

Conservation and Utilization of Plant Genetic Resources for Food and Agriculture in Regions of Monsoon Asia

Makoto KAWASE

National Institute of Agrobiological Sciences
2-1-2, Kan'nondai, Ibaraki 305-8602, Japan
kawase@affrc.go.jp

Abstract: Monsoon Asia, which covers a vast area of countries in South Asia, Southeast Asia, and East Asia, is characterized by rich agricultural biodiversity as well as relevant traditional culture and knowledge. The rich biological diversity has been brought up through diverse natural and cultural conditions there. Nevertheless, it has been confronted with rapid genetic erosion in recent years. Genetic resources of the regions that have potential for future utilization should be studied in detail and will be used for crop improvement particularly for the regions. Plant genetic resources have been collected, conserved, evaluated and used in each country, and by regional and international organizations. Since there are a lot of information and tools developed by advanced plant genome studies but actually we do not understand the diversity in detail, we have to pay much more attention to and analyze genetic variation in cultivated plants and their relatives, and also genetic changes that have been involved in crop evolution. Having established strong collaborative relationships among many countries over the past decades in relation to plant genetic resources for food and agriculture, people in the regions have to seek to extend linkages to each other by helping capacity building and importantly understanding plant genetic resources and developing safe sustainable means of their conservation.

Keywords: plant genetic resources for food and agriculture, bio-diversity, conservation

1. Introduction

Monsoon Asia, which covers a vast area of countries in South Asia, Southeast Asia, and East Asia, is characterized by agriculture-based civilization of long history and now has the highest population density of the world. The region, which is rich in agricultural biodiversity as well as traditional culture and knowledge, has been confronted with rapid genetic erosion in recent years. Peoples' life was supported by and well harmonized within the natural environmental system until early 20th century in the regions. The balance between human activity and environment has drastically changed rather recently and environmental system has been disrupted.

This rich agricultural biodiversity can potentially be utilized for human life in the future and should be conserved as plant genetic resources for food and agriculture (PGRFA). The PGRFA may serve as breeding materials, new crop resources, medicinal materials, some research materials, and so on, particularly for the region. Once any plant variety is lost, even the latest biotechnology could not re-produce the same one.

There are two types of conservation strategy of PGRFA: *ex situ* conservation and *in situ* conservation. Capacity of *ex situ* conservation of PGRFA is rather limited physically by storage facilities but it is easy to conserve different genetic resources systematically, while *in situ* conservation is not so easy, because maintenance of wild plant communities is largely influenced by environment and on-going evolution and adaptation processes, and on-farm conservation might force farmers to cultivate old primitive varieties. International and national agricultural research institutes play an important role for *ex situ* conservation of PGRFA.

The author would like to take some aspects of PGRFA in monsoon Asia and stress the importance of field study, conservation and analysis for sustainable utilization of PGRFA in this article.

2. Present Status of PGRFA in Monsoon Asia

South Asia, Southeast Asia and East Asia are regions where a monsoon climate has developed its landscape - vegetation, soil and water system. Diverse ecosystems are found differently at highlands, semi-arid tropics and humid coastal plains in the regions being influenced by climates varying from temperate to tropical. The monsoon rainfall is the main water resource in most areas, which supplies water to agriculture.

The regions are also characterized by agriculture-based civilization of more than five thousand years and now have the highest population density of the world. Rich biological diversity has been brought up through diverse natural and cultural conditions there. Nevertheless, it has been confronted with rapid genetic erosion in recent years.

A large variety of cultivated plants have been grown there, some of which were domesticated inside the regions and others were introduced from other regions. At the same time, huge genetic diversity has been also reported in each crop. For example, it is thought that rice and buckwheat were domesticated in South China or vicinity, soybean and azuki bean in East Asia, bananas, sugarcane, and taro in South East Asia, and eggplant, green gram, black gram, mango, and sponge guard in South Asia.

Modernizations of agriculture and urbanization have caused genetic erosion in agricultural biodiversity in the regions. Diverse crop landraces have largely been replaced with a limited number of newly bred high-yielding

varieties, and wild relatives have faced extinction in destroyed and polluted environment. High variability of monsoon climate causes frequent climate-related disasters, such as cyclone attack, floods, drought and heat waves that might bring about grave damage to local crop varieties in the region. In the prevailing conditions, agricultural biodiversity should be conserved as PGRFA for sustainable utilization of their genetic variations for crop improvement in the future. PGRFA serve as breeding materials, new crop resource, and research materials. Once any crop variety is lost, even the latest biotechnology could not re-produce the same one.

The conservation strategy of PGRFA is classified into two large categories: *ex situ* conservation and *in situ* conservation. *Ex situ* conservation means PGRFA collected from the field are conserved in places away from the original places. Typical example of *ex situ* conservation is that many different crop cultivars are maintained in gene banks, research institutes, and botanical gardens. *In situ* conservation is a process of conserving specific species in its natural habitat, which is usually adopted for wild plant species. The *in situ* conservation has not only applied to wild species but also increasingly to cultivated forms in farmers' field - conservation of indigenous or unique crop varieties by farmers, by local cooperatives and/or unions is called as "on-farm conservation". Generally speaking, capacity of *ex situ* conservation of PGRFA is rather limited by storage facilities but it is easy to conserved different genotypes systematically. On the contrast, *in situ* conservation is not easy, because maintenance of wild plant communities is largely influenced by environment and on-going evolution and adaptation processes, and on-farm conservation might force farmers to cultivate old primitive varieties. On-farm conservation is often attracted in campaigns of green tourism, local production for local consumption, slow food, food mileage, and others.

For conserving PGRFA, international and national agricultural research institutes are playing an important role. International Rice Research Institute (IRRI, located at Los Baños in the Philippines) conserves more than 109,000 accessions of cultivated and wild rice species, most of which are traditional varieties belonging to *Oryza sativa* L. International Crops Research Institute for the Semi-arid Tropics (ICRISAT, headquarters located at Patancheru, Andhra Pradesh, India) conserves more than 118,000 accessions of crops including sorghum, pigeon pea, pearl millet, chickpea and groundnut and the World Vegetable Center (widely known as AVRDC, headquarters at Shan-Hua, Taiwan) conserves more than 56,000 accessions of vegetables and pulses. The Bioversity International, which was first established for international coordination on PGRFA as the International Board for Plant Genetic Resources (IBPGR), then, the International Plant Genetic Resources Institute (IPGRI) and was reorganized together with the International Network for Improvement of Banana and Plantain (INIBAP), is the world's largest non-profit agricultural research and training organization devoted solely to the study and promotion of agricultural biodiversity.

Many countries in the regions have their own policy on PGRFA, most of which manage gene banks for conservation of PGRFA and facilitation of their use in agricultural research. More than 240,000 accessions are conserved in the NIAS Genebank Project of Japan, more than 391,000 under the Chinese Academy of Agricultural Sciences (CAAS) of China, and more than 366,000 in the National Bureau of Plant Genetic Resources (NBPGR) of India.

3. NIAS Genebank Project of Japan and its International Relations

3.1. NIAS Genebank Project

The Ministry of Agriculture, Forestry and Fisheries (MAFF) of Japan initiated Genebank Project in 1985 to focus on conservation and sustainable utilization of genetic resources related to food and agriculture. The National Institute of Agrobiological Sciences (NIAS) implements the NIAS Genebank Project as the "center-bank" in cooperation with "sub-banks" as follows: the National Agriculture and Food Research Organization (NARO), the Japan International Research Center for Agricultural Sciences (JIRCAS), the National Center for Seeds and Seedlings (NCSS), the National Livestock Breeding Center (NLBC), and the National Institute for Agro-Environmental Science (NIAES). The major activities of Genebank are 1) introduction of genetic resources, field survey and diversity studies, 2) characterization and evaluation of genetic resources toward increased active collection, 3) development of genetic and breeding materials by using genetic resources, 4) durable preservation of genetic resources, quality control and improved multiplication and preservation methods, and 5) advanced information management and disclosure system to facilitate use of genetic resources in order to accomplish the Project purpose. Concerning PGRFA, the Project conserves 241,507 accessions (data on 30 November 2008) and 15,714 samples of the PGRFA were distributed upon request to domestic and/or foreign users for breeding, research and/or educational purposes. Up-to-date passport and evaluation data of distributable accessions have been uploaded onto and disclosed at the website [1]

3.2. International Relations

There are four international cooperation programs incorporated into the NIAS Genebank Project – joint exploration, cooperative research program especially related to *in situ* conservation of PGRFA, overseas seed multiplication and evaluation of PGRFA, and international workshops on PGRFA in addition to distribution of

PGRFA and their information. The Project dispatches researchers overseas to do cooperative exploration/field research every year to survey and collect PGRFA in accordance with the Convention for Biological Diversity (CBD), international community norms and national regulations. Activities of such missions are reported in the Annual Reports on Exploration and Introduction of Plant Genetic Resources (NIAS) [2]. The plant materials collected in a counterpart country are always divided into at least two sets: one set is conserved in the country and another set is transferred to Japan based on a material transfer agreement (MTA) between Japan and the country. Secure duplicated conservation of genetic resources is beneficial to researchers in both countries. This has always been the practice since the beginning of the Genebank Project. Such joint exploration enhances conservation and understanding of PGRFA, increases mutual understanding, and provides a good basis for further research cooperation.

Regarding the conservation of wild species, it is often difficult to preserve their diversity *ex situ* at a gene bank and *in situ* conservation is needed. The NIAS Genebank Project implemented a special program to encourage researchers in developing countries to survey the status of populations in the field and monitor them in cooperation with Japanese scientists at the sites as well as analysis of the populations by molecular techniques at NIAS and related institutions. This reciprocal approach helps *in situ* conservation of PGRFA, especially wild relatives of cultivated plants, and also assists capacity building of researchers in collaborating countries. The *in situ* conservation research activities of the NIAS on wild legumes and wild rice were started in collaboration with the Plant Genetic Resource Centre (PGRC) of Sri Lanka in 2000. Japanese researchers joined the missions in Sri Lanka to monitoring genetic structure of wild *Vigna* species and wild *Oryza* species and learnt much from Sri Lankan scientists, while Sri Lankan researchers who participated in the program could learn various molecular techniques in Japan as well as join collecting missions in Japan [3]. An *in situ* conservation project on *Fagopyrum* species sponsored by IPGRI was conducted in Nepal from 1999 to 2001 in a similar manner. Genetic diversity of the wild species *F. cymosum* successfully identified the populations most suitable for *in situ* conservation of this species [4]. Indonesian and Korean researchers have participated in a similar program on sweet potato and *Perilla* species, respectively.

International workshops on PGRFA serve as a good opportunity for researchers worldwide to exchange up-to-date information and to initiate future research cooperation. For example, the International Genetic Resources Workshop supported by the Genebank Project of Japan titled as “The Genus *Oryza*” was held at Tsukuba, Japan in September, 2003 [5]. In 2006 an international symposium supported by the Genebank Project and OECD on crop domestication and super-domestication was held at Tsukuba [6].

3.3. PGRFA activities in JICA Schemes

The Japan International Cooperation Agency (JICA) has implemented a series of grants-in-aid and technical cooperation projects as official development aid (ODA) of Japan in relation to PGRFA. It contributed to the establishment of gene banks in Sri Lanka, Chile, Pakistan, and Myanmar as well as scientific capacity building. As the responsible institute on PGRFA in Japan, NIAS has always participated in feasibility studies at project sites, the detailed project planning, and research coordination for smooth implementation and fruitful achievements of the JICA undertakings.

For example, Plant Genetic Centre (PGRC) of Sri Lanka was established in 1989, a technical cooperation program was done specifically for the provision of long term and short term Japanese experts, training opportunities for Sri Lankan scientists in Japan and for procuring equipments, which was initially agreed for 5 years, subsequently extended for additional 2 years and completed in 1995. Chile received support from the Inter-American Development Bank (IDB) in 1986 for equipment for plant genetic resource research, and a JICA project-type technical cooperation was done in Chilean National Agriculture and Livestock Research Institute (INIA) from 1989 to 1993, subsequently extended for additional 2 years. In Pakistan, a facility for Genetic Resource Preservation and Research Laboratory that is now called “Plant Genetic Resources Institute (PGRI)” was established through the JICA collaboration scheme in 1993. A project-type technical cooperation was done for 5 years (1993 to 1998), which was followed by an aftercare technical cooperation program (2001 to 2003). In Myanmar construction of a Seed Bank and a relevant technical cooperation project was planned based on collaboration between Japan and Myanmar under a scheme of JICA to collect, evaluate, and conserve agricultural PGRFA in Myanmar and to promote their use in breeding programs. The Myanmar Seed Bank was constructed within the Central Agriculture Research Institute (CARI) at Yezin in 1990, and a technical cooperation project was implemented as “Myanmar Seed Bank Project” from 1997 after a suspended period and completed in 2002. In all cases, the countries’ staff and Japanese experts collaborated well to set up and improve the PGRFA management systems in the countries. All these gene banks actively are functioning as national centers for PGRFA activities.

JICA and NIAS provide a six-month training course on PGRFA, which originally started in 1983, and more than 200 people from different countries has participated in the program.

3.4. Cooperation within International Framework

The Government of Japan started assistance to Bioversity International (former IBPGR/IPGRI) in 1979, and has been one of the main financial supporters since 1987. Japan also supported several international projects organized by Bioversity International. The NIAS Genebank was assigned by Bioversity International to be the global base gene bank for Japonica cultivar group of rice.

Japanese scientists have been dispatched to carry out collaborative exploration for PGRFA in Nepal, Pakistan, Vietnam, Mongolia and other countries based on the special funds provided by the Ministry of Foreign Affairs (MOFA) of Japan to Bioversity International. The materials collected were divided into three sets for conservation by the countries explored, Japan, and Bioversity International.

Bioversity International and Japanese agricultural research institutes have cooperated for holding international meetings. For example, the NIAS cooperated with Bioversity International in holding international symposia on several underutilized crop genetic resources (e.g. [7]). The Japan International Research Center for Agricultural Sciences (JIRCAS) and Bioversity International co-sponsored an international symposium on Cryopreservation of Tropical Plant Germplasm, held at Tsukuba [8].

4. Research Development on PGRFA

4.1 Crop Genetic Resources and Genomics-based Biological Resources

Seasonally different directions of the monsoon in mainland part of Southeast Asia and in South Asia cause clear alternative dry and wet seasons every year. There are savannas in South Asia, rain green forests in lowlands in mainland part of Southeast Asia, and lucidophyllus forests in hilly areas of mainland part of Southeast Asia and East Asia depending on the amount of the rainfall that differs from area to area. A huge diversity in cultivated crop varieties has been developed in such ecological conditions. The archipelago part of Southeast Asia receives wet winds from different direction, and therefore, obtains rainfall all year round to form a tropical rain forest. Different climatic zones are distributed in the region of monsoon Asia, which reflect biological diversity not only at species level but also at intraspecific level.

For example, Asian cultivated rice, *Oryza sativa* L., is a typical major cereal domesticated somewhere in monsoon Asia and has a long history of cultivation there. Diverse rice cultivars adaptive to different ecological conditions such as slash-and-burn cultivation, irrigated paddy fields and in rain-fed conditions were developed through the crop evolution in which natural selection of various mutants were involved. At the same time, you may find diversity in some characters as the fruit of cultural selection. Waxy rice is an example. Northern part of Southeast Asia is a core area of strong food preference to waxy (sticky or glutinous) rice which has spread widely to East Asia. Waxy rice has no amylase content in endosperm starch like other cereals, non-waxy type has about 25% amylase or more, and there are various intermediates between them. There was reported a very wide and continuous frequency distribution of amylose content controlling stickiness of rice grain among rice cultivars in Myanmar, while bimodal (non-waxy and waxy) or trimodal distribution in other areas (non-waxy, waxy and an intermediate type in addition) [9]. People recognize four different categories of amylose content of endosperm starch in rice that correspond with respective traditional uses for food preparations there [10].

Recent advancement of genome studies has enabled characterization and evaluation of rice cultivars at DNA molecular level. Gene flow was reported from modern cultivars to traditional landraces in northern Thailand based on studies of isozymes and DNA markers [11]. The NIAS Genebank distributes upon request “core collections” that were selected by means of DNA diversity studies to consist of the least numbers of accessions that can cover most of the existing diversity –Rice Diversity Research Set (RDRS) [12], a set of 69 cultivars for global-wide diversity and a set of 50 cultivars for Japanese landraces [13]. Almost all cultivars of the former set were from monsoon Asia. Uga *et al.* (2009) [14] analyzed four anatomical traits and two morphological traits of rice root using RDRS.

NIAS has also developed and distributes to scientists’ community a large number of knocked-out mutant lines (mutant panel) induced using *Tos17*, a transposable element [15], several sets of backcross inbred lines (BILs), and chromosome segment substitution lines (CSSLs) in rice based on genome studies [16]. Those newly established biological resources have been and will be used for a wide range of studies including cloning of specific genes. In turn, the genome information obtained using those biological resources will serve as tools for evaluation, classification, gene mining, and other purposes in using and managing PGRFA.

4.2 Crop Wild Relatives in Monsoon Asia

Considering the importance of Asian cultivated rice, *O. sativa* L., its wild relatives are interesting PGRFA widely distributed in monsoon Asia. Scientists have focused on them for a long time as gene pools to explore tolerance and/or resistance to biotic or abiotic stresses for rice breeding. It is not so easy to transfer useful traits from wild relatives without excluding inappropriate ones in ordinary breeding programs. Genome-wide variation studies have

been overcoming such an obstacle. Some institutes such as IRRI [17] and the National Institute of Genetics (NIG) [18] in Japan conserve a good systematic collection of and knowledge has been accumulated about wild rice species [19][5]. Vaughan (1994) [19] well reviewed and summarized the relationships and nomenclature of *Oryza* species, and indicated their potential and difficulties for evaluation, breeding or experimental purposes. We realize, however, that what we understand about wild rice is limited and we should study more about the diversity and ecogenetics of wild rice population. On the other hand, major habitats of wild rice in tropical regions are rapidly decreasing due to land development and modernization of agriculture in recent years.

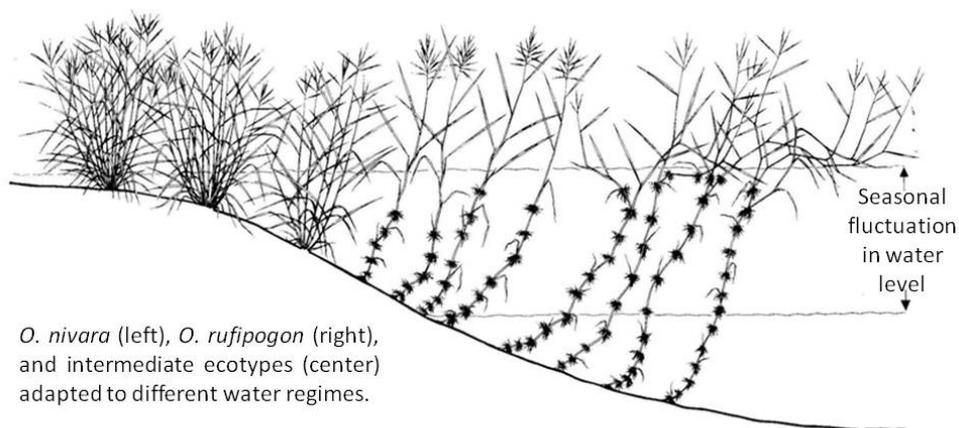


Fig.1. A wide range of variation ranging from perennial type (typical “rufipogon” type) to annual type (“nivara” type) is differentiated being adapted to different water regimes in *O. rufipogon* Griff. in a large sense (Vaughan 1994 [18])

A wide range of variation ranging from perennial type (typical “rufipogon” type) to annual type (“nivara” type) has been differentiated being adapted to different water regimes in *O. rufipogon* Griff., the presumed wild ancestor of *O. sativa* (Fig.1) [19]. Genetic structure of wild rice populations based on morphological data [20] and DNA polymorphism [21] suggested the necessity of *in situ* conservation, and also indicated some gene flow from cultivated *O. sativa* to wild *O. rufipogon* [22]. It is suggested that wild populations of *O. rufipogon* are well maintained under the influence of human activities, e.g. grazing of domesticated animals such as water buffalo [23].

The Department of Agricultural Research (DAR) of Myanmar and the NIAS Genebank Project did cooperative field research of wild rice focusing on *O. rufipogon* in Myanmar [24][25]. They surveyed and collected materials from sites throughout the country (Fig. 2). Random sampling from populations was also tried in several sites. The perennials grow in a stable deepwater habitat and are characterized by taller plants at heading stage, low seed fertility, and high regenerating ability. By contrast, the annuals grow in disturbed habitats and are characterized by shorter plants, high seed fertility, and low regenerating ability. In this study, another type was observed in Myanmar. Floating perennials having both high regenerating ability and seed fertility were found in floating wild rice grown spontaneously in Indawgyi Lake, the largest lake in Myanmar. Genetic studies based on DNA polymorphism suggested that *O. rufipogon* is a continuum including those different types and intermediates adapted to various habitats (Fig. 2).

4.3 Crop Evolution Studies in Monsoon Asia

Recent genome studies have enabled precise analysis of gene structures, which is well applicable to crop evolution research. Shomura *et al.* [26] cloned *qSW5*, a quantitative trait locus (QTL) for seed width in *O. sativa*, and revealed that a deletion of *qSW5* resulted in a significant increase in sink size, which have most likely been selected by humans. They discussed genotypic variations found on *qSW5*, *Waxy* gene loci that controls starch amylase content, and *qSH1*, another QTL controlling seed shattering habit and proposed a new hypothesis of crop evolution process in Japonica cultivar group of rice referring to the probable geographical dispersal in monsoon Asia.

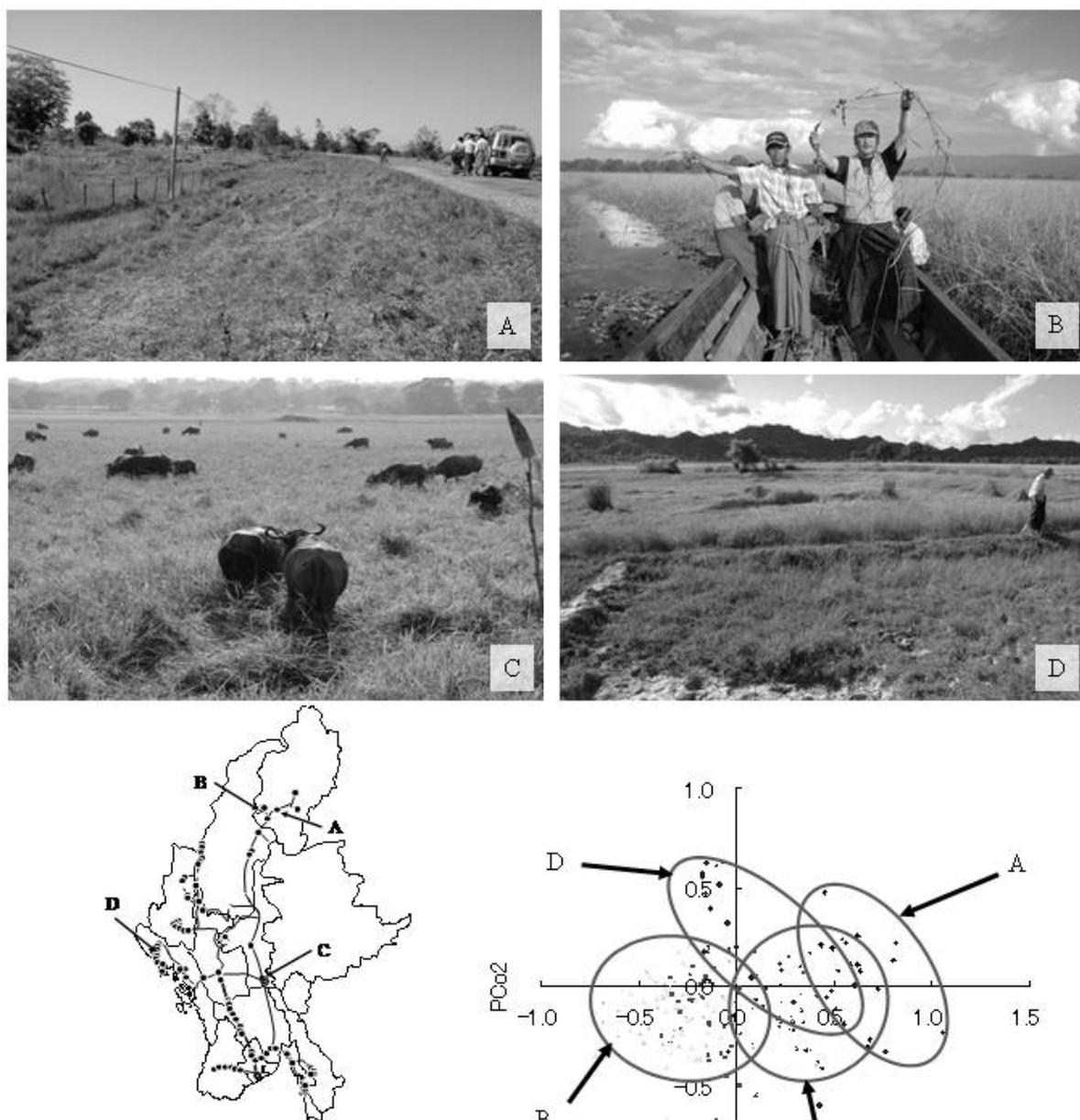


Fig. 2. Above: photographs of wild rice populations in Myanmar (Courtesy of Dr. Y. Uga). A: a population of “nivara” type of *O. rufipogon* in Kachin State; B: a population of long floating perennials on Indawgyi Lake, Kachin State; C: usual “rufipogon” type in Nay-Yaung-Pya-Inn Lake; and D: A: typical “nivara” type in Rakhine State. Left below: field survey routes and collection sites of wild rice and some other PGRFA in Myanmar in 2004 and 2005 (modified from Uga et al. 2005 [18] & 2006 [19]). Right below: scattered diagram of principal coordinate analysis of DNA polymorphism (Yamanaka et al. 2007).

In addition to major crops like rice, rich diversity is found in minor crops in the regions. For example, Asian *Vigna* (subgenus *Ceratotropis*) is a fabaceous taxon to which several cultivated species that are essential component in the diets of a large proportion of monsoon Asia and many related wild species belong. About four thousand nine hundred Asian *Vigna* accessions of 19 taxa including wild relatives have been collected and conserved in the NIAS Genebank. Five different species of this genus were independently domesticated in monsoon Asia - Mung bean, *V. radiata* (L.) Wilczek and black gram, *V. mungo* (L.) Hepper might have been domesticated in semi-arid part of South Asia. *V. aconitifolia* (Jacq.) Marechal was most likely domesticated in drier area of South Asia. *V. umbellate* (Thunb.) Ohwi et Ohashi and Azuki bean, *V. angularis* (Willd.) Ohwi et Ohashi have been cultivated in monsoon Asia. *V. umbellate* has usually twining habit and is often grown in slash-and-burn cultivation, while *V. angularis* is usually erect and widely grown in well prepared fields. Genetic linkage maps were already made in *V. angularis*

and *V. mungo* together with disclosure of markers' information [27][28] and will soon be reported in other species. Comparative genomic studies in four Asian *Vigna* species have suggested that there are some specific domestication-related QTL genes, while others are shared in [29][30]. Based on those genomic information, centers of diversity of putative wild ancestors as well as archaeological evidences, Tomooka [31] hypothesized that *V. angularis* and *V. umbellata* were domesticated in southwestern Japan and in the monsoon forest zone of mainland Southeast Asia, respectively (Figs. 3 & 4).

Another good example of crop evolution in Monsoon Asia was on an endosperm starch character among landraces of cultivated foxtail millet, *Setaria italica* (L.) P. Beauv. ssp. *italica*. Multiple alleles found on *GBSS 1* (*Waxy*) gene that controls starch amylase content was involved in processes of post-domestication crop evolution under the influence of human selection [32]. This crop is at present a minor cereal, but it played an important role in early agriculture, was once widely cultivated in Asia and Europe for a long time, and has even been introduced into other continents until modern times. The waxy endosperm starch type is traditionally grown and preferred to in East Asia and Southeast Asia, while non-waxy type is widely distributed throughout Eurasia. Waxy type has a much stickier texture than non-waxy one when cooked, and is eaten in various forms of sticky grains, cakes made by pounding steamed grains, dumplings made by boiling or steamed dough or batter, or it is used to brew beverages.

Waxy endosperm arise through disrupted expression or loss of function of the *GBSS 1* gene. On the locus, there are Type I allele of non-waxy wild type and 12 mutant alleles detected among landraces of *S. italica* controlling non-waxy type endosperm starch (Type II), low amylase type (Types III, IX, VI, & a recombinant type of II & VI), and waxy type (Types IV, IVa, IVb, V, VII, VIII, & X). Those mutant alleles were induced by the insertions of transposable elements (TEs) onto the locus [32]. A total of 11 TEs (*TSI-1* to *TSI-11*) were found inserted in the gene. Some TEs are inserted in exons and others in introns: the gene is knocked out in the former cases and variable effects occur in the latter (Fig. 5). It is interesting to note diverse probable evolutionary pathways towards various degrees of stickiness of grains from non-sticky wild type in monsoon Asia (Fig. 6).

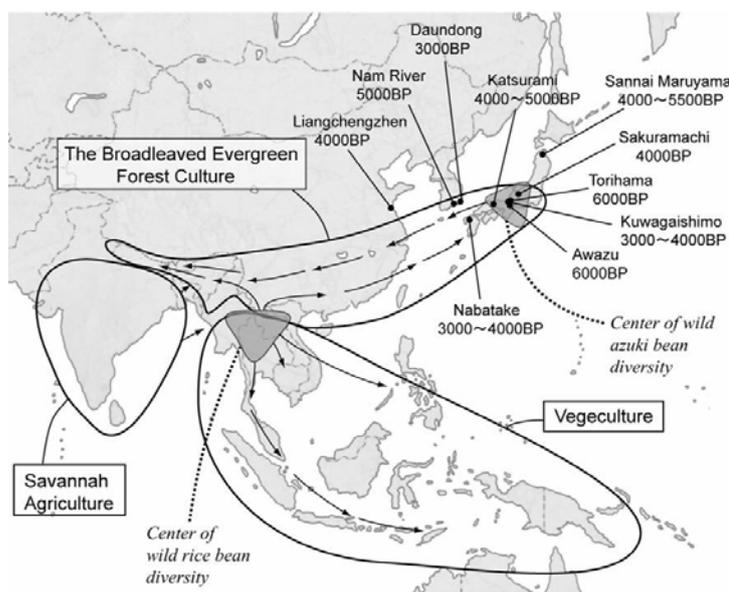


Fig. 3. Early agricultural zones and the archaeological sites where putative azuki bean seeds were found

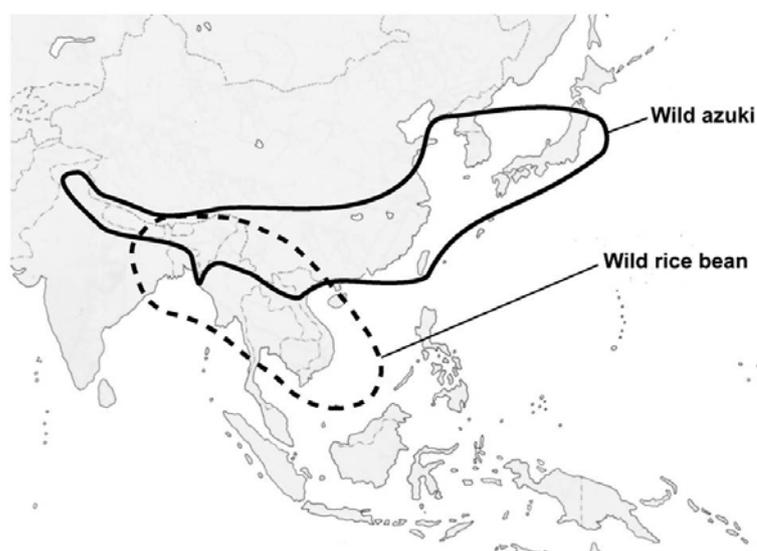


Fig. 4. Natural distribution of wild rice bean and wild azuki bean (Tomooka 2009 [30]).

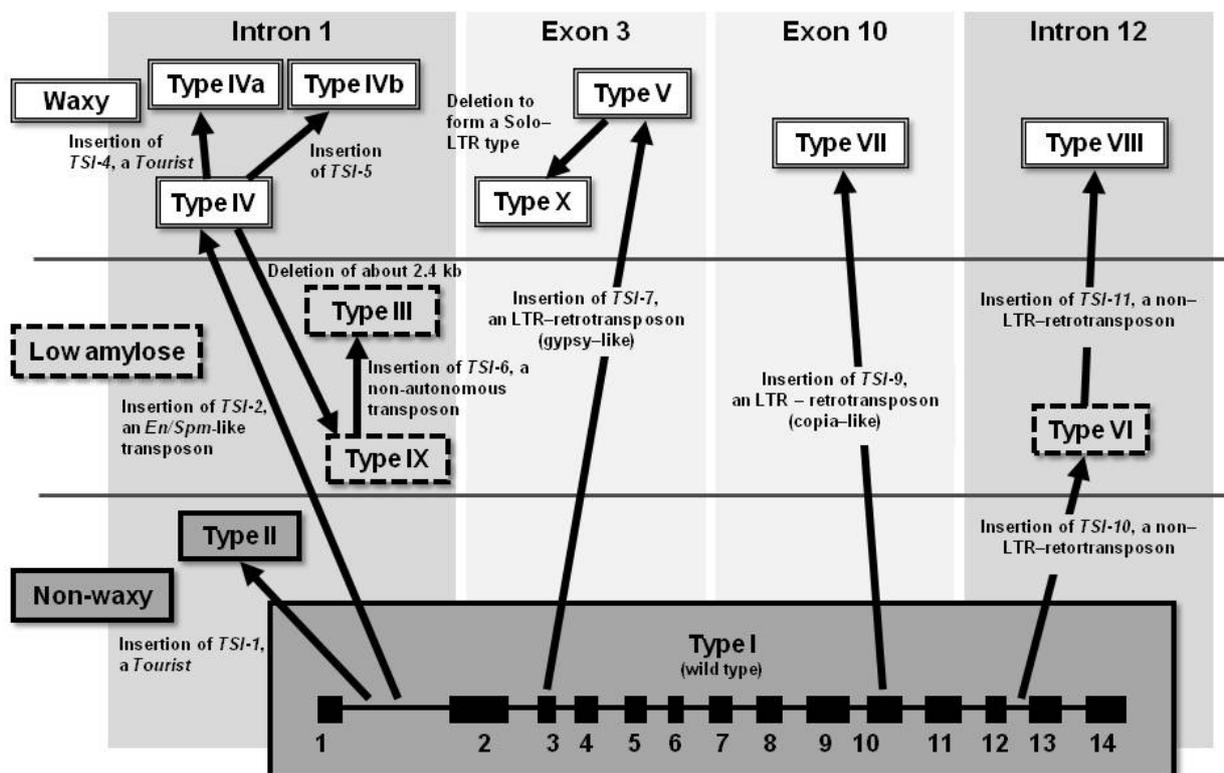


Fig. 5. Schematic drawing of the basic structure of the GBSS 1 gene (Type I, non-waxy shown in the middle) and 12 mutant alleles detected among landraces in *S. italica*. Among the 12 mutant alleles, one controls non-waxy endosperm starch type (Type II), three exhibit low amylose type (Types III, IX, VI, & a recombinant type of II & VI), and seven cause waxy type (Types IV, IVa, IVb, V, VII, VIII, & X). Those mutant alleles were induced by 11 insertions (TSI-1 to TSI-11) onto the locus (modified from Kawase et al. 2005 [31])

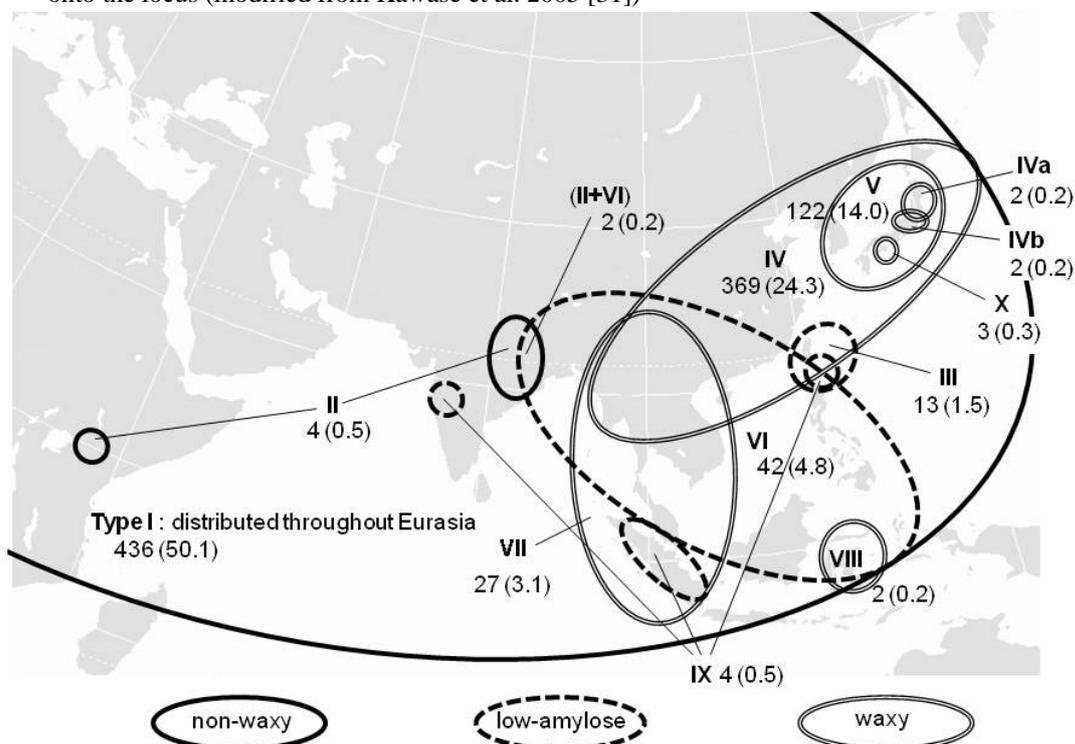


Fig. 6. Geographical distribution of waxy and low-amylose types in *S. italica* (modified from Kawase et al. 2005 [31]).

5. Conclusions - towards fruitful cooperation on PGRFA in Monsoon Asia

As mentioned above, the regions of monsoon Asia are rich in genetic diversity in PGRFA, which should have resulted from the long history of agriculture under various natural and cultural influences there. Yet we do not understand the diversity well, although it has been lost quite rapidly. PGRFA in monsoon Asia should be explored, studied and conserved for the future utilization, for which further international cooperation have to take place.

The global consensus related to PGRFA is changing particularly after CBD. The International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) came into force in 2004. Governing Body and multilateral system has been established for to facilitate access and benefit sharing of PGRFA in a fair and equitable manner. Also there is established the Global Crop Diversity Trust (GCDDT), an independent international organization to ensure the conservation of PGRFA through a partnership between the Food and Agriculture Organization (FAO) in the United Nations and the Consultative Group on International Agricultural Research (CGIAR) [33].

Having established strong collaborative relationships among many countries over the past decades in relation to PGRFA, people in the regions have to seek to extend these linkages to each other by helping capacity building and importantly understanding plant genetic resources and developing safe sustainable means of their conservation. Japan donates a project, “Capacity Building and Enhanced Regional Collaboration for the Conservation and Sustainable Use of Plant Genetic Resources in Asia” (GCP /RAS/240/JPN) of FAO.

Japan is generally considered to be a gene-poor country. However, it was germplasm developed in Japan, wheat cv. Norin 10, which provided vital genes for the “Green Revolution”. This illustrates that so-called gene-rich and gene-poor countries depends very much on what you are looking for in germplasm [34]. The NIAS Genebank project Japan has been and will be an active partner in all the major international developments related to PGRFA and biodiversity.

Acknowledgement

The author wishes to express his sincere gratitude to all the organizers, sponsors and supporters of the Workshop to provide him an opportunity to present this article and to make mutual discussions internationally on different aspects of PGRFA among scientists in the regions of monsoon Asia.

References

- [1] URL: NIAS Genebank Project. Available at <http://www.gene.affrc.go.jp/>
- [2] URL: The Annual Reports on Exploration and Introduction of Plant Genetic Resources issued by NIAS Genebank Project. Available at <http://www.gene.affrc.go.jp/publications.php?section=plant&type=report>
- [3] Jayasuriya, A. H. M. and D. A. Vaughan (eds.) 2003. Conservation and use of crop wild relatives. ISBN 4-931511-08-2
- [4] Okuno, K., K. Shirata, T. Niino and M. Kawase 2004. Plant Genetic Resources in Japan: Platforms and Destinations to Conserve and Utilize Plant Genetic Diversity. *JARQ* 39 (1): 231 – 237.
- [5] NIAS 2003. Proceedings of the International Genetic Resources Workshop on the Genus *Oryza* 24-26 September 2003 Tsukuba, Japan (NIAS). ISBN 4-931511-09-0.
- [6] *Annals of Botany Special Issue*. October 2007. 100(5) 893-1115.
- [7] IBPGR 1992. *International Crop Network*. Series no. 6. Workshop on Buckwheat Genetic Resources in East Asia, Tsukuba, Japan. (IBPGR, Rome) ISBN 92-9043-213-6.
- [8] Engelmann, F. and H. Takagi (eds.) 2000. Cryopreservation of tropical plant germplasm. *Current research progress and application*. JIRCAS International Agriculture Series no. 8. ISBN 92-9043-428-7.
- [9] Nakagahra, M., T. Nagamine and K. Okuno 1986. Spontaneous occurrence of low amylose genes and geographical distribution of amylose content in Asian rice. *Rice Genetic Newsletter* 3: 46-47.
- [10] Ye Tint Tun, K. Irie, H. Toyohara, F. Kikuchi, and H. Fujimaki 2006. Diverse utilization of Myanmar rice with varied amylose contents. *Japan. J. Trop. Agric.* 50(1): 42-50.
- [11] Ishikawa1, R., S. Yamanaka, Y. Fukuta, S. Chitrakon, C. Bounphanousay, K. Kanyavong, L.-H. Tang, I. Nakamura, T. Sato and Y.-I. Sato 2006. *Genetic Resources and Crop Evolution* 53: 245–252.

- [12] Kojima, Y., K. Ebana, S. Fukuoka, T. Nagamine and M. Kawase 2005. Development of an RFLP-based Rice Diversity Research Set of Germplasm. *Breeding Science* 55(4) 431-440.
- [13] Ebana, K., Y. Kojima, S. Fukuoka, T. Nagamine and M. Kawase 2008. Development of mini core collection of Japanese rice landrace. *Breeding Science* 58(3): 281-291.
- [14] Uga, Y., K. Ebana, J. Abe, S. Morita, K. Okuno, and M. Yano 2009. Variation in root morphology and anatomy among accessions of cultivated rice (*Oryza sativa* L.) with different genetic backgrounds. *Breeding Science* 59: 87-93.
- [15] Hirochika, H. 2001. Contribution of the *Tos17* retrotransposon to rice functional genomics. *Current Opinion in Plant Biol.* 4: 118-122.
- [16] **URL:** Detailed information is available from Genome Resources Center at <http://www.rgrc.dna.affrc.go.jp/stock.html>
- [17] **URL:** Information of Genetic Resources Center of the International Rice Research Institute is available at http://beta.irri.org/seeds/index.php?option=com_wrapper&Itemid=3
- [18] **URL:** Information of the National Institute of Genetics is available at <http://www.shigen.nig.ac.jp/rice/oryzabase/top/top.jsp>
- [19] Vaughan, D. A., 1994. The Wild Relative of Rice. *A Genetic Resources Handbook* (IRRI) pp.137. ISBN 971-22-0057-4.
- [20] Kuroda, Y., H. Urairong, and Y.-I. Sato 2002. Population genetic structure of wild rice (*Oryza rufipogon*) in mainland Southeast Asia as revealed by microsatellite polymorphisms. *Tropics* 12(2): 159-170.
- [21] Kuroda, Y., Y.-I. Sato, C. Bounphanousay, Y. Kono, and K. Tanaka 2007. Genetic structure of three *Oryza* AA genome species (*O. rufipogon*, *O. nivara* and *O. sativa*) as assessed by SSR analysis on the Vientiane Plain of Laos. *Conserv. Genet.* 8: 149-158.
- [22] Gene flow from cultivated rice (*Oryza sativa* L.) to wild *Oryza* species (*O. rufipogon* Griff. and *O. nivara* Sharma and Shastry) on the Vientiane plain of Laos. *Euphytica* 142: 75-83.
- [23] Kuroda, y., S. Appa Rao, C. Bounphanousay, K. Kingphanh, A. Iwata, K. Tanaka, and Y.-I. Sato 2006. Diversity of wild and weedy rice in Laos. *In Rice in Laos* (J. M. Schiller, M. B. Chanphengxay, B. Linquist, and S. Appa Rao eds., IRRI) chapter 15. 215-233.
- [24] Uga, Y., Tin Maw Oo, Win Twa and M. Kawase 2005. Exploration and collection of wild rice in northern and western region of Myanmar, 2004. *Annual Report on Exploration and Introduction of Plant Genetic Resources* 21: 117~133. PDF is available at http://www.gene.affrc.go.jp/plant/pdf/report/parts/2004_2-1.pdf
- [25] Uga, Y., Than Sein and M. Kawase 2006. Exploration and Collection of Wild Rice in Northwestern and Southeastern Regions of Myanmar, 2005. *Annual Report on Exploration and Introduction of Plant Genetic Resources* 22: 63-77. PDF is available at http://www.gene.affrc.go.jp/plant/pdf/report/parts/2005_2-2.pdf
- [26] Shomura, A., T. Izawa, K. Ebana, T. Ebitani, H. Kanegae, S. Konishi, and M. Yano 2008. Deletion in a gene associated with grain size increased yields during rice domestication. *Nature Genetics* 40(8): 1023-1028.
- [27] Han, O. K., A. Kaga, T. Isemura, X. W. Wang, N. Tomooka, and D. A. Vaughan 2005. A genetic linkage map for azuki bean [*Vigna angularis* (Willd.) Ohwi & Ohashi] *Theor. Appl. Genet.* 111: 1278-1287
- [28] Chaitieng, B., A. Kaga, N. Tomooka, T. Isemura, Y. Kuroda and D. A. Vaughan 2006. Development of a black gram [*Vigna mungo* (L.) Hepper] linkage map and its comparison with an azuki bean [*Vigna angularis* (Willd.) Ohwi and Ohashi] linkage map. *Theor. Appl. Genet.* 113: 1261-1269.
- [29] Isemura T, A. Kaga, S. Konishi, T. Ando, N. Tomooka, O. K. Han, and D. A. Vaughan 2007. Genome dissection of traits related to domestication in azuki bean (*Vigna angularis*) and comparison with other warm-season legumes. *Annals of Botany* 100(5): 1053-1071.
- [30] Kaga A., T. Isemura, N. Tomooka, and D. A. Vaughan 2008. The genetics of domestication of the azuki bean (*Vigna angularis*). *Genetics* 178(2): 1013-1036.
- [31] Tomooka N. 2009. The origins of rice bean (*Vigna umbelata*) and azuki bean (*V. angularis*): The evolution of two lesser-known Asian beans. *An Illustrated Eco-history of the Mekong River Basin.* (T. Akimichi ed., The Research Institute for Humanity and Nature, Kyoto). (White Lotus Co. Ltd., Bangkok) pp.33-35.
- [32] Kawase, M., K. Fukunaga, and K. Kato 2005. Diverse origins of waxy foxtail millet crops in East and Southeast Asia mediated by multiple transposable element insertions. *Mol. Gen. Genomics* 274: 131-140.

[33] **URL:** Global Crop Diversity Trust, information available at <http://www.croptrust.org/>

[34] Kawase, M and D. A. Vaughan 2008. The present status and future prospects of the NIAS Genebank Project in Japan. *APEC-ATCWG Workshop (2008) - Capacity Building for Risk Management Systems on Genetic Resources* 135-143.

[35] Yamanaka, S., Y. Uga, G. Ahmad, Tin Maw Oo, Win Twa, and M. Kawase 2007. Diversity study for wild rice populations in Kachin State, Rakhine State and Mandalay Division of Myanmar. *Breed. Science* 57(extra vol. 2): p.242.