

# Jiri Macas

## List of Publications by Year in descending order

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124  
papers

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28274

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49909

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129  
docs citations

129  
times ranked

5773  
citing authors

#	ARTICLE	IF	CITATIONS
1	Fine structure and transcription dynamics of bread wheat ribosomal DNA loci deciphered by a multi-omics approach. <i>Plant Genome</i> , 2022, , e20191.	2.8	10
2	The ecology of palm genomes: repeat-associated genome size expansion is constrained by aridity. <i>New Phytologist</i> , 2022, 236, 433-446.	7.3	10
3	Impact of parasitic lifestyle and different types of centromere organization on chromosome and genome evolution in the plant genus <i>Cuscuta</i> . <i>New Phytologist</i> , 2021, 229, 2365-2377.	7.3	22
4	Complex sequence organization of heterochromatin in the holocentric plant <i>Cuscuta europaea</i> elucidated by the computational analysis of nanopore reads. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2179-2189.	4.1	9
5	Limitation of current probe design for oligo-cross-FISH, exemplified by chromosome evolution studies in duckweeds. <i>Chromosoma</i> , 2021, 130, 15-25.	2.2	9
6	Characterization of repeat arrays in ultra-long nanopore reads reveals frequent origin of satellite DNA from retrotransposon-derived tandem repeats. <i>Plant Journal</i> , 2020, 101, 484-500.	5.7	76
7	Mitotic Spindle Attachment to the Holocentric Chromosomes of <i>Cuscuta europaea</i> Does Not Correlate With the Distribution of CENH3 Chromatin. <i>Frontiers in Plant Science</i> , 2020, 10, 1799.	3.6	37
8	Repeat-sequence turnover shifts fundamentally in species with large genomes. <i>Nature Plants</i> , 2020, 6, 1325-1329.	9.3	87
9	Global analysis of repetitive DNA from unassembled sequence reads using RepeatExplorer2. <i>Nature Protocols</i> , 2020, 15, 3745-3776.	12.0	144
10	Chromosome-scale genome assembly for the duckweed <i>Spirodela intermedia</i> , integrating cytogenetic maps, PacBio and Oxford Nanopore libraries. <i>Scientific Reports</i> , 2020, 10, 19230.	3.3	23
11	Super-Resolution Microscopy Reveals Diversity of Plant Centromere Architecture. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3488.	4.1	42
12	<i>Pisum sativum</i> (Pea). <i>Trends in Genetics</i> , 2020, 36, 312-313.	6.7	5
13	Extraordinary Sequence Diversity and Promiscuity of Centromeric Satellites in the Legume Tribe Fabae. <i>Molecular Biology and Evolution</i> , 2020, 37, 2341-2356.	8.9	42
14	Differential Genome Size and Repetitive DNA Evolution in Diploid Species of <i>Melampodium</i> sect. <i>Melampodium</i> (Asteraceae). <i>Frontiers in Plant Science</i> , 2020, 11, 362.	3.6	37
15	The Repetitive Content in Lupin Genomes. <i>Compendium of Plant Genomes</i> , 2020, , 161-186.	0.5	2
16	A reference genome for pea provides insight into legume genome evolution. <i>Nature Genetics</i> , 2019, 51, 1411-1422.	21.4	363
17	The Dark Matter of Large Cereal Genomes: Long Tandem Repeats. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2483.	4.1	19
18	Accessing a Russian Wheat Aphid Resistance Gene in Bread Wheat by Long-Read Technologies. <i>Plant Genome</i> , 2019, 12, 180065.	2.8	15

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19	Genome invasion by a hypomethylated satellite repeat in Australian crucifer <i>Ballantinia antipoda</i> . <i>Plant Journal</i> , 2019, 99, 1066-1079.	5.7	3
20	Nondisjunction and unequal spindle organization accompany the drive of <i>Aegilops speltoides</i> B chromosomes. <i>New Phytologist</i> , 2019, 223, 1340-1352.	7.3	26
21	Systematic survey of plant LTR-retrotransposons elucidates phylogenetic relationships of their polyprotein domains and provides a reference for element classification. <i>Mobile DNA</i> , 2019, 10, 1.	3.6	265
22	Satellite DNA in <i>Vicia faba</i> is characterized by remarkable diversity in its sequence composition, association with centromeres, and replication timing. <i>Scientific Reports</i> , 2018, 8, 5838.	3.3	66
23	Dating the Species Network: Allopolyploidy and Repetitive DNA Evolution in American Daisies ( <i>Melampodium</i> sect. <i>Melampodium</i> , Asteraceae). <i>Systematic Biology</i> , 2018, 67, 1010-1024.	5.6	54
24	TAREAN: a computational tool for identification and characterization of satellite DNA from unassembled short reads. <i>Nucleic Acids Research</i> , 2017, 45, e111-e111.	14.5	222
25	Karyotypes and Distribution of Tandem Repeat Sequences in <i>Brassica nigra</i> ; Determined by Fluorescence in situ Hybridization. <i>Cytogenetic and Genome Research</i> , 2017, 152, 158-165.	1.1	10
26	Centromeric and non-centromeric satellite DNA organisation differs in holocentric <i>Rhynchospora</i> species. <i>Chromosoma</i> , 2017, 126, 325-335.	2.2	59
27	Epigenetic Histone Marks of Extended Meta-Polycentric Centromeres of <i>Lathyrus</i> and <i>Pisum</i> Chromosomes. <i>Frontiers in Plant Science</i> , 2016, 7, 234.	3.6	31
28	Repeat Composition of CenH3-chromatin and H3K9me2-marked heterochromatin in Sugar Beet ( <i>Beta</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	3.6	32
29	<i>Plantago lagopus</i> B Chromosome Is Enriched in 5S rDNA-Derived Satellite DNA. <i>Cytogenetic and Genome Research</i> , 2016, 148, 68-73.	1.1	20
30	Haplotype Detection from Next-Generation Sequencing in High-Ploidy-Level Species: 45S rDNA Gene Copies in the Hexaploid <i>Spartina maritima</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 29-40.	1.8	29
31	Centromere and telomere sequence alterations reflect the rapid genome evolution within the carnivorous plant genus <i>Genlisea</i> . <i>Plant Journal</i> , 2015, 84, 1087-1099.	5.7	41
32	Analysis of the giant genomes of <i>Fritillaria</i> ( <i>Liliaceae</i> ) indicates that a lack of <i>DNA</i> removal characterizes extreme expansions in genome size. <i>New Phytologist</i> , 2015, 208, 596-607.	7.3	122
33	Comparative Genome Analysis Reveals Divergent Genome Size Evolution in a Carnivorous Plant Genus. <i>Plant Genome</i> , 2015, 8, eplantgenome2015.04.0021.	2.8	45
34	Chromatin organization and cytological features of carnivorous <i>Genlisea</i> species with large genome size differences. <i>Frontiers in Plant Science</i> , 2015, 6, 613.	3.6	5
35	Centromeres Off the Hook: Massive Changes in Centromere Size and Structure Following Duplication of <i>CenH3</i> Gene in <i>Fabeae</i> Species. <i>Molecular Biology and Evolution</i> , 2015, 32, 1862-1879.	8.9	69
36	A Set of Cytogenetic Markers Allows the Precise Identification of All A-Genome Chromosomes in Diploid and Polyploid Wheat. <i>Cytogenetic and Genome Research</i> , 2015, 146, 71-79.	1.1	69

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37	Holocentromeres in <i>Rhynchospora</i> are associated with genome-wide centromere-specific repeat arrays interspersed among euchromatin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13633-13638.	7.1	96
38	Genomic Repeat Abundances Contain Phylogenetic Signal. <i>Systematic Biology</i> , 2015, 64, 112-126.	5.6	126
39	Genes on B chromosomes: Old questions revisited with new tools. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2015, 1849, 64-70.	1.9	68
40	In Depth Characterization of Repetitive DNA in 23 Plant Genomes Reveals Sources of Genome Size Variation in the Legume Tribe Fabaeae. <i>PLoS ONE</i> , 2015, 10, e0143424.	2.5	172
41	Differential amplification of satellite PaB6 in chromosomally hypervariable <i>Prospero autumnale</i> complex (Hyacinthaceae). <i>Annals of Botany</i> , 2014, 114, 1597-1608.	2.9	58
42	Boom-Bust Turnovers of Megabase-Sized Centromeric DNA in <i>Solanum</i> Species: Rapid Evolution of DNA Sequences Associated with Centromeres. <i>Plant Cell</i> , 2014, 26, 1436-1447.	6.6	73
43	Genome-Wide Analysis of Repeat Diversity across the Family Musaceae. <i>PLoS ONE</i> , 2014, 9, e98918.	2.5	54
44	The holocentric species <i>Caenorhabditis elegans</i> shows interplay between centromere and large-scale genome organization. <i>Plant Journal</i> , 2013, 73, 555-565.	5.7	86
45	Diploidization and genome size change in allopolyploids is associated with differential dynamics of low- and high-copy sequences. <i>Plant Journal</i> , 2013, 74, 829-839.	5.7	112
46	High-copy sequences reveal distinct evolution of the rye B chromosome. <i>New Phytologist</i> , 2013, 199, 550-558.	7.3	75
47	Flow Sorting and Sequencing Meadow Fescue Chromosome 4F. <i>Plant Physiology</i> , 2013, 163, 1323-1337.	4.8	27
48	RepeatExplorer: a Galaxy-based web server for genome-wide characterization of eukaryotic repetitive elements from next-generation sequence reads. <i>Bioinformatics</i> , 2013, 29, 792-793.	4.1	619
49	Contrasting Patterns of Transposable Element and Satellite Distribution on Sex Chromosomes (XY1Y2) in the Dioecious Plant <i>Rumex acetosa</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 769-782.	2.5	55
50	Stretching the Rules: Monocentric Chromosomes with Multiple Centromere Domains. <i>PLoS Genetics</i> , 2012, 8, e1002777.	3.5	127
51	Selfish supernumerary chromosome reveals its origin as a mosaic of host genome and organellar sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13343-13346.	7.1	173
52	Next-Generation Sequencing Reveals the Impact of Repetitive DNA Across Phylogenetically Closely Related Genomes of Orobanchaceae. <i>Molecular Biology and Evolution</i> , 2012, 29, 3601-3611.	8.9	82
53	Survey Sequencing Reveals Elevated DNA Transposon Activity, Novel Elements, and Variation in Repetitive Landscapes among Vesper Bats. <i>Genome Biology and Evolution</i> , 2012, 4, 575-585.	2.5	38
54	Why size really matters when sequencing plant genomes. <i>Plant Ecology and Diversity</i> , 2012, 5, 415-425.	2.4	27

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55	Repeatless and Repeat-Based Centromeres in Potato: Implications for Centromere Evolution. <i>Plant Cell</i> , 2012, 24, 3559-3574.	6.6	221
56	Nondisjunction in Favor of a Chromosome: The Mechanism of Rye B Chromosome Drive during Pollen Mitosis. <i>Plant Cell</i> , 2012, 24, 4124-4134.	6.6	77
57	Next generation sequencing analysis reveals a relationship between rDNA unit diversity and locus number in <i>Nicotiana</i> diploids. <i>BMC Genomics</i> , 2012, 13, 722.	2.8	60
58	Pea ( <i>Pisum sativum</i> L.) in the Genomic Era. <i>Agronomy</i> , 2012, 2, 74-115.	3.0	172
59	Independent, Rapid and Targeted Loss of Highly Repetitive DNA in Natural and Synthetic Allopolyploids of <i>Nicotiana tabacum</i> . <i>PLoS ONE</i> , 2012, 7, e36963.	2.5	77
60	Next Generation Sequencing-Based Analysis of Repetitive DNA in the Model Dioecious Plant <i>Silene latifolia</i> . <i>PLoS ONE</i> , 2011, 6, e27335.	2.5	97
61	Organization and Evolution of Subtelomeric Satellite Repeats in the Potato Genome. <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 85-92.	1.8	75
62	A widespread occurrence of extra open reading frames in plant Ty3/gypsy retrotransposons. <i>Genetica</i> , 2011, 139, 1543-1555.	1.1	23
63	Plant centromeric retrotransposons: a structural and cytogenetic perspective. <i>Mobile DNA</i> , 2011, 2, 4.	3.6	186
64	Diverse retrotransposon families and an AT-rich satellite DNA revealed in giant genomes of <i>Fritillaria</i> lilies. <i>Annals of Botany</i> , 2011, 107, 255-268.	2.9	78
65	Next Generation Sequencing Reveals Genome Downsizing in Allotetraploid <i>Nicotiana tabacum</i> , Predominantly through the Elimination of Paternally Derived Repetitive DNAs. <i>Molecular Biology and Evolution</i> , 2011, 28, 2843-2854.	8.9	150
66	Graph-based clustering and characterization of repetitive sequences in next-generation sequencing data. <i>BMC Bioinformatics</i> , 2010, 11, 378.	2.6	403
67	Repetitive part of the banana ( <i>Musa acuminata</i> ) genome investigated by low-depth 454 sequencing. <i>BMC Plant Biology</i> , 2010, 10, 204.	3.6	90
68	Global sequence characterization of rice centromeric satellite based on oligomer frequency analysis in large-scale sequencing data. <i>Bioinformatics</i> , 2010, 26, 2101-2108.	4.1	43
69	Evolutionary conserved lineage of Angela-family retrotransposons as a genome-wide microsatellite repeat dispersal agent. <i>Heredity</i> , 2009, 103, 157-167.	2.6	52
70	Hypervariable 3' UTR region of plant LTR-retrotransposons as a source of novel satellite repeats. <i>Gene</i> , 2009, 448, 198-206.	2.2	70
71	Survey of repetitive sequences in <i>Silene latifolia</i> with respect to their distribution on sex chromosomes. <i>Chromosome Research</i> , 2008, 16, 961-976.	2.2	99
72	Experimental evidence for splicing of intron-containing transcripts of plant LTR retrotransposon <i>Ogre</i> . <i>Molecular Genetics and Genomics</i> , 2008, 280, 427-36.	2.1	9

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73	Survey of extrachromosomal circular DNA derived from plant satellite repeats. <i>BMC Plant Biology</i> , 2008, 8, 90.	3.6	86
74	Ogre elements – A distinct group of plant Ty3/gypsy-like retrotransposons. <i>Gene</i> , 2007, 390, 108-116.	2.2	55
75	Isolation and characterization of the highly repeated fraction of the banana genome. <i>Cytogenetic and Genome Research</i> , 2007, 119, 268-274.	1.1	22
76	Repetitive DNA in the pea ( <i>Pisum sativum</i> L.) genome: comprehensive characterization using 454 sequencing and comparison to soybean and <i>Medicago truncatula</i> . <i>BMC Genomics</i> , 2007, 8, 427.	2.8	256
77	<i>Arabidopsis</i> CBF5 interacts with the H/ACA snoRNP assembly factor NAF1. <i>Plant Molecular Biology</i> , 2007, 65, 615-626.	3.9	33
78	Chromosome analysis and sorting in <i>Vicia sativa</i> using flow cytometry. <i>Biologia Plantarum</i> , 2007, 51, 43-48.	1.9	26
79	Sequence homogenization and chromosomal localization of VicTR-B satellites differ between closely related <i>Vicia</i> species. <i>Chromosoma</i> , 2006, 115, 437-447.	2.2	35
80	Retand: a novel family of gypsy-like retrotransposons harboring an amplified tandem repeat. <i>Molecular Genetics and Genomics</i> , 2006, 276, 254-263.	2.1	63
81	PRINS on Plant Chromosomes. , 2006, 334, 133-140.		3
82	Transcription and Evolutionary Dynamics of the Centromeric Satellite Repeat CentO in Rice. <i>Molecular Biology and Evolution</i> , 2006, 23, 2505-2520.	8.9	62
83	Significant Expansion of <i>Vicia pannonica</i> Genome Size Mediated by Amplification of a Single Type of Giant Retroelement. <i>Genetics</i> , 2006, 173, 1047-1056.	2.9	119
84	Loading of <i>Arabidopsis</i> Centromeric Histone CENH3 Occurs Mainly during G2 and Requires the Presence of the Histone Fold Domain. <i>Plant Cell</i> , 2006, 18, 2443-2451.	6.6	181
85	Chromosome Flow Sorting and Physical Mapping. , 2005, , 151-171.		6
86	PIGY, a new plant envelope-class LTR retrotransposon. <i>Molecular Genetics and Genomics</i> , 2005, 273, 43-53.	2.1	19
87	Sobo, a Recently Amplified Satellite Repeat of Potato, and Its Implications for the Origin of Tandemly Repeated Sequences. <i>Genetics</i> , 2005, 170, 1231-1238.	2.9	71
88	Characterization of Stowaway MITEs in pea ( <i>Pisum sativum</i> L.) and identification of their potential master elements. <i>Genome</i> , 2005, 48, 831-839.	2.0	24
89	Long-range organization of plant satellite repeats investigated using strand-specific FISH. <i>Cytogenetic and Genome Research</i> , 2005, 109, 58-62.	1.1	6
90	Flow cytogenetics and plant genome mapping. <i>Chromosome Research</i> , 2004, 12, 77-91.	2.2	65

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91	Development of a composite map in <i>Vicia faba</i> , breeding applications and future prospects. <i>Theoretical and Applied Genetics</i> , 2004, 108, 1079-1088.	3.6	58
92	Multicolor FISH mapping of the dioecious model plant, <i>Silene latifolia</i> . <i>Theoretical and Applied Genetics</i> , 2004, 108, 1193-1199.	3.6	66
93	Highly abundant pea LTR retrotransposon Ogr is constitutively transcribed and partially spliced. <i>Plant Molecular Biology</i> , 2003, 53, 399-410.	3.9	92
94	Sequence subfamilies of satellite repeats related to rDNA intergenic spacer are differentially amplified on <i>Vicia sativa</i> chromosomes. <i>Chromosoma</i> , 2003, 112, 152-158.	2.2	51
95	Zaba: a novel miniature transposable element present in genomes of legume plants. <i>Molecular Genetics and Genomics</i> , 2003, 269, 624-631.	2.1	14
96	Karyotype Analysis of Four <i>Vicia</i> Species using In Situ Hybridization with Repetitive Sequences. <i>Annals of Botany</i> , 2003, 91, 921-926.	2.9	61
97	PlantSat: a specialized database for plant satellite repeats. <i>Bioinformatics</i> , 2002, 18, 28-35.	4.1	118
98	Chromosome sorting and PCR-based physical mapping in pea ( <i>Pisum sativum</i> L.). <i>Chromosome Research</i> , 2002, 10, 63-71.	2.2	69
99	Development and Characterization of Microsatellite Markers from Chromosome 1-Specific DNA Libraries of <i>Vicia Faba</i> . <i>Biologia Plantarum</i> , 2002, 45, 337-345.	1.9	87
100	Molecular and cytogenetic analysis of repetitive DNA in pea ( <i>Pisum sativum</i> L.). <i>Genome</i> , 2001, 44, 716-728.	2.0	46
101	Sorting of plant chromosomes. <i>Methods in Cell Biology</i> , 2001, 64, 3-31.	1.1	18
102	Microarray-based survey of repetitive genomic sequences in <i>Vicia</i> spp. <i>Plant Molecular Biology</i> , 2001, 45, 229-244.	3.9	37
103	Molecular and cytogenetic analysis of repetitive DNA in pea (&lt;i>Pisum sativum&/i> L.). <i>Genome</i> , 2001, 44, 716-728.	2.0	28
104	Two new families of tandem repeats isolated from genus <i>Vicia</i> using genomic self-priming PCR. <i>Molecular Genetics and Genomics</i> , 2000, 263, 741-751.	2.4	49
105	Nuclear Dynamics in <i>Arabidopsis thaliana</i> . <i>Molecular Biology of the Cell</i> , 2000, 11, 2733-2741.	2.1	124
106	Cloning and Characterization of New Repetitive Sequences in Field Bean ( <i>Vicia faba</i> L.). <i>Annals of Botany</i> , 2000, 85, 157.	2.9	0
107	Development of a genetic composite map of <i>Vicia faba</i> using F2 populations derived from trisomic plants. <i>Theoretical and Applied Genetics</i> , 1999, 98, 736-743.	3.6	54
108	The <i>Agrobacterium tumefaciens</i> C58-6b gene confers resistance to N <sup>6</sup> -benzyladenine without modifying cytokinin metabolism in tobacco seedlings. <i>Planta</i> , 1999, 209, 453-461.	3.2	14

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109	Cloning and Characterization of New Repetitive Sequences in Field Bean ( <i>Vicia faba</i> L.). <i>Annals of Botany</i> , 1999, 83, 535-541.	2.9	21
110	Green Fluorescent Protein Targeted to the Nucleus, a Transgenic Phenotype Useful for Studies in Plant Biology. <i>Annals of Botany</i> , 1999, 83, 645-654.	2.9	79
111	Flow Analysis and Sorting of Plant Chromosomes. <i>Current Protocols in Cytometry</i> , 1999, 9, Unit 5.3.	3.7	3
112	Analysis of T-DNA-mediated translational beta-glucuronidase gene fusions. <i>Plant Molecular Biology</i> , 1998, 36, 205-217.	3.9	8
113	A combined PRINS-FISH technique for simultaneous localisation of DNA sequences on plant chromosomes. <i>Biologia Plantarum</i> , 1998, 41, 293-296.	1.9	5
114	Nuclear expressed sequence tag (NEST) analysis: A novel means to study transcription through amplification of nuclear RNA. <i>Cytometry</i> , 1998, 33, 460-468.	1.8	20
115	Isolation of chromosomes from <i>Pisum sativum</i> L. hairy root cultures and their analysis by flow cytometry. <i>Plant Science</i> , 1998, 137, 205-215.	3.6	40
116	Subtraction with 3' Modified Oligonucleotides Eliminates Amplification Artifacts in DNA Libraries Enriched for Microsatellites. <i>BioTechniques</i> , 1998, 25, 32-38.	1.8	50
117	Analysis of Nuclear DNA Content and Ploidy in Higher Plants. <i>Current Protocols in Cytometry</i> , 1997, 2, Unit 7.6.	3.7	46
118	Mapping of repeated DNA sequences in plant chromosomes by PRINS and C-PRINS. <i>Theoretical and Applied Genetics</i> , 1997, 94, 758-763.	3.6	62
119	Construction of chromosome-specific DNA libraries covering the whole genome of field bean ( <i>Vicia</i> ) Tj ETQq1 1 0.784314 rgBT/Overlo	2.2	52
120	Primed in situ labelling facilitates flow sorting of similar sized chromosomes. <i>Plant Journal</i> , 1995, 7, 1039-1044.	5.7	44
121	The effect of an elevated cytokinin level using the <i>ipt</i> gene and N 6-benzyladenine on single node and intact potato plant tuberization in vitro. <i>Journal of Plant Growth Regulation</i> , 1995, 14, 143-150.	5.1	32
122	Genetics of sex determination in flowering plants. <i>Genesis</i> , 1994, 15, 214-230.	2.1	142
123	Localization of seed protein genes on flow-sorted field bean chromosomes. <i>Chromosome Research</i> , 1993, 1, 107-115.	2.2	76
124	Localization of vicilin genes via polymerase chain reaction on microisolated field bean chromosomes. <i>Plant Journal</i> , 1993, 3, 883-886.	5.7	28