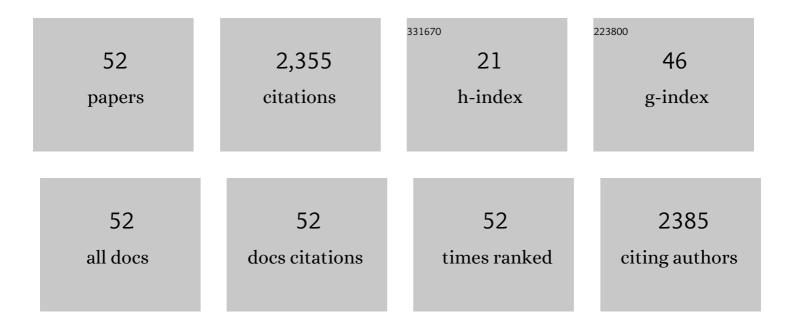
## **Rajinder Singh**

List of Publications by Year in descending order

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RAUNDER SINCH

#	Article	IF	CITATIONS
1	Oil palm genome sequence reveals divergence of interfertile species in Old and New worlds. Nature, 2013, 500, 335-339.	27.8	468
2	Loss of Karma transposon methylation underlies theÂmantled somaclonal variant of oil palm. Nature, 2015, 525, 533-537.	27.8	405
3	The oil palm SHELL gene controls oil yield and encodes a homologue of SEEDSTICK. Nature, 2013, 500, 340-344.	27.8	167
4	Microsatellite-based high density linkage map in oil palm (Elaeis guineensis Jacq.) Theoretical and Applied Genetics, 2005, 110, 754-765.	3.6	130
5	Variation in oil palm (Elaeis guineensis Jacq.) tissue culture-derived regenerants revealed by AFLPs with methylation-sensitive enzymes. Theoretical and Applied Genetics, 2001, 102, 971-979.	3.6	125
6	Mapping quantitative trait loci (QTLs) for fatty acid composition in an interspecific cross of oil palm. BMC Plant Biology, 2009, 9, 114.	3.6	101
7	QTL detection by multi-parent linkage mapping in oil palm (Elaeis guineensis Jacq.). Theoretical and Applied Genetics, 2010, 120, 1673-1687.	3.6	93
8	Oil palm (Elaeis guineensisJacq.) tissue culture ESTs: Identifying genes associated with callogenesis and embryogenesis. BMC Plant Biology, 2008, 8, 62.	3.6	83
9	High density SNP and SSR-based genetic maps of two independent oil palm hybrids. BMC Genomics, 2014, 15, 309.	2.8	70
10	The oil palm VIRESCENS gene controls fruit colour and encodes a R2R3-MYB. Nature Communications, 2014, 5, 4106.	12.8	67
11	SSR mining in oil palm EST database: application in oil palm germplasm diversity studies. Journal of Genetics, 2010, 89, 135-145.	0.7	60
12	Somaclonal variation in micropropagated oil palm. Characterization of two novel genes with enhanced expression in epigenetically abnormal cell lines and in response to auxin. Tree Physiology, 2006, 26, 585-594.	3.1	55
13	Exploiting an oil palm EST database for the development of gene-derived SSR markers and their exploitation for assessment of genetic diversity. Biologia (Poland), 2008, 63, 227-235.	1.5	54
14	Identification of QTLs Associated with Callogenesis and Embryogenesis in Oil Palm Using Genetic Linkage Maps Improved with SSR Markers. PLoS ONE, 2013, 8, e53076.	2.5	43
15	In silico characterization and expression profiling of the diacylglycerol acyltransferase gene family (DGAT1, DGAT2, DGAT3 and WS/DGAT) from oil palm, Elaeis guineensis. Plant Science, 2018, 275, 84-96.	3.6	37
16	Elaeis oleifera Genomic-SSR Markers: Exploitation in Oil Palm Germplasm Diversity and Cross-Amplification in Arecaceae. International Journal of Molecular Sciences, 2012, 13, 4069-4088.	4.1	33
17	Fine-mapping and cross-validation of QTLs linked to fatty acid composition in multiple independent interspecific crosses of oil palm. BMC Genomics, 2016, 17, 289.	2.8	32
18	Characterization of a defensin gene expressed in oil palm inflorescences: induction during tissue culture and possible association with epigenetic somaclonal variation events. Journal of Experimental Botany, 2002, 53, 1387-1396.	4.8	30

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#	Article	IF	CITATIONS
19	Genetic Linkage Map of a High Yielding FELDA Deli×Yangambi Oil Palm Cross. PLoS ONE, 2011, 6, e26593.	2.5	26
20	Non-tenera Contamination and the Economic Impact of SHELL Genetic Testing in the Malaysian Independent Oil Palm Industry. Frontiers in Plant Science, 2016, 7, 771.	3.6	26
21	Analyses of Hypomethylated Oil Palm Gene Space. PLoS ONE, 2014, 9, e86728.	2.5	26
22	Multiple locus genome-wide association studies for important economic traits of oil palm. Tree Genetics and Genomes, 2017, 13, 1.	1.6	24
23	Evaluation of Reference Genes for Quantitative Real-Time PCR in Oil Palm Elite Planting Materials Propagated by Tissue Culture. PLoS ONE, 2014, 9, e99774.	2.5	21
24	QTLs for oil yield components in an elite oil palm (Elaeis guineensis) cross. Euphytica, 2016, 212, 399-425.	1.2	18
25	Opportunities for the Oil Palm via Breeding and Biotechnology. , 2009, , 377-421.		18
26	Comparative genomic and transcriptomic analysis of selected fatty acid biosynthesis genes and CNL disease resistance genes in oil palm. PLoS ONE, 2018, 13, e0194792.	2.5	16
27	Development of SNP markers and their application for genetic diversity analysis in the oil palm (Elaeis) Tj ETQq1	1 0,7843 0.2	14 rgBT /Ove
28	Coconut, Date, and Oil Palm Genomics. , 2012, , 299-351.		14
29	Genomic diversity and genome-wide association analysis related to yield and fatty acid composition of wild American oil palm. Plant Science, 2021, 304, 110731.	3.6	12
30	Variation for heterodimerization and nuclear localization among known and novel oil palm SHELL alleles. New Phytologist, 2020, 226, 426-440.	7.3	11
31	Early nodulin 93 protein gene: essential for induction of somatic embryogenesis in oil palm. Plant Cell Reports, 2020, 39, 1395-1413.	5.6	8
32	Characterization of a defensin gene expressed in oil palm inflorescences: induction during tissue culture and possible association with epigenetic somaclonal variation events. Journal of Experimental Botany, 2002, 53, 1387-96.	4.8	8
33	Putative regulatory candidate genes for QTL linked to fruit traits in oil palm (Elaeis guineensis Jacq.). Euphytica, 2018, 214, 1.	1.2	6
34	Detection of ploidy and chromosomal aberrations in commercial oil palm using high-throughput SNP markers. Planta, 2021, 253, 63.	3.2	6
35	Recycling of superfine resolution agarose gel. Genetics and Molecular Research, 2013, 12, 2360-2367.	0.2	5
36	Differential gene expression during flowering in the oil palm ( Elaeis guineensis ). Plant Cell Reports, 2000, 19, 804-809.	5.6	4

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#	Article	IF	CITATIONS
37	Expression of fatty acid and triacylglycerol synthesis genes in interspecific hybrids of oil palm. Scientific Reports, 2020, 10, 16296.	3.3	4
38	An integrated linkage map of interspecific backcross 2 (BC2) populations reveals QTLs associated with fatty acid composition and vegetative parameters influencing compactness in oil palm. BMC Plant Biology, 2020, 20, 356.	3.6	4
39	Candidate genes linked to QTL regions associated with fatty acid composition in oil palm. Biologia (Poland), 2021, 76, 267-279.	1.5	4
40	Chromosome identification in oil palm (Elaeis guineensis) using in situ hybridization with massive pools of single copy oligonucleotides and transferability across Arecaceae species. Chromosome Research, 2021, 29, 373-390.	2.2	4
41	Association mapping analysis of oil palm interspecific hybrid populations and predicting phenotypic values via machine learning algorithms. Plant Breeding, 2021, 140, 1150-1165.	1.9	4
42	Comparison of quantitative trait loci (QTLs) associated with yield components in two commercial Dura × Pisifera breeding crosses. Euphytica, 2021, 217, 1.	1.2	3
43	Molecular authentication of the traditional Chinese medicinal plant Angelica sinensis based on internal transcribed spacer of nrDNA. Electronic Journal of Biotechnology, 2010, 13, .	2.2	2
44	Elaeis. , 2011, , 113-124.		2
45	Oil Palm Genomics. , 2012, , 59-86.		2
46	Optimal set of microsatellite markers required to detect illegitimate progenies in selected oil palm ( <i>Elaeis guineensis</i> Jacq.) breeding crosses. Breeding Science, 2021, 71, 253-260.	1.9	2
47	Oil Palm Genome: Strategies and Applications. Compendium of Plant Genomes, 2020, , 83-115.	0.5	2
48	A genetic platform for predicting and reducing non-tenera contamination in oil palm (Elaeis) Tj ETQq0 0 0 rgBT $/$	Overlock 1 1.6	10 Tf 50 302
49	Biodiversity and Conservation of Elaeis Species. Sustainable Development and Biodiversity, 2017, , 245-272.	1.7	1
50	Anchoring a genetic map of an interspecific backcross two family to the genome builds of Elaeis. Journal of Genetics, 2021, 100, 1.	0.7	1
51	Molecular Genetics and Breeding. , 2017, , 225-282.		1

<sup>52</sup> Overexpression of Oil Palm Early Nodulin 93 Protein Gene (EgENOD93) Enhances In Vitro Shoot Regeneration in Arabidopsis thaliana. Molecular Biotechnology, 2022, , 1.

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