

## REVIEW

# Technology Development for Stable Agricultural Production under Adverse Environments and Changing Climate Conditions

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### Abstract

The second of the United Nations' 17 Sustainable Development Goals aims to end hunger, achieve food security and improve nutrition, and promote sustainable agriculture. However, it is well known that the agricultural potential in developing regions including Africa has not been fully realized because adverse environments and changing climate conditions impose abiotic (e.g., low soil fertility, droughts) and biotic (e.g., pests, diseases) stresses on plant growth and development. To ensure food and nutrition security in such regions, the Environmental Stress-tolerant Crops project, the High-yielding Biomass Crops project and the Pest and Disease Control project in the Program for Stable Agricultural Production at the Japan International Research Center for Agricultural Sciences aimed to develop technologies and crops with high productivity and adaptability to adverse environments and changing climate conditions. In order to develop crops with environmental stress tolerance and disease resistance, we have clarified and used the genes and loci involved in these traits toward the development of breeding materials. And in order to develop technology for effectively controlling transboundary pests, we have elucidated the ecology of their occurrence and developed pest management technology based on that information. We hope that these materials and technologies will contribute to achieving food and nutrition security in developing regions.

**Discipline:** Crop Science

**Additional key words:** biomass, breeding, rice, soybean, sugarcane

### Introduction

There are concerns that global strains on the supply and demand for food may occur in the medium to long term, owing to the increase in global population, chronic malnutrition in developing countries, projected economic growth in emerging countries, and increasingly abnormal weather (United Nations 2019, World Food Programme 2020). The second of the 17 Sustainable Development Goals (SDGs) developed by the UN calls on all nations to “end hunger, achieve food security and improved nutrition, and promote sustainable agriculture.” In developing regions such as the tropics, many agricultural lands face such adverse environmental conditions as low fertility, high temperature, drought, and salinity, and are

particularly vulnerable to the adverse effects of climate change. For instance, droughts occur frequently around the world. In the past, crops such as rice and soybean have been severely damaged due to drought stress, and there are rising concerns about the adverse effects of climate change (Kim et al. 2019). It is thus necessary to promote sustainable agricultural production activities in developing regions where the potential for agricultural production has not been fully realized.

Recent estimates indicate that damage to crops due to plant pests accounts for 20%-40% of losses in global food production (FAO 2019a). Climate change, global warming, and the globalized movement of people and goods contribute to the spread of transboundary plant pests and diseases, worsening the damage that is creating

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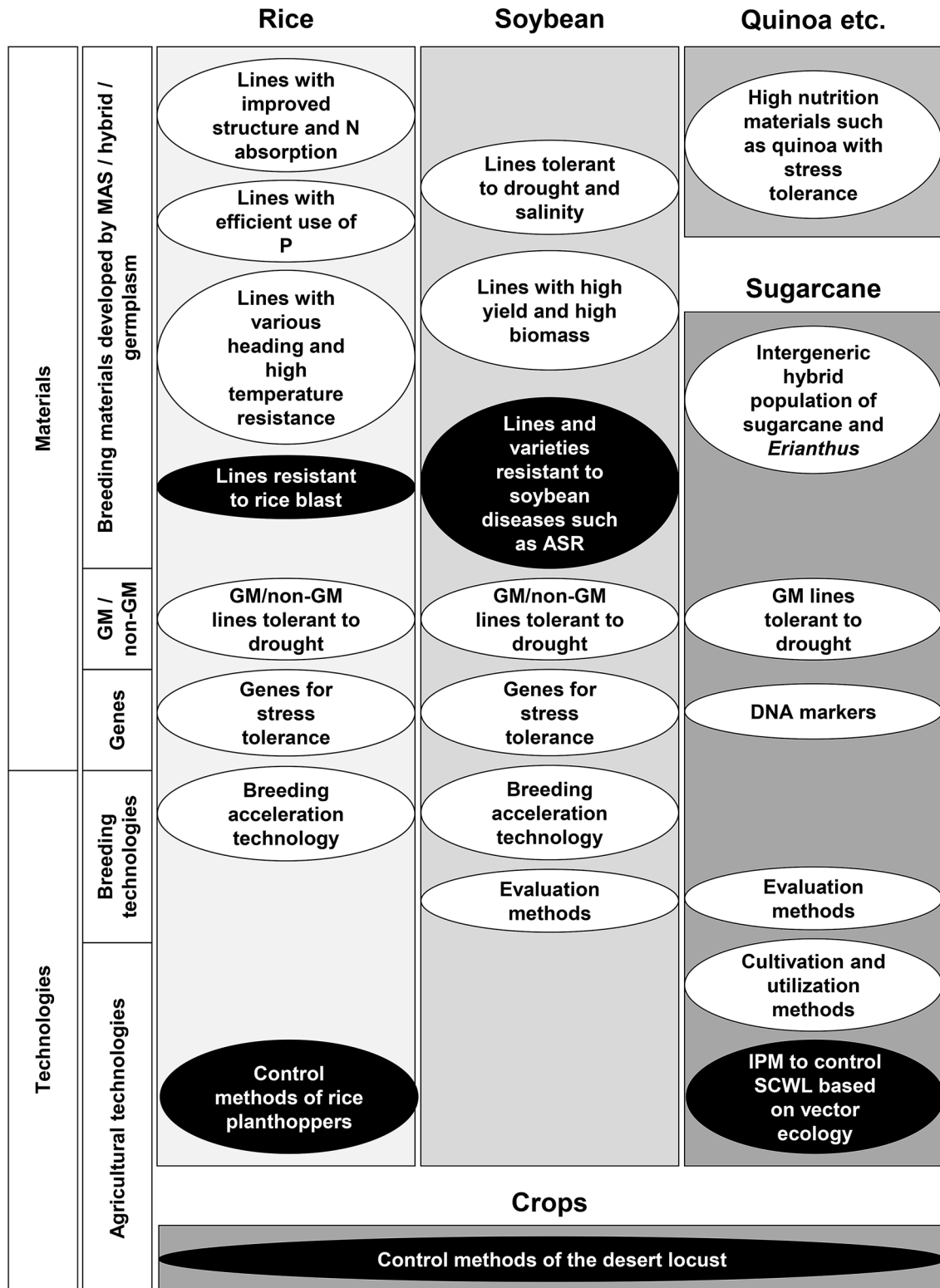


Fig. 1. Main research outputs of the Environmental Stress-tolerant Crops project, High-yielding Biomass Crops project, and Pest and Disease Control project

White ellipse: abiotic stress-related output; black ellipse: biotic stress-related output.

ASR: Asian soybean rust; GM: genetically modified; IPM: integrated pest management; MAS: marker-assisted selection; N: nitrogen; P: phosphorus; SCWL: sugarcane white leaf.

worldwide global public concern. It is difficult for any country to combat pests and diseases alone, thereby necessitating cooperation with neighboring countries.

In order to work towards achieving the second of the SDGs and establish the stable and sustainable production of agricultural crops in developing regions vulnerable to climate change and such adverse environmental conditions as drought, high salinity, and poor soil, we have promoted projects in the Program for Stable Agricultural Production in the Tropics developed at the Japan International Research Center for Agricultural Sciences (JIRCAS) (JIRCAS 2016) (2016-2020) (Fig. 1). This includes Africa and regions with adverse environments. In the Environmental Stress-tolerant Crops project, we have worked on the development of breeding materials and basic breeding technologies for highly productive crops adaptable to such adverse environments. In the High-yielding Biomass Crops project, we have also developed basic technology for the breeding and utilization of promising high-yielding crops, especially sugarcane, which can adapt to adverse environments such as low fertility and drought. Moreover, in the Pest and Disease Control project, we have developed plant pest management technologies based on the ecology of outbreaks and vector insects for the effective control of transboundary crop pests, which may have invaded and proliferated in Japan. Additionally, we are developing disease-resistant varieties of rice and soybean using the research networks established by JIRCAS. In this review, we introduce the representative research results obtained from the projects mentioned above and consider opportunities for work in the future.

### The Environmental Stress-tolerant Crops project

Research on the genetic improvement of crops to withstand adverse environments, such as those with high temperatures, frequent droughts, and high salinity, has been promoted. *qEMF3*—a quantitative trait locus (QTL) for the early morning flowering trait of wild rice (*Oryza officinalis*)—can be exploited to escape heat stress at the flowering stage in rice under future hotter climates (Hirabayashi et al. 2015). In addition, the *DEEPER ROOTING 1 (DROI)* gene, which regulates root angle to obtain water from deep soil, was discovered and used to improve rice yield under drought (Uga et al. 2013). Moreover, root angle modifications regulated by a *DROI* homolog improved rice yield in saline paddy fields (Kitomi et al. 2020). In this project, we have developed breeding materials and basic breeding technologies for highly productive crops that are adaptable to adverse

environments. For rice, breeding materials that have high temperature resistance, drought tolerance, phosphate deficiency resistance, and high nitrogen use efficiency have been developed using marker-assisted selection (Gamuyao et al. 2012, Hirabayashi et al. 2015, Obara et al. 2014). For soybean, breeding materials that are tolerant to drought and high salinity have been developed using marker-assisted selection (Do et al. 2016). In addition, we have developed genetic modification (GM) techniques, such as the optimization of stress-inducible promoters and stress tolerance-related genes for rice and soybean, as well as non-GM techniques, such as genome editing using CRISPR/Cas9 for rice (Ishizaki 2016, Nakashima 2020, Selvaraj et al. 2017, 2020). Furthermore, we have worked on the evaluation and utilization of genetic resources such as tomato, amaranth, and quinoa for the development of crops with high nutritional value and tolerance to adverse environments (Pham et al. 2020, Mizuno et al. 2020, Yasui et al. 2016). We introduce some of the representative results below.

#### 1. *SPIKE*, a quantitative trait locus for increasing the number of spikelets per panicle, enhances rice grain yield under low-yield conditions

Rice is an important food source in Asia and Africa where nutrient-poor soils are predominant, and farmers lack the finances to purchase sufficient fertilizer. Therefore, it is necessary to develop genetically improved rice varieties with high nutrient-use efficiencies. *SPIKELET NUMBER (SPIKE)*, a QTL for increasing the number of spikelets per panicle, has been identified (Fujita et al. 2013). We found that the near-isogenic line for *SPIKE* in the IR64 genetic background (*NIL-SPIKE*) tended to be superior to IR64 for grain yield under low-N application (45 kg N/ha), while the difference disappeared under high-N application (180 kg N/ha) (Takai et al. 2019). The number of spikelets per panicle of *NIL-SPIKE* was significantly higher (about a 20% increase) than that of IR64 under low-N application, but was not significantly different from that of IR64 under high-N application. From these results, we considered that the yield of *NIL-SPIKE* under low-N application was superior to that of IR64, due to the higher number of spikelets of *NIL-SPIKE*. The use of *SPIKE* can be expected to increase the productivity of rice even in environments with low soil fertility and low fertilizer input. The results indicate that *SPIKE* should be used in regions where soil fertility is poor, or where farmers cannot purchase adequate fertilizer (Takai et al. 2019). We conducted this research in collaboration with the International Rice Research Institute (IRRI), one of the Consultative Group on International Agricultural Research (CGIAR) centers

in the Philippines.

## **2. Overexpression of *AtGols2*, an *Arabidopsis* galactinol synthase gene, increases grain yield in rice under drought stress in the field**

Plant biotechnology holds promise to meet the societal demand for increased global crop production (Gupta et al. 2020), and we have developed a GM crop production technology to improve drought tolerance (Nakashima & Suenaga 2017, Nakashima et al. 2018, Nakashima 2020). We generated transgenic rice lines that express *AtGols2*, an *Arabidopsis* galactinol synthase gene, in two upland varieties—Curinga and NERICA4. Curinga is a local Brazilian variety and NERICA4 is a popular variety in African countries. Experiments showed that each transgenic line accumulated significantly higher amounts of galactinol than non-transgenic rice plants. Three consecutive field trials under drought stress identified transgenic lines that consistently had higher grain yields than each non-transgenic variety. For example, compared to non-transgenic Curinga, the transgenic Curinga line (2580) showed a yield increase of 50%, 157%, and 20% at 31, 39, and 19 rain-free days, respectively. *AtGols2* can thus be a useful biotechnological tool for reducing grain yield losses in rice under drought stress in the field (Selvaraj et al. 2017). Recently, we also elucidated that expression of the rice CCCH-tandem zinc finger protein gene *OstZF5*, under a stress-inducible promoter, mitigates the effect of drought stress on rice grain yield under field conditions (Selvaraj et al. 2020). We have also shown that soybeans carrying genes related to drought tolerance show excellent performance in the field (Nakashima 2020). In field conditions with a water deficit, a soybean transgenic line (1Ea2939) expressing transcription factor AREB1 showed a higher total number of pods and seeds, and increased dry seed matter compared to non-transgenic wild-type plants (BR16 conventional cultivar). Moreover, in two representative seasonally dry regions of Brazil, we showed that transgenic sugarcane plants exhibiting stress-induced overexpression of the *Arabidopsis* transcription factor AtDREB2A CA showed higher cane yield per hectare and sugar productivity than non-transformed plants under drought in the field conditions (de Souza et al. 2019). These results indicate that the overexpression of genes involved in stress tolerance might be a suitable strategy to develop drought-tolerant cultivars.

## **3. Draft genome sequence of an inbred line of quinoa, an allotetraploid pseudocereal crop with high nutritional properties and tolerance to abiotic stresses**

Quinoa, a pseudocereal originating from the Andes region of South America, is emerging as an important crop with the potential to contribute toward global food security due to its great nutritional value and tolerance of adverse environments. However, since quinoa is one of the orphan crops, research on it was delayed. Molecular analysis of quinoa is limited by its genome complexity derived from allotetraploidy and its genetic heterogeneity due to outcrossing. Here, we established the inbred quinoa accession ‘Kd,’ presented the draft genome sequence of ‘Kd’ using next-generation sequencing, and constructed the free-access Quinoa Genome Data Base (Yasui et al. 2016, Kazusa DNA Research Institute 2016). Similarly, by sequencing two diploids from the ancestral gene pools of quinoa, Jarvis et al. (2017) identified the sub-genomes of this crop and the reduced-coverage genomes of 22 additional samples of the allotetraploid goosefoot complex. The genome information provides insights into the mechanisms underlying the agronomically important traits of quinoa. Based on this achievement, we recently initiated international joint research to strengthen resilience in arid agro-ecosystems vulnerable to climate change through research on plant resources and technological applications in Bolivia, as a project of the Science and Technology Research Partnership for Sustainable Development (SATREPS) of the Japan Science and Technology Agency (JST)/Japan International Cooperation Agency (JICA). Recently, our group has built a collection of 136 pure quinoa lines and revealed the diversity therein (Mizuno et al. 2020). Some lines were also found to germinate in saline water with the same level of salt content as seawater. These results have paved a way to elucidate the molecular mechanisms underlying the high environmental adaptability and superior nutritional value of quinoa. This is expected to accelerate the breeding of quinoa varieties with excellent nutritional characteristics and adaptability to severe environments.

In addition to these achievements, we have also achieved the excellent results described below. Although the genetic improvement of rice plant types has been widely promoted in breeding research, little progress has been made in terms of improving the root types with drought and salinity tolerance and high nutrient uptake. This could be attributed to the difficulties in evaluating the underground roots. To analyze root type variation across diverse genetic resources and large hybrid populations, we developed a method of evaluating root

angle distribution at the seedling stage in rice (Tomita et al. 2017). And through a genome-wide association study, we identified a QTL associated with lateral root development in rice (Wang et al. 2018). Furthermore, we developed wild soybean chromosome segment substitution lines (CSSLs) for studying important genetic traits (Liu et al. 2018a, 2018b). The seed weight-associated QTL *qSW12.1* and the flowering time-associated QTL *qFT12.1* were detected in these wild soybean CSSLs. We succeeded in enhancing drought tolerance in soybean plants by downregulating *GmERAI* genes using a virus-induced gene silencing technique (Ogata et al. 2017). We also reported the enhancement of ozone resistance by adjusting the stomatal aperture on the leaf surface (Nagatoshi et al. 2016). Moreover, we established novel breeding technologies such as the genome editing of rice cultivars and strategies for producing desired homozygous mutants (Ishizaki 2016). CO<sub>2</sub> supplementation under appropriate light and temperature accelerated soybean cultivation from immature seeds in compact growth chambers, producing up to five generations per year with efficient crossing as compared with only one or two generations that can be produced using current field and/or greenhouse-based cultivation methods (Nagatoshi & Fujita 2019).

As a short-term outcome, local institutes will genetically improve locally cultivated varieties in the Philippines, China, and Brazil by utilizing the developed breeding materials with resistance to adverse environments through collaborative research. As a long-term outcome, production of the environmental stress-tolerant crops developed is expected to increase and stabilize productivity in developing countries, which will contribute to world food security. In the situation of global warming, high-temperature-tolerant crops may contribute to food security in Japan. In developing regions, crops are important not only as a source of calories but also in the formation of a healthy body with a well-balanced nutritional profile and immune system. Therefore, improving and utilizing not only rice and soybeans but also vegetables and minor grains in the future will prove to be effective. Although breeding takes time, crops that are resilient to climate change and adverse environments are very effective for smallholder farmers in developing regions, and strengthen their food production systems without any additional investment. Therefore, we believe that ongoing research to develop environmental stress-tolerant crops in the future is important. Advanced technologies such as genome breeding, genome editing, and phenotyping, which have made remarkable progress in recent years (Eshed & Lippman 2019, Gupta et al. 2020, Yang et al. 2020), are

expected to accelerate the development of crops resilient to the adverse effects of climate change by enabling appropriate growth and flowering in adverse environments.

### The High-yielding Biomass Crops project

Along the world's growing population, such problems as inadequate food and strained energy supplies have also arisen. Hence, low agricultural productivity in the fields should be improved, and food and energy production must be increased. Sugarcane was chosen as the target crop in our project concerning important biomass crops, because it can produce food and energy from its sugar and fiber. Sugar is a food and a source of bioethanol as well, while bagasse (a fibrous byproduct from sugarcane) can be used to generate electricity. Thailand is the world's fourth largest producer of sugarcane and the second largest exporter of sugar. In northeastern Thailand—the main production area of sugarcane—agricultural production is unstable due to drought and low soil fertility; therefore, stable and sustainable food and energy production using high biomass crops that can adapt to poor environments are essential. We have studied sugarcane in Thailand while working toward stable sugarcane production in Asia. We have also promoted research on the development and use of such crops including sugarcane for more effective use of the genetic resources of biomass crops in Japan, in collaboration with Japan's National Agriculture and Food Research Organization (NARO). We previously developed multi-purpose sugarcane varieties with good yields of both sugar and fiber derived from interspecific hybrids between sugarcane and its wild sugarcane species (*Saccharum spontaneum*) in northeastern Thailand, where sugarcane productivity is low due to severe drought and infertile soils (JIRCAS 2015). These new interspecific hybrids have been registered as sugarcane varieties by Thailand's Department of Agriculture, Ministry of Agriculture and Cooperatives. In this project, we have conducted research to develop sustainable cultivation methods utilizing byproducts from sugar factories and mechanical harvest technologies to increase the productivity of high-yielding biomass crops, such as multipurpose sugarcane.

The stagnation of genetic improvement arising from the narrow genetic diversity of cultivars and breeding materials in the world has become an issue in sugarcane breeding, thereby making it necessary to expand genetic diversity by using unused genetic resources such as *Erianthus*. A close relative of sugarcane, *Erianthus* shows considerable potential as a breeding material for

sugarcane improvement, given its high biomass productivity and exceptional adaptability to abiotic stresses such as drought. We are developing new breeding materials that produce high biomass yield in several adverse environments such as drought and low fertility through intergeneric hybridization between sugarcane and *Erianthus*, and backcrossing with sugarcane. We have also established techniques for evaluating such important characteristics as root penetration ability, relative to the biomass production of *Erianthus* under stress conditions, and for selecting intergeneric hybrids using DNA markers. We introduce some of the representative results below.

### **1. Development of interspecific hybrids between sugarcane and its wild sugarcane species *S. spontaneum* and intergeneric hybrids between sugarcane and *Erianthus***

As mentioned above, we have developed new multipurpose sugarcane varieties with good yields of both sugar and fiber derived from interspecific hybrids in Thailand. ‘Harunoogi’ is also a new sugarcane variety for Japan derived from the interspecific hybrids, jointly developed by NARO and JIRCAS (Hattori et al. 2019a, 2019b). To further improve sugarcane for high productivity, even in an environment with water shortages and low fertility, and obtain intergeneric hybrids, we developed a method to synchronize the flowering periods of sugarcane and *Erianthus* by treating *Erianthus* materials with a long day in the field (Tagane et al. 2011, Terajima et al. 2017). Thus, intergeneric hybrids between sugarcane and *Erianthus* were successfully developed, and the resulting cytogenetic and agronomic characteristics revealed a varying number of *Erianthus* chromosomes in the hybrids and a significant positive correlation with some yield-related characteristics, but not quality-related characteristics (Babil et al. 2018). Breeding materials with strong root penetration for growing deep roots (even on hard soils with water and fertility problems) and large biomass production were selected as promising intergeneric lines between sugarcane and *Erianthus* in both Thailand and Japan. Sugarcane is sensitive to low temperatures, and there are many production areas where low temperature is a major constraint on production, including Japan. Therefore, improving its adaptability to low-temperature environments has been an important breeding target for sugarcane. *Miscanthus* spp. (a sugarcane-related genus) is highly adapted to low-temperature environments given its cold tolerance during photosynthetic activity, and thus attracts attention as a biomass crop in cold-climate regions. We also developed intergeneric hybrids between

sugarcane and *Miscanthus* and studied the low-temperature resistance of the hybrids (Kar et al. 2019a, 2019b).

### **2. Research and variety registration of *Erianthus* in Japan**

In Japan, we have been collaborating with NARO to characterize our *Erianthus* genetic resources and develop varieties, with the aim of reducing greenhouse gas emissions by expanding the use of biofuels produced from biomass crops. In this project, we studied the phylogeny of *Erianthus arundinaceus* in Japan (Tsuruta et al. 2017a, 2017b, 2017c). A review of *Erianthus* in a temperate zone in Japan has also been published (Matsunami et al. 2018). For biomass use, we registered two *Erianthus* varieties—JES1 (Gau et al. 2019a) and JEC1 (Gau et al. 2019b)—that were jointly developed by JIRCAS and NARO. Pellet fuel made from JES1 has been commercially used in Tochigi prefecture, Japan.

We hope that new varieties in the future that utilize the beneficial characteristics of sugarcane-related genetic resources such as *Erianthus*, as well as associated sustainable cultivation and versatile application technologies, including harvesting methods to increase biomass productivity, will spread to areas with adverse environments in Thailand and neighboring countries. The productivity of such biomass crops as sugarcane in the region is expected to be improved, and management by farmers will be stabilized by using the developed sustainable cultivation methods utilizing byproducts from sugar factories and mechanical harvesting technologies, combined with the developed biomass crops. We expect that the developed high-yielding biomass crops can be used not only for food production but also for renewable energy production, and will thus contribute to the decarbonization of energy use toward avoiding devastating climate change. Sugarcane genome sequences have recently been reported (Garsmeur et al. 2018, Sauza et al. 2019), and sugarcane genome information should accelerate genome breeding in this crop.

### **The Pest and Disease Control project**

Transboundary insect pests and plant diseases spread to several countries, reach epidemic rates, cause significant losses to farmers, threaten food security, and damage local biodiversity and the environment (Xia et al. 2019). For instance, locust plague is one of the three major natural disasters in history (i.e., droughts, floods, locust). Desert locusts are the most devastating and often cause damage in more than 50 countries, particularly in

Africa and Central Asia. Fall armyworms are another recently emerged notorious pest, and are now widespread in over 65 countries in Africa, the Middle East, and Asia. In addition, wheat rust is a serious threat worldwide. Banana Fusarium wilt caused by *Fusarium oxysporum* is a serious disease in almost every banana-producing country in the world. The vector-borne pathogen *Xylella fastidiosa* can lead to the death of infected plants, and thus is a threat to agriculture, the environment, and economy. We have pursued an extensive project on plant pest control in collaboration with several countries in the tropics and regions with adverse environments, where these insects continue to cause significant losses to farmers. Our focus was on two of the world's most destructive migratory insects: the desert locust and rice planthoppers. We also focus on vector leafhoppers, which transmit sugarcane white leaf (SCWL) disease. Our strategy entailed investigating the ecology of these insects in the field to look for vulnerabilities in their life cycles, and then developing such eco-friendly control measures as integrated pest management (IPM), in collaboration with the countries or regions affected by the migration of these insects. Among the transboundary diseases, we focused on rice blast and Asian soybean rust (ASR) in conjunction with the Rice Blast Research Network (established in 2006 in a JIRCAS research project) and the Soybean Disease Research Network (established in 2007 in a JIRCAS research project). For these transboundary diseases, we identified effective resistance genes in the target countries and regions, and developed resistant varieties of the crop with the corresponding international research networks. We introduce some of the representative results below.

### 1. Development of control technology based on the ecology of migrating pests and vectors

The desert locust is a major threat to agricultural production in Africa, western Asia, and South Asia, threatening the livelihood of at least one-tenth of the world's population. The locust shows phase polyphenism at a high population density, with a solitarious phase transforming into a gregarious phase that can cause serious economic damage. As little is known about the ecological behavior of locust in the field, chemical insecticides are used as major control measures, thereby causing much concern regarding the adverse effects on health and the environment. To reduce these risks, we revealed the spatiotemporal distribution patterns of the desert locust in Africa through field observations (Maeno & Ould Babah Ebbe 2018, Maeno et al. 2018). Recently, Maeno et al. (2021) reported that desert locust larvae migrated in the Sahara Desert during the day and

regulated their body temperature in response to ambient temperature. Based on this observation, the regulation of body temperature was inferred to accelerate foraging and digestion rate. Moreover, a locust-specific model enabled the estimation of body temperature and the prediction of behavior in these insects. We are currently developing an effective survey method and a preventive control system for desert locust in cooperation with Mauritania and the French Agricultural Research Centre for International Development. Recently, Guo et al. (2020) have revealed that 4-vinylanisole is an aggregation pheromone in migratory locusts. This finding provides insights for the development of novel control strategies for locusts, and this locust aggregation pheromone could be used to control desert locust plague in Africa.

Rice planthoppers occur year-round in Southeast Asia and seasonally in East Asia, including Japan. The area around northern Vietnam is considered the point of origin for the migration of planthoppers to China and Japan (Otuka et al. 2008). Rice planthoppers are a major pest in East Asia including Japan, because they carry viral diseases to rice in addition to the plant damage they cause by sucking. Since 2005, outbreaks of rice planthoppers have occurred in such East Asian countries as Vietnam, China, and Japan, and have been closely related to the development of insecticide resistance in these regions (Mastumura & Sanada-Morimura 2010, Matsumura et al. 2018). As the improper use of insecticides at the point of origin could lead to planthoppers acquiring insecticide resistance, there are concerns that such resistance may migrate along with the insects to Japan via China. We are thus pursuing the development of an IPM system in cooperation with Vietnam, Cambodia, and NARO in Japan, in order to manage insecticide resistance. We have evaluated the usage and methods of spraying insecticides on rice planthoppers in northern Vietnam (Matsukawa-Nakata et al. 2019a, 2019b). Appropriate usage and insecticide spraying methods are now being considered for incorporation into the IPM system.

SCWL is an insect-transmitted and seed-cane-borne disease that severely affects sugarcane production in Southeast Asia, especially in Thailand (CABI 2019). To reduce the damage caused by the disease and prevent its spread to sugar production fields in disease-free areas, technology for the mass production of healthy seed stems is necessary. Consequently, a study was conducted in Thailand to establish an IPM system to reduce the risk of pathogen invasion into healthy seed cane production fields based on the ecology of vector insects. The use of appropriate insecticides and sugarcane varieties resistant to vector insects are key components of the IPM system.

We have developed a method of evaluating the resistance against vector insects in sugarcane, and have revealed an effective pesticide against the dominant vector insect of SCWL disease (Hanboonsong & Kobori 2017). Experimental results suggest that the proper use of insecticides for the production of healthy seed cane would reduce SCWL disease prevalence on sugarcane stands. We have published a manual for production of healthy seed cane and method of its distribution to the Thai government, sugar mills, and research institutions in neighboring countries (Hanboonsong et al. 2021).

## 2. Development of control technology using disease resistance

Rice blast is among the most serious diseases worldwide, due to its extensive distribution and destructive ability under favorable conditions. We have successfully established a differential system to facilitate the accurate identification of pathogenic races and resistance genes in rice varieties (Fukuta 2019, 2020). Information obtained using the system helps us select suitable resistance genes and develop rice breeding lines with durable resistance to blast by combining true and field resistance genes. The rice blast research network established by JIRCAS comprises NARO in Japan, national agricultural research stations in Bangladesh, Vietnam, the Philippines, and Indonesia, and CGIAR centers such as AfricaRice and IRRI. Through this network, we have identified races of the pathogen that differ by country and region, as well as possible risks due to a breakdown of resistance from the migration of pathogens from neighboring countries (Fukuta 2019, 2020). For instance, we have revealed genetic variation in resistance in rice germplasm and the differentiation of blast races in Bangladesh (Khan et al. 2016, 2017).

ASR has caused serious yield loss in soybeans. In areas where this disease is common (e.g., Brazil), yield losses can be up to 80%. For this reason, farmers tend to use a lot of fungicides to reduce the damage. We have conducted research to identify effective resistance genes and found that three soybean varieties highly resistant to Asian soybean rust carry the resistance gene *Rpp1-b* (Hossain et al. 2015, Yamanaka et al. 2015, 2016; JIRCAS 2020). We have been developing soybean varieties that are highly resistant to ASR by evaluating the pathogenic diversity of ASR pathogens and pyramiding effective resistance genes in association with the ASR research network, which includes Mexico, Brazil, Argentina, Paraguay, Uruguay, and Bangladesh. Thus far, in collaboration with a research group in Paraguay, we have successfully developed two highly resistant varieties with three resistance genes against ASR (JIRCAS 2019, Lemos

et al. 2011). Information on pathogenic diversity obtained through this research network is also useful for minimizing the risk of a possible breakdown in resistance against ASR in network countries.

Transboundary pests know no borders. The upsurge in desert locust in 2019-2020 developed through back-and-forth locust migrations between East Africa and India, and there are concerns over repeated agricultural damage in large areas. And in recent years, the fall armyworm (a serious polyphagous pest) has spread rapidly worldwide. Although originating in the Americas, this pest crossed Africa just one year after its invasion and advanced east to Asia, reaching Japan in July 2019 (FAO 2019b). The United Nations General Assembly has declared 2020 the International Year of Plant Health (FAO 2019c). This creates a once in a lifetime opportunity to raise global awareness about how plant health protection can help end hunger, reduce poverty, protect the environment, and boost economic development. International cooperation is clearly needed to combat transboundary plant pests.

## Conclusion

To ensure food and nutrition security, we have developed technologies and crops with high productivity and adaptability to adverse environments and changing climate conditions. We have developed breeding materials with stress tolerance in such crops as soybean and rice using marker-assisted selection and biotechnologies, including GM and non-GM technologies. The developed materials will be optimized for each site in collaboration with local research institutions and companies.

The new coronavirus infectious disease (COVID-19) that was confirmed in December 2019 is now affecting the world. COVID-19 is exposing the vulnerability and weaknesses of our already fragile food systems, which were already stressed by increasing climate extremes (Development Initiatives 2020). Efforts to achieve stable food production and reduce malnutrition are increasingly important. Our research should be promoted for stable agricultural production so that it can contribute to achieving food, nutrition, and energy security in developing regions.

Similar to the novel coronavirus that has spread worldwide and caused great damage, certain insect pests and plant diseases have also spread across boundaries and damaged crop production. The mitigation of transboundary insect pests and plant diseases requires concerted efforts and the pooling of resources among the affected countries and regions. It is important for research institutions to implement effective actions through



international research collaborations across the countries concerned. These joint activities will enable early detection, prevention, and prompt control. Under a strategic program aimed at addressing transboundary insect pests and plant diseases, we could contribute more to promoting global efforts toward realizing sustainable food production and environmental conservation, as well as achieving sustainable development goals.

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