Masanori Yamasaki

List of Publications by Year in Descending Order

55 papers	4,877 citations	19 h-index	58 g-index
58 ext. papers	6,200 ext. citations	7.2 avg, IF	4.78 L-index

#	Paper	IF	Citations
55	Genetic Background Negates Improvements in Rice Flour Characteristics and Food Processing Properties Caused by a Mutant Allele of the PDIL1-1 Seed Storage Protein Gene.. *Rice*, **2022**, 15, 13	5.8	1
54	Development of an -Derived Nested Association Mapping (-NAM) Population in Rice. *Plants*, **2021**, 10,	4.5	11
53	Choosing the optimal population for a genome-wide association study: A simulation of whole-genome sequences from rice. *Plant Genome*, **2020**, 13, e20005	4.4	4
52	Predicting biomass of rice with intermediate traits: Modeling method combining crop growth models and genomic prediction models. *PLoS ONE*, **2020**, 15, e0233951	3.7	9
51	Coupling day length data and genomic prediction tools for predicting time-related traits under complex scenarios. *Scientific Reports*, **2020**, 10, 13382	4.9	6
50	Genetic and epistatic effects for grain quality and yield of three grain-size QTLs identified in brewing rice (Oryza sativa L.).. *Molecular Breeding*, **2020**, 40, 1	3.4	2
49	Landraces of temperate japonica rice have superior alleles for improving culm strength associated with lodging resistance. *Scientific Reports*, **2020**, 10, 19855	4.9	1
48	Predicting Rice Heading Date Using an Integrated Approach Combining a Machine Learning Method and a Crop Growth Model. *Frontiers in Genetics*, **2020**, 11, 599510	4.5	3
47	Predicting biomass of rice with intermediate traits: Modeling method combining crop growth models and genomic prediction models **2020**, 15, e0233951		
46	Predicting biomass of rice with intermediate traits: Modeling method combining crop growth models and genomic prediction models **2020**, 15, e0233951		
45	Predicting biomass of rice with intermediate traits: Modeling method combining crop growth models and genomic prediction models **2020**, 15, e0233951		
44	Predicting biomass of rice with intermediate traits: Modeling method combining crop growth models and genomic prediction models **2020**, 15, e0233951		
43	Predicting biomass of rice with intermediate traits: Modeling method combining crop growth models and genomic prediction models **2020**, 15, e0233951		
42	Predicting biomass of rice with intermediate traits: Modeling method combining crop growth models and genomic prediction models **2020**, 15, e0233951		
41	Predicting biomass of rice with intermediate traits: Modeling method combining crop growth models and genomic prediction models **2020**, 15, e0233951		
40	Validation of a quantitative trait locus for the white-core expression rate of grain on chromosome 6 in a brewing rice cultivar and development of DNA markers for marker-assisted selection. *Breeding Science*, **2019**, 69, 401-409	2	4
39	Whole genome sequencing data of L. cv. Takanari. *Data in Brief*, **2019**, 27, 104546	1.2	

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38	Genetic and phenotypic assessment of sugar beet (L. subsp.) elite inbred lines selected in Japan during the past 50 years. *Breeding Science*, **2019**, 69, 255-265	2	4
37	QTL analysis of resistance to bacterial wilt caused by in potato. *Breeding Science*, **2019**, 69, 592-600	2	6
36	Identification of QTLs for rice grain size using a novel set of chromosomal segment substitution lines derived from Yamadanishiki in the genetic background of Koshihikari. *Breeding Science*, **2018**, 68, 210-218	2	13
35	Ethylene-gibberellin signaling underlies adaptation of rice to periodic flooding. *Science*, **2018**, 361, 181-186	39.3	89
34	A novel Rice QTL qOPW11 Associated with Panicle Weight Affects Panicle and Plant Architecture. *Rice*, **2018**, 11, 53	5.8	9
33	Description of grain weight distribution leading to genomic selection for grain-filling characteristics in rice. *PLoS ONE*, **2018**, 13, e0207627	3.7	16
32	Differences in glucose yield of residues from among varieties of rice, wheat, and sorghum after dilute acid pretreatment. *Bioscience, Biotechnology and Biochemistry*, **2017**, 81, 1650-1656	2.1	2
31	Genetic dissection of grain traits in Yamadanishiki, an excellent sake-brewing rice cultivar. *Theoretical and Applied Genetics*, **2017**, 130, 2567-2585	6	8
30	Genetic Tracing of L. from Its Mesoamerican Origin to the World. *Frontiers in Plant Science*, **2017**, 8, 1539	6.2	17
29	Genome-wide association study using whole-genome sequencing rapidly identifies new genes influencing agronomic traits in rice. *Nature Genetics*, **2016**, 48, 927-34	36.3	326
28	Natural variation in the glucose content of dilute sulfuric acid-pretreated rice straw liquid hydrolysates: implications for bioethanol production. *Bioscience, Biotechnology and Biochemistry*, **2016**, 80, 863-9	2.1	3
27	Uncovering a Nuisance Influence of a Phenological Trait of Plants Using a Nonlinear Structural Equation: Application to Days to Heading and Culm Length in Asian Cultivated Rice (Oryza Sativa L.). *PLoS ONE*, **2016**, 11, e0148609	3.7	8
26	Island-Model Genomic Selection for Long-Term Genetic Improvement of Autogamous Crops. *PLoS ONE*, **2016**, 11, e0153945	3.7	11
25	Rare allele of a previously unidentified histone H4 acetyltransferase enhances grain weight, yield, and plant biomass in rice. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 76-81	11.5	156
24	Exploring the areas of applicability of whole-genome prediction methods for Asian rice (Oryza sativa L.). *Theoretical and Applied Genetics*, **2015**, 128, 41-53	6	44
23	Natural Variation in the Flag Leaf Morphology of Rice Due to a Mutation of the NARROW LEAF 1 Gene in Oryza sativa L. *Genetics*, **2015**, 201, 795-808	4	12
22	Changes in Lignin and Polysaccharide Components in 13 Cultivars of Rice Straw following Dilute Acid Pretreatment as Studied by Solution-State 2D 1H-13C NMR. *PLoS ONE*, **2015**, 10, e0128417	3.7	21
21	Glucose content in the liquid hydrolysate after dilute acid pretreatment is affected by the starch content in rice straw. *Bioresource Technology*, **2013**, 149, 520-4	11	15

#	Reference	IF	Cit
20	OsLG1 regulates a closed panicle trait in domesticated rice. *Nature Genetics*, **2013**, 45, 462-5, 465e1-2	36.3	128
19	Development of INDEL markers to discriminate all genome types rapidly in the genus Oryza. *Breeding Science*, **2013**, 63, 246-54	2	33
18	Population structure in Japanese rice population. *Breeding Science*, **2013**, 63, 49-57	2	27
17	Diversity and population structure of black soybean landraces originating from Tanba and neighboring regions. *Breeding Science*, **2012**, 61, 593-601	2	8
16	Artificial selection for a green revolution gene during japonica rice domestication. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 11034-9	11.5	132
15	Variation in biomass properties among rice diverse cultivars. *Bioscience, Biotechnology and Biochemistry*, **2011**, 75, 1603-5	2.1	17
14	Population structure of wild wheat D-genome progenitor Aegilops tauschii Coss.: implications for intraspecific lineage diversification and evolution of common wheat. *Molecular Ecology*, **2010**, 19, 999-1013	5.7	88
13	Allelic interaction at seed-shattering loci in the genetic backgrounds of wild and cultivated rice species. *Genes and Genetic Systems*, **2010**, 85, 265-71	1.4	30
12	Biological control for rice blast disease by employing detachment action with gelatinolytic bacteria. *Biological Control*, **2010**, 55, 85-91	3.8	24
11	DNAAlignEditor: DNA alignment editor tool. *BMC Bioinformatics*, **2008**, 9, 154	3.6	9
10	Empirical Analysis of Selection Screens for Domestication and Improvement Loci in Maize by Extended DNA Sequencing. *Plant Genome*, **2008**, 1,	4.4	4
9	Genomic screening for artificial selection during domestication and improvement in maize. *Annals of Botany*, **2007**, 100, 967-73	4.1	53
8	A unified mixed-model method for association mapping that accounts for multiple levels of relatedness. *Nature Genetics*, **2006**, 38, 203-8	36.3	2595
7	The effects of artificial selection on the maize genome. *Science*, **2005**, 308, 1310-4	33.3	634
6	A large-scale screen for artificial selection in maize identifies candidate agronomic loci for domestication and crop improvement. *Plant Cell*, **2005**, 17, 2859-72	11.6	202
5	Genetic basis of ovicidal response to whitebacked planthopper (Sogatella furcifera Horváth) in rice (Oryza sativa L.). *Molecular Breeding*, **2003**, 12, 133-143	3.4	44
4	Mapping of Quantitative Trait Loci of Ovicidal Response to Brown Planthopper (Nilaparvata lugens Stal) in Rice (Oryza sativa L.).. *Breeding Science*, **2000**, 50, 291-296	2	19
3	Quantitative Trait Locus Mapping of Ovicidal Responsein Rice (Oryza sativa L.) against Whitebacked Planthopper (Sogatella furcifera Horváth). *Crop Science*, **1999**, 39, 1178-1183	2.4	28

LIST OF PUBLICATIONS

2   A novel index to evaluate resource allocation pattern in panicles in Japanese rice cultivars. *Plant Production Science*,1-16   2.4

1   Coupling Day Length Data and Genomic Prediction tools for Predicting Time-Related Traits under Complex Scenarios   1