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Editorial

Rice Genetics: Trends and Challenges for the Future Crops Production

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Twenty-first-century agriculture faces serious challenges in every country on the planet due to global population growth, declining genetic resources, climate change, farmland loss due to urbanization, and stagnant crop yields [1]. According to the United Nations' population growth projections, the world's population is projected to reach 9.6 billion by 2050, from 7 billion in 2021. For rice, it has become increasingly urgent to develop ultra-high-yielding varieties as well as varieties highly resistant to pathogens and climate change as a major staple food holding more than 3 billion people worldwide. As a potential solution to this problem, various genomic studies have been reported that may lead the future use of biotechnology directly in agriculture [2,3]. To date, many genes and single nucleotide polymorphisms (SNPs) involved in agronomically important traits have been identified by comparative genomics, GWAS, and OMICS-based approaches [4–7]. Recent studies provide in-depth technical and market insight into the different genetic technologies used in crop agriculture, including genetically modified organisms (GMOs), genome editing techniques (CRISPR, TALEN, ZFN, etc.), and breeding strategies [8]. Genome editing technology is revolutionizing crop improvement compared to conventional technologies as a fast, efficient, and simple strategy for modification of target genes. A deeper understanding of plant mechanisms that increase yields in diverse environments can be facilitated by genetic diversity analysis and implemented by genome-scale breeding, fine-tuned genetic engineering, and more precise agricultural management practices. Thus, trait-based analysis selection is essential to derive the benefits needed to improve crops. This Special Issue will provide a platform to present and discuss related topics of research progress and trends in the genetics, genomics, and breeding of rice.

Recent genetic research trends in rice aim to explore and apply important agronomical traits-related genes and molecular networks such as grain yield, grain quality, stress tolerance, disease resistance, nutrient use efficiency, and reproductive processes. In rice, various molecular research tools have been well established since the sequenced rice whole genome was reported in 2005 [9]. So far, a lot of information on factors affecting agricultural characteristics has been accumulated through field studies such as mutation breeding, MAB (marker assisted backcross) breeding, genetics, transcriptomics, proteomics, epigenetics, and metabolomics [10,11]. Through these achievements, it will be possible to develop new varieties with excellent agronomic characteristics to respond to climate change. The rice genome contains more than 37,000 annotated genes. However, despite the achievements of many studies, the individual molecular functions of most genes with a function are still unknown [10]. Therefore, functional analysis of individual genes controlling agronomically important traits is required to elucidate molecular mechanisms as well as networks of genes. Increasing grain yields is the overarching goal of any rice breeding program.

Grain yield is composed of very complex networks such as the number of panicles, the number of grains per panicle, and grain weight by controlling the tiller and panicle [12,13]. Moreover, the grain quality depends on four factors such as appearance, cooking, milling and nutritional quality [14]. In addition, the grain shape is a key factor in determining

quality and yield characteristics. Grain chalkiness in rice is an undesirable trait that negatively affects the appearance, cooking, milling, and nutrition qualities as well as the head rice rate [15]. Eating and cooking quality of rice grain is generally determined by three physicochemical indices containing amylase content (AC), gel consistency (GC), and gelatinization temperature (GT) [14,16]. Rice grain nutritional quality mainly comprises the grain protein content (GPC), and contents of fats, amino acids, vitamins, and other micronutrients [17–19]. These research efforts will be able to contribute to improving the quality of rice grains in future breeding programs by acquiring the basic genetic knowledge of grain components. In addition to grain yield and quality, resistance characteristics to biotic and abiotic stresses to climate change are important goals for crop breeders [20]. A large number of pathogens, such as fungi, bacteria, viruses, and nematodes, cause diseases in rice, resulting in serious yield losses worldwide [21,22]. In the past decades, more than 100 stress-responsive genes and QTLs have been identified in rice through either forward or reverse genetics approach [2,23,24]. Recent research trends have revealed important knowledge about the biological interactions between rice and pathogens. Resistance genes to blast disease and bacterial blight disease have been identified in rice [25]. Many studies have been reported to elucidate the molecular mechanisms of immune response processes such as pathogen recognition, signal transduction and susceptibility to pathogens in rice [26]. As a result of overexpression of the *OsAAA-ATPase1* gene, it was reported that the expression of pathogenesis related genes, brassinosteroid signaling response and the salicylic acid (SA)-mediated defense response and resistance to rice blast disease were enhanced [27,28]. The pyramiding lines developed using five bacterial blight resistance genes (*xa4*, *xa5*, *xa7*, *xa13*, *xa21*) showed not only high levels of resistance to bacterial blight disease, but also improved grain quantity and quality [29]. In addition, many researchers have isolated and functionally characterized salinity and osmosis-related genes (*DEP1*, *qLTG3-1*, *OsSAP16*, *qDOM3.1*, *OsWRKY*, and *OsCIPK*) to significantly improve grain yield and quality [30–32]. To date, the great progress has been achieved in uncovering the mechanisms of how rice senses and responds to external nutrients [33]. Rice absorbs and transports ammonium nitrogen and nitrate nitrogen through ammonium transporters (AMTs) and nitrate transporters (NRTs), respectively [34,35]. Male sterility is a major subject of research on reproductive development in rice for both basic biology and breeding application [36,37].

Functional genomic understanding of an agronomic trait refers to characterization of the genes (including non-coding sequences) and their regulatory networks, which collectively determine the formation and development of the trait [38,39]. The formation of any trait involves a large array of genes, and the majority of the genes that participate in many processes thus affect the development of many traits (or pleiotropic effects) [40,41]. Data and literature accumulated to date have already clearly depicted such a "net-like" structure between genes and traits [42]. In addition, formation and development of traits are greatly influenced by environmental conditions and also to some extent by field management practices [42]. For functional genomic understanding of agronomic traits, a complex trait such as yield may be divided into sub traits, which in turn are subdivided into components and biological processes, which may be specified by pathways [38]. Genes and regulatory networks then would be characterized for each component trait and process [43]. Thus, it is necessary to plan and pursue systematic efforts and strategies in future studies that are solidly based on the present findings, keeping in mind the net-like structure of the relationship between the genome and traits. The important research mentioned in this Special Issue demonstrates experimental results that will help us understand and explain the molecular basis of agronomically important characteristics in rice. To develop new rice varieties that can respond to climate change in the future, it is necessary to identify more important genes, explain their molecular functions, and design desirable genotypes.

Conflicts of Interest: The authors declare no conflict of interest.

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