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Review

Phenotypic Variations, Environmental Effects and Genetic Basis Analysis of Grain Elemental Concentrations in Rice (*Oryza sativa* L.) for Improving Human Nutrition

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Abstract: Rice (*Oryza sativa* L.) is primary dietary source for half of the global population that comprising both essential nutrients and toxic heavy metal elements for human health. A number of nutrients are required within the diet and generally lacking in human diets, and need to biofortify into the rice grains, such as iron (Fe), zinc (Zn), calcium (Ca), potassium (K), sodium (Na), magnesium (Mg), phosphorus (P), copper (Cu), iodine (I), selenium (Se), and Sulphur (S). Meanwhile, some elements are toxic to human, including arsenic (As), cadmium (Cd), chromium (Cr), cobalt (Co), mercury (Hg), manganese (Mn), nickel (Ni), and lead (Pb) which need to be eliminated from the rice grains. This article reviews the aspects of phenotypic variation of grain elemental concentration in the diverse rice genotypes, relationship of environmental conditions and rice grain elemental accumulation, correlation between rice grain elemental content and others agronomic traits, and also genetic basis of grain elemental concentration in rice. All of these aspects are important to develop rice varieties with a balanced elemental nutrients and lower toxic heavy metal elements. Enhancing the concentration of essential mineral elements and reducing the accumulation of toxic elements in the rice grain are important to improve the rice quality for human health in addressing mineral deficiency and toxicity that could be accomplished by using plant breeding, agronomic, and genetic engineering approaches.

Keywords: rice; nutrient elements; toxic elements; phenotypic variance; genetic basis

Introduction

Rice (*Oryza sativa* L.) is an important staple food for half of the world population and provides carbohydrate, protein, vitamins, and other mineral elements [1,2]. Human requires at least 49 mineral elements for their health that can be supplied from the appropriate diet [3]. Generally, rice grain is not belong to be mineral-rich diet, but it can still be minerals source for humans due to the high rice consumption reaching 190 kg/capita/year [4,5,6]. The composition of mineral elements in rice grain is determined by genetic factor and environmental conditions [7,8]. Seven mineral elements that often lacking in the human diets and do not concentrated in the rice grains, commonly added into the rice grain by biofortification process, including iron (Fe), zinc (Zn), copper (Cu), calcium (Ca), magnesium (Mg), selenium (Se), and iodine (I) [9,10,11]. These mineral elements play important roles in the human health. Fe is the primary constituent in haemoglobin of the red blood cells. Zn is important element for enzymes that involved in the cell division, growth, and protein synthesis [12,13]. Ca is important element for the development of the skeleton [14]. The recommended dietary intake for Fe is 10–15 mg/kg, while the polished rice only contains Fe around 2 mg/kg [15]. Similarly, the recommended intake for Zn is 12–15 mg/kg, whereas the polished rice only contains 12 mg/kg [16]. Rice grains only contain 12 mg/kg of Se, while the recommended daily intake for Se is 55 mg/kg [17,18].

Deficiencies or insufficient intake of these mineral elements may lead to diseases and dysfunctions in human body [19]. Mineral deficiency mostly happened in the rice-eating populations [20]. Anemia is caused by Fe deficiency affects 60% of the global population particularly in the developing countries [21,22]. More than 30% of the world's population have Zn deficient in their diet that associated with immune system disfunction, growth and mental retardation [23,24,25,26,27]. Approximately 15% of the population have diets that are Se deficient and correlated with various types of cancer [28]. About three million people more than 50 years old mostly in developing countries suffer from osteoporosis due to Ca deficiency [29,30]. A total of 30% global population have diets that are iodine deficient [31,32]. Thus, it is important to increase these mineral element concentrations in the rice grain because of its staple role for human normal development and growth [3]. Rice biofortification with these seven minerals is one of the most effective approach and economical solution to develop rice varieties with balanced nutrient concentrations when milled [33].

Conventional rice breeding and genetic engineering methods can be used in the rice biofortification to improve nutritional quality in rice [33,34]. The highest Fe and Zn concentrations in the rice grain were identified in some aromatic rice varieties, including Zuchem, Jalmagna, and Xua Bue Nuo [35]. The example of the rice varieties with high Zn concentration in the grain are Chattishgarh Zinc Rice-1, CR Dhan 311, and DRR Dhan 45 that developed in India [15]. Several rice varieties such as Annada, Nagina22, HKR126, Dragon Eyeball 100, CH45, and ASD16 have high Fe and Norungan has high Zn concentration more than 30 mg/kg [36]. Cheng et al. (2009) [37] reported that japonica rice have higher Fe concentration compared to indica rice variety. Brown rice had higher grain Fe and Zn concentration than polished rice [38]. The most abundant Fe and Zn concentration are in the aleurone layer of grain that measured by using histochemical techniques and X-ray fluorescence [39,40,41]. Wild rice accessions showed higher Fe and Zn concentration than cultivated rice, indicating wild species are a better source for biofortification of popular rice varieties by using non-transgenic approaches [36,42]. Rice variety with the highest Ca concentration is Gopalbhog (98.23 mg/kg) [43]. Manipuri Black Rice variety contains several essential elements in high concentrations, including Zn (17.98 mg/kg), Fe (37.6 mg/kg), and Mg (173.23 mg/kg) [43]. The highest Na (63.21 mg/kg) and K (503.2 mg/kg) concentration was recorded in Setabhog rice variety [43]. Remigeli contains the highest Cu concentration (15.87 mg/kg) [43].

Rice grains also contain some elements that are toxic to human, including arsenic (As), cadmium (Cd), chromium (Cr), cobalt (Co), mercury (Hg), manganese (Mn), nickel (Ni), aluminum (Al), and lead (Pb) [44,45,46,47]. According to the Codex Alimentarius Commission of Food and Agriculture Organization and World Health Organization (2006) [48], the maximum Cd concentration in polished rice grain is 0.4 mg/kg for human intake. Consumption of high level heavy metal element diets, such as high level of As affects blood vessels and nervous system leading cancer [49,50]. Consumption high level of Cd may lead to have Itai-Itai disease [51,52,53]. These toxic elements concentration are generally influenced by the contamination of environmental growing conditions that leading to serious problems [54]. It is important to develop rice varieties with lower toxic heavy metal elements in the rice grain for human food safety [1,55]. Toxic element concentration in rice grain is influenced by genetic and environmental conditions [56]. Developing rice varieties with high-yield and low toxic heavy metal contamination is challenging for rice breeders because of the lack genetic knowledge. Diverse rice accessions provide genetic variation in uptake, accumulation, and tolerant to toxic heavy metal elements in the contaminated soil that indicating a large genetic sources for developing rice variety with lower toxic elements [57-65]. Therefore, selection process of rice variety with low accumulation of heavy metal elements (e.g., As and Cd) considered to be selected in contaminated soil [66]. The anaerobic flooded field conditions accelerate mobilization of As

[67,68]. Hybrid rice more accumulate As compared to non-hybrid rice [69,70]. Nipponbare, Koshihikari, Sasanishiki, and Hu-Lotao are low Cd-accumulating rice cultivar. Kasalath rice cultivar is categorized as medium Cd-accumulation. Meanwhile, Anjana Dhan, Milyang23, Habataki, and Peh-kuh-tsao-tu belong to the high Cd-accumulating rice cultivars [71]. Cd uptake from contaminated soil in indica rice cultivars is higher than japonica cultivars [72]. Selection of rice varieties with low Cd and As accumulation is difficult [55]. Rice productivity is less in the acid soils due to Al toxicity and several rice varieties are tolerant to the Al [73].

Heavy metal elements contamination, such as As, Cd, Mn, and Ni in soil frequently from anthropogenic activities and application of fertilizers and pesticides [74,75,76]. Contaminated soil with heavy metal elements reduce rice yield due to the limiting plant growth and development [77,78]. Heavy metal elements in contaminated soil were uptake by the rice plants and accumulate in rice grain, lead to rice grain contamination, subsequently enter the food chain and risk human health [54,79,80]. Rice grain could accumulate higher heavy metal element concentration than others cereal crops, such as maize, wheat, and barley [81]. Thus, minimizing translocation heavy metal elements of contaminated soil from roots to grains is important to reduce rice grain contamination [82]. Most of the polished rice in U.S. grocery stores is fortified with essential mineral elements by adding in external surface of the polished rice grain [83]. Rice biofortification by using genetic improvement approach could include both enhancing desirable essential elements concentration (e.g., Fe, Zn, Se, Ca, I, etc) and decreasing toxic elements concentration (e.g., As, Cd, Pb, etc) and also could improve rice marketing strategies for value-added rice products [84].

Understanding the genetic control of mineral accumulation in rice grain is important to develop rice varieties with a balanced elemental nutrients and lower toxic heavy metal elements [1]. Grain elemental concentrations (GEC) in rice are belong to the complex quantitative traits due to a wide range of phenotypic variation for GEC among diverse rice genotypes [1,85]. Therefore, quantitative trait loci (QTL) mapping, association mapping, and genome wide association study (GWAS) has been widely conducted to identify loci or genes correlated to the GEC by using various rice mapping population. A large rice mapping population can have a great power to identify alleles correlated to the GEC. The power of allele detection can be increased by adding sample size of the rice mapping population [86]. For example, GWAS by using the Rice Diversity Panel 1 (RDP1) consists of 421 rice accessions and 36,901 single nucleotide polymorphisms (SNPs) in four different environmental conditions to detect genomic regions correlated to GEC, including Zn, Cu, Mo, and As [46,87,88]. Plant breeding is one of the effective and sustainable approach for fighting nutrient deficiency [35,89]. Bioavailability of the essential mineral elements in rice grains can be improved by plant breeding and also toxic elements in the rice grain can be decreased by plant breeding. Thus, GEC has become an important selection trait in rice breeding [90].

Among the rice genotypes there is a wide phenotypic variation in GEC that provide opportunities to select genotypes with higher essential mineral element contents or lower heavy metal elements [35,91,92]. Screening of rice germplasm, varieties, and elite lines that having higher essential mineral element contents or lower heavy metal elements are important to be used as donor parents in the rice plant breeding programs [93,94]. Several landraces and wild varieties of rice are frequently contain maximum essential mineral element [95]. For example, *O. nivara, O. latifolia,* and *O. officinalis* contained high Fe and Zn concentration [36,96]. GWAS to identify genomic regions association with GEC by using 517 Chinese landraces [97]. A number of studies have shown the exploitation of genetic variation associated with GEC among the rice genotypes to identify genomic regions controlling elemental concentrations in rice due to the abundance of genetic recombination events [35,36]. In recent year, rice genetic improvement correlated to GEC have been done to overcome mineral nutrient deficiencies [99,100]. Several QTLs for Fe, Zn, Mn, and

P in the rice grain have been identified by using doubled-haploid population under controlled conditions [99]. Some QTLs for Fe, Zn, Mn, Cu, Ca, Mg, K, and P in the rice grain also identified by using introgression lines population under field environment [100]. The genetics investigation associated with GEC, demonstrating that additive and dominant gene and also environmental conditions affect the elemental concentration traits. Scientists developed rice varieties with enhanced essential mineral concentrations without negative effect on the grain yield by using marker-assisted selection [35,101]. GEC trait showed a positive correlation with grain yield, thus an improved essential mineral trait can be combined with high grain yield trait. IRRI testing program demonstrated a cross between rice variety with high Fe concentration (IR68144-3B-2-2-3) and high yielding rice variety (IR72), resulting rice cultivar with high Fe concentration and high grain yield 10% below IR72 [35].

Parent preferences are important in the crossing rice varieties to develop improved GEC. For example, progenies with higher Fe grain concentration are resulted from a female parent of rice variety Tong Lang Mo Mi than a male parent [35]. Appropriate selection method also important in rice breeding for developing higher GEC. Single-seed descent by using the F5 generation is more appropriate method to develop higher Fe grain concentration compared to the earlier generation due to less dominance effect in the F5. An optimum environmental condition such as appropriate application of N and P also influence the developing higher GEC. Agronomic approaches were used to increase the essential elements and decrease toxic elements concentration in rice grains by fertilizer application with optimum solubility and mobility in the soil that linked to the ability of rice plants to translocate and accumulate the elements in grains [47].

Identification of functional genomics, transcriptomics, and proteomics associated with GEC has been supported by advanced technologies and tools, including next-generation sequencing (NGS) technologies [102,103,104,105,106,107,108], genome-guided RNA-seq [109,110,111,112,113], sequencing-by-synthesis (SBS) [114,115], whole genome SNP array [82,116,117,118,119], genome-wide association mapping [97,103,119,120,121,122,123,124,125], map-based cloning method [126,127,128,129], and transcriptome profiling [11,115,130]. By combining phenotypic and genotypic characteristics of GEC, molecular mechanisms coordinating the absorption, translocation, and accumulation of elements in rice grain could exploit [131]. Detection of candidate genes controlling the GEC is the initial step in developing marker-assisted selection for GEC. This selection method is highly accurate, fast, and inexpensive. The polygenic genes controlling mineral elements in rice grains are difficult to map by using a biparental population [1,20,132,133,134].

Enhancing the concentration of essential mineral elements and reducing the accumulation of toxic elements in the rice grain are important to improve the rice quality for human health in addressing mineral deficiency and toxicity that could be accomplished by using plant breeding, agronomic, and genetic engineering approaches. Several programs have been applied for mineral deficiency solution, such as HarvestPlus program that trying to increase the essential mineral concentration in rice grain and improve bioavailability of the elements in human diets [9]. This article reviews the aspects of phenotypic variation of GEC in the diverse rice genotypes, relationship of environmental conditions and rice grain elemental accumulation, correlation between rice grain elemental content and others agronomic traits, and also genetic basis of GEC in rice. All of these aspects are important to develop rice varieties with a balanced elemental nutrients and lower toxic heavy metal elements.

Phenotypic Variation of Grain Elemental Compositions in Rice

The composition of mineral elements in rice grain is determined by genetic factors, environmental conditions, and their interactions [7]. A number studies showed that a wide phenotypic variation in GEC among the rice accessions that consist of essential minerals and toxic elements (Table 1). All GEC displayed a normal or continuous distribution and a transgressive segregation in the rice mapping population in different environmental conditions [90]. It is provide possibility to select the rice genotypes with high essential minerals and low toxic elements. These elements including silver (Ag), aluminum (Al), arsenic (As), boron (B), calcium (Ca), cadmium (Cd), cobalt (Co), chromium (Cr), copper (Cu), iron (Fe), potassium (K), magnesium (Mg), manganese (Mn), molybdenum (Mo), nitrogen (N), sodium (Na), nickel (Ni), phosphorus (P), lead (Pb), rubidium (Rb), sulfur (S), selenium (Se), strontium (Sr), and zinc (Zn) that have been measured in many studies by using variety mapping rice population (Table 1). Several methodologies have been used to determine the contents of elements in rice grains, such as inductively coupled plasma mass spectrometry (ICP-MS) and an energy dispersive X-ray fluorescence spectrometer (ED-XRF) [7]. The average of K, Mn, and Cu concentration in brown rice is higher than polished/milled rice. Indica rice showed higher K, Mn, and Cu concentration compared to japonica rice. Concentration of Na and Cu in non-glutinous rice varieties were higher than glutinous rice. Meanwhile, the concentration of K and Mn in non-glutinous rice were lower than glutinous ones. Polished rice from white brown rice showed higher K, Ca, and Mg concentration than red brown rice. Additionally, polished rice of white brown rice also have higher Ca compared to black brown rice. Zn concentration between polished white and red brown rice, or between polished rice of red and black brown rice are also significantly different [135]. This phenotypic variation is important in rice nutrient breeding.

Phenotypic variation explained by genotype called as broad sense heritability (H^2). According to Pinson et al. (2015) [84], 14 elements such as Mg, K, S, Ca, As, Cd, Co, Cu, Fe, Mn, Mo, Rb, Sr, and Zn showed high broad sense heritability ($H^2 > 0.5$) under both flooded and unflooded conditions that accelerate rice nutrient breeding program. Meanwhile, Ni (H^2, 0.24) and P (H^2, 0.3) exhibited low broad sense heritability under both flooded and unflooded conditions indicating the rice nutrient breeding progress for Ni and P become slower. In Fe and Zn grain concentration showed a normal distribution and a polygenic inheritance demonstrating multi-factorial and complex inheritance of Fe and Zn, indicating possibility of the improvement Fe and Zn in rice grain simultaneously [20,132].

Variation of GEC among rice accessions due to genetic and geographic origins, indicating they share a heritable mechanism [84]. A large phenotypic differences of GEC showed in indica, japonica, and aus accessions, suggesting different genetic factors controlling the traits [86]. Indica accession harbor greater allelic diversity compared to japonica. Generally, japonica accessions accumulated higher element minerals than indica. Aus accessions tend to accumulate As in higher concentration compared to tropical or temperate japonica [136]. Temperate japonica exhibited low grain As and Cd concentrations across different environment conditions than indica, suggesting these accessions could be introduced into rice nutrient breeding program with the goal for developing low grain As cultivars. Hybrid rice can accumulate higher As and Cd compared with non-hybrids [70,137]. Additionally, indica tend to accumulate Zn in the lowest concentration than japonica and aus. Five rice cultivars that have been identified accumulate high Zn are belong to temperate japonica and aus, including Bulgare (temperate japonica), DZ 192 (aus), Khao Tot Long 227 (aus), Jamir (aus), and Estrela (admix) [136]. These rice cultivars have a great potential to be exploited in rice nutrient breeding program to increase Zn concentration in rice grain for the solution of human Zn deficiency. The U.S. rice cultivars tend to have higher Cu and Cd concentration, while low in Ca, K, S, Sr, and As [84]. Meanwhile, rice cultivars from Malaysia and Brunei have high Mo concentration. These phenotypic and genotypic variations between indica and japonica indicating a great potential in rice nutrient breeding by crossing different rice accessions for better GEC. It is important to understand the molecular mechanism of elements accumulation in rice grain.

Table 1. Grain elemental concentrations in many studies

Elements in the Rice Grains	Rice Grain Elemental Concentration (mg/kg)	Rice Accessions	References
Ag	0.00017	Diverse rice genotypes	Yang et al., 2018 [7]
Al	5.2 – 9.3	F6 RIL population derived from a cross between Bala (an indica) and Azucena (a japonica)	Norton et al., 2010 [138]
As	0.058 – 1.835	Diverse rice genotypes	Meharg and Rahman, 2003 [139]
	0.032 – 0.046	Diverse rice genotypes	Duxbury and Zavala, 2005 [140]
	0.034 – 0.090	Japonica rice genotypes	Cheng et al., 2006 [141]
	0.04 – 0.92	Diverse rice genotypes	Williams et al., 2006 [142]
	0.15 – 0.59	Diverse rice genotypes	Ohno et al., 2007 [143]
	0.08 – 0.43	Diverse rice genotypes	Williams et al., 2007 [81]
	0.16 – 0.95	Doubled-haploid (DH) population derived from a cross between CJ06 (a japonica) and TN1 (an indica)	Zhang et al., 2008 [144]
	0.2	Mutant rice	Ma et al., 2008 [145]
	0.2	Hybrid rice variety	Rahman et al., 2007 [70]
	0.2 – 0.25	Japonica rice genotypes	Xu et al., 2008 [68]
	0.54	Diverse rice genotypes	Lombi et al., 2009 [146]
	0.01 – 0.82	Diverse rice genotypes	Meharg et al., 2009 [147]
	0.10 – 0.17	Diverse rice genotypes and Landraces	Norton et al., 2009a [58]
	0.07 – 0.74	Diverse rice genotypes and Landraces	Norton et al., 2009b [148]
	0.38 – 0.51	Diverse rice genotypes	Panaullah et al., 2009 [77]
	0.126 – 0.151	F6 RIL population derived from a cross between Bala (an indica) and Azucena (a japonica)	Norton et al., 2010 [138]
	0.10 – 0.22	Indica and aromatic accessions	Ahmed et al., 2011 [56]
	0.045 – 0.676	Aus, indica, and tropical and temperate japonicas	Norton et al., 2010 [138]
	0.628	Aus, indica, and tropical and temperate japonicas	Norton et al., 2010 [138]
	0.041 – 0351	Diverse rice genotypes	Kuramata et al., 2013 [149]
	0.15 – 0.45	Indica, Japonica, and Hybrid accessions	Hu et al., 2013 [82]
	0.10 – 1.30	RIL population derived from a cross between Lemont (a japonica) and TeQing (an indica)	Zhang et al., 2014 [45]
	0.945	Diverse rice genotypes	Pinson et al., 2015 [84]
	0.025 – 0.487	Diverse rice genotypes	Naito et al., 2015 [150]
	0.11 – 0.44	Diverse rice genotypes	Duan et al., 2017 [55]
	0.27	Diverse rice genotypes	Yang et al., 2018 [7]
	0.090 – 0.437	Diverse rice genotypes	Atiaga et al., 2020 [151]
	0.196 – 0.334	Diverse rice genotypes	Moulick et al., 2022 [152]
B	1.56	Diverse rice genotypes	Yang et al., 2018 [7]
Ca	65.81	Diverse rice genotypes	Wang et al., 2002 [153]

	42.27 – 341.70	Diverse rice genotypes	Jiang et al., 2007 [91]
	18.99	RIL population derived from a cross between indica cultivar Zhengshan 97 and Minghui 63	Lu et al., 2008 [154]
	56.6 – 145.3	Introgression lines (IL) population derived from Teqing (an indica) as a recipient parent and wild rice *Oryza rufipogon* as donor parent	Garcia-Oliveira et al., 2009 [100]
	61.8 – 488	Landraces	Zeng et al., 2010 [155]
	35 – 198	Doubled-haploid (DH) population derived from a cross between CJ06 (a japonica) and TN1 (an indica)	Du et al., 2013 [90]
	73 – 241	RIL population derived from a cross between Lemont (a japonica) and TeQing (an indica)	Zhang et al., 2014 [45]
	129.4	Diverse rice genotypes: USDA Rice Mini-Core Collection consists of 211 *O. sativa*, 5 *O. glaberrima*, 2 *O. rufipogon*, and 1 *O. nivara* accession	Nawaz et al., 2015 [156]
	129.4	Diverse rice genotypes	Pinson et al., 2015 [84]
	160	Diverse rice genotypes	Yang et al., 2018 [7]
	98.23	Aromatic and non-aromatic rice accessions	Nath et al., 2022 [43]
Cd	0.002 – 0.027	Japonica, Indica, Javanica, and Indica-Japonica hybrid-bred rice	Morishita et al., 1987 [65]
	0.87 – 2.70	Diverse rice genotypes	Liu et al., 2003 [60]
	0.025 – 0.185	Japonica rice genotypes	Cheng et al., 2006 [141]
	0.17 – 1.76	Diverse rice genotypes	Moraes et al., 2010 [157]
	0.021 – 0.036	F6 RIL population derived from a cross between Bala (an indica) and Azucena (a japonica)	Norton et al., 2010 [138]
	0.38 – 2.31	Backcross inbred lines (BIL) derived from a cross between the low-Cd-accumulating cultivar Sasanishiki (japonica) and high-Cd-accumulating cultivar Habataki (indica)	Ishikawa et al., 2010 [158]
	0.002 – 5.9	An F2 population, derived from a cross between a high Cd-accumulating cultivar (Anjana Dhan) as a female parent and a low Cd-accumulating cultivar (Nipponbare) as a male parent	Ueno et al., 2010 [76]
	0.27 – 3.65	A doubled haploid population derived from a cross between japonica JX17 and indica ZYQ8 rice cultivars	Zhang et al., 2011 [159]
	3	Wild type and transgenic rice of japonica cultivar Tsukinohikari	Masuda et al., 2012 [160]
	0.02 – 1.39	Diverse rice genotypes	Hu et al., 2013 [82]
	0.001 – 0.056	RIL population derived from a cross between Lemont (a japonica) and TeQing (an indica)	Zhang et al., 2014 [45]

	0.010	Diverse rice genotypes	Pinson et al., 2015 [84]
	0.125	Diverse rice genotypes	Huang et al., 2015 [1]
	0.7 – 4.2	Diverse rice genotypes	Arao et al., 2003 [61]
	0.010 – 0.099	Diverse rice genotypes	Meharg et al., 2013 [161]
	0.03 – 0.42	Diverse rice genotypes	Duan et al., 2017 [55]
	0.035	Diverse rice genotypes	Yang et al., 2018 [7]
	0.10	Doubled-haploid (DH) population derived from a cross between Tainan1 (TN1) and Chunjiang06 (CJ06)	Luo et al., 2018 [162]
	0.20 – 0.44	Diverse rice genotypes	Zhang et al., 2022a [163]
Co	0.014 – 0.017	F6 RIL population derived from a cross between Bala (an indica) and Azucena (a japonica)	Norton et al., 2010 [138]
	0.013 – 0.087	RIL population derived from a cross between Lemont (a japonica) and TeQing (an indica)	Zhang et al., 2014 [45]
	0.052	Diverse rice genotypes	Pinson et al., 2015 [84]
	0.094	Diverse rice genotypes	Yang et al., 2018 [7]
Cr	0.29 – 0.98	Japonica rice genotypes	Cheng et al., 2006 [141]
	1.76	Diverse rice genotypes	Yang et al., 2018 [7]
Cu	2.21	Diverse rice genotypes	Wang et al., 2002 [153]
	3.16 – 24.58	Diverse rice genotypes	Jiang et al., 2007 [91]
	0.826	RIL population derived from a cross between two indica cultivars Zhengshan 97 and Minghui	Lu et al., 2008 [154]
	1.5	Wild type and transgenic rice accessions	Lee et al., 2009 [164]
	1.3 – 19.3	Introgression lines (IL) population derived from Teqing (an indica) as a recipient parent and wild rice *Oryza rufipogon* as donor parent	Garcia-Oliveira et al., 2009 [100]
	6.68 – 8.46	F6 RIL population derived from a cross between Bala (an indica) and Azucena (a japonica)	Norton et al., 2010 [138]
	3.11 – 6.04	Backcross inbred lines (BIL) derived from a cross between the low-Cd-accumulating cultivar Sasanishiki (japonica) and high-Cd-accumulating cultivar Habataki (indica)	Ishikawa et al., 2010 [158]
	0.10 – 59.1	Landraces	Zeng et al., 2010 [155]
	6.9 – 8.4	Wild type and transgenic rice of japonica cultivar Nipponbare	Johnson et al., 2011 [165]
	3.767	Rice diversity panel (RDP) population	Norton et al., 2012 [166]
	1.5	Wild type and transgenic rice of japonica cultivar Tsukinohikari	Masuda et al., 2012 [160]
	2.0 – 5.6	RIL population derived from a cross between Lemont (a japonica) and TeQing (an indica)	Zhang et al., 2014 [45]

	6.007	Diverse rice genotypes: USDA Rice Mini-Core Collection consists of 211 *O. sativa*, 5 *O. glaberrima*, 2 *O. rufipogon*, and 1 *O. nivara* accession	Nawaz et al., 2015 [156]
	3.340	Diverse rice genotypes	Pinson et al., 2015 [84]
	5.47	Diverse rice genotypes	Yang et al., 2018 [7]
	2.04 – 3.86	Diverse rice genotypes	Moulick et al., 2022 [152]
	15.87	Aromatic and non-aromatic rice accessions	Nath et al., 2022 [43]
	5 – 7.1	Diverse rice genotypes	Zhang et al., 2022b [167]
Fe	6.3 – 24.4	Diverse rice genotypes	Graham et al., 1999 [24]
	6.03	Diverse rice genotypes	Wang et al., 2002 [153]
	6.5 – 15.6	Diverse rice genotypes	Prom-u-thai et al., 2003 [39]
	37.02 – 51.99	Diverse rice genotypes	Zhang et al., 2004 [98]
	0.98 – 26.78	Diverse rice genotypes	Jiang et al., 2007 [91]
	18.93	RIL population derived from a cross between two indica cultivars Zhengshan 97 and Minghui	Lu et al., 2008 [154]
	4.9 – 20	Introgression lines (IL) population derived from Teqing (an indica) as a recipient parent and wild rice *Oryza rufipogon* as donor parent	Garcia-Oliveira et al., 2009 [100]
	10	Wild type and transgenic rice accessions	Lee et al., 2009 [164]
	14.5 – 31.4	Diverse rice genotypes	Moraes et al., 2010 [157]
	29.1 – 30.6	F6 RIL population derived from a cross between Bala (an indica) and Azucena (a japonica)	Norton et al., 2010 [138]
	7.80 – 14.6	Backcross inbred lines (BIL) derived from a cross between the low-Cd-accumulating cultivar Sasanishiki (japonica) and high-Cd-accumulating cultivar Habataki (indica)	Ishikawa et al., 2010 [158]
	18	An F2 population, derived from a cross between a high Cd-accumulating cultivar (Anjana Dhan) as a female parent and a low Cd-accumulating cultivar (Nipponbare) as a male parent	Ueno et al., 2010 [76]
Fe	0.40 – 147	Landraces	Zeng et al., 2010 [155]
	25 – 56	Wild type and transgenic rice of japonica (Nipponbare)	Johnson et al., 2011 [165]
	6.2 – 71.6	Diverse rice genotypes	Anuradha et al., 2012 [36]
	0.2 – 224	F6 recombinant inbred lines (RILs) derived from the cross Madhukar × Swarna	Anuradha et al., 2012 [36]
	0.9	Wild type and transgenic rice of japonica cultivar Tsukinohikari	Masuda et al., 2012 [160]
	11.2 – 16.1	Diverse rice genotypes	Yuan et al., 2011 [168]

	5 – 18	Doubled-haploid (DH) population derived from a cross between CJ06 (a japonica) and TN1 (an indica)	Du et al., 2013 [90]
	0 – 150	An F2 population derived from the cross between high-yielding (PAU201) and iron-rich (Palman 579) indica rice varieties	Kumar et al., 2014 [169]
	7.3 – 22.0	RIL population derived from a cross between Lemont (a japonica) and TeQing (an indica)	Zhang et al., 2014 [45]
	17.35	Diverse rice genotypes: USDA Rice Mini-Core Collection consists of 211 *O. sativa*, 5 *O. glaberrima*, 2 *O. rufipogon*, and 1 *O. nivara* accession	Nawaz et al., 2015 [156]
	19.44	Diverse rice genotypes	Huang et al., 2015 [1]
	11.45	Diverse rice genotypes	Pinson et al., 2015 [84]
	2 – 13	Wild type and transgenic rice	Trijatmiko et al., 2016 [21]
	8.1 – 16.7	Diverse rice genotypes	Zhang et al., 2008 [66]
	119.26	Diverse rice genotypes	Yang et al., 2018 [7]
	1.6 – 22.2	Two BC2F3 mapping populations derived from the crosses of *O. sativa* cv Swarna with two different accessions of *O. nivara*	Swamy et al., 2018 [132]
	23.1	Diverse rice genotypes	Bollinedi et al., 2020 [20]
	6.9 – 22.3	Diverse rice genotypes	Maganti et al., 2019 [171]
	0.561 – 4.48	Landraces and diverse rice genotypes	Pradhan et al., 2020 [15]
	6.63 – 9.23	Diverse rice genotypes	Moulick et al., 2022 [152]
	37.6	Aromatic and non-aromatic rice accessions	Nath et al., 2022 [43]
K	302.71 – 1832.75	Diverse rice genotypes	Jiang et al., 2007 [91]
	1503 – 3201	Introgression lines (IL) population derived from Teqing (an indica) as a recipient parent and wild rice *Oryza rufipogon* as donor parent	Garcia-Oliveira et al., 2009 [100]
	1130 – 3830	Landraces	Zeng et al., 2010 [155]
	583 – 1634	Doubled-haploid (DH) population derived from a cross between CJ06 (a japonica) and TN1 (an indica)	Du et al., 2013 [90]
	1800 – 3600	RIL population derived from a cross between Lemont (a japonica) and TeQing (an indica)	Zhang et al., 2014 [45]
	2919	Diverse rice genotypes: USDA Rice Mini-Core Collection consists of 211 *O. sativa*, 5 *O. glaberrima*, 2 *O. rufipogon*, and 1 *O. nivara* accession	Nawaz et al., 2015 [156]
	2940	Diverse rice genotypes	Pinson et al., 2015 [84]
	3760	Diverse rice genotypes	Yang et al., 2018 [7]
	503.2	Aromatic and non-aromatic rice accessions	Nath et al., 2022 [43]
	400 – 800	Diverse rice genotypes	Zhang et al., 2022b [167]

Mg	63.31 – 539.35	Diverse rice genotypes	Jiang et al., 2007 [91]
	4.11 – 79.87	Diverse rice genotypes	Jiang et al., 2008 [135]
	896.0 – 1480	Introgression lines (IL) population derived from Teqing (an indica) as a recipient parent and wild rice *Oryza rufipogon* as donor parent	Garcia-Oliveira et al., 2009 [100]
	864 – 2020	Landraces	Zeng et al., 2010 [155]
	800 – 1694	Doubled-haploid (DH) population derived from a cross between CJ06 (a japonica) and TN1 (an indica)	Du et al., 2013 [90]
	1200 – 1860	RIL population derived from a cross between Lemont (a japonica) and TeQing (an indica)	Zhang et al., 2014 [45]
	1406	Diverse rice genotypes: USDA Rice Mini-Core Collection consists of 211 *O. sativa*, 5 *O. glaberrima*, 2 *O. rufipogon*, and 1 *O. nivara* accession	Nawaz et al., 2015 [156]
	1566	Diverse rice genotypes	Pinson et al., 2015 [84]
	1670	Diverse rice genotypes	Yang et al., 2018 [7]
	173.23	Aromatic and non-aromatic rice accessions	Nath et al., 2022 [43]
	100 – 300	Diverse rice genotypes	Zhang et al., 2022b [167]
Mn	9.92	Diverse rice genotypes	Jiang et al., 2002 [172]
	40.99 – 61.82	RIL population derived from a cross between Lemont (a japonica) and TeQing (an indica)	Zhang et al., 2004 [98]
	4.89 – 25.97	Diverse rice genotypes	Jiang et al., 2007 [91]
	14.99	RIL population derived from a cross between two indica cultivars Zhengshan 97 and Minghui	Lu et al., 2008 [154]
	30	Wild type and transgenic rice accessions	Lee et al, 2009 [164]
	8.4 – 28.2	Introgression lines (IL) population derived from Teqing (an indica) as a recipient parent and wild rice *Oryza rufipogon* as donor parent	Garcia-Oliveira et al., 2009 [100]
	13.0 – 35.0	Backcross inbred lines (BIL) derived from a cross between the low-Cd-accumulating cultivar Sasanishiki (japonica) and high-Cd-accumulating cultivar Habataki (indica)	Ishikawa et al., 2010 [158]
	8.43 – 8.44	F6 RIL population derived from a cross between Bala (an indica) and Azucena (a japonica)	Norton et al., 2010 [138]
	6.7 – 26.6	Landraces	Zeng et al., 2010 [155]
	14.2 – 16.6	Wild type and transgenic rice of japonica (Nipponbare)	Johnson et al., 2011 [165]
	7.9	Wild type and transgenic rice of japonica cultivar Tsukinohikari	Masuda et al., 2012 [160]
	17 – 18	Doubled-haploid (DH) population derived from a cross between CJ06 (a japonica) and TN1 (an indica)	Du et al., 2013 [90]

	16 – 64	RIL population derived from a cross between Lemont (a japonica) and TeQing (an indica)	Zhang et al., 2014 [45]
	31.44	Diverse rice genotypes: USDA Rice Mini-Core Collection consists of 211 *O. sativa*, 5 *O. glaberrima*, 2 *O. rufipogon*, and 1 *O. nivara* accession	Nawaz et al., 2015 [156]
	24.72	Diverse rice genotypes	Pinson et al., 2015 [84]
	38.60 – 58.85	Recombinant inbred lines (RILs) from the cross of 93–11 (low grain Mn) with PA64s (high grain Mn)	Liu et al., 2017 [173]
	50.01	Diverse rice genotypes	Yang et al., 2018 [7]
Mo	1.35 – 1.73	F6 RIL population derived from a cross between Bala (an indica) and Azucena (a japonica)	Norton et al., 2010 [138]
	1.554	Rice diversity panel (RDP) population	Norton et al., 2012 [166]
	0.15 – 0.69	RIL population derived from a cross between Lemont (a japonica) and TeQing (an indica)	Zhang et al., 2014 [45]
	0.429	Diverse rice genotypes	Pinson et al., 2015 [84]
	0.458	Diverse rice genotypes	Yang et al., 2018 [7]
N	17760	Diverse rice genotypes	Yang et al., 2018 [7]
Na	4.10 – 79.87	Diverse rice genotypes	Jiang et al., 2007 [91]
	63.31 – 539.351	Diverse rice genotypes	Jiang et al., 2008 [135]
	8.99	Diverse rice genotypes	Yang et al., 2018 [7]
	10.9	Aus, indica, and japonica rice accessions	Chen et al., 2021 [174]
	63.21	Aromatic and non-aromatic rice accessions	Nath et al., 2022 [43]
	40 - 100	Diverse rice genotypes	Zhang et al., 2022b [167]
Ni	0.43 – 0.62	Japonica rice genotypes	Cheng et al., 2006 [141]
	1.46 – 1.48	F6 RIL population derived from a cross between Bala (an indica) and Azucena (a japonica)	Norton et al., 2010 [138]
	2.3 – 2.35	Wild type and transgenic rice of japonica (Nipponbare)	Johnson et al., 2011 [165]
	0.0 – 1.8	RIL population derived from a cross between Lemont (a japonica) and TeQing (an indica)	Zhang et al., 2014 [45]
	1.573	Diverse rice genotypes	Pinson et al., 2015 [84]
P	3330 – 4370	Diverse rice genotypes	Zhang et al., 2004 [98]
	2405.0 – 3767.0	Introgression lines (IL) population derived from Teqing (an indica) as a recipient parent and wild rice *Oryza rufipogon* as donor parent	Garcia-Oliveira et al., 2009 [100]
	3878 – 4025	F6 RIL population derived from a cross between Bala (an indica) and Azucena (a japonica)	Norton et al., 2010 [138]
	2160 – 5500	Landraces	Zeng et al., 2010 [155]
	1721 – 4128	Doubled-haploid (DH) population derived from a cross between CJ06 (a japonica) and TN1 (an indica)	Du et al., 2013 [90]

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	3100 – 4600	RIL population derived from a cross between Lemont (a japonica) and TeQing (an indica)	Zhang et al., 2014 [45]
	3475.27	Diverse rice genotypes: USDA Rice Mini-Core Collection consists of 211 *O. sativa*, 5 *O. glaberrima*, 2 *O. rufipogon*, and 1 *O. nivara* accession	Nawaz et al., 2015 [156]
	3792	Diverse rice genotypes	Pinson et al., 2015 [84]
	4050	Diverse rice genotypes	Yang et al., 2018 [7]
	600 - 950	Diverse rice genotypes	Zhang et al., 2022a [163]
Pb	0.037 – 0.114	Japonica rice genotypes	Cheng et al., 2006 [141]
	0.06 – 0.12	F6 RIL population derived from a cross between Bala (an indica) and Azucena (a japonica)	Norton et al., 2010 [138]
	0.046	Diverse rice genotypes	Huang et al., 2015 [1]
	0.19	Diverse rice genotypes	Yang et al., 2018 [7]
Rb	4.7 – 19.0	RIL population derived from a cross between Lemont (a japonica) and TeQing (an indica)	Zhang et al., 2014 [45]
	10.78	Diverse rice genotypes	Pinson et al., 2015 [84]
S	620 – 1550	RIL population derived from a cross between Lemont (a japonica) and TeQing (an indica)	Zhang et al., 2014 [45]
	1171	Diverse rice genotypes	Pinson et al., 2015 [84]
	300 – 400	Diverse rice genotypes	Zhang et al., 2022b [167]
Se	0.02	Diverse rice genotypes	Wang et al., 2002 [153]
	15 – 115	Diverse rice genotypes	Moraes et al., 2010 [157]
	0.104 – 0.144	F6 RIL population derived from a cross between Bala (an indica) and Azucena (a japonica)	Norton et al., 2010 [138]
	0.09	Diverse rice genotypes	Huang et al., 2015 [1]
Sr	0.15 – 1.20	RIL population derived from a cross between Lemont (a japonica) and TeQing (an indica)	Zhang et al., 2014 [45]
	0.555	Diverse rice genotypes	Pinson et al., 2015 [84]
Zn	13.5 – 58.4	Diverse rice genotypes	Graham et al., 1999 [24]
	7.99	Diverse rice genotypes	Wang et al., 2002 [153]
	53.53 – 83.66	Diverse rice genotypes	Zhang et al., 2004 [98]
	0.47 – 0.79	RIL population derived from a cross between two indica cultivars IR74 and Jalmagna	Wissuwa et al., 2006 [175]
	13.32 – 43.65	Diverse rice genotypes	Jiang et al., 2007 [91]
	22.33	RIL population derived from a cross between two indica cultivars Zhengshan 97 and Minghui	Lu et al., 2008 [154]
	13.7 – 22	Diverse rice genotypes	Liang et al., 2008 [176]
	13.3 – 60.1	Introgression lines (IL) population derived from Teqing (an indica) as a recipient parent and wild rice *Oryza rufipogon* as donor parent	Garcia-Oliveira et al., 2009 [100]

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	23	Wild type and transgenic rice	Lee et al., 2009 [164]
	24.4 – 44.7	Diverse rice genotypes	Moraes et al., 2010 [157]
	29.7 – 36.5	F6 RIL population derived from a cross between Bala (an indica) and Azucena (a japonica)	Norton et al., 2010 [138]
	19.6 – 47.5	Backcross inbred lines (BIL) derived from a cross between the low-Cd-accumulating cultivar Sasanishiki (japonica) and high-Cd-accumulating cultivar Habataki (indica)	Ishikawa et al., 2010 [158]
	44	An F2 population, derived from a cross between a high Cd-accumulating cultivar (Anjana Dhan) as a female parent and a low Cd-accumulating cultivar (Nipponbare) as a male parent	Ueno et al., 2010 [76]
	15.1 – 124	Landraces	Zeng et al., 2010 [155]
	40 – 59	Wild type and transgenic rice of japonica (Nipponbare)	Johnson et al., 2011 [165]
	9.56 – 15.89	A doubled haploid population derived from a cross between japonica JX17 and indica ZYQ8 rice cultivars	Zhang et al., 2011 [159]
	30.017	Rice diversity panel (RDP) population	Norton et al., 2012 [166]
	26.2 – 67.3	Diverse rice genotypes	Anuradha et al., 2012 [36]
	0.4 – 104	F6 recombinant inbred lines (RILs) derived from the cross Madhukar × Swarna	Anuradha et al., 2012 [36]
	12	Wild type and transgenic rice of japonica cultivar Tsukinohikari	Masuda et al., 2012 [160]
	19.3 – 24	Diverse rice genotypes	Yuan et al., 2011 [168]
	13 – 42	Doubled-haploid (DH) population derived from a cross between CJ06 (a japonica) and TN1 (an indica)	Du et al., 2013 [90]
	4.4 – 157.4	An F2 population derived from the cross between high-yielding (PAU201) and iron-rich (Palman 579) indica rice varieties	Kumar et al., 2014 [169]
	18.0 – 33.0	RIL population derived from a cross between Lemont (a japonica) and TeQing (an indica)	Zhang et al., 2014 [45]
	32.36	Diverse rice genotypes: USDA Rice Mini-Core Collection consists of 211 *O. sativa*, 5 *O. glaberrima*, 2 *O. rufipogon*, and 1 *O. nivara* accession	Nawaz et al., 2015 [156]
Zn	24.29	Diverse rice genotypes	Pinson et al., 2015 [84]
	28.7	Diverse rice genotypes	Huang et al., 2015 [1]
	16 – 28	Wild type and transgenic rice	Trijatmiko et al., 2016 [21]
	7.1 – 64.7	Two BC2F3 mapping populations derived from the crosses of *O. sativa* cv Swarna with two different accessions of *O. nivara*	Swamy et al., 2018 [132]

25.69	Diverse rice genotypes	Yang et al., 2018 [7]
19.7 – 23.3	Diverse rice genotypes	Zhang et al., 2008 [66]
47.0	Diverse rice genotypes	Bollinedi et al., 2020 [20]
14.5 – 35.3	Diverse rice genotypes	Maganti et al., 2019 [171]
9.7 – 26.96	Landraces and diverse rice genotypes	Pradhan et al., 2020 [15]
3.15 – 5.54	Diverse rice genotypes	Moulick et al., 2022 [152]
17.98	Aromatic and non-aromatic rice accessions	Nath et al., 2022 [43]

A significant positive correlation was observed within all GEC in rice [156]. Between Fe and Zn concentration in rice grain showed a strong positive correlation, suggesting that higher Fe and Zn concentrations may occur simultaneously in rice grain [1]. Meanwhile, no close correlations were identified between Se and Fe or Zn concentration in rice grain. Fe, Zn, and Mn concentration in rice grain also displayed a positive correlation [91]. A significant negative association showed in Cu and K or Mg grain concentrations. There was no significant correlation between Fe and Cd. A strong positive correlation was found between Pb and Fe or Zn or Cd. Between As and Cd concentration in rice grain displayed a significant negative correlation [55]. There was a strong correlation between grain and straw As or Cd concentrations. The interaction between essential nutrient elements and toxic elements are needed further investigation to increase uptake desirable elements effectively and to reduce uptake undesirable elements. Elements with similar chemical characteristics may compete in absorption, transport, and function mechanisms in rice plant tissues. For example, heavy metal elements (Cu, Cd, Hg, Ni, and Pb) might make substitution of Mg in the central atom of chlorophyll, leading interruption in photosynthesis [177]. Absorption of Cu from the soil will be decreased by the presence of K [178]. Fe grain concentration was strongly correlated with Ca, Na, Mg, and K. Mn concentration in rice grain showed closely associated with Ca, Mg, and K. There was also positively relationship between Zn and Ca or Mg. Positively relationship were also found between Ca and Fe, Mg, Mn, Na, or Zn. Since Mg showed a positive association with other elements, suggesting Mg regulated other elements in the rice plants. Correlation analysis also showed close association between As and Cd, Cr and Ni, and As and Pb concentration in rice grains. These results suggest that high As and Cd grain concentrations would likely happen simultaneously. Meanwhile, Ni and Zn displayed a negative correlation [141].

Phloem transport of mineral elements from flag leaf to the grain during grain filling stage [179]. Molecular mechanisms or genes controlling the root uptake and/or transport and partitioning of elements between rice plant tissues and rice grains are influenced the accumulation patterns and GEC [84]. Under flooded conditions, Ca and Mn shared intracellular transporter at the early stages of grain formation, indicating Ca and Mn concentration in rice grain showed a significant positive correlation. Meanwhile, P, K, and Mg do not share uptake mechanisms under flooded and unflooded field conditions. Phytate concentration in rice grain showed strong correlation with P-Mg-K concentration in aleurone layer of rice grain [180].

Grain Elemental Concentration in Rice and Environmental Conditions

Environmental conditions also determined the composition and concentration of mineral nutrient elements and toxic elements in rice grains. These environmental conditions, including pH, salinity, water availability (drought, rainfall, etc), commercial fertilizers application, manures, and other contaminants caused by industry and mining [181,182,183,184]. When rice plants were grown at different location with variety environmental conditions, the heritability for most elements in rice grain was low [7]. The availability of elements in soil have a direct or indirect effect on the metabolism of rice plants, such as uptake, transport, mobilization, and accumulation in grains. Most of the mineral elements in rice grains have been supplied by root uptake and translocation from vegetative plant tissues to developing rice grains during grain filling stage [185,186,187]. Rice nutrient breeding program become slow due to lack understanding of the network of regulatory and physicochemical process controlling the directing elements uptake by roots from the soils or water and translocation of the elements through vegetative tissues and loaded into developing rice grains during grain filling stage. Fe concentration in rice grains is strongly affected by environment, genotype, and interaction of genotype and the environmental factors [171]. A number of studies showed that agricultural practices such as fertilizers application could influence the elements composition and concentration in rice grains. For example, nitrogen fertilizer application influenced Fe and Zn contents in rice grains [135]. Fe and Zn concentrations in rice grains can be improved by spraying Fe and Zn fertilizer to the leaves [168].

GEC is affected by the soil and other environmental factors in different countries and geographical regions with various conditions. This indicates that rice variety adapted to geographical regions which a particular element is excess or lacking, that may express special genes to enhance ability to absorb or detoxify specific elements. For example, deficiency of Fe, Ca, K, and Mo and toxicity of As and Cd are more specific to certain geographical regions with various soil conditions and water availability. Landraces and rice cultivars adapted to these particular regions may demonstrate improved ability to absorb desired elements and detoxify toxic elements to develop balanced rice varieties [84]. Extreme environments including drought, saline, and acid soils also affected Fe and Zn concentrations in rice grains among diverse rice accessions [35]. Water availability alters GEC in rice. For example, under flooded field condition, As concentration in rice grains showed 30 times higher concentrations than under unflooded condition. Meanwhile, Cd and Ni concentrations in rice grains under flooded condition showed 10 times lower compared with unflooded conditions [84]. Rice accessions from Malaysia and Brunei that belong to tropical japonica have high Mo concentration in their grains due to the soil conditions in this geographical regions having low pH and acidic soils. These rice accessions from Malaysia and Brunei also may share a heritable regulating mechanism which improved Mo concentrations in rice grains [84]. Several rice accessions, such as aus, indica and temperate japonica originated from East Europe when grown unflooded conditions, the Cd grain concentration exceeded the limit of 0.4 mg/g. None of the rice accessions from East Europe were found high for both Cd and Co concentration in rice grains [84].

Toxic heavy metal elements are found in both contaminated and uncontaminated soils and water. All of the heavy metal elements at higher concentrations are toxic to rice plants and human health [181,188]. Heavy metal elements that generally toxic to both plants and humans are As, Cd, Cr, Ni, and Pb. Heavy metals are showing significantly negative effects to rice plant growth by causing oxidative stress, displacing important elements in enzymes or pigments with heavy metals, leading to disruption many metabolism process (e.g., photosynthesis), and resulting decreasing plant growth and grain yield [189,190,191,192,193]. Al toxicity generally occurred in highly acidic soil conditions with pH 5.0, that is phytotoxic and causing root growth inhibition, leading impairment water and nutrients uptake [73]. Entering heavy metal elements to human food chain because of the uptake and accumulation in rice grains and affect to human health [194,195,196].

Mechanisms involved in accumulating As in rice grain from As contaminated soil, including As uptake, efflux from roots, loading into xylem, transport, partitioning, arsenate reduction, As sequestration in vacuoles, and As accumulation in grains. Among rice accessions, there were a diverse ability in As accumulation that provide possibility to select rice variety with low As accumulation. Identification of genes involved in As uptake, transport, and accumulation in rice grains is important that can accelerate the development of rice variety with low As accumulation safer for agriculture in As contaminated environments [197]. Cd uptake from soil to rice plants is strongly affected by soil conditions such as organic carbon content, clay content, cation exchange capacity, pH, and the coexistence of other heavy metals [158] [243]. Cd bioavailability is influenced by soil redox potential which varies in the field depending on water availability [198]. Cd accumulation in rice grains is positively correlated with the transport of essential trace elements, such as Cu, Mn, and Zn [158, 244, 247]. Se concentration in the xylem sap was significantly reduced with increasing Fe concentration in the rice rhizosphere [199]. Phloem sap loading and unloading rates during the grain filling stage affect Fe and Zn concentrations in rice grains [36]. Soil properties, such as organic matter content, pH, and Fe or Zn availability in soils also influence the grain Fe and Zn concentration [36]. Optimizing Fe availability in soils could effectively decrease Cd accumulation in the shoots by immobilizing Cd in the roots [163]. Rice grain characteristics, such as aleurone layer number, embryo and caryopsis size, nutrient availability in the rhizosphere, and molecular mechanism for elements uptake, transport and accumulation in grains, also determines the GEC [169].

Fe application in soil increase defense system of the rice plants [200]. Fe and Zn deficiency in soil leads to reduce plant growth, grain yield, and also Zn concentration in rice grain [84,201]. Application of Zn to the soil decrease disease severity due to Zn has toxic effect on the pathogen [36]. Na and K are macronutrients for rice plant growth and affect element concentrations in rice grains. The balance of Na and K in soil or water is important for normal rice plant growth and play an important role in adaptation of rice plants to salinity stress. Salt stress is one of major constraint to rice production worldwide [202]. Approximately 960 million hectares of agricultural area affected by salt [203]. The mechanism of salinity tolerance in rice plants are reduce Na uptake and increase absorption of K to maintain the balance of Na and K in rice plants [204,174]. Understanding the mechanism of Na and K accumulation in rice grains is important to provide useful information for developing rice variety with balanced concentration of Na and K in the grains. N and P concentrations in soil also affected many elements concentrations in rice grains [7]. Deficiency of N and P in the rice plants may affect transcription mechanism of many genes and change the root morphology, finally affect elements concentrations in rice grains [205]. Thus, soil fertility and climate condition might be the important factors affecting elemental accumulation in rice grains.

A number of mitigation approaches or management strategies that can be employed to reduce toxic elements (e.g., As and Cd) accumulation in rice grains [206–221]. These include (1) field water management; (2) liming of acidic soils with fly ash, limestone, calcium silicate, and calcium magnesium phosphate; (3) silicon (Si), bentonite, and gypsum application; (4) compost, manure, and biochar amendments; (5) exogenous application of microbes, (6) hormones (e.g., abscisic acid, salicylic acid, glutathione, jasmonic acid, nitric oxide, phytochelatins, polyamines, and brassinosteroids), and osmolytes; (7) phytoremediation; (8) crop rotation; and (9) breeding by using rice cultivars with low accumulation of toxic elements in the grains. Water management affects As and Cd accumulation differently among rice accessions. With increasing water availability in the field from aerobic, intermittent irrigation, conventional irrigation, until flooded field conditions increases As accumulation in rice grains, but decrease Cd accumulation in the grains [67,82,207,245]. During vegetative stage, anaerobic conditions of flooded field and the soil has a low redox potential, can effectively reduce Cd but increase As in rice grains [67]. Thus, aerobic conditions decrease As accumulation in rice grains. It is important to investigate mitigating approaches to decrease both As and Cd accumulation in rice grains simultaneously by water management. Maintaining water management both before and after the tillering stage affected As and Cd accumulation in the rice grains. Under flooded and unflooded conditions, the accumulation of Cd, Mo, and Rb in rice grains are significantly correlated [54]. Mo and Rb accumulation in rice grains are consistent under both flooded and unflooded conditions [54]. Balancing water management and selecting proper rice cultivars could produce low heavy metal concentrations in rice grains [82]. Liming reduces Cd uptake by the rice plants [222,223]. Phytoremediation has been effective to cleaning up toxic elements in small scale contaminated field, but remains uncertain in large scale field [224,225,226]. Breeding by using rice cultivars with low accumulation of toxic elements in the grains is effective method due to exist wide genetic variations among rice accessions [84,149,166,227].

Polishing, cooking, and storing of rice grains affect the toxic element concentrations. Toxic heavy metal elements in rice grains could be reduced through cooking methods of rice [197]. Rinsing the raw rice with excess water can decrease the As concentration up to 83%. Water-to-rice ratio (1:6 and above) also decreases As concentration up to 50%. As the water-to-rice ratio increases, the As concentration of cooked rice reduces [151]. Washing the raw rice with deionized water were decreased As concentration up to 84%. Polishing the rice grains by removing 10% bran by grain weight were decrease As concentration up to 70% in brown rice and up to 66% in white rice [150]. Storing the rice grains for one year do not reduce the As concentration [150].

Grain Elemental Compositions and their Relationship with other Agronomic Traits

A significant correlation was observed between GEC and flowering time, indicating that flowering time regulates the accumulation of elements in rice grains [156,166]. Accumulation of Rb in rice grains under flooded and unflooded conditions is strongly correlated with flowering time [54]. As concentration in rice grain is also determined by flowering time [136]. GEC is influenced by heading date. Heading date is an crucial agronomic trait for adaptation of the rice plants to various growth environmental conditions. Generally, rice genotypes with later heading date have longer vegetative stage, which have a longer time to uptake mineral elements from the soils, potentially accumulate the mineral elements in vegetative tissues followed by remobilization to the grains during grain filling stage, and also resulting higher grain yield. Extending the vegetative stage of the rice plants might be one of the effective approach for enhancing desired element concentrations in the grains considered mobility of the elements within the plants [84]. A significant positive correlation was found between heading date and the concentrations of Cd, Mn, and Pb [7,55]. Meanwhile, strongly negative correlation was detected between heading date and the grain concentrations of As, B, Ca, Cu, Fe, K, N, and P; which poorly remobilized within plants, resulting these elements accumulated in vegetative tissues and unavailable in the grains [7]. Mo concentration in rice grain is not determined by heading date [84]. The concentration of N in shoots of the rice plants is associated with heading date [7]. There was no significantly correlation between Fe and Zn concentrations in rice grains with any agronomical traits, including grain yield per plant, panicle length, grain weight, productive tiller number per plant, and plant height [169]. Meanwhile, Cd concentration in rice grain showed a significantly positive correlation with grain yield, but there was a negative correlation between As concentration and grain yield [55].

GEC was not showed to be a significantly correlated with grain shape, such as grain length, grain weight, and ratio of grain length and weight across 1763 diverse rice accessions [84]. Under unflooded condition, Fe was found weakly correlated with grain weight [84]. Meanwhile, Anuradha et al. (2012) [36] reported that Zn concentration exhibited significantly correlated to grain elongation. According to Zhang et al. (2004) [98] several elements in rice grains displayed positive correlation with the grain shape. For example, positive correlations were found between Fe content with 100-grain weight; Fe, Mn, and Zn contents with grain width; Mn and P contents with grain length; and P content with grain shape. Meanwhile, negative associations were detected between Mn and P contents with 100-grain weight; Zn content with grain length; Fe, Mn, and Zn content with grain shape. The content of several elements in rice grains depend on the grain size. Fe content in aromatic long grain basmati variety is high. Zn, Mn, and P content in narrow grains are higher than long grains. Fe and Mn contents are higher than short grains. Zn and P contents are higher in short grains than longer grains. P content is higher in bigger grain weight [36]. Phytate (inositol-hexa-phosphate) in rice grains have a significant positive correlation with the concentration of P, Cu, Fe, Mn, and Zn in grains [99].

Fe concentration in rice grains also associated with grain color. For example, purple-bran rice grains showed higher Fe concentration than the white grains [84]. Time of grain milling also affected Fe concentration. As milling time increase, Fe concentration in red pericarp varieties (e.g., Tong Lang Mo Mi, Xua Bue Nuo, and Jalmagna) became less. Decreased Fe concentration along with the changes color of red pericarp grain due to milling process from 15 to 45 minutes [35]. By milling process for 15 minutes, the Fe concentration of brown rice IR64 as a popular commercial rice variety decreased 30%. Thus, Fe accumulates in the outer layer of the rice grains [35]. During milling process, about 70% of nutrient elements are lost [40]. Different thickness of aleurone layer also associated with the GEC because of differences ability among the rice genotypes to translocate mineral elements from aleurone to endosperm [20].

Grain Elemental Compositions and Quality Traits of Rice

A significantly correlation was found between GEC and quality traits of rice, such as gel consistency, amylose content, alkali spreading value, amino acid contents, and aroma. Cu, K, and Mn concentration of polished grains were significantly associated with gel consistency. Mn concentration was related to gelatinization temperature. The concentration of Cu, K, Mg, Mn, and Na in rice grains were closely related to amylose content. Ca, Mg, and Mn grain concentrations had strongly positive correlations with alkali spreading value. The relationship among Ca, Cu, Fe, K, Mg, Mn, Na, and Zn concentrations in polished rice had significant correlations with amino acid contents. Ca, Mg, and Zn concentrations had obvious associations with 17 amino acid contents (proline, arginine, histidine, lysine, phenylalanine, tyrosine, leucine, isoleucine, methionine, valine, cysteine, alanine, glycine, glutaminic acid, serine, threonine, and aspartic acid). Meanwhile, Na concentration only correlated with aspartic acid. K concentration only has positive correlation with proline, histidine, tyrosine, methionine, cysteine, serine, and aspartic acid. Fe concentration showed closely association with tyrosine, methionine, cysteine, and alanine. Cu concentration was strongly positively correlated with alanine, but negatively associated with methionine and cysteine. Mn concentration was closely positively correlated with histidine, tyrosine, methionine, cysteine, and serine. These results indicated that these mineral elements might be increased with some amino acid contents and involved in N. Additionally, Cu, Mg, Mn, Na, and Zn concentrations showed significant relationship with protein content of rice [91]. Fe concentration exhibited a slight correlation with aroma of rice. Mg/K ratio of brown rice grains showed significant relationships with cooking quality. As concentration in rice grain was positively related to amylose content, cooking time, and gruel solid loss [152]. These relationships assist selection of appropriate rice varieties for specific desired nutritional contents.

The association between GEC and quality traits of rice indicating the physiological function of the minerals in metabolism mechanism of rice plants. For example, Mg is a component of chlorophyll structure, which is important in photosynthesis. Mg also essential for carbohydrate metabolism. Cu and Mn as enzyme cofactors which to be involved in chlorophyll formation. Cu also involved in protein synthesis. K has important roles in carbohydrate metabolism by translocate starches and sugars among plants organs. It is crucial to increase understanding of the correlation between GEC and rice quality to select rice genotypes for nutrient breeding program. Ca acts in carbohydrate transport and nitrogen uptake from soils. Zn also essential for carbohydrate metabolism and controlling sugar consumption. Mn is involved in nitrogen metabolism and carbohydrate breakdown [91]. These results suggested that a wide opportunity to develop rice variety with rich desired mineral nutrients by indirect selection.

Genomic Regions of Grain Elemental Concentrations in Rice

Genotypic factors, environmental conditions, and their interaction regulating the phenotypic variation of GEC [7,84]. A number of genes controlling the uptake, translocation, and accumulation of elements in rice grains have been detected. Identifying genes/quantitative trait loci (QTL) by integrating classical breeding, molecular markers, and transgenic assisted breeding methods will be useful to develop rice varieties with high desired elements and low toxic elements concentrations in the grains [131]. Bioinformatics analysis also an effective method to detected the genes associated with GEC. GEC trait belongs to the complex agronomical trait, thereby QTL analysis is an effective tool for identifying the genes regulating the complex traits. Identification of QTLs leading to the identification of the genes governing the GEC, such as Os-HKT1 transporter genes for Na, NRT1.11B for N, Os-HMA3 for Cd, and Os-HMA4 for Cu [76,229,230,231,232]. Validation of candidate genes within the QTL regions are important by using overexpressing and knock out candidate genes, yeast mutant, and gene expression analysis [7]. Gene networks regulating the GEC are important to be elucidated. Genetic variation for GEC have been studied [98,233]. Exploitation of genetic basis for enhancement in GEC have been employed not only cultivated rice but also wild rice to enrich favorable alleles controlling desired elements and reducing toxic elements accumulation in rice grains [90,100].

Numerous landraces, popular rice varieties, breeding lines, recombinant inbred line (RIL) population, doubled-haploid (DH) population, introgression lines (IL) population, backcross population, and other biparental populations collected all over the world have been used. Application of single nucleotide polymorphism (SNP) has been widely used to cover entire rice genome, that would identify genomic regions governing the GEC [20]. These favorable alleles are distributed in different rice accessions [1]. Recently, numerous QTLs, genes, and gene networks have been identified to be involved in regulating grain elemental concentrations by performing QTL mapping, genome-wide association study (GWAS), and transgenic approaches (Table 2). Genetic basis of 22 elements in rice grains provide in table 2, including arsenic (As), boron (B), calcium (Ca), cadmium (Cd), cobalt (Co), chromium (Cr), copper (Cu), iron (Fe), potassium (K), magnesium (Mg), mangan (Mn), molybdenum (Mb), nitrogen (N), sodium (Na), nickel (Ni), phosphor (P), lead (Pb), rubidium (Rb), sulphur (S), selenium (Se), strontium (Sr), and zinc (Zn).

Lu et al. (2008) [154] identified QTLs regulating Fe, Ca, Cu, Mn, and Zn concentration in rice grains on seven chromosomes and several of these QTLs are co-localized with loci controlling for plant height, grain yield, biomass, and sheath blight resistance. These results indicating that genes regulating GEC might be involved in the grain yield and developmental process of rice plants. A total of 41 QTLs accounting for 17 essential elements and 3 toxic elements (As, Cd, and Pb) in rice grains have been identified [138]. QTLs might be pleiotropy, which several loci correlated with more than one trait, and form clustered QTLs. Clustered QTLs that one loci controlled different elements provide important information for enhancing several different desired elements in rice grains simultaneously. Pleiotropy of these genes governed the metabolism of several elements. Zhang et al. (2014) [45], detected 39 clustered QTLs correlated with 16 elements in rice grains from 134 QTLs. A total of 14 QTLs associated with Fe and Zn concentration in rice grains and identified candidate genes within the QTL regions, such as *OsMTP1* and *OsYSL1* controlling Fe concentration, and *OsNAS1, OsNAS2, OsIRT1,* and *OsARD2* regulating Zn accumulation in rice grains [36]. Co-localized QTLs regulated both Fe and Zn concentrations in rice grains were found on chromosome 7 and 12 [36]. Additionally, co-localizations of QTLs for Fe, K, Mg, Mn, P, and Zn were identified on chromosome 8 and 9 [90]. Co-localization of QTLs for different element accumulations in rice grains were observed, including Mg and Mn on chromosome 6, Mg and P on chromosome 6, Mn and Z on chromosome 3, Pb and Zn on chromosome 7, Pb and Cd on chromosome 5, and Pb and Se on chromosome 11 [1,90]. OsNRAMP5 has been identified as a gene which responsible for Cd and Mn uptake from soils. By regulating the gene expression of OsNRAMP5 could be used for developing rice varieties with high Mn and low Cd concentrations in rice grains [173]. QTL regulating

Cd concentration in rice grains was found on chromosome 7 [158, 246]. Identification for new QTLs for GEC is necessary to support rice biofortification breeding program [1].

GWAS use diverse rice genotypes to identify genetic basis for phenotypic variation of elements accumulation in rice grains and to exploit molecular mechanism of GEC in rice grains, such as elements uptake from the soils and their accumulation in the grains. GWAS accelerated identifying genomic regions and candidate genes associated with GEC. GWAS data also more accurate than other mapping studies [45,103,236]. Bollinedi et al. (2020) [20] used GWAS to identify genomic regions associated with Fe and Zn concentrations in rice grains by using 192 rice accessions, including popular rice varieties, landraces, Basmati accessions, and breeding lines from elite parent that provide donor alleles. Identifying genes related to Fe and Zn concentrations in rice grains by using GWAS also done by Anuradha et al. (2012) [36], which use 168 RILs derived from crossing Madhukar x Swarna. Several candidate genes were identified, including *OsMTP1* and *OsYSL1* regulating Fe; *OsNAS1, OsNAS2, OsIRT1,* and *OsARD2* controlling Zn. Several studies also used GWAS to identify genomic regions controlling As, Cu, Mo, and Zn accumulation in rice grains [136]; Fe, Ca, Cu, K, Mg, Mn, P, and Zn accumulation in brown rice [156]; and Al tolerance [73]. Genomic regions associated with 17 elements (As, B, Ca, Cd, Cu, Co, Cr, Fe, K, Mg, Mn, Mo, N, Na, P, Pb, and Zn) in rice grains also identified by GWAS using 529 diverse rice genotypes and 6.4 million SNP markers [7]. OsWRKY102 was identified as the regulator of Cd uptake from soils and accumulate in rice grains [54]. Cd concentration in rice grains might be decreased by suppressing the gene expressing level of OsHMA2 [237]. Comparative element mapping based on GWAS data of rice and Arabidopsis provides important information about the genetic architecture in natural element variations of rice and other plant species [7]. More than 200 new genomic regions associated with GEC were identified in the rice genome [54]. Candidate genes within the genomic regions were identified and analyze their gene expression.

Table 2. Genetic basis of grain elemental concentrations in rice

Elements in the Rice Grains	Chromosome	Loci	References
As	2	-	(Zhang et al., 2014) [45]
	3	-	(Zhang et al., 2014) [45]
	5	-	(Norton et al., 2014) [136]
		-	(Zhang et al., 2014) [45]
	6	-	(Zhang et al., 2008) [66]
		-	(Kuramata et al., 2013) [149]
	8	-	(Zhang et al., 2008) [66]
		-	(Kuramata et al., 2013) [149]
		LOC_Os08g37600	(Yang et al., 2018) [7]
		LOC_Os08g37950	(Yang et al., 2018) [7]
	9	-	(Zhang et al., 2014) [7]
		LOC_Os09g37300	(Yang et al., 2018) [7]
		LOC_Os09g37610	(Yang et al., 2018) [7]
	11	-	(Zhang et al., 2014) [45]
B	4	LOC_Os04g02720	(Yang et al., 2018) [7]
	9	LOC_Os09g36040	(Yang et al., 2018) [7]
Ca	1	-	(Garcia-Oliveira et al., 2009) [100]
	2	-	(Nawaz et al., 2015) [156]
	3	-	(Du et al., 2013) [90]
		-	(Zhang et al., 2014) [45]
		-	(Nawaz et al., 2015) [156]
		LOC_Os03g07600	(Yang et al., 2018) [7]
		LOC_Os03g08070	(Yang et al., 2018) [7]
		LOC_Os03g08230	(Yang et al., 2018) [7]
		LOC_Os03g08380	(Yang et al., 2018) [7]

	4	-	(Lu et al., 2008) [154]
		-	(Garcia-Oliveira et al., 2009) [100]
		-	(Zhang et al., 2014) [45]
	5	-	(Lu et al., 2008) [154]
		-	(Garcia-Oliveira et al., 2009) [100]
	8	LOC_Os08g43120	(Yang et al., 2018) [7]
	9	-	(Lu et al., 2008) [154]
		-	(Garcia-Oliveira et al., 2009) [100]
		LOC_Os09g03310	(Yang et al., 2018) [7]
	10	-	(Garcia-Oliveira et al., 2009) [100]
		-	(Du et al., 2013) [90]
		-	(Zhang et al., 2014) [45]
	11	-	(Garcia-Oliveira et al., 2009) [100]
		-	(Du et al., 2013) [90]
	12	-	(Garcia-Oliveira et al., 2009) [100]
		-	(Zhang et al., 2014) [45]
Cd	1	-	(Norton et al., 2010) [136]
		-	(Zhang et al., 2014) [45]
		OsWRKY102	(Liu et al., 2020) [54]
	2	-	(Ishikawa et al., 2010) [158]
		-	(Norton et al., 2010) [138]
		-	(Zhang et al., 2014) [45]
		-	(Luo et al., 2018) [162]
		LOC_Os02g53490	(Yang et al., 2018) [7]
		CAL1	(Liu et al., 2020) [54]
	3	-	(Norton et al., 2010) [138]
		-	(Ueno et al., 2010) [76]
		-	(Zhang et al., 2011) [159]
		-	(Zhang et al., 2014) [45]
		-	(Huang et al., 2015) [1]
	4	-	(Zhang et al., 2011) [159]
		-	(Luo et al., 2018) [162]
		-	(Liu et al., 2020) [54]
	5	-	(Zhang et al., 2014) [45]
		-	(Huang et al., 2015) [1]
		OsWRKY75	(Liu et al., 2020) [54]
	6	-	(Ueno et al., 2010) [76]
		-	(Zhang et al., 2011) [159]
		-	(Zhang et al., 2014) [45]
		OsMan07	(Liu et al., 2020) [54]
		OsHMA2	(Liu et al., 2020) [54]
	7	-	(Ueno et al., 2010) [76]
		-	(Ishikawa et al., 2010) [158]
		-	(Norton et al., 2010) [138]
		-	(Liu et al., 2020) [54]
	8	-	(Ueno et al., 2010) [76]
		-	(Zhang et al., 2014) [45]
		LOC_Os08g08070	(Yang et al., 2018) [7]
		-	(Liu et al., 2020) [54]
	9	-	(Norton et al., 2010) [138]
		-	(Zhang et al., 2014) [45]
		gcc9	(Liu et al., 2020) [54]
	10	-	(Norton et al., 2010) [138]
	11	-	(Luo et al., 2018) [162]
		qcd11	(Liu et al., 2020) [54]
		rgMT	(Liu et al., 2020) [54]
	12	-	(Liu et al., 2020) [54]

Co	1	-	(Zhang et al., 2014) [45]
		-	(Liu et al., 2020) [54]
	2	-	(Liu et al., 2020) [54]
	3	-	(Norton et al., 2010) [138]
		-	(Liu et al., 2020) [54]
	5	LOC_Os05g40740	(Yang et al., 2018) [7]
	6	-	(Zhang et al., 2014) [45]
		-	(Liu et al., 2020) [54]
	7	-	(Zhang et al., 2014) [45]
	8	-	(Zhang et al., 2014) [45]
	9	-	(Liu et al., 2020) [54]
	10	-	(Liu et al., 2020) [54]
	11	-	(Zhang et al., 2014) [45]
		-	(Liu et al., 2020) [54]
Cr	6	LOC_Os06g30730	(Yang et al., 2018) [7]
		LOC_Os06g30950	(Yang et al., 2018) [7]
	7	LOC_Os07g48760	(Yang et al., 2018) [7]
		LOC_Os07g48980	(Yang et al., 2018) [7]
	11	LOC_Os11g38160	(Yang et al., 2018) [7]
Cu	1	-	(Norton et al., 2010) [138]
		-	(Norton et al., 2014) [136]
		-	(Zhang et al., 2014) [45]
	2	-	(Lu et al., 2008) [154]
		-	(Norton et al., 2010) [138]
		-	(Zhang et al., 2014)[45]
	3	-	(Zhang et al., 2014) [45]
		-	(Nawaz et al., 2015) [156]
	4	-	(Zhang et al., 2014) [45]
	5	-	(Zhang et al., 2014) [45]
		-	(Norton et al., 2014) [136]
	6	-	(Garcia-Oliveira et al., 2009) [100]
	7	-	(Zhang et al., 2014) [45]
		LOC_Os07g15370	(Yang et al., 2018) [7]
		LOC_Os07g15460	(Yang et al., 2018) [7]
		-	(Liu et al., 2020) [54]
	8	-	(Zhang et al., 2014) [45]
		LOC_Os08g05820	(Yang et al., 2018) [7]
		LOC_Os08g05910	(Yang et al., 2018) [7]
		LOC_Os08g06010	(Yang et al., 2018) [7]
	9	-	(Zhang et al., 2014) [45]
	11	-	(Zhang et al., 2014) [45]
		-	(Liu et al., 2020) [54]
	12	-	(Zhang et al., 2014) [45]
		-	(Liu et al., 2020) [54]
		-	(Norton et al., 2010) [138]
Fe	1	-	(Lu et al., 2008) [154]
		-	(Norton et al., 2010) [138]
		LOC_Os01g13710 (*OsYSL1*)	(Anuradha et al., 2012) [36]
		-	(Du et al., 2013) [90]
		-	(Zhang et al., 2014) [45]
		-	(Nawaz et al., 2015) [156]
		LOC_Os01g0503400 (*OsNRAMP6*)	(Swamy et al., 2018) [132]
		LOC_Os01g0238700 (*OsYSL1*)	(Swamy et al., 2018) [132]
	2	-	(Stangoulis et al., 2007) [99]
		-	(Garcia-Oliveira et al., 2009) [100]
		-	(Kumar et al., 2014) [169]
		-	(Zhang et al., 2014) [45]

		-	(Nawaz et al., 2015) [156]
		LOC_Os02g0306401 (*OsNAAT1*)	(Swamy et al., 2018) [132]
		-	(Bollinedi et al., 2020) [20]
	3	-	(Norton et al., 2010) [138]
		-	(Kumar et al., 2014) [169]
		-	(Zhang et al., 2014) [45]
		-	(Nawaz et al., 2015) [156]
		LOC_Os0307200 (*OsNAS2*)	(Swamy et al., 2018) [132]
		LOC_Os03g0307300 (*OsNAS1*)	(Swamy et al., 2018) [132]
		OsMIT	(Bollinedi et al., 2020) [20]
		-	(Pradhan et al., 2020) [15]
Fe	4	-	(Ishikawa et al., 2010) [158]
		-	(Norton et al., 2010) [138]
		-	(Zhang et al., 2014) [45]
		LOC_Os04g0444800 (*OsFRO1*)	(Swamy et al., 2018) [132]
		LOC_Os04t0578600-02 (*OsFRO2*)	(Swamy et al., 2018) [132]
		LOC_Os04g0542800 (*OsYSL16*)	(Swamy et al., 2018) [132]
		LOC_Os04g39380	(Yang et al., 2018) [7]
	5	LOC_Os05g03780 (*OsMTP1*)	(Anuradha et al., 2012) [36]
		LOC_Os05g07210 (*OsZIP6*)	(Anuradha et al., 2012) [36]
		LOC_Os05g10940 (*OsZIP7*)	(Anuradha et al., 2012) [36]
		LOC_Os05g16290 (*OsYSL4*)	(Anuradha et al., 2012) [36]
		-	(Zhang et al., 2014) [45]
		-	(Huang et al., 2015) [1]
		LOC_Os04g39380	(Yang et al., 2018) [7]
	6	-	(Du et al., 2013) [90]
		-	(Zhang et al., 2014) [45]
		LOC_Os04g39380	(Yang et al., 2018) [7]
		OsNRAMP3	(Bollinedi et al., 2020) [20]
	7	-	(Norton et al., 2010) [138]
		LOC_Os07g48980 (*OsNAS3*)	(Anuradha et al., 2012) [36]
		LOC_Os07g15460 (*OsNRAMP1*)	(Anuradha et al., 2012) [36]
		LOC_Os07g43040	(Anuradha et al., 2012) [36]
		LOC_Os07g12890 (*OsZIP8*)	(Anuradha et al., 2012) [36]
		-	(Kumar et al., 2014) [169]
		-	(Zhang et al., 2014) [45]
		LOC_Os04g39380	(Yang et al., 2018) [7]
		-	(Bollinedi et al., 2020) [20]
		-	(Pradhan et al., 2020) [15]
	8	-	(Stangoulis et al., 2007) [99]
		-	(Du et al., 2013) [90]
		-	(Zhang et al., 2014) [45]
		LOC_Os08g0207500 (*OsZIP4*)	(Swamy et al., 2018) [132]
		LOC_Os08g0290300 (*OsYSL17*)	(Swamy et al., 2018) [132]
		-	(Pradhan et al., 2020) [15]
	9	-	(Lu et al., 2008) [154]
		-	(Garcia-Oliveira et al., 2009) [100]
		-	(Huang et al., 2015) [1]
	10	-	(Kumar et al., 2014) [169]
		-	(Zhang et al., 2014) [45]
		LOC_Os10g02340	(Yang et al., 2018) [7]
	11	LOC_Os11g0184900 (*OsNAC5*)	(Swamy et al., 2018) [132]
	12	-	(Stangoulis et al., 2007) [99]
		LOC_Os12g39860 (*APRT*)	(Anuradha et al., 2012) [36]
		-	(Kumar et al., 2014) [169]
		-	(Huang et al., 2015) [1]
		LOC_Os10g02340	(Yang et al., 2018) [7]

		-	(Pradhan et al., 2020) [15]
K	1	-	(Garcia-Oliveira et al., 2009) [100]
		-	(Zhang et al., 2014) [45]
		LOC_Os01g62070	(Yang et al., 2018) [7]
		OsMKK6	(Liu et al., 2020) [54]
		OsNPKL1	(Chen et al., 2021) [174]
		OsNPKL2	(Chen et al., 2021) [174]
		OsNPKL3	(Chen et al., 2021) [174]
		OsNPKL4	(Chen et al., 2021) [174]
	2	-	(Du et al., 2013) [90]
		-	(Zhang et al., 2014) [45]
		OsSKIPa	(Chen et al., 2021) [174]
	3	LOC_Os03g08230	(Yang et al., 2018) [7]
		LOC_Os03g08380	(Yang et al., 2018) [7]
	4	-	(Garcia-Oliveira et al., 2009) [100]
		-	(Zhang et al., 2014) [45]
		-	(Liu et al., 2020) [54]
		OsCPKI3	(Chen et al., 2021) [174]
	5	-	(Zhang et al., 2014) [45]
	6	-	(Du et al., 2013) [90]
	7	-	(Norton et al., 2010) [138]
		-	(Zhang et al., 2014) [45]
		SAPK2	(Chen et al., 2021) [174]
	8	-	(Garcia-Oliveira et al., 2009) [100]
		-	(Du et al., 2013) [90]
	9	-	(Garcia-Oliveira et al., 2009) [100]
		-	(Du et al., 2013) [90]
		-	(Zhang et al., 2014) [45]
		-	(Nawaz et al., 2015) [156]
	11	-	(Zhang et al., 2014) [45]
		LOC_Os11g40540	(Yang et al., 2018) [7]
		-	(Liu et al., 2020) [54]
Mg	1	-	(Garcia-Oliveira et al., 2009) [100]
	2	-	(Zhang et al., 2014) [45]
	3	-	(Norton et al., 2010) [138]
		-	(Nawaz et al., 2015) [156]
	4	-	(Norton et al., 2010) [138]
	5	-	(Garcia-Oliveira et al., 2009) [100]
		-	(Zhang et al., 2014) [45]
	6	-	(Du et al., 2013) [90]
		-	(Zhang et al., 2014) [45]
		LOC_Os06g06440	(Yang et al., 2018) [7]
	7	-	(Zhang et al., 2014) [45]
	8	-	(Du et al., 2013) [90]
	9	-	(Garcia-Oliveira et al., 2009) [100]
		-	(Norton et al., 2010) [138]
		-	(Du et al., 2013) [90]
	10	-	(Norton et al., 2010) [138]
		-	(Zhang et al., 2014) [45]
	11	-	(Norton et al., 2010) [138]
		-	(Zhang et al., 2014) [45]
		LOC_Os11g05010	(Yang et al., 2018) [7]
		LOC_Os11g05390	(Yang et al., 2018) [7]
	12	-	(Garcia-Oliveira et al., 2009) [100]
		-	(Zhang et al., 2014) [45]
Mn	1	-	(Stangoulis et al., 2007) [99]
		-	(Lu et al., 2008) [154]

		-	(Garcia-Oliveira et al., 2009) [100]
		-	(Ishikawa et al., 2010) [158]
	2	-	(Garcia-Oliveira et al., 2009) [100]
		-	(Ishikawa et al., 2010) [158]
		-	(Zhang et al., 2014) [45]
	3	-	(Garcia-Oliveira et al., 2009) [100]
		-	(Du et al., 2013) [90]
		-	(Zhang et al., 2014) [45]
	4	-	(Zhang et al., 2014) [45]
		-	(Nawaz et al., 2015) [156]
	6	-	(Zhang et al., 2014) [45]
	7	-	(Ishikawa et al., 2010) [158]
		-	(Zhang et al., 2014) [45]
		OsNRAMP5	(Liu et al., 2017) [173]
		LOC_Os07g15370	(Yang et al., 2018) [7]
		LOC_Os07g15460	(Yang et al., 2018) [7]
		LOC_Os07g15460	(Yang et al., 2018) [7]
	8		(Du et al., 2013) [90]
		-	(Zhang et al., 2014) [45]
	9	-	(Du et al., 2013) [90]
		LOC_Os09g16290	(Yang et al., 2018) [7]
	10	-	(Norton et al., 2010) [138]
		-	(Garcia-Oliveira et al., 2009) [100]
	11	-	(Norton et al., 2010) [138]
		-	(Zhang et al., 2014) [45]
		LOC_Os11g43860	(Yang et al., 2018) [7]
		LOC_Os11g47809	(Yang et al., 2018) [7]
	12	-	(Ishikawa et al., 2010) [158]
		-	(Zhang et al., 2014) [45]
Mo	1	-	(Norton et al., 2010) [138]
		-	(Zhang et al., 2014) [45]
		-	(Liu et al., 2020) [54]
	2	-	(Norton et al., 2010) [138]
		-	(Zhang et al., 2014) [45]
		-	(Liu et al., 2020) [54]
	3	-	(Norton et al., 2010) [138]
		-	(Zhang et al., 2014) [45]
		LOC_Os03g32630	(Yang et al., 2018) [7]
		LOC_Os03g37411	(Yang et al., 2018) [7]
		-	(Liu et al., 2020) [54]
	5	-	(Liu et al., 2020) [54]
	6	-	(Liu et al., 2020) [54]
	7	-	(Zhang et al., 2014) [45]
		-	(Liu et al., 2020) [54]
	8	-	(Zhang et al., 2014) [45]
		LOC_Os08g01030	(Yang et al., 2018) [7]
		LOC_Os08g01120	(Yang et al., 2018) [7]
		LOC_Os08g03350	(Yang et al., 2018) [7]
		LOC_Os08g04110	(Yang et al., 2018) [7]
		-	(Liu et al., 2020) [54]
	9	-	(Norton et al., 2010) [138]
		-	(Liu et al., 2020) [54]
	10	-	(Norton et al., 2014) [136]
		-	(Zhang et al., 2014) [45]
	12	-	(Liu et al., 2020) [54]
N	6	LOC_Os06g05860	(Yang et al., 2018) [7]
		LOC_Os06g05980	(Yang et al., 2018) [7]

		LOC_Os06g30730	(Yang et al., 2018) [7]
	12	LOC_Os12g39990	(Yang et al., 2018) [7]
Na	1	LOC_Os01g20160	(Yang et al., 2018) [7]
		OsHSP17.0	(Chen et al., 2021) [174]
		OsHKT1;5	(Chen et al., 2021) [174]
	2	*OsCAX4*	(Chen et al., 2021) [174]
		SRZ1	(Chen et al., 2021) [174]
		LOC_Os02g32490	(Chen et al., 2021) [174]
		Lip9	(Chen et al., 2021) [174]
		OsFAD2-1	(Chen et al., 2021) [174]
	3	*OSEDR1*	(Chen et al., 2021) [174]
		OsA3	(Chen et al., 2021) [174]
	5	*OsNHX3*	(Chen et al., 2021) [174]
		OsBURP06	(Chen et al., 2021) [174]
		OsBURP02	(Chen et al., 2021) [174]
		OsBURP08	(Chen et al., 2021) [174]
		OsP5CS1	(Chen et al., 2021) [174]
		OsPP2C49	(Chen et al., 2021) [174]
	6	*OsDREB1C*	(Chen et al., 2021) [174]
		OsABF2	(Chen et al., 2021) [174]
	7	*OsAPX2*	(Chen et al., 2021) [174]
	11	*OsCCX5*	(Chen et al., 2021) [174]
		OsSAE1a	(Chen et al., 2021) [174]
		OsNHX2	(Chen et al., 2021) [174]
	12	*OsCBL6*	(Chen et al., 2021) [174]
		OsHSP23.7	(Chen et al., 2021) [174]
Ni	1	-	(Zhang et al., 2014) [45]
	2	-	(Zhang et al., 2014) [45]
	3	-	(Zhang et al., 2014) [45]
	4	-	(Liu et al., 2020) [54]
	5	-	(Zhang et al., 2014) [45]
	6	-	(Liu et al., 2020) [54]
	8	-	(Zhang et al., 2014) [45]
		-	(Liu et al., 2020) [54]
	9	-	(Norton et al., 2010) [138]
P	1	-	(Garcia-Oliveira et al., 2009) [100]
		-	(Norton et al., 2010) [138]
		-	(Zhang et al., 2014) [45]
	2	-	(Norton et al., 2010) [138]
		-	(Du et al., 2013) [90]
		-	(Zhang et al., 2014) [45]
	3	-	(Garcia-Oliveira et al., 2009) [100]
		-	(Zhang et al., 2014) [45]
		-	(Nawaz et al., 2015) [156]
	4	-	(Norton et al., 2010) [138]
	5	-	(Zhang et al., 2014) [45]
	6	-	(Norton et al., 2010) [138]
		-	(Du et al., 2013) [90]
		-	(Zhang et al., 2014) [45]
	7	-	(Zhang et al., 2014) [45]
		LOC_Os07g37890	(Yang et al., 2018) [7]
		LOC_Os07g38070	(Yang et al., 2018) [7]
	8	-	(Garcia-Oliveira et al., 2009) [100]
		-	(Du et al., 2013) [90]
	9	-	(Garcia-Oliveira et al., 2009) [100]
		-	(Norton et al., 2010) [138]
		-	(Du et al., 2013) [90]

	11	-	(Zhang et al., 2014) [45]
		LOC_Os11g38810	(Yang et al., 2018) [7]
	12	-	(Garcia-Oliveira et al., 2009) [100]
		-	(Zhang et al., 2014) [45]
Pb	1	-	(Norton et al., 2010) [138]
		-	(Huang et al., 2015) [1]
	3	-	(Huang et al., 2015) [1]
	4	-	(Norton et al., 2010) [138]
		LOC_Os04g46940	(Yang et al., 2018) [7]
		LOC_Os04g47930	(Yang et al., 2018) [7]
	5	-	(Huang et al., 2015) [1]
	6	-	(Norton et al., 2010) [138]
	7	-	(Huang et al., 2015) [1]
	9	LOC_Os09g29430	(Yang et al., 2018) [7]
	11	-	(Huang et al., 2015) [1]
	12	-	(Norton et al., 2010) [138]
Rb	4	-	(Liu et al., 2020) [54]
	6	-	(Liu et al., 2020) [54]
	9	-	(Liu et al., 2020) [54]
	11	-	(Liu et al., 2020) [54]
S	1	-	(Zhang et al., 2014) [45]
	2	-	(Zhang et al., 2014) [45]
	3	-	(Zhang et al., 2014) [45]
	4	-	(Zhang et al., 2014) [45]
	5	-	(Zhang et al., 2014) [45]
	6	-	(Zhang et al., 2014) [45]
	7	-	(Zhang et al., 2014) [45]
	8	-	(Zhang et al., 2014) [45]
	9	-	(Zhang et al., 2014) [45]
	10	-	(Zhang et al., 2014) [45]
Se	1	-	(Norton et al., 2010) [138]
	3	-	(Norton et al., 2010) [138]
	6	-	(Norton et al., 2010) [138]
		-	(Huang et al., 2015) [1]
	7	-	(Norton et al., 2010) [138]
	8	-	(Huang et al., 2015) [1]
	9	-	(Norton et al., 2010) [138]
	10	-	(Huang et al., 2015) [1]
	11	-	(Huang et al., 2015) [1]
Sr	6	-	(Liu et al., 2020) [54]
	9	-	(Liu et al., 2020) [54]
	11	-	(Liu et al., 2020) [54]
Zn	1	-	(Norton et al., 2014) [136] & (Nawaz et al., 2015) [156] & (Bollinedi et al., 2020) [20] & (Liu et al., 2020) [54]
		-	(Stangoulis et al., 2007) [99]
		LOC_Os01g0816100 (*OsNAC4*)	(Swamy et al., 2018) [132]
		LOC_Os01g0834400 (*OsHAP3*)	(Swamy et al., 2018) [132]
	2		(Kumar et al., 2014) [169]
			(Bollinedi et al., 2020) [20]
			(Pradhan et al., 2020) [15]
	3	LOC_Os03g19420 (*OsNAS2*)	(Anuradha et al., 2012) [36]
		LOC_Os03g19427 (*OsNAS1*)	(Anuradha et al., 2012) [36]
		LOC_Os03g06620 (*OsARD2*)	(Anuradha et al., 2012) [36]
		LOC_Os03g46470 (*OsIRT1*)	(Anuradha et al., 2012) [36]
		LOC_Os03g19427 (*OsNAS1*)	(Anuradha et al., 2012) [36]
		LOC_Os03g19420 (*OsNAS2*)	(Anuradha et al., 2012) [36]

		-	(Du et al., 2013) [90]
		-	(Norton et al., 2014) [136] & (Nawaz et al., 2015) [156] & (Bollinedi et al., 2020) [20] & (Liu et al., 2020) [54]
		-	(Pradhan et al., 2020) [15]
	4	-	(Zhang et al., 2011) [159]
		-	(Huang et al., 2015) [1]
		OsZIP3	(Bollinedi et al., 2020) [20]
	5	-	(Lu et al., 2008) [154]
		-	(Garcia-Oliveira et al., 2009) [100]
		LOC_Os05g0111300	(Swamy et al., 2018) [132]
		LOC_Os05g41070	(Yang et al., 2018) [7]
		-	(Bollinedi et al., 2020) [20]
	6	-	(Norton et al., 2010) [138]
		-	(Zhang et al., 2011) [159]
		-	(Huang et al., 2015) [1]
		LOC_Os06g0676000 (*OsNRAMP3*)	(Swamy et al., 2018) [132]
		LOC_Os06g39960	(Yang et al., 2018) [7]
		-	(Bollinedi et al., 2020) [20]
		-	(Liu et al., 2020) [54]
Zn	7	-	(Lu et al., 2008) [154]
		-	(Norton et al., 2010) [138]
		LOC_Os07g48980 (*OsNAS3*)	(Anuradha et al., 2012) [36]
		LOC_Os07g15460 (*OsNRAMP1*)	(Anuradha et al., 2012) [36]
		LOC_Os07g43040	(Anuradha et al., 2012) [36]
		LOC_Os07g12890	(Anuradha et al., 2012) [36]
		-	(Huang et al., 2015) [1]
		LOC_Os06g39960	(Yang et al., 2018) [7]
		-	(Bollinedi et al., 2020) [20]
		qZN-7	(Liu et al., 2020) [54]
		-	(Pradhan et al., 2020) [15]
	8	-	(Garcia-Oliveira et al., 2009) [100]
		-	(Du et al., 2013) [90]
		LOC_Os06g39960	(Yang et al., 2018) [7]
		-	(Bollinedi et al., 2020) [20]
		-	(Liu et al., 2020) [54]
		-	(Pradhan et al., 2020) [15]
	9	-	(Du et al., 2013) [90]
		-	(Huang et al., 2015) [1]
		LOC_Os06g39960	(Yang et al., 2018) [7]
		-	(Bollinedi et al., 2020) [20]
	10	-	(Norton et al., 2010) [138]
		-	(Kumar et al., 2014) [169]
		-	(Bollinedi et al., 2020) [20]
		qZN10.1	(Liu et al., 2020) [54]
	11	-	(Lu et al., 2008) [154]
		-	(Huang et al., 2015) [1]
		-	(Liu et al., 2020) [54]
	12	-	(Garcia-Oliveira et al., 2009) [100]
		LOC_Os12g39860 (*APRT*)	(Anuradha et al., 2012) [36]
		-	(Stangoulis et al., 2007) [99]
		Myb transcription factor	(Swamy et al., 2018) [132]
		-	(Liu et al., 2020) [54]
		-	(Pradhan et al., 2020) [15]

A number of genes which have been detected as being associated with the uptake, translocate, and accumulation of Fe, Cd, Cu, Mg, and Zn in rice plants. These genes including NRAMPs (Natural Resistance Associated Macrophage Proteins), copper chaperone proteins, metallotheioneins, COPT (COPper Transporter)/Ctr (Copper transporter) family, MTPs (metal tolerance proteins), HMA (heavy metal transporting ATPase) family, YSL (yellow stripe-like) proteins, Iron-regulated transporter (IRT)-like protein family, and ZIP (Zinc-regulated transporter). There were six ZIP genes, such as ZIP1, 3, 4, 5, 71, and 8 which involved in Zn transport in rice plants [136]. Based on microarray and northern blot analysis, OsZIP4 showed highly expression in shoots and roots especially in phloem cells under Zn deficiency conditions [27]. Under Zn deficiency environments, OsZIP4 was more abundant than OsZIP1 and OsZIP3 which were revealed by real-time-PCR. Thus, OsZIP4 plays an important role in translocation of Zn in rice plants. Overexpression of OsZIP8 disturbed the Zn transportation in rice plants, resulting an increase Zn in the roots, and low Zn accumulation in shoots and mature grains [238]. Balanced Zn contents in rice plants is important to normal growth and development of rice plants. COPT family genes that associated with Cu transport in rice plants, consist of six genes, including COPT1, 2, 3, 4, 5, 6, and 7. COPT1 (LOC_Os01g56420) and COPT2 (LOC_Os01g56430) located on chromosome 1 [136]. Nicotianamine synthase (NAS) family genes, such as OsNAS1 and OsNAS2 have been identified to be associated with increasing Fe and Zn in rice grains [156]. Activation and overexpression of NAS genes resulted in highly increasing Fe and Zn concentrations in rice grains [164,165].

Fe concentration in rice grains could be increased by overexpression genes which involved in Fe uptake from soils, translocation from root, shoot, to flag leaf, and accumulation in rice grains. Many genes showed pleiotropic of Fe and Zn, including Nicotianamine Synthase (NAS) genes. Activation or overexpression of NAS genes (OsNAS1 (LOC_Os03g19427), OsNAS2 (LOC_Os03g19420), and OsNAS3 (LOC_Os07g48980)) resulted in enhancement of Fe and Zn 2-to 3-fold higher Fe and Zn in unpolished and polished rice grains. Fe and Zn concentration in unpolished rice grains showed positive correlation with nicotianamine concentration [165,248]. By overexpression of multiple genes could enhanced mineral elements concentration in rice grains and provide solution to mineral deficiently worldwide [131,249,250].

Os-HKT1 has been shown to be involved in Na transportation in rice plants [7]. Os-MOLYBDATE transporter correlated with Mo transportation, grain number, heading date, and plant height [7]. By using knockdown mutants, OsMIT on chromosome 3 has been detected to be associated with Fe accumulation in rice grains [20]. Genome editing method, such as CRISPR/Cas9 has been applied for Fe bio-fortification in rice grains [21,160,239,240,241]. Four candidate genes which identified by GWAS, including OsFAD2_1, LOC_Os02g32490, OsNHX2, and OsHKT1;5 related to Na and K concentration in rice grains [174]. OsNHX2 regulates accumulation of toxic Na in bundle sheath and leaf mesophyll, resulting in improved salt tolerance [242]. These candidate genes are useful for developing rice varieties with lower Na concentration and enhanced salt tolerance. Accumulation of Cd in rice grains associated with the genes OsWRKY102 (LOC_Os01g0182700), OsWRKY75 (LOC_Os05g0321900), OsHMA3, and OsMan07 (LOC_Os06g0311600) [54,55]. OsHMA3 located on chromosome 7 encoding Cd translocation to the tonoplast in vacuoles of root cells, indicating lower Cd accumulation in rice grains. Knockout of OsHMA3 leading to the high Cd accumulation in the rice grains [55]. Identification of genes which limit Cd accumulation in rice grains is important for developing rice varieties with lower Cd accumulation.

Conclusion

Rice varieties with balanced elemental nutrients and lower toxic heavy metal elements could be developed by using several approaches, including plant breeding and genetic engineering. In plant breeding method, phenotypic variation of GEC in diverse rice genotypes, relationship of environmental conditions and rice grain elemental accumulation, correlation between rice grain elemental content and others agronomic traits could be used to select potential parental rice genotypes. Genetic basis of GEC in rice, including QTLs or candidate genes associated with grain elemental accumulation could be used in genetic engineering method by overexpress or knockout the genes.

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