

Improvement of the eating and cooking qualities of rice: a review

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ABSTRACT: Yet rice feeds the largest number of people in the world. At the same time rice is very flexible and grows practically all over the world. The demand for superior grain quality represents a major issue in rice (*Oryza sativa* L.) breeding. Eating and cooking qualities (ECQs) are important determinants of cooked rice grain quality. ECQs comprise three physical and chemical characteristics of starch in the endosperm: amylose content (AC), gel consistency (GC) and gelatinization temperature (GT). Nowadays, scientists and breeders are more and more focused on improving the quality of rice for different purposes and markets. For instance, people in the Far East prefer sticky and soft rice, while in India, a non-sticky type is preferred. Consumers from developed countries ask mainly for grain with good cooking quality and eating characteristics, but in many developing regions, nutritional value is crucial as rice is the most consumed staple food. Grain quality is a general concept which covers many characteristics ranging from physical to biochemical and physiological properties. Improving grain-quality is an important goal in rice breeding programs. One vital step is to find major quantitative trait loci (QTLs) for quality related traits and then investigate the relationships among them.

Quantitative trait locus (QTL) analysis that entails genome-wide mapping has been a widely applied strategy for 20 years. Using various rice populations, researchers have identified many QTLs for quality traits in rice.

Keywords: Rice (*Oryza sativa* L.), Eating and cooking quality, conventional breeding, Quantitative trait loci (QTL)

INTRODUCTION

Oryza Sativa L (Rice) is a vital worldwide agriculture product. It is one of the leading food crops of the world as more than half of the world's population relies on rice as the major daily source of calories and protein (Rohit , 2011). Botanically, cultivated rice belongs to the Poaceae family and includes two species: *Oryza sativa* L. (commonly known as Asian rice) and *Oryza glaberrima* Steud. (commonly known as African rice) (Linares, 2002). rice in this review and many other papers refers to *O. sativa* only, unless otherwise specified. *O. sativa* is comprised of two subspecies, *indica* and *japonica* (Liu , 2013). But, with the achievement of production goals, acquisition of better intrinsic quality of rice has been identified as one of the possible avenues and challenges of the next decade (Abeywickrama , 2010). With the increasing awareness, people tend to be more health conscious and more interested on nutritional quality of food (Abesekara , 2008). The eating and cooking qualities (ECQs) of rice are important in determining its economic value in the export market and for consumer acceptance (Pingali , 1997). The

preferences for rice eating and cooking qualities within a certain region and culture may not be accepted by other cultures. In general, the Japanese prefer short grain, sticky rice that is usually used in making sushi. Conversely, in India, Pakistan and the Middle East, Basmati rice is well-liked due to its fragrance and its elongated, dry grains when cooked (Suwannaporn and Linnemann, 2007). Rice grain quality is a complex characteristic including many components such as appearance, cooking qualities and eating qualities (Rabiei , 2004). Rice bran is an underutilised by-product of rice milling, despite being a nutrient-dense product and a rich source of protein, fat, carbohydrate, and a number of micronutrients such as vitamins, minerals, antioxidants, and phytosterols (Schramm , 2007; Iqbal , 2005; Renuka and Arumughan, 2007). QTL mapping was introduced as a method for understanding the molecular and genetics mechanisms of rice quality (Li , 2003; Fan , 2005; Sun , 2006). Many QTLs for rice quality have been detected. Twelve main-effect QTLs were identified for rice quality using a RIL population using a seed descent method (Li , 2003; Fan , 2005). Wendy (2014) identified 12 main-effect QTLs for rice ECQs using a doubled haploid (DH) population derived from a cross between two indica varieties. Conventional breeding has developed traditional varieties with improved eating and cooking qualities. intensive genetic studies have pinpointed the genes that control eating and cooking quality traits. Advances in genetic studies have developed molecular techniques, thereby allowing marker-assisted breeding (MAB) for improved eating and cooking qualities in rice (Wendy , 2014).

THE GENUS ORYZA

Rice belongs to the genus *Oryza* and family Poaceae tribe Oryzaceae. It originated in Asia (*O. sativa* L.) and West Africa (*Oryza glaberrima* Steud) (Vaughan et al., 2003). According to Vaughan (2004) the genus *Oryza* is made up of 23 species, with two species being cultivated (*O. sativa* and *O. glaberrima*), while the other 21 are not domesticated. The *O. sativa* has further three subspecies; indica Kato, japonica Kato and javanica (Roschevitz, 1931). The subspecies japonica has two strains, namely tropical and temperate which is commonly sticky rice due to high amylopectin content. Indica are found in tropica land sub-tropical regions, while javanica are mainly grown in Indonesia and japonica are found in temperate regions. In terms of grain characteristics; the indica varieties have long grains. While, japonica have short grains and javanica have broad grains (Jones , 1997; Khush, 2005).

Grain Quality in Rice

Rice grain quality is determined by its physical and physicochemical properties. Physical properties include kernel size, shape, milling recovery, degree of milling and grain appearance (Cruz and Khush, 2000). Physicochemical properties of rice are determined based on amylose content, gel consistency and gelatinization temperature (Rohilla , 2000). In rice, eating and cooking qualities are mainly controlled by the physicochemical properties which greatly influence the consumer's affinity (Rohilla , 2000). Therefore, eating and cooking quality can be considered as a vital intrinsic quality component of rice grains that have to be focused in future rice breeding programmes to meet market demands at both local and international level. Volume expansion over cooking is another quality parameter which influences the edible volume which is the final output after cooking (Rebeira , 2014).

conventional breeding for eating and cooking qualities in rice

Conventional breeding was implemented in the past to improve and develop varieties with better eating and cooking qualities. Conventional breeding has undeniably wrought significant contributions. Jennings (1979) stressed that conventional backcrossing is useful for selecting traits that are controlled by a single gene. However, grain quality is controlled by quantitative trait loci (QTL), which show continuous phenotypic variation and lack discrete phenotypic segregation in the progeny (Yano and Sasaki, 1997). In addition, due to the triploid endospermic nature of the genotypes, genetic complexity and interactions between genotypes and the environment, users of the conventional breeding techniques have encountered difficulties in improving the cooking and eating quality traits (Wendy , 2014).

a- Improvement by backcrossing method

One effort of the International Rice Research Institute (IRRI) is the conventional backcrossing program between Peta, which was released in 1940, and Belle Patna, released in 1961 (Jennings , 1979). Peta has chalky endosperm and a low gelatinization temperature, whereas Belle Patna has clear endosperm and an intermediate gelatinization temperature. In a conventional backcrossing program, selection is based on the phenotype of the progenies. Individuals with eating and cooking qualities similar to Belle Patna will be selected and crossed with Peta. After a series of backcrosses, the end products are lines with a morphology similar to that of Peta, besides having grains similar to those of Belle Patna (Wendy , 2014).

b- Improvement by pedigree method

Another example of a cultivar with superior cooking, eating and processing quality is Newrex. Newrex was released in Texas during 1979, and is an example of a variety developed using the conventional pedigree method (Bollich , 1979; Hodges , 1979). Newrex was developed from a selection in the F₅ generation from Beaumont cross No. B686A (Bollich , 1979; Hodges ,1979).

Quantitative trait loci for grain-appearance quality traits

This trait for appearance is generally defined according to grain length (GL), grain width (GW), grain thickness (GT), and chalkiness of the endosperm (Juliano and Villareal, 1993). However, quality is a complex quantitative trait controlled by numerous genes that have low heritability and expression that is significantly influenced by the environment (Lou , 2009). Using various rice populations, researchers have identified many QTLs for appearance traits and thousand-grain weights (TGW) (Hittalmani , 2002; Li , 2004b; Rabiei , 2004; Wan , 2005; Yoon , 2006; Bai , 2010). Moreover, some major effect QTLs for grain size and weight have been reported. They include GS3, controlling grain length and TGW (Fan , 2006), GW2, for grain width and TGW (Song , 2007), qSW5/GW5, for seed width, as found on Chromosome 5 (Shomura , 2008; Wan 2008; Weng 2008), and GIF1 and OsSPL14, also for TGW (Wang , 2008; Jiao , 2010). Later, GS5 was cloned on Chromosome 5, it controls grain size by regulating grain width, filling and weight (Li , 2011). In addition, qPGWC-7, the first finely mapped QTL for grain chalkiness, has been located to a 44-kb DNA fragment containing 13 genes (Zhou , 2009). Finally, several other QTLs for grain shape (grain weight) have been fine-mapped, e.g., gw3.1, gw8.1, and gw9.1 (Li , 2004a).

Improving quality by QTL pyramiding in rice

Large numbers of quantitative trait loci (QTL) affecting rice quality traits have been identified and mapped in various mapping populations (Xing and Zhang, 2010), in order to apply marker assisted selection (MAS) to improve breeding efficiency. Several QTL with major effect on agriculturally important traits such as grain number (Gn1a), grain size (GS3), grain weight (qSW5/GW5), and heading date (Hd1, Hd3a), and a major QTL (i.e., Ghd7) with large pleiotropic effects on heading date, plant height, and number of spikelets per panicle have been cloned (Yano , 2000; Kojima , 2002; Ashikari , 2005; Fan et 2006; Song , 2007; Weng , 2008; Shomura , 2008; Xue , 2008). With the accumulated information on these cloned QTL and their closely linked markers affecting traits of agronomic importance in rice, accumulating beneficial genes using MAS has become a straightforward approach for improving target traits in rice (Ashikari , 2005; Ashikari and Matsuoka, 2006; Ando , 2008). Peng (2012) developed near-isogenic lines (NIL) containing one or more target genes by marker-assisted transfer of '93-11' alleles at qHD8, qHD7, and qHD6.1, and the GS3 gene for grain size into 'Zhenshan97'. The pyramid line NIL (qHD8+GS3) had higher longer grains, and a more suitable heading date than 'Zhenshan97'. Comparison of the NIL showed existence of epistasis between alleles at different loci and background effect on qHD8, which are very important for pyramiding of desirable alleles at the target QTL.

Allelic variation for candidate genes, responsible for grain shape in rice

Grain shape, as defined by its length, width and their ratio, is an important measure of end-use quality in rice. Both grain length and width are polygenically inherited and controlling loci have been identified on each of the 12 rice chromosomes. Some of them (qGL7, qGL7-2, GW2, qSW5, GW5, GS3 and GS5) have been fine mapped and even isolated in recent years (Tan , 2000). Both qGL7 and qGL7-2 underlie the determination of grain length, separated from one another by 13.2 cM on the long arm of chromosome 7, and their locations have each been narrowed to within a *300-kb segment (Bai , 2010; Shao , 2010). The genomic location of the grain shape QTLGS7 was narrowed to lie within a 4.8-kb segment on chromosome 7 (Shao , 2012)

mapping of grain length QTLs in rice

Grain dimensions (length, breadth and length/ breadth ratio) are quantitatively inherited, it is difficult for the breeders to efficiently improve grain appearance using conventional selection methods (Mckenzie and Rutger, 1983; Tan , 2000). For rice millers, the proportion of head and broken rice on milling is an important attribute which is affected by the grain shape and size (Singh , 2002). Lin (1995) identified twelve QTLs for grain dimensions, including five for grain length, two for grain breadth, and five for grain thickness on chromosomes 5, 6 and 7. A consistent QTL for grain length has been mapped on rice chromosome 7 (grl7-1, qGL7, qGL7-2) using three different mapping populations (Amaravathi , 2008; Bai , 2010; Shao , 2010). Singh (2012) identified two significant quantitative trait loci (QTL) intervals on chromosomes 1 and 7 for grain dimensions in Basmati rice using a population of recombinant inbred lines (RILs) from cross between Basmati variety Pusa 1121 and a short grain non-aromatic variety Pusa 1342.

For fine mapping of these QTLs, 184 F6 RILs were grown and phenotyped in the normal rice growing season at two different locations.

Amylose content (AC) in rice

Waxy rice has near zero amylose, and is used for special foods such as desserts and snacks. High amylose cultivars (>25%) are common in indica rice, and are dry and fluffy on cooking, often becoming hard after cooling. Low amylose cultivars (15–20%) are soft and sticky, and include nearly all temperate japonica cultivars. Intermediate amylose (20–25%) rice is soft but not sticky, and is widely preferred by most consumers. AAC is largely genetically controlled by the *Wx* locus on chromosome 6, or specifically by the amount of *Wx* protein present (Wang, 1995). Therefore, high AC will lead to the deterioration of viscosity, softness, luster, and palatability, but AC does not absolutely determine the texture of cooked rice because the palatability of cooked rice with similar AC may vary greatly. However, the rapid viscosity analyzer (RVA) profile characteristics of rice endosperm starch can make up for the deficiency in using AC to appraise the palatability of cooked rice. Namely, RVA, breakdown viscosity (BDV) and setback viscosity (SBV) can be used to evaluate the palatability differences of cooked rice with similar ACs (Shu, 1998; Wu, 2001). By using nine segregating populations derived from the hybrid combinations of high or intermediate AC × low AC rice varieties, several research groups have detected one major gene controlling AC in the *Wx* gene on chromosome 6 (He, 1999; Tan, 1999; Lanceras, 2000; Bao, 2003; Li, 2003; Septiningsih, 2003; Aluko, 2004; Tian, 2005). Meanwhile, three genetic populations derived from the hybrid combinations of high or intermediate AC × low AC rice varieties were used to detect quantitative trait loci (QTLs) for BDV and SBV. It was found that BDV and SBV are mainly controlled by the *Wx* gene (Bao, 2000). Therefore, the *Wx* gene can affect BDV and SBV through controlling AC in rice. However, it's not yet known why BDV and SBV can be used to effectively appraise the palatability of cooked rice with similar AC.

Gelatinization temperature (GT) in rice

Gelatinization temperature (GT) is another important quality predictor in determining the cooking quality of rice. Low GT rice needs less energy input during cooking than high GT rice. GT in rice is mainly controlled by the starch synthase IIa (*SSIIa*) gene which is located on chromosome 6 (Umamoto, 2002, 2004; Waters, 2006). Functional single nucleotide polymorphisms (SNPs) found in the *SSIIa* closely associate with GT and amylopectin structure (Umamoto, 2002, 2004; Waters, 2006). Especially, two contiguous SNPs (GC/TT) in *SSIIa* have a very strong association with GT (Waters, 2006).

gel consistency in rice

In order to enable rice improvement programmes to select for soft-textured rices, the gel consistency test was developed as an indirect method for routine screening of cooked rice hardness for rices with amylose above 25% (Juliano, 1985). The gel consistency test measures the distance travelled, after 1 h, of a gel made from rice flour and KOH. For rices with a hard texture, the gel is short, travelling only a small distance, but for those with soft texture, the gel is viscous and travels up to 10 cm within the hour (Cagampang, 1973). Gel consistency (GC) is a standard assay used in rice improvement programmes to determine whether rice cultivars/breeding lines of high amylose content are soft or firm textured when cooked (Tran, 2011). A number of studies, using different mapping populations, have located the gene for gel consistency at the *Wx* locus (Bao, 2002; Bao, 2003; He, 2006; Lanceras, 2000; Li, 2003; Tang, 1991; Tian, 2005; Wang, 2007), which encodes the enzyme responsible for amylose synthesis. Single nucleotide polymorphisms (SNPs) have been found at the splice site of exon 1 (Cai, 1998; Isshiki, 1998; Wang, 1995), exon 4 (Mikami, 2008), exon 6 (Chen, 2008a; Larkin and Park, 2003; Mikami, 2008) and exon 10 (Chen, 2008b; Larkin and Park, 2003; Mikami, 2008), of the *Wx* gene. Different haplotypes of the *Wx* gene, based on the SNPs at exon 1, 4 and 6, determine the different classes of amylose (Chen, 2008b; Mikami, 2008). However, both states of the SNP on exon 10 are found in the high amylose class, and this SNP associates with the firming of the gel as the temperature cools from 95 to 50 °C in a rapid visco analyser (RVA) (Chen, 2008b).

In a study, Tran (2011) showed that sequence variation in exon 10 of the *Waxy* (*Wx*) gene associated with GC using RILs derived from parents with high amylose content that differ in GC. The association was validated using a diverse set of traditional varieties, selected on the basis of amylose content, from the generation challenge programme.

Aroma in rice

Aroma in cultivated rice (*Oryza sativa* L.) is being appreciated more and more by many people and represents a high-value-added trait. Also, high milling returns and good cooking quality are often associated with aromatic or

scented rice (Nagaraju , 1975; Tripathi and Rao, 1979). Many studies on the genetic control of the aroma trait in rice have been reported (Ahn , 1992; Lin, 1990; Nagaraju , 1975; Raghuram and Sathyanarayanaiah, 1980; Sood and Siddiq, 1978; Tripathi and Rao,1979; Yano ,1992). Some of the authors concluded that the trait under goes monogenic inheritance, while others favoured the idea that two or three recessive or dominant genes participate in the construction of the trait. Thus, the problem seemed to be an interesting one to investigate with tools permitting an intensive study of the genetics of aroma, and notably, to locate the gene(s) involved in the expression of this character. Ahn (1992) were the first investigators to combine the utilisation of molecular markers with that of near-isogenic lines (NILs), in order to locate a gene controlling aroma in rice. They found that the gene is located at the end of a linkage group belonging to chromosome 8, at 4.5 cM (centimorgans) from the restriction fragment length polymorphism (RFLP) marker RG 28. Buttery (1983) identified 2-acetyl-1-pyrroline (AcPy) as the major component of rice aroma. The aroma of both aromatic and non-aromatic rice cultivars consists of a complex mixture of odor-active compounds. Several authors have studied the composition of the cooked rice volatile fraction, identifying a large number of components and defining several key-aroma compounds (Bryant , 2011; Champagne, 2008; Jezussek , 2002; Widjaja ,1996a; Yang ,2008; Zeng , 2008). These include saturated and unsaturated aldehydes, alcohols, and cyclic compounds; in particular, hexanal, 1-octen-3-ol and 2-pentylfuran are markers of both quality and ageing, while 2-acetyl pyrroline (2-AP) is one of the aroma quality markers for aromatic rice (Buttery,1988; Champagne, 2008; Grimm, 2001; Laguerre , 2007; Mahatheeranon,2001; Widjaja , 1996a). Additional information on release of key-aroma compounds was also obtained from quantitation and its dependence on grain shape and chemical composition. Heptanal/1-octen-3-ol and heptanal/octanal ratios were also defined as characterising the aroma quality indices of the six Italian rice cultivars investigated (Alessandra , 2015).

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