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Chapter

Rice Grain Quality: Current Developments and Future Prospects

Neerja Sharma and Renu Khanna

Abstract

Grain quality of rice is more complex than other cereals, since it is mostly consumed as whole grain in countries where it serves as a staple food. Quality characteristics are major determinants of market price and include milling, physical appearance, cooking, sensory, palatability, and nutritional value. A better understanding of the factors that control these quality characteristics will be useful for developing new breeding strategies. In this chapter, we will review the progress made toward improvement of important grain quality traits along with their genetic basis. This chapter will also give innovative insights into the knowledge gained through new tools that integrate grain quality with high yield in the present scenario of diminishing natural resources and environmental fluctuations.

Keywords: rice, cooking traits, sensory quality, appearance quality, genetic basis, nutritional quality

1. Introduction

Rice is the staple food of half of human population globally and fulfills over 21% calorific requirement of world population. About 90% of the rice is produced and consumed in Asia. During 1960s to 1970 when the major rice producing countries relied on rice as a subsistence crop, the major emphasis was on high yield. As these countries attained food security and standard of living of the rice eating population improved, consumers became conscious about grain quality. Their potential as exporters of surplus rice produced, gave a further impetus to grain quality research. The world population is expected to reach 9.8 billion from the current 7.6 billion by 2050 (The *World Population Prospects: The 2017 Revision*, published by the UN Department of Economic and Social Affairs). The current challenge to rice improvement programs is to feed the ever-growing population with diminishing natural resources and environmental fluctuations on one-hand and varieties that have grain quality that the consumer demands, on the other. The economic value and the consumer acceptance/preference of a rice variety depend on rice grain quality [1–3]. Rice grain quality is a complex trait and is therefore difficult to define comprehensively. Rice quality comes from a polygenic group of traits that are affected by environmental factors, crop management and the resulting interactions among these. It involves the physical appearance, milling quality, cooking, sensory and nutritional value. The emphasis laid on each of these traits depends

on regional consumer preference, market demand, and intended functional use. For instance, consumers in North Asia prefer short and bold rice grains with low amylose, whereas in several states of India, most parts of Pakistan and Iran prefer long, slender grains having intermediate amylose content [4]. One of the major challenges facing the rice improvement programs is to have simple, robust, high throughput methods for assessing various quality traits that can reflect consumer preference. We review here the key grain quality traits and the classical and modern methods used in rice improvement programs to evaluate them. A comprehensive list of quality evaluation methods for different parameters is given in **Table 1**.

S. No.	Quality parameter	Recent quality evaluation method(s)
Cooking and eating quality		
1.	Apparent amylose content	HPLC-SEC [5] DSC [6] NIRS [7, 8]
2.	Cooking time	Measured indirectly by estimating gelatinization temperature using DSC [6]
3.	Kernel elongation	None
4.	Grain volume expansion	None
5.	Gelatinization temperature	Measurement of starch gelatinization by DSC, photometric method, alkali photometry, or RVA pasting curve [9]
6.	Pasting properties	Brabender visco-amylograph, micro Visco-analyzer [10, 11]
Textural and sensory quality		
7.	Gel consistency	None
8.	Texture profiling	Instron hardness testing. Parallel plate plastometer, consistometer, texturometer, hardness tester, viscoelastograph, tensipresser, surface tensiometer, Kramer shear or texture press, extrusion and back extrusion, puncture test
9.	Sensory evaluation	None
10.	Aroma profiling	Detection and quantification of 2-acetyl-1-pyrroline by GC-MS [3] Detection of total volatile metabolome by GC-MS
11.	Rancidity test	Detection of free fatty acids by titration or colorimetry [12]
Nutritional quality		
12.	Protein content	NIRS [13]
13.	Lipid content	Metabolomics approach using LC-MS [14] or GC-MS
14.	Resistant starch content	None
15.	Nonstarch polysaccharide content and dietary fiber content	CE [15], HPLC coupled with mass spec detector
16.	Micronutrients	AAS, ICP-OES, ICP-MS [16, 17], XRF
17.	Digestibility	Time-resolved NMR [18]

Table 1.
Summary of evaluation methods used for determining rice quality.

2. Rice quality traits

2.1 Appearance quality

Major factors determining market value are immediately discernible by the consumers and include physical properties like, whiteness, translucence, uniform shape and yield of edible polished grain. Visual characters of rice grains like grain dimensions, chalk, color and whole grain recovery are important attributes that affect the choice of consumers' and millers. Therefore, these are among some of the first selection criteria in varietal improvement programs [19–21]. Grain size depends on the length of the grain in its greatest dimension, while grain shape is based on length-to-breadth ratio [20]. The classification of rice samples based on size and shape is not standardized across different countries and different marketing areas [22, 23]. The routine classification system used by the International Rice Research Institute (IRRI) breeding programs for grain size is as follows: short (≤5.50 mm), medium/intermediate (5.51–6.60 mm), long (6.61–7.50 mm), and very long (>7.50 mm). Similarly, the grain shapes of rice can be described based on the length-to breadth ratio values, and the classification used in IRRI is: bold (≤2.0), medium (2.1–3.0), and slender (>3.0) [23]. Chalky areas in rice grains present on the dorsal (white belly), ventral side (white back) or in the center are opaque white parts of the endosperm and generally, associated with poor quality in many rice markets thus these grains have lower market acceptability [24]. Classification of the grains is based on the proportion of the grain that is chalky: none (0%), small (<10%), medium (10–20%), and large (>20%) [23, 25, 26]. The starch granules in the chalky areas of the grain have air spaces between them, are small and less compact compared to bigger and tightly packed granules in translucent areas and hence are more prone to breakage during milling [27, 28]. Chalk thus affects both the esthetic value and head rice yield decreasing the marketability of rice. Chalk is caused by both environment and genetic factors. Increase in nighttime air temperatures during grain filling stage can increase chalk and reduce head rice yields [29, 30]. Rice grain dimensions are conventionally measured using transparent rulers, vernier calipers and photographic enlargers [31], while the proportion of grain that is chalky is visually scored. Measuring of grain dimensions using manual methods is both labor intensive and time-consuming. Moreover, visual scoring of chalk involves subjectivity. Now-a-days, image analysis methods are being used in advanced laboratories that are very convenient and objective [31–33].

Yin et al. [34] divided the dimensions of grain shape into grain length, grain width, length-to-width ratio, grain area, grain circumference, grain diameter, and grain roundness. Several important genes have been characterized in previous studies that control grain shape traits, e.g., GS3 [35] affecting grain length, qSW5/GW5/GSE5 [14, 36, 37] affecting grain width, GL7/GW7 [38] shaping both grain length and grain width. In various studies across different environments and genetic backgrounds, a major effect quantitative trait loci (QTL) for grain length, *GS3* was identified near the centromeric region of chromosome 3 [12, 35, 39, 40]. However, a functional marker in the second exon of GS3 was identified that explains 80–90% of the kernel length variation [41]. Bai et al. [42] identified four QTLs for grain length on chromosomes 3 and 7; and 10 QTLs for grain width and 9 QTLs for grain thickness on chromosomes 2, 3, 5, 7, 9 and 10, respectively. A total of 28 QTLs were detected, of which numerous were reported for the first time. Four major and six minor QTLs for grain shape were also identified in their study. Later on, *qGL7* was narrowed down to an interval covering a 258 kb region in the Nipponbare genome between InDel marker RID711 and SSR marker RM6389, and co-segregated with

InDel markers RID710 and RID76. The dimensions of grain shape were dissected by Yin et al. [34] into grain length, grain width, length-to-width ratio, grain area, grain circumference, grain diameter, and grain roundness. By contrast, a few QTLs for grain chalkiness have been finely mapped and characterized functionally. *Chalk5* was the first cloned and functionally characterized gene that controls rice grain chalkiness which encodes a vacuolar H+-translocating pyrophosphatase [43]. Two methods are commonly applied for genetic dissection of these complex traits: QTL mapping in bi-parental recombinant populations and genome-wide association studies (GWAS) using diverse varieties. In general, genetic diversity and mapping resolution are limitations in the bi-parental linkage approach, while conventional GWAS is often mystified by complicated population structure and low power to map the low-frequency alleles [44, 45]. Genome-wide high-resolution mapping for the traits of grain shape and grain chalkiness was performed by Gong et al. [46] in hybrid rice using multiple collaborative populations for joint analyses.

2.2 Milling quality

Milling yield is an important quality character especially from the commercial standpoint [47]. It includes milled rice yield and head rice yield. Milling yield is the estimate of the quantity of total milled rice obtained from a unit of rough rice (paddy) and produced by removing the hulls, germ, and most of the bran. It includes intact and broken kernels and generally expressed as percentage [48]. Head rice is the intact or "whole" kernels and includes milled kernels having equal to or more than three-fourth length. The economic value of broken kernels is only 50–60% that of head rice, supporting the immense impact it has on marketability. Bran consists of several layers of outer covering of the endosperm. These layers include the pericarp, testa (seed coat), the nucellus and the aleurone, including the germ, are collectively called bran. Both, the degree of milling, which is an estimate of the degree to which the bran layers are removed from the endosperm, and fissuring of grains contribute to the percentage of broken kernels and hence, determine the overall milling quality [49]. Fissures or cracks in the grains weaken the strength of the grain and predispose them to break when exposed to mechanical forces during milling process [50]. Post-harvest drying of rice is one of the greatest factors that affect the percentage of broken kernels. Alternate wetting and drying of grains, drying at high temperatures and non-equilibrated grains before polishing lead to a decrease in head rice recovery [51–55]. Milling quality is determined with the help of laboratory-sized mills. They include dehuskers that remove husk, polishers or Test Rice Whitening Machine and graders, indent cylinders and shaker tables to segregate broken kernels from milled rice. Lam and Proctor [56] determined that linoleic and oleic acids were the main fatty acids released during milled rice surface lipids hydrolysis. Limited number of QTLs has been identified for milling quality. Two have been fine mapped but none has been cloned so far [57].

2.3 Cooking and sensory quality

Rice is mainly consumed as polished grain in contrast to other staple cereals like wheat and maize that are consumed after the grain is ground to flour. Therefore, the quality characters of rice grain assume greater importance. The chief component of milled rice grain is starch which constitutes approximately 78% (14% moisture) or 90% (dry weight) of the endosperm [58]. Thus, the properties of starch mainly determine the cooking and eating quality of rice grains. Three important traits of starch that determine the cooking and organoleptic properties of rice grain are: apparent amylose content (AAC), gelatinization temperature (GT) and gel consistency.

The amylose fraction, essentially the linear polymer of glucose, forms only a small component of starch. The other major form of starch is the highly branched amylopectin molecule. Amylose is an important quality trait of rice and is considered as an indirect predictor of cooking and sensory quality [59–61]. Iodine-binding assay, generally used for measuring amylose content, also detects long-chain amylopectin in addition to 'true' amylose [62]. Hence, amylose is referred to as apparent amylose content (AAC). AAC of starch ranges from 0.8 to 1.3% in waxy rice, whereas it constitutes 8–37% [58] in non-waxy rice, the rest being amylopectin. AAC is directly proportional to water absorption, volume expansion, fluffiness, hardness and inversely proportional to cohesiveness, tenderness, stickiness and glossiness of cooked rice. Based on AAC, rice can be classified as: waxy (0–2%), very low (3–9%), low (10–19%), intermediate (20–25%), and high (>25%) [10]. Despite overestimating the actual amylose content and other limitations, iodine—binding assay that produces blue iodine—amylose complex when iodine binds to gelatinized rice flour which is quantified using a spectrophotometer, remains the method of choice for determining AAC. The two methods approved for the estimation of amylose content in milled rice are: the AACCI Method61-03.01 and ISO Method 6647-1:2015 [63, 64]. Auto-analyzers are also being used for routine amylose estimations in several rice improvement programs [65].

In general, the AAC is related to sensory quality of cooked rice however, there are varieties that have the same AAC but differ in their cooked rice hardness [66]. To account for such differences, a complementary test called gel consistency (GC) is routinely used [32]. It measures the length moved by rice flour gel, before it sets. Rice is classified into three GC groups based on gel length: hard and very flaky (≤40 mm), medium and flaky (41–60 mm), and soft (>61 mm). The differences in GC groups are explained on the basis of the proportion of hot water soluble amylose compared to that of insoluble amylose. The varieties with higher proportion of hot water insoluble amylose exhibit hard GC [67, 68]. Studies have indicated that long-chain amylopectin that remains in the gelatinized starch granule is probably the hot water insoluble amylose [69, 70]. According to Matsue et al. [71], amylose and protein content, amylographic characteristics, and even palatability showed significant difference depending on the position of spikelets in a panicle.

Conventional genetic studies have revealed that AAC is under the control of one major gene with several modifiers [56]. Among non-waxy parents, high amylose is completely dominant over low or intermediate amylose, and intermediate is dominant over low [72]. With the advent of molecular marker technology, it is now easy to apprehend complex quantitative traits [73]. Amylose content is reported to be mainly controlled by the waxy gene locus (*Wx*) present on chromosome 6, which encodes the granule-bound starch synthase (GBSS) [74].This enzyme is required for amylose synthesis, and several alleles are encoded by the *Wx* locus [75, 76]. Three alleles of the *waxy* gene—*Wx*, Wx^a and Wx^b are known, which exist in waxy (sticky) rice, *indica* and *japonica* sub-species, respectively. The activity of the encoded protein, GBSS differs in different genetic backgrounds [77]. A single nucleotide polymorphism (SNP) at the splice site of intron 1 differentiates low amylose varieties from intermediate and high varieties. This SNP defines the Wx^a and Wx^b alleles for high and low amylose, respectively [78]. In the Wx^{in} allele [76] it was identified that an SNP in exon 6, results in an amino acid substitution from serine to tyrosine that distinguishes high and intermediate amylose varieties [75].

Gelatinization temperature (GT) is another important physicochemical parameter that ranges from 55 to 80°C and provides information regarding the cooking time of rice and its texture [79]. The temperature at which the semi-crystalline structure of starch begins to melt in hot water with loss of birefringence is termed GT [1]. GT is classified into three classes: low (55–69°C), intermediate (70–74°C) or high

(75–79°C) [27]. GT is dependent on the amylopectin fine structure of starch with higher proportion of short chains (DP 6–12) decreasing the GT [80, 81]. Consumer preferences are varied throughout the world but varieties with intermediate GT are mostly preferred [82]. The two most commonly used methods for GT determination are: alkali spreading value (ASV) and Differential Scanning Calorimetry (DSC). ASV is based on the disintegration of starch granules present in milled rice grains in dilute KOH. The extent of disintegration is numerically scored on a scale of 1–7 [31, 68]. Though ASV is a high throughput method for the determination of GT, it is an indirect and subjective test. In contrast, DSC is an instrumental method based on measuring in real time, the first peak of the endotherm as the starch granules gelatinize [6, 83, 84]. DSC is a precise but an expensive method for measuring GT and cannot be routinely used to screen thousands of breeding lines in rice improvement programs. GT is also determined by an amylograph method [85] which tracks the viscosity changes that take place when rice flour-water slurry is heated with continuous stirring and was approved as the AACCI Method 61-01.01. The temperature at which the viscosity of 20% slurry begins to rise, determines the GT. The instrument used extensively in advanced rice quality labs is Rapid Viscoamylograph (RVA) [1]. It determines the viscosity changes during the heating and cooling of relatively small rice flour samples (6 g) AACCI Method 61-02.01.

A QTL corresponding to the *alk* locus was identified by Fan et al. [35], having a major effect on alkali spreading value. *Alk/alk* codes for starch synthase IIa (SSIIa) which is responsible for the vital differences in amylopectin chain length distribution [81]. Specifically, four haplotypes are able to distinguish between low and high GT. But a marker which is able to identify genotypes with the intermediate class of GT has yet to be discovered. GT is classified into two groups by allelic variation in SSIIa [81, 86]. The SNPs in SSIIa define four haplotypes [87, 88] and two haplotypes associate with high and two with low GT. Varieties having intermediate GT are found in all haplotype groups [89], thereby suggesting that another locus interacts with SSIIa to produce the intermediate phenotype. SNP mutations in the rice *alk* gene have been shown to alter the amylose content in grains [88]. Although several alleles of *Waxy/waxy* and *Alk/alk* genes linked with different forms of starch have been identified [87], other starch biosynthesis genes in addition to *Waxy/waxy* and *Alk/alk* also affect rice cooking and eating quality. However, starch structure does not clarify all the variation in rice grain quality parameters present in all rice germplasm [90].

Aroma is a prized sensory trait of cooked rice that increases its market value. Among more than 100 identified volatile compounds, 2-acetyl-1-pyrroline (2-AP) is the major chemical compound contributing to the fragrance of Basmati rice, Jasmine rice and Pandanus leaves [91–94]. Aroma is traditionally detected by smelling after reaction with 0.1 M KOH. However, this method is subjective and is also harmful to the nasal cavity of the analyst upon continuous and prolonged exposure. To solve this problem, gas chromatography coupled with flame ionization detector (GC-FID) or mass spectrometry (GC-MS) is being used in advanced rice breeding facilities. However, these methods are expensive and involve high running and maintenance costs. Therefore, molecular markers related to 2-AP are routinely used in rice breeding programs working on aroma.

Genetics studies of aroma have been an attractive research topic and many researchers studied it by employing various sensory tests. A few scientists like Reddy and Reddy [95] described two to three recessive or dominant genes that determine the fragrance, but most researchers believe that Basmati fragrance is under the control of a single recessive gene [96, 97]. Almost two decades of attempts to know the genetics of aroma at molecular level concluded in mapping of a single locus (*fgr*) on chromosome 8. QTL mapping [98, 99] followed by fine mapping [94], sequence

analysis and complementation test [100] have helped to determine that Betaine Aldehyde Dehydrogenase (BADH2) gene possessing 15 exons and 14 introns is the fragrance causing gene (*fgr*). Several studies have suggested that a recessive allele of BADH2 carrying fragment deletions, *badh2* includes 7 bp deletion in 2nd exon, an 8 bp deletion in 7th exon and an 803 bp deletion between exons 4 and 5 [101, 102]. This characterization of fragrant and non-aromatic rice varieties suggested that these events might have occurred after the divergence of aromatic and non-aromatic varieties from the common ancestor. On the other hand, the functional *BADH2* converts AB-ald (presumed 2-AP precursor) into GABA (4-aminobutyraldehyde) in non-fragrant rice and the non-functional BADH2 causes accumulation of AB-ald and thereby enhances 2-AP biosynthesis in fragrant rice [100]. A study by Kovach *et al* [103] suggested that Basmati cultivars were nearly identical to the ancestral japonica haplotype across 5.3 Mb region flanking BADH2 thereby, demonstrating the close evolutionary relationship of Basmati cultivars with japonica varietal group. Due to instability in expression of *Badh2* gene and complexity in fragrance determination, marker assisted selection (MAS) is considered to be a useful tool for screening this trait.

Detailed studies were done by Sood and Siddiq [104] on the geological distribution of kernel elongation gene(s) in rice and reported that varieties showing high kernel elongation on cooking were known to be traditionally cultivated in the northwest part of undivided India. Kernel elongation upon cooking is an endosperm character significantly influenced by factors like environment, aging, etc. Basmati rices are characterized by doubling of kernel length upon cooking. Despite being an important trait, not many reports are available on the inheritance of kernel elongation on cooking. Among the limited number of studies on this trait, one study had reported identification of a QTL between two RFLP markers *viz*., RZ323 and RZ562 and mapped it at a distance of 14.6 cM on chromosome 8 [105].

2.4 Nutritional quality

Rice is consumed as a staple for providing sustenance to its consumers'. With improving purchasing power of the rice consumers' post green revolution, nutritional quality of rice gained importance. As starch is the main constituent of milled rice grain, it is the major source of energy and affects its nutritional quality. It has been reported that starch is digested at different rates in human gastro-intestinal tract [106]. The digestibility of starch is measured by estimating the rise in blood glucose level of humans upon consumption of a food containing 50 g available carbohydrates compared to a standard solution containing 50 g glucose [107–109]. This glycemic response is reported as glycemic index (GI). However, estimation of GI involves low-throughput and expensive clinical assays, therefore, it is not routinely used in screening for low GI rices [110]. In vitro estimation of nutritional fractions of starch can be carried out by estimating the content of total sugars, total starch, rapidly digestible starch, slowly digestible starch and resistant starch [111, 112]. Apart from starch, the other major macronutrients present in milled rice grain are: storage proteins (7%), storage lipids (<1%) and non-starch polysaccharides (NSPs, trace amounts). These macronutrients significantly affect the nutritional quality, textural and sensory traits, and functional properties [113] even though they constitute minor components of milled rice grain. Storage proteins are major source of proteins in developing countries, are hypoallergenic and possess superior amino acid composition [114]. The Kjeldahl method with modifications to accommodate smaller sample sizes (AACCI Method 46-13.01) [63] is widely used method for the estimation of total proteins. Individual amino acids can be quantified after acid hydrolysis using pre-column derivatization with a fluorescent derivatizing reagent

followed by HPLC separation [115, 116]. Rice lipids serve nutritional and functional role. They provide protection against cardiovascular diseases and cancer [117] and also affect the pasting properties. Crude fat in rice grains is routinely analyzed using a standard method (AACCI Method 30-10.01). The fatty acid composition of the bran layer can also be analyzed using gas-liquid chromatography (GLC) [118]. NSPs are concentrated in the bran layer and only trace amounts are detected in the milled rice grains but have nutritional importance because of their unique composition compared to other cereals [109].

Nutritional components such as minerals, vitamins and phytochemicals are concentrated in the bran layer and are either absent or present at low levels in milled grains. The iron and zinc content are generally low and some of which is lost during milling. So a modest increase in these levels in rice would provide a significant nutritional boost to the hundreds of millions of people who depend on it. Hence there is an imperative need for a shift in emphasis toward development of nutritionally high quality rice. This is achieved by evaluating the available germplasm lines for micro nutrient content and by generation of knowledge regarding their inheritance pattern to use in future breeding programs. Micronutrients are being quantified by using atomic absorption spectroscopy (AAS), X-ray fluorescence spectrometry (XRF), inductively coupled plasma-mass spectrometry (ICP-MS), laser-induced breakdown spectroscopy (LIBS), and inductively coupled plasma-optical emission spectrometry (ICP-OES) [16, 17].

Integration of marker assisted breeding with conventional breeding creates a possibility to track the introgression of nutritional quality associated QTLs and genes into a popular/elite cultivar from various germplasm sources [119]. Two consistent QTLs for protein content in milled rice were reported by Zhong et al. [120] as *qPr1* and *qPr7* and located in the marker interval of RM493-RM562 and RM445-RM418 on chromosome 1 and 7, respectively. Gande et al. [121] identified 24 candidate genes namely OsNAC, OsZIP8a, OsZIP8c and OsZIP4b showed significant phenotypic variance of 4.5, 19.0, 5.1 and 10.2%, respectively. The QTL associated with increased grain protein content has been cloned and designated as Gpc-B1 [122].

3. Future prospects

Rice quantity and quality are directly or indirectly influenced by decrease in suitable arable land due to increase in urbanization, urban migration, soil deterioration and problems relating to climate fluctuations. Rice eating and cooking quality traits appear to be simple but the genetic machinery is too complex and needs to be deciphered. Rice appearance quality is a complex trait and involves interaction between quality and yield and also between quality and environment. Grain chalkiness is of primary concern since it affects milling, appearance, eating and cooking qualities [123]. To reduce chalkiness, genotypes with low chalk formation at high temperature after heading can be identified and utilized through MAS. Biochemical, physiological and molecular mechanisms have to be worked out by identifying and cloning chalkiness functional genes. The most challenging issue facing milling industry is to obtain high head rice recovery, since it is directly related to profitability to both the farmers and millers. Genetic understanding of milling quality is still limited [57]. Improvement of milling quality requires (i) search for QTLs with large effect (ii) robust and accurate analytical tools to measure the trait (iii) improvement in postharvest handling and storage techniques (iv) Breeding efforts through MAS. With the expeditious progress in functional genomics and development of high throughput genotyping technologies, more number of rice functional genes will be cloned in the future.

Increased awareness among the rice consuming population toward sensory and nutritional traits makes it necessary to develop evaluation techniques that can directly correlate with the consumer perception. To improve eating and sensory quality of rice it is important to integrate methods in textural analysis and rheology with taste and flavor metabolomics. Nutritional quality of rice is another trait that needs to be included in rice improvement programs. Rice has an important role to play to mitigate the impact of non-communicable diseases like diabetes. Since starch forms about 90% of milled rice grain weight, its structure (amylose content, branching pattern) and digestibility (resistant starch) affect its nutritional quality. Clinical evaluation of rice digestibility is difficult, therefore, methods for accurate *in vitro* estimations should be developed and validated *in vivo*. Available germplasm can be screened for resistant starch, amylose content, digestibility, and other health-promoting properties [110]. Cooking and processing methods have a major impact on digestibility and eating quality [33]. Further research is needed to assess how these cooking and processing techniques affect the structural, physical-chemical, and mechanical properties of rice. Robust and innovative modeling approaches that link the physical-chemical changes that occur during cooking (amylose leaching, gelatinization, water absorption) with rice grain digestibility and nutritional value and consumer demands could help in identifying the key determinants of rice grain cooking and sensory quality.

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