

Tzen-Yuh Chiang

List of Publications by Year in descending order

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93
papers

2,513
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236925

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2717
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#	ARTICLE	IF	CITATIONS
1	Microbial Communities Along 2,3,7,8-tetrachlorodibenzodioxin Concentration Gradient in Soils Polluted with Agent Orange Based on Metagenomic Analyses. <i>Microbial Ecology</i> , 2023, 85, 197-208.	2.8	3
2	Metagenomics: Potential for bioremediation of soil contaminated with heavy metals. <i>Ecological Genetics and Genomics</i> , 2022, 22, 100111.	0.5	7
3	Metagenomics analyses of microbial dynamics associated with putative flavor development in mash fermentation of sake. <i>LWT - Food Science and Technology</i> , 2022, 163, 113570.	5.2	5
4	Endophytic Microbiome of Biofuel Plant <i>Miscanthus sinensis</i> (Poaceae) Interacts with Environmental Gradients. <i>Microbial Ecology</i> , 2020, 80, 133-144.	2.8	9
5	Behavioral and brain- transcriptomic synchronization between the two opponents of a fighting pair of the fish <i>Betta splendens</i> . <i>PLoS Genetics</i> , 2020, 16, e1008831.	3.5	22
6	Title is missing!. , 2020, 16, e1008831.		0
7	Title is missing!. , 2020, 16, e1008831.		0
8	Title is missing!. , 2020, 16, e1008831.		0
9	Title is missing!. , 2020, 16, e1008831.		0
10	Title is missing!. , 2020, 16, e1008831.		0
11	Title is missing!. , 2020, 16, e1008831.		0
12	Revegetation on abandoned salt ponds relieves the seasonal fluctuation of soil microbiomes. <i>BMC Genomics</i> , 2019, 20, 478.	2.8	9
13	Highly diverse endophytes in roots of <i>Cycas bifida</i> (Cycadaceae), an ancient but endangered gymnosperm. <i>Journal of Microbiology</i> , 2018, 56, 337-345.	2.8	39
14	Comparative phylogeography of two codistributed endemic cyprinids in southeastern Taiwan. <i>Biochemical Systematics and Ecology</i> , 2017, 70, 283-290.	1.3	10
15	Common Stress Transcriptome Analysis Reveals Functional and Genomic Architecture Differences Between Early and Delayed Response Genes. <i>Plant and Cell Physiology</i> , 2017, 58, pxx002.	3.1	13
16	Frequent gene flow blurred taxonomic boundaries of sections in <i>Lilium L.</i> (Liliaceae). <i>PLoS ONE</i> , 2017, 12, e0183209.	2.5	7
17	Cross-Species, Amplifiable EST-SSR Markers for <i>Amentotaxus</i> Species Obtained by Next-Generation Sequencing. <i>Molecules</i> , 2016, 21, 67.	3.8	27
18	Students' knowledge of, and attitudes towards biotechnology revisited, 1995â€“2014: Changes in agriculture biotechnology but not in medical biotechnology. <i>Biochemistry and Molecular Biology Education</i> , 2016, 44, 475-491.	1.2	13

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19	Comparative transcriptome analysis of <i>Gastrodia elata</i> (Orchidaceae) in response to fungus symbiosis to identify gastrodin biosynthesis-related genes. <i>BMC Genomics</i> , 2016, 17, 212.	2.8	39
20	<i>Miscanthus</i> as an example of ecological genetics and genomics for nonmodel species. <i>Ecological Genetics and Genomics</i> , 2016, 1, 6-7.	0.5	1
21	Multilocus Analyses Reveal Postglacial Demographic Shrinkage of <i>Juniperus morrisonicola</i> (Cupressaceae), a Dominant Alpine Species in Taiwan. <i>PLoS ONE</i> , 2016, 11, e0161713.	2.5	7
22	Draft genome of <i>Myxosarcina</i> sp. strain G11, a baeocyctous cyanobacterium associated with the marine sponge <i>Terpios hoshinota</i> . <i>Standards in Genomic Sciences</i> , 2015, 10, 28.	1.5	9
23	Alleviation of allelochemical juglone-induced phytotoxicity in tobacco plants by proline. <i>Journal of Plant Interactions</i> , 2015, 10, 167-172.	2.1	12
24	Ecological genomics in <i>Xanthomonas</i> : the nature of genetic adaptation with homologous recombination and host shifts. <i>BMC Genomics</i> , 2015, 16, 188.	2.8	23
25	Highly diversified fungi are associated with the achlorophyllous orchid <i>Gastrodia flavilabella</i> . <i>BMC Genomics</i> , 2015, 16, 185.	2.8	19
26	Biogeography of the <i>Phalaenopsis amabilis</i> species complex inferred from nuclear and plastid DNAs. <i>BMC Plant Biology</i> , 2015, 15, 202.	3.6	13
27	Genetic Divergence and Biogeographical Patterns in <i>Amentotaxus argotaenia</i> Species Complex. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 264-280.	1.8	28
28	Temperate origin and diversification via southward colonization in <i>Fatsia</i> (Araliaceae), an insular endemic genus of the West Pacific Rim. <i>Tree Genetics and Genomes</i> , 2014, 10, 1317-1330.	1.6	10
29	Analysis of microsatellites in the vulnerable orchid <i>Gastrodia flavilabella</i> : the development of microsatellite markers, and cross-species amplification in <i>Gastrodia</i> . , 2014, 55, 72.		15
30	Complete mitochondrial genome of <i>Microphysogobio alticorpus</i> (Cypriniformes, Cyprinidae). <i>Mitochondrial DNA</i> , 2014, 25, 173-174.	0.6	5
31	Adaptive divergence with gene flow in incipient speciation of <i>Miscanthus floridulus</i> / <i>M. sinensis</i> complex (Poaceae). <i>Plant Journal</i> , 2014, 80, 834-847.	5.7	17
32	Taming the wild: resolving the gene pools of non-model <i>Arabidopsis</i> lineages. <i>BMC Evolutionary Biology</i> , 2014, 14, 224.	3.2	61
33	Deciphering mycorrhizal fungi in cultivated <i>Phalaenopsis</i> microbiome with next-generation sequencing of multiple barcodes. <i>Fungal Diversity</i> , 2014, 66, 77-88.	12.3	24
34	Development and characterization of nine polymorphic microsatellite markers from the sword prawn <i>Parapenaeopsis hardwickii</i> using PCR-based isolation of microsatellite arrays (PIMA). <i>Conservation Genetics Resources</i> , 2014, 6, 547-549.	0.8	1
35	Volatilized myrcene inhibits growth and activates defense responses in rice roots. <i>Acta Physiologiae Plantarum</i> , 2013, 35, 2475-2482.	2.1	16
36	Diverse processes shape deep phylogeographical divergence in <i>Cobitis sinensis</i> (Teleostei). <i>Trends in Ecology and Evolution</i> , 2013, 24, 110-118.	1.4	30

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37	Characterization of 42 Microsatellite Markers from Poison Ivy, <i>Toxicodendron radicans</i> (Anacardiaceae). <i>International Journal of Molecular Sciences</i> , 2013, 14, 20414-20426.	4.1	17
38	Isolation and Characterization of Polymorphic Microsatellite Loci from <i>Metapenaeopsis barbata</i> Using PCR-Based Isolation of Microsatellite Arrays (PIMA). <i>International Journal of Molecular Sciences</i> , 2012, 13, 2763-2768.	4.1	4
39	Footprints of natural and artificial selection for photoperiod pathway genes in <i>Oryza</i> . <i>Plant Journal</i> , 2012, 70, 769-782.	5.7	40
40	Inferring Multiple Refugia and Phylogeographical Patterns in <i>Pinus massoniana</i> Based on Nucleotide Sequence Variation and DNA Fingerprinting. <i>PLoS ONE</i> , 2012, 7, e43717.	2.5	30
41	Population Structure in the Endangered Cyprinid Fish <i>Pararasbora moltrechti</i> in Taiwan, Based on Mitochondrial and Microsatellite DNAs. <i>Zoological Science</i> , 2011, 28, 642-651.	0.7	15
42	Conservation genetics and phylogeography of endangered and endemic shrub <i>Tetraena mongolica</i> (Zygophyllaceae) in Inner Mongolia, China. <i>BMC Genetics</i> , 2011, 12, 1.	2.7	92
43	Characterization of Expressed Sequence Tags from Flower Buds of Alpine <i>Lilium formosanum</i> using a Subtractive cDNA Library. <i>Plant Molecular Biology Reporter</i> , 2011, 29, 88-97.	1.8	16
44	Population structure of <i>Nouelia insignis</i> (Asteraceae), an endangered species in southwestern China, based on chloroplast DNA sequences: recent demographic shrinking. <i>Journal of Plant Research</i> , 2011, 124, 221-230.	2.4	27
45	Genetic population structure of the alpine species <i>Rhododendron pseudochrysanthum sensu lato</i> (Ericaceae) inferred from chloroplast and nuclear DNA. <i>BMC Evolutionary Biology</i> , 2011, 11, 108.	3.2	14
46	Development of 12 genic microsatellite loci for a biofuel grass, <i>Miscanthus sinensis</i> (Poaceae). <i>American Journal of Botany</i> , 2011, 98, e201-3.	1.7	17
47	Multilocus analysis of genetic divergence between outcrossing <i>Arabidopsis</i> species: evidence of genome-wide admixture. <i>New Phytologist</i> , 2010, 188, 488-500.	7.3	18
48	Population history in <i>Arabidopsis halleri</i> using multilocus analysis. <i>Molecular Ecology</i> , 2010, 19, 3364-3379.	3.9	11
49	Phylogeography of <i>Hemibarbus labeo</i> (Cyprinidae): secondary contact of ancient lineages of mtDNA. <i>Zoologica Scripta</i> , 2010, 39, 23-35.	1.7	10
50	Isolation and characterization of polymorphic microsatellite loci from <i>Areca catechu</i> (Arecaceae) using PCR-based isolation of microsatellite arrays. <i>Molecular Ecology Resources</i> , 2009, 9, 658-660.	4.8	3
51	Phylogenetic relationships of diploid and polyploid species in <i>Ludwigia</i> sect. <i>Isnardia</i> (Onagraceae) based on chloroplast and nuclear DNAs. <i>Taxon</i> , 2009, 58, 1216-1226.	0.7	8
52	Isolation and characterization of polymorphic microsatellite loci in <i>Candidia barbata</i> (Cyprinidae) using PCR-based isolation of microsatellite arrays (PIMA). <i>Conservation Genetics</i> , 2009, 10, 503-505.	1.5	2
53	Isolation and characterization of 15 microsatellite loci from <i>Caridina gracilipes</i> (Atyidae, Decapoda). <i>Conservation Genetics</i> , 2009, 10, 1065-1068.	1.5	4
54	Isolation and characterization of microsatellite loci from a potential biofuel plant <i>Miscanthus sinensis</i> (Poaceae). <i>Conservation Genetics</i> , 2009, 10, 1377-1380.	1.5	38

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55	Isolation and characterization of eight polymorphic microsatellite loci from <i>Ludwigia polycarpa</i> (Onagraceae), a threaten herb in North America. <i>Conservation Genetics</i> , 2009, 10, 1381-1383.	1.5	1
56	Isolation and characterization of polymorphic microsatellite DNA makers for <i>Euphrasia nankotaizanensis</i> (Orobanchaceae) and cross amplification in another <i>Euphrasia</i> L.. <i>Conservation Genetics</i> , 2009, 10, 1163-1165.	1.5	2
57	Isolation and characterization of microsatellite loci in <i>Taxus sumatrana</i> (Taxaceae) using PCR-based isolation of microsatellite arrays (PIMA). <i>Conservation Genetics</i> , 2008, 9, 471-473.	1.5	29
58	Isolation and characterization of microsatellite loci in the endangered freshwater fish <i>Parasbora moltrechti</i> (Cyprinidae) using PCR-based isolation of microsatellite arrays (PIMA). <i>Conservation Genetics</i> , 2008, 9, 945-947.	1.5	9
59	Isolation and characterization of microsatellite loci of <i>Lycopodium fordii</i> Bak. (Lycopodiaceae). <i>Tj ETQq1 1 0.784314 rgBT / Overlock 107</i>	1.5	2
60	Isolation and characterization of 11 microsatellite loci from <i>Camellia sinensis</i> in Taiwan using PCR-based isolation of microsatellite arrays (PIMA). <i>Conservation Genetics</i> , 2008, 9, 779-781.	1.5	24
61	Isolation and characterization of 11 polymorphic microsatellite loci from <i>Fatsia polycarpa</i> (Araliaceae), an element of evergreen forests in Taiwan. <i>Conservation Genetics</i> , 2008, 9, 1333-1335.	1.5	3
62	Isolation and characterization of 12 microsatellite loci from <i>Suzukia shikikunensis</i> (Lamiaceae), a genus endemic to Taiwan and Ryukyus. <i>Conservation Genetics</i> , 2008, 9, 1337-1339.	1.5	2
63	Isolation and characterization of microsatellite loci in <i>Pedicularis verticillata</i> L. using PCR-based isolation of microsatellite arrays (PIMA). <i>Conservation Genetics</i> , 2008, 9, 1389-1391.	1.5	3
64	Isolation and characterization of microsatellite loci in the commercially important mudshrimp <i>Austinoergia edulis</i> (Upogebiidae) using PCR-based isolation of microsatellite arrays (PIMA). <i>Conservation Genetics</i> , 2008, 9, 1653-1655.	1.5	3
65	Isolation and characterization of microsatellite loci in the endangered freshwater fish <i>Varicorhinus alticorpus</i> (Cyprinidae). <i>Conservation Genetics</i> , 2008, 9, 1399-1401.	1.5	10
66	Development of 15 polymorphic microsatellite loci from <i>Garrulax morrisonianus</i> (Timaliidae), an endemic avian species of Taiwan. <i>Conservation Genetics</i> , 2008, 9, 1711-1713.	1.5	2
67	Diverse selective modes among orthologs/paralogs of the chalcone synthase (Chs) gene family of <i>Arabidopsis thaliana</i> and its relative <i>A. halleri</i> ssp. <i>gemmifera</i> . <i>Molecular Phylogenetics and Evolution</i> , 2007, 44, 503-520.	2.7	14
68	Isolation and characterization of polymorphic microsatellite loci in <i>Hemibarbus labeo</i> (Cyprinidae) using PCR-based isolation of microsatellite arrays (PIMA). <i>Molecular Ecology Notes</i> , 2007, 7, 788-790.	1.7	10
69	High Genetic Diversity vs. Low Genetic Differentiation in <i>Nouelia insignis</i> (Asteraceae), a Narrowly Distributed and Endemic Species in China, Revealed by ISSR Fingerprinting. <i>Annals of Botany</i> , 2006, 98, 583-589.	2.9	99
70	Phylogeography of plants in Taiwan and the Ryukyu Archipelago. <i>Taxon</i> , 2006, 55, 31-41.	0.7	96
71	Phylogeography of Asian wild rice, <i>Oryza rufipogon</i> , reveals multiple independent domestications of cultivated rice, <i>Oryza sativa</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 9578-9583.	7.1	640
72	Contrasting phylogeographical patterns between mainland and island taxa of the <i>Pinus luchuensis</i> complex. <i>Molecular Ecology</i> , 2006, 15, 765-779.	3.9	84

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73	Population structure of wild bananas, <i>Musa balbisiana</i> , in China determined by SSR fingerprinting and cpDNA PCR-RFLP. <i>Molecular Ecology</i> , 2005, 14, 933-944.	3.9	68
74	Phylogeography and conservation genetics of <i>Hygrophila pogonocalyx</i> (Acanthaceae) based on atpB/rbcL noncoding spacer cpDNA. <i>Journal of Plant Research</i> , 2005, 118, 1-11.	2.4	23
75	Low genetic diversity and significant population structuring in the relict <i>Amentotaxus argotaenia</i> complex (Taxaceae) based on ISSR fingerprinting. <i>Journal of Plant Research</i> , 2005, 118, 415-422.	2.4	56
76	Isolation and characterization of microsatellite loci in <i>Acrossocheilus paradoxus</i> (Cyprinidae) using PCR-based isolation of microsatellite arrays (PIMA). <i>Conservation Genetics</i> , 2004, 5, 113-115.	1.5	23
77	Range expansion leading to departures from neutrality in the nonsymbiotic hemoglobin gene and the cpDNA trnL-trnF intergenic spacer in <i>Trema dielsiana</i> (Ulmaceae). <i>Molecular Phylogenetics and Evolution</i> , 2004, 31, 929-942.	2.7	18
78	Phylogeography of <i>Varicorhinus barbatulus</i> (Cyprinidae) in Taiwan based on nucleotide variation of mtDNA and allozymes. <i>Molecular Phylogenetics and Evolution</i> , 2004, 31, 1143-1156.	2.7	62
79	Coalescent processes and relaxation of selective constraints leading to contrasting genetic diversity at paralogs AtHVA22d and AtHVA22e in <i>Arabidopsis thaliana</i> . <i>Molecular Phylogenetics and Evolution</i> , 2004, 32, 616-626.	2.7	7
80	Contrasting selection modes at the <i>Adh1</i> locus in outcrossing <i>Miscanthus sinensis</i> vs. inbreeding <i>Miscanthus condensatus</i> (Poaceae). <i>American Journal of Botany</i> , 2003, 90, 561-570.	1.7	54
81	Characterization and adaptive evolution of β -tubulin genes in the <i>Miscanthus sinensis</i> complex (Poaceae). <i>American Journal of Botany</i> , 2003, 90, 1513-1521.	1.7	9
82	Nucleotide Sequence Diversity at the Methionine Synthase Locus in Endangered <i>Dunnia sinensis</i> (Rubiaceae): An Evaluation of the Positive Selection Hypothesis. <i>Molecular Biology and Evolution</i> , 2002, 19, 1367-1375.	8.9	10
83	Genetic variation and population differentiation of <i>Michelia formosana</i> (Magnoliaceae) based on cpDNA variation and RAPD fingerprints: relevance to post-Pleistocene recolonization. <i>Journal of Plant Research</i> , 2002, 115, 203-216.	2.4	30
84	Title is missing!. <i>Conservation Genetics</i> , 2002, 3, 351-362.	1.5	38
85	Population differentiation and phylogeography of <i>Hygrophila pogonocalyx</i> based on RAPDs fingerprints. <i>Aquatic Botany</i> , 2001, 70, 269-280.	1.6	8
86	Chloroplast DNA phylogeography of <i>Cunninghamia konishii</i> (Cupressaceae), an endemic conifer of Taiwan. <i>Genome</i> , 2001, 44, 797-807.	2.0	63
87	Experimental Hybridization Reveals Biased Inheritance of the Internal Transcribed Spacer of the Nuclear Ribosomal DNA in <i>Begonia taipeiensis</i> . <i>Journal of Plant Research</i> , 2001, 114, 343-351.	2.4	23
88	Chloroplast DNA phylogeography of <i>Cunninghamia konishii</i> (Cupressaceae), an endemic conifer of Taiwan. <i>Genome</i> , 2001, 44, 797-807.	2.0	28
89	Lineage sorting accounting for the disassociation between chloroplast and mitochondrial lineages in oaks of southern France. <i>Genome</i> , 2000, 43, 1090-1094.	2.0	21
90	Molecular evolution and phylogeny of the atpB-rbcL spacer of chloroplast DNA in the true mosses. <i>Genome</i> , 2000, 43, 417-426.	2.0	18

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91	Genetic variability and phylogeography of <i>Miscanthus sinensis</i> var. <i>condensatus</i> , an apomictic grass, based on RAPD fingerprints. <i>Canadian Journal of Botany</i> , 2000, 78, 1262-1268.	1.1	31
92	Cloning and genetic variability of a HindIII repetitive DNA in <i>Acrossocheilus paradoxus</i> (Cyprinidae). <i>Genome</i> , 1999, 42, 780-788.	2.0	9
93	Within- and between-individual length heterogeneity of the rDNA-IGS in <i>Miscanthus sinensis</i> var. <i>glaber</i> (Poaceae): Phylogenetic analyses. <i>Genome</i> , 1999, 42, 1088-1093.	2.0	21