## Silvina C Pessino

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The Auxin-Response Repressor IAA30 Is Down-Regulated in Reproductive Tissues of Apomictic Paspalum notatum. Plants, 2022, 11, 1472.	3.5	1
2	A study of the heterochronic sense/antisense RNA representation in florets of sexual and apomictic Paspalum notatum. BMC Genomics, 2021, 22, 185.	2.8	6
3	How to Become an Apomixis Model: The Multifaceted Case of Paspalum. Genes, 2020, 11, 974.	2.4	15
4	Small RNA-seq reveals novel regulatory components for apomixis in Paspalum notatum. BMC Genomics, 2019, 20, 487.	2.8	33
5	A Portion of the Apomixis Locus of Paspalum Simplex is Microsyntenic with an Unstable Chromosome Segment Highly Conserved Among Poaceae. Scientific Reports, 2019, 9, 3271.	3.3	32
6	A Plant-Specific TGS1 Homolog Influences Gametophyte Development in Sexual Tetraploid Paspalum notatum Ovules. Frontiers in Plant Science, 2019, 10, 1566.	3.6	15
7	The vesicle trafficking regulator PN_SCD1 is demethylated and overexpressed in florets of apomictic Paspalum notatum genotypes. Scientific Reports, 2018, 8, 3030.	3.3	16
8	Structure, target-specificity and expression of PN_LNC_N13, a long non-coding RNA differentially expressed in apomictic and sexual Paspalum notatum. Plant Molecular Biology, 2018, 96, 53-67.	3.9	13
9	The MAP3K-Coding QUI-GON JINN (QGJ) Gene Is Essential to the Formation of Unreduced Embryo Sacs in Paspalum. Frontiers in Plant Science, 2018, 9, 1547.	3.6	36
10	Temporal and spatial expression of genes involved in DNA methylation during reproductive development of sexual and apomictic Eragrostis curvula. Scientific Reports, 2017, 7, 15092.	3.3	22
11	A reference floral transcriptome of sexual and apomictic Paspalum notatum. BMC Genomics, 2017, 18, 318.	2.8	39
12	An apomixis-linked <i>ORC3</i> -like pseudogene is associated with silencing of its functional homolog in apomictic <i>Paspalum simplex</i> . Journal of Experimental Botany, 2016, 67, 1965-1978.	4.8	53
13	Repetitive sequences in Eragrostis curvula cDNA EST libraries obtained from genotypes with different ploidy. Biologia Plantarum, 2016, 60, 55-67.	1.9	7
14	First insight into divergence, representation and chromosome distribution of reverse transcriptase fragments from L1 retrotransposons in peanut and wild relative species. Genetica, 2015, 143, 113-125.	1.1	33
15	Increased apomixis expression concurrent with genetic and epigenetic variation in a newly synthesized Eragrostis curvula polyploid. Scientific Reports, 2015, 4, 4423.	3.3	23
16	PnTgs1-like expression during reproductive development supports a role for RNA methyltransferases in the aposporous pathway. BMC Plant Biology, 2014, 14, 297.	3.6	59
17	Development of a modified transformation platform for apomixis candidate genes research in Paspalum notatum (bahiagrass). In Vitro Cellular and Developmental Biology - Plant, 2014, 50, 412-424.	2.1	26
18	A methylation status analysis of the apomixis-specific region in Paspalum spp. suggests an epigenetic control of parthenogenesis. Journal of Experimental Botany, 2014, 65, 6411-6424.	4.8	57

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19	Genetic response of Paspalum plicatulum to genome duplication. Genetica, 2014, 142, 227-234.	1.1	2
20	Characterization and expression analysis of SOMATIC EMBRYOGENESIS RECEPTOR KINASE (SERK) genes in sexual and apomictic Paspalum notatum. Plant Molecular Biology, 2014, 84, 479-495.	3.9	55
21	A succinate dehydrogenase flavoprotein subunit-like transcript is upregulated in llex paraguariensis leaves in response to water deficit and abscisic acid. Plant Physiology and Biochemistry, 2013, 65, 48-54.	5.8	41
22	Harnessing apomictic reproduction in grasses: what we have learned from Paspalum. Annals of Botany, 2013, 112, 767-787.	2.9	163
23	Sequence characterization, in silico mapping and cytosine methylation analysis of markers linked to apospory in Paspalum notatum. Genetics and Molecular Biology, 2012, 35, 827-837.	1.3	37
24	Identification of Candidate Genes Related to Polyploidy and/or Apomixis in <i>Eragrostis curvula</i> . American Journal of Plant Sciences, 2012, 03, 403-416.	0.8	28
25	Evaluation of different methods for assessing the reproductive mode of weeping lovegrass plants, Eragrostis curvula (Schrad.) Nees. Australian Journal of Botany, 2011, 59, 253.	0.6	30
26	Eragrostis. , 2011, , 135-151.		4
27	Expression of lorelei-like genes in aposporous and sexual Paspalum notatum plants. Plant Molecular Biology, 2011, 77, 337-354.	3.9	34
28	Characterization of retrotransposon sequences expressed in inflorescences of apomictic and sexual Paspalum notatum plants. Sexual Plant Reproduction, 2011, 24, 231-246.	2.2	70
29	Variation in cytosine methylation patterns during ploidy level conversions in Eragrostis curvula. Plant Molecular Biology, 2009, 70, 17-29.	3.9	30
30	Expressed sequence tag analysis and development of gene associated markers in a near-isogenic plant system of Eragrostis curvula. Plant Molecular Biology, 2008, 67, 1-10.	3.9	51
31	Gene expression in diplosporous and sexual Eragrostis curvula genotypes with differing ploidy levels. Plant Molecular Biology, 2008, 67, 11-23.	3.9	53
32	Gene expression analysis at the onset of aposporous apomixis in Paspalum notatum. Plant Molecular Biology, 2008, 67, 615-628.	3.9	63
33	Genome rearrangements derived from autopolyploidization in Paspalum sp Plant Science, 2007, 172, 970-977.	3.6	52
34	Genome polymorphisms and gene differential expression in a â€~back-and-forth' ploidy-altered series of weeping lovegrass (Eragrostis curvula). Journal of Plant Physiology, 2007, 164, 1051-1061.	3.5	28
35	A genetic map of tetraploid Paspalum notatum Flügge (bahiagrass) based on single-dose molecular markers. Molecular Breeding, 2007, 20, 153-166.	2.1	92
36	Novel genotypes of the subtropical grass Eragrostis curvula for the study of apomixis (diplospory). Euphytica, 2006, 151, 263-272.	1.2	14

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37	Genetic characterization of Paspalum notatum accessions by AFLP markers. Plant Systematics and Evolution, 2006, 258, 147-159.	0.9	32
38	A comprehensive analysis of gene expression alterations in a newly synthesized Paspalum notatum autotetraploid. Plant Science, 2005, 169, 211-220.	3.6	46
39	A Genetic Map of the Apospory-Region in Brachiaria Hybrids: Identification of two Markers Closely Associated with the Trait. Hereditas, 2004, 128, 153-158.	1.4	70
40	The Molecular Genetics of Gametophytic Apomixis. Hereditas, 2004, 130, 1-11.	1.4	33
41	Isolation of cDNA Clones Differentially Expressed in Flowers of Apomictic and Sexual Paspalum Notatum. Hereditas, 2004, 134, 35-42.	1.4	63
42	Genetic diversity in sexual diploid and apomictic tetraploid populations of Paspalum notatum situated in sympatry or allopatry. Plant Systematics and Evolution, 2004, 244, 189-199.	0.9	60
43	Tetraploid races of Paspalum notatum show polysomic inheritance and preferential chromosome pairing around the apospory-controlling locus. Theoretical and Applied Genetics, 2004, 109, 186-191.	3.6	90
44	Effect of Pollination Timing on the Rate of Apomictic Reproduction Revealed by RAPD Markers in Paspalum notatum. Annals of Botany, 2002, 89, 165-170.	2.9	61
45	A Genetic Linkage Map of Diploid Paspalum notatum. Crop Science, 2001, 41, 823-830.	1.8	22
46	A rise of ploidy level induces the expression of apomixis in Paspalum notatum. Sexual Plant Reproduction, 2001, 13, 243-249.	2.2	191
47	Non-radioactive mRNA fingerprinting to visualise gene expression in mature ovaries of Brachiaria hybrids derived from B. brizantha, an apomictic tropical forage. Plant Science, 1997, 126, 49-58.	3.6	34
48	Identification of a maize linkage group related to apomixis in Brachiaria. Theoretical and Applied Genetics, 1997, 94, 439-444.	3.6	101
49	Genetic fingerprinting for determining the mode of reproduction in Paspalum notatum, a subtropical apomictic forage grass. Theoretical and Applied Genetics, 1997, 95, 850-856.	3.6	90
50	Structure and characterization of the gene encoding the ferredoxin-NADP reductase-binding protein from Zea mays L. Gene, 1994, 147, 205-208.	2.2	5