Review of abiotic stress tolerance of African rice (Oryza glaberrima)

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Abstract

The utilization of *Oryza glaberrima* in a number of abiotic stresses such as drought iron toxicity, submergence, salt tolerance and weed competitiveness and ability to grow under low input soil condition has been reported in several literatures. Despite its utilization, hybridization between *O. glaberrima* and *O. sativa* hampered by high sterility phenomenon in interspecific F_1 and in early progenies development. Though, African rice species (*Oryza glaberrima*) has been used in interspecific hybridization with *Oryza sativa* with combine yield traits and resistant to some abiotic stresses that are uniquely adapted to Africa growing environment. The high rate of sterility in the crosses between (*O. sativa x O. glaberrima*) have been confirmed to reduce the required maximum breakthrough in interspecific hybridization of these species. Thus, information on crossing barrier and hybrid sterility phenomenon expressed in *O. sativa x O. glaberrima* crosses, led to the recent development in breeding and molecular markers and linkage map approach of *O. glaberrima* which provides the opportunity to rationalize introgressions between the two cultivated rice species (*O. glaberrima* x *O. sativa*). Genetic models for the female sterility between the two cultivated species for their full utilization in rice improvement for abiotic stress tolerance have been proposed. The recent achievements in marker assisted selection using molecular tools for introgression of desirable traits and the development of such introgressed desirable traits of interests and elimination of sterility genes through interspecific hybridization and backcrossing represents a very high potential to create new genetic and transgressive variation that with be useful for developing rice tolerant to various abiotic stresses. In this effort, several approaches to abiotic stress tolerance have been developed starting from field screening and use of molecular tools. The interspecific and backcross breeding methodology is anticipated to make this approach feasible. It is expected that the results will produce complimentary breeding techniques that will provide (i) water information of field phenotyping and systematic assessment of the useful heritable resources exhibit by *Oryza glaberrima*, (ii) substantiate on empirical data on *Oryza glaberrima* for drought tolerance breeding and (iii) tools for genetic analysis of *O. glaberrima* germplasm. Though, the overall goal for the use of *O. glaberrima* in breeding rice for abiotic stress tolerance is challenging, but promising if we understand the genetic base of the two cultivated species, this can be widened for its exploitation in developing rice with higher yield and tolerant in abiotic stresses under harsh environmental conditions of Africa.

Key words: Abiotic, Breeding, Drought, Genome, Germplasm, Interspecific, Oryza, Species, Stress

Introduction

Rice is one of the most important and strategic commodities in Africa. It is consumed widely in all countries of sub-regions of the continent and is cultivated in almost all African countries under diverse ecosystem and a wide variety of climatic and soil conditions (rain-fed lowland, irrigated lowland, mangrove swamps and upland ecosystems). Since the major portion of area under rice is rainfed, production is strongly linked to the distribution of rainfall. Drought and flood often occur regularly in the

same year in many regions of Africa, and this limit rice productivity in these areas. Iron toxicity is also a major problem in parts of sub-Saharan Africa (SSA). In addition to insect pests, diseases and related abiotic stresses, weeds are becoming a major factor that is constraining rice productivity and profitability in rainfed areas of SSA. Most of the farmers in such areas are rural poor who cannot afford necessary inputs in their rice farms for full exploitation of the yield potential of improved rice varieties. In addition, herbicides for the control of insect pests are hazard to human health and are often not affordable by poor farmers. In SSA, there was a tremendous increase in the growth rate during 2007-2012 (8%) compared to 2001-2007 (4%). Paddy production is estimated at 19 million tons in 2012 in SSA. If investments in rice production are maintained, especially breeding for drought tolerant rice and related abiotic stresses, SSA countries are on target for doubling production in 2018.

Oryza glaberrima Steud (African rice) has been identified to have many useful agronomic traits of interests such as drought tolerance, weed competitiveness, submergence tolerance, iron toxicity, salt tolerance, acidity and low input responsive nature unique to rice varieties, thus, no valid data have been provided by scientific literatures in this regard, but these traits have been reported (Sarla and Swamy, 2005) very important and of interests and can be introgressed into the elite varieties of *Oryza saliva* in order to improve the yield and other agronomic characteristics, while improving the sexual barriers of hybridization between *Oryza sativa* and *Oryza glaberrima* and sterility of the F1 hybrids (www.scienceinafrica.co.za/nerica.htm). The recent effort on improving high-yielding rice varieties as reported by Sarla and Swamy (2005) was obtained from crosses between African rice *(O. glaberrima)* and Asian rice *(O. sativa).* This approach led to the development of rice varieties that is well known to African and sub regions tagged "New Rice for Africa" (NERICA), by West African Rice Center (AfricaRice). These NERICAs have tremendously increased high yield potential by 50% above the local cultivated varieties in both lowland and upland ecosystem of Africa. The NERICA varieties substituted the low-yielding, lodging and shattering-prone *0. glaberrima* that has been cultivated over the years.

In 1990s, about 300 lines were developed from the interspecific breeding between the two cultivated rice species *(0. glaberrima x O.sativa)* and many of these varieties have been released and are being grown by farmers in West African countries. The new rice for Africa varieties are high yielding compared to the existing local varieties as this new varieties combined drought and pest resistant. They adapt widely to the unique growing conditions of West Africa, and the high yield potential under good agronomic management have benefited more than 20 million farmers in the region (Sarla and Swamy, 2005). This success of NERICA rice has led to the award by the World Food Prize with Monty Jones in 2004 (www.warda.org/warda1/main/Achievements/nerica.htm; www.worldfoodprice.org/). In this review, we present the available information on African rice species (0. *glaberrima)* and provide a general overview describing the problems associated with the utilization of 0. *glaberrima* in rice improvement and its prospects in abiotic stress tolerance when used in interspecific hybridization with 0. *saliva* to produce rapidly high yielding rice varieties that will withstand various abiotic stresses in African environment. For example, abiotic stresses such as iron toxicity have limited rice yield and productivity in many rice production environments (Sikirou et.al., 2018; Sikirou et.al., 2015; Swamy *et.al.,* 2016; Sahebi *et.al.,* 2018; Melandri *et.al.,* 2021; Kirk *et.al.,* 2021), and drought (Shaibu *et.al.,* 2018). Iron toxicity is recognized as one of the most widely distributed nutritional disorders in rice production systems, and the most important constraint to rice productivity (Kirk *et.al.,* 2021). Although there are several approaches breeding and selection for tolerance cultivars from African rice species and phytohormones plant regulator that is considered an important factor in rice defense system under iron toxicity stress. Iron toxicity has been reported as significant yield reduction in rice, and under severe conditions, total crop failure is experienced (Audebert and Sahrawat, 2000). Reduction in yield could be as high as 90% due to iron toxicity (Audebert and Fofana 2009; Cherif *et.al.,* 2009). It has been documented that excess iron in the soil causes oxidative bursts which is toxic to the root of the rice plant, and can affect the uptake of some nutrients, such as copper, zinc and phosphorus, (De Dorlodot et al. 2005). Hence, iron caused yield reduction in rice is often associated with poor soil nutrient status (Ottow *et.al.,* 1983). Absorption of excess iron by the rice plant has also been reported to reduce the root and shoot length (Verma and Pandey, 2017). Accumulation of iron result in the disruption of plant membrane (Verma and Pandey 2017), thereby reducing the effectiveness of photosystem (Li *et.al.,* 2019) this leads to loss of biomass, reduced the grain yield in rice crop and results in whole plant death.
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Evolution and origin of *Oryza glaberrima* in West Africa

As reported by Nayar (2012), rice belongs to the genus *Oryza* L., family Poaceae (https://www.researchgate.net/publication/228453823_Origin_of_African_rice_from_Asian_rice).

The genus Oryza is believed to have originated in Gondwanaland (Chang, 1976), covering south America, Australia, India and Africa. It is a small genus of 20-25 species with tropical and sub-tropical distribution. Two species of the genus are cultivated including *Oryza sativa,* the universally cultivated Asian rice, and *0. glaberrima,* the West African cultivated rice. *Oryza glaberrima,* African monocarpic annual rice derived from *Oryze barthii,* is grown in traditional rice producing wetland areas of West Africa. *Oryza saliva,* an Asian rice that varies from annual to perennial, is derived from *Oryza rufipogon* (Sakagami *et.al.,* 1999). Genotypes of *0. glaberrima* (AA genome, 2n = 24) are inherently cultivated rice species of Africa origin with two major

ecotypes which include 1: floating photosensitive ecotype grown in deep water and coastal mangrove areas of sub Saharan Africa, and 2: early erect ecotype grown in upland or in moderately inundated lowland conditions (Sarla and Swamy, 2005; Besancon *et.al.,* 1984). The genotype of Asian rice species (0. *saliva*) belong to the same genome group (AA genome, 2n = 24) but spread widely around the world and more diverse and widely cultivated than *0. glaberrima* and lower yielding than those of *0. saliva* and are therefore cultivated in fewer areas (Linares, 2002). It is well known that Oriza glaberrima can grow and tolerate harsh African environment with multiple stress. *Oryza glaberrima* Steud, is the scientific name for African rice, a cultivated grain distinct from that of Asian rice (*Oryza sativa).* The two cultivated rice species are considered to have evolved by independent and parallel evolutionary process in Asian and African continents (Sarla and Swamy, 2005). *0. sativa* is broadly divided into two sub species; indica and japonica. These two strains of *0. saliva (Oryza japonica* and *Oryza indica)* were domesticated independently, both probably in China (Porteres, 1956, 1962). *0. Glaberrima* originated around 1500 BC in the swampy basins of the upper river delta of Niger in West Africa, identified as the primary centre of origin of this species (Chang, 1976; Porteres, 1956). Two major secondary centres of diversification have been reported in Guinea coast around 1000 BC (Sarla and Swamy, 2005; Chang, 1976; Porteres, 1956) and the theory of lines of development of these two species confirmed by cytological studies (Fukui and Fijima, 1991; Ohmido and Fukui, 1995). Scientific evidence showed that the major chromosomes positions of *0. glaberrima* could not be differentiated from that of *0. saliva,* and the organization of chromosome were found to be similar (Ohmido and Fukui, 1995). However, going by the records and report of Sarla and Swamy (2005), the two species have been classified within the same A-genome group as confirmed by molecular marker results (Ge, *et.al.,* 1999; Joshi, *et.al.,* 1999). Results from molecular marker (Ge *et.al.,* 1999; Ren *et.al.,* 2003; Joshi *et.al.,* 1999), show similarities (Park *et.al.,* 2003) that support the scientific assumption. The two species may have evolved from an unknown common ancestor following a sequence from wild perennial to wild annual to cultivated annual ancestors. Recent studies on *0. glaberrima* genome has been used as a reference to unravel the sequence of *0. saliva* subspecies (Ma and Bennetzen, 2004). For example, similarities and variations (Sarla and Swamy, 2005; Park *et.al.,* 2003) were observed in studies using miniature inverted transposable element amplified fragment length polymorphism (MITE-AFLP).

The family species

Generally, there are five wild *Oryza* species that occur in Africa, including *0. barthii, 0. longistaminata, 0. brachyantha, 0. eichingeri* Peter and *0. punctata* Kotschy ex Steud, and these could only have originated indigenously from Africa (Vaughan, 1994). The last three species are usually ruled out as putative ancestral species of *0. glaberrima* because of their different genomic composition (BB, CC cf. AA of African rice). Asian rice was also not generally reckoned as a putative ancestral species, because it is widely held as a recent introduction. It was established that *0. barthii* is the progenitor of *0. glaberrima* (Sarla and Swamy, 2005). Roschevicz (1931) was the first to propose *0. barthii* as the progenitor of the African rice (https://doi.org/10.2135/cropsci2010.10.0605), was reported by Nayar (2012). Further, Porteres (1945, 1962, 1976) and Morishima *et.al* (1963) supported this proposal. Brar and Khush (2003) report also confirmed that *0. Barthii* is the progenitor of *0. glaberrima* and both have been confirmed to be restricted to West Africa, while *0. longistaminata* is derived from *0. barthii* and is widely distributed in Africa while *0. rufipogon* and *0. nivara* gave rise to *0. saliva* (Porteres, 1956; Ishii *et.al.,* 2001; Bautista *et.al.,* 2001; Cheng *et.al.,* 2002; Khush, 1997). The three species, *Oryza barthil; 0. longistaminata* and *0. glaberrima* are AA genome widely distributed mainly to Africa, and the two cultivated rice species (Table 1) can be distinguished by some specific traits (Sarla and Swamy, 2005).

Germplasm collection

Africa contains the largest diversity of *Oryza* species in the world, the management and in-depth understanding of the genetic resources and diversity of African rice germplasm is of great importance for breeding progress towards improving rice for abiotic stress tolerance for sustainable rice production in sub–Saharan Africa (Guimaraes, 2002). Thus, Africa is endowed with enormous genetic resources which on improvement can contribute substantially to the broadening of rice genetic base that will adapt to abiotic and biotic stress tolerance in African environment. Currently, it was reported that the diversity of African rice species is hindered by some social and environmental factors are involved (Kiambi *et.al.,* 2008). Various types of accessions of African rice and landraces have been collected between 1973 and 1978 (Abifarin, 1988), and geographical pattern of some landraces evaluated in some countries of Africa (Sani *et.al.,* 2008) from the mangrove swamp and irrigated ecologies in some parts of Africa. Sani *et.al.,* (2013), reported that at Africa Rice Center gene bank, several accessions 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 the Food and Agricultural Organization (FAO) as part of the global ex-situ collections and conservation (Table 2).

Table 1. Distinguishing characters between *O. glaberrima* and *O. sativa*

Character	*O. sativa*	*O. glaberrima*
Distribution	cosmopolitan	prevalent in west Africa
Habitat	essentially perennial	annual
Varietal differences	high variation	limited variation
Lodging	rare	frequently lodge
Drought resistance	rare	high
Ligules	long, 40-45mm, pointed thin	short, 6mm, oblong, thick
Panicle branching	many	non or few
Grain number	high up to 250 grain/panicle	low, 74-100 grain/panicle
Grain	easy to mill	difficult to mill
Seed dormancy	low	high
Seed shattering	low	high
Protein	low	high

Source: Adapted from Sarla and Swamy (2005)

Valuable agronomic traits of *Oryza glaberrima*

Some scientific evidence has pointed out the usefulness of *O. glaberrima* in rice improvement. Some valuable traits of interests in Africa rice species (Oryza *glaberrima)* have been identified with attribute of drought tolerance, weed competitiveness and ability to respond to low input condition of fertilization and resistant to various pests and diseases (Sarla and Swamy, 2005). It has been established that these traits are unique in *0. Glaberrima* species. It had the ability to thrive in a varied range of harsh environmental conditions such as rainfed hilly and unpredictable rainfall areas, deep-water floating conditions and coastal mangrove areas. The unique features in *0. glaberrima* species in terms of weed competitive ability as reported by Sarla and Swamy (2005) is attributed to the early vigour of rapid growth, low extinction coefficient, high light use efficiency, high specific leaf area leading to high canopy growth for given amount of assimilate including droopy leaves that prevents excess sunshine from reaching the soil surface. 0. *glaberrima* has the ability to produce tillers (up to 8-1 O tillers/hill) between 40 and 70 days after planting (Sarla and Swamy, 2005), and similar observations (Jones *et.al.,* 1997), have been reported. The short circle vegetative stage and the ability to produce more biomass within a short period allow *0. glaberrima* to be unique and compete with weeds. Some accessions of 0. *glaberrima* have been identified as weed competitive lines (Jones *et.al.,* 1997), and other 0. *glaberrima* accessions have been used as a source of resistance to many pests and diseases found in West Africa. Drought is one of the abiotic stresses among the major stress that affects rice yields and 0. *glaberrima* has been identified to have a number of droughts escaping mechanisms. It has the ability to mature early and synchronized maturity towards the end of growth cycle is unique attribute. In addition to its ability to withstand drought, it has the capability to recover very fast on receipt of moisture. Although, *0. glaberrima* are inherently lower yielding than those of *0. saliva* and are therefore cultivated in fewer areas (Linares, 2002). It is well known that Oryza glaberrima grow favorably under varied conditions and can tolerate harsh African environment even under severe stress. The thin leaves roll quickly to retain water and thin roots penetrate effectively in close contact with the soil particles to effectively extract water and nutrients (Dingkuhn, *et.al.,* 1999; Bagachi, *et.al.,* 1995; Maji, *et.al.,* 2001). These traits are useful in breeding for drought tolerance in rice (Bagach *et.al.,* 1995; Maji, *et.al.,* 2001). *0. glaberrima* is also a source of resistance to other abiotic stresses such as its ability to tolerate acidic conditions, iron and aluminum toxicity. It has been reported that 0. *glaberrima* showed a remarkable tolerance to iron toxicity (Sahrawat and Sika, 2002), and show high nitrogen use and photosynthetic efficiency (Tagawa *et.al.,* 2000), high specific leaf area, rapid canopy architecture and establishment along with droopy leaves (Jones, *et. al,* 1997; Dingkuhn and Asch, 1999; Heuer *et.al.,* 2003), and high biomass (Bagachi, *et. al,* 1995). Some accessions of *0. glaberrima* has been identified to be resistant to lodging (Jones, *et.al.,* 1997) including useful cooking quality traits for feeding and weaning babies, genes to enhance milling with good cooking quality (http://www.Unu.edu/enu/plec). Although, *0. glaberrima* while lacking many of the agronomic and quality traits found in Asian rice, *Oryza glaberrima* is significantly unique for traits of abiotic stress tolerance. Sarla and Swamy (2005), and Tagawa, *et.al.,* (2000) reported that under low input condition, high nitrogen efficiency, high photosynthetic efficiency and specific leaf area with rapid canopy establishment, droopy leaves (Jones, et.al., 1997; Dingkuhn and Asch, 1999; Heuer, *et.al.,* 2003) and high root biomass (Bagachi, *et.al.,* 1995) in *0. glaberrima* accessions are traits that could be exploited to develop new plant types for both rainfed and irrigated areas of rice production ecologies. Sarla and Swamy (2005) reported that interspecific

crosses between African and Asian rice have produced cultivars with improved yield and quality traits adopted by many farmers in African countries to meet the growing need for rice as a staple food crop. From a scientific point of view, the genome of 0. *glaberrima* will provide insight into the comparative genetic basis of domestication and other traits by finding commonalities and differences with *Oryza saliva*. Similar to Asian rice, Africa rice carries the AA-type genome, having 12 chromosomes and an estimated size of 358 Mbp. Other agronomic traits of valuable interest could be exploited to develop new plant genotypes.

Utilization of *O. glaberrima* for abiotic stress response

Africa in general is affected by various stresses including water unavailability, soil nutrient deficiencies, salinity, iron toxicity, drought and submergence. Under this condition, the productivity of rice sub–Saharan Africa areas is seriously affected by various abiotic stresses and rice production in this region is mainly dependent on rainfall, but these areas are often affected by periodic, unpredicted and erratic rainfall pattern during early to middle rice growth stage. Rice plants are often partially or completely affected by drought for more than a month especially during critical growth period of rice at vegetative and reproductive stages. Such prolonged lack of rain often triggers crop failures. Farmers in low rainfall areas prefer to cultivate 0. *glaberrima* fields with prolonged unstable rainfall distribution because of such advantageous traits of drought tolerance. For example, coastal or lowland areas are heavily affected by submergence during the rainy season. Rice plants are often partially or completely submerged for more than a month, and such prolonged submergence often triggers crop failures. Given the success of interspecific breeding that brought about the success of NERICA varieties in Africa, *Oryza glaberrima* therefore has gained renewed interest by rice scientists. Thus, several literatures have reported the useful traits in 0. *glaberrima* species and their resistance to both biotic and abiotic stresses (Table 3), as reported by Sarla and Swamy (2005). Even though there has not been valid data to support this assumption, but various opinion and literatures have supported its utilization for abiotic stress tolerance including drought, iron toxicity, acidity, submergence and low input soil conditions (Sano *et.al.,* 1984; Jones *et.al.,* 1997) and ability to grow under a wide range of unfavorable environmental conditions of Africa (Sarla and Swamy, 2005). In the past at AfricaRice, only four *Oryza glaberrima* accessions were used to develop the NERICA varieties for both lowland and upland ecosystem, and with more than 2500 germplasm accessions maintained in AfricaRice gene bank. This is an indication that there is therefore a tremendous amount of genetic diversity traits of interests that have not been exploited and utilized for genetic improvement in the primary gene pool of 0. *glaberrima*. It was reported that several 0. *glaberrima* lines have been identified for use as donor parents for drought tolerance (Ndjiondjop *et.al.,* 2007; Bimpong *et.el.,* 2011a). Similarly, good sources of salinity tolerance have been identified within 0. *glaberrima* accessions and these alleles can effectively combine with Saito! to breed salt tolerant rice varieties. Consequently, CG 14 reported to have remarkable tolerance to iron toxicity stress (Sahrawat and Sika, 2002) while further progress has been made towards interspecific breeding to avoid spikelet sterility due to heat stress (Yoshida *et.al.,* 1981; Manneh *et.al.,* 2007). Thus, the major limitations in the use of 0. *glaberrima* for the improvement of 0. *saliva* was the interspecific hybrid sterility that routinely occurs between these crosses (Ghesquiere *et.al.,* 1997), even though there is major breakthrough in the development of interspecific NERICAs, the introgression of useful traits from 0. *glaberrima* still remain tedious and time consuming exercise to achieve results within time frame becomes more difficult and slow.

Sterility in F1 hybrids

Hybrid inviability and sterility (Matsubara *et.al.,* 2003) are major obstacles in rice improvement for the comprehensive utilization of closely related species in rice breeding programs, and therefore impairing the exploitation of the rich genetic diversity found within the *Oryza saliva* complex (known as genome group AA), and the beneficial effect of the high level of heterosis observed in the F1 plants. One of the most commonly known relevant examples of this strong limitation comes from the African cultivated rice species (0. *glaberrima* Steud). This species represents an interesting source of genetic diversity and drought tolerance (Sarla and Swamy 2005), weed competitiveness (Dingkuhn *et.al.,* 1998), and nematode and virus resistances (Ndjiondjop *et.al.,* 1999; Soriano *et.al.,* 1999). There is a high rate of hybrid sterility in interspecific hybridization between 0. *glaberrima* x 0. *saliva* crosses despite both are AA genome species, normal chromosome pairing, and gamete formation are not hindered in the hybrids (Nayar, 1973). Though, high rate of sterility is reported as the general rule in the crosses between 0. *saliva* and 0. *glaberrima* F1 hybrids, irrespective of combination of varieties (Chang, 1976; Pham and Bougerol, 1993) used as parents. Various causes have been confirmed to be meiotic irregularities (Heuer *et.al.,* 2003; Peltier, 1953; Gopal *et.al.,* 1964). This irregularity is attributed to be low proportion of viable pollen, low pollen germination, cytoplasm and its interaction effects from male side and early elimination of female gametes and zygotes from female side have been reported and described as sterility (Porteres, 1956; Kitampura, 1962). Pollen development in F1 in interspecific hybrids is arrested at the microspore stage. Three types of pollen have been identified and reported as empty, intermediate and fully stained and has been reported based on staining with iodine solution (l2KI). Pollen studies in some hybrids showed pollen sterility up to 80% as reported by (Sarla and Swammy, 2005). It was reported to contribute to the reproductive barriers between two cultivated species (Sano *et. al,* 1979; Sano, 1986) of (0. *glaberrima* and 0. *saliva)*. A sterility locus causing hybrid sterility has been well studied (Sano, 1990), and a number of sterility loci on chromosomes have also been reported (Doi *et.al.,* 1998; *Doi et.al.,* 1999). Several of these traits have

already been mapped (Lorieux *et.al.,* 2003; Ndjiondjop *et.al.,* 2003); however, their introduction to *0. saliva* has been hampered by the strong sterility barrier between the two species (Sano *et.al.,* 1979; Morinaga *et.al.,* 1957 Morishima *et.al.,* 1962, Morishima *et.al.,* 1963, Chu *et.al.,* 1969, Jones *et.al.,* 1997, Sano 1983, Tao *et.al.,* 1997). This barrier is the result of several loci that might interact or act separately to render the F1 hybrids pollen sterile and partially female fertile (Andrea *et.al.,* 2010). Among these, the *S1* locus has the strongest effect over the fertility of hybrids (Sano, 1990). Despite the strong hybrid sterility (Andrea *et.al.,* 2010), obtaining fertile plants derived from *O. saliva* x *0. glaberrima* crosses have been possible by performing successive backcrosses followed by selfing (Ghesquie're *et.al.,* 1997). Nevertheless, this fertility recovery is associated with the presence of homozygote *0. glaberrima S1* allele (S19) and lost again when re-crossing with *0. saliva* (Heuer and Miezan, 2003). Further, a strong transmission ratio distortion (TRD) of markers linked with *S1,* in favor of the *0. Glaberrima* alleles, results as a consequence of the systematic elimination of the *0. saliva* alleles from the descendants (Ghesquie're *et.al.,* 1997; Doi *et.al.,* 1998b; Lorieux *et.al.,* 2000; Aluko *et.al.,* 2004). Andrea *et.al* (2010) reported that S1 is the most important locus acting as a reproductive barrier between the two cultivated species hybridization *(Oryza saliva* and *0. glaberrima).* It has been described that it is a complex locus, with factors that possibly will affect male and female fertility separately (Andrea *et.al.,* 2010). Their recent study has indicated that the component causing the allelic elimination of pollen was fine mapped. However, the position and nature of the component causing female sterility are yet to be identified. To fine map the factor of the S1 locus affecting female fertility, Andrea et.al, (2010), developed a mapping approach based on the evaluation of the degree of female transmission ratio distortion (fTRD) of markers. The methodology was implemented in four *0. saliva* x *0. glaberrima* crosses. the female component of the S1 locus was mapped into a 27.8-kb (0. saliva) and 50.3-kb (0. glaberrima) region included within the interval bearing the male component of the locus, and more evidence of an additional factors interacting with S1 was also found. The analysis of their available data show that a model where incompatibilities in epistatic interactions between S 1 and the additional factors are the main cause of the female sterility barrier between *0. saliva* and *0. glaberrima.* This was developed to explain the female sterility and the TRD mediated by S 1. According to (Andrea *et.al.,* 2010) on the model developed, the recombination ratio and allelic combinations between these factors would determine the final allelic frequencies observed for a given cross. TRD and its association with interspecific sterility loci (Andrea *et.al.,* 2010), described those different processes such as the nonrandom segregation of chromosomes during meiosis (meiotic drive) (Fishman and Willis, 2005), abortion of haploid gametes (as in hybrid sterility) (Orr and Irving, 2005), or abortion of zygotes after fertilization (as in hybrid inviability), as reported by Matsubara *et.al,* (2003). The strong association between markers showing TRD and pollen sterility QTL has been reported in some interspecific cross of tomato (Moyle and Graham, 2006). This association shows that hybrid sterility may occur from incompatibilities.

In the study of genetic map (Andrea *et.al.,* 2010), the interpolated positioning of genes and QTL causing *0. saliva* x *0. glaberrima* hybrid sterility evidences their colocalization with markers showing fTRD (reference). Presently, there is an on-going alternative intended to unlock the full potential of *0. glaberrima* to rice breeding, titled "iBridges" project, supported by the Generation Challenge Program (http://www.generationcp.org) aims to develop a set of *0. saliva* x *0. glaberrima* hybrids that would be fertile when crossed with *0. saliva.* To develop these interspecific bridges, genetic factors affecting their fertility will be identified and characterized so as to better understand the nature of the sterility barrier (Andrea *et.al.,* 2010). For example, percent spikelet fertility was ranked following the ranking of INGER (1996) as follows; highly fertile (90%), fertile (75-89%), partly sterile (50-74%), highly sterile (50% to trace), and completely sterile (0%). These results will definitely slow down breeding progress towards developing abiotic stress tolerant rice. Recently, the complex nature of the S1 locus was suggested, and the male component was mapped to an interval equivalent to 45 kb on the genome of *0. Saliva* cv. Nipponbare (Koide *et.al.,* 2008c). New breeding progress towards reducing interspecific barriers and hybrid sterility between *0. saliva* and *0. glaberrima* and identification of sterility genes using molecular marker approach will help to abate this negative trend between the hybridization barriers and sterility of the two cultivated species.
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Table 2. Rice Gemplasm accessions in the AfricaRice gene bank as of April 2012

Origin	O. glaberrima	O. sativa	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

Source: Adapted from K.A. Sani *et. al.,* (2012) diversity of rice and related wild species

Table 3. Abiotic and biotic stress tolerance of African rice (*Oryza glaberrima*)

Stresses	Relevant Reference
A. Abiotic stress	
Acidity	Sano *et.al.* 1984
Aluminum Toxicity	Baggie *et al*. 2002
Drought tolerance	Jones *et al*, 1997: Maj et.al, 2001
Iron toxicity	Sakrawat and Sika (2002)
Salt tolerance	Linares *et al,* 2002
Submergence tolerance	Watarai and Inoye (1998)
Weed competition	Johnson *et al*. 1998
B. Biotic stress	
African rice gall midge	Nwlene *et al*, 2002
Bacterial leaf blight	Kuldeep Sing, pers commun
Blast	Silue and Nottenghem (1991)
Nematode	PlowRight *et al*, 1999
Rice yellow motte virus	IIT (1988)
Sheath blight	Wasano and Hirota, 1986
Stem bore and hispa	Sauphanor (1985)
Stalked eyes fly	Joshi *et al*. 1991

Breeding approach for abiotic drought stress

The main objective of breeding program is not only to breed diverse genotypes, but to identify and develop genotypes that adapt to certain environmental conditions. Therefore, plant science must make accurate predictions and strategies about how various rice genotypes will perform in various environmental conditions. These predictions will be used to precisely design and develop rice genotypes for specific environments. With a better understanding of the mechanism of stress tolerance, breeders are now using precise breeding approaches to develop crop varieties tolerant to abiotic stresses. The main breeding approach is to breed for high yield under optimum or nominal environmental conditions (water, stress and free) condition because the nominal maximum genetic potential is expected to be realized under optimum environmental condition and crop performance under optimum and stress conditions should be highly and positively correlated (Johnson and Frey, 1967). It has been reported that a genotype superior under optimum level will also yield relatively well under drought conditions (Jiban, 2001). However, the concept of expression of maximum genetic potential in optimum condition is debated as genotype by environment interaction may restrict the high yielding genotype to perform well under drought condition. Breeding under actual drought condition has been suggested (Hurd, 1971), but this approach may suffer from the intensity of drought as it is highly variable from year to

year and as a consequence environmental selection on breeding materials may possibly change drastically from one generation to another (Jiban, 2001). This may compound many problems that will be associated with low heritability of yield (Roy and Murty, 1970), and may complicate and slow down breeding program activities targeted to develop varieties tolerant to abiotic stresses within time frame. An alternative approach has been suggested to improve drought resistance in high yielding genotypes (Jiban, 2001) through incorporation of traits of interests. However, it has been reported (Jiban, 2001), transferring drought resistance in high yielding genotype can sometimes be complicated due to lack of understanding of the physiological and genetic basis of adaptation in drought conditions. Improving the yield potential of an already resistant material may be a more promising approach provided there is genetic variation within such materials. Different approaches have been used in breeding for abiotic stresses. For example, pedigree and bulk method could be used for self-pollinated crops and recurrent selection for cross pollinated. However, the success of any breeding and crop improvement program depends on the germplasm resources at hand and methods and understanding of crop improvement. Several breeding approaches for abiotic stress resistance have evolve, for example direct selection for gran yield under drought has been reported (Venuprasad *et.al.,* 2008; Kumar *et.al.,* 2008), breeding strategies to overcome the interspecific barriers and sterility in F, hybrids (Jones et. al, 1997; Heuer et. al, 2003; Sano, 1986). In this way, the first step is to identify parental lines of *0. glaberrima* accessions which produce fertile F, using the approach as described by (Sarla and Swamy, 2005). Repeated backcrossing (Ishii *et.al.,* 2001; Johnson *et.al.,* 1998; Wasano and Hirota, 1986) can restore fertility if embryo sacs are fertile in F, using the strategies adapted from Sarla and Swamy (2005) in (Figure 1). The level of fertility restoration has been reported to vary from 30 to 65% and between 90 and 98% (Sarla and Swamy, 2005). Though, crossability in *0. glaberrima* is still limited to a few parental accessions and sometimes desirable traits are lost in the process of restoring fertility.

Screening methods for abiotic stress tolerance

Any breeding effort directed towards genetic improvement of abiotic stresses such as drought, iron toxicity, salinity, submergence tolerance and biotic such as disease resistance requires efficient screening methods for evaluating plant performance at certain developmental stages. Screening using a large population size with a good experimental design has been reported (Johnson, 1980). Several literatures have proposed that a combination of different traits could be used as selection criteria for screening appropriate ideotype, or a combination of traits of direct relevance, rather than a single trait, should be used as selection criteria (Singh and Sarkar, 1991). The earlier approach of improving grain yield under drought through selection on secondary traits such as root architecture, leaf water potential, panicle water potential, osmotic adjustment, and relative water content (Fukai *et.al.,* 1999; Price and Courtois, 1999; Jongdee *et.al.,* 2002; Pantuwan *et.al.,* 2002a,b,c) did not give the expected results to improve yield under drought. Recent studies as reported (Bernier *et.al.,* 2007; Venuprasad *et.al.,* 2007; Kumar *et.al.,* 2008) have shown moderate to high heritability of grain yield under reproductive stage drought stress (Bernier *et.al.,* 2007; Venuprasad *et.al.,* 2007; Kumar *et.al.,* 2008), and thus opening a new area for direct selection for grain yield instead of secondary traits. The study by Venuprasad *et.al.,* (2007) also emphasized the importance of using highly tolerant parents as donors if the objective is to make gains under severe drought stress. Direct selection for grain yield under drought has been reported effective (Kumar *et.al.,* 2008; Venuprasad *et.al.,* 2008) and the possibility of combining high yield under drought (Kumar *et.al.,* 2008; Venuprasad *et.al.,* 2008). For example, Ludlow and Muchow (1990) ranked the merit of various traits conferring drought resistance. McCree *et.al.,* (1990) and Johnson *et.al.,* (1991) provided a framework for evaluating plant materials under drought stress. Venuprasad *et.al* (2002) reported that plant breeding for drought-prone habitats envisages a favourable combination of grain yield and drought tolerance. Though several mechanisms enhancing drought tolerance have been identified in rice, their association with grain yield under low-moisture stress have been established in few instances and reported (Venuprasad *et.al.,* 2002). For example, loss of yield is the main concern in rice improvement; therefore, yield performance under moisture stress condition is imperative. A drought resistance index which provides a measure of drought based on loss of yield under drought stress condition in comparison to moist condition has been used for screening drought tolerant genotypes (Clark *et.al.,* 1984; Ndunguru *et.al.,* 1995). An artificially created water-stress environment (Mai-Kodomi *et.al.,* 1999; Jiban, 2001) is used to provide the opportunity in selecting superior genotypes out of a large population. This technique has been adopted by many plant breeders working on drought resistance in field crops. Shaibu *et.al.,* (2018), identified four *Oryza glaberrima* accessions with higher grain yield under drought stress out of 2000 accessions screened.
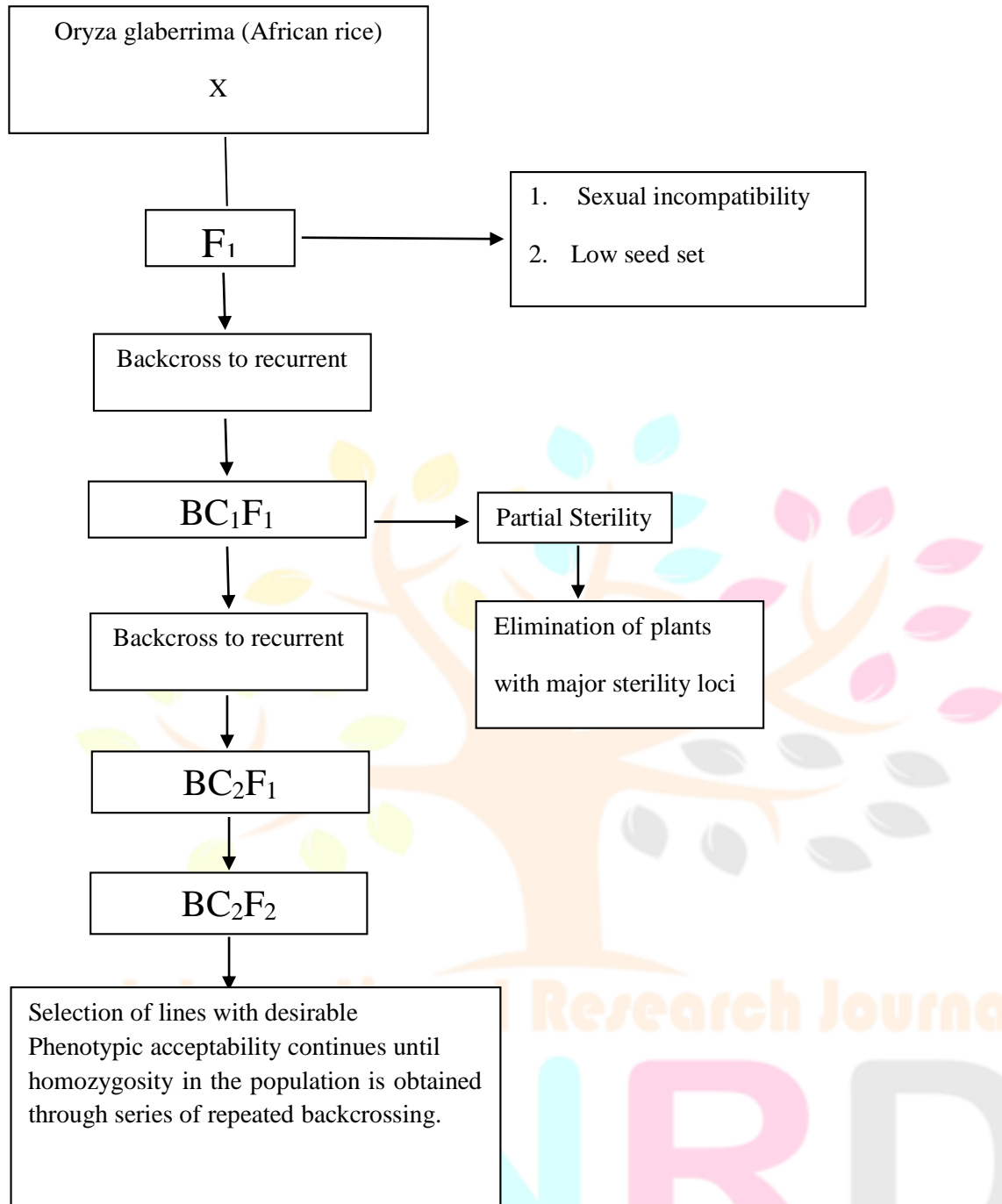
Oryza glaberrima (African rice)

X

F_1

1. Sexual incompatibility

2. Low seed set

Backcross to recurrent

BC_1F_1

Partial Sterility

Backcross to recurrent

Elimination of plants

with major sterility loci

BC_2F_1

BC_2F_2

Selection of lines with desirable
Phenotypic acceptability continues until
homozygosity in the population is obtained
through series of repeated backcrossing.

Figure 1. Proposed breeding scheme to obtain fertile lines from interspecific hybridization between *(O. glaberrima x O. sativa)* crosses.

Constraints to abiotic stress tolerance in rice

African rice species reported to have many important traits of interests that could be exploited and introgressed into elite cultivars through conventional breeding and molecular. Reproductive barriers between the two species as reported by Sarla and Swamy (2005) have been studied and genetic models proposed for its better utilization. Repeated backcrossing (Ishii *et al*, 2001, Johnson, *et al*. 1998; Wasino and Hirota, 1986), anther culture and double haploid plants have been obtained from isolated microspore culture in rice and this culture has open up new possibilities for transformation, mutation and selection making it more useful for breeding. A molecular approach (Ghesquiere, *et al*, 1997) has been adopted, and embryo rescue (Jena and Khush, 1984) techniques have been helpful and applied to combat sterility barriers in few instances. Many other scientific investigations have proffer solution to abiotic stresses tolerance and have proposed many possible different information linked to drought resistance that could be used in selection and genetic variability that exist in different crops (Blum, 1983; Jayalakshmi *et.al.* 1998) The success rate in obtaining resistant genotypes to different abiotic stresses such as drought, iron toxicity, submergence tolerance has been very slow. The lack of success may be due to (1) lack of precise proprietary technology to handle abiotic stresses thoroughly in many breeding and research programs (2) technical know-how of the multidisciplinary approach to understand the complex genetic mechanism that control abiotic stresses such as drought (3) limitation in genetic engineering information, its application and genetic factors controlling abiotic stress tolerance (4) lack of precise and screening techniques.

Genetic research

Understanding the evolution of genetic research of plant at DNA level will greatly increase knowledge of genome structure and function because of the diverse approaches scientists take in studying different species (Van Deynze et.al, 1995a). Comparative genetics of abiotic stress such as drought tolerance will continue to evolve as new technologies, methods, and information become available. For example, current) and future research will focus on genes and their expression under drought conditions across species using sequence and map-based tools that will characterize evolutionary trends in these genes at both the structural and functional levels (Van Deynze *et.al.,* 19956). For example, comparative maps allow transfer of information about genetic control of traits from species with small diploid genome, such as rice (Oryza sativa L.). The earlier study on Gramineae family encompasses a diverse group of species that have been classified into two major clades based on molecular phylogenetic studies (Clark *et.al.,* 1995; Soreng and Davis, 1990). The Panicoideas subfamily including maize, sugarcane (Saccharum, sorghum, and millet (Penniseturn) make up one clade while the other clade contains the Pooideae subfamily wheat, barley, rye, and oat. Rice and wild rice, belong to the subfamily Oryzoidese. The genome of cultivated rice is reported to resemble an ancestral grass genome with a high base chromosome number (x-12) and relatively small genome size of 430MB (Argumuganathan and Earle, 1991). Molecular markers have been used to develop comparative chromosome maps for several members of the Gramineae (Moore *et.al,* 1995: Devos and Gale, 1997) and these have been used for the identification of genes that are vital across species (Snape and Laurie, 1998). For example, study on crop species of the Poaceae display a remarkable level of genetic similarity despite their evolutionary divergence 65 million years ago (Bennetzen and Freeling, 1993, Paterson et al, 1995). Large segments of the genomes of maize, sorghum, rice, wheat, and barley conserve gene content and order (Hulbert et al, 1990: Ahnand Tanksley, 1993; Ahn ef at. 1993: Kurata et.al. 1994: Van Deynze etal. 1995a,b,c: Gale and Davos, 1998), although the correspondence has been modified by chromosome duplications, inversions, and translocations. For the domesticated grasses, the conserved linkage blocks and their relationships with rice linkage groups provides insight into the basic organization of the ancestral grass genome (Moore *et.al.,* 1995; Wilson *et.al,* 1999). Most comparative mapping among the grasses before now has relied on RFLP probes (cDNAs or genomic clones) to establish gross gene orders and distance in specific chromosome segments. Only to a limited extent have researchers employed cloned genes, ESTs, mutant phenotype loci or QTLs in comparative genomics (McCouch and Doerge, 1995). Despite the progress in comparative mapping, McCouch and Doerge (1995) reported that the application of this technology, especially for rice will not be realized unless scientifically sound strategies for studying abiotic stress such as drought tolerance are devised that allow researchers to utilize genetic tools and information developed for model species. This will require more detailed comparative genetic analysis from the DNA sequence of genes all the way to comparative analysis of QTL (Van Deynze *et.al.,* 1995c). The research reviews as reported by Van Deynze *et.al.,* (1995a,b) on drought tolerance among grass species with comparative genetics perspective has provided with new technologies for evaluating, dissecting, and mapping components of drought tolerance as well as transfer of this information among species is accelerating the understanding of this phenomenon. In addition, exploitation of the genetic variation and evolutionary benefits of certain species (Ray *et.al,* 1996) can enhance our knowledge and provide source of genes for transfer to other species.

Genetics of abiotic stress tolerance

Crop productivity is drastically reduced by abiotic stresses such as salinity, temperature, and drought. It has been estimated that crops attain only about 25% of their potential yield because of the damaging effects of environmental stress (Boyer, 1982). The

abiotic stresses have been reported to be location-specific, exhibiting variation in frequency, intensity, and duration (Turner, 1979). Several definitions have been ascribed to drought which include precipitation, evapotranspiration, potential evapotranspiration, temperature, humidity and other factors individually or in combination (Renu and Suresh, 1998). Drought has been reported as the primary abiotic stress causing not only differences between the mean yield and the potential yield but also causing variation from year to year (yield instability). Selection for genotypes with increased productivity in drought environments has been an important aspect of many plant breeding programs, but the biological basis for drought tolerance is still poorly understood (Turner, 1979). In addition, drought stress is highly heterogeneous in time (over the seasons and years) and space (between and within sites) and is unpredictable. This makes it difficult to satisfactorily identify or simulate a representative drought stress condition. It has been predicted that in the coming years rainfall patterns might shift due to an increase in the global temperature caused by burning of fossil fuels and the corresponding increase in atmospheric dioxide (Guido and Paul, 1994). Consequently, farming communities could become increasingly dependent on drought tolerant varieties. Crop productivity in a water-limited environment derives from mechanisms that either permit tolerance of occurrences of cellular dehydration or that minimize water loss and thereby maintain a favourable water status for leaf development. Different mechanisms may render a plant drought tolerant: (i) the ability of a plant to escape stages of drought, especially during the most sensitive stages of plant development; (ii) the ability of a plant to recover from a dry period by producing new leaves from buds that were able to tolerate the dry spell and (iii) the ability of a plant to endure or withstand a dry period by conserving a favourable internal water balance under drought condition. Thus, it was reported that selection for drought tolerance while maintaining maximum productivity under optimal conditions has been challenging (Rosenow *et.al.,* 1983; Clarke *et.al.,* 1992; Zavala-Garcia *et.al.,* 1992). It has been reported also that photosynthesis and several other related physiological traits differed significantly between drought tolerant and drought susceptible genotypes (Gummuluru *et.al.,* 1989). Several characteristics have been considered important in adaptation to abiotic stress. For example, osmotic adjustment, in which the plant increases the concentration of organic molecules in the cell water solution to "bind" water (Turner, 1979; Yancy *et.al.,* 1982), is one example of a mechanism that alleviates some of the injurious effects of water stress by promoting both avoidance and tolerance (Blum, 1989). Study on leaf water growing under drought stress (Morgan and LeCain, 1991), has received attention. In addition, a thicker layer of waxy material at the plant surface and more extensive and deeper rooting (Morgan, 1984) are others. Physiological and biochemical traits that might enhance drought tolerance have been proposed (Morgan, 1984; Good and Zaplachinski, 1994, Ludlow and Muchow, 1990). The identification of genes responsible for morphological and physiological traits and their location on chromosomes have not been possible but their inheritance pattern and nature of genes and their actions have been well reported. Ekanayake *et.al.,* (1985) reported on polygenic inheritance of root characters. It was reported that the long root and high root numbers are controlled by dominant alleles and thick root tip by recessive alleles (Armento-Soto *et.al.,* 1983). However, leaf rolling (Singh *et.al.,* 1991) and osmotic adjustment (Morgan, 1991) have shown monogenic inheritance. A drought resistant gene (Drt1) in rice was reported (Tomar and Prasad, 1996) linked to plant height, pigmentation, hull colour and awn with pleiotropic effect on the root system. Drought resistance in cowpea was reported to be controlled by a single dominant gene (Mai Kodomi *et.al.,* 1999). In addition to morphological and physiological changes (Jiban, 2001), biochemical changes involving induction of compatible solute biosynthesis is one way to impart drought (Mccue and Hanson, 1990).

Mapping quantitative traits

Several studies examining the mapping of quantitative trait loci that are associated with abiotic stress tolerance such as drought and related trait has been demonstrated and confirmed that this trait is affected by several loci of which each have reasonably small effect (McCouch and Doerge, 1995; Quarrie, 1996). It has been reported that several studies have mapped loci associated with morphological traits under drought conditions (Agrama and Moussa, 1996; Ribaut, *et al.,* 1996; Ribaut, *et.al.,* 1997). A study was conducted on an early QTL in rice and more than 45 QTL found associated with leaf rolling under field drought stress and root morphology traits {Champoux *et.al.,* 1995). The twelve (12) out of the 14 QTLs associated with leaf rolling were also associated with root thickness, root/shoot ratio, or root dry weight per tiller. Using the same mapping population (Ray *et.al.,* 1996), evaluated and examine root penetration, and it was found that some of these QTLs also corresponded to QTL of root morphology. Further, the results of the two studies were later extended by evaluating osmotic adjustment and relative water content. QTL for root morphology and leaf rolling in the homoeologous chromosome region in rice was mapped (Champoux *et.al.,* 1995), and Teulat *et.al.,* {1997) mapped QTL for controlling relative water content and number of leaves under water stress. However, a major gene mapped in wheat for osmoregulation (Morgan and Tan, 1996) appears to be distal to this region based on rice wheat comparative map (Van Deynze *et.al.,* 1995c). It was reported by Lilley *et.al.,* (1996) that the E_94 locus osmoregulation genes in Barley also correspond with rice chromosome segmented reported to be associated with lethal osmotic potential in rice (Lilley et.al, 1996), and several root growth characteristics and genetic dissection in rice was evaluated (Price *et.al.,* 1997; Price and Thomas, 1997). A more comprehensive approach to studying abiotic stress tolerance such as drought using proteomics has been advanced (De Vienne *et.al.,* 1999; Prioul *et.al.,* 1999). Further, there has been substantial progress in identifying genes for resistance to various abiotic stresses such as temperature, salinity and drought. It has been reported that

some transgenic plants for improved drought tolerance using genes that have been isolated and tested as drought resistance genes including alanine aminotransferase and D-myo-inositol methyltransferase (Muench and Good, 1994), and transgenic approach to investigate the function of the HVA1 protein in stress protection (Xu *et.al.,* 1996) have been adopted. This approach may aid in the detection of regulatory genes and in identifying candidate genes for studying various abiotic stress tolerance in rice species.

Molecular marker

A thorough molecular analysis of the plant genome and the events that occur during stress and their genetic control is essential to define which genes are regulatory, or which are primary gene products that are positively contributing to stress tolerance. With a better understanding of the mechanisms of genetics of stress tolerance, breeders are now using more precise molecular breeding approaches for rice improvement. For example, marker assisted backcrossing (MASC) is one approach towards rice improvement. Many QTLs genes have been identified and mapped for some abiotic stress tolerance in rice (Jena and Mackill, 2008; Ismail and Thomson, 2011), and with the aid of marker assisted breeding approach to incorporate high yielding varieties has yielded positive results. Though, improving stress tolerance of rice has been hindered by low level of genetic variability coupled with complex inheritance of trait and difficulty to accurately measure the level of tolerance. Recently, various molecular approaches have been applied to rice improvement and many QTLs have been identified. For example, leaf rolling (Laffite *et.al.,* 2006), QTLs related to better yield under drought (Venuprasad *et.al.,* 2009; Vikram *et.al.,* 2011; *Bernier et.al.,* (2007). QTLs (*ql/2. 1* and *DTY 3. 1),* associated with yield under drought in upland and lowland has been reported (Bernier *et.al.,* 2007; Venuprasad *et.al.,* 2009). Sarla and Swamy (2005) reported the Contig line concept (Ghesquiere *et.al.,* 1997) was proposed to bypass sporogametic interaction for monitoring sterility loci using molecular marker approach was developed, but effort to transfer Rice yellow mottle virus (RYMV) resistance from a variety of *0. glaberrima* was not successful. The linkage map of *0. Glaberrima* developed using 129 markers representing 112 discrete loci (Sarla and Swamy, 2005) permits the identification, location and introgression of various genes of interest to a new genetic background, and several of these traits have been already mapped (Lorieux *et.al.,* 2002; Lorieux *et.al.,* 2003).

Conclusion and outlook

The present review provided some evidence in the utilization of African rice species (*O. glaberrima)* in rice improvement for abiotic stress tolerance. Though, from several information gathered, its utilization has been widely recognized, but access to the gene pool of the cultivated African rice has so far been limited. Hybridization between the two cultivated species (0. *glaberrima* x *0. saliva)* has been attempted since the last fifty years, but the issues of interspecific incompatibility still remain unanswered as the sterility of the F1 hybrids and semi sterility in subsequent generations still remain a major problem of rice improvement that demands research responsiveness. Consistent effort is required to identify compatible *0. glaberrima* and *0. saliva* accessions for interspecific hybridization that would facilitate broader access to the African rice gene pool utilization in breeding. The development of large backcross population may increase the likelihood of obtaining fertile progenies as a result of frequent recombination process. Though anther culture has been used to speed up this process in the past, and these procedures would enable quick recovery of useful recombinants to reduce the occurrence of sterility in the hybrids. Double haploid lines have been used to develop NERICAs and map agronomically useful traits that are very important and promising, but this is not enough to meet the challenging climate change scenarios that are facing agricultural and economic activities today. Based on genome-wide linkage disequilibrium microsatellite markers, about 198 accessions of *0. glaberrima* were reported grouped into five subgroups. With the relevant information in this paper, it is important that the accessions of *0. glaberrima* be conserved for genetic exploitation because for its unique qualities and as a subsistence crop that can withstand environmental stresses. Introgression from 0. *saliva* is reported to have influenced the genetic structure of 0. *glaberrima* populations in West Africa (Semon *et.al.,* 2005). Nevertheless, an initiative to genetically characterize the important traits of interests in African rice species and incorporation through conventional breeding and molecular markers, develop models to identify compatible donors that will constitute the new plant types as well as screening techniques that will address various abiotic stresses such as drought tolerance, submergence tolerance, acidity, iron toxicity, salt tolerance is a necessary step. A thorough analysis of the physiological events that occur during stress period and their genetic control is essential to define which gene is regulatory and which are primary gene products positively contributing to stress tolerance, which genes may serve as markers for the physiological stage of plant development, and which gene product may be considered as secondary stress induced metabolites. However, comparative genetic analysis can greatly facilitate the discovery of genes that contribute to this complex trait by allowing scientists to transfer information between species. Further, genetic variation for components of abiotic stress tolerance may differ widely among species and this genetic variation is crucial to understanding the underlying mechanisms of abiotic stresses. The crossbreeding of *Oryza glaberrima* and *Oryza saliva* should continue in aiming at the transfer of genome fragments in association with *in-situ* maintenance of genetic resources of wild and cultivated rice of African origin, aiming at increased yield, tolerant to various biotic and abiotic stresses. The recent improvement in anther culture success in rice, and by drawing parallels to their involvement, pinpoint factors that either have or could be examine further. The recent improvements in

molecular breeding and marker assisted selection (MAS) provide an obvious new area for investigation of abiotic stress tolerance in rice. Cultivated rice (Oryza *sativa* L. *2n* = 24) has a wide genetic diversity and well-characterized genetic base is a useful model for the study of hybrid sterility in plants.

Highlights

- Some studies from this review have identified *O. glaberrima* accessions as a source of tolerant genes for abiotic stresses in rice.
- These genes are valuable source of tolerance to many abiotic stresses and can be used in the development of climate-resilient rice varieties adapted to African environment.
- Some of these accessions selected for different abiotic stresses will probably contribute to widening the genetic base of the lowland rice breeding program gene pool.
- Consistent effort is therefore required in breeding to develop new rice varieties adaptable to the emerging climate change.
- New Rice for Africa (NERICA) was developed from double haploid lines with promising agronomic traits of importance.
- New breeding progress towards reducing interspecific barriers and hybrid sterility between *0. saliva* and *0. glaberrima* and identification of sterility genes using molecular marker approach will help in the hybridization barriers and sterility of the two cultivated species.

Conflict of Interest

The authors declare that there is no conflict of interest.

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