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Genomics-Centric Approach: An Insight into the Role of Genomics in Assisting GM-Rice Varieties With-in a Paradigm of Future Climate-Change Mitigation, Food Security, and GM Regulation

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Abstract

Genomics, in the context of crop science, is an emerging field with great potential to establish a deeper insight into staple crops, such as rice. Rice, as a global food commodity, faces the effects of climate change. Abiotic stresses, such as those associated with drought and salt tolerance, will require a genomics-centric approach in order to better scrutinise those QTL regions and SNPs associated with climatic change. Moreover, an improved analysis on trade, GM-rice varieties, and marketing will be required, from global agricultural authorities such as the FAO, which can effectively, and successfully, address the inevitable shift from non-GM to GM rice varieties.

Keywords: Crops; Rice, Genomics; Genetic diversity; Breeding; Abiotic stress; Climate change; DNA

Introduction

With an increasing demand for food throughout the developed and developing world improved approaches of identifying and utilizing rice genes, along with modifying existing ones involved in abiotic stress, should be more associated to a reliance of genomic tools. This demand for applying improved, and better resolving, genomic tools will need to coincide with an unprecedented population growth to 9 billion people, which will also signal a need to produce 70-100% more food by 2050.

In particular, the FAO in their recent 2016 report developed a likelihood of scenario outcomes (FAO, 2016) based on food price increases. In four climate change scenarios of low population growth and high income, it was predicted that by 2050 projected mean price increase of 31% for rice alone (FAO, 2016). The presently occurring shift in global climate will undoubtedly impact agriculture [1].

The FAO: Save and Grow guidelines detail, and address, the need of improved crop varieties. Looking specifically at Chatter 4, Crops and varieties, the report clearly highlights the need to prioritize sustainable crop production intensification (SCRI). They report stresses the need to increase genetic diversity of crop species in order to evade climate change outcomes such as those posing abiotic stresses, whilst at the same time improving adaptability. What is interesting is that the Save and Grow guidelines for improving crop varieties is also geared towards increasing farmer participation, involving the public sector on improved crop varieties, and supporting local, and private seed companies that spans markets and value chains.

Cultivated rice (Oryza sativa) [2], as one crucial crop responsible for feeding around 50% of the population [3], and providing 20% of the world’s caloric intake and over 50% in Asian countries [2], is cultivated across the world on available arable land [4]. It has been calculated that by 2035, 116 million tons of rice production, globally, will need to be met [5]. This increase will need to be from smallholder farmers in developing countries. Currently, there exists two cultivated species of rice, along with 22 wild species [6].

The relationship between relevant climate-linked traits and crop diversity can be adequately linked to genomics [7]. Additionally, the mapping and characterization of eventual SNPs in rice climate-linked QTL regions can allow an insight into the molecular and biochemical basis of their expression profiles [7], which can be used to predict phenotype.

Overall, the essential mapping of rice genes modelled within future climatic shifts, can prime genetic engineering approaches which can produce GM-rice varieties with strengthened traits to cope with an ever-changing global environment. These climate impacts, namely abiotic stresses, pest and disease outbreaks, from the overall effect of climate change, projected to considerably effect rice yields in tropical regions than temperate regions (FAO, 2016), will require careful stitching of new rice crop varieties [8].

One goal of abiotic stress research in rice is to improve its characteristics via the method of diversification [9]. It has been suggested that the use of crop wild relatives (CWRs) can support the building strengthened rice varieties [9]. Since crop wild-relatives might be less variable from a lack of human selection parameters, they nonetheless contain a broad range of exploitable traits which can be screened using GWAS and GS.

Genomics is leading the way in rice crop research by:

- Providing a platform to discover the ongoing effects of climate change on rice varieties through re-sequencing;
- Enabling a larger pool of genes from CWR to be determined, and utilized, in downstream genetic engineering processes;
- Providing a strong scientific knowledge-base for the seed industry (SMEs and government agencies) that can also assist in developing new agricultural guidelines catering for GM-rice, and,
- Efficiently storing and re-using known rice germ-plasm/ genotypes which can efficiently streamline the processes of creating new GM-rice varieties which can withstand predicted climate shifts; shortening the lag time between climate-induced abiotic stress to elite rice variety engineering.

This perspective and mini-review will firstly explain the brief background of some NGS-genomics strategies, discussing their likely impacts on creating new rice varieties. Genomics will then be explained within a context of climate change and food security, exemplified from using the major staple crop, rice. Lastly, a discussion on the aspects and difficulties of commercializing new elite GM-rice varieties along with the inclusion and discussion of current FAO assessments, and other authorized agricultural documents will be mentioned.

Frameworks that harmonize aspects of current rice genomics with food security/guidelines outlined in the recent 2016 FAO report, The State of Food and Agriculture, will also be discussed. This section will also bring into light the issues surrounding trade, commercialization, policy, and industry relevance and responsibility, from a post-genomics era viewpoint.

Along with these insights, the review suggests a genomic-centric perspective that seeks to recommend strategies to appropriately consider GM-rice varieties, and the paramount adaption to future shifting climate, that will lead to strengthened food security.

Genomic Tools Used in Rice Improvement

Precise selection of multiple traits can be uncovered using present day genomics [10]. Uncovering such genetic information relating to agronomically important crop traits represents a critical step in understanding phenotypic variation which can lead to improving crops [11], along with a better understanding of abiotic stress effects on developing varieties well-suited to handle difficult environments [10]. With widely-used Next Generation Sequencing (NGS) approaches and its association with sequencing large populations, heightening the resolution of QTL discovery, and uncovering SNP markers for plant crop analysis many biological hypotheses have nowadays become open for further investigation [12].

Genomics-assisted breeding represents a range of holistic approaches [13] wherein a phenotype can be predicted from a genotype from the incorporation of genomic analysis.

Marker-assisted selection (MAS) tools that can specifically investigate the basis of genetic variations in rice [3] will require further application in order to characterize the other >37, 000 protein coding genes in its genome [3]. Genomics-assisted breeding [12] represents an effective approach that can decode rice crop traits from seedling stage, and potentially eliminate multi-location trials, without the lengthy process of phenotypic evaluation over stretches of time.

Prior to the popularity of NGS technologies, a limitation with the number of available markers necessary for marker-breeding strategies was a barricade that disqualified the identification of valuable agronomic traits outside continuously utilized genomic regions [12].

Thus, NGS technologies have allowed entire genomes to be annotated for agronomically-valuable traits based on precise nucleotide positions. Additionally, reverse genetics techniques such as Eco-TILLING have also been developed for use in discovering drought and salinity tolerant genes [12] in economically important crops, such as rice.

Furthermore, the application of a GWAS (genome-wide association studies) and Genome-sequencing (GS) will greatly improve mapping resolution and genetic diversity data, as it efficiently identifies a magnitude of allelic variations [11] through nucleotide polymorphisms, and the subsequent variability in phenotypes [11].

Genotyping-by-Sequencing (GBS) is an off-shoot of NGS wherein plant populations can be genotyped for their SNP attributes [7,14] used a genome-wide SNP analysis to study polymorphism patterns in 395 rice accessions. The study analyzed amylose content and grain length to uncover complex traits, and genetic elements that were functionally important, based on their population genetics approaches using the SNPs [14].

Wedged between full-length cDNA sequence data and functional genomics is the highly crucial role of DNA microarray technology. The imperativeness of DNA microarray applications lies in its utilization in comparative experimentation. Its yielding transcript data reveals vital information that can indicate gene expression based upon the experimental/abiotic pressure in question. Discrepancies between microarray data and gel-based analyses is a major drawback to the validity and accuracy of applying this approach to derive plant transcriptomic data.

The overall adoption of genomics to its application within a crop improving context will open new pathways which will lead to discoveries and produce data based on;

- Screening crop communities from varying environmental climates;
- Comparing the results of improved heterozygosity, heterosis, and its impacts on crop domestication;
- Developing new, or improving existing molecular, techniques that can derive important patterns and processes at the plant- and community-level which can subsequently provide relevant bio-marker data[3].

In order to mine for existing and new functional traits in rice, which can be utilized in cultivar improvement such as improving yield, drought tolerance, and/or synthesizing heat tolerant lines, statistical models used in GWAS and GS would be required to explain, for example, population history more accurately. Genomic resources that pertain to QTL linked to drought-tolerant rice are crucial in climate-resilient lines [15] however their trait complexities are hampered by genetic linkages and interactions. The researcher described the possibility of linkages between QTLs from flowering and plant height, to drought-grain QTLs [15]. They subsequently utilized a marker-assisted approach to infer improve grain yield under drought street conditions.

These approaches should also screen for consumer-friendly factors/genes such as those associated with sensory attributes [16], for example fragrance, along with cooking characteristics, such as the amylose content [17]. Both fragrance and amylose content are also important characteristics which influence consumer choice. Depending on the consumer preference in question, selecting sensory and physical attributes is an interesting aspect of rice quality that can be investigated, and exploited, through the use of genomics approaches.

Genomics offers the capacity to not only uncover these unknown genes and/or gene regions, but also to facilitate further downstream developmental processes that could determine physiological traits for improved crop resilience to abiotic stresses, at the whole crop level. Thus, the aim of research in this post-genomic era is to identify the functions of these unknown genes that could further be available throughout online public databases. By assessing SNPs conferring changes at the gene level from external pressures such as drought and/or heat stress, a gradual building of enhanced holistic crop-models can be developed fusing biological changes happening at the gene/biochemical level to providing detailed information on rice-climate interactive responses at the whole-crop level.

In a study that utilized chloroplast sequence data, [18] were able to uncover 122 polymorphisms in a wild rice relative, matching this to a reference cultivated rice genome. This chloroplast barcoding approach can be further applied to GM-rice varieties, which will be discussed in the next section accordingly, along with possibly eliminating amplification steps that would otherwise interfere with genotypes [18] from different plants. Another example of whole chloroplast gene sequencing is described by [19]. In their study, the evolutionary and phylogenetic relationships of the AA Oryza genome generated a primary gene pool that allowed the authors to conclude relationships between cultivated and wild rice relatives, and potentially exploit these wild genetic resources for rice improvement [19].

Table 1 Save and Grow recommended measures (SCPI) taken from Chapter 4 of the Save and Grow guidelines, with relevant genomics inputs aligned.

Measures	**Genomics-derived approaches**
Strengthening linkages between the conservation of PGR and the use of diversity in plant breeding	Providing genomics databases to store and utilize large datasets
Increasing the participation of farmers in conservation, crop improvement and seed supply	Educating smallholder farmers in genomic-platform technologies and opportunities with communication of risk-assessments
Improving policies and legislation for variety development and release, and seed supply	Integrating genomics technologies into policy-maker decisions that can rationally lead legislation into adopting NGS approaches as standardized methods for developing elite varieties; based on the intended design and its purpose within a climate-mitigating context.
Strengthening capacity: creating skill workers to assist enhanced breeding	Training skilled workers in matters regarding land intensification and additional benefits of using GM-varieties from genomics-derived been pools.
Revitalizing public sector: expanding its roles in developing new crop varieties	Investing into the development of improved NGS platforms; funding research centers into NGS research.
Supporting the emergence of local, private sector seed enterprises	Using genomics-based modelling from a climate-change perspective, to explain economic advantages, ROI, and human well-being, rom developing SME opportunities.
Coordinating linkages with other essential components of SCPI	Implementing a reasonable model that incorporates economics, climate-change science, sociological and geographical factors, and regulation/IP to further enhance the SCPI approach.

Exploratory genomic techniques applied to rice draft genomes can help identify functional elements in non-coding DNA regions, along with characterizing genome-wide SNPs in rice. Fitness maps provide mutation-variation data and estimate probability functions which help determine the effect of that mutation within a crop-genome context.

Genomics based breeding is becoming more popular as ongoing genomic discoveries are made. The ability to genotype an abundance of SNPs, in breeding new rice varieties, has led to more accurate marker-assisted trait selection providing improved genome coverage of commercially vital stable crops, such as rice. If a more defined genomics pipeline is applied, identifying consumer-/climate-important traits for consumer preference and climate mitigation, a reduction in rice breeding costs will be apparent in the near future. Overall, the continuing use of NGS technologies, especially those associated with genomics data mining and processing, will allow for a much better characterized trait-pool from crop gene resources. For example, the application of NGS to sequence total plant DNA can lead to chloroplast barcoding [18], which can in turn accommodate the streamlined plant identification from an apparent diversity-lacking across closely related plant species [20].

NGS technologies will also permit previously undefined and neglected gene banks to become utilized by plant breeders. This should be aligned with the FAO's Save and Grow guidelines, mentioned in the beginning of this article. **Table 1** describes this alignment through matching genomics approaches with the Save and Grow: The Way Forward key points of consideration. These genomics-FAO matches could support further policy formulation by interested policy-makers.

Continually working towards, and within, a bio-informational framework of uncovering genetic data will nonetheless facilitate a growing number of virtual-laboratory based scientists that will need to better handle this incoming informatics data. This can only occur if genomics-based approaches can simultaneously manage and interpret incoming genomic datasets.

Genomics: Adapting, or Diversifying, New and Existing Crop Species to Climate Change

The FAOs recent report outlines several strategies to mitigate climate change through improved agricultural practices, and also through enabling genetic diversity (FAO, 2016). Climate change influences and modifies agriculture both directly and indirectly upon society [21]. These effects can be modelled from the IPCC's Special Report on Emissions Scenarios (SRES), which include four families of socio-economic development. Aligned it these SRES's is the FAO's food security dimensions [21], which focuses on the monetary and non-monetary resources of current food insecurity; seeking to avoid an inadequacy of food supplies as its overall goal.

Since crop-stress environments are highly variable [22], the incorporation of a plant-response to its stress-mediated environment would involve a series of changes at the DNA level which follow on to non-specific changes at the expression level. There is still a persisting problem of addressing abiotic stresses such as drought exposure [23], salinity stress [24] and temperature stress [25].

Genomics can help inform on past trends of extreme climate events (ECEs) on crop populations and demographics [23].

What is of equal importance is the need to finely describe gene-expression data resulting from abiotic-stress environments [26], and use this data to design abiotic-tolerant rice varieties. Since drought stress involves molecular, cellular, and physiological level changes [27], genomics can help reveal small individual changes across a large number of genes. Genomic information can uncover the combined traits leading to drought-stress crop changes and conclude a map of QTL.

Nonetheless, a more holistic approach [13] is needed in order to combine abiotic-stress genomics data [27] to other equally important approaches such as understanding complex regulatory networks using metabolomics [11], proteomics and transcriptomics [28] and crop phenotyping. An additional approach utilized in rice studies, phytochemical genomics, seeks to uncover metabolites pertaining to biosynthetic enzymes [11].

These combined approaches can provide the elementary and necessary datasets needed to design improved agriculture production systems which can then feedback to engineering GM-rice varieties which can both be productive and provide a platform for investigating SNPs information, also based upon stress conditions.

The rapidity of designing cultivars with enhanced tolerance to abiotic stresses and/or improving rice varieties with stably agronomic performance [13] is becoming increasingly important in designing climate-resilient rice crops.

The importance of breeding climate-resilient rice is globally imperative in order to counteract the effects of this growing climate danger. In line with this, the adaption of crops to this climatic shift, namely heat and drought, will be an essential element to maintaining rice quality [29].

1. Defining regional climate, based on establishing criteria: In the case of drought-tolerance or water deficiency, a short-term and gradual, water shortage will cause physiological changes to the plant crop:

- Shortening life-cycle
- Optimizing resources
- Metabolic protection
- Maintaining high tissue water potential.

1. Characterizing plant crop genes/alleles changes (SNPs); from (1),
2. Mapping genes, using genomics, which are up-regulated and favoured from conditions within a (1) scenario,
3. Excising candidate gene(s) from (2,3) for strengthened crop variety, gene engineering approaches, and phenotyping in field studies to preclude the damage from severe drought events.
4. Using genome data from (3) and improved crop varieties from (4) to develop new production systems which positively support physiological and phenological responses from plants in a (1) scenario.

Another possible strategy which could be independent or dependent on currently utilized crop improvements is the idea of domesticating new rice species [29] under diversification programs. This approach makes use of Crop Wild Relatives (CWRs), which can provide a future safety-net and readily-exploitable [10] genetic resource for phylogentically similar crops.

For example, Oryza sativa (rice) can be rearranged if rapid adaption to abiotic stresses is necessary by employing genomics to map the 155 CWRs [17] associated within its predefined group [17]. This would assist by discovering possible abiotic-stress related genes that can recover a specific abiotic stress phenotype, depending of course on the environmental stress in question.

Aligned to this, NGS technologies [13] can provide the necessary genomic information which could assist in developing available genomic resources for improving existing domesticated rice varieties. This includes developing drought-tolerant lines

This will also strengthen food security [29] as it alleviates reliance on the current major rice varieties, increasing the likelihood of securing rice for further generations, through diversification with CWR versions.

The combination and implementation of crop adaption strategies and/or new crops species management can only be directed by modelling climate change behavior with a readily available genetic resource of engineered rice varieties. Efforts should also be guided towards population characteristics; i.e. how rice is consumed in society, and the various physical and nutritional preferences that humans may have. This presents an additional layer of consumer-information which might suggest that along with climate change, the likely change(s) in human response(s) to available functional foods may need to be concurrently taken into consideration, based on key cultural and sociological indicators. Together, a clearer picture of changing climatic events can be aligned to better understanding climate responses in rice species. Mitigating undesirable climate change effects in this major staple crop, for example, should encompass adaption strategies [30], not only focused on agricultural systems but also geographic indicators.

Unfavorable climatic conditions driven by climate change will hamper, and decrease [31], the productivity of economically important agricultural crops, which have only a short production opportunity to thrive in a given climatic window. Conclusively, genomics technologies and genomic-based crop improvements will provide identification of a larger gene pool, for plant breeders, to create elite crops that can greatly assist future food supply and security.

Genomics Leading to Secure Food Supplies

Food security and genomics

Food security, represented in this case by agricultural productivity and food pricing [32,33], will be subsequently affected by climate change, which sit within the four FAO elements of food security. Food security can be maintained from the indirect action of appropriately applying NGS-genomic studies, which can tackle food insecurity as is being faced by those in developing countries.

Food insecurity is nonetheless a serious problem, with the FAO identifying the need for agricultural biotechnology implementation to address this growing issue [33]. Therefore, the importance of commercializing new rice crop innovations, usually GM, will assist developing countries and their desire to shift into, and maintain, a nutritionally sustainable diet.

An increase in rice crop productivity has been the resulting trend from the ongoing operation of traditional production systems, namely the unchanged farming simplification and intensification procedures. It is now acceptable to assume that changes in how current rice crop harvesting strategies are approached should be remodelled accordingly.

The FAO has established a Save and Grow setup for addressing crop management practices [33].

Researchers described three important challenges which must be circumvented in regard to gene loss [32];

- Shifting focus on a selection criteria which accounts for stress adaption;
- Confirming the existence, through genomics, of stress-related genes which can be utilized for further breeding programs; and,
- Accounting for minor rice crops, along with major ones, which might have already-adapted characteristics which will require less input.

A combination of sufficient food availability, an economically feasible access to food, and an appropriate and adequate nutritional content [34] from consumed foods, are all relevant to ensuring food security.

Referring back to the Save and Grow guidelines, and also the Hague conference climate-Smart report (2010); in both instances policies and institutions are described [35]. The Climate-Smart approach, with regards to enabling food security, proposes that a significant transformation must be initiated to address food security challenges. Additionally, their key findings suggest that investment in developing technologies and methodologies to fill present research knowledge gaps is mandatory to fully enable the proposed climate-smart approach. [35]. Genomics can assist efforts in researching into knowledge gaps, such that the climate-smart approach can account for scientific platforms, offered by NGS. FAO's Save and Grow guidelines, also addressing policies and institutions, base their outcomes on their developed Sustainable crop production intensification (SCPI) goal [35]. It interprets seed sector regulation, plant genetic resources, technologies and information, and agricultural investments as key factors that will support their SCPI intentions. Enabling institutions, as an additional SCPI function, presents two main functions: 1) Ensuring key resources (natural, inputs, knowledge, financial, and, 2) ensuring small farmers can access those resources.

Genomics technologies can adequately support the Save and Grow SCPI program, through providing accessible crop genetic data that can be disseminated appropriately to smallholder farmers, provided knowledge is also communicated.

GM-Rice commercialization

GM-rice has been mentioned as a new-comer in the GM-market [36], which will no doubt yield some interesting products for both industry and community. The reasons for this emergence into cultivating GM-rice varieties is from the simultaneous problems affected rice yields and a need to manage abiotic-stresses more readily. Scientists identified some 3.6 million SNPs from the sequencing of 517 rice landraces, using GWAS on 14 agronomic traits in a subspecies of O. sativa indica [14]. The same authors concluded that such a GWAS approach showcases the possibility of uncovering complex traits in rice, where this strategy can be used as a resource for further, and alongside, breeding strategies [14].

Consumer preferences are also leaking into R&D pipelines, hence affecting how new GM-rice varieties could be marketed. An effective approach could be to design and market nutritional traits. These modifications to the nutritional profile of rice would require public opinion and a disclosure of the technology used, to gain mainstream community acceptance.

Genomics-based trait identification as a means to identify resilient-genes and QTL regions in rice cannot be the end-all-be-all to progress these engineered varieties with subsequent improved phenotypes to farm-scale. An appropriate commercialization platform must be set-up and readily implemented. Commercializing GM-rice varieties will require a strict approach to detecting GM events [37]. A high-throughput system, such as genomics, will lead to an advanced system wherein UGM can be detected, and conformations of authorized GM traits are mapped. Minor differences in GM-non-GM crops will become increasingly difficult to identify [37], and so NGS technologies-genomics platforms will better handle this growing GM complexity in the future.

Commercialization strategies have previously approved crops which contain minor modifications that provide resistance against herbicides and pesticides [10]. A current dilemma exists within the relationship between IP rights, biotechnology, and public discourse on matters relating to GM crops. The interrelationship of trust and public perception must be aligned to an overall agreement if genomic technologies can start exploiting large pools of genetic data and material, and use these in a context of developing drought- and/or -temperature resilient rice varieties. Overall, a lengthy and usually expensive process [38] is required to bring a GM-product from lab to shelf.

If improved GM-rice varieties are to be invested and sold within this paradigm of biotechnology regulation, then it is of equal importance to develop and include existing genomics protocols/techniques which can lead to a better defined agricultural development plan, for both policy and industry. Inclusively, policy-makers must also ensure that GM technologies are suitable for those nations in need of poverty reduction, and, consider the potential of GM crops [34], such as GM-rice varieties. Researcher outlined that the several opportunities from utilizing GM techniques/ technologies can enable improved GM crops based on a 3 dimensional framework consisting of, Physical, Economical, and Food safety attributes [34]. Importantly, GM technologies can help raise small farmer incomes. An improvement in food safety from genomics adaptions will also need to overcome regulatory obstacles. This is contrary to the intended purposes of applying genomics, for example re-sequencing and WGS, as their purpose is to provide precise mapping of genetic changes. Therefore, these approaches would depend on institute and policy elements, rather than on their benefits of speeding-up commercialization, and simultaneously strengthening regulation of high-risk labelled GM.

Markets, trade, and genomics approaches

There is however another aspect of commercializing new GM-rice varieties that will curtail such adverse effects from climate change; that is, investment options and opportunities. Market size is crucial in this regard, and only sustainable markets will be appealing to those large companies that can maintain their position within their existing position within such markets.

Market size, in the context of GM-approved rice varieties that will mitigate climatic change effects, will also depends on the risk(s), regulatory position of importing/exporting countries, and public perception, or a lack thereof, associated with continuing with pipeline processes, from lab GM-trait development to supply-chain.

How will genomics assist in this overall process involving the many risk-associated steps of commercializing GM-rice varieties? Genomics approaches can lower the risk level when designing GM-rice varieties by providing sufficient genetic resources for the regulator and investor. The precision of NGS technologies can also provide a model-simulated approach that can help explain spatial and temporal consequences by mapping RNA transcripts indicating a time-, geographical- scale change in GM-rice varieties. Due to the large dataset generated from genomics/NGS technologies, there is currently no application of genomics approaches in GMs [39]. If genomics were applied, however, then it would require an improvement in the NGS analysis, along with a complete assessment of the currently used GM detection method, using qPCR [39]. Therefore, the way in which GM detection laboratories assess GM-derived products could be tightened by using genomics technologies.

Genomics will also assist plant breeders. A plant breeder can utilize, with increased confidence, genome-wide datasets of known rice varieties/species to understand which chromosomal fragment(s) might be involved in cross-over events, thereby increasing confidence of their marker-placement along genetic maps. This approach also enables the more precise transfer of QTL or chromosome regions from one cultivar to another. Additionally, if specific QTLs are involved in metabolic engineering pathways, then genomics will paint a clearer picture of which genes should be excised and transferred to produce strengthened varieties. Genomics-assisted breeding, in this regard, might utilize rice CWRs.

Trade is a critical aspect of agriculture. Using genomics-based methods might also lower the risk of GM-rice trade, i.e. import/ export. This stage relates to the necessary regulatory framework that ensures access to genetic resources [26], derived from MAB and/or WGS data, which should be communicated and provided between trading nations. Additionally, policy frameworks should be developed; regulating access to these genetic resources. Currently, the EU member states (MS) have complicated this trade process by their decision to take a zero-tolerance approach to trading partners exporting GM-traits [33]. In doing so, those countries, such as within sub-Saharan Africa, may lose their market- positions from investments into GM-based productive crops.

Genomics-based approaches can avoid the stigma surrounding GM-crops in certain EU MS. If policy-makers and regulators of the EU formulate a collaborative effort to provide its public groups and government access to interpreted, user-friendly, genomics data and/or knowledge courses, outlining associated benefits, then perhaps genomics could lead the way in lowering risks associated with GM-rice varieties in the future, especially alleviating perceived risks involved in investing into adaption of GM-crops varieties. Regulation would then be an appropriate measure in the detection of GMO traces in GM-crops [40]. The researcher described the additional advantage of implementing NGS, targeting sequencing and WGS, in GM traceability, as one that allows new PCR markers to be synthesized, however is based on an unknown a priori GM sequence [40]. This study noted that difficulties in adopting NGS in enforcement laboratories relates to high-costs and inadequacies in computer and expertise infrastructures [40]. Nonetheless, the high-throughout of NGS can be applied to GM varieties via the screening of unique barcodes.

This leads into another aspect of the genomics revolution; sharing genetic resource information. Extending the aforementioned example, a GM-rice-adopting country in Asia, such as in China or India (R), will be better-equipped to share NGS data: WGS and/or MAS information, to its export GM-allowing countries, in the foreseeable future.

By enforcing adequate guidelines and monitoring systems from GM-adapting states to non-GM allowing states [37], and for SMEs to remain viable within their markets, the use of a re-sequencing approach, for example, should be a mandatory element of quality assurance (QA) in order to segregate GM and non-GM varieties, ensuring trade isn't hampered and further investment decisions are not affected.

Although the examples provided signify a much longer-term strategy for GM-rice varieties, it is still important that policy-makers and state GM regulators are aware of the challenges that lie ahead regarding abiotic-stress traits in rice, heralded from climate change events.

Secondly, can genomics-assisted technology applied to producing GM-rice cultivar development increase the amount of positive investment in these carefully constructed varieties? In the long-term, genomics mapping of GM-rice of economically traits will greatly assist and enable stronger agricultural productivity in developing nations where food insecurity persists. This will serve as a basis for, and feed into, policy-maker decisions, which will in turn affect country-to-country legislation on GM related decisions.

New breeding outcomes, from adopting genomics-based methodologies, will only be accepted in mainstream perception when food and agricultural authorities, such as the FAO, can realize their ambitions of eliminating food insecurity by challenging current viewpoints, such as those currently harboured by the EU [33]. The FAO might also enlist as part of its objectives and mission to tackle global food insecurity the growing genomics revolution, in progress, with already published results that will greatly enhance confidence in WGS-based studies, and resolve a greater number of genetic resources/markers.

The additional commercial advantage of combining traits from genomics technologies is of particular interest. Not only will genomics, and its complementary holistic approaches, provide appropriate genetic and chromosomal maps for industry to exploit and design, with improved resolution, elite rice varieties; but genomics-assisted breeding strategies can work within a paradigm of selecting and combining traits that can overcome complicated farming environments [41]. This should be viewed as a significant subset of mitigating climate-change.

Scientific publications from genomics studies should be transcribed for public readability, and disclosed accordingly, to trigger public-GM acceptance [42] that is malleable to rational suggestion upon anticipated public discourse. GM-trust concerns, perhaps relating to long term GM-rice cultivation, should also account for the need to protect and improve global food production and security. A skillful approach from policy and private agro-companies should span the science, in this case NGS-genomics, the need for climate adaptive GM-crops, an education on climate change effects on crops such as rice, and a focus on the benefits to the local farm-owner (R); so that farmer advantages outweigh the benefits yielded from private and public organizations.

State and Federal government should work to reformat and redefine key terminologies to the relevant food standards, for example FSANZ (Food Standards Australia and New Zealand 2016), and GM consultancy, for example with the OGTR (Office of the Gene Regulator), in an Australian context. This could adequately characterize and define new GM-rice varieties projected to mitigate climate change effects, based on IPCC and FAO objectives (IPCC 2014;FAO 2016), and summaries for policy makers.

Private sector stakes in GM-initiated rice projects should not be monopolized solely towards their own commercial interests, and should allow room for other agri-startups and SMEs to innovate. State governance remains the key limiting factor in these scenarios, which must encourage and support innovative genomic technologies/methodologies, and their application, that complement production systems and which can harmonize these in favor of providing suitable return on investments for private players. A simulated study of GM economics conducted by [43] revealed that a loss of 10 years from not applying golden-rice would have resulted in millions of damaged eye sights. The authors concluded that it is unjustified to delay GM technologies if their adoption is greater than the expected damages. From a social welfare perspective, GM technology adaption can improve social standing [43]. What this suggests is that an additional economical limiting factor, that is economic benefits from GM technologies, could also influence government decision towards being more precaution-orientated rather than accepting the economical- social and -agricultural rewards with accepting NGS-genomics technologies [44-46].

Large and SME agri-businesses should also work collaboratively [42] and incorporate developing nations/rural farmers into their strategic ventures in order to communicate the use of genomic technologies and methodologies and associated outputs based on gene bank databases, for example. In unison, governments should position themselves towards reviewing regulation, educating public to ensure confidence in their perception(s), and working with large and SME organizations to evolve policy and incentives that favors food security, through a new agricultural model; that should incorporate NGS - genomics to generate public interest in biotechnology [47]. This will ensure the local farmer is considered, educated, and well-informed of, climate-mitigated GM-approved crop varieties which can only be effective if their socio-cultural factors are considered in governmentally regulated frameworks and policies.

Scientists described the concerns associated with commercialization barriers. In their study, they pointed out that other factors such as market availability and viability, regulatory systems, and economic aspects of commercialization are fundamental for companies to understand if they are to continue investing into their R&D agricultural products [36].

The same study addresses products, GM traits in staple crops, and explains their barriers to commercialization which might be due to unfavorable market platforms, the failure to transition GM events to a large-scale and/or under-performing, and the discouragement from public consensus that offsets further progression towards commercialization [48].

Furthermore, risks of investing large sums of money into product pipelines can be, depending on the R&D stage, associated with stringent and expensive regulatory outlines. From a large business perspective the costs may seem manageable; conversely, a SME or public organization would need to invest more during the early stages of their R&D pipeline. In the case of a long-term SME with promising GM-rice variety cultivars that can tolerate drought and temperature stress, initiating the genomics-driven results to large-scale trials might seem feasible and within budget, however this could breakdown at regulatory step(s) where over-spending might become an apparent issue. Together, these strategies will pave a way forward for new agricultural systems from GM-crop genome to farmer satisfaction that should only be marketed and sold to farmers based on their needs, not for the purpose of stand-alone profitability.

Conclusion

The obvious relationship between existing and emerging genomics approaches, climate change outlooks, and their translational output in designing GM-rice varieties which can withstand changing socio-economic and climatic terrain, will represent the next phase in rice research. Problems currently exist within managing a suitable agricultural development plan which accounts for the improved genomics approaches that can mitigate human-induced environmental threats in most staple crops across the globe. The Save and Grow, and Hague conference reports both offer suitable plans that address climate change, and agricultural intensification processes; however they do not take into account the potential of NGS technologies that can offer a valid rationale for their ‘agricultural transformation’ ambitions. These new advances in NGS, and biotechnology, must be considered by regulators in order to account for the many more GM events that will undoubtedly occur. These regulatory concerns should keep up with the growing number of molecular markers, for example, which will explain the complexity of stress-related traits, and which will require GM to address climate-change effects.

Chapter five of the 2016 FAO has listed an ‘inefficient use of resources’ as a prime concern influencing productivity and climate change, and resilience. It could well be the role of genomics, such as WGS, GS, GWAS, and/or re-sequencing, that can fill certain ‘knowledge gaps’ which can provide the initial data surrounding the development of climate-resilient rice varieties. By improving this knowledge base using a genomic-derived platform, a more scientifically-defined approach to establishing relevant policy can be materialized and implemented.

The example of FAOs Save and Grow approach provides a well-developed paradigm that also includes several suggested strategies that address the need of improved and adapted varieties. Agricultural assessment will need to address not only the implementation of the improvement in rice phenotypes to its transfer to food security and policy, but also to maintain a focus on what consumers’ desire, i.e. nutritional content.

Modifying the existing framework of how rice varieties become commercially sold and grown, by industry to farmers, consequently to consumer, will explicitly call in strict food safety criteria that will need to address, and meet, end-use quality processes in a globally-demanding food outlook.

The challenge in the near future is not only developing more resilient rice varieties that can mitigate abiotic effects, but also managing and implementing a minimally-timed process of commercializing elite rice varieties with functional traits that don't run the risk of a lengthy time-to-market pipeline. Thus it is necessary that GM regulation is properly educated to avoid a further politicization of the GM debate. Developing nations will be the beneficiaries in genomics-applied GM-rice varieties, and so major reform is required. This will undoubtedly herald the need for economists to explain cost-risk analysis, and the advantage of adaption to genomics (GM) technologies.

Genetic engineering is needed to produce elite rice varieties which can synergistically work within a redefined and scientifically-acceptable paradigm of food security, government policy, and confident investment. However, GM varieties are not a complete replacement, but a substitution which will bring a whole myriad of other benefits.

The additional value of including new plant breeding techniques (NPBT) signals the process of developing end-products with consumer-beneficial traits. The challenges that NPBT, in a genomics context, faces is a standardized legal framework for which authorities will decide upon. As a result, these policy-driven decisions will affect timeframes from lab to market, and to consumer.

The FAO has announced its urgent agenda to address food insecurity and so, food insecurity involves a multitasked effort to incorporate domestic food policy and science. This will influence the end-result of food volatility and have an overall net effect on further climate change outcomes, which can be, as evidenced throughout this article, assessed from a genomics-centric perspective

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