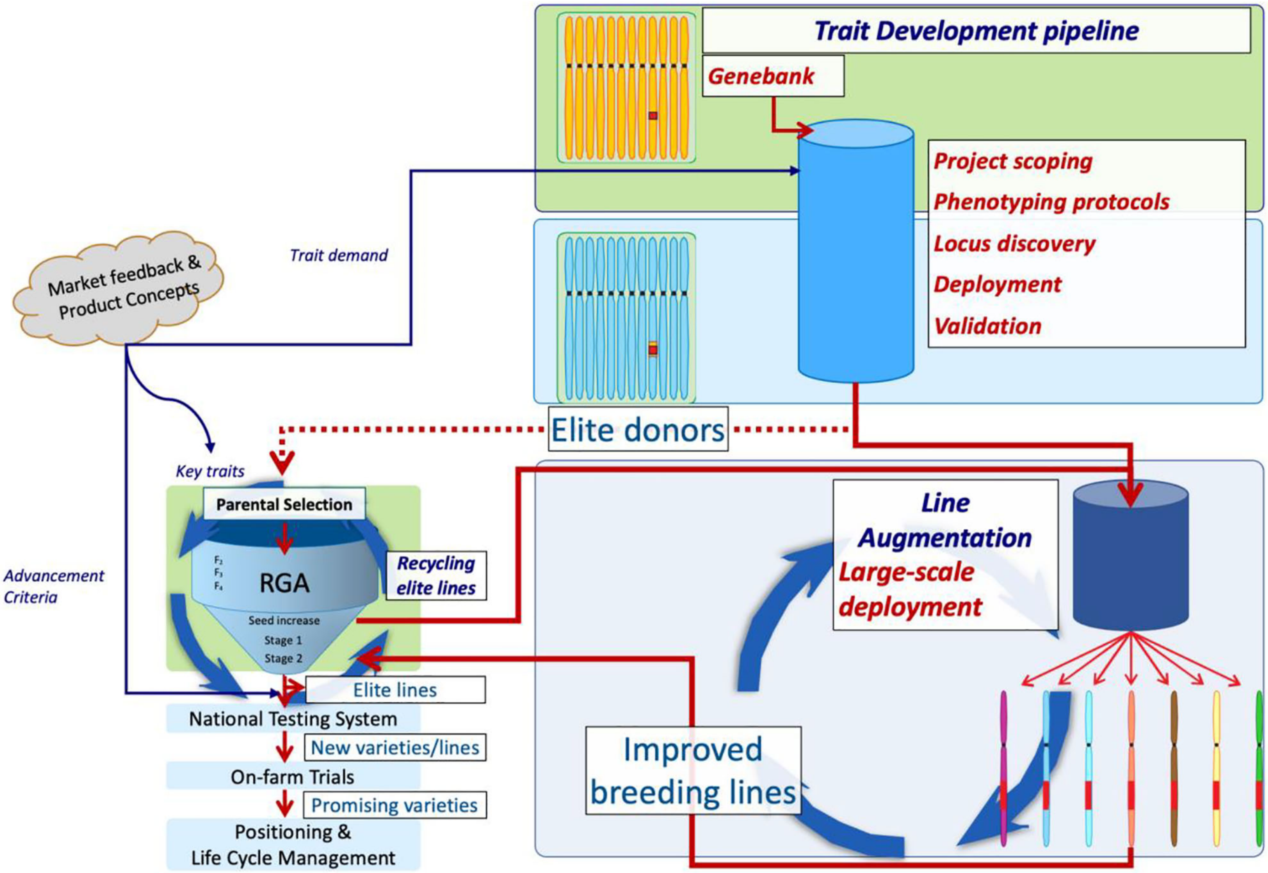


FIGURE 4 Strategy for incorporation of novel alleles of major genes into the elite material. A two-stage process is followed: deployment involves producing a single high-quality introgression of a target locus into an elite background. Augmentation utilizes the deployment product to rapidly diversify the elite backgrounds containing a new gene. Together these allow new genes to be deployed at significant scale in the elite breeding program without compromising yield or genetic gains. RGA, rapid generation advance.

pyramids designed to produce durable resistance to major diseases (blast, bacterial blight, RYMV, and others) and abiotic stresses (drought and salinity).

5.2 | Line augmentation

The deployment of new genes into an elite background is thus progressing rapidly at IRRI, and the outputs of deployment activities can be used directly in the mainstream crossing program. However, due to resource constraints and the need to focus efforts on producing high-quality introgressions, it is not possible for deployment activities to produce a wide diversity of elite donors. To date, deployment has focused on a single, general-purpose background (IRRI 154) that can serve as a bridge into a wide variety of breeding programs. This is suboptimal for two reasons: excessive crossing with a single genetic background will produce a skew in the haplotype frequencies in a breeding program, reducing genetic variation. Second, while IRRI 154 is widely adapted and is considered to be a good general-purpose background, by the same token it is necessarily something of a compromise and may not be among the top performers for any given breeding program, and has some undesirable characteristics (notably in grain quality) for certain market segments.

Ideally, every individual breeding program requires specific new genes in a variety of elite backgrounds (and local haplotypes) so that the value of the gene can be captured separately and independently of the genomic background and local haplotypic diversity. To address this, a different form of introgression program is being established, which is called Line Augmentation. The focus of this effort will be to produce early-generation (BC_1F_4) conversions of as many elite backgrounds as possible to rapidly increase the frequency and diversity of elite material containing new genes. Since speed and quantity are the primary focus areas, there will be insufficient bandwidth to focus on quality; however, since augmentation activities can start with high-quality elite lines from the deployment pipeline as input donor material, the major genomic penalties typically associated with trait donors have already been eliminated. Recipient lines to be upgraded with new genes are sourced from the best of the current elite material (Stage 2, or Stage 1 predictions; see below) produced by mainstream breeding programs. Genomic quality of augmentation products is further improved by applying selection for GEBV during the BC_1F_1, BC_1F_2, and in some cases BC_1F_3 generations (Platten & Fritsche-Neto, 2023). Thus, this two-stage process of Native Trait Deployment and Line Augmentation enables breeding programs to gain both high quality and large quantities of donor material well-suited to their individual efforts.

6 | PRODUCT TESTING AND ADVANCEMENT

6.1 | Evaluation of breeding lines in the TPE

It is essential to evaluate the variation generated in the crosses through segregation before the selection process (Lynch, 1998). Testing of new germplasm developed through the breeding process is done by conducting multi-environment trials (METs) under field conditions across the TPE. Data generated from these field trials are used to select lines as parents, advancement products for release, and inform commercialization steps. Consequently, accurate and comprehensive multi-location trial data are crucial to the success of breeding programs. The accuracy of selection, which is a square root of the heritability of the trait, is influenced by the quality of data collected from the trials for the trait of interest. Several factors influence trial quality, including the number of locations, the experimental design, plot size, replications, and the inclusion of checks. With the advancements in the fields of statistics, quantitative genetics, and genotyping, the breeders now have the power to estimate the genetic values of individuals through a combination of the phenotype and genotype data (Meuwissen et al., 2001).

One of the fundamental transformations at IRRI has been that all of its early-stage (hereafter referred as Stage 1) and late-stage (hereafter referred as Stage 2) breeding trials are now conducted with NARES partners in the respective TPEs. TPEs are the environments under which each breeding pipeline makes selections and advances the genotypes. Previously, all of the early-stage and late-stage trials were previously conducted mostly in one location, IRRI Headquarters (HQ), Philippines. The development of a comprehensive network of trial locations is one of the key factors enabling reliable improvement of rice germplasm. The implementation of these networks in the breeding program has been almost uniquely enabled by the multinational nature of CGIAR centers such as IRRI, which can aggregate data from similar environments across countries to provide more accurate predictions. Having a sufficient number of locations allows the breeding pipeline to sample the TPE more comprehensively and better estimate G × E effects. The TPE for IRRI breeding pipelines/product concepts covers countries in South Asia, East and Southern Africa, and Southeast Asia. Therefore, after the breeding lines exit the RGA, a seed increase step is performed for each pipeline and shipped to the corresponding NARES partner in the regions. Population development is thus decoupled from testing.

SOPs for Stage 1 and Stage 2 trialing have been outlined and shared with national partners for uniform evaluation across locations (Supporting Information 2). For a 1X breeding pipeline, the number of trial sites required is greater than six. Experimental designs, either fully or partially replicated, are fixed and homogenized across all locations for uniformity. Minimum plot sizes of 5 m^2 are recommended in all the trials to minimize the error component in the single trial and multi-location trial analysis (Gomez, 1972). Apart from test entries, every trial should include about 10 checks where some act as connectivity checks across trials and years, and some act as benchmark checks for the target market segment.

Under the OneRice Breeding Framework, the IRRI breeding programs have been testing a larger number of Stage 1 breeding materials than previously in multiple locations directly in the TPE. The total number of entries tested in each of the Stage 1 and Stage 2 locations is determined based on the NARES partner testing capacity. In the Stage 1 trial, around 200 breeding lines are evaluated in each location. A sparse testing approach is followed, and hence a different but partially overlapping set of 200 lines (replicated at 1.2x) is evaluated in each location allowing most of the lines to be tested at least in one environment. The genomic information is then coupled with phenotypic data to compute GEBVs, and then GS is carried out (see below). The best lines from the Stage 1 evaluation are selected using a selection index to be recycled as parents and also advanced to Stage 2 (late-stage testing) trials. Around 25 breeding lines are tested in Stage 2 trials for product extraction in the following year at the same locations in the TPE. The best lines from the Stage 2 based on their phenotypic performance are nominated to national level testing in the respective countries, and subsequent evaluation is managed by the national varietal testing programs.

6.2 | Genomic selection

GS is a powerful tool for plant breeding to increase the rates of genetic gain (Crossa et al., 2017). Numerous studies have implemented genomic prediction in rice, many of which examine the accuracy of different prediction models using breeding populations (Arbelaez et al., 2019; Azodi et al., 2019; Banerjee et al., 2020; Berro et al., 2019; e Sousa et al., 2019; Gao et al., 2017, 2018; Matias et al., 2017; Monteverde et al., 2019, 2018; Spindel et al., 2016, 2015). Despite the proven benefits, only a few rice breeding programs have implemented GS routinely in their breeding programs.

The OneRice Breeding Framework is designed to enable GS. Mid-density genotyping is carried out prior to field evaluation of Stage 1 material, and GS is implemented using the phenotype data from the Stage 1 trials to reduce the cycle time and increase the intensity without an increase in cost. IRRI is one of the few public rice breeding programs that has integrated GS and routinely implements it in its breeding programs (Bartholomé et al., 2022). The process makes use of a medium density marker panel (the 1k RiCA) for genotyping (Arbelaez et al., 2019), a defined base population for genetic connectivity (Juma et al., 2021), full adoption of the Enterprise Breeding System (EBS) data management system for seamless multi-year analysis, and a semi-automated analytical and reporting workflow (Bartholomé et al., 2022; Hussain et al., 2022) to perform routine data analysis and make breeding selections over recurrent cycles.

At IRRI, all the breeding lines are DNA fingerprinted using a 1k RiCA custom-designed single nucleotide polymorphism panel at the seed amplification stage (Arbelaez et al., 2019) and implemented at Agriplex and DArT. These data generated are used to build the genomic relationship matrix of the breeding lines to select a training set for genomic prediction models and to predict the performance of the entire Stage 1 breeding cohort in every pipeline. Training set selection enables testing of a portion of the Stage 1 lines in order to predict the remaining untested lines. Therefore, a NARES partner who can test no more than a few 100 lines at a time in a particular trial site will be able to receive breeding values of all the 1200 Stage 1 lines generated through genomic prediction.

The primary output of a breeding pipeline is to identify top-performing breeding lines to nominate for each respective market segment. The optimal numbers outlined in the OneRice Breeding Framework are derived through Mendelian and population genetics concepts, the number of breeding lines needed for nomination, and also the capacity of the breeding operations unit (BOU). These numbers are further corroborated by previous stochastic simulation studies performed in a cassava (*Manihot esculenta*) breeding program (Covarrubias-Pazaran et al., 2022). Our current numbers fall well within the recommended range considering both short-term and long-term breeding time frames.

6.3 | Parental re-cycling and product extraction

Shorter breeding cycles and the use of GS for recycling parents will enhance the rates of genetic gain. However, pursuing higher rates of genetic gain will also accelerate the depletion of genetic variation compared to conventional phenotypic selection (Seck et al., 2024). To overcome this, breeders need to adopt methods to maintain the genetic variation in their breeding pool and also to achieve genetic gain, such as through optimal contribution approach (Kinghorn, 2011).

Parental recycling under the OneRice Breeding Framework is done after Stage 1 evaluations by using GEBVs. Lines are selected based on multiple traits, and thus some sort of selection index method is required. Since it is challenging to obtain exact weights for each trait, the desired gain approach is used to select lines for multiple traits (Pešek & Baker, 1969). Under the OneRice Breeding Framework, parental recycling is implemented at the F5 generation, producing a breeding cycle time equivalent to 3 years.

Decisions on which lines to recycle as parents are made during joint annual advancement meetings between IRRI and NARES partners for each breeding pipeline addressing a market segment. Advancement criteria are based on the product concepts, and decisions are made collectively by breeding teams and NARES partners. The joint annual advancement meetings are conducted physically in the corresponding regions involving all the associated NARES partners and the associated IRRI breeders. The aim of the advancement meeting is to select lines from Stage 1 to Stage 2 using GEBV, and from Stage 2 to the national testing system using phenotypic best linear unbiased predictions (BLUP) and parental selections from Stage 1 using GEBV. Prior to the advancement meeting, the single trial and MET analysis summaries generated using all the Stage 1 and Stage 2 data of the evaluation year are shared with the NARES partners. A typical summary report contains breeding values of individual quantitative traits, selection index scores, and trait marker profiles of all the breeding lines (both tested and predicted). In addition, the summaries are consolidated into short interactive HTML format for uniformity and better understanding.

7 | PRODUCT DELIVERY

For the breeding lines advanced from Stage 2 trials, there is a need to validate their performance and adaptability across a large number of representative locations of the TPE. This is a critical step before the positioning efforts are made to scale the products in the seed chain to ensure access and adoption.

Under the OneRice Breeding Framework, product evaluation and positioning are carried out by conducting a large number of on-farm trials (OFT) across the TPE. The number of test locations is 30 or more to generate statistically robust evidence of the product's performance. The products (either newly released or advanced lines closer to release) are nominated across the breeding pipelines or leveraged market segments. Nomination of products (advanced breeding lines) is generally the prerogative of the national coordinators from the NARES breeding network, working closely and in unison with the IRRI pipeline and regional breeding leads. While IRRI's Seed System and Product Management Unit plays a neutral catalytic role, product nominations from any pipeline are a blindfolded exercise repeated every season/year. In the process, non-IRRI lines are included as entrants, depending on merit. This increases the competitive value of the product pool that is advancing to the OFT. This essentially provides better choices against varietal replacement targets.

A typical OFT layout (under one pipeline/market segment) consists of —five to six candidate varieties (nominated new lines or varieties), a replacement target/farmer check (older varieties), and also a promising benchmark for that segment. While farmer checks can vary from site to site given the diversity of rice varieties in the regions targeted, the benchmark and the candidate test varieties remain constant within each pipeline across all the sites. The farmer's check is an older product, still popular in the market and grown by farmers widely, which serves as a replacement target. The benchmark is a relatively newer product with a strong performance track record. The candidate varieties are the choices available from breeding programs. The OFT results (yield and other agronomic traits measured) provide the data to select the best product from the candidate pool. A general scale of more than 10% average yield advantage over both the benchmark and farmer checks is considered as a minimal requirement to advance/position the new product in the seed chain. A minimum of 15–20 trials are conducted for each pipeline under each targeted region. In a country like India where varietal release systems and seed markets have federal regulatory systems and associated opportunities, replications (trials) are often counted at the state (province) level (targeting state release and seed markets), and a holistic picture is also taken at the national level combining all state results (targeting national release systems). The NARES who operate in technology delivery and scaling domains are partnered, trained, and capacitated around the protocols of the OFT. The biometrics team of Rice Breeding Innovations (RBI) Department at IRRI supports NARES in data analysis, result consolidation, and interpretation before efforts on product positioning start, targeting formal and informal seed systems.

8 | CENTRALIZED BREEDING OPERATIONS

Most, if not all, breeding programs operate under finite resources, and therefore, achieving scale and efficiency per dollar spent becomes an important element for a breeding program's success. In addition, it is not efficient for any research organization to maintain multiple breeding teams with overlapping expertise who are independently working on similar activities. Instead, field operations can be managed as centralized services and executed by pooled technicians following the standard operating protocols. This way of organization allows consolidation of research activities, mechanization, and thus generation of high-quality genetic materials and field data. Many private research companies have implemented this model so that breeders can focus on decisions related to breeding rather than spending the majority of their time on managing routine day-to-day field activities.

At IRRI, the BOU is composed of the Cross Cutting Operations (CCO), IRRI Service Laboratories (ISL), Zeigler Experiment Station (ZES), and Seed Health Unit (SHU). BOU exists to provide research services at optimal cost through operational excellence supporting the OneRice Breeding Framework. BOU operations encompass performing crosses of elite lines, genotyping of materials, advancing generations in the RGA, conducting yield trials, and collecting phenotypic data at the IRRI HQ.

The SHU at IRRI handles all of the seed shipment processes from IRRI HQ to the breeding network locations in the TPE. This includes obtaining the necessary government permits from the importing country, preparation of seeds at IRRI HQ, screening for the presence of regulated pathogens, seed treatment and phytosanitary certification, and shipment to the NARES partners via host country quarantine agencies as applicable. After clearance and release of the seeds, the NARES partners will sow the planned trials in the TPEs in the main season following the IRRI standard trialing protocols.

8.1 | Forecasting of breeding activities

Oftentimes breeding programs do not know the exact cost involved in completing a breeding cycle, posing a critical challenge for resource optimization. This necessitates the need for a breeding costing tool through which a breeding program can calculate the cost for each of its breeding pipelines (e.g., https://aussorgm.org.au/downloads/breeding-costing-tool/). Only when the costs are estimated with reasonable accuracy can the breeding programs know the gain per dollar investment and appropriately optimize the breeding schemes.

After the implementation of the OneRice Breeding Framework, it became feasible for IRRI breeding programs to forecast seasonal and yearly activities from crossing up to shipment based on the respective pipeline sizes. Standardizing the activity-based costing of all breeding steps has enabled the breeding teams to arrive at the research budget needed for the calendar year ahead. This allowed the BOU team to better estimate the resources needed for IRRI breeding pipelines and to recommend adjustments as per the available research budget.

8.2 | Data management and analysis

Digitization of breeding data and using a breeding data management system have already become essential to safely store and retrieve data at any place and at any time. IRRI's breeding program uses EBSs, which is an open source breeding informatics software (https://ebs.excellenceinbreeding.org/). All stages of the breeding process are supported by the EBS, which acts as a centralized data repository and analysis suite. All of the breeding pipelines have fully adopted EBS, which allows breeders to (i) create and manage germplasm, trials, and nurseries; (ii) collect and upload trial data digitally; (iii) connect to genotyping, quality, and phytosanitary (shipping) services; and (iv) perform basic analysis of single and multiple location trials.

As breeding programs are conducting multi-location trials, genotyping the breeding lines, and using GS every year for the selection process, there is a strong need for a data analytical workflow and pipeline to efficiently use the phenotype and genotype data in complex statistical models. Over the years, IRRI has evolved from using semi-automated data analytical workflows (Bartholomé et al., 2022; Hussain et al., 2022) to an advanced, fully automated analytical workflow (https://cgiar-market-intelligence.shinyapps.io/bioflow/). The analytical workflow allows breeders to perform the single trial analysis to correct for experimental design factors and spatial variation, multi-location analysis where the phenotype and genotype data are combined to generate breeding values, build selection indices, design the crosses through optimal contribution selection, and generate interactive reports. The yearly analyzed data and the advancement summaries are also deposited on the RBI microsite (https://rbi.irri.org/rbi-at-a-glance) for the breeding teams and the collaborators to revisit and use them.

9 | PARTNER NETWORK MANAGEMENT

The NARES partners network is crucial for all breeding programs at IRRI and other CGIAR breeding programs. Previously the NARES network was created and managed through a research project-based approach, and the network activities ended when the project ended. This approach was disadvantageous for breeding programs that adopt population improvement approaches, where testing is required for multiple breeding cycles, which often exceed the duration of a given research project.

To strengthen the IRRI-NARES network, a network management strategy was developed as part of the OneRice Breeding Framework. The hub and spoke model was chosen to connect and promote two-way interaction with the NARES partners in South Asia, Southeast Asia, and East and Southern Africa regions (Figure 5). Relevant NARES partners are identified based on the active market segment and the network is maintained in a project-agnostic fashion for long-term benefits. The NARES network is actively involved right from early-stage testing to the OFT and in joint advancement of breeding products to the national release systems. Routine capacity-building exercises on modern breeding methods, data analysis, and seed systems are conducted to empower NARES partners in the regions of interest. A detailed division of labor for IRRI and NARES partners has been developed for effective functioning of the network (Table S2).

10 | IMPLEMENTATION OF THE ONERICE BREEDING FRAMEWORK AT IRRI

All of the active breeding pipelines from early, medium, and late maturity breeding programs have fully adopted and implemented the OneRice Breeding Framework. The breeding cycle time has been gradually reduced to 3 years. One full breeding cycle using elite by elite by crosses is completed while the crosses for the next cycle are currently in the generation advance step. Further reduction of cycle length is planned and potential breeding schemes are simulated to determine the best scheme (Seck et al., 2024). The parental recycling and product extraction steps are clearly decoupled in the breeding scheme. Genomic prediction is routinely performed in all of the breeding pipelines, and the parents are recycled purely based on the GEBV from the Stage 1 trials. Product advancement is done using the phenotypic BLUP from the Stage 2 trials. A higher rate of realized genetic gain (∼1%) than the historic estimate has already been observed for one of the pipelines that has at least 5 years of data (https://www.cgiar.org/initiative/accelerated-breeding/?section=results). This increase could be attributed to the disciplined breeding practices as outlined in the OneRice Breeding Framework. When the segregants of the next breeding cycle will be tested, genetic gain numbers will be calculated and updated for all the breeding pipelines.

11 | CONCLUSIONS

Modernization efforts of the IRRI breeding programs started in 2012 through the Transforming Rice Breeding project funded by the Bill and Melinda Gates Foundation (BMGF). Rice breeding prior to 2014 was characterized by separate, discrete breeding programs based generally around ecosystems, grain quality aspects, and specific stress targets (irrigated, rainfed, salinity, submergence, biofortification, hybrids, Green Super Rice). There was limited early-stage multi-location testing, and crossing involved significant use of landrace parents. Initially, the focus of breeding modernization was implementing rapid line fixation, a central database for curating germplasm information and phenotype data (development of B4R), developing a multi-location early-stage testing in the Philippines, and a focus on variety replacement and genetic gains as metrics of program

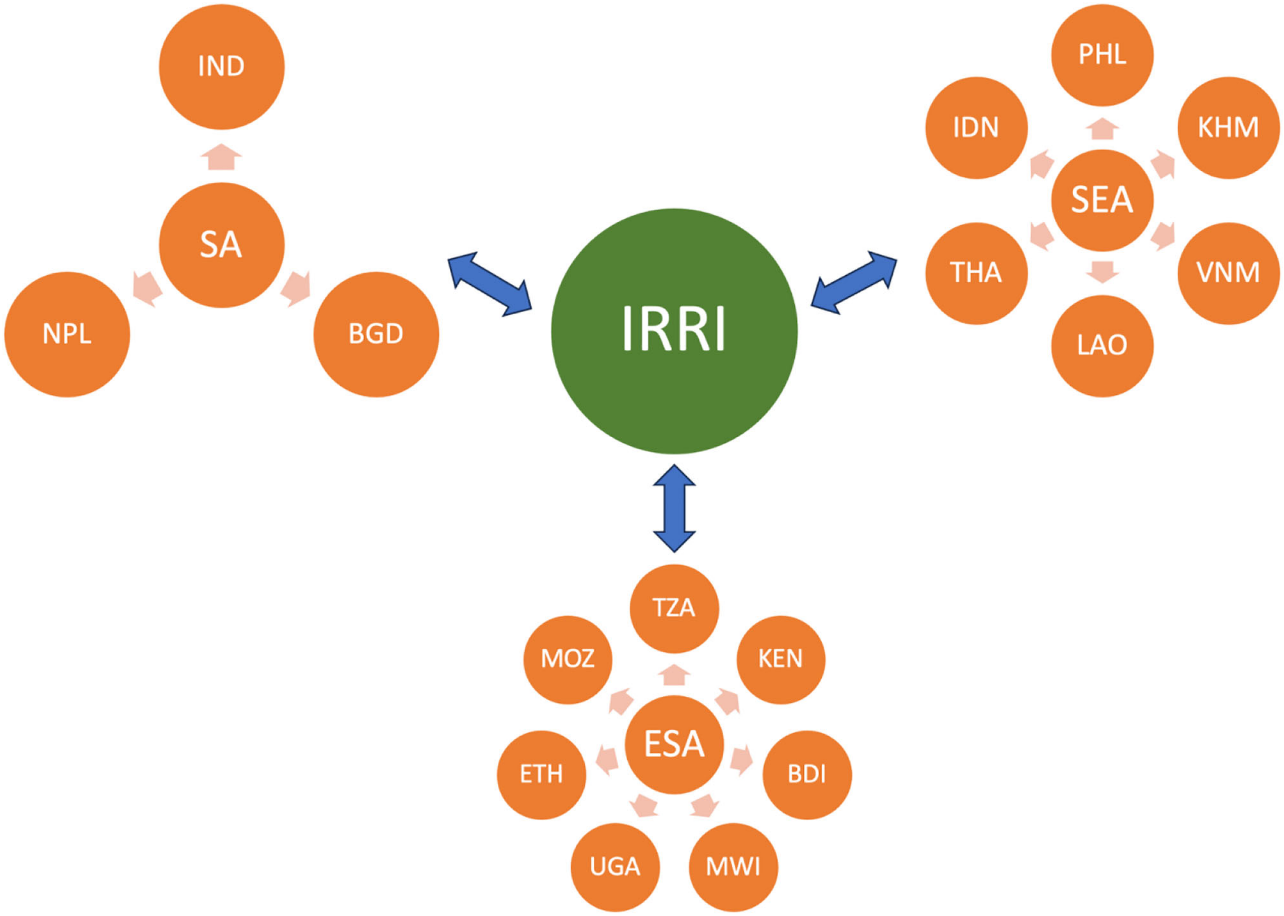


FIGURE 5 The hub-and-spoke model of the International Rice Research Institute-National Agricultural Research and Extension System (IRRI-NARES) network with multiple partners within the South Asia (SA), Southeast Asia (SEA), and East and Southern Africa (ESA) regions. The regional breeding leads work and interact on a regular basis with NARES partners in different countries (smaller circles) within the regions. The countries represented are India (IND), Bangladesh (BGD), Nepal (NPL), Tanzania (TZA), Kenya (KEN), Burundi (BDI), Malawi (MWI), Uganda (UGA), Ethiopia (ETH), Mozambique (MOZ), Philippines (PHL), Indonesia (IDN), Thailand (THA), Lao People's Democratic Republic (LAO), Vietnam (VNM), and Cambodia (KHM). IRRI's partner network is not just limited to the countries mentioned in this figure.

success. The focus of modernization initiatives has progressed to include a much more comprehensive set of changes addressing all aspects of the breeding process. These are often driven by standard operating processes proven in the private seed industry, while some have been developed in-house at IRRI.

Despite these positive changes, the IRRI breeding programs still required a unified strategy and framework to adhere to as a standard way of elite inbred creation, strict focus on population improvement to sustain genetic gains, centralized pre-breeding, quick development and dissemination of germplasm, and rigorous multi-location testing and life cycle management in a close cooperation with partner NARES partners. The breeding efforts were reported on a project-by-project basis leading to the creation of silos resulting in variable use of high-value materials (genes/donors/elite lines). It was a challenge to evaluate the progress of breeding programs due to the absence of common framework and key performance indicators. All of this could be attributed to the lower and variable rates of genetic gains in the breeding programs. At the same time, investment expectations in CGIAR programs have changed to a more accountable role of delivering the rate of genetic gain in farmers' fields. Therefore, the IRRI breeding programs urgently needed a unified framework to organize the way of working and gear up to meet the evolving expectations.

Although this review on the OneRice Breeding Framework focuses primarily on breeding inbred lines, it is easy to extend the principles to hybrid rice breeding programs or other crops with similar reproduction biology. For instance, in the hybrid rice program, the male and the female breeding components could adopt the inbred breeding scheme (Figure 3) with minor modifications such as evaluating top crosses at Stage 1 trial rather than just the inbreds, use of non-additive effects in the GS model, and so on. In cases where the same product concept is targeted by both inbred and hybrid breeding programs, the elite lines from inbred breeding pipelines can be shared with the hybrid breeding pipeline to be tested in hybrid combinations (Figure S1), expanding the scope of products.

The OneRice Breeding Framework establishes an end-to-end system of creating and disseminating improved rice varieties faster. The system takes into account the division of rice geographies into meaningful pieces (market segments) in which critical trait information is captured into product concept documents that provide a target to guide centralized pre-breeding and breeding processes using the central service platform of IRRI to drive the economics of scale. Once high-value fixed lines are created, they are tested in the target environments with NARES partners, and a GS process is implemented to predict the performance of the entire breeding cohort to generate GEBVs; these high-value lines then enter national testing and release systems. Subsequently, the seed systems and product management component of the OneRice Breeding Framework provides catalytic support to the seed systems and the varietal dissemination by providing leadership in creating product profiles and database resources of major attributes of leading mega and promising varieties, which are the replacement targets through an active engagement with NARES and seed system players. In summary, the OneRice Breeding Framework is an end-to-end system that provides a clear and effective framework for teamwork through proactive engagement and capacity building of NARES partners to create a stronger foundation for the product development. The OneRice Breeding Framework can serve as a guide for public crop breeding programs to increase the rate of genetic gains to address global food security.

AUTHOR CONTRIBUTIONS

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CONFLICT OF INTEREST STATEMENT

The authors declare no conflicts of interest

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