

# Yoosook Lee

## List of Publications by Year in descending order

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78  
papers

2,138  
citations

257450

24  
h-index

289244

40  
g-index

86  
all docs

86  
docs citations

86  
times ranked

2072  
citing authors

#	ARTICLE	IF	CITATIONS
1	Adaptive introgression in an African malaria mosquito coincident with the increased usage of insecticide-treated bed nets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 815-820.	7.1	204
2	Next-generation gene drive for population modification of the malaria vector mosquito, <i>Anopheles gambiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 22805-22814.	7.1	157
3	Development of a confinable gene drive system in the human disease vector <i>Aedes aegypti</i> . <i>ELife</i> , 2020, 9, .	6.0	156
4	Relationship Between <i>kdr</i> Mutation and Resistance to Pyrethroid and DDT Insecticides in Natural Populations of <i>Anopheles gambiae</i> . <i>Journal of Medical Entomology</i> , 2008, 45, 260-266.	1.8	97
5	Spatiotemporal dynamics of gene flow and hybrid fitness between the M and S forms of the malaria mosquito, <i>Anopheles gambiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19854-19859.	7.1	95
6	Relationship Between <i>kdr</i> Mutation and Resistance to Pyrethroid and DDT Insecticides in Natural Populations of <i>Anopheles gambiae</i> . <i>Journal of Medical Entomology</i> , 2008, 45, 260-266.	1.8	81
7	The Genetic Basis of Host Preference and Resting Behavior in the Major African Malaria Vector, <i>Anopheles arabiensis</i> . <i>PLoS Genetics</i> , 2016, 12, e1006303.	3.5	76
8	Asymmetric introgression between the M and S forms of the malaria vector, <i>Anopheles gambiae</i> , maintains divergence despite extensive hybridization. <i>Molecular Ecology</i> , 2011, 20, 4983-4994.	3.9	70
9	Identification and Functional Analysis of Light-Responsive Unique Genes and Gene Family Members in Rice. <i>PLoS Genetics</i> , 2008, 4, e1000164.	3.5	69
10	Core commitments for field trials of gene drive organisms. <i>Science</i> , 2020, 370, 1417-1419.	12.6	67
11	Evidence for subdivision within the M molecular form of <i>Anopheles gambiae</i> . <i>Molecular Ecology</i> , 2006, 16, 639-649.	3.9	64
12	Complex genome evolution in <i>Anopheles coluzzii</i> associated with increased insecticide usage in Mali. <i>Molecular Ecology</i> , 2015, 24, 5145-5157.	3.9	47
13	Genome-wide divergence among invasive populations of <i>Aedes aegypti</i> in California. <i>BMC Genomics</i> , 2019, 20, 204.	2.8	44
14	Ecological and genetic relationships of the Forest-M form among chromosomal and molecular forms of the malaria vector <i>Anopheles gambiae sensu stricto</i> . <i>Malaria Journal</i> , 2009, 8, 75.	2.3	37
15	Surveillance, insecticide resistance and control of an invasive <i>Aedes aegypti</i> (Diptera: Culicidae) population in California. <i>F1000Research</i> , 2016, 5, 194.	1.6	37
16	Mosquito community composition in South Africa and some neighboring countries. <i>Parasites and Vectors</i> , 2018, 11, 331.	2.5	36
17	Desiccation Resistance Among Subpopulations of <i>Anopheles gambiae</i> s. From Selinkenyi, Mali. <i>Journal of Medical Entomology</i> , 2009, 46, 316-320.	1.8	35
18	Surveillance, insecticide resistance and control of an invasive <i>Aedes aegypti</i> (Diptera: Culicidae) population in California. <i>F1000Research</i> , 2016, 5, 194.	1.6	35

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19	Diversity, Differentiation, and Linkage Disequilibrium: Prospects for Association Mapping in the Malaria Vector <i>Anopheles arabiensis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 121-131.	1.8	33
20	Identification of three single nucleotide polymorphisms in <i>Anopheles gambiae</i> immune signaling genes that are associated with natural <i>Plasmodium falciparum</i> infection. <i>Malaria Journal</i> , 2010, 9, 160.	2.3	28
21	Altitudinal genetic and morphometric variation among populations of <i>Culex theileri</i> Theobald (Diptera: Culicidae) from northeastern Turkey. <i>Journal of Vector Ecology</i> , 2012, 37, 197-209.	1.0	28
22	Chromosome Inversions, Genomic Differentiation and Speciation in the African Malaria Mosquito <i>Anopheles gambiae</i> . <i>PLoS ONE</i> , 2013, 8, e57887.	2.5	28
23	Abundance of conserved CRISPR-Cas9 target sites within the highly polymorphic genomes of <i>Anopheles</i> and <i>Aedes</i> mosquitoes. <i>Nature Communications</i> , 2020, 11, 1425.	12.8	28
24	Morphological Differentiation May Mediate Mate-Choice between Incipient Species of <i>Anopheles gambiae</i> s.s.. <i>PLoS ONE</i> , 2011, 6, e27920.	2.5	28
25	A DNA extraction protocol for improved DNA yield from individual mosquitoes. <i>F1000Research</i> , 2015, 4, 1314.	1.6	27
26	An analysis of two island groups as potential sites for trials of transgenic mosquitoes for malaria control. <i>Evolutionary Applications</i> , 2013, 6, 706-720.	3.1	26
27	A new multiplex SNP genotyping assay for detecting hybridization and introgression between the <i>M</i> and <i>S</i> molecular forms of <i>Anopheles gambiae</i> . <i>Molecular Ecology Resources</i> , 2014, 14, 297-305.	4.8	26
28	Differential <i>Plasmodium falciparum</i> infection of <i>Anopheles gambiae</i> s.s. molecular and chromosomal forms in Mali. <i>Malaria Journal</i> , 2012, 11, 133.	2.3	25
29	Sequencing of <i>Tuta absoluta</i> genome to develop SNP genotyping assays for species identification. <i>Journal of Pest Science</i> , 2019, 92, 1397-1407.	3.7	24
30	The fate of genes that cross species boundaries after a major hybridization event in a natural mosquito population. <i>Molecular Ecology</i> , 2018, 27, 4978-4990.	3.9	23
31	Colonization of malaria vectors under semi-field conditions as a strategy for maintaining genetic and phenotypic similarity with wild populations. <i>Malaria Journal</i> , 2015, 14, 10.	2.3	21
32	Speciation in <i>Anopheles gambiae</i> – The Distribution of Genetic Polymorphism and Patterns of Reproductive Isolation Among Natural Populations. , 2013, , .		20
33	Characterization of the complete mitogenome of <i>Anopheles aquasalis</i> , and phylogenetic divergences among <i>Anopheles</i> from diverse geographic zones. <i>PLoS ONE</i> , 2019, 14, e0219523.	2.5	20
34	Population genomics of <i>Drosophila suzukii</i> reveal longitudinal population structure and signals of migrations in and out of the continental United States. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	19
35	<i>Culex pipiens</i> Ssensu Lato in California: A Complex Within a Complex?. <i>Journal of the American Mosquito Control Association</i> , 2012, 28, 113-121.	0.7	18
36	Complete <i>Anopheles funestus</i> mitogenomes reveal an ancient history of mitochondrial lineages and their distribution in southern and central Africa. <i>Scientific Reports</i> , 2018, 8, 9054.	3.3	18

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37	Population genetic structure of <i>Anopheles arabiensis</i> and <i>Anopheles gambiae</i> in a malaria endemic region of southern Tanzania. <i>Malaria Journal</i> , 2011, 10, 289.	2.3	17
38	The genetic structure of <i>Aedes aegypti</i> populations is driven by boat traffic in the Peruvian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007552.	3.0	16
39	High Degree of Single Nucleotide Polymorphisms in California <i>Culex pipiens</i> (Diptera: Culicidae) sensu lato. <i>Journal of Medical Entomology</i> , 2012, 49, 299-306.	1.8	15
40	A Multi-detection Assay for Malaria Transmitting Mosquitoes. <i>Journal of Visualized Experiments</i> , 2015, e52385.	0.3	15
41	Transcontinental dispersal of <i>Anopheles gambiae</i> occurred from West African origin via serial founder events. <i>Communications Biology</i> , 2019, 2, 473.	4.4	13
42	Malaria Vectors and Vector Surveillance in Limpopo Province (South Africa): 1927 to 2018. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 4125.	2.6	13
43	A preliminary investigation of the relationship between water quality and <i>Anopheles gambiae</i> larval habitats in western Cameroon. <i>Malaria Journal</i> , 2013, 12, 225.	2.3	12
44	Frequency of sodium channel genotypes and association with pyrethrum knockdown time in populations of Californian <i>Aedes aegypti</i> . <i>Parasites and Vectors</i> , 2021, 14, 141.	2.5	12
45	Mitochondrial genomes of <i>Anopheles arabiensis</i> , <i>An. gambiae</i> and <i>An. coluzzii</i> show no clear species division. <i>F1000Research</i> , 2018, 7, 347.	1.6	12
46	<i>Plasmodium falciparum</i> infection rates for some <i>Anopheles</i> spp. from Guinea-Bissau, West Africa. <i>F1000Research</i> , 2014, 3, 243.	1.6	11
47	Single-Nucleotide Polymorphisms for High-Throughput Genotyping of <i>Anopheles arabiensis</i> in East and Southern Africa. <i>Journal of Medical Entomology</i> , 2012, 49, 307-315.	1.8	10
48	High endemism of mosquitoes on São Tomé and Príncipe Islands: evaluating the general dynamic model in a worldwide island comparison. <i>Insect Conservation and Diversity</i> , 2019, 12, 69-79.	3.0	10
49	<i>Plasmodium falciparum</i> infection rates for some <i>Anopheles</i> spp. from Guinea-Bissau, West Africa. <i>F1000Research</i> , 2014, 3, 243.	1.6	10
50	Mitochondrial genomes of <i>Anopheles arabiensis</i> , <i>An. gambiae</i> and <i>An. coluzzii</i> show no clear species division. <i>F1000Research</i> , 2018, 7, 347.	1.6	9
51	Introgression between <i>Anopheles gambiae</i> and <i>Anopheles coluzzii</i> in Burkina Faso and its associations with <i>kdr</i> resistance and <i>Plasmodium</i> infection. <i>Malaria Journal</i> , 2019, 18, 127.	2.3	8
52	Microsatellite-Based Parentage Analysis of <i>Aedes aegypti</i> (Diptera: Culicidae) Using Nonlethal DNA Sampling. <i>Journal of Medical Entomology</i> , 2012, 49, 85-93.	1.8	7
53	Complete mitogenome sequence of <i>Aedes</i> ( <i>Stegomyia</i> ) <i>aegypti</i> derived from field isolates from California and South Africa. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 994-995.	0.4	7
54	The origin of island populations of the African malaria mosquito, <i>Anopheles coluzzii</i> . <i>Communications Biology</i> , 2021, 4, 630.	4.4	7

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55	Evidence of Local Extinction and Reintroduction of <i>Aedes aegypti</i> in Exeter, California. <i>Frontiers in Tropical Diseases</i> , 2021, 2, .	1.4	7
56	The Knockdown Resistance Mutation and Knockdown Time in <i>Anopheles gambiae</i> Collected from Mali Evaluated Through a Bottle Bioassay and a Novel Insecticide-Treated Net Bioassay. <i>Journal of the American Mosquito Control Association</i> , 2012, 28, 119-122.	0.7	6
57	Absence of <i>kdr</i> resistance alleles in the Union of the Comoros, East Africa. <i>F1000Research</i> , 2015, 4, 146.	1.6	6
58	Identification and Characterization of Single Nucleotide Polymorphisms (SNPs) in <i>Culex theileri</i> (Diptera: Culicidae). <i>Journal of Medical Entomology</i> , 2012, 49, 581-588.	1.8	5
59	Comparing efficacy of a sweep net and a dip method for collection of mosquito larvae in large bodies of water in South Africa. <i>F1000Research</i> , 2016, 5, 713.	1.6	5
60	Ethanol as a potential mosquito sample storage medium for RNA preservation. <i>F1000Research</i> , 2019, 8, 1431.	1.6	5
61	<i>Anopheles darlingi</i> polytene chromosomes: revised maps including newly described inversions and evidence for population structure in Manaus. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2016, 111, 335-346.	1.6	4
62	A Magnetic-Bead-Based Mosquito DNA Extraction Protocol for Next-Generation Sequencing. <i>Journal of Visualized Experiments</i> , 2021, . .	0.3	4
63	Mosquito Control Priorities in Florida—Survey Results from Florida Mosquito Control Districts. <i>Pathogens</i> , 2021, 10, 947.	2.8	4
64	Evidence for Divergent Selection on Immune Genes between the African Malaria Vectors, <i>Anopheles coluzzii</i> and <i>A. gambiae</i> . <i>Insects</i> , 2020, 11, 893.	2.2	3
65	Complete mitogenome sequences of <i>Aedes</i> ( <i>Howardina</i> ) <i>busckii</i> and <i>Aedes</i> ( <i>Ochlerotatus</i> ) <i>taeniorhynchus</i> from the Caribbean Island of Saba. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1163-1164.	0.4	3
66	Profiling Transcriptional Response of Dengue-2 Virus Infection in Midgut Tissue of <i>Aedes aegypti</i> . <i>Frontiers in Tropical Diseases</i> , 2021, 2, .	1.4	3
67	Surveillance, insecticide resistance and control of an invasive <i>Aedes aegypti</i> (Diptera: Culicidae) population in California. <i>F1000Research</i> , 0, 5, 194.	1.6	3
68	Spontaneous mutation rate estimates for the principal malaria vectors <i>Anopheles coluzzii</i> and <i>Anopheles stephensi</i> . <i>Scientific Reports</i> , 2022, 12, 226.	3.3	3
69	Defining Genetic, Taxonomic, and Geographic Boundaries Among Species of the <i>Psorophora confinnis</i> (Diptera: Culicidae) Complex in North and South America. <i>Journal of Medical Entomology</i> , 2015, 52, 907-917.	1.8	2
70	TWO NOVEL SINGLE NUCLEOTIDE POLYMORPHISMS IN THE VOLTAGE-GATED SODIUM CHANNEL GENE IDENTIFIED IN <i>AEDES AEGYPTI</i> MOSQUITOES FROM FLORIDA. <i>Journal of the Florida Mosquito Control Association</i> , 2022, 69, .	0.3	2
71	Multiple Novel Clades of Anopheline Mosquitoes Caught Outdoors in Northern Zambia. <i>Frontiers in Tropical Diseases</i> , 2021, 2, .	1.4	2
72	Complete mitogenome sequence of <i>Anopheles coustani</i> from São Tomé island. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3376-3378.	0.4	1

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73	Genetically Modified Mosquitoes. <i>Edis</i> , 2021, 2021, .	0.1	1
74	Grammar Structure and the Dynamics of Language Evolution. <i>Lecture Notes in Computer Science</i> , 2005, , 624-633.	1.3	1
75	Supplementary data for: High Degree of Single Nucleotide Polymorphisms in California <i>Culex pipiens</i> (Diptera: Culicidae) sensu lato. <i>Journal of Medical Entomology</i> , 2012, 49, .	1.8	0
76	The Population Genomics of <i>Aedes aegypti</i> : Progress and Prospects. <i>Population Genomics</i> , 2021, , .	0.5	0
77	The Population Genomics of <i>Anopheles gambiae</i> Species Complex: Progress and Prospects. <i>Population Genomics</i> , 2021, , 1.	0.5	0
78	Perfect association between spatial swarm segregation and the X-chromosome speciation island in hybridizing <i>Anopheles coluzzii</i> and <i>Anopheles gambiae</i> populations. <i>Scientific Reports</i> , 2022, 12, .	3.3	0