Breeding for Rice Aroma and Drought Tolerance: A Review

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Abstract: Aroma is one of the main characteristics that guide rice purchases worldwide. Aromatic rice varieties are generally less adapted to biotic and abiotic stresses. Among the abiotic constraints, drought stress causes considerable yield losses. This review describes advances in breeding for aroma and drought tolerance in rice and investigates the possibility of combing these traits in one variety. Some of the major quantitative trait loci that have been discovered for drought tolerance were recently introgressed into aromatic varieties. However, more details on the performance of developed lines are still needed. Furthermore, there are not yet any published reports on the release of aromatic drought-tolerant rice varieties.

Keywords: badh2 gene; aroma; quantitative trait loci (QTLs); drought tolerance; yield

1. Introduction

Rice (*Oryza sativa* L.) is an important source of calories and of some proteins for more than half of the world's population [1]. Rice provides energy and essential nutrients, such as thiamine, riboflavin, niacin, vitamin E, zinc, potassium, iron and fibre, making it a very useful food [2]. Consumer preferences may vary across countries in terms of grain quality, but aroma is the first factor that influences rice purchases among most consumers in the markets of East African countries [1]. Aroma is an important trait that provides significant profits for farmers who grow aromatic rice varieties worldwide [3]. India, the main exporter of basmati rice to the global market, sold more than 44 million metric tons, corresponding to 4.7 billion United States dollars, in 2018 [4]. Fragrance in rice is mainly controlled by genetic factors but its expression is heavily influenced by environmental conditions [5].

Rice production in 2020 was estimated to be 756,743,722 metric tons worldwide, with a harvested area of 164,192,164 hectares (ha) [6]. Almost 90% of the world's rice is grown in Asia, especially South Asia, where more than 24.5 million ha are dedicated to rice production [7]. In Africa, with a harvested area of 17,174,644 ha, rice production was estimated to be 37,889,802 tons in 2020 [6]. Rice production faces biotic and abiotic constraints, among which drought stress is the major one in rain-fed ecosystems [8]. In East African countries, rice ecologies are subjected to severe drought, as in Asia [1,9]. In Burundi, failure to produce rice twice per year is mainly due to unsuccessful water management, for which coordination is very difficult [10]. In a study conducted by Gahungu [11] in Burundi, the major constraints on rice production were inputs, flooding and drought, which accounted for 41%, 30% and 29%, respectively. Estimated rice production in Burundi in 2020 was 150,000 metric tons harvested across 47,184 ha [6].

Trends in climate change predict a further increase in drought intensity [8]. The use of water for irrigation is a common approach to managing drought stress in lowland ecologies. However, investment in irrigation infrastructures for rice production is very expensive [10]. Therefore, growing drought-tolerant varieties may be the best option.

As drought tolerance is a complex trait subject to strong environmental influence, the best strategy is to select for a particular environment based on physiological or morphological traits and through the use of molecular markers [12]. This review attempts to assess the progress in breeding for drought and aroma and discover whether it has been possible to combine these traits in one rice variety.

2. Rice Consumer Preferences and Rice Fragrance

2.1. Preferences of Rice Consumers

Diverse agro-climatic, behavioural and sociocultural factors influence the preferences regarding traits of rice varieties, which change according to season, location, gender and market segment [13]. In general, low-income consumers like cheap rice that is homogeneous; they have less noticeable preferences for the physical and chemical characteristics of rice compared to high-income consumers [14].

A study conducted by Muhammad [15] in Indonesia showed that high-income consumers like rice with a good taste, medium-income consumers like rice cakes and low-income consumers prefer head rice. Rice attributes can either be extrinsic to the product, such as packaging, brand or label, or intrinsic, such as taste, kernel elongation after cooking, amylose content, gelatinization temperature, percentage of broken grains, colour and fragrance [14].

National and international markets have revealed an increasing demand for aromatic rice [16]. Aroma is the first factor guiding rice purchases among most consumers in markets in East Africa countries. Ugandans prefer rice that is aromatic, non-sticky, whole-grained and white. The urban consumers in Rwanda prefer aromatic and long-grain rice. Consumers in Tanzania prefer local aromatic rice [1]. In Burundi, urban consumers prefer good-quality rice that is aromatic with large grains [10], which is imported from Tanzania [17]. However, rural people and those in boarding schools, the military and police camps eat the cheapest medium-quality rice, which is produced in Burundi [10].

2.2. Aroma of Rice

The quality of rice can be described using its commercial value, its nutritional value or its organoleptic value [16]. Aroma is a superior rice grain quality trait that leads to a high price in national and international markets [18,19]. Volatile organic compounds are responsible for the characteristic features of aromatic rice varieties [20]. Aroma can be defined as a complex mixture of more than 500 volatile chemical compounds that influence rice fragrance [16]. Among these biochemical compounds, 2 acetyl-1-pyrroline (2AP) has been reported to be the most important for flavour in rice [18,21]. The 2AP compound is found in high concentrations in leaves during the early growth stage, reaching its peak at the booting stage and decreasing in the leaves at reproductive stage [19]. 2AP is actually transported from the leaves and stem sheath and accumulates in grains of aromatic varieties [21].

Different techniques are used for the isolation and quantification of 2AP concentration in rice. Among them, simultaneous distillation extraction (SDE) is a traditional and normalized method. Solid-phase microextraction (SPME) and supercritical fluid extraction (SFE) are new, very simple, rapid, efficient and mostly solvent-free methods [16]. These methods are currently combined with gas chromatography with flame ionization detection (GC-FID), gas chromatography–mass spectrometry (GC-MS), gas chromatography-olfactometry (GC-O) and sensory evaluation [18]. The levels of 2AP among different varieties are provided in Table 1.

Table 1. Levels of 2AP among different genotypes worldwide.

Genotype	Origin	Mean 2AP (%)	Aroma Status	Author
Agra 41	AfricaRice, Benin	0.1520 ± 0.0370	2.86 *	[22]
Agra 55	CRI, Ghana	0.1595 ± 0.0159	2.14 *	[22]
Ambemohar 157	India	0.0662 ± 0.0000	a	[18,23]
Basmati	India	0.0000113 ± 0.0000	a	[24]
Basmati 370	India	0.0451 ± 0.0000	a	[18,23]
IR 64	IRRI, Philippines	0.0000 ± 0.0000	na	[18,23,25]
Jasmine	-	0.0000146 ± 0.0000	a	[24]
Kala Jeera	IRRI, South Asia	0.00000005 ± 0.0000	a	[25]
Kala Namak-2	South Asia	0.00000009 ± 0.1000	a	[25]
Komboka	IRRI, Philippines	0.0957 ± 0.0354	2.21 *	[22]
Namche 2	NaCRRI, Uganda	0.0031 ± 0.0029	1.50 *	[22]
Nerica 4	AfricaRice, Ivory Coast	0.0000 ± 0.0000	1.14 *	[22]
Pusa Basmati 1	IRRI, South Asia	0.0000 ± 0.0000	a	[25]
Sintanur	-	0.000008 ± 0.0000	a	[24]
Supa 5	IRRI, Philippines	0.2445 ± 0.0268	2.79 *	[22]
Yasmin Aromatic	Egypt	0.3195 ± 0.0576	2.29 *	[22]

* = aroma score on a scale of 1–4 (1 = no aroma, 2 = slight aroma, 3 = moderate aroma and 4 = high aroma), a = aromatic, na = non-aromatic, CRI = Crops Research Institute, NaCRRI = National Crops Resources Research Institute, IRRI = International Rice Research Institute, - = unknown.

The 2AP concentration is influenced by many factors, including differences in rice varieties and environmental influences, such as temperature during ripening and soil type [26]. The factors that influence rice flavour and other rice characteristics are provided in Table 2.

Table 2. Factors influencing flavour and other rice grain attributes.

Attributes	Factors Influencing the Attribute (s)	Author
Aroma	Volatile organic compounds, including 2AP	[23,25]
Aroma	QTLs/genes	[27–29]
Flavour, aroma and taste	Timing of field draining, harvest time during ripening, harvest moisture content and final moisture content after drying, serving temperature of cooked rice	[29]
Flavour, taste and aroma	Milled rice storage temperature and time, degree of milling, evaluation methods, cultural practices, time of heating and cooking operations (washing, soaking, water-to-rice ratio)	[4,25,29]
Aroma/2AP	Deep application of fertilizers at 10 cm	[30]
Aroma/2AP	Optimum temperatures (20 to 30 °C) in area where rice is grown	[28]
Gel hardness and flavour	Growing location	[31]
Aroma, flavour and sweet taste-induced illusion	Rice surface colours	[32]

2.3. Molecular and Genetic Bases of Rice Aroma

Volatile organic compounds (VOCs) are reported to be responsible for flavour in basmati and jasmine rice [21]. More than 500 volatile chemical compounds have been reported to influence rice fragrance [16]. One of these, 2AP, is a strong flavour component that is present at higher concentrations in aromatic compared to non-aromatic varieties [21]. Thus, 2AP has been considered the key compound influencing aroma in rice [5]. Ocan et al. [33] recently found 41 VOCs to be significantly correlated with 2AP in 37 lines that are commonly grown in Uganda.

Some genetic studies have revealed a single recessive gene to be responsible for rice aroma, others discovered a dominant gene [26,34] or many genes controlling this trait [35]. Three quantitative trait loci (QTLs) have been reported to be associated with aroma in rice. The most significant QTL related to this trait is qaro8.1, located on chromosome 8 [26]. Another significant QTL for aroma, named qaro3-1, was mapped on rice chromosome

3 [35]. Furthermore, specific alleles of the badh1 gene located on chromosome 4 within the QTL qaro4.1 showed an association with aroma in rice varieties [26].

However, the major gene for fragrance was found in non-aromatic varieties in homozygote form [34]. A non-functional allele of the badh2 gene coding for the enzyme betaine aldehyde dehydrogenase was reported to be the main factor controlling aroma in rice. The functional allele of badh2 is responsible for the absence of aroma in some rice varieties [3,26]. Nineteen alleles of the badh2 gene have so far been reported to be associated with aroma in rice varieties. Among these alleles, the badh2-E7 allele was the most abundant in the evaluated aromatic rice varieties in Uganda [36]. Nevertheless, the badh2-p allele was reported to show the highest occurrence in aromatic rice varieties in India, higher than the badh2-E7 allele. This allele, badh2-p, was found in both indica and japonica types [3]. One functional marker of aromatic rice has been reported to be 8 bp deletion in exon 7, which is found in aromatic rice varieties all over the world.

However, some aromatic lines showed a 3 bp addition in exon 13 instead of the 8 bp deletion [37]. The deletions and additions are found in most of the reported alleles for the badh2 gene [36]. Bindusree et al. [3] reported that an 8 bp insertion in the promoter region of the badh2 gene was responsible for fragrance in Seeragasamba, an indica-type aromatic rice variety with short grains. Two important mutation events (A to T and T to A), followed by the 8 bp deletion "GATTAGGC", are also associated with aroma in rice [37]. In a study conducted by Akwero et al. in Uganda [36], 20 out of 23 aromatic accessions had the badh2-E7 allele with an 8 bp deletion and 3 SNPs.

3. Molecular Markers and Selection of Aromatic Rice Varieties

3.1. Markers Used in Crop Improvement

Different methods of screening for traits of interest have been implemented by breeders, using either classical markers or DNA/molecular markers [38]. Classical markers include morphological, cytological and biochemical markers. They have some disadvantages, including their limited number, the influence of the plant growth stages and various environmental factors.

Molecular markers are sequences of nucleotides and can be investigated through the polymorphisms between the nucleotide sequences of studied individuals [39]. Molecular markers allow greater selection accuracy with lower labour and time inputs and enable combinations of different target traits controlled by quantitative trait loci (QTLs) into a single cultivar [40].

The most commonly used molecular markers include restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism (AFLP), randomly amplified polymorphic DNA (RAPD), inter-simple sequence repeat (ISSR), simple sequence repeat (SSR), single-nucleotide polymorphism (SNP), retrotransposons and diversity arrays technology (DArT) markers [39].

These markers are useful for high-resolution genotyping for association studies and genomic selection, as well as QTL mapping and marker-assisted selection (MAS) [41]. For example, 54 random SNPs helped to divide rice cultivars into two groups, where aromatic genotypes belonged to the japonica group [42]. A competitive allele-specific polymorphism chain reaction (KASP) SNP enabled Addison et al. [43] to distinguish between aromatic and non-aromatic rice varieties in the United States of America. SSR markers were used by Singh et al. [35] to map three significant QTLs for rice aroma in recombinant inbred lines developed from a cross between aromatic and non-aromatic varieties in India.

Each kind of molecular marker has advantages and disadvantages depending on the specific purposes. SSRs, relatively speaking, have most of the desirable features and are consequently most commonly chosen for many crops [44,45]. However, SNPs are also considered an important type for marker-assisted breeding, even if they require more detailed knowledge about the specific single-nucleotide changes responsible for genetic variation among studied individuals [45]. SNPs are rapidly replacing SSRs because they are

more abundant, stable, amenable to automation and efficient and increasingly cost-effective. More details on these markers are provided in Table 3.

Table 3. Comparison of molecular markers most commonly used in crop improvement.

Marker *	Asset	Weaknesses
AFLP	Reliable, more instructive, highly reproducible	Dominant, requires high-quality DNA
DArT	Cost-effective, high throughput, high polymorphism, previous sequence information not needed, highly reproducible	Dominant, expensive to develop
Isozymes	Specific instrument not needed, easy to use, co-dominant	Lower polymorphism, influence of environment
ISSR	High polymorphism, simple and easily used, prior sequence information not needed	Poorly reproducible, requires high-quality DNA, fragments are differently sized
RAPD	Easily used, requires lower quantity of DNA, polymorphic	Dominant, requires high-quality DNA, poorly reproducible, not locus-specific
Retrotransposons	Simple, easily used, prior sequence information not used, highly reproducible	Dominant
RFLPs	Co-dominant, prior sequence information not needed	Takes a long time, requires high-quality DNA, expensive
SNP	Cost-effective, wide distribution in genome, previous sequence information not needed, highly reproducible, co-dominant	Expensive to develop
SRAP	Simple, reliable, bands isolated easily	Dominant, moderate-to-high throughput ratio
SSRs	Co-dominant, requires lower quantity of DNA, highly reproducible	Expensive to develop, presence of more null alleles, occurrence of homoplasy

* This table was constructed based on information from Iqbal et al. [46], Jiang [45] and Nadeem et al. [39].

3.2. Breeding for Aroma in Rice

It is difficult to select for aroma due to low selection efficiency, the weak contributions of individual QTLs and strong environmental influences [26]. The level of aroma expression in rice is affected by genetic factors, weather and soil conditions, agricultural practices and processing and storage factors [5]. Rice aroma is a complex trait for which expression is influenced by environmental factors. The same variety grown in different environments may reveal significant differences in levels of aroma expression [26].

Different methods have been used by researchers to select aromatic lines or varieties. These methods include sensory evaluation, electronic nose, near-infrared spectroscopy and gas chromatography methods [5]. Aroma strength can be analysed using gas chromatography, which is used to assess the amount of 2AP content in rice leaves and grains [18,33]. Aroma can be smelt after soaking rice grains in KOH solution [33,36,47]. However, KOH inhalation may damage nasal passages if too many samples are evaluated [36]. Sensory evaluation of aroma and other flavour attributes, such as taste, can be performed by cooking rice samples in a rice cooker [48].

DNA markers linked to aroma can be effectively used in breeding programs to target aroma gene [47]. Molecular markers made it possible to map three significant QTLs for aroma in a rice population developed from a cross between aromatic and non-aromatic varieties [35]. Finely mapped genes, such as badh2, may help breeders in developing aromatic lines [26]. A breeding approach integrating both phenotypic and genotypic selection was approved as being most efficient in plant selection [49]. Sensory analysis combined with the use of functional markers can help to accurately select rice genotypes that may be used to develop highly aromatic varieties [36].

4. Advances in Breeding for Drought Tolerance in Rice

Most of the work that has been done on rice drought-tolerance was conducted in Asian countries where several drought-tolerant varieties were released by the International Rice Research Institute (IRRI) [49–51]. In contrast, very few studies have so far been conducted on rice drought-tolerance in Africa [52–54].

4.1. Effect of Drought on Rice Growth and Production

Drought is one of the most destructive abiotic stresses and can cause yield losses up of to 10%, 50% and 100% in cases of mild, moderate and severe drought, respectively [9]. Drought stress affects rice at the morphological, physiological, biochemical and molecular levels. Its effects on rice include reduced germination, plant height, plant biomass, numbers of tillers, chlorophyll content, leaf number and size [55]. The morphological, molecular, physiological and biochemical responses of rice plants to drought stress induce delayed flowering with reduced yields due to reduced tillering, grain filling rates, spikelet fertility, numbers and sizes of panicles and grain size and weight [56]. Drought increases leaf rolling and drying and accumulation of osmo-protectants, such as proline, sugars, polyamines and antioxidants [55]. For many soils, it takes at least two weeks without rainfall to produce marked differences in drought sensitivity during the vegetative stage and at least seven days without rainfall during the reproductive stage to cause severe drought injury [57].

4.2. Genetic Basis of Rice Drought-Tolerance

Drought tolerance is a quantitative trait with complex phenotypes that are often further complicated by plant phenology [12]. In a study conducted by Swamy et al. [58], broad-sense heritability reached up to 78% for grain yield under drought. Many genes controlling drought tolerance have been reported.

These include OsALDH2–1 (LOC_Os01g40860), OsALDH2–2 (LOC_Os01g40870), OsWRKY45 (LOC_Os05g25770), dOsMSOD1 (LOC_Os05g25850), OsRCN1 (Os11g05470), OsbZIP79 (Os11g05480), OsbZIP80 (Os11g05640) and Os11g12530 [59].

Several quantitative trait loci associated with drought tolerance have been reported and their numbers vary from author to author depending on the types of trait and experimental conditions [12]. For example, there were 14 detected QTLs for the leaf relative water content, 9 for the slope of the relative water content, 12 for drought sensitivity, 3 for recovery ability and 1 for the relative crop growth rate in a study by Hoang et al. [59]. Sabar et al. [60] found two QTLs for total water uptake, two for the leaf drying score, one for the leaf dry weight, two for the deep root surface area, three for the deep root length, one for the leaf dry weight, one for tillers per plant and two for plant height. Swamy et al. [61] reported the presence of qDTY12.1 in 85% of evaluated lines, followed by qDTY4.1 in 79% of the lines and qDTY1.1 in 64% of the lines. These QTLs are common in drought-tolerant donors. Bernier et al. [62] found the qDTY12.1 on chromosome 12 in the Vandana/Way Rarem population explained about 51% of the genetic variance for yield under severe upland drought stress.

Kumar et al. [63] reported qDTY1.1 as major QTL for grain yield under lowland drought stress in the CT9993/IR62266 population on chromosome 1, explaining 32% of the genetic variance. Later, this QTL was reported to explain, on average, 58% of the genetic variation in the Apo/3*IR64 and Vandana/3*IR64 populations in an upland ecosystem [64].

4.3. Breeding for Rice Drought Tolerance

Breeding for drought tolerance is very complicated because different types of environmental stresses, such as high irradiance, high temperatures, nutrient deficiencies and toxicities, may challenge crops simultaneously [12]. Drought-tolerant genotypes can be directly selected based on their grain yield under drought conditions [50]. However, some traits that have strong positive relationships with yield have been highlighted and suggested for indirect selection to improve grain yield under drought stress [54].

Selection of drought-tolerant genotypes may consider the targeted rice growth stage [65]. Screening under drought stress conditions allows selection of the drought-tolerant plants within each line. Single plant selection was recommended to be performed in the F3 generation when developing pure lines [50]. Traditional breeding approaches emphasize phenotypic traits, but they are only partially successful because direct selection is hindered by low heritability and genotype selection is hindered by environmental interactions and genetic interactions, such as epistasis and polygenic effects [12].

Modified conventional breeding approaches involve an integrative and sequential phenotyping, genotyping and selection strategy to screen many genotypes, improving the assessment of plant response to drought stress [49]. Genotypic selection saves time and has been used as an important method to predict genotype performance [45]. However, QTL x genotype background interactions remain a big issue in drought tolerance improvement [38]. Sandhu and Kumar [49] recommended selecting parents for use in breeding programs based on their breeding values, utilizing best linear unbiased predictions (BLUPs). BLUPs were recently confirmed to be the most effective prediction method among the commonly used approaches in plant selection [66].

Advances in molecular biology have provided new opportunities for breeders to identify QTLs, refine them through fine mapping and move those regions into drought-susceptible varieties [50]. According to the IRRI, several QTLs with significant effects may be used to improve varieties in terms of grain yield. These are qDTY1.1, qDTY2.2, qDTY3.1, qDTY3.2 and qDTY12.1 for reproductive-stage drought in lowland ecosystems and qDTY2.3, qDTY3.2 and qDTY12.1 in upland ecosystems [50]. More information about these QTLs is provided in Table 4.

Table 4. Major QTLs for rice drought-tolerance recommended by the IRRI in lowland and upland ecologies for grain yield and reported QTLs for aroma.

QTL Name *	Cross between	Marker Interval	LOD	R^2	Ecology	Chr	Author
qDTY1.1	N22 and IR64	RM11943–RM12091	2.5	16.9	Lowland	1	[67]
qDTY2.2	IR646 and Aday Sel.	RM236/RM279–RM555	6.5	11.2	Lowland	2	[68]
qDTY2.3	Kali Aus and IR64	RM573–RM213	-	9	Lowland	2	[69]
qDTY2.3	Kali Aus and IR64	RM263–RM573	-	7.4	Upland	2	[70]
qDTY3.1	IR55419-04 and TDK1	RM168–RM468	6.3	7.9	Lowland	3	[71]
qDTY3.1	IR55419-04 and TDK1	RM168–RM468	3.5	15	Upland	3	[58]
qDTY3.2	Sel. and Sabitri	RM569–RM517	10.1	23.4	Lowland	3	[72]
qDTY3.2	Moroberekan and Swarna	id3000019–id3000946	-	19	Upland	3	[50]
qDTY12.1	Vandana and Way Rarem	RM28048–RM511	34	33	Upland	12	[49,62]
qDTY12.1	IR74371-46-1-1 and Sabitri	RM28166–RM28199	-	23.8	Lowland	12	[73]
qaro8.1	Pusa 1121 and Pusa1342	RM223–RM80	11.54	0.189	-	8	[74]
qaro3-1	Pusa 1121 and Pusa1342	RM5474–RM282	3.20	0.103	-	3	[74]
qaro4-1	Pusa 1121 and Pusa1342	RM5633–RM273	3.30	0.061	-	4	[74]

* = The first 10 quantitative trait loci (QTLs) are for rice drought-tolerance while the last 3 are for aroma. LOD = likelihood of odds, R^2 = percentage of yield phenotypic variance explained by the QTL, - = missing information, Chr = chromosome.

Recently, high-density linkage maps helped to identify two novel consistent QTLs (qDTY2.4 and qDTY3.3), along with qDTY1.1, that are free from any undesirable linkages to tall plant height/early maturity [75]. The yields of grown varieties can be appreciably improved by pyramiding three or more major QTLs with a consistent effect [38,50]. Dhawan et al. [51] successfully introgressed qDTY1.1 from Nagina 22, a pure line, into Pusa Basmati 1, a popular cultivar in India. The performance of the near-isogenic lines developed was good under drought stress and the mean yield varied between 0.57 t/ha and 1.72 t/ha. Lines with good performance were selected based on indices calculated using the yield BLUP.

Improved lines with different QTLs for drought tolerance have been identified and released, mostly in Asia but also in a few countries in Africa. The plant height of the released varieties varied between 90 and 130 cm, their days to maturity varied between 105 and 125 and their potential yield varied between 197 and 3831 kg/ha under drought stress [49,50]. For example, IR74371-54-1-1, IR79913-B-176-B-4, IR81412-B-B-82-1, IR81023-B-116-1-2, IR72667-16-1-B-B-3 and IR81047-B-106-2-4 were released in the Philippines between 2009 and 2013 [50]. IR 86857-101-2-1-3, IR 83383-B-B-129-4, IR 86781-3-3-1-1 and IR 84878-B-60-4-1 were also released in the Philippines between 2014 and 2016 [49]. Between 2010

and 2011, IR74371-46-1-1, IR79971-B-191-B-B and IR74371-70-1-1 were released in Nepal, Indonesia, India and Bangladesh, respectively [50]. IR 55423-01, IR 83388-B-B-108-3 and IR 82635-B-B-75-2 were released in India, Nepal and Bangladesh, respectively, and 2012 and 2014 [49]. IR 82589-B-B-84-3 was released in Bangladesh for drought tolerance in lowland ecosystems [49].

In Africa, IR77080-B-B-34-3 and IR74371-54-1-1 were released in Mozambique and Nigeria, respectively, in 2013 [50]. IR 82077-B-B-71-1 and IR 80411-B-49-1 were released in Malawi in 2015. A study was conducted in Egypt in which potentially drought-tolerant rice lines were identified [52].

NERICA 4 and NERICA 10, followed by NARIC-2, were identified to be the most drought-tolerant among widely grown upland varieties in East Africa [53]. However, there is no information about their use in breeding programs.

5. Development of Aromatic Drought-Tolerant Rice Varieties

Market-led breeding is an approach targeting location-specific varieties based on the preferences of consumers, producers and other value-chain actors [13].

In general, non-aromatic rice varieties have appreciable agronomic performance and are high yielding, adapted to environmental conditions and grown in most rice-producing countries. The opposite can be observed for aromatic rice varieties [76]. Information about combining both aroma and drought tolerance in one rice variety is limited. In Burundi, previous research work aimed to improve blast resistance in aromatic varieties, including Supa 234 [77]. There are no published reports on the improvement of drought tolerance in these varieties. Luzi-Kihupi et al. [78] reported that the rice breeding program in Tanzania was emphasizing different traits, including drought tolerance and aroma. However, there are not yet any reports on combining these traits in one rice variety. Studies conducted in Uganda revealed that genotypes MET 3, SUPA 1052, Namche 1, ART-4 and BASMATI 370 exhibited stable 2AP levels. These genotypes were recommended for further use in breeding programs for aroma improvement [79]. Aroma is the main rice characteristic that guides the adoption of varieties, especially in Kenya and Tanzania. Nevertheless, the drought tolerance levels of most of the aromatic varieties that were released in these countries up to 2013 have not been reported [80].

Sabar et al. [60] produced a cross between Super Basmati, an aromatic rice variety sensitive to water stress, and IR55419-04, a non-aromatic variety that is drought-tolerant. However, they did not report the aroma status in the developed progenies. Steele et al. [81] reported the presence of aroma in near-isogenic lines developed from a cross between Azucena and Kalinga III. However, they did not conduct any formal analysis for aroma in these lines. Waheed et al. [65] reported one QTL on chromosome 7 and another on chromosome 11 for shoot dry weight and water uptake under drought conditions in recombinant inbred lines (RILs) developed from a cross between Super Basmati, an aromatic variety, and Azucena, a drought-tolerant cultivar. Nevertheless, they did not determine the aroma status in these lines. Biolistic transformation enabled Ganguly et al. [82] to develop transgenic rice from Pusa Sugandhi 2 (PS2), an aromatic indica rice cultivar. Transgenic plants that were grown in pots exhibited tolerance to drought stress. However, their performance in the field was not reported.

In personal communication, Bashir et al. [83] stated that improved plants based on local basmati varieties performed better under drought stress compared to the control, but no variety has yet been approved for release to farmers. In another study, near-isogenic lines developed from a cross between Pusa Basmati 1, an aromatic parent, and N22, a non-aromatic parent, had good cooking grain quality and were as aromatic as the Basmati parent, scoring 2 with the panel. Furthermore, these lines were drought-tolerant and were proved to successful introgress the major quantitative trait loci qDTY1.1 into a basmati variety [51]. In a study conducted by Arsa et al. [84], drought stress increased 2AP compound content and related aroma scores compared to control. In fact, aroma is expected to increase due

to increases in 2AP content in areas affected by drought compared to places with normal rainfall [85].

6. Concluding Remarks

Aroma is one of the grain quality characteristics that attract consumers around the world. This trait is mainly controlled by the badh2 gene, but its expression is strongly influenced by environmental factors.

Sensory evaluation combined with the use of functional markers seems to be the best approach to successfully select aromatic rice varieties. Aromatic rice varieties are reported to be low yielding and less adapted to environmental conditions, including drought stress. Researchers have tried to identify major QTLs for drought tolerance in rice and introgress them into varieties with other preferred traits, such as high yield and high grain quality. The IRRI has recommended QTLs for drought tolerance improvement in lowland and upland ecosystems. More details on the performance of the developed lines are still needed. Most of the research on drought tolerance has been undertaken in Asia, and there is very little information about breeding for rice drought-tolerance in Africa. Most African countries, including Burundi, have no published reports on rice drought-tolerance. However, in Burundi, the rice breeding program aims to improve aromatic varieties for drought tolerance for further release to farmers. It has been demonstrated that it is possible to combine drought tolerance and aroma in one variety. However, there are not yet any published reports on the release of aromatic drought-tolerant rice varieties. Future breeding programs could focus on improving aromatic rice varieties for drought tolerance to meet the preferences of both farmers and consumers in Africa.

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