

7 Diversity of Rice and Related Wild Species in Africa

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Introduction

In-depth understanding and wise management of genetic resources and genetic diversity is of great importance to progress in rice breeding and sustainable production (Guimaraes, 2002). Africa possesses an enormous wealth of rice genetic resources which can contribute to the broadening of the genetic base of rice varieties grown in farmers' fields to ensure that they become better adapted to the multiple biotic and abiotic stresses in Africa. This diversity is under threat from both environmental and socio-economic factors, such as urbanization and climate change (Kiambi *et al.*, 2008).

Rice belongs to the genus *Oryza*, classified under the tribe *Oryzae*, sub-family *Oryzoideae* (*Ehrhartoideae*) of the grass family *Poaceae* (*Gramineae*). The *Oryza* genus was named by Linnaeus (1753). The taxonomy of the genus has undergone numerous revisions. Vaughan *et al.* (2003) recognized 23 species. GRIN Taxonomy (USDA, ARS, National Genetic Resources Program, 2012), a standard widely adopted by the genetic-resources community, now recognizes 26 species. Of these, two are cultivated in Africa, *O. sativa* and

O. glaberrima, both of which are diploid (genome AA, $2n = 24$).

Oryza sativa was introduced to East Africa, probably in the first century AD, via traders from India (Harlan and Stemler, 1976; Ng *et al.*, 1991) and subsequently to West Africa by the Portuguese in about AD 1500 (Portères, 1962).

According to Portères (1962, 1976), *O. glaberrima* was first domesticated from the wild ancestor *O. barthii* (formerly known as *O. breviligulata*) by people living in the inland delta of the upper Niger River about 3500 years BP. The species spread to two secondary centres of domestication, one along the coast of The Gambia, Casamance (Senegal) and Guinea-Bissau and the second in the Guinea forest between Sierra Leone and the western part of Côte d'Ivoire. However, Harlan and Stemler (1976) suggest that *O. glaberrima* was domesticated from *O. barthii* in several different localities within the vast forest and savannah areas. Many studies have confirmed that *O. barthii* is the progenitor of *O. glaberrima* and both are restricted to West Africa, while *O. longistaminata* (from which *O. barthii* is derived) is widely distributed in Africa (Brar and Khush, 2003).

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Oryza also contains 24 wild species distributed throughout the tropics and sub-tropics and representing 10 genome types (AA, BB, CC, BBCC, CCDD, EE, FF, GG, HHJJ and HHKK) (Vaughan *et al.*, 2003). Africa is home to representatives of five of these genome types: AA (*O. longistaminata*, *O. barthii*, *O. glaberrima* and *O. sativa*), BB (*O. punctata*), BBCC (*O. schweinfurthiana*), CC (*O. eichingeri*) and FF (*O. brachyantha*) (Vaughan *et al.*, 2003).

The collection, conservation and utilization of genetic diversity of these rice resources and related wild species in Africa were entrusted to the Africa Rice Center (AfricaRice) and resources are kept in trust for humanity under the auspices of the Food and Agriculture Organization of the United Nations (FAO). This chapter provides an overview of efforts by AfricaRice and partners since 1970 to build up an *ex-situ* collection. The current status of knowledge with respect to these accessions is presented. The chapter concludes with a discussion of the challenges remaining for expansion, characterization and more effective use of the collection.

Collection Efforts and Conservation

Between 1973 and 1977, AfricaRice received collections from national and international research institutes working on rice in Africa, including the Office de la Recherche Scientifique et Technique d'Outre-Mer (ORSTOM), Institut de Recherches Agronomiques Tropicales (IRAT) and the International Institute for Tropical Agriculture (IITA) (Abifarin, 1988). Since 1978, it has continued to receive materials from various collaborators and has also organized its own missions to collect landraces from all rice-growing environments, mostly in West Africa. The mangrove-swamp rice station in Rokupr (Sierra Leone) collected landraces from the mangrove-swamp environment; the then irrigated rice station based in Saint-Louis (Senegal) collected lowland rice; the station based in Mopti (Mali) collected deep-water/floating rice and the upland station based in M'bé/Bouaké (Côte d'Ivoire) collected upland landraces. Between 2000 and 2008, collections were made through various missions by AfricaRice scientists and partners in Burkina Faso, Côte d'Ivoire, Niger, Sierra Leone and Togo.

About 20,000 accessions of rice are being conserved in the gene bank of AfricaRice, made up of both cultivated (*O. glaberrima* and *O. sativa*) and wild species (*O. barthii*, *O. longistaminata*, *O. punctata*, *O. brachyantha* and *O. eichingeri*) from all across the world, with over 80% of the germplasm accessions from Africa (Table 7.1). AfricaRice, the International Rice Research Institute (IRRI) and national partners are now collaborating to expand the germplasm collection to include entries from North, Central, East and Southern Africa (Table 7.1).

The accessions conserved in the AfricaRice gene bank are from about 85 countries and are kept in trust for humanity under the Multi-Lateral System (MLS) of access and benefit sharing within the purview of the International Treaty on Plant Genetic Resources for Food and Agriculture of FAO as part of the global *ex-situ* collections. These accessions are kept in a medium-term storage at 5°C at the temporary headquarters of AfricaRice in Cotonou (Benin) and in a long-term conservation facility at -18°C at IITA in Ibadan (Nigeria). Two safety duplications are also maintained at the National Center for Genetic Resources Preservation (NCGRP), Fort Collins, USA and Svalbard Global Seed Vault (SGSV), Norway in collaboration with Global Crop Diversity Trust as part of the global effort for crop diversity security.

Seeds of cultivated species are multiplied during the dry season when good-quality seeds (free from disease and pest attack) can be produced. Wild species are grown in pots in a quarantined screen house. After harvest, seeds are partially dried, threshed and hand cleaned. Seeds are then brought to a cool drying room maintained at 18°C and 20% relative humidity to attain a moisture content of 6% before medium- and long-term conservation. The temperature and humidity of the storage rooms are monitored daily, and the viability of the seeds in medium-term storage is monitored every 5 years for each accession.

AfricaRice has established a database for the accessions stored in its gene bank, which is being bar-coded. Data associated with each accession consist of passport information and phenotypic and genotypic data.

Table 7.1. Number of rice germplasm accessions per region in the AfricaRice gene bank as of April 2012.

Origin	<i>O. glaberrima</i>	<i>O. sativa</i>	Wild species	Total
Central Africa	83	190	101	374
East Africa	14	743	13	770
North Africa	0	53	0	53
West Africa	2,400	12,025	311	14,736
Southern Africa	0	869	53	922
Total Africa	2,497	17,033	482	20,012
Others	0	3,153	4	3,157

Current Status of Knowledge

Molecular diversity analysis

The population structure of *O. glaberrima* was analysed using 93 simple sequence repeat (SSR) markers on 198 accessions by Semon *et al.* (2004). The accessions were selected among 1136 accessions in the AfricaRice gene bank to maximize geographical and morphological diversity. Five genetically distinct groups were identified. Two of those groups (groups 4 and 5) shared ancestry with the two subspecies of *O. sativa* (*indica* and *japonica*, respectively). It was suggested that the three other groups corresponded to the three ecotypes reported by Portères (1970). Group 1 contained plants that were relatively tall and was found throughout West Africa. This group may represent the ancestral floating type first domesticated in the inland delta of the upper Niger River. Group 2, mostly from Nigeria, consisted of late-maturing entries. This group represented the non-floating (lowland) rice type that migrated to Nigeria along the Niger River. The third group originated from Liberia and was characterized by a larger number of tillers per plant and longer grain, corresponding phenotypically to the upland rice type.

Barry *et al.* (2007) used 11 SSR markers to characterize 26 *O. glaberrima* and 144 *O. sativa* accessions collected in maritime Guinea. They revealed the existence of two major ecotypes – floating and erect – among the *O. glaberrima* accessions. Moreover, they detected an original genetic compartment, highlighting the occurrence of *O. glaberrima* × *O. sativa* hybridization.

Dramé *et al.* (2011) used a highly polymorphic set of 30 SSR markers to characterize 74 accessions of *O. glaberrima* collected from various

ecosystems in eight countries. They differentiated the two major ecotypes – a floating photosensitive type grown in deep water, including coastal mangrove areas, and an early erect ecotype grown in upland or moderately inundated lowlands (Ghesquière *et al.*, 1997) – and an intermediate group between *O. sativa* and *O. glaberrima*.

Morphological characterization

Guei *et al.* (2005) assessed the genetic diversity of 434 *O. sativa* landraces from Côte d'Ivoire using morphological traits such as plant height, leaf length, number of days to heading and maturity, tillering ability, panicle length and grain size (weight, length and width) as the principal discriminatory characteristics. The accessions were classified into seven groups, each with specific traits. This information could be used by breeders in making parental selection based on their traits of interest.

Sanni *et al.* (2008) analysed the geographical patterns of phenotypic diversity of 880 *O. sativa* landraces of upland rice collected from the four main rice-production regions in Côte d'Ivoire: Gagnoa (west-central), Touba (north-western), Boundiali (northern) and Danané (western). Variation was observed across the geographical zones and ecological regions with respect to the 13 traits measured. The majority of accessions from the north and north-west were early maturing, a sign of adaptation to the short rainfall period in these zones. Meanwhile, most accessions from the west and west-central regions were late maturing.

Jones *et al.* (1999) studied 1300 *O. glaberrima* accessions and reported considerable variation in seedling vigour. More than 90% of the accessions

showed very high seedling vigour, and 15% also had very rapid vegetative growth and produced a large number of tillers and droopy lower leaves within 20 to 30 days after sowing, resulting in rapid ground cover and good weed suppression.

AfricaRice has initiated a comprehensive morphological characterization of the whole *O. glaberrima* collection (about 2500 accessions) in order to understand its diversity, as well as to make the information available for breeding activities.

Trait Identification in *O. glaberrima*

Oryza glaberrima constitutes a rich reservoir of adaptive traits essential for new rice varieties for Africa. It has sources of resistance to African rice gall midge (Nwilene *et al.*, 2002), for weed competitiveness (Rodenburg *et al.*, 2009), for tolerance to iron toxicity (Sahrawat and Sika, 2002), and for drought tolerance (Ndjiondjop *et al.*, 2010; Bimpong, 2011; Bocco, 2012).

New screening, inspired by identification of a source of resistance to Rice yellow mottle virus (RYMV) among *O. sativa*, *O. glaberrima* and *O. barthii* (Thottappilly and Rossel, 1993), led to the identification of new resistant accessions. Among these accessions, TOG5681 and TOG5672 exhibited two new resistance alleles (*rymv1-3* and *rymv1-4*, respectively), different from the resistance allele *rymv1-2* first identified in an *O. sativa* accession Gigante (Albar *et al.*, 2006). Furthermore, using 337 *O. glaberrima* accessions, covering a wider geographic area in Africa, a new gene named RYMV2, different from RYMV1, was identified (Thiémiélé *et al.*, 2010).

Screening a set of 107 *O. glaberrima* accessions, selected on the basis of their geographical origin, for resistance to African strains of *Xanthomonas oryzae*, Djedatin *et al.* (2011) identified 20 accessions showing resistance to strains from Mali.

Challenges for More Effective Use of Genetic Resources

Enhancing use

Arguably the greatest challenge facing gene bank managers is how to facilitate effective use

of the germplasm. Germplasm without information about its major characteristics has little value, hindering its wide use. AfricaRice has worked with Bioversity International and IRRI to define standards for characterizing rice (Bioversity International *et al.*, 2007). However, it is neither practically nor economically feasible to evaluate all accessions in a gene bank for agriculturally important traits. Even if it were feasible, much of the genetic variation present in germplasm collections is hidden by factors such as epistasis and epigenetics – valuable traits may be expressed in the progeny of crosses between accessions in ways that cannot be predicted simply by evaluating the accessions. Traditionally, gene bank managers have characterized their accessions for highly heritable traits that are simple enough to record for all accessions; however, most such traits have little agronomic relevance.

To overcome this problem, the concept of ‘core collections’ (van Hintum *et al.*, 2000) has become established as an effective ‘entry point’ to start exploring the potential value of collections. A core collection consists of a sub-set of the germplasm believed to provide a reasonable representation of the genetic diversity of a particular species, and small enough to be evaluated in detail. In most cases, however, a core set has been derived from a sub-set of the germplasm, but not the entire collection. Furthermore, traits evaluated have usually been limited. A core set should be derived from an entire collection of a particular species, and be evaluated for the majority of agriculturally important traits.

Thanks to rapid advances in genomics, molecular markers such as SSRs and single nucleotide polymorphisms (SNPs) can be used to characterize the diversity of rice germplasm at reasonable cost, and the information can be used to define more representative core collections for detailed evaluation. Development of core sets of wild species and landraces is an urgent task in Africa. Realizing the importance of this, AfricaRice – in collaboration with Institut de recherche pour le développement (IRD) – has started to develop core sets of *O. glaberrima* and *O. barthii* based on SNP markers and will subsequently evaluate them for major agronomic traits including disease resistance.

However, the core collection concept itself suffers limitations. First, although intended as an

entry point to explore the collection, mechanisms have not been developed to go beyond the core to explore the rest of the collection. Second, since core collections are constructed to represent the greatest possible diversity in a reasonably small sub-set regardless of the trait(s) of interest, they are by definition a generic entry point; for the user with a specific breeding or research objective, it is often possible and suitable to construct a sub-set better tailored to their specific needs.

One proven alternative is the ecogeographic approach to select use-specific sub-sets (Sackville Hamilton *et al.*, 2002; Mackay and Street, 2004). Assuming that accessions are adapted to the environment they came from, we may use knowledge of the distribution of accession origins to predict probable patterns of variation. However, creating such a sub-set requires intensive analysis. There is a need to mainstream this approach so that gene bank curators or even users can more easily select tailor-made sub-sets designed to better meet the specific needs of each user.

A new approach that brings the promise of radically improving the effectiveness of using germplasm collections, is the genomics approach (McCouch *et al.*, 2012; McCouch *et al.*, Chapter 9, this volume). In the 3 years from 2008, the cost per raw megabase of DNA sequence decreased from approximately US\$500 to less than \$0.10. We can now envision that in the future the genome of every accession present in the collection will be sequenced. Having sequence information of every accession, discovery of new alleles for agronomically important traits can be done by association analysis based on available phenotypic data (McCouch *et al.*, 2012).

The keys to this approach will be to tie all phenotyping to genotyping or sequencing, and to involve gene banks more in gene discovery. For that, gene bank curators should no longer characterize independently of other phenotyping efforts; for rice, this work should be integrated into the phenotyping network of the Global Rice Science Partnership (GRiSP).

Collection of germplasm from under-represented regions

Since 1978, AfricaRice has organized collection missions with national (NARS) partners to

collect landraces and wild species from all rice-growing environments, mostly in West Africa (Burkina Faso, Côte d'Ivoire, Niger, Sierra Leone and Togo). NARS scientists have also collected in Côte d'Ivoire, Mali, Senegal and Sierra Leone. Collection efforts are under way with NARS partners and IRRI in East Africa.

However, there may still be areas and countries that are under-represented in the AfricaRice gene bank. We intend to check the gene bank database for under-represented areas and, when needed, establish collection programmes with NARS partners in compliance with their national priorities, policies and regulations on collecting germplasm and traditional knowledge. Complete information associated with the collected germplasm (e.g. geographical origin, including latitude, longitude and altitude) will be recorded.

It will be essential to plan the further collection of African rice in the context of the global rice strategy (Hay and Sackville Hamilton, 2010). Compared with many other crops, the rice gene pool is already relatively well conserved *ex situ*, with over 500,000 accessions in gene banks worldwide. Annual investment in conservation is high. The additional cost of adding a new accession to a collection is much higher than the recurrent annual cost of conserving the accession (Shands *et al.*, 2011). Thus, it is becoming increasingly important to ensure that efforts to collect additional germplasm genuinely add additional diversity.

However, no methodology exists to address this need systematically, or to estimate when a collection can be considered 'complete'. As genotyping and sequencing become ever more affordable, it is now possible – as well as increasingly important – to develop such a methodology: to determine how much genetic novelty is added to a collection when new accessions are added; to quantify the diminishing rate of return on sequentially adding more accessions; and to devise the cost–benefit relationships to guide how much more collecting is needed. We will rely on the geographic information system- (GIS-) based global gap analysis of the Global Crop Diversity Trust (Hijmans *et al.*, 2001; Ramírez-Villegas *et al.*, 2010) to establish priorities for collection of the wild relatives of rice.

Up-to-date databases

A wide range of information about rice accessions is recorded by various stakeholders. This includes information on their genealogy and origins, conservation status, availability and use, genetic and phenotypic characteristics, agronomic adaptation, performance and quality, and the performance of their progeny. Much of this information is generated through scientific research by those who receive germplasm from gene banks, and much is in the domain of traditional knowledge held by the indigenous communities that originally grew landraces now conserved in the gene bank. For effective conservation and use of accessions, all this information should ideally be integrated and made available. However, the task of collating and publishing it is beyond the capacity of any gene bank or any other laboratory. One effective strategy to help fill a critical component of the information gap is based on recognizing that the most important scientific knowledge generated by recipients of accessions is typically published in scientific journals. Information in a published journal can be incorporated into the germplasm database. With a large proportion of the scientific literature now available electronically, it would be possible (as well as desirable) to organize a systematic survey of journals, augmented by enquiries to the germplasm recipients. Such surveys should lead to an increase in the available information, thereby increasing the value of accessions.

Information on rice germplasm conserved in the AfricaRice gene bank is stored in a database called AfricaRice Genebank Information System (ARGIS) and made available to users online (www.africarice.org/argis). Likewise, information newly gained through internal research activities as well as that obtained from the recipients will be stored and managed in this system. Here, the accuracy of information and

data for each accession is the most important. These data are now being integrated into IRIS (International Rice Information System, <http://iris.irri.org>). A key priority for the future development of IRIS will be to develop improved mechanisms for seamlessly sharing data, to facilitate collaboration among the many different partners involved in GRiSP.

Conclusions

The rational exploitation of the genetic diversity existing among the 20,000 accessions held in the AfricaRice gene bank represents one of the basic components of efforts to improve rice production in Africa. To enhance this exploitation, service to stakeholders needs to be improved in three areas:

- The information associated with each accession conserved in the gene bank: there is a need to complete the identification of key descriptors for each accession in collaboration with experts for target traits. This will enable the formation of sub-sets for targeted traits and users. There is also a need to genotype/sequence the accessions in the selected sub-sets and associate the genotypic and phenotypic data, to enhance their use.
- Conservation methods and equipment: regeneration methods that avoid genetic drift are needed to ensure the maintenance of the genetic integrity of accessions.
- Management and use of information from the gene bank: it is important to update the information on a regular basis. Within the framework of GRiSP, AfricaRice, IRRI and the International Center for Tropical Agriculture (CIAT) will collaborate to ensure the accessibility, through IRIS, of all available information on rice gene bank accessions worldwide.

References

- Abifarin, A.O. (1988) West Africa Rice Development Association (WARDA) activities in rice germplasm collection, conservation and utilization. In: *Proceedings of an International Conference on Crop Genetic Resources of Africa*, Ibadan, Nigeria, 17–20 October 1988, pp. 35–40.
- Albar, L., Angratz-Reyser, M., Hébrard, E., Ndjiondjop, M.-N., Jones, M. and Ghesquière, A. (2006) Mutations in the eIF(iso)4G translation initiation factor confer high resistance of rice to *Rice yellow mottle virus*. *The Plant Journal* 47, 417–426.

- Barry, M.B., Pham, J.L., Noyer, A.J.L., Billot, A.C., Courtois, A.B. and Ahmad, A.N. (2007) Genetic diversity of the two cultivated rice species (*O. sativa* and *O. glaberrima*) in maritime Guinea. Evidence for inter-specific recombination. *Euphytica* 154, 127–137.
- Bimpong, I.K., Serraj, R., Chin, J.H., Mendoza, E.M.T., Hernandez, J. and Mendiolo, M.S. (2011) Determination of genetic variability for physiological traits related to drought tolerance in African rice (*Oryza glaberrima*). *Journal of Plant Breeding and Crop Science* 3(4), 60–67.
- Bioversity International, IRRI and WARDA (2007) *Descriptors for Wild and Cultivated Rice (Oryza spp.)*. Bioversity International, Rome, Italy; International Rice Research Institute, Los Baños, Philippines; Africa Rice Center, Cotonou, Benin.
- Bocco, R., Lorieux, M., Seck, P.A., Futakuchi, K., Manneh, B. and Baimey, H. (2012) Agro-morphological characterization of a population of introgression lines derived from crosses between IR 64 (*Oryza sativa indica*) and TOG 5681 (*Oryza glaberrima*) for drought tolerance. *Plant Science* 183, 65–76.
- Brar, D.S. and Khush, G.S. (2003) Utilization of wild species of genus *Oryza* in rice improvement. In: Nanda, J.S. and Sharma, S.D. (eds) *Monograph on Genus Oryza*. Science Publishers, Enfield, New Hampshire, pp. 283–309.
- Djedatin, G., Ndjiondjop, M., Mathieu, T., Vera Cruz, C.M., Sanni, A., Ghesquière, A. and Verdier, V. (2011) Evaluation of African cultivated rice *Oryza glaberrima* for resistance to bacterial blight. *Plant Disease* 95(4), 441–447.
- Dramé, K.N., Sanchez, I., Gregorio, G. and Ndjiondjop, M. (2011) Suitability of a selected set of simple sequence repeats (SSR) markers for multiplexing and rapid molecular characterization of African rice (*Oryza glaberrima* Steud.). *African Journal of Biotechnology* 10(35), 6675–6685.
- Ghesquière, A., Séquier, J., Second, G. and Lorieux, M. (1997) First steps towards a rational use of African rice, *Oryza glaberrima*, in rice breeding through a 'contig line' concept. *Euphytica* 96, 31–39.
- Guei, R.G., Sanni, K.A., Abamu, F.J. and Fawole, I. (2005) Genetic diversity of rice (*Oryza sativa* [L.]). *Agronomie Africaine* 5, 17–28.
- Guimaraes, E.P. (2002) Genetic diversity of rice production in Brazil. In: Nguyen, V.N. (ed.) *Genetic Diversity in Rice Production, Case Studies from Brazil, India and Nigeria*. Food and Agriculture Organization of the United Nations (FAO), Rome, Italy, pp. 11–35.
- Harlan, J.R. and Stemler, A. (1976) The races of sorghum in Africa. In: Harlan, J.R., De Wet, J.M. and Stemler, A.B. (eds) *Origin of African Plant Domestication*. Mouton, The Hague, Netherlands.
- Hay, F.R. and Sackville Hamilton, R. (2010) Global strategy for the *ex situ* conservation of rice genetic resources. International Rice Research Institute, Manila, Philippines. www.croptrust.org/documents/cropstrategies/Rice%20Strategy.pdf.
- Hijmans, R.J., Guarino, L., Cruz, M. and Rojas, E. (2001) Computer tools for spatial analysis of plant genetic resources data: 1. DIVA-GIS. *Plant Genetic Resources Newsletter* 127, 15–19.
- Jones, M.P., Nwanza [sic], K.F., Miezán, K.M., Singh, B.N. and Guei, R.G. (1999) Rice germplasm evaluation and enhancement at WARDA. In: Rutger, J.N., Robinson, J.F. and Dilday, R.H. (eds) *Proceedings of the International Symposium on Rice Germplasm Evaluation and Enhancement*, Stuttgart, Arkansas, USA, 30 August to 2 September 1998. *Special Report* 195. Arkansas Agricultural Experiment Station, Fayetteville, USA, pp. 29–37.
- Kiambi, D.K., Newbury, H.J., Maxted, N. and Ford-Lloyd, B.V. (2008) Molecular genetic variation in the African wild rice *Oryza longistaminata* A. Chev. et Roehr. and its association with environmental variables. *African Journal of Biotechnology* 7(10), 1446–1460.
- Linnaeus, C. (1753) *Species plantarum: exhibentes plantas rite cognitatas, ad genera relatas, cum differentiis specificis, nominibus trivialibus, synonymis selectis, locis natalibus, secundum systema sexuale digestas*. Laurentius Salvius, Stockholm, Sweden.
- Mackay, M.C. and Street, K.A. (2004) Focused identification of germplasm strategy – FIGS. In: Black, C.K., Panozzo, J.F. and Rebetzke, G.J. (eds) *Cereals 2004: Proceedings of the 54th Australian Cereal Chemistry Conference and the 11th Wheat Breeders' Assembly*, Canberra, ACT, Australia, 21–24 September 2004. Royal Australian Chemical Institute, Melbourne, Australia, pp. 138–141.
- McCouch, S.R., McNally, K.L., Wang, W. and Sackville Hamilton, R. (2012) Genomics of gene banks: a case study in rice. *American Journal of Botany* 99(2), 1–17.
- Ndjiondjop, M.N., Manneh, B., Cissoko, M., Drame, N.K., Kakai, R.G., Bocco, R., Baimey, H. and Wopereis, M. (2010) Drought resistance in an interspecific backcross population of rice (*Oryza* spp.) derived from the cross WAB56-104 (*O. sativa*) × CG14 (*O. glaberrima*). *Plant Science* 179, 364–373.
- Ng, N.Q., Chang, T.T., Vaughan, D.A. and Zunbo-Alto Versos, C. (1991) African rice diversity: conservation and prospects for crop improvement. In: Ng, N.Q., Perrino, P., Attere, F. and Zedan, H. (eds) *Crop*

- Genetic Resources of Africa*. Proceedings International Conference on Crop Genetic Resources of Africa, Ibadan, Nigeria, 17–20 October 1988, Vol. 2. International Institute of Tropical Agriculture, Ibadan, Nigeria, pp. 213–227.
- Nwilene, F.E., Williams, C.T., Ukwangwu, M.N., Dakouo, D., Nacro, S., Hamadoun, A., Kamara, S.I., Okhidiebe, O., Abamu, F.J. and Adam, A. (2002) Reactions of differential genotypes to African gall midge in West Africa. *International Journal of Pest Management* 48, 195–201.
- Portères, R. (1962) Berceaux agricoles primaires sur le continent africain. *Journal of African History* 3(2), 195–210.
- Portères, R. (1970) Primary cradles of agriculture in the African continent. In: Fage, J.D. and Olivier, R.A. (eds) *Papers in African Prehistory*. Cambridge University Press, Cambridge, UK, pp. 43–58.
- Portères, R. (1976) African cereals: eleusine, fonio, black fonio, teff, *Brachiaria*, *Paspalum*, *Pennisetum*, and African rice. In: Harlan, J.R., de Wet, J.M.J. and Stemler, A.B.L. (eds) *The Origin of African Plant Domestication*. Mouton, The Hague, Netherlands, pp. 409–452.
- Ramírez-Villegas, J., Khoury, C., Jarvis, A., Debouck, D.G. and Guarino, L. (2010) A gap analysis methodology for collecting crop gene pools: a case study with *Phaseolus* beans. *PLoS ONE* 5(10), e13497. doi:10.1371/journal.pone.0013497 (accessed 13 February 2013).
- Rodenburg, J., Saito, K., Kakai, R.G., Touré, A., Mariko, M. and Kiepe, P. (2009) Weed competitiveness of the lowland rice varieties of NERICA in the southern Guinea savanna. *Field Crops Research* 114(3), 411–418.
- Sackville Hamilton, N.R., Skøt, L., Chorlton, K.H., Thomas, I.D. and Mizen, S. (2002) Molecular genealogy of temperature response in *Lolium perenne*: 1. Preliminary analysis to reduce false positives. *Molecular Ecology* 11(9), 1855–1863.
- Sahrawat, K.L. and Sika, M. (2002) Comparative tolerance of *O. sativa* and *O. glaberrima* rice cultivars for iron toxicity in West Africa. *International Rice Research Notes* 27, 30–31.
- Sanni, K.A., Fawole, I., Guei, R.G., Ojo, D.K., Somado Eklou, A., Sanchez, I., Ogunbayo, S.A. and Tia, D.D. (2008) Geographical patterns of phenotypic diversity in *Oryza sativa* landraces of Côte d'Ivoire. *Euphytica* 160, 389–400.
- Semon, M., Nielsen, R., Jones, M. and McCouch, S.R. (2004) The population structure of African cultivated rice *Oryza glaberrima* (Steud.): evidence for elevated levels of LD caused by admixture with *O. sativa* and ecological adaptation. *Genetics* 169, 1639–1647.
- Shands, H., Hawtin, G. and MacNeil, G. (2011) The cost to the CGIAR Centers of maintaining and distributing germplasm. In: Consortium Board of Trustees. Financial Support to the CGIAR Center Genebanks in 2011. Proposal to the Fund Council, Annex 4, pp. 15–91. www.cgiarfund.org/cgiarfund/sites/cgiarfund.org/files/Documents/PDF/fc4_funding_proposal_CGIAR_Genebanks.pdf (accessed 13 June 2012).
- Thiémiélé, D., Boisnard, A., Ndjondjop, M.-N., Chéron, S., Séré, Y., Aké, S., Ghesquière, A. and Albar, L. (2010) Identification of a second major resistance gene to *Rice yellow mottle virus*, *RYMV2*, in the African cultivated rice species, *O. glaberrima*. *Theoretical and Applied Genetics* 121, 169–179.
- Thottappilly, G. and Rossel, H.W. (1993) Evaluation of resistance to *Rice yellow mottle virus* in *Oryza* species. *Indian Journal of Virology* 9, 65–73.
- USDA, ARS, National Genetic Resources Program (2012) Germplasm Resources Information Network – (GRIN) [Online Database]. National Germplasm Resources Laboratory, Beltsville, Maryland. www.ars-grin.gov/cgi-bin/npgs/html/index.pl (accessed 11 June 2012).
- van Hintum, T.J.L., Brown, A.H.D., Spillane, C. and Hodgkin, T. (2000) Core collections of plant genetic resources. *IPGRI Technical Bulletin* No. 3. International Plant Genetic Resources Institute, Rome, Italy.
- Vaughan, D.A., Morishima, H. and Kadowaki, K. (2003) Diversity in the *Oryza* genus. *Current Opinion in Plant Molecular Biology* 6, 139–146.