Copy Number Variation of Multiple Genes at Rhg1 Mediates Nematode Resistance in Soybean

Science

338, 1206-1209

DOI: 10.1126/science.1228746

Citation Report

#	Article	IF	Citations
1	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. Genome Biology, 2013, 14, R58.	3.8	125
2	Homo-dimerization and ligand binding by the leucine-rich repeat domain at RHG1/RFS2 underlying resistance to two soybean pathogens. BMC Plant Biology, 2013, 13, 43.	1.6	14
3	Engineered resistance and hypersusceptibility through functional metabolic studies of 100 genes in soybean to its major pathogen, the soybean cyst nematode. Planta, 2013, 237, 1337-1357.	1.6	72
4	Cbf14 copy number variation in the A, B, and D genomes of diploid and polyploid wheat. Theoretical and Applied Genetics, 2013, 126, 2777-2789.	1.8	17
5	Userâ€friendly markers linked to <scp>F</scp>usarium wilt race 1 resistance <scp>Fw</scp> gene for markerâ€assisted selection in pea. Plant Breeding, 2013, 132, 642-648.	1.0	22
6	Estimating DNA polymorphism from next generation sequencing data with high error rate by dual sequencing applications. BMC Genomics, 2013, 14, 535.	1.2	13
7	High presence/absence gene variability in defense-related gene clusters of Cucumis melo. BMC Genomics, 2013, 14, 782.	1.2	36
8	Overexpression of a soybean salicylic acid methyltransferase gene confers resistance to soybean cyst nematode. Plant Biotechnology Journal, 2013, 11, 1135-1145.	4.1	61
9	Insights from the Soybean (Glycine max and Glycine soja) Genome. Advances in Agronomy, 2013, , 177-204.	2.4	13
10	War of the worms: how plants fight underground attacks. Current Opinion in Plant Biology, 2013, 16, 457-463.	3.5	30
11	Fine mapping and identification of candidate genes controlling the resistance to southern root-knot nematode in PI 96354. Theoretical and Applied Genetics, 2013, 126, 1825-1838.	1.8	46
12	Copy number variation in potato â€“ an asexually propagated autotetraploid species. Plant Journal, 2013, 75, 80-89.	2.8	39
13	Impacts of Resistance Gene Genetics, Function, and Evolution on a Durable Future. Annual Review of Phytopathology, 2013, 51, 291-319.	3.5	131
14	An Atypical Kinase under Balancing Selection Confers Broad-Spectrum Disease Resistance in Arabidopsis. PLoS Genetics, 2013, 9, e1003766.	1.5	117
15	A comparison of the molecular organization of genomic regions associated with resistance to common bacterial blight in two Phaseolus vulgaris genotypes. Frontiers in Plant Science, 2013, 4, 318.	1.7	14
16	Hard Selective Sweep and Ectopic Gene Conversion in a Gene Cluster Affording Environmental Adaptation. PLoS Genetics, 2013, 9, e1003707.	1.5	77
17	Quantitative trait loci for partial resistance to P seudomonas syringae pv. maculicola in A rabidopsis thaliana. Molecular Plant Pathology, 2013, 14, 828-837.	2.0	12
18	Recent Achievement in Gene Cloning and Functional Genomics in Soybean. Scientific World Journal, The, 2013, 2013, 1-7.	0.8	28

#	Article	IF	Citations
19	Potential of Association Mapping and Genomic Selection to Explore PI 88788 Derived Soybean Cyst Nematode Resistance. Plant Genome, 2014, 7, plantgenome2013.11.0039.	1.6	63
20	Comparative Mapping of the Wild Perennial Glycine latifolia and Soybean (G. max) Reveals Extensive Chromosome Rearrangements in the Genus Glycine. PLoS ONE, 2014, 9, e99427.	1.1	15
21	Novel MiRNA and PhasiRNA Biogenesis Networks in Soybean Roots from Two Sister Lines That Are Resistant and Susceptible to SCN Race 4. PLoS ONE, 2014, 9, e110051.	1.1	25
22	Structural variations in plant genomes. Briefings in Functional Genomics, 2014, 13, 296-307.	1.3	176
23	Adaptive genomic structural variation in the grape powdery mildew pathogen, Erysiphe necator. BMC Genomics, 2014, 15, 1081.	1.2	162
24	Genome Resilience and Prevalence of Segmental Duplications Following Fast Neutron Irradiation of Soybean. Genetics, 2014, 198, 967-981.	1.2	53
25	Digital Genotyping of Macrosatellites and Multicopy Genes Reveals Novel Biological Functions Associated with Copy Number Variation of Large Tandem Repeats. PLoS Genetics, 2014, 10, e1004418.	1.5	49
26	Extensive Copy-Number Variation of Young Genes across Stickleback Populations. PLoS Genetics, 2014, 10, e1004830.	1.5	70
27	Distinct Copy Number, Coding Sequence, and Locus Methylation Patterns Underlie Rhg1-Mediated Soybean Resistance to Soybean Cyst Nematode Â Â. Plant Physiology, 2014, 165, 630-647.	2.3	136
28	Resistance to phytopathogens e tutti quanti: placing plant quantitative disease resistance on the map. Molecular Plant Pathology, 2014, 15, 427-432.	2.0	135
29	Comparative Analysis of Gene Expression Profiling Between Resistant and Susceptible Varieties Infected With Soybean Cyst Nematode Race 4 in Glycine max. Journal of Integrative Agriculture, 2014, 13, 2594-2607.	1.7	7
30	A Roadmap for Functional Structural Variants in the Soybean Genome. G3: Genes, Genomes, Genetics, 2014, 4, 1307-1318.	0.8	42
31	Genome-wide association mapping of quantitative resistance to sudden death syndrome in soybean. BMC Genomics, 2014, 15, 809.	1.2	164
32	Plant genomics in view of plant genetic resources â€“ an introduction. Plant Genetic Resources: Characterisation and Utilisation, 2014, 12, S6-S8.	0.4	4
33	Copy number polymorphism in plant genomes. Theoretical and Applied Genetics, 2014, 127, 1-18.	1.8	215
34	Introgression of homeologous quantitative trait loci (QTLs) for resistance to the root-knot nematode [Meloidogyne arenaria (Neal) Chitwood] in an advanced backcross-QTL population of peanut (Arachis hypogaea L.). Molecular Breeding, 2014, 34, 393-406.	1.0	39
35	Joint linkage QTL analyses for partial resistance to Phytophthora sojae in soybean using six nested inbred populations with heterogeneous conditions. Theoretical and Applied Genetics, 2014, 127, 429-444.	1.8	33
36	Legumes in the Omic Era. , 2014, , .		12

#	Article	IF	Citations
37	Genomeâ€<scp>w</scp>ide patterns of largeâ€<scp>s</scp>ize presence/<scp>a</scp>bsence variants in sorghum. Journal of Integrative Plant Biology, 2014, 56, 24-37.	4.1	22
38	Insights into the Effects of Long-Term Artificial Selection on Seed Size in Maize. Genetics, 2014, 198, 409-421.	1.2	38
39	Unraveling Genomic Complexity at a Quantitative Disease Resistance Locus in Maize. Genetics, 2014, 198, 333-344.	1.2	51
40	Nucleotide polymorphism and copy number variant detection using exome capture and nextâ€generation sequencing in the polyploid grass P anicum virgatum. Plant Journal, 2014, 79, 993-1008.	2.8	39
41	Genome Structures and Transcriptomes Signify Niche Adaptation for the Multiple-Ion-Tolerant Extremophyte Schrenkiella parvula. Plant Physiology, 2014, 164, 2123-2138.	2.3	77
42	Fine mapping of Co-x, an anthracnose resistance gene to a highly virulent strain of Colletotrichum lindemuthianum in common bean. Theoretical and Applied Genetics, 2014, 127, 1653-1666.	1.8	59
43	Effects of stacked quantitative resistances to downy mildew in lettuce do not simply add up. Theoretical and Applied Genetics, 2014, 127, 1805-1816.	1.8	17
44	Syntaxin 31 functions in Glycine max resistance to the plant parasitic nematode Heterodera glycines. Plant Molecular Biology, 2014, 85, 107-121.	2.0	39
45	Identification and characterization of transcript polymorphisms in soybean lines varying in oil composition and content. BMC Genomics, 2014, 15, 299.	1.2	49
46	Arabidopsis genes, AtNPR1, AtTGA2 and AtPR-5, confer partial resistance to soybean cyst nematode (Heterodera glycines) when overexpressed in transgenic soybean roots. BMC Plant Biology, 2014, 14, 96.	1.6	65
47	Genomic variation in Helianthus: learning from the past and looking to the future. Briefings in Functional Genomics, 2014, 13, 328-340.	1.3	10
48	The Activation and Suppression of Plant Innate Immunity by Parasitic Nematodes. Annual Review of Phytopathology, 2014, 52, 243-265.	3.5	171
49	Manipulation of two Î±â€endoâ€Î²â€1,4â€glucanase genes,AtCel6andGmCel7, reduces susceptibility toHeterodera glycinesin soybean roots. Molecular Plant Pathology, 2014, 15, 927-939.	2.0	10
50	Exploration of presence/absence variation and corresponding polymorphic markers in soybean genome. Journal of Integrative Plant Biology, 2014, 56, 1009-1019.	4.1	21
52	Diversity and population structure of northern switchgrass as revealed through exome capture sequencing. Plant Journal, 2015, 84, 800-815.	2.8	47
53	Two Decades of Molecular Markerâ€Assisted Breeding for Resistance to Soybean Sudden Death Syndrome. Crop Science, 2015, 55, 1460-1484.	0.8	15
54	The distribution and impact of common copy-number variation in the genome of the domesticated apple, Malus x domestica Borkh. BMC Genomics, 2015, 16, 848.	1.2	21
55	Genomic consequences of selection and genome-wide association mapping in soybean. BMC Genomics, 2015, 16, 671.	1.2	121

#	Article	IF	Citations
56	Diversity in boron toxicity tolerance of Australian barley (Hordeum vulgare L.) genotypes. BMC Plant Biology, 2015, 15, 231.	1.6	15
57	A genomeâ€wide survey reveals abundant rice blast RÂgenes in resistant cultivars. Plant Journal, 2015, 84, 20-28.	2.8	42
58	The dynamics of cereal cyst nematode infection differ between susceptible and resistant barley cultivars and lead to changes in (1,3;1,4)â€î²â€glucan levels and <scp>HvCslF</scp> gene transcript abundance. New Phytologist, 2015, 207, 135-147.	3.5	40
59	New Soybean Accessions Evaluated for Reaction to Heterodera glycines Populations. Crop Science, 2015, 55, 1236-1242.	0.8	11
60	Fine Mapping and Characterization of Candidate Genes that Control Resistance to Cercospora sojina K. Hara in Two Soybean Germplasm Accessions. PLoS ONE, 2015, 10, e0126753.	1.1	27
61	A SNARE-Like Protein and Biotin Are Implicated in Soybean Cyst Nematode Virulence. PLoS ONE, 2015, 10, e0145601.	1.1	41
62	Sequence composition of BAC clones and SSR markers mapped to Upland cotton chromosomes 11 and 21 targeting resistance to soil-borne pathogens. Frontiers in Plant Science, 2015, 6, 791.	1.7	22
63	Resistance genes against plant-parasitic nematodes: a durable control strategy?. Nematology, 2015, 17, 249-263.	0.2	39
64	Durable Resistance of Crops to Disease: A Darwinian Perspective. Annual Review of Phytopathology, 2015, 53, 513-539.	3.5	246
65	Meloidogyne incognita nematode resistance QTL in carrot. Molecular Breeding, 2015, 35, 1.	1.0	23
66	Understanding Plant Immunity as a Surveillance System to Detect Invasion. Annual Review of Phytopathology, 2015, 53, 541-563.	3.5	440
67	Quantitative Resistance to Biotrophic Filamentous Plant Pathogens: Concepts, Misconceptions, and Mechanisms. Annual Review of Phytopathology, 2015, 53, 445-470.	3.5	201
68	Multiply to conquer: Copy number variations at Ppd-B1 and Vrn-A1 facilitate global adaptation in wheat. BMC Genetics, 2015, 16, 96.	2.7	90
69	A revolution in plant metabolism: Genome-enabled pathway discovery. Plant Physiology, 2015, 169, pp.00976.2015.	2.3	26
70	Dynamics of Copy Number Variation in Host Races of the Pea Aphid. Molecular Biology and Evolution, 2015, 32, 63-80.	3.5	55
71	The syntaxin 31-induced gene, LESION SIMULATING DISEASE1 (LSD1), functions inGlycine maxdefense to the root parasiteHeterodera glycines. Plant Signaling and Behavior, 2015, 10, e977737.	1.2	18
72	Whole-genome resequencing: changing the paradigms of SNP detection, molecular mapping and gene discovery. Molecular Breeding, 2015, 35, 1.	1.0	35
73	Resequencing 302 wild and cultivated accessions identifies genes related to domestication and improvement in soybean. Nature Biotechnology, 2015, 33, 408-414.	9.4	1,023

#	Article	IF	Citations
74	Enhanced resistance to soybean cyst nematode Heterodera glycines in transgenic soybean by silencing putative <scp>CLE</scp> receptors. Plant Biotechnology Journal, 2015, 13, 801-810.	4.1	59
75	Suppression of Plant Defences by Plant-Parasitic Nematodes. Advances in Botanical Research, 2015, , 325-337.	0.5	24
76	Introductory Chapter on the Basic Biology of Cyst Nematodes. Advances in Botanical Research, 2015, 73, 33-59.	0.5	21
78	Copy number variation at the GL7 locus contributes to grain size diversity in rice. Nature Genetics, 2015, 47, 944-948.	9.4	485
79	Resistance to Gray Leaf Spot of Maize: Genetic Architecture and Mechanisms Elucidated through Nested Association Mapping and Near-Isogenic Line Analysis. PLoS Genetics, 2015, 11, e1005045.	1.5	86
81	Small-Scale duplication as a genomic signature for crop improvement. Journal of Crop Science and Biotechnology, 2015, 18, 45-51.	0.7	2
82	Whole-genome gene expression profiling revealed genes and pathways potentially involved in regulating interactions of soybean with cyst nematode (Heterodera glycines Ichinohe). BMC Genomics, 2015, 16, 148.	1.2	43
83	SNP identification and marker assay development for high-throughput selection of soybean cyst nematode resistance. BMC Genomics, 2015, 16, 314.	1.2	86
84	Gaining insight into soybean defense responses using functional genomics approaches: Figure 1. Briefings in Functional Genomics, 2015, 14, 283-290.	1.3	18
85	Fine-mapping of a major QTL controlling angular leaf spot resistance in common bean (Phaseolus) Tj ETQq1 1 0.784314 rgBT /Overlock	1.8	54
86	Identification of quantitative trait loci underlying resistance to southern root-knot and reniform nematodes in soybean accession PI 567516C. Molecular Breeding, 2015, 35, 131.	1.0	34
87	Genetic characteristics of soybean resistance to HG type 0 and HG type 1.2.3.5.7 of the cyst nematode analyzed by genome-wide association mapping. BMC Genomics, 2015, 16, 598.	1.2	104
88	Evolution and selection of <scp>R</scp>hg1, a copyâ€number variant nematodeâ€resistance locus. Molecular Ecology, 2015, 24, 1774-1791.	2.0	66
89	A System for Dosage-Based Functional Genomics in Poplar. Plant Cell, 2015, 27, 2370-2383.	3.1	70
90	Macrotene chromosomes provide insights to a new mechanism of high-order gene amplification in eukaryotes. Nature Communications, 2015, 6, 6154.	5.8	13
91	Genetic architecture of cyst nematode resistance revealed by genome-wide association study in soybean. BMC Genomics, 2015, 16, 593.	1.2	111
92	CNV and Structural Variation in Plants: Prospects of NGS Approaches. , 2015, , 211-232.		8
93	A gene cluster encoding lectin receptor kinases confers broad-spectrum and durable insect resistance in rice. Nature Biotechnology, 2015, 33, 301-305.	9.4	299

#	Article	IF	Citations
94	Identification and evaluation of quantitative trait loci underlying resistance to multiple HG types of soybean cyst nematode in soybean PI 437655. Theoretical and Applied Genetics, 2015, 128, 15-23.	1.8	33
95	Integrated views in plant breeding: from the perspective of biotechnology. , 2015, , 467-486.		2
96	Integrated signaling networks in plant responses to sedentary endoparasitic nematodes: a perspective. Plant Cell Reports, 2015, 34, 5-22.	2.8	31
98	Dissecting the Genetic Basis of Resistance to Soybean Cyst Nematode Combining Linkage and Association Mapping. Plant Genome, 2016, 9, plantgenome2015.04.0020.	1.6	27
99	Arabidopsis thaliana population analysis reveals high plasticity of the genomic region spanning MSH2, AT3G18530 and AT3G18535 genes and provides evidence for NAHR-driven recurrent CNV events occurring in this location. BMC Genomics, 2016, 17, 893.	1.2	16
100	Copy number variation contributes to cryptic genetic variation in outbreak lineages of Cryptococcus gattii from the North American Pacific Northwest. BMC Genomics, 2016, 17, 700.	1.2	36
101	The Current Status of the Soybean-Soybean Mosaic Virus (SMV) Pathosystem. Frontiers in Microbiology, 2016, 7, 1906.	1.5	43
102	Single and multiple resistance QTL delay symptom appearance and slow down root colonization by Aphanomyces euteiches in pea near isogenic lines. BMC Plant Biology, 2016, 16, 166.	1.6	35
103	Genome-Wide Association Study of Resistance to Soybean Cyst Nematode (Heterodera glycines) HG Type 2.5.7 in Wild Soybean (Glycine soja). Frontiers in Plant Science, 2016, 7, 1214.	1.7	68
104	QTLomics in Soybean: A Way Forward for Translational Genomics and Breeding. Frontiers in Plant Science, 2016, 7, 1852.	1.7	29
105	Highâ€Ðensity Mapping of Resistance QTL Toward Phytophthora sojae, Pythium irregulare, and Fusarium graminearum in the Same Soybean Population. Crop Science, 2016, 56, 2476-2492.	0.8	41
106	A Plasmodiumâ€like virulence effector of the soybean cyst nematode suppresses plant innate immunity. New Phytologist, 2016, 212, 444-460.	3.5	47
107	An efficient method for measuring copy number variation applied to improvement of nematode resistance in soybean. Plant Journal, 2016, 88, 143-153.	2.8	31
108	The genome of black raspberry (Rubus occidentalis). Plant Journal, 2016, 87, 535-547.	2.8	111
109	Molecular Soybean-Pathogen Interactions. Annual Review of Phytopathology, 2016, 54, 443-468.	3.5	67
110	Quantitative disease resistance to the bacterial pathogen <scp>X</scp>anthomonas campestris involves an <scp>A</scp>rabidopsis immune receptor pair and a gene of unknown function. Molecular Plant Pathology, 2016, 17, 510-520.	2.0	53
111	Rapid evolutionary dynamics in a 2.8â€Mb chromosomal region containing multiple prolamin and resistance gene families in Aegilops tauschii. Plant Journal, 2016, 87, 495-506.	2.8	33
112	Using Genotyping by Sequencing to Map Two Novel Anthracnose Resistance Loci inSorghum bicolor. G3: Genes, Genomes, Genetics, 2016, 6, 1935-1946.	0.8	29

#	Article	IF	Citations
113	Recent breeding programs enhanced genetic diversity in both desi and kabuli varieties of chickpea (Cicer arietinum L.). Scientific Reports, 2016, 6, 38636.	1.6	77
114	Characterization of Disease Resistance Loci in the USDA Soybean Germplasm Collection Using Genome-Wide Association Studies. Phytopathology, 2016, 106, 1139-1151.	1.1	91
115	Different responses of soybean cyst nematode resistance between two RIL populations derived from Peking Ã— 7605 under two ecological sites. Journal of Genetics, 2016, 95, 975-982.	0.4	0
116	Mechanisms of quantitative disease resistance in plants. Seminars in Cell and Developmental Biology, 2016, 56, 201-208.	2.3	70
117	Genome and transcriptome analysis of the Mesoamerican common bean and the role of gene duplications in establishing tissue and temporal specialization of genes. Genome Biology, 2016, 17, 32.	3.8	166
118	Gene duplication confers enhanced expression of 27-kDa Î³-zein for endosperm modification in quality protein maize. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 4964-4969.	3.3	67
119	Plant innate immunity in rice: a defense against pathogen infection. National Science Review, 2016, 3, 295-308.	4.6	57
120	Impact of Rhg1 copy number, type, and interaction with Rhg4 on resistance to Heterodera glycines in soybean. Theoretical and Applied Genetics, 2016, 129, 2403-2412.	1.8	32
121	Fine mapping and candidate gene analysis of two loci conferring resistance to Phytophthora sojae in soybean. Theoretical and Applied Genetics, 2016, 129, 2379-2386.	1.8	54
122	1,10-Phenanthroline and its derivatives are novel hatching stimulants for soybean cyst nematodes. Bioorganic and Medicinal Chemistry Letters, 2016, 26, 5240-5243.	1.0	8
123	The <scp>A</scp>rabidopsis immune regulator <scp>SRFR</scp>1 dampens defences against herbivory by <scp>S</scp>podoptera exigua and parasitism by <scp>H</scp>eterodera schachtii. Molecular Plant Pathology, 2016, 17, 588-600.	2.0	11
124	Molecular Markers and Their Applications. , 2016, , 137-157.		3
125	Soybean Resistance to the Soybean Cyst Nematode Heterodera glycines: An Update. Phytopathology, 2016, 106, 1444-1450.	1.1	101
126	Belowground Defence Strategies Against Sedentary Nematodes. Signaling and Communication in Plants, 2016, , 221-251.	0.5	2
127	Molecular aspects of plant-nematode interactions. Indian Journal of Plant Physiology, 2016, 21, 477-488.	0.8	11
128	In Situ Hybridization in Rice (Oryza sativ a). Current Protocols in Plant Biology, 2016, 1, 89-106.	2.8	2
129	Soybean (Glycine max) Mutant and Germplasm Resources: Current Status and Future Prospects. Current Protocols in Plant Biology, 2016, 1, 307-327.	2.8	9
130	Belowground Defence Strategies in Plants. Signaling and Communication in Plants, 2016, , .	0.5	6

#	Article	IF	Citations
131	Disease resistance through impairment of Î±-SNAPâ€“NSF interaction and vesicular trafficking by soybean Rhg1. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E7375-E7382.	3.3	71
132	Advancements in breeding, genetics, and genomics for resistance to three nematode species in soybean. Theoretical and Applied Genetics, 2016, 129, 2295-2311.	1.8	44
133	Draft Assembly of Elite Inbred Line PH207 Provides Insights into Genomic and Transcriptome Diversity in Maize. Plant Cell, 2016, 28, 2700-2714.	3.1	183
134	The impact and origin of copy number variations in the Oryza species. BMC Genomics, 2016, 17, 261.	1.2	30
135	Construction of high resolution genetic linkage maps to improve the soybean genome sequence assembly Glyma1.01. BMC Genomics, 2016, 17, 33.	1.2	137
136	Genes and Small RNA Transcripts Exhibit Dosage-Dependent Expression Pattern in Maize Copy-Number Alterations. Genetics, 2016, 203, 1133-1147.	1.2	12
137	Transgenic soybean overexpressing Gm<scp>SAMT</scp>1 exhibits resistance to multipleâ€<scp>HG</scp> types of soybean cyst nematode Heterodera glycines. Plant Biotechnology Journal, 2016, 14, 2100-2109.	4.1	23
138	Genome-wide identification of SNPs and copy number variation in common bean (Phaseolus vulgaris L.) using genotyping-by-sequencing (GBS). Molecular Breeding, 2016, 36, 1.	1.0	87
139	Copy number variation at the HvCBF4â€“HvCBF2 genomic segment is a major component of frost resistance in barley. Plant Molecular Biology, 2016, 92, 161-175.	2.0	45
140	Identification of haplotypes at the Rsv4 genomic region in soybean associated with durable resistance to soybean mosaic virus. Theoretical and Applied Genetics, 2016, 129, 453-468.	1.8	37
141	Copy number variation of a gene cluster encoding endopolygalacturonase mediates flesh texture and stone adhesion in peach. Journal of Experimental Botany, 2016, 67, 1993-2005.	2.4	100
142	Towards plant pangenomics. Plant Biotechnology Journal, 2016, 14, 1099-1105.	4.1	203
143	Genome Reduction Uncovers a Large Dispensable Genome and Adaptive Role for Copy Number Variation in Asexually Propagated Solanum tuberosum. Plant Cell, 2016, 28, 388-405.	3.1	163
144	A remorin gene is implicated in quantitative disease resistance in maize. Theoretical and Applied Genetics, 2016, 129, 591-602.	1.8	56
145	Two Tightly Linked Genes at the hsa1 Locus Cause Both F 1 and F 2 Hybrid Sterility in Rice. Molecular Plant, 2016, 9, 221-232.	3.9	53
146	Genomic-assisted phylogenetic analysis and marker development for next generation soybean cyst nematode resistance breeding. Plant Science, 2016, 242, 342-350.	1.7	78
147	Soybean domestication: the origin, genetic architecture and molecular bases. New Phytologist, 2017, 214, 539-553.	3.5	162
148	Fine mapping of the SCN resistance QTL cqSCN-006 and cqSCN-007 from Glycine soja PI 468916. Euphytica, 2017, 213, 1.	0.6	22

#	Article	IF	Citations
149	Quantitative Disease Resistance: Dissection and Adoption in Maize. Molecular Plant, 2017, 10, 402-413.	3.9	91
150	Genome-wide association study for soybean cyst nematode resistance in Chinese elite soybean cultivars. Molecular Breeding, 2017, 37, 1.	1.0	22
151	Characterization of the Soluble NSF Attachment Protein gene family identifies two members involved in additive resistance to a plant pathogen. Scientific Reports, 2017, 7, 45226.	1.6	69
152	Gene expression profiling describes the genetic regulation of Meloidogyne arenaria resistance in Arachis hypogaea and reveals a candidate gene for resistance. Scientific Reports, 2017, 7, 1317.	1.6	32
153	Nitrate analogs as attractants for soybean cyst nematode. Bioscience, Biotechnology and Biochemistry, 2017, 81, 1542-1547.	0.6	10
154	Impact of Soybean Cyst Nematode Resistance on Soybean Yield. Crop Science, 2017, 57, 1373-1382.	0.8	27
155	Genetics and Adaptation of Soybean Cyst Nematode to Broad Spectrum Soybean Resistance. G3: Genes, Genomes, Genetics, 2017, 7, 835-841.	0.8	23
156	A PP2C-1 Allele Underlying a Quantitative Trait Locus Enhances Soybean 100-Seed Weight. Molecular Plant, 2017, 10, 670-684.	3.9	144
157	The soybean GmSNAP18 gene underlies two types of resistance to soybean cyst nematode. Nature Communications, 2017, 8, 14822.	5.8	91
158	Components of the SNARE-containing regulon are co-regulated in root cells undergoing defense. Plant Signaling and Behavior, 2017, 12, e1274481.	1.2	25
159	Structural Variation and the Soybean Genome. Compendium of Plant Genomes, 2017, , 57-72.	0.3	0
160	Impact of Genomic Research on Soybean Breeding. Compendium of Plant Genomes, 2017, , 111-129.	0.3	2
161	Copy number variation and disease resistance in plants. Theoretical and Applied Genetics, 2017, 130, 2479-2490.	1.8	53
162	Gene copy number variations in adaptive evolution: The genomic distribution of gene copy number variations revealed by genetic mapping and their adaptive role in an undomesticated species, white spruce (Picea glauca). Molecular Ecology, 2017, 26, 5989-6001.	2.0	25
163	Enhanced post wash retention of combed DNA molecules by varying multiple combing parameters. Analytical Biochemistry, 2017, 536, 45-50.	1.1	1
164	RNA-seq data comparisons of wild soybean genotypes in response to soybean cyst nematode () Tj ETQq1 1 0.784314 rgBT /Overlock	1.3	21
165	Systematic Mutagenesis of Serine Hydroxymethyltransferase Reveals an Essential Role in Nematode Resistance Â. Plant Physiology, 2017, 175, 1370-1380.	2.3	43
166	Extensive genome heterogeneity leads to preferential allele expression and copy numberâ€dependent expression in cultivated potato. Plant Journal, 2017, 92, 624-637.	2.8	54

#	Article	IF	Citations
167	Quantitative trait loci with additive and epistatic effects underlying resistance to two <scp>HG</scp> types of soybean cyst nematode. Plant Breeding, 2017, 136, 720-727.	1.0	8
168	Hairy Root Composite Plant Systems in Root-Microbe Interaction Research. , 2017, , 17-44.		3
169	Assessment of gene copy number variation of Scots pine thaumatin-like protein gene using real-time PCR based methods. Tree Genetics and Genomes, 2017, 13, 1.	0.6	4
170	Genomic structural variation-mediated allelic suppression causes hybrid male sterility in rice. Nature Communications, 2017, 8, 1310.	5.8	124
171	CNVs into the wild: screening the genomes of conifer trees (Picea spp.) reveals fewer gene copy number variations in hybrids and links to adaptation. BMC Genomics, 2017, 18, 97.	1.2	32
172	Loci and candidate genes conferring resistance to soybean cyst nematode HG type 2.5.7. BMC Genomics, 2017, 18, 462.	1.2	37
173	Development and utilization of a new chemicallyâ€induced soybean library with a high mutation density. Journal of Integrative Plant Biology, 2017, 59, 60-74.	4.1	46
174	Characterization of Soybean WRKY Gene Family and Identification of Soybean WRKY Genes that Promote Resistance to Soybean Cyst Nematode. Scientific Reports, 2017, 7, 17804.	1.6	92
175	Production of Plant Derived Natural Compounds through Hairy Root Culture. , 2017, , .		6
176	Pyramiding of Alleles from Multiple Sources Increases the Resistance of Soybean to Highly Virulent Soybean Cyst Nematode Isolates. Crop Science, 2017, 57, 2932-2941.	0.8	13
177	Increase in Soybean Cyst Nematode Virulence and Reproduction on Resistant Soybean Varieties in Iowa From 2001 to 2015 and the Effects on Soybean Yields. Plant Health Progress, 2017, 18, 146-155.	0.8	67
178	MLPA-Based Analysis of Copy Number Variation in Plant Populations. Frontiers in Plant Science, 2017, 8, 222.	1.7	16
179	Genetic Interaction between Arabidopsis Qpm3.1 Locus and Bacterial Effector Gene hopW1-1 Underlies Natural Variation in Quantitative Disease Resistance to Pseudomonas Infection. Frontiers in Plant Science, 2017, 8, 695.	1.7	6
180	Quantitative Disease Resistance under Elevated Temperature: Genetic Basis of New Resistance Mechanisms to Ralstonia solanacearum. Frontiers in Plant Science, 2017, 8, 1387.	1.7	36
181	Quantitative Resistance to Plant Pathogens in Pyramiding Strategies for Durable Crop Protection. Frontiers in Plant Science, 2017, 8, 1838.	1.7	182
182	QTL Analysis of Transgressive Nematode Resistance in Tetraploid Cotton Reveals Complex Interactions in Chromosome 11 Regions. Frontiers in Plant Science, 2017, 8, 1979.	1.7	17
183	Parallel evolution of the POQR prolyl oligo peptidase gene conferring plant quantitative disease resistance. PLoS Genetics, 2017, 13, e1007143.	1.5	38
184	Bringing New Plant Varieties to Market: Plant Breeding and Selection Practices Advance Beneficial Characteristics while Minimizing Unintended Changes. Crop Science, 2017, 57, 2906-2921.	0.8	57

#	Article	IF	Citations
185	Gene duplication and dosage effects during the early emergence of C4 photosynthesis in the grass genus Alloteropsis. Journal of Experimental Botany, 2018, 69, 1967-1980.	2.4	29
186	Integration of sudden death syndrome resistance loci in the soybean genome. Theoretical and Applied Genetics, 2018, 131, 757-773.	1.8	19
187	Efficient genome-wide genotyping strategies and data integration in crop plants. Theoretical and Applied Genetics, 2018, 131, 499-511.	1.8	62
188	The transcriptomic changes of Huipizhi Heidou (Glycine max), a nematode-resistant black soybean during Heterodera glycines race 3 infection. Journal of Plant Physiology, 2018, 220, 96-104.	1.6	16
189	An atypical N-ethylmaleimide sensitive factor enables the viability of nematode-resistant Rhg1 soybeans. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4512-E4521.	3.3	58
190	Mapping of new quantitative trait loci for sudden death syndrome and soybean cyst nematode resistance in two soybean populations. Theoretical and Applied Genetics, 2018, 131, 1047-1062.	1.8	13
191	Identification of the dwarf gene GmDW1 in soybean (Glycine max L.) by combining mapping-by-sequencing and linkage analysis. Theoretical and Applied Genetics, 2018, 131, 1001-1016.	1.8	50
192	Update on amino acid transporter functions and on possible amino acid sensing mechanisms in plants. Seminars in Cell and Developmental Biology, 2018, 74, 105-113.	2.3	99
193	Glyphosate Resistance and EPSPS Gene Duplication: Convergent Evolution in Multiple Plant Species. Journal of Heredity, 2018, 109, 117-125.	1.0	71
194	Comprehensive description of genomewide nucleotide and structural variation in shortâ€season soya bean. Plant Biotechnology Journal, 2018, 16, 749-759.	4.1	46
195	The limited role of differential fractionation in genome content variation and function in maize (Zea mays L.) inbred lines. Plant Journal, 2018, 93, 131-141.	2.8	42
196	Chemical mutagenesis and soybean mutants potential for identification of novel genes conferring resistance to soybean cyst nematode. Journal of Integrative Agriculture, 2018, 17, 2734-2744.	1.7	9
197	The Maize Pan-Genome. Compendium of Plant Genomes, 2018, , 13-29.	0.3	8
198	Molecular and Genomic Approaches to Peanut Improvement. , 2018, , 57-76.		0
199	Mapping Quantitative Trait Loci for Tolerance to Pythium irregulare in Soybean (Glycine max L.). G3: Genes, Genomes, Genetics, 2018, 8, 3155-3161.	0.8	14
200	Biology, Ecology and Management of Plant Parasitic Nematodes in Minnesota. Sustainability in Plant and Crop Protection, 2018, , 125-155.	0.2	0
201	The Untapped Genetic Reservoir: The Past, Current, and Future Applications of the Wild Soybean (Glycine soja). Frontiers in Plant Science, 2018, 9, 949.	1.7	79
202	Evaluation of Soybean Germplasm for Resistance to Multiple Nematode Species: Heterodera glycines , Meloidogyne incognita , and Rotylenchulus reniformis. Crop Science, 2018, 58, 2511-2522.	0.8	21

#	Article	IF	Citations
203	Detection of large sequence insertions by a hybrid approach that combine de novo assembly and resequencing of medium-coverage genome sequences. Genome, 2018, 61, 745-754.	0.9	2
204	Genome sequences of two diploid wild relatives of cultivated sweetpotato reveal targets for genetic improvement. Nature Communications, 2018, 9, 4580.	5.8	181
205	Adult plant resistance in maize to northern leaf spot is a feature of partial loss-of-function alleles of Hm1. PLoS Pathogens, 2018, 14, e1007356.	2.1	16
206	Variability of CP4 EPSPS expression in genetically engineered soybean (Glycine max L. Merrill). Transgenic Research, 2018, 27, 511-524.	1.3	10
207	Current Research Status of Heterodera glycines Resistance and Its Implication on Soybean Breeding. Engineering, 2018, 4, 534-541.	3.2	21
208	Full-length RNA sequencing reveals unique transcriptome composition in bermudagrass. Plant Physiology and Biochemistry, 2018, 132, 95-103.	2.8	50
209	Genetically Diverse Soybean Cyst Nematodeâ€"Resistant Fullâ€Sib Soybean Germplasm Lines AR4SCN, AR5SCN, AR6SCN, AR7SCN, and AR8SCN. Journal of Plant Registrations, 2018, 12, 124-131.	0.4	1
210	QTL mapping and epistatic interaction analysis of field resistance to sudden death syndrome (Fusarium) Tj ETQq1 1 0.784314 rgBT /Ove	1.8	14
211	Genomic Sequencing of Japanese Plum (Prunus salicina Lindl.) Mutants Provides a New Model for Rosaceae Fruit Ripening Studies. Frontiers in Plant Science, 2018, 9, 21.	1.7	55
212	Analysis of Extreme Phenotype Bulk Copy Number Variation (XP-CNV) Identified the Association of rp1 with Resistance to Goss's Wilt of Maize. Frontiers in Plant Science, 2018, 9, 110.	1.7	23
213	Aldaulactone â€" An Original Phytotoxic Secondary Metabolite Involved in the Aggressiveness of Alternaria dauci on Carrot. Frontiers in Plant Science, 2018, 9, 502.	1.7	13
214	Large-Scale Investigation of Soybean Gene Functions by Overexpressing a Full-Length Soybean cDNA Library in Arabidopsis. Frontiers in Plant Science, 2018, 9, 631.	1.7	7
215	Tandem Duplicate Genes in Maize Are Abundant and Date to Two Distinct Periods of Time. G3: Genes, Genomes, Genetics, 2018, 8, 3049-3058.	0.8	13
216	A population genomic characterization of copy number variation in the opportunistic fungal pathogen Aspergillus fumigatus. PLoS ONE, 2018, 13, e0201611.	1.1	26
217	Copy Number Variation in Fungi and Its Implications for Wine Yeast Genetic Diversity and Adaptation. Frontiers in Microbiology, 2018, 9, 288.	1.5	63
219	Sequence analysis of European maize inbred line F2 provides new insights into molecular and chromosomal characteristics of presence/absence variants. BMC Genomics, 2018, 19, 119.	1.2	27
220	Marker-Assisted Breeding for Disease Resistance in Crop Plants. , 2018, , 41-57.		4
221	Sequence and Analysis of the Black Raspberry (Rubus occidentalis) Genome. Compendium of Plant Genomes, 2018, , 185-197.	0.3	3

#	Article	IF	Citations
222	The Genomes of Rosaceous Berries and Their Wild Relatives. Compendium of Plant Genomes, 2018, , .	0.3	17
223	Registration of â€˜IAR1902 SCNâ€™ Cultivar Resistant to Soybean Cyst Nematode and Brown Stem Rot. Journal of Plant Registrations, 2019, 13, 334-344.	0.4	1
224	Soybean Resistance Locus Rhg1 Confers Resistance to Multiple Cyst Nematodes in Diverse Plant Species. Phytopathology, 2019, 109, 2107-2115.	1.1	16
225	A Species-Wide Inventory of NLR Genes and Alleles in Arabidopsis thaliana. Cell, 2019, 178, 1260-1272.e14.	13.5	265
226	Cloning of Genes Underlying Quantitative Resistance for Plant Disease Control. , 2019, , 21-44.		0
227	Copy number variation of Ppd-B1 is the major determinant of heading time in durum wheat. BMC Genetics, 2019, 20, 64.	2.7	30
228	Effective identification of soybean candidate genes involved in resistance to soybean cyst nematode via direct whole genome re-sequencing of two segregating mutants. Theoretical and Applied Genetics, 2019, 132, 2677-2687.	1.8	18
229	Construction of genetic linkage map and identification of a novel major locus for resistance to pine wood nematode in Japanese black pine (Pinus thunbergii). BMC Plant Biology, 2019, 19, 424.	1.6	17
230	Identification of a candidate gene underlying qKRN5b for kernel row number in Zea mays L.. Theoretical and Applied Genetics, 2019, 132, 3439-3448.	1.8	12
232	Identification of MicroRNAs That Respond to Soybean Cyst Nematode Infection in Early Stages in Resistant and Susceptible Soybean Cultivars. International Journal of Molecular Sciences, 2019, 20, 5634.	1.8	18
233	Nonallelic homologous recombination events responsible for copy number variation within an RNA silencing locus. Plant Direct, 2019, 3, e00162.	0.8	14
234	The rhg1â€a (Rhg1 lowâ€copy) nematode resistance source harbors a copiaâ€family retrotransposon within the Rhg1â€encoded Î±â€SNAP gene. Plant Direct, 2019, 3, e00164.	0.8	27
235	Deep genotyping of the gene GmSNAP facilitates pyramiding resistance to cyst nematode in soybean. Crop Journal, 2019, 7, 677-684.	2.3	10
236	Molecular Basis of Soybean Resistance to Soybean Aphids and Soybean Cyst Nematodes. Plants, 2019, 8, 374.	1.6	12
237	Exploring and Exploiting Pan-genomics for Crop Improvement. Molecular Plant, 2019, 12, 156-169.	3.9	172
238	Wholeâ€genome reâ€sequencing reveals the impact of the interaction of copy number variants of the rhg1 and Rhg4 genes on broadâ€based resistance to soybean cyst nematode. Plant Biotechnology Journal, 2019, 17, 1595-1611.	4.1	65
239	Polar bear evolution is marked by rapid changes in gene copy number in response to dietary shift. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 13446-13451.	3.3	56
240	A comprehensive genomic scan reveals gene dosage balance impacts on quantitative traits in Populus trees. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 13690-13699.	3.3	23

#	Article	IF	Citations
241	Structural variants in 3000 rice genomes. Genome Research, 2019, 29, 870-880.	2.4	112
242	Fluorescence in situ hybridization in plants: recent developments and future applications. Chromosome Research, 2019, 27, 153-165.	1.0	142
243	Overexpression of Wild Arachis Lipocalin Enhances Root-Knot Nematode Resistance in Peanut Hairy Roots. Plant Molecular Biology Reporter, 2019, 37, 74-86.	1.0	6
244	Genome-Wide Association Analysis Pinpoints Additional Major Genomic Regions Conferring Resistance to Soybean Cyst Nematode (Heterodera glycines Ichinohe). Frontiers in Plant Science, 2019, 10, 401.	1.7	32
245	The HuangZaoSi Maize Genome Provides Insights into Genomic Variation and Improvement History of Maize. Molecular Plant, 2019, 12, 402-409.	3.9	41
246	The mitogen activated protein kinase (MAPK) gene family functions as a cohort during the Glycine max defense response to Heterodera glycines. Plant Physiology and Biochemistry, 2019, 137, 25-41.	2.8	44
247	Copy Number Variation in Domestication. Trends in Plant Science, 2019, 24, 352-365.	4.3	131
248	Genome wide association study discovers genomic regions involved in resistance to soybean cyst nematode (Heterodera glycines) in common bean. PLoS ONE, 2019, 14, e0212140.	1.1	14
249	Phenotypic Characterization of a Major Quantitative Disease Resistance Locus for Partial Resistance to Phytophthora sojae. Crop Science, 2019, 59, 968-980.	0.8	11
250	Genome-wide association study and genomic selection for soybean chlorophyll content associated with soybean cyst nematode tolerance. BMC Genomics, 2019, 20, 904.	1.2	29
251	The future of legume genetic data resources: Challenges, opportunities, and priorities. , 2019, 1, e16.		30
252	Connecting genome structural variation with complex traits in crop plants. Theoretical and Applied Genetics, 2019, 132, 733-750.	1.8	97
253	Genome-wide association and genomic prediction identifies soybean cyst nematode resistance in common bean including a syntenic region to soybean Rhg1 locus. Horticulture Research, 2019, 6, 9.	2.9	36
254	Landscape of gene transpositionâ€“duplication within the Brassicaceae family. DNA Research, 2019, 26, 21-36.	1.5	19
255	The role of genomic structural variation in the genetic improvement of polyploid crops. Crop Journal, 2019, 7, 127-140.	2.3	54
256	An updated gene atlas for maize reveals organâ€specific and stressâ€induced genes. Plant Journal, 2019, 97, 1154-1167.	2.8	114
257	The soybean Rhg1 amino acid transporter gene alters glutamate homeostasis and jasmonic acidâ€induced resistance to soybean cyst nematode. Molecular Plant Pathology, 2019, 20, 270-286.	2.0	26
258	Gene copy number variations involved in balsam poplar (Populus balsamifera L.) adaptive variations. Molecular Ecology, 2019, 28, 1476-1490.	2.0	31

#	Article	IF	Citations
259	Early transcriptional responses to soybean cyst nematode HG Type 0 show genetic differences among resistant and susceptible soybeans. Theoretical and Applied Genetics, 2020, 133, 87-102.	1.8	17
260	Super-Pangenome by Integrating the Wild Side of a Species for Accelerated Crop Improvement. Trends in Plant Science, 2020, 25, 148-158.	4.3	177
261	Comparative genomics of six Juglans species reveals diseaseâ€associated gene family contractions. Plant Journal, 2020, 102, 410-423.	2.8	25
262	Genetics and Cytogenetics of theÂPotato. , 2020, , 219-247.		11
263	Comparison of Arachis monticola with Diploid and Cultivated Tetraploid Genomes Reveals Asymmetric Subgenome Evolution and Improvement of Peanut. Advanced Science, 2020, 7, 1901672.	5.6	43
264	Integrated Management of Important Soybean Pathogens of the United States in Changing Climate. Journal of Integrated Pest Management, 2020, 11, .	0.9	41
265	An integrated peach genome structural variation map uncovers genes associated with fruit traits. Genome Biology, 2020, 21, 258.	3.8	77
266	Prospects of next generation sequencing in lentil breeding. Molecular Biology Reports, 2020, 47, 9043-9053.	1.0	10
267	Large tandem duplications affect gene expression, 3D organization, and plantâ€“pathogen response. Genome Research, 2020, 30, 1583-1592.	2.4	31
268	Plant Immune Mechanisms: From Reductionistic to Holistic Points of View. Molecular Plant, 2020, 13, 1358-1378.	3.9	82
269	Plant pan-genomes are the new reference. Nature Plants, 2020, 6, 914-920.	4.7	302
270	tâ€SNAREs bind the Rhg1 Î±â€SNAP and mediate soybean cyst nematode resistance. Plant Journal, 2020, 104, 318-331.	2.8	24
271	Identification of copy number variation and population analysis of the sacred lotus (Nelumbo) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262	0.6	1
272	Proteome-Wide Analyses Provide New Insights into the Compatible Interaction of Rice with the Root-Knot Nematode Meloidogyne graminicola. International Journal of Molecular Sciences, 2020, 21, 5640.	1.8	6
273	Targeted suppression of soybean BAG6â€induced cell death in yeast by soybean cyst nematode effectors. Molecular Plant Pathology, 2020, 21, 1227-1239.	2.0	9
274	Structural Variations Affecting Genes and Transposable Elements of Chromosome 3B in Wheats. Frontiers in Genetics, 2020, 11, 891.	1.1	16
275	Wholeâ€genome de novo assemblies reveal extensive structural variations and dynamic organelleâ€toâ€nucleus DNA transfers in African and Asian rice. Plant Journal, 2020, 104, 596-612.	2.8	19
276	Pangenomics in Crop Plants. Population Genomics, 2020, , 1.	0.2	1

#	Article	IF	Citations
277	An Overview of Duplicated Gene Detection Methods: Why the Duplication Mechanism Has to Be Accounted for in Their Choice. Genes, 2020, 11, 1046.	1.0	65
278	Sequence Composition of Bacterial Chromosome Clones in a Transgressive Root-Knot Nematode Resistance Chromosome Region in Tetraploid Cotton. Frontiers in Plant Science, 2020, 11, 574486.	1.7	3
279	Dynamics of Population Density and Virulence Phenotype of the Soybean Cyst Nematode as Influenced by Resistance Source Sequence and Tillage. Plant Disease, 2020, 104, 2111-2122.	0.7	8
280	Fluopyram Suppresses Population Densities of Heterodera glycines in Field and Greenhouse Studies in Michigan. Plant Disease, 2020, 104, 1305-1311.	0.7	11
281	Epigenetic Mechanisms in Nematodeâ€“Plant Interactions. Annual Review of Phytopathology, 2020, 58, 119-138.	3.5	32
282	Map-based cloning of a novel QTL qBN-1 influencing branch number in soybeanÂ[Glycine maxÂ(L.) Merr.]. Crop Journal, 2020, 8, 793-801.	2.3	10
283	Plant Genome Editing and the Relevance of Off-Target Changes. Plant Physiology, 2020, 183, 1453-1471.	2.3	68
284	Coinfection of soybean plants with Phytophthora sojae and soybean cyst nematode does not alter the efficacy of resistance genes. Plant Pathology, 2020, 69, 1437-1444.	1.2	3
285	Pan-Genome of Wild and Cultivated Soybeans. Cell, 2020, 182, 162-176.e13.	13.5	508
286	Characterization of Pingliang xiaoheidou (ZDD 11047), a soybean variety with resistance to soybean cyst nematode Heterodera glycines. Plant Molecular Biology, 2020, 103, 253-267.	2.0	9
287	Gynoecy instability in cucumber (Cucumis sativus L.) is due to unequal crossover at the copy number variation-dependent Femaleness (F) locus. Horticulture Research, 2020, 7, 32.	2.9	25
288	Biotic stress-tolerant plants through small RNA technology. , 2020, , 435-468.		4
289	Exploiting Broad-Spectrum Disease Resistance in Crops: From Molecular Dissection to Breeding. Annual Review of Plant Biology, 2020, 71, 575-603.	8.6	125
290	Mutations at the Serine Hydroxymethyltransferase Impact Its Interaction with a Soluble NSF Attachment Protein and a Pathogenesis-Related Protein in Soybean. Vaccines, 2020, 8, 349.	2.1	18
291	A genome-wide survey of copy number variations reveals an asymmetric evolution of duplicated genes in rice. BMC Biology, 2020, 18, 73.	1.7	7
292	AÂspontaneous complex structural variant in rcan-1 increases exploratory behavior and laboratory fitness of Caenorhabditis elegans. PLoS Genetics, 2020, 16, e1008606.	1.5	9
293	The Mungbean Genome. Compendium of Plant Genomes, 2020, , .	0.3	23
294	A pathogenesisâ€related protein GmPR08â€Bet VI promotes a molecular interaction between the GmSHMT08 and GmSNAP18 in resistance to Heterodera glycines. Plant Biotechnology Journal, 2020, 18, 1810-1829.	4.1	29

#	Article	IF	Citations
295	Pan-genomics of plants and its applications. , 2020, , 285-306.		2
296	Exploring the genetic base of the soybean germplasm from Africa, America and Asia as well as mining of beneficial allele for flowering and seed weight. 3 Biotech, 2020, 10, 195.	1.1	4
297	Characterizing resistance to soybean cyst nematode in PI 494182, an early maturing soybean accession. Crop Science, 2020, 60, 2053-2069.	0.8	15
298	Soybean cyst nematode-resistance: Gene identification and breeding strategies. Crop Journal, 2020, 8, 892-904.	2.3	23
299	Genomic Profiling of Virulence in the Soybean Cyst Nematode Using Single-Nematode Sequencing. Phytopathology, 2021, 111, 137-148.	1.1	20
300	Fine-mapping and characterization of qSCN18, a novel QTL controlling soybean cyst nematode resistance in PI 567516C. Theoretical and Applied Genetics, 2021, 134, 621-631.	1.8	13
301	QTL mapping of qSCN3-1 for resistance to soybean cyst nematode in soybean line Zhongpin 03-5373. Crop Journal, 2021, 9, 351-359.	2.3	6
302	A copy number variant at the HPDAâ€Ð12 locus confers compact plant architecture in cotton. New Phytologist, 2021, 229, 2091-2103.	3.5	27
303	Resistance Gene Pyramiding and Rotation to Combat Widespread Soybean Cyst Nematode Virulence. Plant Disease, 2021, 105, 3238-3243.	0.7	9
304	Progress in Biological Activity and Synthesis of Nematode Hatching Pheromone Glycinoeclepin A. Chinese Journal of Organic Chemistry, 2021, 41, 553.	0.6	1
305	How the pan-genome is changing crop genomics and improvement. Genome Biology, 2021, 22, 3.	3.8	142
306	Transcriptional analysis reveals the response mechanism of soybean (Glycine max) Kangxian 2 to soybean cyst nematode (Heterodera glycines) HG Type 0. Crop and Pasture Science, 2021, 72, 44.	0.7	0
307	Genomicsâ€assisted lentil breeding: Current status and future strategies. , 2021, 3, e71.		22
309	Resisting Potato Cyst Nematodes With Resistance. Frontiers in Plant Science, 2021, 12, 661194.	1.7	28
310	Molecular and Cellular Mechanisms Involved in Host-Specific Resistance to Cyst Nematodes in Crops. Frontiers in Plant Science, 2021, 12, 641582.	1.7	18
311	Dissecting nematode resistance regions in soybean revealed pleiotropic effect of soybean cyst and reniform nematode resistance genes. Plant Genome, 2021, 14, e20083.	1.6	12
312	Novel resistance strategies to soybean cyst nematode (SCN) in wild soybean. Scientific Reports, 2021, 11, 7967.	1.6	20
313	RNA-seq-based identification of potential resistance genes against the soybean cyst nematode (Heterodera glycines) HG Type 1.2.3.5.7 in â€˜Dongnong L-10â€™. Physiological and Molecular Plant Pathology, 2021, 114, 101627.	1.3	10

#	Article	IF	Citations
314	Transgressive resistance to Heterodera glycines in chromosome segment substitution lines derived from susceptible soybean parents. Plant Genome, 2021, 14, e20091.	1.6	5
315	Crop breeding for a changing climate: integrating phenomics and genomics with bioinformatics. Theoretical and Applied Genetics, 2021, 134, 1677-1690.	1.8	38
316	Comparative transcriptome profiling identifies maize line specificity of fungal effectors in the maizeâ€“Ustilago maydis interaction. Plant Journal, 2021, 106, 733-752.	2.8	12
317	Meta-GWAS for quantitative trait loci identification in soybean. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	23
318	Evaluation of antixenosis in soybean against Spodoptera litura by dual-choice assay aided by a statistical analysis model: Discovery of a novel antixenosis in Peking. Journal of Pesticide Sciences, 2021, 46, 182-188.	0.8	0
319	A rhomboidâ€like protease gene from an interspecies translocation confers resistance to cyst nematodes. New Phytologist, 2021, 231, 801-813.	3.5	8
320	Structural variations in papaya genomes. BMC Genomics, 2021, 22, 335.	1.2	11
321	Combining targeted metabolite analyses and transcriptomics to reveal the specific chemical composition and associated genes in the incompatible soybean variety PI437654 infected with soybean cyst nematode HG1.2.3.5.7. BMC Plant Biology, 2021, 21, 217.	1.6	14
322	Genomic patterns of structural variation among diverse genotypes of Sorghum bicolor and a potential role for deletions in local adaptation. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	9
323	A Qa-SNARE complex contributes to soybean cyst nematode resistance via regulation of mitochondria-mediated cell death. Journal of Experimental Botany, 2021, 72, 7145-7162.	2.4	12
324	Status and advances in mining for blackleg (Leptosphaeria maculans) quantitative resistance (QR) in oilseed rape (Brassica napus). Theoretical and Applied Genetics, 2021, 134, 3123-3145.	1.8	7
325	Copy Number Quantification for the Soybean Cyst Nematode Resistance Locus rhg1 in the Soybean Varieties of Taiwan. Agronomy, 2021, 11, 1346.	1.3	3
326	Identification of genomic loci conferring broad-spectrum resistance to multiple nematode species in exotic soybean accession PI 567305. Theoretical and Applied Genetics, 2021, 134, 3379-3395.	1.8	10
327	Creation and judicious application of a wheat resistance gene atlas. Molecular Plant, 2021, 14, 1053-1070.	3.9	66
328	Increased copy number of gibberellin 2â€oxidase 8 genes reduced trailing growth and shoot length during soybean domestication. Plant Journal, 2021, 107, 1739-1755.	2.8	24
329	Genomic variation within the maize stiffâ€stalk heterotic germplasm pool. Plant Genome, 2021, 14, e20114.	1.6	14
330	Next-Generation Breeding Strategies for Climate-Ready Crops. Frontiers in Plant Science, 2021, 12, 620420.	1.7	61
331	Identification and validation of a novel locus, Qpm-3BL, for adult plant resistance to powdery mildew in wheat using multilocus GWAS. BMC Plant Biology, 2021, 21, 357.	1.6	14

#	Article	IF	Citations
333	Homoeologous chromosome exchange explains the creation of a QTL affecting soilâ€borne pathogen resistance in tobacco. Plant Biotechnology Journal, 2022, 20, 47-58.	4.1	12
334	Soybean Cyst Nematode Resistance Quantitative Trait Locus cqSCN-006 Alters the Expression of a Î³-SNAP Protein. Molecular Plant-Microbe Interactions, 2021, 34, 1433-1445.	1.4	10
335	Progress in soybean functional genomics over the past decade. Plant Biotechnology Journal, 2022, 20, 256-282.	4.1	76
336	Advances in omics technology for improving crop yield and stress resilience. Plant Breeding, 2021, 140, 719-731.	1.0	13
337	Soybean cyst nematodes: a destructive threat to soybean production in China. Phytopathology Research, 2021, 3, .	0.9	11
338	Conserved oligomeric Golgi (COG) complex genes functioning in defense are expressed in root cells undergoing a defense response to a pathogenic infection and exhibit regulation my MAPKs. PLoS ONE, 2021, 16, e0256472.	1.1	5
339	High quality haplotypeâ€resolved genome assemblies of Populus tomentosa Carr., a stabilized interspecific hybrid species widespread in Asia. Molecular Ecology Resources, 2022, 22, 786-802.	2.2	19
340	WI12_{Rhg1} interacts with DELLAs and mediates soybean cyst nematode resistance through hormone pathways. Plant Biotechnology Journal, 2022, 20, 283-296.	4.1	17
341	Network organization of the plant immune system: from pathogen perception to robust defense induction. Plant Journal, 2022, 109, 447-470.	2.8	38
342	Characterization of PmHHXM, a New Broad-Spectrum Powdery Mildew Resistance Gene in Chinese Wheat Landrace Honghuaxiaomai. Plant Disease, 2021, 105, 2089-2096.	0.7	7
343	Classification methods and identification of reniform nematode resistance in known soybean cyst nematode resistant soybean genotypes. Plant Disease, 2021, , .	0.7	3
344	Genome-wide association study for resistance to the Meloidogyne javanica causing root-knot nematode in soybean. Theoretical and Applied Genetics, 2021, 134, 777-792.	1.8	15
345	Genetic characterization of qSCN10 from an exotic soybean accession PI 567516C reveals a novel source conferring broad-spectrum resistance to soybean cyst nematode. Theoretical and Applied Genetics, 2021, 134, 859-874.	1.8	10
346	Common Bean Genomics and Its Applications in Breeding Programs. , 2014, , 185-206.		4
347	Soybean [Glycine max (L.) Merr.] Breeding: History, Improvement, Production and Future Opportunities. , 2019, , 431-516.		36
348	RNA-Seq-based identification of potential resistance mechanism against the soybean cyst nematode (Heterodera glycines) HG Type 0 in soybean (Glycine max) cv. Dongnong L-204. Crop and Pasture Science, 2020, 71, 539.	0.7	9
349	Impaired folate binding of serine hydroxymethyltransferase 8 from soybean underlies resistance to the soybean cyst nematode. Journal of Biological Chemistry, 2020, 295, 3708-3718.	1.6	13
351	Mapping soybean rhg2 locus, which confers resistance to soybean cyst nematode race 1 in combination with rhg1 and Rhg4 derived from PI 84751. Breeding Science, 2020, 70, 474-480.	0.9	8

#	Article	IF	Citations
352	Systematic Application of DNA Fiber-FISH Technique in Cotton. PLoS ONE, 2013, 8, e75674.	1.1	25
353	Diversification of spatiotemporal expression and copy number variation of the echinoid hbox12/pmar1/micro1 multigene family. PLoS ONE, 2017, 12, e0174404.	1.1	9
354	GWAS of a soybean breeding collection from South East and South Kazakhstan for resistance to fungal diseases. Vavilovskii Zhurnal Genetiki I Selektsii, 2018, 22, 536-543.	0.4	11
355	A New Race (X12) of Soybean Cyst Nematode in China. Journal of Nematology, 2017, 49, 168-176.	0.4	15
356	Cataloging Plant Genome Structural Variations. Current Issues in Molecular Biology, 2018, 27, 181-194.	1.0	6
357	The Glycine max Conserved Oligomeric Golgi (COG) Complex Functions During a Defense Response to Heterodera glycines. Frontiers in Plant Science, 2020, 11, 564495.	1.7	11
358	Optimization of a Virus-Induced Gene Silencing System with Soybean yellow common mosaic virus for Gene Function Studies in Soybeans. Plant Pathology Journal, 2016, 32, 112-122.	0.7	15
359	Impact des changements climatiques sur les interactions molÃ©culaires entre le nÃ©matode Ã kyste du soya (Heterodera glycines) et son hÃ´te principal, le soya (Glycine max). Phytoprotection, 0, 95, 41-47.	0.3	2
360	Genome-wide analysis of deletions in maize population reveals abundant genetic diversity and functional impact. Theoretical and Applied Genetics, 2021, 135, 273.	1.8	4
361	Screening of Early Maturing Soybean Accessions for Resistance against HG Type 2.5.7 of Soybean Cyst Nematode, Heterodera glycines. Plant Health Progress, 0, , .	0.8	0
369	Response of soybean genotypes from Northeast China to Heterodera glycines races 4 andÂ5, and characterisation of rhg1Âand Rhg4 genes for soybean resistance. Nematology, 2021, 24, 333-345.	0.2	3
370	Detection of rare nematode resistance Rhg1 haplotypes in Glycine soja and a novel Rhg1 Î±â€šSNAP. Plant Genome, 2021, , e20152.	1.6	1
372	Future Prospects and Challenges. Compendium of Plant Genomes, 2020, , 181-191.	0.3	1
376	A New Race (X12) of Soybean Cyst Nematode in China. Journal of Nematology, 2017, 49, 321-326.	0.4	3
377	Soybean cyst nematode (Heterodera glycines) resistant cultivar rotation system impacts nematode population density, virulence, and yield. Crop Protection, 2021, 153, 105864.	1.0	1
378	Reprogramming microbial populations using a programmed lysis system to improve chemical production. Nature Communications, 2021, 12, 6886.	5.8	13
379	RNA-Seq analysis of resistant and susceptible soybean genotypes in response to stress from soybean cyst nematode (Heterodera glycines) HG type 1.2.3.5.7. Crop and Pasture Science, 2021, , .	0.7	1
380	A Broad Review of Soybean Research on the Ongoing Race to Overcome Soybean Cyst Nematode. Biology, 2022, 11, 211.	1.3	8

#	Article	IF	Citations
381	Broadening the horizon of crop research: a decade of advancements in plant molecular genetics to divulge phenotype governing genes. Planta, 2022, 255, 46.	1.6	9
382	Essential Roles of Cupredoxin Family Proteins in Soybean Cyst Nematode Resistance. Phytopathology, 2022, 112, 1545-1558.	1.1	3
383	Phased, chromosome-scale genome assemblies of tetraploid potato reveal a complex genome, transcriptome, and predicted proteome landscape underpinning genetic diversity. Molecular Plant, 2022, 15, 520-536.	3.9	72
384	Improvement of Soybean; A Way Forward Transition from Genetic Engineering to New Plant Breeding Technologies. Molecular Biotechnology, 2023, 65, 162-180.	1.3	24
386	Dissection of the practical soybean breeding pipeline by developing ZDX1, a high-throughput functional array. Theoretical and Applied Genetics, 2022, 135, 1413-1427.	1.8	10
387	The conserved oligomeric Golgi (COG) complex, a window into plant-pathogen interactions. Journal of Plant Interactions, 2022, 17, 344-360.	1.0	1
388	Impact of multiple selective breeding programs on genetic diversity in soybean germplasm. Theoretical and Applied Genetics, 2022, 135, 1591-1602.	1.8	7
389	Combined use of Oxford Nanopore and Illumina sequencing yields insights into soybean structural variation biology. BMC Biology, 2022, 20, 53.	1.7	10
390	Identification of Candidate Genes Controlling Soybean Cyst Nematode Resistance in â€œHandou 10â€•Based on Genome and Transcriptome Analyzes. Frontiers in Plant Science, 2022, 13, 860034.	1.7	1
391	SoySNP618K array: A highâ€resolution single nucleotide polymorphism platform as a valuable genomic resource for soybean genetics and breeding. Journal of Integrative Plant Biology, 2022, 64, 632-648.	4.1	7
392	Integrated analysis of the lncRNA/circRNA-miRNA-mRNA expression profiles reveals novel insights into potential mechanisms in response to root-knot nematodes in peanut. BMC Genomics, 2022, 23, 239.	1.2	5
393	Physiological mechanisms of stress-induced evolution. Journal of Experimental Biology, 2022, 225, .	0.8	14
394	Genomic structural variation in tomato and its role in plant immunity. Molecular Horticulture, 2022, 2, .	2.3	4
395	Genomic Variations and Mutational Events Associated with Plantâ€“Pathogen Interactions. Biology, 2022, 11, 421.	1.3	5
396	Modern plant biotechnology as a strategy in addressing climate change and attainingÂfood security. Agriculture and Food Security, 2022, 11, .	1.6	48
397	Epistatic interaction between Rhg1-a and Rhg2 in PI 90763 confers resistance to virulent soybean cyst nematode populations. Theoretical and Applied Genetics, 2022, 135, 2025-2039.	1.8	7
398	Mapping of partial resistance to Phytophthora sojae in soybean PIs using wholeâ€genome sequencing reveals a major QTL. Plant Genome, 2022, 15, e20184.	1.6	11
399	Fluorescent Soybean Hairy Root Construction and Its Application in the Soybeanâ€“Nematode Interaction: An Investigation. Biology, 2021, 10, 1353.	1.3	3

#	Article	IF	Citations
400	Breeding a Soybean Cultivar Heinong 531 with Peking-Type Cyst Nematode Resistance, Enhanced Yield, and High Seed-Oil Contents. Phytopathology, 2022, 112, 1345-1349.	1.1	5
401	Bacteriophage self-counting in the presence of viral replication. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	8
403	CNVs with adaptive potential in Rangifer tarandus: genome architecture and new annotated assembly. Life Science Alliance, 2022, 5, e202101207.	1.3	7
404	Opposite Beet Cyst Nematode-Infection Phenotypes of Transgenic Arabidopsis between Overexpressing GmSNAP18 and AtSNAP2 and between Overexpressing GmSHMT08 and AtSHMT4. Phytopathology, 2022, , .	1.1	5
443	Genetic and Genomic Resources for Soybean Breeding Research. Plants, 2022, 11, 1181.	1.6	5
444	Glycine max Homologs of DOESN'T MAKE INFECTIONS 1, 2, and 3 Function to Impair Heterodera glycines Parasitism While Also Regulating Mitogen Activated Protein Kinase Expression. Frontiers in Plant Science, 2022, 13, .	1.7	0
445	Novel Fusarium wilt resistance genes uncovered in natural and cultivated strawberry populations are found on three non-homoeologous chromosomes. Theoretical and Applied Genetics, 2022, 135, 2121-2145.	1.8	8
446	Exploring Soybean Resistance to Soybean Cyst Nematode. Annual Review of Phytopathology, 2022, 60, 379-409.	3.5	10
447	Full-Length Transcriptional Analysis of the Same Soybean Genotype With Compatible and Incompatible Reactions to Heterodera glycines Reveals Nematode Infection Activating Plant Defense Response. Frontiers in Plant Science, 2022, 13, .	1.7	4
448	The Key to the Future Lies in the Past: Insights from Grain Legume Domestication and Improvement Should Inform Future Breeding Strategies. Plant and Cell Physiology, 2022, 63, 1554-1572.	1.5	13
450	Identification of Candidate Genes for a Major Quantitative Disease Resistance Locus From Soybean PI 427105B for Resistance to Phytophthora sojae. Frontiers in Plant Science, 0, 13, .	1.7	2
451	The heterologous expression of conserved Glycine max (soybean) mitogen activated protein kinase 3 (MAPK3) paralogs suppresses Meloidogyne incognita parasitism in Gossypium hirsutum (upland) Tj ETQq1 1 0.784314 rgBT /Overlock	1.34	0
452	Transcriptomic Reprogramming and Genetic Variations Contribute to Western Hemlock Defense and Resistance Against Annosus Root and Butt Rot Disease. Frontiers in Plant Science, 0, 13, .	1.7	0
453	The GmSNAP11 Contributes to Resistance to Soybean Cyst Nematode Race 4 in Glycine max. Frontiers in Plant Science, 0, 13, .	1.7	3
454	Interactions among Heterodera glycines, Macrophomina phaseolina, and soybean genotype. Plant Disease, 0, , .	0.7	0
455	Breeding for disease resistance in soybean: a global perspective. Theoretical and Applied Genetics, 2022, 135, 3773-3872.	1.8	42
456	Beet cyst nematode HsSNARE1 interacts with both AtSNAP2 and AtPR1 and promotes disease in Arabidopsis. Journal of Advanced Research, 2022, , .	4.4	2
457	Identification of Heat-Tolerant Genes in Non-Reference Sequences in Rice by Integrating Pan-Genome, Transcriptomics, and QTLs. Genes, 2022, 13, 1353.	1.0	2

#	Article	IF	Citations
458	A mutant allele of the <scp> flowering promoting factor 1 </scp> gene at the tomato <scp> BRACHYTIC </scp> locus reduces plant height with high quality fruit. Plant Direct, 2022, 6, .	0.8	6
459	â€œLateâ€•effectors from Leptosphaeria maculans as tools for identifying novel sources of resistance in Brassica napus. Plant Direct, 2022, 6, .	0.8	2
460	Mining alleles for tar spot complex resistance from CIMMYT's maize Germplasm Bank. Frontiers in Sustainable Food Systems, 0, 6, .	1.8	1
461	GmIAA27 Encodes an AUX/IAA Protein Involved in Dwarfing and Multi-Branching in Soybean. International Journal of Molecular Sciences, 2022, 23, 8643.	1.8	12
462	An evolutionary look into the history of lentil reveals unexpected diversity. Evolutionary Applications, 2022, 15, 1313-1325.	1.5	6
463	Fertility, genome stability, and homozygosity in a diverse set of resynthesized rapeseed lines. Crop Journal, 2022, , .	2.3	3
464	Functional analysis of soybean cyst nematode-inducible synthetic promoters and their regulation by biotic and abiotic stimuli in transgenic soybean (Glycine max). Frontiers in Plant Science, 0, 13, .	1.7	3
466	Quantitative trait loci and gene-specific markers associated with resistance to soybean cyst nematode HG type 2.5.7. Molecular Breeding, 2022, 42, .	1.0	4
467	Timeâ€ordering japonica/geng genomes analysis indicates the importance of large structural variants in rice breeding. Plant Biotechnology Journal, 2023, 21, 202-218.	4.1	5
468	Improvement of resistance to pod shattering and the soybean cyst nematode in the high-yielding soybean variety â€˜Fukuibukiâ€™ through marker-assisted selection and back-crossing. Ikushugaku Kenkyu, 2022, , .	0.1	0
469	The soybean ubiquitinâ€proteasome system: Current knowledge and future perspective. Plant Genome, 0, , .	1.6	2
470	Copy Number Variation among Resistance Genes Analogues in Brassica napus. Genes, 2022, 13, 2037.	1.0	4
471	Comparisons of constitutive resistances to soybean cyst nematode between PI 88788- and Peking-type sources of resistance in soybean by transcriptomic and metabolomic profilings. Frontiers in Genetics, 0, 13, .	1.1	0
472	The prevalence of deleterious mutations during the domestication and improvement of soybean. Crop Journal, 2023, 11, 523-530.	2.3	3
473	Quantitative disease resistance: Multifaceted players in plant defense. Journal of Integrative Plant Biology, 2023, 65, 594-610.	4.1	4
474	Multi-omics revolution to promote plant breeding efficiency. Frontiers in Plant Science, 0, 13, .	1.7	10
475	Ideal Type 1 is caused by a point mutation in the Î±-tubulin gene that affects microtubule arrangement in soybean. Crop Journal, 2022, , .	2.3	0
476	Six decades of soybean breeding in Ontario, Canada: a tradition of innovation. Canadian Journal of Plant Science, 2023, 103, 333-352.	0.3	5

#	Article	IF	Citations
477	Understandings and future challenges in soybean functional genomics and molecular breeding. Journal of Integrative Plant Biology, 2023, 65, 468-495.	4.1	14
478	Genetic architecture of fresh-market tomato yield. BMC Plant Biology, 2023, 23, .	1.6	2
479	Transcriptome analysis of aphid-resistant and susceptible near isogenic lines reveals candidate resistance genes in cowpea (Vigna unguiculata). BMC Plant Biology, 2023, 23, .	1.6	3
480	Development of SNP molecular markers associated with resistance to reniform nematode in soybean using KASP genotyping. Euphytica, 2023, 219, .	0.6	0
481	Weighted gene co-expression network analysis identifies genes related to HG Type 0 resistance and verification of hub gene GmHg1. Frontiers in Plant Science, 0, 13, .	1.7	2
482	Dynamic Genomes - Mechanisms and consequences of genomic diversity impacting plant-fungal interactions. Physiological and Molecular Plant Pathology, 2023, 125, 102006.	1.3	3
483	Discovering and prioritizing candidate resistance genes against soybean pests by integrating GWAS and gene coexpression networks. Gene, 2023, 860, 147231.	1.0	3
484	Genomic structural variation: A complex but important driver of human evolution. American Journal of Biological Anthropology, 2023, 181, 118-144.	0.6	3
485	Soybean transporter AAT Rhg1 abundance increases along the nematode migration path and impacts vesiculation and ROS. Plant Physiology, 2023, 192, 133-153.	2.3	2
488	Identification of resistant sources from Glycine max against soybean cyst nematode. Frontiers in Plant Science, 0, 14, .	1.7	0
489	Deciphering the genetic basis of resistance to soybean cyst nematode combining IBD and association mapping. Theoretical and Applied Genetics, 2023, 136, .	1.8	1
492	Identification of QTL, QTL-by-environment interactions, and their candidate genes for resistance HG Type 0 and HG Type 1.2.3.5.7 in soybean using 3VmrMLM. Frontiers in Plant Science, 0, 14, .	1.7	1
508	Research progress on the functional study of host resistance-related genes against Heterodera glycines. , 2023, 1, .		0
517	Plant Breeding Strategies and Methods for Food Security: Review on the Technology. , 2023, , 213-254.		0
522	Soybean Improvement and the Role of Gene Editing. , 2024, , 271-289.		0
533	Lentil breeding in postgenomic era. , 2024, , 307-324.		0
535	Lentil genome sequencing: Establishing a comprehensive platform for molecular breeding. , 2024, , 217-236.		0