
Securing Diversity for Food Security: The Case of Conservation and Use of Rice Genetic Resources

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Abstract

Producing enough food, fiber, and fuel, in this case, the second most important global crop called rice, remains a continuing challenge as global population increases and various production constraints ensue. Plant breeding scientists prefer using elite rice lines but also infuse new genetic resources into the parental genepool for desirable traits, such as resistance to pests and diseases, good flavor, and high nutritional quality on top of high-yielding potential. Prior research studies reveal the importance of germplasm resources including wild rice relatives as excellent sources of desirable traits in new crop breeds. Advances in molecular and genomics approaches (QTLs, GWAS, OMICS technologies) have identified and transferred genes, genomes, loci among other important genetic materials that are sought for. As knowledge builds up with these biotechniques, more rice genetic resources can be characterized at the molecular and systems levels for further utility in breeding better cultivars. Information generated from innovative approaches must be documented and processed as germplasm characterization data and must remain accessible at genebanks that exist centrally to conserve biodiversity. Development of germplasm information should be a collaborative effort of scientists who share similar interests in exploiting the valuable and novel genes within germplasm resources that are essential for crop improvement.

Keywords: rice genetic resources, diversity, molecular approaches, OMICS technologies, genomic-assisted breeding

1. Introduction

Food-production systems are greatly affected by increasing demand of a burgeoning world population on top of production constraints as such water availability, soil degradation, dwindling

arable lands, and abrupt changes in climate. Commitments to uphold the fundamental right of people to have adequate food and to be free from hunger were made during the Rome Declaration on World Food Security in 1996 and the United Nations Millennium Summit in 2000. These included commitments of participating countries to implement policies on eradication of inequality and poverty through improved economic and physical access to sufficient, safe, and nutritious food supply. Despite these efforts, almost 1000 million people experience malnutrition and hunger, of which 15 million who are predominantly children die every year [1]. Producing enough food becomes more crucial considering that population is expected to grow to about 8.3 billion by 2030 where about 90% of the increase emanates from developing countries [2]. Considering such pressures, one must remember that food security is interlinked with wise use of agricultural biodiversity and genetic resources including their conservation and exchange [1].

Plant genetic resources for food and agriculture (PGRFA) are crucial for food production and sustainable agriculture as they become foundations for breeders, biotechnologists and farmers engaged in developing new plant varieties that can address growing food demands, unpredictable human needs, and changing environmental conditions [1]. Although significant to human survival, PGRFA is dwindling at an alarming rate. For example, hundreds of thousands of heterogeneous plant varieties and landraces have been developed for generations in farmers' fields until the beginning of the 20th century [1]. It is also important to note that socioeconomic perspective in agriculture varies by region. About 50% of the populations in Africa and Asia depend on agriculture, while only a meager 1.9% does in North America, and that half of the world's population chiefly draws income from agricultural production [2].

2. Germplasm banks and functions

Worldwide, central to conserving agricultural diversity are about 1700 genebanks including 11 international genebanks that spend about US\$18 million a year [3] to maintain, manage and share germplasm collections. These 11 international genebanks are managed by the consortium of international agricultural research centers (CGIAR, formerly the Consultative Group for International Agricultural Research). Collectively, CGIAR genebanks hold 730,000 accessions in 35 collections, available as seeds, plants maintained in screenhouses or fields, in cryopreservation, in tissue culture, and as DNA samples [4]. In recent years, germplasm distribution reported an overall increase estimated at almost 40,000 samples yearly between 1985 and 2009 [5] and almost 92,000 samples yearly between 2012 and 2014 [4]. The considerable upsurge in value and demand for diversity will ensue owing to present-day advances in high-throughput sequencing and phenotyping, disease indexing, and screening data [6].

Although genebanks exist as germplasm repositories, farmers and farmers' groups, or organizations also exert efforts to save seeds of crop species and have been custodians of landraces and traditional varieties as well [7, 8]. Additionally, genebanks exist to conserve the genetic diversity of wild and cultivated plants that people rely on as a source of food, fuel, and fiber [3]. Maintaining biodiversity in both plants and animals has become a central principle in

formulating strategies for sustainable agriculture advancement [7]. Diversity is important in progressing nutritional quality, productivity, and sustainability [3] of plants and animals. Diversity shown in crop wild relatives (CWRs) means beneficial traits such as resistance to biotic and abiotic stresses and adaptation to a wide range of habitats or environments [9–11], which are important attributes to curb the effects of climate change-induced variations [12] affecting crop growth and development parameters.

Throughout time, scientists and researchers including the public have witnessed and realized the long-term benefits derived from conserving and securing biological diversity [7]. The biodiversity conserved in genebanks helps advance global plant breeding programs [3]. In rice, for example, a study found out that *Oryza nivara*, a wild rice species conferred protection against grassy stunt virus to almost all tropical rice varieties in Asia [7]. Additionally, a genomics study [6] on more than 4300 rice varieties worldwide reported that 100% of the varieties from the international rice research institute (IRRI) and 90% of non-IRRI varieties have in their pedigrees at least one accession from the international rice genebank (IRG).

As of January 2017, IRRI reports that IRG maintains more than 127,916 rice accessions and 4647 wild relatives including 44 wild *Oryza* species and nine species from seven related genera [13]. This makes the Philippines as the country repository having the largest in number and most diverse rice genetic resources (Figure 1) as shown in Genesys, a global portal to information about PGRFA. IRG's holdings come from various rice-growing countries that transmit to IRG the seeds of rice cultivars for safeguarding and sharing as public goods [13].

Considering agricultural diversity as a public good strengthens global interdependence and proactive upkeep of plant genetic resources [14]. One of the deep-rooted forms of interdependence is the reliance of foreign genetic resources as exhibited by the spread of common

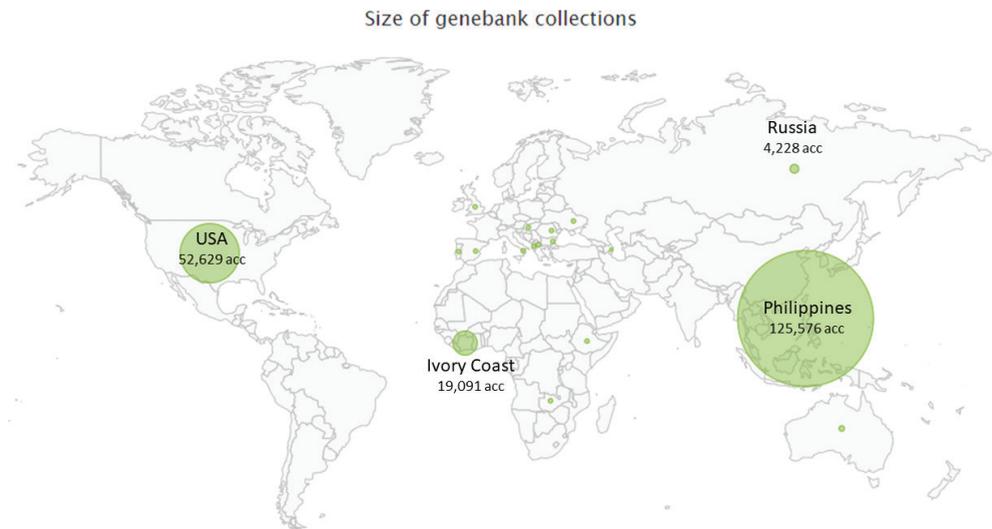


Figure 1. Genebank holdings of rice germplasm around the world (data from Genesys database <https://goo.gl/xPFzSE>).

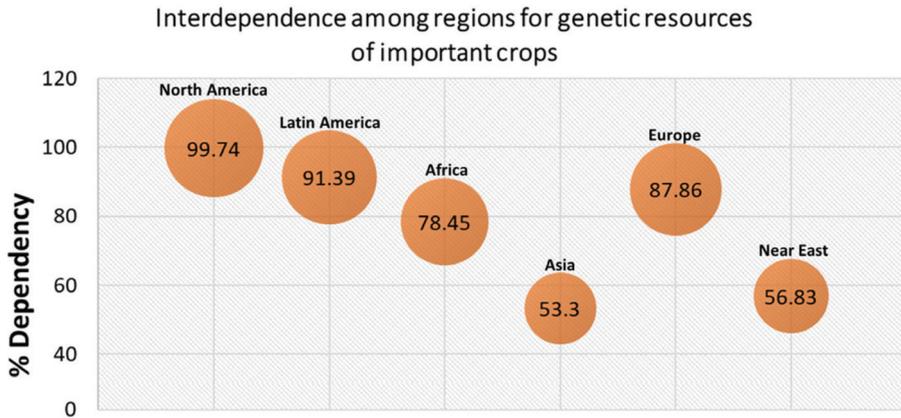


Figure 2. Estimate of the degree of interdependence of major regions on genetic resources of important crops.

crops from centers of origin to the rest of the world [1]. About 70% is the estimated average of interdependence degree of countries (**Figure 2**) on the most important crops worldwide [1]. These relate to the function of genebanks as worldwide distributors of crop germplasm to help sustain the availability of food, fiber, and fuel, strengthen on-farm crop diversity and crop productivity. The dependency of most countries and their farmers on modern, improved varieties of rice, corn, wheat, and other crops [15] existed then and likely on the rise owing to productivity concerns brought by global climate change. For example, at the top of its popularity, IR36 rice variety was planted to 10% of the world's rice area which is about 11 million hectares [16]. Moreover, modern varieties are usually created using genetic resources sourced from various countries that demonstrate the interdependence on the availability and accessibility of plant genetic resources [16] for sustainable agriculture and food security.

3. Rice production systems and constraints

Rice ranks second to maize among the most important cereals globally produced in the world [17]. Global rice production was forecasted at a record high of 481.3 million tons in 2017 with the bulk of production coming from Asia (**Figure 3A**) [18]. Rice is chiefly consumed in the developing countries (**Figure 3B**) with about 340 metric tons (Mt) and 392 Mt. (15% increase) consumed in 2002–2004 and in 2012–2014, respectively, [19] and projected to reach 449 Mt. in 2024, a 32% increase from 2004 consumption level [19]. In contrast, developed countries consumed 17 Mt. of rice in 2002–2004 and about 3% more (17.5 Mt) in 2012–2014 and the consumption is expected to reach 18.2 Mt. [19].

The South Asia region is a global major rice producer yet 75% of rice growers from this region are smallholders [20]. Smallholding farmers are key food producers in developing countries contributing about 70–80% of the food produce in Africa and in sub-Saharan Africa, respectively [20]. Due to their major role in food production in developing countries, smallholder farmers

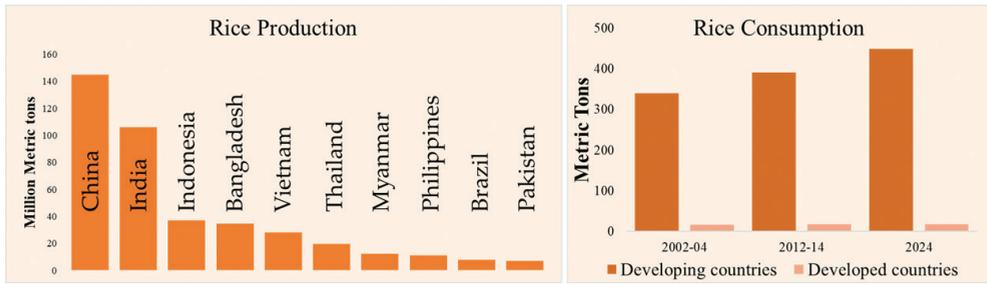


Figure 3. Rice production and consumption in the world. (A). Top 10 rice producing countries in the world. (B). Rice consumption in developing and developed countries (data from (Childs, 2017) and OECD/FAO, 2015).

are crucial contributors to food security and produce more than 50% of the food requirement to feed 9 billion people in 2050 [21]. However, these groups of farmers are highly vulnerable to production constraints, which include socio-economic, biotic, abiotic, and management-related factors (**Figure 4**) [20]. Studies have shown that 18–21% and 22–23% of yield losses are attributed to biotic and abiotic factors [20, 22]. Another major biotic factor to yield loss is weed competition contributing up to 7% yield loss in rice production of small-scale farmers [20]. Studies on no weed control in rice production incurred as high as 94–96% yield loss during the wet and dry season of 2009, respectively [23]. Insect pest that accounts 5% yield loss among smallholder farmers [20] have caused 20% loss in sub-Saharan in 2008 [24]. Socio-economic factors contributed 22% to yield loss from which 4.5% is due to difficulty in access to sufficient irrigation water [20].

Shifts in global climatic conditions also pose threats of limiting crop yields and water-supply availability among other factors that threaten the bumper food supply. In the United States, USDA-ERS reports that climate change can limit average yields in various crops including rice in both dryland and irrigated production by 2020 [25]. The projected decline in US rice production is 2.2% by 2020 to as much as 6.1% by 2080 [25].

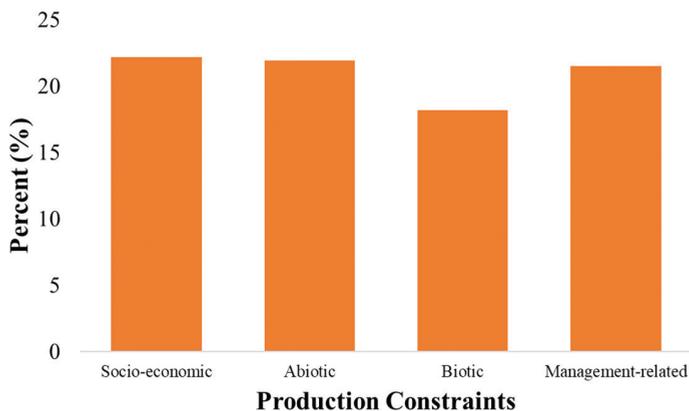


Figure 4. Major factors affecting rice production in south Asian farmers.

4. Importance of rice genetic resources

Smallholder farmers have contributed to and unknowingly preserved the diversity of rice genetic resources throughout time as they cultivated, selected, and nurture their favorite cultivars owing to favorable yield and quality of product. These cultivars comprised of landraces and traditional varieties are vast sources of important genetic traits that can further improve future rice varieties [8]. Historical accounts on rice breeding, for instance, show the discovery and development of high-yielding cultivars that can withstand environmental stresses, such as varieties having excellent genes for submergence tolerance and having significant yield increases owing to NAL1 allele [8]. One variety dubbed miracle rice, IR8 released in 1966 served as a source of desirable traits and reportedly is associated to 92% of the 67 rice varieties released in the Philippines between 1960 and 1994 and that the varieties have 57 more parental lines in commonality [26]. Moreover, 19 ancestral parents comprise the genetic core of all Philippine rice cultivars developed from 1960 to 1994 [26, 27].

Genetic diversity of the 193 rice cultivars collected from 19 countries was studied toward developing an international rice molecular program [27]. A cluster analysis using SSR data of the 193 accessions showed four prominent groups: classical *indica* (Group I), classical japonica (Group IV), and a mix of modern cultivars, traditional *japonica*, and diverse landraces (Groups II and III) of which Group I showed the highest level of diversity [27]. Among 632 alleles shown in the study, only 5% was prevalent alleles, which were consistent with the known knowledge that 95% of the rice gene pool was seldom used in rice breeding programs [27].

Other notable results of the study include the possible existence of differentiation between the temperate and tropical indica that may not be exhaustive as those in japonica cultivars in same regions [27]. Additionally, the study revealed that high genetic diversity between Chinese *indica* maintainer lines and the tropical restorer line developed at the Philippine-based IRRI highly influenced the hybrid vigor of Chinese hybrids [27]. The study further suggested that molecular breeding of *japonica-indica* variation be explored to further increase the genetic diversity of rice cultivars that may improve production sustainability and help break the yield ceiling [27].

A recent genomics research study underscores the importance of genetic conservation in rice. Using 13 reference genomes of modern and related-rice species, the study found rapid species diversification reflected by lineage-specific emergence and turnover of various novel elements, consisting of potential new coding and noncoding genes and transposons among others [28]. Analyzed genomes were new *Oryza* species' chromosome-level reference assemblies, either long- or short-read technologies were derived from seven wild species (*O. barthii*, *O. glumaepatula*, *O. meridionalis*, *O. nivara*, *O. rufipogon*, *O. punctata*, and *Leersia perrieri*) and two domesticated varieties (*O. sativa* vg. *aus* [N22] and vg. *indica* [cv IR8] or miracle rice) in addition to previously published assemblies of *O. brachyantha*, *O. glaberrima*, *O. sativa* vg. *japonica* and *O. sativa* vg. *indica* [93–11]. Majority of the cultivars have AA genome, except for *O. punctata* (BB), *O. brachyantha* (FF), and *L. perrieri* (unknown), a closely related outgroup species.

The study identified a possible strong candidate and long-pursued Pi-ta2 locus [28] that can provide broad-specificity resistance to rice blast diseases upon interaction with Pi-ta (Bryan et al.,

2000). Among many blast disease pathogens, *Magnaporthe oryzae* pose major threats to global rice production of which yearly losses can potentially feed about 60 million people [28]. Overall, the accessibility of 13 high-quality reference genome assemblies will allow in-depth exploration of major orthologous loci and genomic regions of genotypes: AA, BB, FF, and *L. perrieri*.

5. The extent of rice genetic diversity

As previously discussed, several studies have shown the importance of germplasm resources in rice improvement and breeding programs for higher yields, better resistance to biotic and abiotic factors including the incidence of pests and diseases. Germplasm resources comprised of wild relatives, traditional, and modern cultivars among others are excellent sources of desirable traits in breeding programs. **Table 1** shows available information about useful and

Species	Genome	Characteristics/traits
<i>O. barthii</i>	AA	Resistance to BB, GLH; tolerance to heat and drought; drought avoidance
<i>O. glaberrima</i>	AA	Resistance to nematodes, rice yellow mottle virus, stem borers, African gall midge, iron toxicity, drought; tolerance to waterlogging; cultigen; crude protein content; weed competitiveness; high adaptability to acidic soils showing low levels of phosphorus availability
<i>O. glumaepatula</i>		Tolerance to heat; source of CMS; elongation ability
<i>O. meridionalis</i>		Tolerance to heat and drought; drought avoidance; elongation ability
<i>O. nivara</i>	AA	Resistance to BB, grassy stunt virus
<i>O. rufipogon</i>		Resistance to blast, Tungro virus, BB, BPH; moderately tolerant to Shb; increased elongation under deep water; Source of yield-enhancing loci and CMS; tolerance to aluminum and soil acidity
<i>O. punctata</i>	BB	Resistance to zigzag leaf hopper, BB, BPH; tolerance to heat and drought
<i>O. brachyantha</i>	FF	Resistance to YSB, BB, whorl maggot, leaf-folder; tolerance to laterite soil
<i>Leersia perrieri</i>	unknown	Stoloniferous; shade tolerance

Abbreviations: BB-bacterial blight; BPH-brown planthopper; CMS-cytoplasmic male sterility; GLH-green leafhopper; Shb-sheath blight; YSB-yellow stem borer.

Table 1. Important and useful genomic characteristics or traits in wild *Oryza* species with available reference genomes (sources: [33, 34]).

important traits in wild rice species. With reliable reference genome assemblies made available (like those studied in [28]), useful and important traits in wild *Oryza* species can be extensively used in wild hybridization and gene introgression toward breeding high-yield varieties expressing significant characteristics such as tolerance or resistance to biotic and abiotic stress factors that limit crop productivity in general.

In modern plant breeding, scientists repetitively rely on a continuous infusion of genetic resources to develop crops with superior resistance to diseases and pests, with better yield quantity and with the high quality of produce including flavor and nutritional values [10, 29–31].

Wild species	Key traits	Gene	Rice Variety
<i>O. barthii</i>	Drought-or heat-related traits	unknown	
<i>O. glaberrima</i>	Resistance to blast	unknown	Yun Dao, China-YAAS
	Tolerance to iron toxicity	unknown	many NERICA lines/varieties, Africa
	Drought-or heat-related traits	QTLs	
	Tolerance to acidic conditions	unknown	
	Tolerance to P deficiency	unknown	
	Tolerance to abiotic stresses, high yield, weed competitive ability, earliness		
<i>O. glumaepatula</i>	Cytoplasmic male sterility	unknown	
	Drought-or heat-related traits	unknown	
<i>O. meridionalis</i>	Drought-or heat-related traits	unknown	Arkansas rice varieties (2), USA
<i>O. nivara</i>	Resistance to grassy stunt	GS	many Asian rice varieties
	Resistance to bacterial blight	<i>Xa38</i>	
<i>O. rufipogon</i>	Resistance to bacterial blight	<i>Xa23</i>	Dhanarasi, India
	Resistance to blast	unknown	Matatag 9, Philippines
	Cytoplasmic male sterility	unknown	AS 996, Vietnam (acid sulfate)
	Tolerance to Tungro virus	unknown	BRRIdhan55, Bangladesh (salt)
	Tolerance to iron toxicity	unknown	
	Tolerance to aluminum toxicity	QTL	
	Tolerance to acidic conditions	unknown	
	Tolerance to P deficiency	unknown	
	Yield-enhancing loci	QTL, <i>yl1</i> , <i>yl2</i>	
	Increased elongation ability	unknown	
<i>O. punctata</i>	NO DATA		
<i>O. brachyantha</i>	Resistance to bacterial blight	unknown	
<i>Leersia perrieri</i>	NO DATA		

Table 2. Key traits of select wild *Oryza* species transferred in modern rice varieties through gene introgression and wide hybridization (source: [33]).

Conversely, scientists favor to employ existing cultivars or called elite or advanced breeding materials owing to previous experience in ease of intermating these cultivars and proven high productivity [31]. Aside from the difficulty of transferring outstanding traits, another major reason breeding scientists do not resort to using wild relatives in rice breeding is because of the inferior characteristics of wild relatives particularly, poor plant type and more grass-like appearance, poor grain type that shatters in nature, and low grain yield [31–33].

Nevertheless, successful breeding of wild rice species into modern rice varieties has been achieved through advances in tissue culture and molecular approaches [33] that complement conventional breeding methods. **Table 2** shows key traits from select wild rice species that have been transferred in modern rice varieties through gene introgression and wild hybridization.

Some examples of biotechniques used to explore favorable alleles in rice germplasm are employing advanced backcross populations to detect quantitative trait loci (QTL) associated with enhanced performance in rice as well as clone genes underlying key QTLs of interest (McCouch [30]) as well as use of backcross inbred lines (BILs) and chromosome segment substitution lines (CSSLs) and high-density single nucleotide polymorphism (SNP) arrays [32]. These research achievements further illustrate the importance of rice genetic resources in breeding new crops with highly desirable traits on top of high yield potential.

6. Molecular biotechniques to enhance rice breeding activities

Recent advances in molecular biology and biotechniques increase the chances of utilizing rice genetics resources that have not been explored in previous rice breeding programs. The availability of genomic, phenotypic, geographical, and ecological information among other sequence data, when analyzed all-together, can help researchers to strategically plan experiments based on developed models predicting plant performance [3].

Molecular approaches used in modern rice breeding include molecular marker technology and marker-assisted selection (MAS), molecular mapping of genes and QTLs and production of hybrids and alien introgression lines (AILs) [33] to name a few. One method of genomic-assisted breeding, MAS (**Figure 5**), utilizes molecular markers that map QTLs or specific genes known to be linked with phenotypes or target traits to choose individuals that exhibit desirable alleles for traits of interest [35]. Compared to conventional phenotypic selection, MAS has primary advantages, such as it is simpler than phenotypic screening, selection can be done at the seedling stage, and a single plant can be selected based on its genotype [36].

Another type of genomic-assisted breeding, called genomic selection (GS) utilizes all available marker data for a population as predictors of breeding value [35]. To generate a prediction model, GS combines marker data from a training population (TP) with phenotypic data as well as available pedigree data and then the model produces genomic estimated breeding values (GEBVs) of all TP-genotyped individuals [35]. GEBVs calculate the possible performance of a genotype as a potential parent in a breeding pipeline [35].

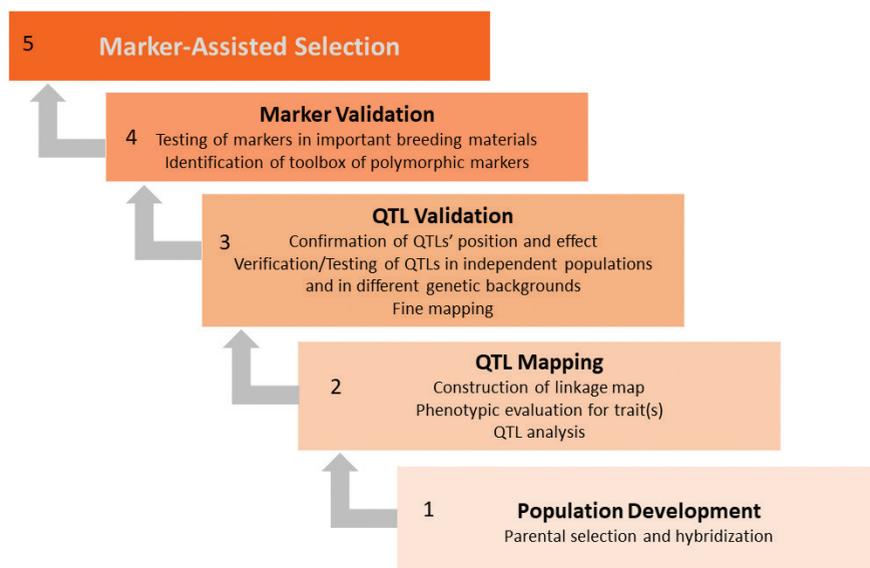


Figure 5. The process of marker development (adapted from [36]).

As modern plant biology further advances, other technology options like OMICs sciences or systems biology approaches become exploitable to pinpoint genomes (genomics) [37], genes (transcriptomics), metabolites (metabolomics), proteins (proteomics), and interactions (interactomics of protein-protein or protein-DNA) [38] among other complex biological systems that can revolutionize the improvement of crop productivity. For instance, metabolomics helps determine the differences between a healthy and a disease-infected plant through analysis of various levels of their thousands of molecules (ISAAA leaflet) [39]. Metabolomics can also identify plant defense metabolites and nutritional values as shown in a study that detected metabolites useful as molecular markers for drought stress tolerance for species related to tobacco and soybean [39].

In genomics research, present-day advances that made multi-layer genomic data derived from sequencing of both DNA and RNA now provide information on gene expressions, differential isoforms, alternative splicing methods, messenger RNA, non-coding RNA, and DNA polymorphism [37]. In short, current genomics is far ahead and progressive compared to traditional genomics that studies the function, structure, and sequence of a genome.

Recent studies in rice involving OMICs approaches have shown promise in scaling down the rice breeding process by focusing on the discovery of and engineering of desirable traits or genes. In China, scientists had integrated analyses of rice omics and biotechnological applications toward improving rice agronomic traits through molecular breeding approaches [40]. Integrated data analyzed include 220 functional genes that were cloned and identified, sequencing data of chromosome 4 of japonica rice Nipponbare and whole genome shotgun sequencing of Indica rice 9311 [40]. Additionally, the testing of comprehensive annotation platform for

functional exploration of rice multi-omics data (CARMO) provided multiple web-based analysis tools for in-depth data mining and visualization [41]. CARMO stands for comprehensive annotation of rice multi-omics data. Its performance test showed useful functional insights for supplementary experimental studies and evidence that were previously reported [41].

A combinatorial analysis of data from genome-wide association study (GWAS) and high-throughput phenotyping was used to evaluate the effects of salinity in rice particularly on relative growth rate (RGR), transpiration rate (TR), and transpiration use efficiency (TUE) [42]. Results include the identification of new candidate genes responsible for the early response of rice to salinity stress (**Figure 6**). Through interaction model approach, early response of rice to salt stress was associated with various signaling mechanisms as shown by expressions of signaling-related genes such as *Os03g16130* (encoding a calcium/calmodulin (*Ca/CaM*)-dependent kinase), *Os05g39870* (encoding *OsCIPK28* and *CAMK_KIN1*, *Ca/CaM*-dependent protein kinase), *Os05g39900* (encoding a CBL-interacting serine/threonine-protein kinase 15), *Os05g46320* (encoding *OsFBX173*, an F-box domain-containing protein), and *Os05g47670* (containing a

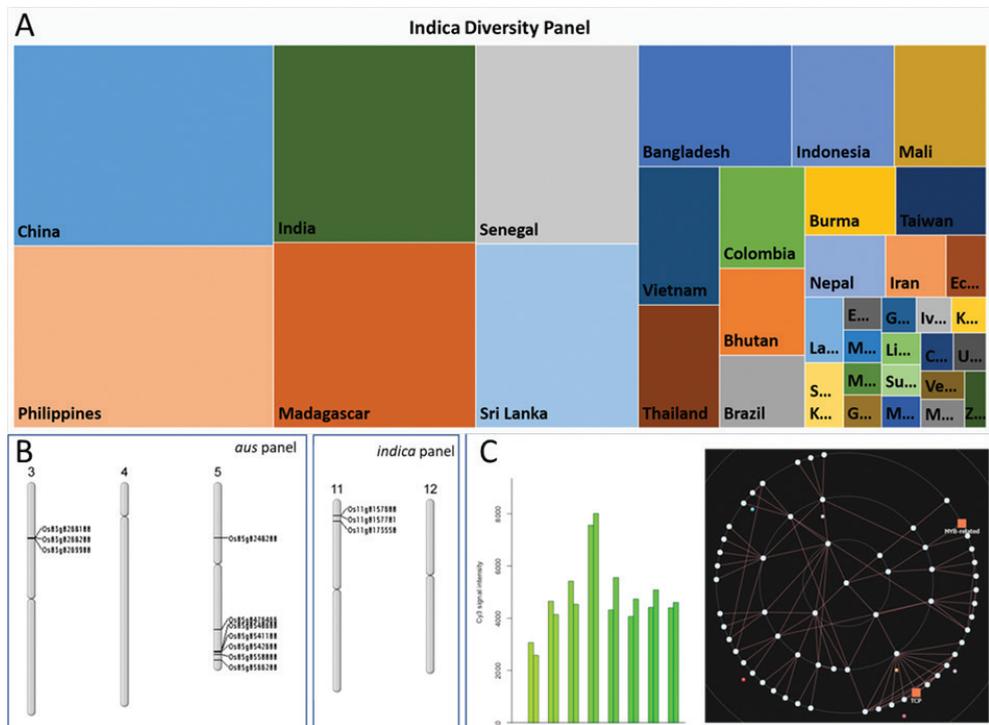


Figure 6. Utilization of rice diversity panel for identification of salinity tolerance loci in the study of Al-Tamini et al. [42]. (A) Blocks represent source countries of germplasm sizes contributed in the diversity panel (data taken from GRiSP global Rice Phenotyping network). (B) Candidate genes involved in early salinity response in aus and indicator panels. (C) Expression profile of *Os03g16130* (calcium/Calmodulin-dependent kinase) in rice inflorescence and co-expression network (expression and network data sourced from RiceXPro [44] and RiceFRIEND [45]).

zinc-finger motif, a C3HC4-type domain-containing protein) [42]. Candidate genes and QTLs can also be detected effectively using GWAS and gene-based association analysis followed by haplotype analysis for forthcoming functional characterization and genetic improvement of protein content, consumption, and cooking quality [43].

7. Rice genetic resources: experiences and prospects

Overall, rice genetic resources have been used to improve modern cultivars, although common knowledge is 95% of the rice gene pool [27] remains untapped and unexploited in rice improvement. Major reasons of breeders for not using a wider gene pool base including wild relatives are inferior traits of wild relatives in terms plant type, grain shattering, and low yield and generally, the difficulty of transferring desirable traits as well [31–33].

As more information about germplasm is available, wider selection and diversity of materials can be exploited for varietal improvement [46]. Generating more usable information becomes more possible with modern biotechniques that can examine and identify specific genes, genomes, QTLs, and proteins among other genetic materials. These techniques target precise genetic materials expressing advantageous traits toward increasing yield and quality, specific resistance to biotic and abiotic factors as well as emerging or future production constraints.

Figure 7 shows a concept framework of molecular- and systems-levels of gene discovery and transfer enabling development of new breeds from a wide gene pool including wild relatives. Various biotechnologies such as GWAS, QTLs, genomic selection, and OMICs approaches

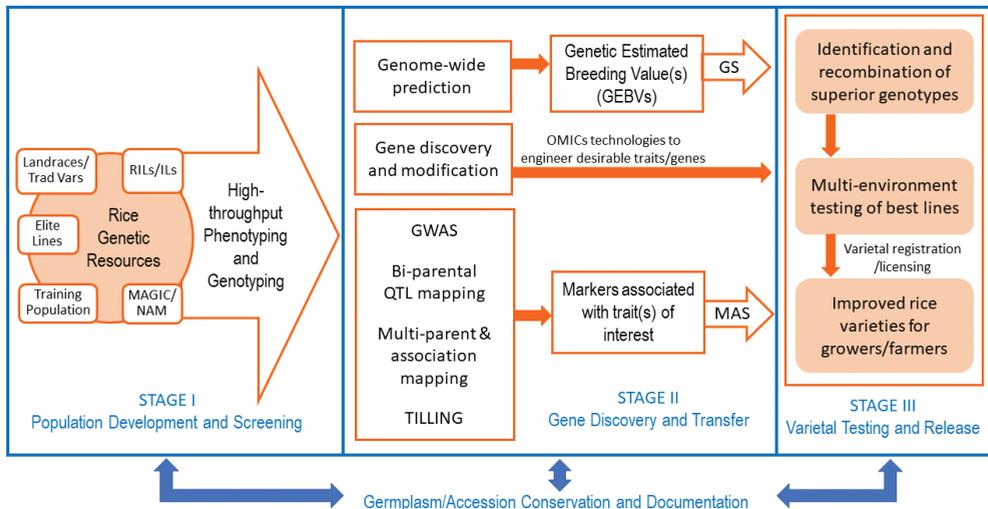


Figure 7. The conceptual framework of the applications of NGS and OMICs technologies for molecular- and systems-level breeding of improved crop varieties. Seeds and information generated from stages 1 to 3 generation and submission of information to genebank for the provision of better passport and characterization data of accessions or germplasm for future breeding use.

among other techniques complementing conventional breeding methods can hasten the discovery and transfer of desired genetic materials toward developing improved varieties.

Compared to yesteryears, these biotechniques are becoming low-cost and easier to use and can now be routinely employed to identify and transfer desirable traits into new crops. In a recent review about genetically engineering crops, OMICs approaches were evaluated to weigh in the intended and unintended effects of genetic engineering (GE) in plant breeding. Results suggest that GE and OMICs technologies have remarkable potentials toward boosting crop improvement initiatives in the twenty-first century in conjunction with conventional breeding techniques [47].

Figure 7 also points out the importance of conserving seeds as germplasm and providing information derived from biotechniques for further use and reference in future breeding programs. For example, genotypic and phenotypic information will further elucidate the values of germplasm resources [6]. Accessibility of integrated germplasm characterization information including molecular markers, genome sequence information, genotype-phenotype relationships will entice breeders to use a wider genepool as potential parent lines and as sources of important traits and characteristics. Development of integrated germplasm information for a germplasm should be a collaborative effort of scientists, such as physiologists, geneticists, pathologists, genebank curators, and breeders, who share parallel and harmonized interests in exploiting the genetic materials of germplasm resources and determining valuable and novel genes for crop improvement.

In summary, advances in complementary plant breeding methods including molecular marker technology, OMICs approaches have allowed rapid developments in basic knowledge of genetics and breeding of plants. Molecular approaches have also provided important information about genetic materials and specific genes and genomes for the development of improved crops. Additionally, these approaches hold promise and help speculate about how their applications can shape the future of rice breeding for beneficial prospects of rice producers and consumers worldwide. The ease of use of these biotechniques coupled with affordability will allow better characterization of genetic resources that can increase their utility to improve crops to address present-day and future production constraints.

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