Identification of candidate markers associated with agr discriminant analysis

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Citation Report

#	Article	IF	CITATIONS
1	Haplotype diversity: the link between statistical and biological association. Trends in Plant Science, 2005, 10, 466-471.	4.3	40
2	Genetic and molecular basis of grain size and grain number and its relevance to grain productivity in higher plants. Genome, 2006, 49, 565-571.	0.9	143
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4	Bayesian association mapping of multiple quantitative trait loci and its application to the analysis of genetic variation among Oryza sativa L. germplasms. Theoretical and Applied Genetics, 2007, 114, 1437-1449.	1.8	47
5	Association mapping of yield and its components in rice cultivars. Molecular Breeding, 2007, 19, 341-356.	1.0	267
6	Genetic diversity, structure and marker-trait associations in a collection of Italian tomato (Solanum) Tj ETQq1 1 ().784314 1.8	rgBT/Overloc
7	Genetic variation in rice. Current Opinion in Plant Biology, 2008, 11, 144-148.	3.5	23
8	Molecular Markers Associated with Resistance toAspergillus flavusin Maize Grain: QTL and Discriminant Analyses. Journal of New Seeds, 2008, 9, 1-18.	0.3	20
9	Rice Molecular Breeding Laboratories in the Genomics Era: Current Status and Future Considerations. International Journal of Plant Genomics, 2008, 2008, 1-25.	2.2	68
10	Application of Association Mapping to Understanding the Genetic Diversity of Plant Germplasm Resources. International Journal of Plant Genomics, 2008, 2008, 1-18.	2.2	221
11	Unraveling the Impact of Nitrogen Nutrition on Cooked Rice Flavor and Texture. Cereal Chemistry, 2009, 86, 274-280.	1.1	64
12	Identification of molecular markers associated with sugar-related traits in a Saccharum interspecific cross. Euphytica, 2009, 167, 127-142.	0.6	29
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15	Analytical Approaches and Population Types for Finding and Utilizing QTL in Complex Plant Populations. Crop Science, 2009, 49, 363-380.	0.8	53
16	Maintaining the yield of edible rice in a warming world. Functional Plant Biology, 2009, 36, 1037.	1.1	120
17	Genetic diversity and marker-trait associations in a collection of Pak-choi (Brassica rapa L. ssp.) Tj ETQq0 0 0 rgB	Γ/Qverloc	k 10 Tf 50 102
18	Multivariate selection of AFLP markers associated with \hat{l}^2 -carotene in sweetpotatoes. Euphytica, 2010, 175, 123-132.	0.6	4

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19	Association mapping of grain quality and flowering time in elite japonica rice germplasm. Journal of Cereal Science, 2010, 51, 337-343.	1.8	30
20	Discovery of Elite Alleles for Seed Vigor Traits in Two Populations of Japonica Rice in Taihu Lake Region. Acta Agronomica Sinica, 2010, 36, 754-763.	0.3	13
21	Profiling and Association Mapping of Grain Metabolites in a Subset of the Core Collection of Chinese Rice Germplasm (<i>Oryza sativa</i> L.). Journal of Agricultural and Food Chemistry, 2011, 59, 9257-9264.	2.4	15
22	Identification of Microsatellite (SSR) and RAPD Markers Linked to Rice Blast Disease Resistance gene in Rice (Oryza sativa L.). African Journal of Biotechnology, 2011, 10, 3301-3321.	0.3	9
23	Genetic parameters of variability, correlation and path-coefficient studies for grain yield and other yield Attributes among rice blast disease resistant genotypes of rice (Oryza sativa L.). African Journal of Biotechnology, 2011, 10, 3322-3334.	0.3	37
24	Phenotypic and QTL analyses of herbage production-related traits in perennial ryegrass (Lolium) Tj ETQq1 1 0.78	4314 rgB1	7/Qyerlock 1
25	Association of molecular markers with cold tolerance and green period in zoysiagrass (<i>Zoysia</i> Willd.). Breeding Science, 2012, 62, 320-327.	0.9	17
26	Identifying loci influencing grain number by microsatellite screening in bread wheat (Triticum) Tj ETQq1 1 0.7843	314.rgBT /	Overlock 10
27	Molecular tagging of a rust resistance gene in cultivated groundnut (Arachis hypogaea L.) introgressed from Arachis cardenasii. Molecular Breeding, 2012, 29, 467-476.	1.0	29
28	Mining Elite Alleles of Growth Duration and Productive Panicle Number per Plant by Association Mapping with Conditional Phenotypic Value in Japonica Rice. Rice Science, 2013, 20, 200-206.	1.7	9
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32	Genetic diversity and association mapping of seed vigor in rice (Oryza sativa L.). Planta, 2014, 239, 1309-1319.	1.6	93
33	Mapping and Validation of Quantitative Trait Loci Associated with Tiller Production in Rice. Crop Science, 2015, 55, 1537-1551.	0.8	8
34	Association Analysis in Rice: From Application to Utilization. Frontiers in Plant Science, 2016, 7, 1202.	1.7	37
35	QTLs for Early Tiller Production and Relationships with Rapid Seedling Growth and Increased Panicle Number in Rice. Crop Science, 2016, 56, 505-519.	0.8	6
36	Application of subtracted gDNA microarray-assisted Bulked Segregant Analysis for rapid discovery of molecular markers associated with day-neutrality in strawberry (Fragaria x ananassa). Scientific Reports, 2016, 6, 32551.	1.6	3

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37	Identification and validation of FaP1D7, a putative marker associated with the biosynthesis of methyl butanoate in cultivated strawberry (Fragaria x ananassa). Scientific Reports, 2017, 7, 17454.	1.6	1
38	Markers Associated with Culm Length and Elongated Internode Length in <i>Japonica</i> Rice. Crop Science, 2017, 57, 2329-2344.	0.8	4
39	Research Article Support vector machines applied to the genetic classification problem of hybrid populations with high degrees of similarity. Genetics and Molecular Research, 2018, 17, .	0.3	1
40	Identification of a specific molecular marker for the rice blast-resistant gene Pigm and molecular breeding of thermo-sensitive genic male sterile leaf-color marker lines. Molecular Breeding, 2018, 38, 1.	1.0	10
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44	Dissecting Genetic Network of Fruit Branch Traits in Upland Cotton by Association Mapping Using SSR Markers. PLoS ONE, 2017, 12, e0162815.	1.1	8
45	Classification of Coffea canephora clones in botanical varieties by discriminant analysis of the k-nearest neighbors. Revista Ceres, 2021, 68, 420-428.	0.1	1
47	Identification of quantitative trait loci for tillering, root, and shoot biomass at the maximum tillering stage in rice. Scientific Reports, 2022, 12, .	1.6	5