

# CITATION REPORT

List of articles citing

## Gene duplication and evolutionary novelty in plants

DOI: 10.1111/j.1469-8137.2009.02923.x  
New Phytologist, 2009, 183, 557-564.

**Source:** <https://exaly.com/paper-pdf/46419457/citation-report.pdf>

**Version:** 2024-04-27

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Paper	IF	Citations
638	Two independent C4 origins in Aristidoideae (Poaceae) revealed by the recruitment of distinct phosphoenolpyruvate carboxylase genes. <b>2009</b> , 96, 2234-9		31
637	Brassica orthologs from BANYULS belong to a small multigene family, which is involved in procyanidin accumulation in the seed. <b>2009</b> , 230, 1167-83		31
636	Specialization of flowers: is floral orientation an overlooked first step?. <i>New Phytologist</i> , <b>2009</b> , 183, 502-506	9.8	60
635	Why red-dominated autumn leaves in America and yellow-dominated autumn leaves in Northern Europe?. <i>New Phytologist</i> , <b>2009</b> , 183, 506-512	9.8	44
634	Darwinism renewed: contemporary studies of plant adaptation. <i>New Phytologist</i> , <b>2009</b> , 183, 497-501	9.8	7
633	Coexistence of diploids and triploids in a Saharan relict olive: evidence from nuclear microsatellite and flow cytometry analyses. <b>2009</b> , 332, 1115-20		25
632	Characterisation of the <i>Vitis vinifera</i> PR10 multigene family. <b>2010</b> , 10, 184		57
631	Dating and functional characterization of duplicated genes in the apple ( <i>Malus domestica</i> Borkh.) by analyzing EST data. <b>2010</b> , 10, 87		19
630	A powerful toolkit for synthetic biology: Over 3.8 billion years of evolution. <b>2010</b> , 32, 304-13		11
629	Homoeologous nonreciprocal recombination in polyploid cotton. <i>New Phytologist</i> , <b>2010</b> , 186, 123-34	9.8	105
628	Evolutionary consequences of autopolyploidy. <i>New Phytologist</i> , <b>2010</b> , 186, 5-17	9.8	442
627	Did gene family expansions during the Eocene-Oligocene boundary climate cooling play a role in Pooideae adaptation to cool climates?. <b>2010</b> , 19, 2075-88		51
626	Parallel polyploid speciation: distinct sympatric gene-pools of recurrently derived allo-octoploid <i>Asplenium</i> ferns. <b>2010</b> , 19, 2916-32		33
625	Speciation genetics: Limits and promises. <b>2010</b> , 59, 1404-1412		2
624	What we still don't know about polyploidy. <b>2010</b> , 59, 1387-1403		225
623	Gene amplification delivers glyphosate-resistant weed evolution. <b>2010</b> , 107, 955-6		44
622	Complete switchgrass genetic maps reveal subgenome collinearity, preferential pairing and multilocus interactions. <b>2010</b> , 185, 745-60		121

621	The five AhMTP1 zinc transporters undergo different evolutionary fates towards adaptive evolution to zinc tolerance in <i>Arabidopsis halleri</i> . <b>2010</b> , 6, e1000911		94
620	Evolutionary genomics of C4 photosynthesis in grasses requires a large species sampling. <b>2010</b> , 333, 577-81		5
619	Molecular basis of trait correlations. <b>2010</b> , 15, 454-61		104
618	Evolutionary studies illuminate the structural-functional model of plant phytochromes. <b>2010</b> , 22, 4-16		86
617	The <i>Chlorella variabilis</i> NC64A genome reveals adaptation to photosymbiosis, coevolution with viruses, and cryptic sex. <b>2010</b> , 22, 2943-55		384
616	The Dawn Angiosperms. <b>2010</b> ,		26
615	Large changes in anatomy and physiology between diploid Rangpur lime ( <i>Citrus limonia</i> ) and its autotetraploid are not associated with large changes in leaf gene expression. <b>2011</b> , 62, 2507-19		105
614	Notes. 177-210		
613	The Genomes of All Angiosperms: A Call for a Coordinated Global Census. <b>2011</b> , 2011, 1-10		6
612	Adaptation to drought in two wild tomato species: the evolution of the <i>Asr</i> gene family. <i>New Phytologist</i> , <b>2011</b> , 190, 1032-1044	9.8	45
611	Neopolyploidy and diversification in <i>Heuchera grossulariifolia</i> . <b>2011</b> , 65, 1667-79		41
610	Defense mechanisms against herbivory in <i>Picea</i> : sequence evolution and expression regulation of gene family members in the phenylpropanoid pathway. <b>2011</b> , 12, 608		32
609	ZINC-INDUCED FACILITATOR-LIKE family in plants: lineage-specific expansion in monocotyledons and conserved genomic and expression features among rice ( <i>Oryza sativa</i> ) paralogs. <b>2011</b> , 11, 20		49
608	Cytochromes p450. <b>2011</b> , 9, e0144		218
607	Specific characteristics of CK2 regulatory subunits in plants. <b>2011</b> , 356, 255-60		7
606	Transcriptional variations mediated by an alternative promoter of the <i>FPR3</i> gene. <b>2011</b> , 22, 621-33		4
605	Molecular evolution of miraculin-like proteins in soybean Kunitz super-family. <b>2011</b> , 73, 369-79		16
604	Discovery and expression assessment of the AP2-like genes in <i>Hordeum vulgare</i> . <b>2011</b> , 33, 1639-1649		8

603	The glutamine synthetase gene family in <i>Populus</i> . <b>2011</b> , 11, 119	50
602	Extensive and heritable epigenetic remodeling and genetic stability accompany allohexaploidization of wheat. <b>2011</b> , 188, 499-510	58
601	Diversification of CYCLOIDEA expression in the evolution of bilateral flower symmetry in Caprifoliaceae and Lonicera (Dipsacales). <b>2011</b> , 107, 1521-32	63
600	Three homologous genes encoding sn-glycerol-3-phosphate acyltransferase 4 exhibit different expression patterns and functional divergence in <i>Brassica napus</i> . <b>2011</b> , 155, 851-65	43
599	Roles of mutation and selection in speciation: from Hugo de Vries to the modern genomic era. <b>2011</b> , 3, 812-29	51
598	The multiple functions of plant serine protease inhibitors: defense against herbivores and beyond. <b>2011</b> , 6, 1009-11	32
597	Expansion mechanisms and functional divergence of the glutathione s-transferase family in sorghum and other higher plants. <b>2011</b> , 18, 1-16	66
596	Gene duplication as a mechanism of genomic adaptation to a changing environment. <b>2012</b> , 279, 5048-57	343
595	From landing lights to mimicry: the molecular regulation of flower colouration and mechanisms for pigmentation patterning. <b>2012</b> , 39, 619-638	168
594	Molecular bases and evolutionary dynamics of self-incompatibility in the Pyrinae (Rosaceae). <b>2012</b> , 63, 4015-32	65
593	Duplications and Expression of RADIALIS-Like Genes in Dipsacales. <b>2012</b> , 173, 971-983	17
592	Genome-wide identification of differentially expressed genes under water deficit stress in upland cotton ( <i>Gossypium hirsutum</i> L.). <b>2012</b> , 12, 90	54
591	Genetic dissection of fruit quality traits in the octoploid cultivated strawberry highlights the role of homoeo-QTL in their control. <b>2012</b> , 124, 1059-77	75
590	The Application of Reverse Genetics to Polyploid Plant Species. <b>2012</b> , 31, 181-200	6
589	A tandem segmental duplication (TSD) in green revolution gene Rht-D1b region underlies plant height variation. <i>New Phytologist</i> , <b>2012</b> , 196, 282-291	9.8 60
588	Is hybridization involved in the evolution of the <i>Chenopodium album</i> aggregate? An analysis based on chromosome counts and genome size estimation. <b>2012</b> , 207, 530-540	23
587	Accelerated evolution and coevolution drove the evolutionary history of AGPase sub-units during angiosperm radiation. <b>2012</b> , 109, 693-708	8
586	Analyses of the sucrose synthase gene family in cotton: structure, phylogeny and expression patterns. <b>2012</b> , 12, 85	56

585	Small RNA-regulated networks and the evolution of novel structures in plants. <b>2012</b> , 77, 221-33	9
584	Transposable Element Exaptation in Plants. <b>2012</b> , 219-251	14
583	Genome-wide analysis of Aux/IAA genes in <i>Vitis vinifera</i> : cloning and expression profiling of a grape Aux/IAA gene in response to phytohormone and abiotic stresses. <b>2012</b> , 35, 365	15
582	Plant Transposable Elements. <b>2012</b> ,	7
581	Developing tools for investigating the multiple roles of ethylene: identification and mapping genes for ethylene biosynthesis and reception in barley. <b>2012</b> , 287, 793-802	9
580	Whole genome duplication affects evolvability of flowering time in an autotetraploid plant. <b>2012</b> , 7, e44784	28
579	Increasing strawberry fruit sensorial and nutritional quality using wild and cultivated germplasm. <b>2012</b> , 7, e46470	59
578	The First Ten Years of Plant Genome Sequencing and Prospects for the Next Decade. <b>2012</b> , 1-15	4
577	A new development: evolving concepts in leaf ontogeny. <b>2012</b> , 63, 535-62	54
576	Levels of biological organization and the origin of novelty. <b>2012</b> , 318, 428-37	50
575	Variation in HMA4 gene copy number and expression among <i>Noccaea caerulescens</i> populations presenting different levels of Cd tolerance and accumulation. <b>2012</b> , 63, 4179-89	85
574	The Impact of Transposable Elements on Gene and Genome Evolution. <b>2012</b> , 35-58	15
573	Phylogeny and Molecular Evolution of the Green Algae. <b>2012</b> , 31, 1-46	582
572	The validation of a 15 STR multiplex PCR for <i>Cannabis</i> species. <b>2012</b> , 126, 601-6	21
571	Tracing the origin and evolutionary history of plant nucleotide-binding site-leucine-rich repeat (NBS-LRR) genes. <i>New Phytologist</i> , <b>2012</b> , 193, 1049-1063	9.8 159
570	Carbonic anhydrase and the molecular evolution of C4 photosynthesis. <b>2012</b> , 35, 22-37	35
569	The multifaceted roles of FLOWERING LOCUS T in plant development. <b>2012</b> , 35, 1742-55	216
568	Emerging knowledge from genome sequencing of crop species. <b>2012</b> , 50, 250-66	30

567	The Y-segment of novel cold dehydrin genes is conserved and codons in the PR-10 genes are under positive selection in <i>Oxytropis</i> (Fabaceae) from contrasting climates. <b>2012</b> , 287, 123-42		5
566	Patterns of Gene Duplication and Their Contribution to Expansion of Gene Families in Grapevine. <b>2013</b> , 31, 852-861		27
565	Molecular characterisation of two homoeologous elicitor-responsive lipin genes in cotton. <b>2013</b> , 288, 519-33		3
564	Gene body methylation shows distinct patterns associated with different gene origins and duplication modes and has a heterogeneous relationship with gene expression in <i>Oryza sativa</i> (rice). <i>New Phytologist</i> , <b>2013</b> , 198, 274-283	9.8	45
563	The rice faded green leaf locus encodes protochlorophyllide oxidoreductase <sup>L</sup> and is essential for chlorophyll synthesis under high light conditions. <b>2013</b> , 74, 122-33		104
562	Polyploidy is genetic hence may cause non-adaptive radiations, whereas pseudopolyploidy is genomic hence may cause adaptive non-radiations. <b>2013</b> , 320, 286-94		7
561	Development of the gene-based SCARs for the Ph-3 locus, which confers late blight resistance in tomato. <b>2013</b> , 164, 9-16		18
560	Divergent evolutionary mechanisms of co-located Tak/Lrk and Glu-D3 loci revealed by comparative analysis of grass genomes. <b>2013</b> , 56, 195-204		2
559	Gene family evolution in green plants with emphasis on the origination and evolution of <i>Arabidopsis thaliana</i> genes. <b>2013</b> , 73, 941-51		82
558	Ascorbate as seen through plant evolution: the rise of a successful molecule?. <b>2013</b> , 64, 33-53		175
557	The evolution, function, structure, and expression of the plant sHSPs. <b>2013</b> , 64, 391-403		228
556	Comprehensive analysis of NAC domain transcription factor gene family in <i>Vitis vinifera</i> . <b>2013</b> , 32, 61-75		120
555	Convergent gene loss following gene and genome duplications creates single-copy families in flowering plants. <b>2013</b> , 110, 2898-903		231
554	A bountiful harvest: genomic insights into crop domestication phenotypes. <b>2013</b> , 64, 47-70		244
553	Sub- and neo-functionalization of APETALA3 paralogs have contributed to the evolution of novel floral organ identity in <i>Aquilegia</i> (columbine, Ranunculaceae). <i>New Phytologist</i> , <b>2013</b> , 197, 949-957	9.8	44
552	The spatial organization of metabolism within the plant cell. <b>2013</b> , 64, 723-46		153
551	Diversification of the monoterpene synthase gene family (TPSb) in <i>Protium</i> , a highly diverse genus of tropical trees. <b>2013</b> , 68, 432-42		12
550	Effect of phosphorus availability on the selection of species with different ploidy levels and genome sizes in a long-term grassland fertilization experiment. <i>New Phytologist</i> , <b>2013</b> , 200, 911-921	9.8	62

549	Evolutionary analysis of CBL-interacting protein kinase gene family in plants. <b>2013</b> , 71, 49-56	21
548	Can resource costs of polyploidy provide an advantage to sex?. <b>2013</b> , 110, 152-9	18
547	Gene divergence of homeologous regions associated with a major seed protein content QTL in soybean. <b>2013</b> , 4, 176	16
546	Natural genetic transformation generates a population of merodiploids in <i>Streptococcus pneumoniae</i> . <b>2013</b> , 9, e1003819	15
545	Evolution of the key alkaloid enzyme putrescine N-methyltransferase from spermidine synthase. <b>2013</b> , 4, 260	20
544	Flower color as a model system for studies of plant evo-devo. <b>2013</b> , 4, 321	73
543	The <i>Tarenaya hassleriana</i> genome provides insight into reproductive trait and genome evolution of crucifers. <b>2013</b> , 25, 2813-30	67
542	PolyCat: a resource for genome categorization of sequencing reads from allopolyploid organisms. <b>2013</b> , 3, 517-25	65
541	Protein change in plant evolution: tracing one thread connecting molecular and phenotypic diversity. <b>2013</b> , 4, 382	10
540	Crop plants as models for understanding plant adaptation and diversification. <b>2013</b> , 4, 290	62
539	Selective acquisition and retention of genomic sequences by Pack-Mutator-like elements based on guanine-cytosine content and the breadth of expression. <b>2013</b> , 163, 1419-32	21
538	Analysis of functional redundancies within the <i>Arabidopsis</i> TCP transcription factor family. <b>2013</b> , 64, 5673-85	83
537	The <i>Brassica rapa</i> FLC homologue FLC2 is a key regulator of flowering time, identified through transcriptional co-expression networks. <b>2013</b> , 64, 4503-16	69
536	Parallel recruitment of multiple genes into c4 photosynthesis. <b>2013</b> , 5, 2174-87	49
535	Genome-wide analysis of the <i>Sus</i> gene family in cotton. <b>2013</b> , 55, 643-53	35
534	Subfunctionalization of cyprinid hypoxia-inducible factors for roles in development and oxygen sensing. <b>2013</b> , 67, 873-82	41
533	Identification of genetic elements associated with EPSPs gene amplification. <b>2013</b> , 8, e65819	41
532	Insights into the loblolly pine genome: characterization of BAC and fosmid sequences. <b>2013</b> , 8, e72439	41

531	High genetic diversity and distinctiveness of rear-edge climate relicts maintained by ancient tetraploidisation for <i>Alnus glutinosa</i> . <b>2013</b> , 8, e75029	38
530	The 2-C-methylerythritol 4-phosphate pathway in melon is regulated by specialized isoforms for the first and last steps. <b>2014</b> , 65, 5077-92	29
529	Gene duplication, population genomics, and species-level differentiation within a tropical mountain shrub. <b>2014</b> , 6, 2611-24	17
528	Neofunctionalization of duplicated <i>Tic40</i> genes caused a gain-of-function variation related to male fertility in <i>Brassica oleracea</i> lineages. <b>2014</b> , 166, 1403-19	15
527	Distinct Copy Number, Coding Sequence, and Locus Methylation Patterns Underlie <i>Rhg1</i> -Mediated Soybean Resistance to Soybean Cyst Nematode. <b>2014</b> , 165, 630-647	90
526	Global dissection of alternative splicing in paleopolyploid soybean. <b>2014</b> , 26, 996-1008	178
525	Stable transformation and reverse genetic analysis of <i>Penium margaritaceum</i> : a platform for studies of charophyte green algae, the immediate ancestors of land plants. <b>2014</b> , 77, 339-51	45
524	Glyphosate resistance: state of knowledge. <b>2014</b> , 70, 1367-77	293
523	Evolution and expression analysis of the soybean glutamate decarboxylase gene family. <b>2014</b> , 39, 899-907	9
522	Protein subcellular relocalization of duplicated genes in <i>Arabidopsis</i> . <b>2014</b> , 6, 2501-15	8
521	New insights on the evolution of <i>Leafy cotyledon1 (LEC1)</i> type genes in vascular plants. <b>2014</b> , 103, 380-7	22
520	<i>LEC1-LIKE</i> paralog transcription factor: how to survive extinction and fit in NF-Y protein complex. <b>2014</b> , 543, 220-33	10
519	Root parasitic plant <i>Orobanche aegyptiaca</i> and shoot parasitic plant <i>Cuscuta australis</i> obtained Brassicaceae-specific strictosidine synthase-like genes by horizontal gene transfer. <b>2014</b> , 14, 19	46
518	Polyploidy and the petal transcriptome of <i>Gossypium</i> . <b>2014</b> , 14, 3	29
517	Conserved CO-FT regulons contribute to the photoperiod flowering control in soybean. <b>2014</b> , 14, 9	51
516	Origin and evolution of alginate-c5-mannuronan-epimerase gene based on transcriptomic analysis of brown algae. <b>2014</b> , 33, 73-85	5
515	The impact of widespread regulatory neofunctionalization on homeolog gene evolution following whole-genome duplication in maize. <b>2014</b> , 24, 1348-55	60
514	Concerted evolution of D1 and D2 to regulate chlorophyll degradation in soybean. <b>2014</b> , 77, 700-12	49



513	Pollen-specific activation of Arabidopsis retrogenes is associated with global transcriptional reprogramming. <b>2014</b> , 26, 3299-313		22
512	Natural compounds as next-generation herbicides. <b>2014</b> , 166, 1090-105		191
511	Identification, characterization, and utilization of single copy genes in 29 angiosperm genomes. <b>2014</b> , 15, 504		21
510	Comparative genetic mapping and genomic region collinearity analysis of the powdery mildew resistance gene Pm41. <b>2014</b> , 127, 1741-51		29
509	Diversity and evolution of transposable elements in Arabidopsis. <b>2014</b> , 22, 203-16		23
508	Molecular evolution and sequence divergence of plant chalcone synthase and chalcone synthase-Like genes. <b>2014</b> , 142, 215-25		15
507	Evolutionary and Expression Analyses of Basic Zipper Transcription Factors in the Highly Homozygous Model Grape PN40024 ( <i>Vitis vinifera</i> L.). <b>2014</b> , 32, 1085-1102		23
506	Are polyploids really evolutionary dead-ends (again)? A critical reappraisal of Mayrose et al. (). <i>New Phytologist</i> , <b>2014</b> , 202, 1105-1117	9.8	107
505	Exploring the evolutionary route of the acquisition of betaine aldehyde dehydrogenase activity by plant ALDH10 enzymes: implications for the synthesis of the osmoprotectant glycine betaine. <b>2014</b> , 14, 149		16
504	Impact of recurrent gene duplication on adaptation of plant genomes. <b>2014</b> , 14, 151		21
503	Genome-wide investigation and expression analysis suggest diverse roles and genetic redundancy of Pht1 family genes in response to Pi deficiency in tomato. <b>2014</b> , 14, 61		59
502	Effects of apomixis and polyploidy on diversification and geographic distribution in Amelanchier ( <i>Rosaceae</i> ). <b>2014</b> , 101, 1375-87		27
501	Phylogenetic analyses provide the first insights into the evolution of OVATE family proteins in land plants. <b>2014</b> , 113, 1219-33		37
500	Evolution of isoprene emission capacity in plants. <b>2014</b> , 19, 439-46		35
499	Structure and expression profile of the sucrose synthase gene family in the rubber tree: indicative of roles in stress response and sucrose utilization in the laticifers. <b>2014</b> , 281, 291-305		49
498	Genomic evidence for adaptation by gene duplication. <b>2014</b> , 24, 1356-62		70
497	A Comprehensive Forage Development Model for Advancing the Agricultural and Rural Economy of Pakistan through Integration of Agronomic and Omics Approaches. <b>2014</b> , 184-201		1
496	The impacts of polyploidy, geographic and ecological isolations on the diversification of <i>Panax</i> ( <i>Araliaceae</i> ). <b>2015</b> , 15, 297		26

495	Using Disease-Associated Coding Sequence Variation to Investigate Functional Compensation by Human Paralogous Proteins. <b>2015</b> , 11, 245-51	
494	Gene structure, phylogeny and expression profile of the sucrose synthase gene family in cacao ( <i>Theobroma cacao</i> L.). <b>2015</b> , 94, 461-72	14
493	Genome-wide investigation and expression analysis of Sodium/Calcium exchanger gene family in rice and <i>Arabidopsis</i> . <b>2015</b> , 8, 54	29
492	Development of two major resources for pea genomics: the GenoPea 13.2K SNP Array and a high-density, high-resolution consensus genetic map. <b>2015</b> , 84, 1257-73	60
491	Genomic limitations to RNA sequencing expression profiling. <b>2015</b> , 84, 491-503	17
490	Evolutionary Analysis of Genes for S-RNase-based Self-incompatibility Reveals S Locus Duplications in the Ancestral Rosaceae. <b>2015</b> , 84, 233-242	19
489	Aquaporins as targets for stress tolerance in plants: genomic complexity and perspectives. <b>2015</b> , 39, 879-886	6
488	The phylogeny and evolutionary history of the Lesion Simulating Disease (LSD) gene family in Viridiplantae. <b>2015</b> , 290, 2107-19	4
487	Genome-wide analysis reveals diverged patterns of codon bias, gene expression, and rates of sequence evolution in picea gene families. <b>2015</b> , 7, 1002-15	46
486	A Time-Calibrated Road Map of Brassicaceae Species Radiation and Evolutionary History. <b>2015</b> , 27, 2770-84	143
485	Duplicate gene divergence by changes in microRNA binding sites in <i>Arabidopsis</i> and <i>Brassica</i> . <b>2015</b> , 7, 646-55	18
484	Genomic patterns of species diversity and divergence in <i>Eucalyptus</i> . <i>New Phytologist</i> , <b>2015</b> , 206, 1378-90,8	18
483	Intraspecific and intergenerational differences in plant-soil feedbacks. <b>2015</b> , 124, 994-1004	23
482	Genome-wide identification and expression analysis of TCP transcription factors in <i>Gossypium raimondii</i> . <b>2014</b> , 4, 6645	53
481	Assignment of homoeologs to parental genomes in allopolyploids for species tree inference, with an example from <i>Fumaria</i> (papaveraceae). <b>2015</b> , 64, 448-71	15
480	Functional evolution of phosphatidylethanolamine binding proteins in soybean and <i>Arabidopsis</i> . <b>2015</b> , 27, 323-36	77
479	Genetic enablers underlying the clustered evolutionary origins of C4 photosynthesis in angiosperms. <b>2015</b> , 32, 846-58	46
478	Discovery of novel genes derived from transposable elements using integrative genomic analysis. <b>2015</b> , 32, 1487-506	38

477	IGMAP: An Interactive Mapping and Clustering Platform for Plants. <b>2015</b> , 8, 818-21		3
476	Identification of a member of the catalase multigene family on wheat chromosome 7A associated with flour b* colour and biological significance of allelic variation. <b>2015</b> , 290, 2313-24		4
475	Evolution of CONSTANS Regulation and Function after Gene Duplication Produced a Photoperiodic Flowering Switch in the Brassicaceae. <b>2015</b> , 32, 2284-301		36
474	Analysis of the sucrose synthase gene family in tobacco: structure, phylogeny, and expression patterns. <b>2015</b> , 242, 153-66		34
473	New insights into the evolutionary history of plant sorbitol dehydrogenase. <b>2015</b> , 15, 101		12
472	Genome-wide identification and characterization of aquaporin gene family in common bean ( <i>Phaseolus vulgaris</i> L.). <b>2015</b> , 290, 1771-85		54
471	An Ancestral Role for CONSTITUTIVE TRIPLE RESPONSE1 Proteins in Both Ethylene and Abscisic Acid Signaling. <b>2015</b> , 169, 283-98		31
470	CATION EXCHANGER1 Cosegregates with Cadmium Tolerance in the Metal Hyperaccumulator <i>Arabidopsis halleri</i> and Plays a Role in Limiting Oxidative Stress in <i>Arabidopsis</i> Spp. <b>2015</b> , 169, 549-59		72
469	Genome-wide identification and characterization of MADS-box family genes related to organ development and stress resistance in <i>Brassica rapa</i> . <b>2015</b> , 16, 178		58
468	Unraveling the evolution and regulation of the alternative oxidase gene family in plants. <b>2015</b> , 225, 331-9		5
467	Parallel subfunctionalisation of PsbO protein isoforms in angiosperms revealed by phylogenetic analysis and mapping of sequence variability onto protein structure. <b>2015</b> , 15, 133		8
466	Population Level Purifying Selection and Gene Expression Shape Subgenome Evolution in Maize. <b>2015</b> , 32, 3226-35		42
465	Anthocyanin leaf markings are regulated by a family of R2R3-MYB genes in the genus <i>Trifolium</i> . <i>New Phytologist</i> , <b>2015</b> , 205, 882-93	9.8	36
464	Ecological transition predictably associated with gene degeneration. <b>2015</b> , 32, 347-54		35
463	<i>Arabidopsis thaliana</i> 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. <b>2016</b> , 17, 893		14
462	Genome-wide identification and expression analysis of CIPK genes in diploid cottons. <b>2016</b> , 15,		7
461	Molecular and Genomic Tools Provide Insights on Crop Domestication and Evolution. <b>2016</b> , 135, 181-223		2
460	Evolutionary Expansion of WRKY Gene Family in Banana and Its Expression Profile during the Infection of Root Lesion Nematode, <i>Pratylenchus coffeae</i> . <b>2016</b> , 11, e0162013		13

459	Genome-Wide Identification and Expression Analysis of Homeodomain Leucine Zipper Subfamily IV (HDZ IV) Gene Family from <i>Musa accuminata</i> . <b>2016</b> , 7, 20	27
458	Glutathione S-Transferase Gene Family in <i>Gossypium raimondii</i> and <i>G. arboreum</i> : Comparative Genomic Study and their Expression under Salt Stress. <b>2016</b> , 7, 139	45
457	Conservation and Expression Patterns Divergence of Ascorbic Acid d-mannose/l-galactose Pathway Genes in <i>Brassica rapa</i> . <b>2016</b> , 7, 778	10
456	Genome-Wide Identification and Expression Profiling of Tomato Hsp20 Gene Family in Response to Biotic and Abiotic Stresses. <b>2016</b> , 7, 1215	51
455	Comparative structural analysis of Bru1 region homeologs in <i>Saccharum spontaneum</i> and <i>S. officinarum</i> . <b>2016</b> , 17, 446	5
454	Species interactions and plant polyploidy. <b>2016</b> , 103, 1326-35	50
453	Comprehensive analysis of TCP transcription factors and their expression during cotton ( <i>Gossypium arboreum</i> ) fiber early development. <b>2016</b> , 6, 21535	32
452	Evolutionary Histories of Gene Families in Angiosperm Trees. <b>2016</b> , 121-137	
451	Evolutionary and functional analysis of mulberry type III polyketide synthases. <b>2016</b> , 17, 540	13
450	Imbalanced positive selection maintains the functional divergence of duplicated DIHYDROKAEMPFEROL 4-REDUCTASE genes. <b>2016</b> , 6, 39031	5
449	Genomic Identification and Comparative Expansion Analysis of the Non-Specific Lipid Transfer Protein Gene Family in <i>Gossypium</i> . <b>2016</b> , 6, 38948	22
448	Between-species differences in gene copy number are enriched among functions critical for adaptive evolution in <i>Arabidopsis halleri</i> . <b>2016</b> , 17, 1034	21
447	Expansion Mechanisms and Evolutionary History on Genes Encoding DNA Glycosylases and Their Involvement in Stress and Hormone Signaling. <b>2016</b> , 8, 1165-84	1
446	Insights into the <i>Prunus</i> -Specific S-RNase-Based Self-Incompatibility System from a Genome-Wide Analysis of the Evolutionary Radiation of S Locus-Related F-box Genes. <b>2016</b> , 57, 1281-94	25
445	Differential Regulation of Protochlorophyllide Oxidoreductase Abundances by VIRESCENT 5A (OsV5A) and VIRESCENT 5B (OsV5B) in Rice Seedlings. <b>2016</b> , 57, 2392-2402	11
444	Drought stress differentially regulates the expression of small open reading frames (sORFs) in <i>Arabidopsis</i> roots and shoots. <b>2016</b> , 11, e1215792	7
443	Functional conservation and divergence of GmCHLI genes in polyploid soybean. <b>2016</b> , 88, 584-596	11
442	Is post-polyploidization diploidization the key to the evolutionary success of angiosperms?. <b>2016</b> , 180, 1-5	98

441	Genome-wide identification of salinity responsive HSP70s in common bean. <b>2016</b> , 43, 1251-1266	18
440	LRR-RLK family from two Citrus species: genome-wide identification and evolutionary aspects. <b>2016</b> , 17, 623	24
439	Genome Analysis of Plants. <b>2016</b> , 1-27	
438	Novel Structures in Plants, Developmental Evolution of. <b>2016</b> , 146-166	
437	Bridging evolution and development in plants. <i>New Phytologist</i> , <b>2016</b> , 212, 827-830	9.8 5
436	pATsi: Paralogs and Singleton Genes from <i>Arabidopsis thaliana</i> . <b>2016</b> , 12, 1-7	8
435	Phylogenetic and Genomic Analyses Resolve the Origin of Important Plant Genes Derived from Transposable Elements. <b>2016</b> , 33, 1937-56	19
434	Genetic Analysis of <i>Physcomitrella patens</i> Identifies ABSCISIC ACID NON-RESPONSIVE, a Regulator of ABA Responses Unique to Basal Land Plants and Required for Desiccation Tolerance. <b>2016</b> , 28, 1310-27	73
433	Plant Evolution: Evolving Antagonistic Gene Regulatory Networks. <b>2016</b> , 26, R493-R495	1
432	Insights into the Ecology and Evolution of Polyploid Plants through Network Analysis. <b>2016</b> , 25, 2644-60	20
431	Genomics-based strategies for the use of natural variation in the improvement of crop metabolism. <b>2016</b> , 242, 47-64	49
430	Repeated Whole-Genome Duplication, Karyotype Reshuffling, and Biased Retention of Stress-Responding Genes in Buckler Mustard. <b>2016</b> , 28, 17-27	28
429	<i>Solidago altissima</i> differs with respect to ploidy frequency and clinal variation across the prairie-forest biome border in Minnesota. <b>2016</b> , 103, 22-32	10
428	A global perspective on Campanulaceae: Biogeographic, genomic, and floral evolution. <b>2016</b> , 103, 233-45	26
427	Integrated mapping and characterization of the gene underlying the okra leaf trait in <i>Gossypium hirsutum</i> L. <b>2016</b> , 67, 763-74	33
426	Biogeography of the Anthropocene: Domestication. <b>2016</b> , 40, 161-174	13
425	The <i>Arabidopsis</i> paralogs, PUB46 and PUB48, encoding U-box E3 ubiquitin ligases, are essential for plant response to drought stress. <b>2017</b> , 17, 8	27
424	Plant Actin-Depolymerizing Factors Possess Opposing Biochemical Properties Arising from Key Amino Acid Changes throughout Evolution. <b>2017</b> , 29, 395-408	29

423	Genome sequencing and population genomic analyses provide insights into the adaptive landscape of silver birch. <b>2017</b> , 49, 904-912	123
422	Evolutionary dynamics of mixed-ploidy populations in an annual herb: dispersal, local persistence and recurrent origins of polyploids. <b>2017</b> , 120, 303-315	27
421	Identification and Characterization of Chalcone Synthase Gene Family Members in <i>Nicotiana tabacum</i> . <b>2017</b> , 36, 374-384	11
420	Autopolyploidy leads to rapid genomic changes in <i>Arabidopsis thaliana</i> . <b>2017</b> , 136, 199-206	11
419	Wild tobacco genomes reveal the evolution of nicotine biosynthesis. <b>2017</b> , 114, 6133-6138	98
418	Identification and expression analysis under abiotic stress of the - genes in <i>L.</i> <b>2017</b> , 23, 503-516	16
417	Partial Order Concepts in Applied Sciences. <b>2017</b> ,	14
416	Coordinated Functional Divergence of Genes after Genome Duplication in. <b>2017</b> , 29, 2786-2800	25
415	Producing Designer Oils in Industrial Microalgae by Rational Modulation of Co-evolving Type-2 Diacylglycerol Acyltransferases. <b>2017</b> , 10, 1523-1539	78
414	Polyploidy: Recent Trends and Future Perspectives. <b>2017</b> ,	0
413	DuplicationDetector , a light weight tool for duplication detection using NGS data. <b>2017</b> , 9-10, 23-28	4
412	Genome-wide dissection of the chalcone synthase gene family in <i>Oryza sativa</i> . <b>2017</b> , 37, 1	10
411	A Highly Specific Genome-Wide Association Study Integrated with Transcriptome Data Reveals the Contribution of Copy Number Variations to Specialized Metabolites in <i>Arabidopsis thaliana</i> Accessions. <b>2017</b> , 34, 3111-3122	5
410	Recent autopolyploidization in a naturalized population of <i>Mimulus guttatus</i> (Phrymaceae). <b>2017</b> ,	4
409	No difference in plasticity between different ploidy levels in the Mediterranean herb <i>Mercurialis annua</i> . <b>2017</b> , 7, 9484	1
408	Pure polyploidy: Closing the gaps in autopolyploid research. <b>2017</b> , 55, 340-352	80
407	Comparative and Evolutionary Genomics of Angiosperm Trees. <b>2017</b> ,	5
406	Functional divergence and intron variability during evolution of angiosperm TERMINAL FLOWER1 (TFL1) genes. <b>2017</b> , 7, 14830	8

405 Polyploidy in Changing Environment. **2017**, 89-99

404 Gene-body CG methylation and divergent expression of duplicate genes in rice. **2017**, 7, 2675 16

403 Next-generation polyploid phylogenetics: rapid resolution of hybrid polyploid complexes using PacBio single-molecule sequencing. *New Phytologist*, **2017**, 213, 413-429 9.8 50

402 Genomic Scans across Three Eucalypts Suggest that Adaptation to Aridity is a Genome-Wide Phenomenon. **2017**, 9, 253-265 21

401 Transcriptome Signatures of Selection, Drift, Introgression, and Gene Duplication in the Evolution of an Extremophile Endemic Plant. **2017**, 9, 3478-3494 2

400 Selective Constraints on Coding Sequences of Nervous System Genes Are a Major Determinant of Duplicate Gene Retention in Vertebrates. **2017**, 34, 2773-2791 24

399 Evolution and expression analysis reveal the potential role of the HD-Zip gene family in regulation of embryo abortion in grapes (*Vitis vinifera* L.). **2017**, 18, 744 29

398 Genome-Wide Analysis of the Sucrose Synthase Gene Family in Grape (*Vitis vinifera*): Structure, Evolution, and Expression Profiles. **2017**, 8, 33

397 Genome-Wide Identification of the MIKC-Type MADS-Box Gene Family in *L.* Unravels Their Roles in Flowering. **2017**, 8, 384 27

396 Identification of TIFY Family Genes and Analysis of Their Expression Profiles in Response to Phytohormone Treatments and Infection in Poplar. **2017**, 8, 493 23

395 Functional Characterization of a Putative in Transgenic Arabidopsis and Its Role during Flowering Control. **2017**, 8, 618 12

394 Genome-Wide Identification and Expression Analysis of the Biotin Carboxyl Carrier Subunits of Heteromeric Acetyl-CoA Carboxylase in. **2017**, 8, 624 10

393 Genome-Wide Identification and Functional Analysis of the Calcineurin B-like Protein and Calcineurin B-like Protein-Interacting Protein Kinase Gene Families in Turnip ( var. ). **2017**, 8, 1191 28

392 Genome-Wide Identification and Characterization of Transcription Factors in. **2017**, 8, 1588 17

391 Hybrid assembly with long and short reads improves discovery of gene family expansions. **2017**, 18, 541 33

390 Genome-wide analysis of DUF221 domain-containing gene family in *Oryza* species and identification of its salinity stress-responsive members in rice. **2017**, 12, e0182469 25

389 Rapid diversification of homothorax expression patterns after gene duplication in spiders. **2017**, 17, 168 9

388 Genome-wide comparative analysis of putative Pth11-related G protein-coupled receptors in fungi belonging to Pezizomycotina. **2017**, 17, 166 9

387	Genome-wide analysis of WOX genes in upland cotton and their expression pattern under different stresses. <b>2017</b> , 17, 113	62
386	Polyamines in the life of Arabidopsis: profiling the expression of S-adenosylmethionine decarboxylase (SAMDC) gene family during its life cycle. <b>2017</b> , 17, 264	18
385	New reference genome sequences of hot pepper reveal the massive evolution of plant disease-resistance genes by retroduplication. <b>2017</b> , 18, 210	142
384	Genome-wide identification of glutathione peroxidase (GPX) gene family and their response to abiotic stress in cucumber. <b>2018</b> , 8, 159	23
383	Phylogenomics reveals an extensive history of genome duplication in diatoms (Bacillariophyta). <b>2018</b> , 105, 330-347	27
382	Papain-like cysteine proteases in <i>Carica papaya</i> : lineage-specific gene duplication and expansion. <b>2018</b> , 19, 26	14
381	Genetic and epigenetic divergence of duplicate genes in two legume species. <b>2018</b> , 41, 2033-2044	15
380	One Hundred Ways to Invent the Sexes: Theoretical and Observed Paths to Dioecy in Plants. <b>2018</b> , 69, 553-575	46
379	New insights into the phylogeny of the TMBIM superfamily across the tree of life: Comparative genomics and synteny networks reveal independent evolution of the BI and LFG families in plants. <b>2018</b> , 126, 266-278	10
378	Characterization of the late embryogenesis abundant (LEA) proteins family and their role in drought stress tolerance in upland cotton. <b>2018</b> , 19, 6	115
377	The unique evolutionary pattern of the Hydroxyproline-rich glycoproteins superfamily in Chinese white pear ( <i>Pyrus bretschneideri</i> ). <b>2018</b> , 18, 36	4
376	Annotation of the Corymbia terpene synthase gene family shows broad conservation but dynamic evolution of physical clusters relative to <i>Eucalyptus</i> . <b>2018</b> , 121, 87-104	10
375	Molecular cytogenetics to characterize mechanisms of gene duplication in pesticide resistance. <b>2018</b> , 74, 22-29	12
374	Glyphosate Resistance and EPSPS Gene Duplication: Convergent Evolution in Multiple Plant Species. <b>2018</b> , 109, 117-125	36
373	Successive evolutionary steps drove Pooideae grasses from tropical to temperate regions. <i>New Phytologist</i> , <b>2018</b> , 217, 925-938	9.8 18
372	Molecular Evolution and Stress and Phytohormone Responsiveness of Genes in. <b>2018</b> , 9, 494	6
371	Regulatory motifs found in the small heat shock protein (sHSP) gene family in tomato. <b>2018</b> , 19, 860	15
370	Characterization of bHLH/HLH genes that are involved in brassinosteroid (BR) signaling in fiber development of cotton ( <i>Gossypium hirsutum</i> ). <b>2018</b> , 18, 304	23



369	Comparative analysis of selection mode reveals different evolutionary rate and expression pattern in <i>Arachis duranensis</i> and <i>Arachis ipaësis</i> duplicated genes. <b>2018</b> , 98, 349-361	8
368	Plastid genome analysis of three Nemaliophycidae red algal species suggests environmental adaptation for iron limited habitats. <b>2018</b> , 13, e0196995	7
367	Factors Influencing Gene Family Size Variation Among Related Species in a Plant Family, Solanaceae. <b>2018</b> , 10, 2596-2613	21
366	Genome-wide identification and expression analyses of the pectate lyase (PEL) gene family in cotton ( <i>Gossypium hirsutum</i> L.). <b>2018</b> , 19, 661	20
365	Whole Genome Analysis of Cyclin Dependent Kinase ( ) Gene Family in Cotton and Functional Evaluation of the Role of Gene in Drought and Salt Stress Tolerance in Plants. <b>2018</b> , 19,	29
364	Chromosome-level reference genome and alternative splicing atlas of moso bamboo ( <i>Phyllostachys edulis</i> ). <b>2018</b> , 7,	48
363	Gene duplicates cause hybrid lethality between sympatric species of <i>Mimulus</i> . <b>2018</b> , 14, e1007130	29
362	Phylogenetics of <i>Camelina</i> Crantz. (Brassicaceae) and insights on the origin of gold-of-pleasure ( <i>Camelina sativa</i> ). <b>2018</b> , 127, 834-842	25
361	Identification of jumonjiC domain containing gene family among the <i>Oryza</i> species and their expression analysis in FL478, a salt tolerant rice genotype. <b>2018</b> , 130, 43-53	10
360	Evolutionary Origin, Gradual Accumulation and Functional Divergence of Gene Family with Plant Evolution. <b>2018</b> , 9, 71	19
359	Different Modes of Gene Duplication Show Divergent Evolutionary Patterns and Contribute Differently to the Expansion of Gene Families Involved in Important Fruit Traits in Pear ( <i></i> ). <b>2018</b> , 9, 161	35
358	Functional Conservation and Divergence of Soybean GmSTOP1 Members in Proton and Aluminum Tolerance. <b>2018</b> , 9, 570	13
357	Identification and transcriptional analysis of dehydrin gene family in cucumber ( <i>Cucumis sativus</i> ). <b>2018</b> , 40, 1	8
356	Focus on putative serine carboxypeptidase-like acyltransferases in grapevine. <b>2018</b> , 130, 356-366	11
355	Tandem Duplicate Genes in Maize Are Abundant and Date to Two Distinct Periods of Time. <b>2018</b> , 8, 3049-3058	8
354	A Dead Gene Walking: Convergent Degeneration of a Clade of MADS-Box Genes in Crucifers. <b>2018</b> , 35, 2618-2638	6
353	Genome-Wide Study of YABBY Genes in Upland Cotton and Their Expression Patterns under Different Stresses. <b>2018</b> , 9, 33	40
352	The Role of Transposable Elements in Speciation. <b>2018</b> , 9,	75

351	Plant Cation-Chloride Cotransporters (CCC): Evolutionary Origins and Functional Insights. <b>2018</b> , 19,	13
350	Evolution and Stress Responses of <i>Gossypium hirsutum</i> SWEET Genes. <b>2018</b> , 19,	22
349	Widespread signatures of selection for secreted peptidases in a fungal plant pathogen. <b>2018</b> , 18, 7	15
348	Terzyme: a tool for identification and analysis of the plant terpenome. <b>2018</b> , 14, 4	17
347	Histone Acetyltransferases (HATs) in Chinese Cabbage: Insights from Histone H3 Acetylation and Expression Profiling of HATs in Response to Abiotic Stresses. <b>2018</b> , 143, 296-303	6
346	Evolutionary dynamic analyses on monocot flavonoid 3'-hydroxylase gene family reveal evidence of plant-environment interaction. <b>2019</b> , 19, 347	8
345	The Diversity of Nutritional Metabolites: Origin, Dissection, and Application in Crop Breeding. <b>2019</b> , 10, 1028	12
344	Genome-wide identification and expression analysis of the BURP domain-containing genes in <i>Gossypium hirsutum</i> . <b>2019</b> , 20, 558	7
343	Molecular identification of the phosphate transporter family 1 (PHT1) genes and their expression profiles in response to phosphorus deprivation and other abiotic stresses in <i>Brassica napus</i> . <b>2019</b> , 14, e0220374	16
342	Combining genome-wide and transcriptome-wide analyses reveal the evolutionary conservation and functional diversity of aquaporins in cotton. <b>2019</b> , 20, 538	13
341	Autopolyploidization in switchgrass alters phenotype and flowering time via epigenetic and transcription regulation. <b>2019</b> , 70, 5673-5686	12
340	Dissecting the Genome-Wide Evolution and Function of R2R3-MYB Transcription Factor Family in. <b>2019</b> , 10,	12
339	Fine-Tuning the Expression of Duplicate Genes by Translational Regulation in and Maize. <b>2019</b> , 10, 534	2
338	Genome-Wide Mining and Identification of Protein Kinase Gene Family Impacts Salinity Stress Tolerance in Highly Dense Genetic Map Developed from Interspecific Cross between <i>G. hirsutum</i> L. and <i>G. darwinii</i> G. Watt. <b>2019</b> , 9, 560	5
337	Independent evolution of rosmarinic acid biosynthesis in two sister families under the Lamiids clade of flowering plants. <b>2019</b> , 294, 15193-15205	20
336	Duplication history and molecular evolution of the <i>rbcS</i> multigene family in angiosperms. <b>2019</b> , 70, 6127-6139	7
335	Identification and Expression Analysis of GRAS Transcription Factors to Elucidate Candidate Genes Related to Stolons, Fruit Ripening and Abiotic Stresses in Woodland Strawberry (). <b>2019</b> , 20,	7
334	MIPS: Functional dynamics in evolutionary pathways of plant kingdom. <b>2019</b> , 111, 1929-1945	10

333	Linking Duplication of a Calcium Sensor to Salt Tolerance in. <b>2019</b> , 179, 1176-1192	12
332	Whole-genome re-sequencing reveals the impact of the interaction of copy number variants of the rhg1 and Rhg4 genes on broad-based resistance to soybean cyst nematode. <b>2019</b> , 17, 1595-1611	36
331	Genetic Consequences of Interspecific Hybridization, Its Role in Speciation and Phenotypic Diversity of Plants. <b>2019</b> , 55, 278-294	10
330	Identification and characterisation of a novel FT orthologous gene in London plane with a distinct expression response to environmental stimuli compared to PaFT. <b>2019</b> , 21, 1039-1051	3
329	Genome-wide analysis of spatiotemporal gene expression patterns during floral organ development in Brassica rapa. <b>2019</b> , 294, 1403-1420	10
328	In silico genome-wide identification and comprehensive characterization of the gene family in soybean. <b>2019</b> , 5, e01868	4
327	Genome-wide analysis of the callose enzyme families of fertile and sterile flower buds of the Chinese cabbage (Brassica rapa L. ssp. pekinensis). <b>2019</b> , 9, 1432-1449	3
326	Comparative Analysis of SUS Gene Family between Saccharum officinarum and Saccharum spontaneum. <b>2019</b> , 12, 174-185	4
325	Homeologous regulation of Frigida-like genes provides insights on reproductive development and somatic embryogenesis in the allotetraploid Coffea arabica. <b>2019</b> , 9, 8446	7
324	Genome-wide identification, characterization and expression analysis of the non-specific lipid transfer proteins in potato. <b>2019</b> , 20, 375	8
323	Genes from Common Bean (L.) Show Broad to Specific Abiotic Stress Responses and Distinct Levels of Nucleotide Diversity. <b>2019</b> , 2019, 9520642	13
322	Meiosis, the master driver of gene duplication in higher plants?. <b>2019</b> , 514, 756-758	1
321	Evolutionary Conservation and Divergence of Genes Encoding 3-Hydroxy-3-methylglutaryl Coenzyme A Synthase in the Allotetraploid Cotton Species. <b>2019</b> , 8,	4
320	Identification of Histone H3 ( ) Genes in Revealed Diverse Expression During Ovule Development and Stress Responses. <b>2019</b> , 10,	18
319	Deep Transcriptome Analysis Reveals Reactive Oxygen Species (ROS) Network Evolution, Response to Abiotic Stress, and Regulation of Fiber Development in Cotton. <b>2019</b> , 20,	17
318	Rapid functional divergence after small-scale gene duplication in grasses. <b>2019</b> , 19, 97	8
317	Effect of paleopolyploidy and allopolyploidy on gene expression in banana. <b>2019</b> , 20, 244	15
316	Genome-wide identification and analysis of the WUSCHEL-related homeobox (WOX) gene family in allotetraploid Brassica napus reveals changes in WOX genes during polyploidization. <b>2019</b> , 20, 317	19

315	Organization and evolution of the chalcone synthase gene family in bread wheat and relative species. <b>2019</b> , 20, 30	5
314	A meta-analysis of whole genome duplication and the effects on flowering traits in plants. <b>2019</b> , 106, 469-476	12
313	Duplication and selection in $\beta$ -ketoacyl-ACP synthase gene lineages in the sexually deceptive <i>Chiloglottis</i> (Orchidaceae). <b>2019</b> , 123, 1053-1066	3
312	Genome-Wide Identification, Sequence Variation, and Expression of the Glycerol-3-Phosphate Acyltransferase (GPAT) Gene Family in. <b>2019</b> , 10, 116	9
311	Herbicide Metabolism: Crop Selectivity, Bioactivation, Weed Resistance, and Regulation. <b>2019</b> , 67, 149-175	35
310	Variation of gene expression in plants is influenced by gene architecture and structural properties of promoters. <b>2019</b> , 14, e0212678	16
309	Transcriptional profiling reveals differentially expressed genes involved in lipid biosynthesis during cacao seed development. <b>2019</b> , 9, 17263	1
308	Genetic Analysis and Gene Mapping for a Short-Petiole Mutant in Soybean ( <i>Glycine max</i> (L.) Merr.). <b>2019</b> , 9, 709	0
307	Dissecting the Genomic Diversification of Late Embryogenesis Abundant (LEA) Protein Gene Families in Plants. <b>2019</b> , 11, 459-471	39
306	Different divergence events for three pairs of PEBPs in <i>Gossypium</i> as implied by evolutionary analysis. <b>2019</b> , 41, 445-458	
305	The role of transposable elements in the evolution of aluminium resistance in plants. <b>2019</b> , 70, 41-54	20
304	Evolution of CYCLOIDEA-like genes in Fabales: Insights into duplication patterns and the control of floral symmetry. <b>2019</b> , 132, 81-89	5
303	Phenotypic plasticity, canalization, and the origins of novelty: Evidence and mechanisms from amphibians. <b>2019</b> , 88, 80-90	28
302	Polyploid plants have faster rates of multivariate niche differentiation than their diploid relatives. <b>2020</b> , 23, 68-78	46
301	Genome-wide identification and transcriptional profiling of small heat shock protein gene family under diverse abiotic stress conditions in <i>Sorghum bicolor</i> (L.). <b>2020</b> , 142, 822-834	23
300	Divergence of duplicated genes by repeated partitioning of splice forms and subcellular localization. <i>New Phytologist</i> , <b>2020</b> , 225, 1011-1022	9.8 9
299	Uncovering the evolutionary origin of blue anthocyanins in cereal grains. <b>2020</b> , 101, 1057-1074	16
298	Variation in the amino acids, volatile organic compounds and terpenes profiles in induced polyploids and in <i>Solanum tuberosum</i> varieties. <b>2020</b> , 180, 112516	4

297	Characterization and Comparative Analysis of RWP-RK Proteins from , , and. <b>2020</b> , 2020, 2568640	
296	Synthesis of icariin in tobacco leaf by overexpression of a glucosyltransferase gene from <i>Epimedium sagittatum</i> . <b>2020</b> , 156, 112841	1
295	In silico characterization of class II plant defensins from <i>Arabidopsis thaliana</i> . <b>2020</b> , 179, 112511	2
294	Genome-Wide Identification of Apple Ubiquitin SINA E3 Ligase and Functional Characterization of MdSINA2. <b>2020</b> , 11, 1109	5
293	ddRAD-seq derived genome-wide SNPs, high density linkage map and QTLs for fruit quality traits in strawberry (x). <b>2020</b> , 10, 353	2
292	Genomics of Evolutionary Novelty in Hybrids and Polyploids. <b>2020</b> , 11, 792	36
291	Genome-Wide Identification of the NHX Genes Reveals that the Endosomal-Type is Critical for the Salt Tolerance of Cotton. <b>2020</b> , 21,	4
290	Genome-wide survey, characterization, and expression analysis of bZIP transcription factors in <i>Chenopodium quinoa</i> . <b>2020</b> , 20, 405	5
289	Next-generation metabolic engineering approaches towards development of plant cell suspension cultures as specialized metabolite producing biofactories. <b>2020</b> , 45, 107635	21
288	Genome-wide identification and expression analysis of NtbHLH gene family in tobacco () and the role of NtbHLH86 in drought adaptation.. <b>2021</b> , 43, 510-522	2
287	Mechanisms of evolved herbicide resistance. <b>2020</b> , 295, 10307-10330	117
286	Genes Encoding Recognition of the Effector Protein Ecp5 Are Encoded at Several Loci in the Tomato Genome. <b>2020</b> , 10, 1753-1763	3
285	Genome-wide identification and functional characterization of cotton ( <i>Gossypium hirsutum</i> ) MAPKKK gene family in response to drought stress. <b>2020</b> , 20, 217	12
284	Phylotranscriptomics reveals extensive gene duplication in the subtribe Gentianinae ( <i>Gentianaceae</i> ). <b>2020</b> ,	6
283	Ab initio GO-based mining for non-tandem-duplicated functional clusters in three model plant diploid genomes. <b>2020</b> , 15, e0234782	
282	Phenotypic plasticity and the origins of novelty. <b>2020</b> , 443-458	1
281	High Resolution Mapping of a -Derived Powdery Mildew Resistance Locus in Barley Using Distinct Homologous Introgression Lines. <b>2020</b> , 11, 225	10
280	Genome-wide analysis of glutathione S-transferase gene family in chickpea suggests its role during seed development and abiotic stress. <b>2020</b> , 47, 2749-2761	5

279	Global Survey and Expressions of the Phosphate Transporter Gene Families in and Their Roles in Phosphorus Response. <b>2020</b> , 21,		8
278	Genome-wide identification and expression analysis of PUB genes in cotton. <b>2020</b> , 21, 213		10
277	Genome-wide expression analysis suggests glutaredoxin genes response to various stresses in cotton. <b>2020</b> , 153, 470-491		21
276	The Hybrid Genome of a New Goldfish-Like Fish Lineage Provides Insights Into the Origin of the Goldfish. <b>2020</b> , 11, 122		4
275	Genome-wide characterization and expression analysis of soybean trihelix gene family. <b>2020</b> , 8, e8753		4
274	Genome-Wide Characterization and Analysis of Gene Family in Two Cultivated Allopolyploid Cotton Species: Sequence Variation, Association with Seed Oil Content, and the Role of. <b>2020</b> , 21,		7
273	The importance and prevalence of allopolyploidy in Aotearoa New Zealand. <b>2020</b> , 50, 189-210		1
272	The persimmon genome reveals clues to the evolution of a lineage-specific sex determination system in plants. <b>2020</b> , 16, e1008566		23
271	Structural evolution drives diversification of the large LRR-RLK gene family. <i>New Phytologist</i> , <b>2020</b> , 226, 1492-1505	9.8	15
270	Duplication and functional divergence of a calcium sensor in the Brassicaceae. <b>2020</b> , 71, 2782-2795		2
269	Genome-Wide Analysis of the MYB Transcription Factor Superfamily in. <b>2020</b> , 21,		17
268	Double mutation of two homologous genes YL1 and YL2 results in a leaf yellowing phenotype in soybean [ <i>Glycine max</i> (L.) Merr]. <b>2020</b> , 103, 527-543		5
267	Natural polymorphisms in a pair of NSP2 homoeologs can cause loss of nodulation in peanut. <b>2021</b> , 72, 1104-1118		3
266	Impact of ploidy changes on secondary metabolites productions in plants. <b>2021</b> , 29-46		2
265	Expansion and expression diversity of genes provides insights into flowering time regulation in roses. <b>2021</b> , 43, 173-179		2
264	New insights into homoeologous copy number variations in the hexaploid wheat genome. <b>2021</b> , 14, e20069		3
263	Genome-Wide Identification, Evolution, and Expression Profile of Aquaporin Genes in <i>Coffea canephora</i> in Response to Water Deficit. <b>2021</b> , 39, 146-162		2
262	Genetic innovations: Transposable element recruitment and de novo formation lead to the birth of orphan genes in the rice genome. <b>2021</b> , 59, 341-351		6

261	In situ dissecting the evolution of gene duplication with different histone modification patterns based on high-throughput data analysis in. <b>2021</b> , 9, e10426	0
260	Whole-genome characterization of <i>Rosa chinensis</i> AP2/ERF transcription factors and analysis of negative regulator RcdREB2B in <i>Arabidopsis</i> . <b>2021</b> , 22, 90	5
259	Response of phytohormone mediated plant homeodomain (PHD) family to abiotic stress in upland cotton ( <i>Gossypium hirsutum</i> spp.). <b>2021</b> , 21, 13	12
258	Genome-wide search and structural and functional analyses for late embryogenesis-abundant (LEA) gene family in poplar. <b>2021</b> , 21, 110	4
257	Comprehensive Genome-Wide Exploration of C2H2 Zinc Finger Family in Grapevine ( <i>L.</i> ): Insights into the Roles in the Pollen Development Regulation. <b>2021</b> , 12,	7
256	Genome-Wide Identification and Comprehensive Analyses of TCP Gene Family in Banana ( <i>Musa L.</i> ). <b>2021</b> , 14, 180-202	2
255	Adaptive evolution driving the young duplications in six Rosaceae species. <b>2021</b> , 22, 112	4
254	Gene expression shapes the patterns of parallel evolution of herbicide resistance in the agricultural weed <i>Monochoria vaginalis</i> .	0
253	Identification and characterization of genes related to salt stress tolerance within segregation distortion regions of genetic map in F2 population of upland cotton. <b>2021</b> , 16, e0247593	4
252	Gene and Transposable Element Expression Evolution Following Recent and Past Polyploidy Events in ( <i>Poaceae</i> ). <b>2021</b> , 12, 589160	3
251	Biosynthesis and Cellular Functions of Tartaric Acid in Grapevines. <b>2021</b> , 12, 643024	6
250	Genome-Wide Analysis, Evolutionary History and Response of Family to Phosphate Starvation in. <b>2021</b> , 22,	
249	Non-specific Lipid Transfer Proteins in Legumes and Their Participation During Root-Nodule Symbiosis. <b>2021</b> , 3,	1
248	Ancient gene duplications, rather than polyploidization, facilitate diversification of petal pigmentation patterns in <i>Clarkia gracilis</i> ( <i>Onagraceae</i> ).	
247	The role of ion-transporting proteins in the evolution of salt tolerance in charophyte algae. <b>2021</b> , 57, 1014-1025	2
246	Stability of EPSPS gene copy number in <i>Hordeum glaucum</i> Steud (barley grass) in the presence and absence of glyphosate selection. <b>2021</b> , 77, 3080-3087	1
245	Polyploidy underlies co-option and diversification of biosynthetic triterpene pathways in the apple tribe. <b>2021</b> , 118,	14
244	Whole-Genome Doubling Affects Pre-miRNA Expression in Plants. <b>2021</b> , 10,	

243	A comparative genome-wide analysis of the ABC transporter gene family among three <i>Gossypium</i> species. <b>2021</b> , 61, 2489		1
242	Molecular Characterisation of Soybean Osmotins and Their Involvement in Drought Stress Response. <b>2021</b> , 12, 632685		3
241	Trajectories of Homoeolog-Specific Expression in Allotetraploid Populations of Independent Origins. <b>2021</b> , 12, 679047		0
240	Genome-wide analysis, identification, evolution and genomic organization of dehydration responsive element-binding (DREB) gene family in. <b>2021</b> , 9, e11647		1
239	Mitogen-Activated Protein Kinase Expression Profiling Revealed Its Role in Regulating Stress Responses in Potato (). <b>2021</b> , 10,		5
238	Annual and perennial <i>Medicago</i> show signatures of parallel adaptation to climate and soil in highly conserved genes. <b>2021</b> , 30, 4448-4465		1
237	Genome-Wide Comparative Analysis of Flowering-Time Genes; Insights on the Gene Family Expansion and Evolutionary Perspective. <b>2021</b> , 12, 702243		0
236	Genome-wide identification of candidate aquaporins involved in water accumulation of pomegranate outer seed coat. <b>2021</b> , 9, e11810		1
235	Cassava ( <i>Manihot esculenta</i> ) defensins: Prospection, structural analysis and tissue-specific expression under biotic/abiotic stresses. <b>2021</b> , 186, 1-12		1
234	Identification and Characterization of SRS Genes in <i>Phaseolus vulgaris</i> Genome and Their Responses Under Salt Stress. <b>2021</b> , 1		1
233	Identification and functional analysis of 9-cis-epoxy carotenoid dioxygenase (NCED) homologs in <i>G. hirsutum</i> . <b>2021</b> , 182, 298-310		2
232	Genome-wide identification and expression analysis of bZIP transcription factors in oil palm ( <i>Elaeis guineensis</i> Jacq.) under abiotic stress. <b>2021</b> , 1		3
231	RetroScan: An Easy-to-Use Pipeline for Retrocopy Annotation and Visualization. <b>2021</b> , 12, 719204		0
230	New insights into the evolution of SPX gene family from algae to legumes; a focus on soybean.		
229	Gene expression shapes the patterns of parallel evolution of herbicide resistance in the agricultural weed <i>Monochoria vaginalis</i> . <i>New Phytologist</i> , <b>2021</b> , 232, 928-940	9.8	3
228	A chromosome-scale assembly of the bilberry genome identifies a complex locus controlling berry anthocyanin composition. <b>2021</b> ,		3
227	Identification and Characterization of the ERF Subfamily B3 Group Revealed Improves Salt Tolerance in Upland Cotton. <b>2021</b> , 12, 705883		2
226	Ancient Gene Duplications, Rather Than Polyploidization, Facilitate Diversification of Petal Pigmentation Patterns in <i>Clarkia gracilis</i> (Onagraceae). <b>2021</b> , 38, 5528-5538		1



225	Genome-wide analysis of R2R3-MYB transcription factors family in the autopolyploid <i>Saccharum spontaneum</i> : an exploration of dominance expression and stress response. <b>2021</b> , 22, 622	2
224	The DUF221 domain-containing (DDP) genes identification and expression analysis in tomato under abiotic and phytohormone stress. <b>2021</b> , 1-14	1
223	Genome-wide identification and expression profile under abiotic stress of the barley non-specific lipid transfer protein gene family and its Qingke Orthologues. <b>2021</b> , 22, 674	1
222	Multiplex knockout of trichome-regulating MYBs in poplar affects light sensitivity and triterpene accumulation.	
221	Gene duplication and rate variation in the evolution of non-photosynthetic pathways in plastids.	0
220	Expression of Two Rye CENH3 Variants and Their Loading into Centromeres. <b>2021</b> , 10,	1
219	Reassessing the evolution of the 1-deoxy-D-xylulose 5-phosphate synthase family suggests a possible novel function for the DXS class 3 proteins. <b>2021</b> , 310, 110960	3
218	ATP-binding cassette transporters expression profiling revealed its role in the development and regulating stress response in <i>Solanum tuberosum</i> . <b>2021</b> , 1	2
217	Morphological and environmental differentiation as prezygotic reproductive barriers between parapatric and allopatric <i>Campanula rotundifolia</i> agg. cytotypes. <b>2021</b> ,	
216	Genome-wide investigation of bHLH genes and expression analysis under different biotic and abiotic stresses in <i>Helianthus annuus</i> L. <b>2021</b> , 189, 72-83	13
215	Using Genomic Approaches to Unlock the Potential of CWR for Crop Adaptation to Climate Change. 268-280	8
214	Haustrorium Initiation and Early Development. <b>2013</b> , 61-74	13
213	Selective constraints on coding sequences of nervous system genes are a major determinant of duplicate gene retention in vertebrates.	1
212	New insights into homoeologous copy number variations in the hexaploid wheat genome.	1
211	Tandem Duplicate Genes in Maize are Abundant and Date to Two Distinct Periods of Time.	1
210	Genes encoding recognition of the <i>Cladosporium fulvum</i> effector protein Ecp5 are encoded at several loci in the tomato genome.	1
209	Evolution, expression differentiation and interaction specificity of heterotrimeric G-protein subunit gene family in the mesohexaploid <i>Brassica rapa</i> . <b>2014</b> , 9, e105771	14
208	Uncovering the differential molecular basis of adaptive diversity in three <i>Echinochloa</i> leaf transcriptomes. <b>2015</b> , 10, e0134419	17

207	Genome-wide analysis of rice dehydrin gene family: Its evolutionary conservedness and expression pattern in response to PEG induced dehydration stress. <b>2017</b> , 12, e0176399	34
206	Comparative genomic study of ALDH gene superfamily in <i>Gossypium</i> : A focus on <i>Gossypium hirsutum</i> under salt stress. <b>2017</b> , 12, e0176733	7
205	Identification and expression analyses of WRKY genes reveal their involvement in growth and abiotic stress response in watermelon ( <i>Citrullus lanatus</i> ). <b>2018</b> , 13, e0191308	32
204	Species-Specific Duplication Event Associated with Elevated Levels of Nonstructural Carbohydrates in. <b>2020</b> , 10, 1511-1520	3
203	Expression Level Dominance and Homeolog Expression Bias in Recurrent Origins of the Allopolyploid Fern <i>Polypodium hesperium</i> . <b>2019</b> , 109, 224	4
202	Chromosome Numbers in Some Cacti of Western North America. <b>2018</b> , 2018, 5	3
201	Genome-Wide Identification and Evolution of Receptor-Like Kinases (RLKs) and Receptor like Proteins (RLPs) in. <b>2020</b> , 10,	9
200	Genome-wide analyses of the bHLH gene family reveals structural and functional characteristics in the aquatic plant. <b>2019</b> , 7, e7153	11
199	Pumpkin () HSP20 Gene Family Identification and Expression Under Heat Stress. <b>2021</b> , 12, 753953	1
198	Genome-Wide Analysis of Major Facilitator Superfamily and Its Expression in Response of Poplar to. <b>2021</b> , 12, 769888	0
197	General Conclusions. <b>2010</b> , 189-194	
196	Evolution and the Environment. 377-393	
195	Analyzing Ethnopharmacological Data Matrices on Traditional Uses of Medicinal Plants with the Contribution of Partial Order Techniques. <b>2017</b> , 251-272	0
194	Wild tobacco genomes reveal the evolution of nicotine biosynthesis.	
193	MITE-based drives to transcriptional control of genome host.	
192	Multiple reference genome sequences of hot pepper reveal the massive evolution of plant disease resistance genes by retroduplication.	0
191	A dead gene walking: convergent degeneration of a clade of MADS-box genes in Brassicaceae.	
190	General Conclusions. <b>2018</b> , 375-384	

- 189 Phylogenomics reveals an extensive history of genome duplication in diatoms (Bacillariophyta).
- 188 Gene duplicates cause hybrid lethality between sympatric species of *Mimulus*. 1
- 187 Factors influencing gene family size variation among related species in a plant family.
- 186 Polyploid plants have faster rates of multivariate climatic niche evolution than their diploid relatives. 1
- 185 Rapid functional divergence of grass duplicate genes.
- 184 The persimmon genome reveals clues to the evolution of a lineage-specific sex determination system in plants. 1
- 183 High resolution mapping of a *Hordeum bulbosum*-derived powdery mildew resistance locus in barley using distinct homologous introgression lines.
- 182 Genome-wide identification and expression analysis of PUB genes in cotton.
- 181 In silico Characterization of Class II Plant Defensins from *Arabidopsis thaliana*.
- 180 DNA methylation signatures of duplicate gene evolution in angiosperms. 1
- 179 Genome-wide identification and expression analysis of PUB genes in cotton.
- 178 Genome-wide identification and expression analysis of PUB genes in cotton.
- 177 Genome-wide identification and expression analysis of PUB genes in cotton.
- 176 Genome-wide identification and expression analysis of PUB genes in cotton.
- 175 *Passiflora organensis* FT/TFL1 gene family and their putative roles in phase transition and floral initiation. **2021**, 1 0
- 174 Genome-wide identification and expression analysis of the xyloglucan endotransglucosylase/hydrolase gene family in poplar. **2021**, 22, 804 3
- 173 *Sorghum* [*Sorghum bicolor* (L.) Moench] Genomunda BES1 Transkripsiyon Faktör Ailesinin Genom Analizi. 0
- 172 The origin and evolution of a two-component system of paralogous genes encoding the centromeric histone CENH3 in cereals. **2021**, 21, 541 0

171	Genome-wide identification and expression analysis of ammonium transporter 1 (AMT1) gene family in cassava (Crantz) and functional analysis of in transgenic .. <b>2022</b> , 12, 4	1
170	Polyploidy promotes divergent evolution across the leaf economics spectrum and plant edaphic niche in the <i>Dianthus broteri</i> complex.	1
169	Understanding the role of SWEET genes in fruit development and abiotic stress in pomegranate ( <i>Punica granatum</i> L.). <b>2021</b> , 1	0
168	Genome-wide identification and expression analysis of GDSL esterase/lipase genes in tomato. <b>2022</b> , 21, 389-406	1
167	Systematic analysis and comparison of ABC proteins superfamily confer structural, functional and evolutionary insights into four cotton species. <b>2022</b> , 177, 114433	1
166	Evolution of RGF/GLV/CLEL Peptide Hormones and Their Roles in Land Plant Growth and Regulation.. <b>2021</b> , 22,	1
165	Genome-Wide Comprehensive Analysis of PtLACs: Prediction and Verification of the Functional Divergence of Tandem-Duplicated Genes. <b>2022</b> , 13, 157	0
164	Identification and expression analysis of histone modification gene (HM) family during somatic embryogenesis of oil palm.. <b>2022</b> , 23, 11	0
163	Genome-wide identification and characterization of the bHLH gene family in an ornamental woody plant <i>Prunus mume</i> . <b>2022</b> ,	0
162	Genome-Wide Identification and Expression Profiling of DUF221 Gene Family Provides New Insights Into Abiotic Stress Responses in Potato.. <b>2021</b> , 12, 804600	0
161	Identification and expression analysis of the sucrose synthase gene family in pomegranate (L).. <b>2022</b> , 10, e12814	0
160	Proteome evaluation of homolog abundance patterns in <i>Arachis hypogaea</i> cv. Tifrunner.. <b>2022</b> , 18, 6	0
159	Genome-wide Characterization of Histone Gene Family and Expression profiling During Microspore Development in Radish ( <i>Raphanus sativus</i> L).. <b>2022</b> , 815, 146180	0
158	Gene duplication and rate variation in the evolution of plastid ACCase and Clp genes in angiosperms.. <b>2022</b> , 168, 107395	1
157	High rates of spontaneous chromosomal duplications are compensated by translational regulation in a photosynthetic unicellular eukaryote.	0
156	Genome-Wide Identification and Characterization of SET Domain Family Genes in L.. <b>2022</b> , 23,	1
155	Two Aquaporin Genes, and , Positively Regulate the Tolerance of Upland Cotton to Salt and Osmotic Stresses.. <b>2021</b> , 12, 780486	0
154	Genome-wide analysis of bromodomain gene family in <i>Arabidopsis</i> and Rice.	0

- 153 Genome-Wide Analysis of HSP70s in Hexaploid Wheat: Tandem Duplication, Heat Response, and Regulation.. **2022**, 11, ○
- 152 Genome-Wide Identification and Expression Profiles of 13 Key Structural Gene Families Involved in the Biosynthesis of Rice Flavonoid Scaffolds.. **2022**, 13, ○
- 151 Genome-Wide Identification and Expression Profiling of Germin-Like Proteins Reveal Their Role in Regulating Abiotic Stress Response in Potato.. **2021**, 12, 831140 ○
- 150 Genome-wide analysis of sucrose synthase family in soybean and their expression in response to abiotic stress and seed development.. **2022**, 17, e0264269 ○
- 149 Multiplex knockout of trichome-regulating MYB duplicates in hybrid poplar using a single gRNA.. **2022**, ○
- 148 Genome-wide identification, evolutionary and expression analyses of LEA gene family in peanut (*Arachis hypogaea* L.).. **2022**, 22, 155 ○
- 147 Comparative transcriptomics of wild and commercial Citrus during early ripening reveals how domestication shaped fruit gene expression.. **2022**, 22, 123 ○
- 146 Genome-wide analysis of trehalose-6-phosphate phosphatases (TPP) gene family in wheat indicates their roles in plant development and stress response.. **2022**, 22, 120 1
- 145 New insights into the evolution of SPX gene family from algae to legumes; a focus on soybean.. **2021**, 22, 915 ○
- 144 Duplication of NRAMP3 gene in poplars generated two homologous transporters with distinct functions. ○
- 143 Genome-Wide Identification, Characterization and Expression Analysis of the Gene Family in Potato (*L.*) and the Role of in Response to Drought and Osmotic Stress.. **2021**, 22, 3
- 142 The impact of whole genome duplications on the human gene regulatory networks. **2021**, 17, e1009638 ○
- 141 Expression profiling of pathogenesis-related Protein-1 (PR-1) genes from *Solanum tuberosum* reveals its critical role in *Phytophthora infestans* infection. **2021**, 161, 105290 ○
- 140 Genome-wide expression analysis of carboxylesterase (CXE) gene family implies GBCXE49 functional responding to alkaline stress in cotton.. **2022**, 22, 194 2
- 139 Understanding Diversity, Evolution, and Structure of Small Heat Shock Proteins in Annelida Through in Silico Analyses.. **2022**, 13, 817272 ○
- 138 Image1.PDF. **2018**,
- 137 Image2.PDF. **2018**,
- 136 Image3.PDF. **2018**,

135 Table1.DOCX. 2018,

134 Table10.DOCX. 2018,

133 Table2.DOCX. 2018,

132 Table3.DOCX. 2018,

131 Table4.DOCX. 2018,

130 Table5.DOCX. 2018,

129 Table6.DOCX. 2018,

128 Table7.XLSX. 2018,

127 Table8.XLSX. 2018,

126 Table9.DOCX. 2018,

125 Image\_1.TIF. 2018,

124 Image\_2.TIF. 2018,

123 Table\_1.DOCX. 2018,

122 Table\_2.DOCX. 2018,

121 Table\_3.DOCX. 2018,

120 Table\_4.DOCX. 2018,

119 Table\_5.docx. 2018,

118 DataSheet\_1.docx. 2020,

117 Image\_1.JPEG. 2019,

116 Image\_2.TIF. 2019,

115 Table\_1.docx. 2019,

114 Table\_2.docx. 2019,

113 Table\_3.xlsx. 2019,

112 Table\_4.xlsx. 2019,

111 Table\_5.docx. 2019,

110 Table\_6.xlsx. 2019,

109 Table\_7.xlsx. 2019,

108 Table\_8.docx. 2019,

107 Image\_1.PDF. 2018,

106 Image\_2.PDF. 2018,

105 Image\_3.PDF. 2018,

104 Image\_4.PDF. 2018,

103 Table\_1.PDF. 2018,

102 DataSheet\_1.docx. 2020,

101 Table\_1.XLSX. 2020,

100 Data\_Sheet\_1.docx. 2019,

99 Data\_Sheet\_2.xlsx. **2019,**

98 DataSheet1.FASTA. **2018,**

97 DataSheet2.FASTA. **2018,**

96 Image1.PDF. **2018,**

95 Image2.PDF. **2018,**

94 Image3.PDF. **2018,**

93 Image4.PDF. **2018,**

92 Presentation1.PDF. **2018,**

91 Table1.XLSX. **2018,**

90 Table2.XLSX. **2018,**

89 Table3.XLSX. **2018,**

88 Table4.XLSX. **2018,**

87 Table5.XLSX. **2018,**

86 Table6.XLSX. **2018,**

85 Data\_Sheet\_1.XLSX. **2018,**

84 Image\_1.PDF. **2018,**

83 Genome-Wide Identification and Expression Profiling of Gene Family in Passion Fruit () Under and Drought Stress Conditions.. **2022**, 13, 872263

1

82 Genetic Divergence of Lineage-Specific Tandemly Duplicated Gene Clusters in Four Diploid Potato Genotypes. **2022**, 13,

0



- 81 Phenotypic responses to light, water, and nutrient conditions in the allopolyploid and its parent species and : Does the allopolyploid outrange its parents?. **2022**, 12, e8915
- 80 Genome-wide identification of SINA gene family in sugarcane and functional analysis of SsSINA1a in drought response.
- 79 Origin, Expansion, and Divergence of ETHYLENE-INSENSITIVE 3 (EIN3)/EIN3-LIKE Transcription Factors During Streptophytes Evolution. **2022**, 13,
- 78 Identification of epitranscriptomic methylation marker genes in Arabidopsis and their expression profiling in response to developmental, anatomical, and environmental modulations. **2022**, 100247 1
- 77 Genome-Wide Identification, Classification, Expression and Duplication Analysis of bZIP Family Genes in *Juglans regia* L. **2022**, 23, 5961 1
- 76 Terpene Synthases in Rice Pan-Genome and Their Responses to *Chilo suppressalis* Larvae Infesting. **2022**, 13,
- 75 Molecular and Biochemical Analysis of Duplicated Cytosolic CuZn Superoxide Dismutases of Rice and in silico Analysis in Plants. **2022**, 13, 0
- 74 Genome-wide identification of ovate family in Citrus and functional characterization of CitOFP19. **2022**, 321, 111328 0
- 73 Interplay between gene expression and gene architecture as a consequence of gene and genome duplications: evidence from metabolic genes of *Arabidopsis thaliana*. **2022**, 28, 1091-1108
- 72 Genome-wide identification and characterization of glutathione S-transferase gene family in *Musa acuminata* L. AAA group and gaining an insight to their role in banana fruit development. 0
- 71 Functional divergence of GhAP1.1 and GhFUL2 associated with flowering regulation in upland cotton (*Gossypium hirsutum* L.). **2022**, 153757
- 70 The fate of drought-related genes after polyploidization in *Arachis hypogaea* cv. Tifrunner. 0
- 69 Functional Heterogeneity of the Young and Old Duplicate Genes in Tung Tree (*Vernicia fordii*). 13, 1
- 68 Genome-wide identification and expression analysis of the NAC transcription factor family in *Saccharum spontaneum* under different stresses. **2022**, 17, 0
- 67 Duplication of NRAMP3 gene in poplars generated two homologous transporters with distinct functions. 0
- 66 Comprehensive Genome-Wide Identification and Expression Profiling of Eceriferum (CER) Gene Family in Passion Fruit (*Passiflora edulis*) Under *Fusarium kyushuense* and Drought Stress Conditions. 13, 0
- 65 Oxytocin/vasopressin system of insects influences parental care in males but not females.
- 64 Genome-Wide Classification and Evolutionary Analysis Reveal Diverged Patterns of Chalcone Isomerase in Plants. **2022**, 12, 961

- 63 Genome-Wide Characterization and Analysis of the bHLH Transcription Factor Family in Suaeda aralocaspica, an Annual Halophyte With Single-Cell C4 Anatomy. 13, 0
- 62 Identifying potential flavonoid biosynthesis regulator in Zanthoxylum bungeanum Maxim. by genome-wide characterization of the MYB transcription factor gene family. **2022**, 21, 1997-2018 1
- 61 Integration of eQTL Analysis and GWAS Highlights Regulation Networks in Cotton under Stress Condition. **2022**, 23, 7564 1
- 60 Polyploidy before and after domestication of crop species. **2022**, 69, 102255 1
- 59 The rubber tree kinome: genome-wide characterization and insights into coexpression patterns associated with abiotic stress responses. 0
- 58 Exploring the genetic makeup and population structure among Capsicum accessions for crop improvement and breeding curriculum insights. **2022**, 20, 0
- 57 Involvement of glutamine synthetase 2 (GS2) amplification and overexpression in Amaranthus palmeri resistance to glufosinate. **2022**, 256, 1
- 56 Double DJ -1 domain containing Arabidopsis DJ-1D is a robust macromolecule deglycase. 1
- 55 Side-chain modifications of phyllobilins may not be essential for chlorophyll degradation in Arabidopsis. **2022**, 6, 0
- 54 Genome-Wide Analysis of the Type-B Authentic Response Regulator Gene Family in Brassica napus. **2022**, 13, 1449 0
- 53 Identification and characterization of three nearly identical linalool/nerolidol synthase from Acorus calamus. **2022**, 202, 113318 1
- 52 Analyses of gene copy number variation in diverse epigenetic regulatory gene families across plants: Increased copy numbers of BRUSHY1/TONSOKU/MGOUN3 (BRU1/TSK/MGO3) and SILENCING DEFECTIVE 3 (SDE3) in long-lived trees. **2022**, 32, 100384 0
- 51 The role of gene duplication in the divergence of the sweet cherry. **2022**, 32, 100379 0
- 50 Diospyros Lotus Genome. **2022**, 65-74 0
- 49 Genome-Wide Characterization of Remorin Genes in Terms of Their Evolution and Expression in Response to Hormone Signals and Abiotic Stresses in Foxtail Millet (Setaria italica). **2022**, 14, 711 0
- 48 Structural changes and adaptative evolutionary constraints in FLOWERING LOCUS T and TERMINAL FLOWER1-like genes of flowering plants. 13, 0
- 47 GhNFYA16 was functionally observed positively responding to salt stress by genome-wide identification of NFYA gene family in cotton. **2022**, 34, 0
- 46 Learning to tango with four (or more): the molecular basis of adaptation to polyploid meiosis. 1

45	A2TEA: Identifying trait-specific evolutionary adaptations. 11, 1137	0
44	Genome-wide identification, characterization and expression of HSP 20 gene family in dove. 13,	0
43	Genome-Wide Identification and Characterization of the Oat ( <i>Avena sativa</i> L.) WRKY Transcription Factor Family. <b>2022</b> , 13, 1918	0
42	Genome-wide identification and comparative analysis of CLE family in rapeseed and its diploid progenitors. 13,	0
41	Transcriptomes of Different Tissues for Expression Characteristics Analysis of MYB gene Family in Kenaf ( <i>Hibiscus cannabinus</i> L.).	0
40	Simultaneous editing of three homoeologs of TaCIPK14 confers broad-spectrum resistance to stripe rust in wheat.	1
39	Accurate identification of de novo genes in plant genomes using machine learning algorithms.	1
38	The bZIP transcription factors in <i>Liriodendron chinense</i> : Genome-wide recognition, characteristics and cold stress response. 13,	0
37	Genomic survey of TCP transcription factors in plants: Phylogenomics, evolution and their biology. 13,	1
36	Genome-wide analysis of the Early Flowering 4 (ELF4) gene family in short-juvenile persimmon <i>Deyangshi</i> ( <i>Diospyros deyangensis</i> ) and its role of DdELF4B during flowering control. <b>2023</b> , 310, 111736	0
35	Identification and Characterization of AP2/ERF Transcription Factors in Yellow Horn. <b>2022</b> , 23, 14991	1
34	Genome-wide identification, molecular evolution and expression analysis of the non-specific lipid transfer protein (nsLTP) family in <i>Setaria italica</i> . <b>2022</b> , 22,	0
33	Genome-wide identification, comprehensive characterization of transcription factors, cis-regulatory elements, protein homology, and protein interaction network of DREB gene family in <i>Solanum lycopersicum</i> . 13,	1
32	Genome-Wide Identification of Common Bean PvLTP Family Genes and Expression Profiling Analysis in Response to Drought Stress. <b>2022</b> , 13, 2394	0
31	Genome-Wide Identification and Expression Analysis of the 14-3-3 (TFT) Gene Family in Tomato, and the Role of SlTFT4 in Salt Stress. <b>2022</b> , 11, 3491	0
30	Kinase regulators evolved into two families by gain and loss of ability to bind plant steroid receptors.	1
29	The LEA gene family in tomato and its wild relatives: genome-wide identification, structural characterization, expression profiling, and role of SlLEA6 in drought stress. <b>2022</b> , 22,	0
28	Genome-wide characterization, chromosome localization, and expression profile analysis of poplar nonspecific lipid transfer proteins. <b>2023</b> , 123226	0

- 27 A chromosome-scale genome assembly of *Artemisia argyi* reveals unbiased subgenome evolution and key contributions of gene duplication to volatile terpenoid diversity. **2023**, 100516 1
- 26 Genome-wide identification, expression analysis, and functional verification of the JMJ (Jumonji) histone demethylase gene family in pear (*Pyrus bretschneideri*). **2023**, 19, 0
- 25 Genome-wide identification and analysis of the IQM gene family in soybean. 13, 0
- 24 Genome-Wide Characterization and Functional Analysis of ABCG Subfamily Reveal Its Role in Cutin Formation in Cotton. **2023**, 24, 2379 0
- 23 Genome-wide in silico identification of glutathione S-transferase (GST) gene family members in fig (*Ficus carica* L.) and expression characteristics during fruit color development. 11, e14406 0
- 22 Comparative gene retention analysis in barley, wild emmer, and bread wheat pangenome lines reveals factors affecting gene retention following gene duplication. **2023**, 21, 0
- 21 Genome-Wide Identification and Analysis of bHLH Transcription Factors Related to Anthocyanin Biosynthesis in *Cymbidium ensifolium*. **2023**, 24, 3825 0
- 20 Genome-Wide Identification and Expression Analysis of the SHI-Related Sequence Family in Cassava. **2023**, 14, 870 0
- 19 The rubber tree kinome: Genome-wide characterization and insights into coexpression patterns associated with abiotic stress responses. 14, 0
- 18 Identification of a Major QTL-Controlling Resistance to the Subtropical Race 4 of *Fusarium oxysporum* f. sp. *cubense* in *Musa acuminata* ssp. *malaccensis*. **2023**, 12, 289 0
- 17 Genome-wide identification and expression analysis of SLAC1 gene family in tomato (*Solanum lycopersicum*) and the function of SLSLAC1B under cold stress. **2023**, 313, 111904 0
- 16 Genome-wide identification and analysis of the molecular evolution and expression of type-A response regulator genes in *Populus deltoids*. **2023**, 194, 116336 0
- 15 Genome-Wide Analysis of the Rhododendron AP2/ERF Gene Family: Identification and Expression Profiles in Response to Cold, Salt and Drought Stress. **2023**, 12, 994 0
- 14 Two soybean homologues of TERMINAL FLOWER 1 control flowering time under long day conditions. **2023**, 0
- 13 Genome-Wide Identification and Expression Analysis of RCC1 Gene Family under Abiotic Stresses in Rice (*Oryza sativa* L.). **2023**, 13, 703 0
- 12 Genome-wide analysis of bromodomain gene family in *Arabidopsis* and rice. 14, 0
- 11 Genome-wide identification of bHLH transcription factors and their response to salt stress in *Cyclocarya paliurus*. 14, 0
- 10 Comprehensive Analysis of Universal Stress Protein Family Genes and Their Expression in *Fusarium oxysporum* Response of *Populus davidiana* [P. alba var. *pyramidalis* Louche Based on the Transcriptome. **2023**, 24, 5405 0

- 9 Asymmetric evolution of protein domains in the leucine-rich repeat receptor-like kinase (LRR-RLK) family of plant developmental coordinators. ○
- 8 Evolutionary history of two evergreen *Rhododendron* species as revealed by chromosome-level genome assembly. 14, ○
- 7 Genome-Wide Identification of the MADS-Box Gene Family during Male and Female Flower Development in Chayote (*Sechium edule*). **2023**, 24, 6114 ○
- 6 Genome-wide identification and expression analysis of DREB family genes in cotton. **2023**, 23, ○
- 5 Genomic diversity of aquaporins across genus *Oryza* provides a rich genetic resource for development of climate resilient rice cultivars. **2023**, 23, ○
- 4 Comprehensive genome-wide identification and characterization of ABC Transporter superfamily in *Cajanus cajan* and its expression profiling under different developmental stages in various anatomical tissues. ○
- 3 A2TEA: Identifying trait-specific evolutionary adaptations. 11, 1137 ○
- 2 Origins and evolution of biological novelty. ○
- 1 DNA methylation signatures of duplicate gene evolution in angiosperms. ○