

1. 3. Hung SHW, Yu MY, Liu CH, Huang TC, Peng JH, Jang NY, (Kuo CH), Yang YL, Ho YN, Chiang EPI, Hwang HH, Huang CC*. [Endophytic biostimulant pyrroloquinoline quinone enhances banana growth and primes immunity against Fusarium wilt](#). Physiologia Plantarum. 178(3), e70913, 2026-04. [\[JCR\]](#) [\[WOS\]](#)
2. Pei SC, Li NP, Li TT, Yang YC, Hung TH*, (Kuo CH)*. [Comparative genomics of a poinsettia-associated phytoplasma and functional validation of its SAP11-homologous effectors that induce plant branching](#). Microbial Genomics. 12(3), 001675, 2026-03. [\[JCR\]](#) [\[WOS\]](#)
3. Huang J, Huyen TNBV, Liu X, Mitra S, Yu M, Zeng Q, Sundin GW, Cox KD, Förster H, Adaskaveg JE, (Kuo CH), Yuan X, Cuhel RL, Yang CH*. [RejuAgro A as an antimicrobial for fire blight control of pome fruits and beyond](#). Nature Communications. 17(1), 2282, 2026-03. [\[JCR\]](#) [\[WOS\]](#)
4. Pei SC, Hsu YY, Lee SK, Chen CY, Liu CT*, (Kuo CH)*. [Complete genome sequences of three Bradyrhizobium strains isolated from root nodules of peanut \(Arachis hypogaea\) cultivar Tainan Select No. 9 collected in Taiwan](#). Microbiology Resource Announcements. 15, e01413-25, 2026-02. [\[JCR\]](#) [\[WOS\]](#)
5. Liu MS, Huang TK, Wang YC, Wang SC, Wu CH, (Kuo CH), Lai EM*. [Floral stage optimization and immune evasion enhance Agrobacterium-mediated genome editing in Arabidopsis](#). New Phytologist. 249, 2125, 2026-02. [\[JCR\]](#) [\[WOS\]](#)
6. Lopez-Agudelo JC, Goh FJ, Tchabashvili S, Huang YS, Huang CY, Lee KT, Wang YC, Wu Y, Chang HX, (Kuo CH), Lai EM, Wu CH*. [Rhizobium rhizogenes A4-derived strains mediate hyper-efficient transient gene expression in Nicotiana benthamiana and other solanaceous plants](#). Plant Biotechnology Journal. 24, 131, 2026-01. [\[JCR\]](#) [\[WOS\]](#)
7. Yen HC, Huang FC, Chien PR, Wu CL, Chen LY, Ho CW, Song GZM, Lin WJ, Lin HJ, Huang CC, Hwang HH*, (Kuo CH)*. [Draft genome sequences of 12 Agrobacterium strains isolated from coastal plants in Taiwan](#). Microbiology Resource Announcements. 14(12), e01046-25, 2025-12. [\[JCR\]](#) [\[WOS\]](#)
8. Yen HC, Huang FC, Chien PR, Wu CL, Chen LY, Ho CW, Song GZM, Lin WJ, Lin HJ, Huang CC, Hwang HH*, (Kuo CH)*. [Draft genome sequences of seven](#)

- [endophytic bacterial strains isolated from the roots of coastal plants in Taiwan](#). Microbiology Resource Announcements. 14(11), e00964-25, 2025-11. [\[JCR\]](#) [\[WOS\]](#)
9. Hung SHW, Liu CH, Kuo CC, Huang CC*, (Kuo CH)*. [Complete genome sequence of *Bacillus velezensis* Tcba05, a biocontrol strain for multiple plant diseases in Taiwan](#). Microbiology Resource Announcements. 14(10), e00212-25, 2025-10. [\[JCR\]](#) [\[WOS\]](#)
 10. Nishino T, Moriyama M*, Mukai H, Tanahashi M, Hosokawa T, Chang HY, Tachikawa S, Nikoh N, Koga R, (Kuo CH), Fukatsu T*. [Defensive fungal symbiosis on insect hindlegs](#). Science. 390(6770), 279-283, 2025-10. [\[JCR\]](#) [\[WOS\]](#)
 11. Chiu YC, Lin YC, Pao SH, Chen YK, Liao PQ, Mejia HM, Sheue CR, (Kuo CH)*, Yang JY*. [Comprehensive genomic and functional characterization of a phytoplasma associated with root retardation, early bolting, witches'-broom, and phyllody in daikon \(*Raphanus sativus* L.\)](#). Frontiers in Microbiology. 16, 1654928, 2025-09. [\[JCR\]](#) [\[WOS\]](#)
 12. Mijatović Scouten J, Hsieh SC, Sung LK, Wen YHV, (Kuo CH), Lai EM, Chang JH*. [Function, Evolution, and Ecology of Type VI Secretion Systems of Plant-Associated Bacteria](#). Annual Review of Phytopathology. 63(1), 333-356, 2025-09. [\[JCR\]](#) [\[WOS\]](#)
 13. Wu Y, Chang HY, Wu CH, Lai EM*, (Kuo CH)*. [Comparative transcriptomics reveals context- and strain-specific regulatory programmes of *Agrobacterium* during plant colonization](#). Microbial Genomics. 11(8), 001485, 2025-08. [\[JCR\]](#) [\[WOS\]](#)
 14. Chen CNN, Lin KM, Lin YC, Chang HY, Yong TC, Chiu YF, (Kuo CH)*, Chu HA*. [Comparative genomic analysis of a novel heat-tolerant and euryhaline strain of unicellular marine cyanobacterium *Cyanobacterium* sp. DS4 from a high-temperature lagoon](#). BMC Microbiology. 25(1), 279, 2025-05. [\[JCR\]](#) [\[WOS\]](#)
 15. Seruga Music M*, Polak B, Drčelić M, Pei SC, (Kuo CH)*. [Sequencing and comparative analyses of 'Candidatus *Phytoplasma solani*' genomes reveal diversity of effectors and potential mobile units](#). Microbial Genomics. 11(4), 001401, 2025-04. [\[JCR\]](#) [\[WOS\]](#)
 16. Yan XH, Pei SC, Yen HC, Blanchard A, Sirand-Pugnet P, Baby V, Gasparich

- GE, (Kuo CH)*. [Delineating bacterial genera based on gene content analysis: a case study of the Mycoplasmatales–Entomoplasmatales clade within the class Mollicutes](#). Microbial Genomics. 10(11), 001321, 2024-11. [[JCR](#)] [[WOS](#)]
17. Gasparich GE*, (Kuo CH), Manso-Silván L, Blanchard A, Balish MF. [International Committee on Systematics of Prokaryotes Subcommittee on the Taxonomy of Mollicutes: minutes of the closed meeting, 7 July 2024, Gran Canaria, Spain](#). International Journal of Systematic and Evolutionary Microbiology. 74, 006576, 2024-11. [[JCR](#)] [[WOS](#)]
18. Chang HY, Yen HC, Chu HA, (Kuo CH)*. [Population genomics of a thermophilic cyanobacterium revealed divergence at subspecies level and possible adaptation genes](#). BOTANICAL STUDIES. 65, 35, 2024-11. [[JCR](#)] [[WOS](#)]
19. Fukatsu T*, Kakizawa S, Harumoto T, Sugio A, (Kuo CH). [Editorial: Spiroplasma, Mycoplasma, Phytoplasma, and other genome-reduced and wall-less mollicutes: their genetics, genomics, mechanics, interactions and symbiosis with insects, other animals and plants](#). Frontiers in Microbiology. 15, 1477536, 2024-08. [[JCR](#)] [[WOS](#)]
20. Yen HC, Wang SC, Chen WM, Lai EM*, (Kuo CH)*. [Complete genome sequence of Sphingomonas sp. strain R1, a bacterium isolated from tomato \(Solanum lycopersicum\)](#). Microbiology Resource Announcements. 13, e00242-24, 2024-07. [[JCR](#)] [[WOS](#)]
21. Yao RB, Yan XH, Yen HC, Lee S, Chu CC, Hong CF*, (Kuo CH)*. [Complete genome sequence of Agrobacterium pusense Bbcg2-2, a strain isolated from blueberry crown gall in Taiwan](#). Microbiology Resource Announcements. 13, e01083-23, 2024-02. [[JCR](#)] [[WOS](#)]
22. Li NP, Yan XH, Pei SC, Hung TH, Chang TC, Bai QZ, Tai CF*, (Kuo CH)*. [Complete genome sequence of Candidatus Phytoplasma australasiaticum WF GM2021, a plant pathogen associated with soybean witches' broom disease in Taiwan](#). Microbiology Resource Announcements. 13, e00993-23, 2024-02. [[JCR](#)] [[WOS](#)]
23. Hung SHW, Yeh PH, Huang TC, Huang SY, Wu IC, Liu CH, Lin YH, Chien PR, Huang FC, Ho YN, (Kuo CH), Hwang HH, Chiang EPI, Huang CC*. [A cyclic](#)

- [dipeptide for salinity stress alleviation and the trophic flexibility of endophyte provide insights into saltmarsh plant–microbe interactions](#). ISME Communications. 4(1), ycae041, 2024-01. [\[JCR\]](#) [\[WOS\]](#)
24. Czajkowski R*, Zhu L, (Kuo CH), Li Z. [Editorial: Insights in microbial symbioses: 2022/2023](#). Frontiers in Microbiology. 15, 1367452, 2024-01. [\[JCR\]](#) [\[WOS\]](#)
25. Fernández FD*, Yan XH, (Kuo CH), Marcone C, Conci LR. [Improving the Comprehension of Pathogenicity and Phylogeny in 'Candidatus Phytoplasma meliae' through Genome Characterization](#). Microorganisms. 12(1), 142, 2024-01. [\[JCR\]](#) [\[WOS\]](#)
26. Hung SHW, Wu IC, Huang CC*, (Kuo CH)*. [Complete genome sequence of Erythrobacteraceae bacterium WH01K, a strain isolated from corals \(Acropora sp.\) in Taiwan](#). Microbiology Resource Announcements. 12(12), e00830-23, 2023-12. [\[JCR\]](#) [\[WOS\]](#)
27. Salazar SRB, Santos MNM*, Palaad J, Yen HC, Castellano JL, Pena LD, Amar EC, Lai EM, (Kuo CH)*. [Complete genome sequence of Vibrio parahaemolyticus strain PH1273, isolated from aquacultured shrimp in the Philippines](#). Microbiology Resource Announcements. 12(11), e00532-23, 2023-11. [\[JCR\]](#) [\[WOS\]](#)
28. Cho ST, Chen AP, Chou SJ, Yan XH, Lin CP*, (Kuo CH)*. [Complete genome sequence of "Candidatus Phytoplasma cynodontis" GY2015, a plant pathogen associated with Bermuda grass white leaf disease in Taiwan](#). Microbiology Resource Announcements. 12(10), e00457-23, 2023-10. [\[JCR\]](#) [\[WOS\]](#)
29. Pei SC, Chen AP, Chou SJ, Hung TH*, (Kuo CH)*. [Complete genome sequence of "Candidatus Phytoplasma pruni" PR2021, an uncultivated bacterium associated with poinsettia \(Euphorbia pulcherrima\)](#). Microbiology Resource Announcements. 12(9), e00443-23, 2023-09. [\[JCR\]](#) [\[WOS\]](#)
30. Weisberg AJ*, Wu Y, Chang JH, Lai EM, (Kuo CH)*. [Virulence and ecology of agrobacteria in the context of evolutionary genomics](#). Annual Review of Phytopathology. 61(1), 1-23, 2023-09. [\[JCR\]](#) [\[WOS\]](#)
31. Li Y, Yan XH, Liu Y, Pei SC, (Kuo CH)*, Huang W*. [Complete genome](#)

[sequence of "Candidatus Phytoplasma aurantifolia" TB2022, a plant pathogen associated with sweet potato little leaf disease in China.](#)

Microbiology Resource Announcements. 12(7), e00308-23, 2023-07. [\[JCR\]](#) [\[WOS\]](#)

32. Yan XH, Lin J, Liu Y, Huang P, Liu J, Hu Q, Li Y#, Pei SC, Huang W*, (Kuo CH)*. [Complete genome sequence of "Candidatus Phytoplasma asteris" QS2022, a plant pathogen associated with lettuce chlorotic leaf rot disease in China.](#) Microbiology Resource Announcements. 12(6), e00306-23, 2023-06. [\[JCR\]](#) [\[WOS\]](#)
33. Wang SC, Chen AP, Chou SJ, (Kuo CH)*, Lai EM*. [Soil Inoculation and Blocker-Mediated Sequencing Show Effects of the Antibacterial T6SS on Agrobacterial Tumorigenesis and Gallobiome.](#) mBio. 14(2), e00177-23, 2023-04. [\[JCR\]](#) [\[WOS\]](#)
34. Hung SHW, Huang TC, Lai YC, Wu IC, Liu CH, Huarng YF, Hwang HH, Chiang EPI, (Kuo CH), Huang CC*. [Endophytic biostimulants for smart agriculture: Burkholderia seminalis 869T2 benefits heading leafy vegetables in-field management in Taiwan.](#) AGRONOMY-BASEL. 13(4), 967, 2023-03. [\[JCR\]](#) [\[WOS\]](#)
35. Liu YH, Tseng TS, Wu CR, Cho ST, (Kuo CH), Huang XJ, Cheng JY, Hsu KH, Lin KF, Liu CC, Yeh CH*. [Rice OsHsp16.9 A interacts with OsHsp101 to confer thermotolerance.](#) Plant Science. 330, 111634, 2023-02. [\[JCR\]](#) [\[WOS\]](#)
36. Lee SK, Chiang MS, Hseu ZY, (Kuo CH)*, Liu CT*. [A photosynthetic bacterial inoculant exerts beneficial effects on the yield and quality of tomato and affects bacterial community structure in an organic field.](#) Frontiers in Microbiology. 13, 959080, 2022-08. [\[JCR\]](#) [\[WOS\]](#)
37. Cheng YI, Lin YC, Leu JY, (Kuo CH)*, Chu HA*. [Comparative analysis reveals distinctive genomic features of Taiwan hot-spring cyanobacterium Thermosynechococcus sp. TA-1.](#) Frontiers in Microbiology. 13, 932840, 2022-08. [\[JCR\]](#) [\[WOS\]](#)
38. Hung SHW, Chiu MC, Huang CC*, (Kuo CH)*. [Complete genome sequence of Curtobacterium sp. C1, a beneficial endophyte with the potential for in-plant salinity stress alleviation.](#) MOLECULAR PLANT-MICROBE INTERACTIONS. online, online, 2022-08. [\[JCR\]](#) [\[WOS\]](#)

39. Bertaccini A*, Arocha-Rosete Y, Contaldo N, Duduk B, Fiore N, Montano HG, Kube M, (Kuo CH), Martini M, Oshima K, Quaglino F, Schneider B, Wei W, Zamorano A. [Revision of the 'Candidatus Phytoplasma' species description guidelines](#). International Journal of Systematic and Evolutionary Microbiology. 72(4), 005353, 2022-04. [\[JCR\]](#) [\[WOS\]](#)
40. Huang CT, Cho ST, Lin YC, Tan CM, Chiu YC, Yang JY*, (Kuo CH)*. [Comparative genome analysis of 'Candidatus Phytoplasma luffae' reveals the influential roles of potential mobile units in phytoplasma evolution](#). Frontiers in Microbiology. 13, 773608, 2022-02. [\[JCR\]](#) [\[WOS\]](#)
41. Chou L, Lin YC, Haryono M, Santos MNM, Cho ST, Weisberg AJ, Wu CF, Chang JH, Lai EM, (Kuo CH)*. [Modular evolution of secretion systems and virulence plasmids in a bacterial species complex](#). BMC Biology. 20, 16, 2022-01. [\[JCR\]](#) [\[WOS\]](#)
42. Castillo AI, Tsai CW, Su CC, Weng LW, Lin YC, Cho ST, Almeida RPP, (Kuo CH)*. [Genetic differentiation of Xylella fastidiosa following the introduction into Taiwan](#). Microbial Genomics. 7(12), 000727, 2021-12. [\[JCR\]](#) [\[WOS\]](#)
43. Tan CM, Lin YC, Li JR, Chien YY, Wang CJ, Chou L, Wang CW, Chiu YC, (Kuo CH)*, JY Yang*. [Accelerating complete phytoplasma genome assembly by immunoprecipitation-based enrichment and MinION-based DNA sequencing for comparative analyses](#). Frontiers in Microbiology. 12, 766221, 2021-11. [\[JCR\]](#) [\[WOS\]](#)
44. (Kuo CH), Huang PY, Sheu SY, Sheu DS, Jheng LC, Chen WM*. [Zophobihabitans entericus gen. nov., sp. nov., a new member of the family Orbaceae isolated from the gut of a superworm Zophobas morio](#). International Journal of Systematic and Evolutionary Microbiology. 71, 005081, 2021-11. [\[JCR\]](#) [\[WOS\]](#)
45. Wu CF, Weisberg AJ, Davis EW, Chou L, Khan S, Lai EM, (Kuo CH), Chang JH*. [Diversification of the Type VI Secretion System in Agrobacteria](#). mBio. 12, e01927-21, 2021-09. [\[JCR\]](#) [\[WOS\]](#)
46. Huang W, MacLean A, Sugio A, Maqbool A, Busscher M, Cho ST, Kamoun S, (Kuo CH), Immink RGH, Hogenhout SA*. [Parasitic modulation of host development by ubiquitin-independent protein degradation](#). Cell. 184, 5201-5214, 2021-09. [\[JCR\]](#) [\[WOS\]](#)

47. Hwang HH*, Huang FC, Chien PR, Hung SH, (Kuo CH), Deng WL, Chiang EPI, Huang CC*. [A plant endophytic bacterium, Burkholderia seminalis strain 869T2, promotes plant growth in Arabidopsis, pai tsai, Chinese amaranth, lettuces and other vegetables](#). Microorganisms. 9(8), 1703, 2021-08. [\[JCR\]](#) [\[WOS\]](#)
48. Weng LW, Lin YC, Su CC, Huang CT, Cho ST, Chen AP, Chou SJ, Tsai CW*, (Kuo CH)*. [Complete genome sequence of Xylella taiwanensis and comparative analysis of virulence gene content with Xylella fastidiosa](#). Frontiers in Microbiology. 12, 684092, 2021-05. [\[JCR\]](#) [\[WOS\]](#)
49. Cho ST, Zwolińska A, Huang W, Wouters RHM, Mugford ST, Hogenhout SA, (Kuo CH)*. [Complete genome sequence of 'Candidatus Phytoplasma asteris' RP166, a plant pathogen associated with the rapeseed phyllody disease in Poland](#). Microbiology Resource Announcements. 9(35), 2020-08. [\[JCR\]](#) [\[WOS\]](#)
50. Cho ST, Kung HJ, Huang W, Hogenhout SA, (Kuo CH)*. [Species boundaries and molecular markers for the classification of 16Srl phytoplasmas inferred by genome analysis](#). Frontiers in Microbiology. 11, 2020-07. [\[JCR\]](#) [\[WOS\]](#)
51. Weisberg AJ, Davis EW, Tabima J, Belcher MS, Miller M, (Kuo CH), Loper JE, Grünwald NJ, Putnam ML, Chang JH*. [Unexpected conservation and global transmission of agrobacterial virulence plasmids](#). Science. 368(6495), 1080-, 2020-06. [\[JCR\]](#) [\[WOS\]](#)
52. Cheng YI, Chou L, Chiu YF, Hsueh HT, (Kuo CH)*, Chu HA*. [Comparative genomic analysis of a novel strain of Taiwan hot-spring cyanobacterium Thermosynechococcus sp. CL-1](#). Frontiers in Microbiology. 11, 82, 2020-01. [\[JCR\]](#) [\[WOS\]](#)
53. Santos MNM, Cho ST, Wu CF, Chang CJ, (Kuo CH), Lai EM*. [Redundancy and Specificity of Type VI Secretion vgrG Loci in Antibacterial Activity of Agrobacterium tumefaciens 1D1609 Strain](#). Frontiers in Microbiology. 10, 3004, 2020-01. [\[JCR\]](#) [\[WOS\]](#)
54. Balish M, Bertaccini A, Blanchard A, Brown DR*, Browning G, Chalker V, Frey J, Gasparich G, Hoelzle L, Knight T, Knox C, (Kuo CH), Manso-Silván L, May M, Pollack JD, Ramirez AS, Spergser J, Taylor-Robinson D, Volokhov D, Zhao Y. [Recommended rejection of the names Malacoplasma gen. nov.,](#)

- [Mesomycoplasma gen. nov., Metamycoplasma gen. nov., Metamycoplasmataceae fam. nov., Mycoplasmoidaceae fam. nov., Mycoplasmoidales ord. nov., Mycoplasmoides gen. nov., Mycoplasmopsis gen. nov. \[Gupta, Sawnani, Adeolu, Alnajjar and Oren 2018\] and all proposed species comb. nov. placed therein](#). International Journal of Systematic and Evolutionary Microbiology. 69(11), 3650-3653, 2019-11. [\[JCR\]](#) [\[WOS\]](#)
55. Acheampong G, Owusu M, Owusu-Ofori A, Osei I, Sarpong N, Sylverken A, Kung HJ, Cho ST, (Kuo CH), Park SE, Marks F, Adu-Sarkodie Y, Owusu-Dabo E*. [Chromosomal and plasmid-mediated fluoroquinolone resistance in human Salmonella enterica infection in Ghana](#). BMC Infectious Diseases. 19(1), 2019-10. [\[JCR\]](#) [\[WOS\]](#)
 56. Gasparich GE*, (Kuo CH). [Genome analysis-based union of the genus Mesoplasma with the genus Entomoplasma](#). International Journal of Systematic and Evolutionary Microbiology. 69(9), 2735-2738, 2019-09. [\[JCR\]](#) [\[WOS\]](#)
 57. Cho ST, Lin CP, (Kuo CH*). [Genomic Characterization of the Periwinkle Leaf Yellowing \(PLY\) Phytoplasmas in Taiwan](#). Frontiers in Microbiology. 10, 2194, 2019-09. [\[JCR\]](#) [\[WOS\]](#)
 58. Pecher P, Moro G, Canale MC, Capdevielle S, Singh A, MacLean A, Sugio A, (Kuo CH), Lopes JRS, Hogenhout SA*. [Phytoplasma SAP11 effector destabilization of TCP transcription factors differentially impact development and defence of Arabidopsis versus maize](#). PLOS Pathogens. 15(9), e1008035, 2019-09. [\[JCR\]](#) [\[WOS\]](#)
 59. Wu CF, Santos MNM, Cho ST, Chang HH, Tsai YM, Smith DA, (Kuo CH*), Chang JH*, Lai EM*. [Plant-Pathogenic Agrobacterium tumefaciens Strains Have Diverse Type VI Effector-Immunity Pairs and Vary in In-Planta Competitiveness](#). Molecular Plant-Microbe Interactions. 32(8), 961-971, 2019-08. [\[JCR\]](#) [\[WOS\]](#)
 60. Haryono M, Cho ST, Fang MJ, Chen AP, Chou SJ, Lai EM, (Kuo CH*). [Differentiations in Gene Content and Expression Response to Virulence Induction Between Two Agrobacterium Strains](#). Frontiers in Microbiology. 10, 1554, 2019-07. [\[JCR\]](#) [\[WOS\]](#)
 61. Chou L, Lee TY, Tsai YM, (Kuo CH*). [Complete Genome Sequence of](#)

- [Spiroplasma alleghenense PLHS-1T \(ATCC 51752\), a Bacterium Isolated from Scorpion Fly \(Panorpa helena\)](#). Microbiology Resource Announcements. 8(17), e00317-19, 2019-04. [\[JCR\]](#) [\[WOS\]](#)
62. Seruga Music M*, Samarzija I, Hogenhout SA*, Haryono M, Cho ST, (Kuo CH*). [The genome of 'Candidatus Phytoplasma solani' strain SA-1 is highly dynamic and prone to adopting foreign sequences](#). Systematic and Applied Microbiology. 42(2), 117-127, 2019-03. [\[JCR\]](#) [\[WOS\]](#)
63. Haryono M, Tsai YM, Lin CT, Huang FC, Ye YC, Deng WL, Hwang HH*, (Kuo CH*). [Presence of an Agrobacterium-type tumor-inducing plasmid in Neorhizobium sp. NCHU2750 and the link to phytopathogenicity](#). Genome Biology and Evolution. 10(12),3188-3195, 2018-12. [\[JCR\]](#) [\[WOS\]](#)
64. Lo WS, Gasparich GE, (Kuo CH*). [Convergent evolution among ruminant-pathogenic Mycoplasma involved extensive gene content changes](#). Genome Biology and Evolution. 10(8), 2130-2139, 2018-08. [\[JCR\]](#) [\[WOS\]](#)
65. Perry BW, Card DC, McGlothlin JW, Pasquesi GIM, Adams RH, Schield DR, Hales NR, Corbin AB, Demuth JP, Hoffmann FG, Vandewege MW, Schott RK, Bhattacharyya N, Chang BSW, Casewell NR, Whiteley G, Reyes-Velasco J, Mackessy SP, Gamble T, Storey KB, Biggar KK, Passow CN, (Kuo CH), McGaugh SE, Bronikowski AM, de Koning J, Edwards SV, Pfrender ME, Minx P, Brodie ED, Brodie ED, Warren WC, Castoe TA*. [Molecular adaptations for sensing and securing prey and insight into amniote genome diversity from the garter snake genome](#). Genome Biology and Evolution. 10(8), 2110-2129, 2018-08. [\[JCR\]](#) [\[WOS\]](#)
66. Lo KJ, Lin SS, Lu CW, (Kuo CH*), Liu CT*. [Whole-genome sequencing and comparative analysis of two plant-associated strains of Rhodopseudomonas palustris \(PS3 and YSC3\)](#). Scientific Reports. 8(1), 12769, 2018-08. [\[JCR\]](#) [\[WOS\]](#)
67. Cho ST, Tsai YM, Chen CY*, (Kuo CH*). [Draft Genome Sequence of Vibrio vulnificus 86573B, a Bacterium Isolated from Diseased Tilapia in Taiwan](#). Microbiology Resource Announcements. 7(1), e00813-18, 2018-07. [\[JCR\]](#) [\[WOS\]](#)
68. Tsai YM, Chang A, (Kuo CH)*. [Horizontal gene acquisitions contributed to genome expansion in insect-symbiotic Spiroplasma clarkii](#). Genome Biology

- and Evolution. 10(6), 1526-1532, 2018-06. [\[JCR\]](#) [\[WOS\]](#)
69. Tsai YM, Lo WS, Wu PS, Cho ST, (Kuo CH*). [Complete genome sequence of *Spiroplasma monobiae* MQ-1T \(ATCC 33825\), a bacterium isolated from the vespid wasp \(*Monobia quadridens*\)](#). Genome Announcements. 6(18), e00347-18, 2018-05. [\[JCR\]](#) [\[WOS\]](#)
 70. Cho ST, Haryono M, Chang HH, Santos MNM, Lai EM, (Kuo CH*). [Complete genome sequence of *Agrobacterium tumefaciens* 1D1609](#). Genome Announcements. 6(16), e00253-18, 2018-04. [\[JCR\]](#) [\[WOS\]](#)
 71. Tsai YM, Wu PS, Lo WS, (Kuo CH*). [Complete genome sequence of *Spiroplasma floricola* 23-6T \(ATCC 29989\), a bacterium isolated from a tulip tree \(*Liriodendron tulipifera* L.\)](#). Genome Announcements. 6(16), e00302-18, 2018-04. [\[JCR\]](#) [\[WOS\]](#)
 72. Owusu M, Marfo KS, Acheampong G, Arthur A, Sarpong N, Im J, Mogeni OD, Annan A, Chiang HY, (Kuo CH), Park SE, Marks F, Owusu-Dabo E*, Adu-Sarkodie Y. [Gonococcal sepsis in a 32-year-old female: a case report](#). BMC Research Notes. 11(1), 253, 2018-04. [\[JCR\]](#)
 73. Cittì C*, Dordet-Frisoni E, Nouvel LX, (Kuo CH), Baranowski E. [Horizontal gene transfers in mycoplasmas \(Mollicutes\)](#). Current Issues in Molecular Biology. 29, 3-22, 2018-04. [\[JCR\]](#) [\[WOS\]](#)
 74. Cho ST, Chen CL, Yang Y, Wang TF*, (Kuo CH*). [Draft genome sequence of *Burkholderia* sp. strain WAC0059, a bacterium isolated from the medicinal fungus *Antrodia cinnamomea*](#). Genome Announcements. 6(6), e00027-18, 2018-02. [\[JCR\]](#) [\[WOS\]](#)
 75. Lo WS, (Kuo CH*). [Horizontal acquisition and transcriptional integration of novel genes in mosquito-associated *Spiroplasma*](#). Genome Biology and Evolution. 9(12), 3246-3259, 2017-12. [\[JCR\]](#) [\[WOS\]](#)
 76. Tsai YM, Lo WS, (Kuo CH*). [Complete genome sequence of *Spiroplasma corruscae* EC-1T \(DSM 19793\), a bacterium isolated from a lampyrid beetle \(*Ellychnia corrusca*\)](#). Genome Announcements. 5(37), e00964-17, 2017-09. [\[JCR\]](#) [\[WOS\]](#)
 77. Huang YY, Cho ST, Haryono M, (Kuo CH*). [Complete chloroplast genome sequence of common bermudagrass \(*Cynodon dactylon* \(L.\) Pers.\) and comparative analysis within the family Poaceae](#). PLOS ONE. 12(6),

- e0179055, 2017-06. [\[JCR\]](#) [\[WOS\]](#)
78. Orlovskis Z, Canale MC, Haryono M, Lopes JR, (Kuo CH*), Hogenhout SA*. [A few sequence polymorphisms among isolates of Maize bushy stunt phytoplasma associate with organ proliferation symptoms of infected maize plants](#). Annals of Botany. 119, 869-884, 2017-03. [\[JCR\]](#) [\[WOS\]](#)
79. Haryono M, Lo WS, Gasparich GE, (Kuo CH*). [Complete Genome Sequence of Spiroplasma sp. NBRC 100390](#). Genome Announcements. 5(10), 2017-03. [\[JCR\]](#) [\[WOS\]](#)
80. Owusu M, Owusu-Dabo E*, Acheampong G, Osei I, Amuasi J, Sarpong N, Annan A, Chiang HY, (Kuo CH), Park SE, Marks F, Adu-Sarkodie Y. [Pseudomonas oryzihabitans sepsis in a 1-year-old child with multiple skin rashes: a case report](#). Journal of Medical Case Reports. 11, 77, 2017-03. [\[JCR\]](#)
81. Lo WS, Haryono M, Gasparich GE, (Kuo CH*). [Complete Genome Sequence of Spiroplasma sp. TU-14](#). Genome Announcements. 5(2), 1465, 2017-01. [\[JCR\]](#) [\[WOS\]](#)
82. Shen WY, Lo WS, Lai YC, (Kuo CH)*. [Complete genome sequence of Spiroplasma helicoides TABS-2T \(DSM 22551\), a bacterium isolated from a horse fly \(Tabanus abactor\)](#). Genome Announcements. 4(5), e01201-16, 2016-10. [\[JCR\]](#) [\[WOS\]](#)
83. Lo WS, Gasparich GE, (Kuo CH)*. [Complete genome sequence of Spiroplasma turonicum Tab4cT, a bacterium isolated from horse flies \(Haematopota sp.\)](#). Genome Announcements. 4(5), e01010-16, 2016-09. [\[JCR\]](#) [\[WOS\]](#)
84. Lo WS, Huang YY, (Kuo CH)*. [Winding paths to simplicity: genome evolution in facultative insect symbionts](#). FEMS Microbiology Reviews. 40(6), 855-874, 2016-08. [\[JCR\]](#) [\[WOS\]](#)
85. Bondage DD, Lin JS, Ma LS, (Kuo CH), Lai EM*. [VgrG C terminus confers the type VI effector transport specificity and is required for binding with PAAR and adaptor-effector complex](#). Proceedings of the National Academy of Sciences of the United States of America. 113(27), E3931-E3940, 2016-07. [\[JCR\]](#) [\[WOS\]](#)
86. Wu WL, Lai SJ, Yang JT, Chern J, Liang SY, Chou CC, (Kuo CH), Lai MC*, Wu

- SH*. [Phosphoproteomic analysis of Methanohalophilus portucalensis FDF1\(T\) identified the role of protein phosphorylation in methanogenesis and osmoregulation](#). Scientific Reports. 6, 29013, 2016-06. [JCR] [WOS]
87. Chang CL, Chung CY, (Kuo CH), Kuo TF, Yang CW*, Yang WC*. [Beneficial Effect of Bidens pilosa on Body Weight Gain, Food Conversion Ratio, Gut Bacteria and Coccidiosis in Chickens](#). PLOS ONE. 11(1), e0146141, 2016-01. [JCR] [WOS]
88. Chang SH, Cho ST, Chen CL, Yang JY*, (Kuo CH)*. [Draft genome sequence of a 16SrII-A subgroup phytoplasma associated with purple coneflower \(Echinacea purpurea\) witches' broom disease in Taiwan](#). Genome Announcements. 3(6), 2015-11. [JCR]
89. Lo WS, Liu PY, (Kuo CH)*. [Complete Genome Sequence of Spiroplasma cantharicola CC-1T \(DSM 21588\), a Bacterium Isolated from Soldier Beetle \(Cantharis carolinus\)](#). Genome Announcements. 3(5), 2015-10. [JCR]
90. Lo WS, Lai YC, Lien YW, Wang TH, (Kuo CH)*. [Complete genome sequence of Spiroplasma litorale TN-1T \(DSM 21781\), a bacterium isolated from a green-eyed horsefly \(Tabanus nigrovittatus\)](#). Genome Announcements. 3(5), e01116-15, 2015-10. [JCR]
91. Cho ST, Chang HH, Egamberdieva D, Kamilova F, Lugtenberg B, (Kuo CH)*. [Genome analysis of Pseudomonas fluorescens PCL1751: a rhizobacterium that controls root diseases and alleviates salt stress for its plant host](#). PLOS ONE. 10(10), e0140231, 2015-10. [JCR] [WOS]
92. Lo WS, Gasparich GE, (Kuo CH)*. [Found and lost: the fates of horizontally acquired genes in arthropod-symbiotic Spiroplasma](#). Genome Biology and Evolution. 7, 2458-2472, 2015-08. [JCR] [WOS]
93. Huang YY, Cho ST, Lo WS, Wang YC, Lai EM, (Kuo CH)*. [Complete genome sequence of Agrobacterium tumefaciens Ach5](#). Genome Announcements. 3(3), pii: e00570-15, 2015-06. [JCR]
94. (Kuo CH)*. [Scrambled and not-so-tiny genomes of fungal endosymbionts](#). Proceedings of the National Academy of Sciences of the United States of America. 112, 7622-7623, 2015-06. [JCR] [WOS]
95. McGaugh SE*, Bronikowski AM*, (Kuo CH)*, Reding DM, Addis EA, Flagel LE, Janzen FJ, Schwartz TS*. [Rapid molecular evolution across amniotes of the](#)

- [IIS/TOR network](#). Proceedings of the National Academy of Sciences of the United States of America. 122, 7055-7060, 2015-05. [[JCR](#)] [[WOS](#)]
96. Paredes JC, Herren JK, Schupfer F, Marin R, Claverol S, (Kuo CH), Lemaitre B*, Beven L*. [Genome sequence of the *Drosophila melanogaster* male-killing *Spiroplasma* strain MSRO endosymbiont](#). mBio. 6(2), pii: e02437-14, 2015-03. [[JCR](#)] [[WOS](#)]
97. Liu AC, Chou CY, Chen LL, (Kuo CH)*. [Bacterial community dynamics in a swine wastewater anaerobic reactor revealed by 16S rDNA sequence analysis](#). Journal of Biotechnology. 194, 124-131, 2015-01. [[JCR](#)] [[WOS](#)]
98. Chang HH, Cho ST, Canale MC, Mugford ST, Lopes JR, Hogenhout SA, (Kuo CH)*. [Complete Genome Sequence of "Candidatus *Sulcia muelleri*" ML, an Obligate Nutritional Symbiont of Maize Leafhopper \(*Dalbulus maidis*\)](#). Genome Announcements. 3(1), pii: e01483-14, 2015-01. [[JCR](#)]
99. Su HJ, Hogenhout SA, Al-Sadi AM, (Kuo CH)*. [Complete chloroplast genome sequence of Omani lime \(*Citrus aurantiifolia*\) and comparative analysis within the rosids](#). PLoS ONE. 9(11), e113049, 2014-11. [[JCR](#)] [[WOS](#)]
100. Lo WS, Chen H, Chen CY, (Kuo CH)*. [Complete genome sequence of *Vibrio vulnificus* 93U204, a bacterium isolated from diseased tilapia in Taiwan](#). Genome Announcements. 2(5), e01005-14, 2014-10. [[JCR](#)]
101. Radjacommaré R, Usharani R, (Kuo CH), Fu H*. [Distinct phylogenetic relationships and biochemical properties of *Arabidopsis* ovarian tumor-related deubiquitinases support their functional differentiation](#). Frontiers in Plant Science. 5, 84, 2014-03. [[JCR](#)] [[WOS](#)]
102. Ku C, Lo WS, (Kuo CH)*. [Molecular evolution of the actin-like MreB protein gene family in wall-less bacteria](#). Biochemical and Biophysical Research Communications. 446(4), 927-932, 2014-03. [[JCR](#)] [[WOS](#)]
103. Tung CH, Cheng YR, Lin CY, Ho JS, (Kuo CH), Yu JK*, Su YH*. [A new copepod with transformed body plan and unique phylogenetic position parasitic in the acorn worm *Ptychodera flava*](#). The Biological Bulletin. 226(1), 69-80, 2014-02. [[JCR](#)] [[WOS](#)]
104. Chang TH, Lo WS, Ku C, Chen LL, (Kuo CH)*. [Molecular evolution of the substrate utilization strategies and putative virulence factors in mosquito-associated *Spiroplasma* species](#). Genome Biology and Evolution. 6(3), 500-

- 509, 2014-02. [\[JCR\]](#) [\[WOS\]](#)
105. Ku C, Lo WS, Chen LL, (Kuo CH)*. [Complete genome sequence of *Spiroplasma apis* B31T \(ATCC 33834\), a bacterium associated with May disease of honeybees \(*Apis mellifera*\)](#). Genome Announcements. 2(1), e01151-13, 2014-01. [\[JCR\]](#)
106. Shelomi M, Lo WS, Kimsey LS, (Kuo CH)*. [Analysis of the gut microbiota of walking sticks \(*Phasmatodea*\)](#). BMC Research Notes. 6(1), 368, 2013-09. [\[JCR\]](#)
107. Ku C, Lo WS, (Kuo CH)*. [Horizontal transfer of potential mobile units in phytoplasmas](#). Mobile Genetic Elements. 3(5), e26145, 2013-08. [\[JCR\]](#)
108. Lo WS, Ku C, Chen LL, Chang TH, (Kuo CH)*. [Comparison of metabolic capacities and inference of gene content evolution in mosquito-associated *Spiroplasma diminutum* and *S. taiwanense*](#). Genome Biology and Evolution. 5(8), 1512-1523, 2013-07. [\[JCR\]](#) [\[WOS\]](#)
109. Kuo PA, (Kuo CH), Lai YK, Graumann PL, Tu J*. [Phosphate limitation induces the intergeneric inhibition of *Pseudomonas aeruginosa* by *Serratia marcescens* isolated from paper machines](#). FEMS Microbiology Ecology. 84(3), 577-587, 2013-06. [\[JCR\]](#) [\[WOS\]](#)
110. Ku C, Chung WC, Chen LL, (Kuo CH)*. [The Complete Plastid Genome Sequence of Madagascar Periwinkle \(*L. G. Don*: Plastid Genome Evolution, Molecular Marker Identification, and Phylogenetic Implications in Asterids](#). PLoS One. 8(6), e68518, 2013-06. [\[JCR\]](#) [\[WOS\]](#)
111. Ku C, Lo WS, Chen LL, (Kuo CH)*. [Complete genomes of two dipteran-associated spiroplasmas provided insights into the origin, dynamics, and impacts of viral invasion in *Spiroplasma*](#). Genome Biology and Evolution. 5(6), 1151-1164, 2013-05. [\[JCR\]](#) [\[WOS\]](#)
112. Chung WC, Chen LL, Lo WS, Lin CP, (Kuo CH)*. [Comparative analysis of the peanut witches'-broom phytoplasma genome reveals horizontal transfer of potential mobile units and effectors](#). PLoS One. 8(4), e62770, 2013-04. [\[JCR\]](#) [\[WOS\]](#)
113. Chung WC, Chen LL, Lo WS, Kuo PA, Tu J, (Kuo CH)*. [Complete Genome Sequence of *Serratia marcescens* WW4](#). Genome Announcements. 1(2), e0012613, 2013-04. [\[JCR\]](#)

114. Ku C, Hu JM, (Kuo CH)*. [Complete Plastid Genome Sequence of the Basal Asterid *Ardisia polysticta* Miq. and Comparative Analyses of Asterid Plastid Genomes](#). PLoS One. 8(4), e62548, 2013-04. [\[JCR\]](#) [\[WOS\]](#)
115. Lo WS, Chen LL, Chung WC, Gasparich GE, (Kuo CH)*. [Comparative genome analysis of *Spiroplasma melliferum* IPMB4A, a honeybee-associated bacterium](#). BMC Genomics. 14(1), 22, 2013-01. [\[JCR\]](#) [\[WOS\]](#)
116. Chen LL, Chung WC, Lin CP, (Kuo CH)*. [Comparative analysis of gene content evolution in phytoplasmas and mycoplasmas](#). PLoS One. 7(3), e34407, 2012-03. [\[JCR\]](#) [\[WOS\]](#)
117. McGaugh SE*, Bowden RM, (Kuo CH), Janzen FJ . [Field-measured heritability of the threshold for sex determination in a turtle with temperature dependent sex determination](#). Evolutionary Ecology Research. 13, 75-90, 2011. [\[JCR\]](#) [\[WOS\]](#)
118. Ochman H*, Worobey M, (Kuo CH), Ndjango JB, Peeters M, Hahn BH, Hugenholtz P. [Evolutionary relationships of wild hominids recapitulated by gut microbial communities](#). PLoS Biology. 8(11), e1000546, 2010. [\[JCR\]](#) [\[WOS\]](#)
119. Joseph SJ, Fernandez-Robledo JA, Gardner MJ, El-Sayed NM, (Kuo CH), Schott EJ, Wang H, Kissinger JC*, Vasta GR*. [The Alveolate *Perkinsus marinus*: biological insights from EST gene discovery](#). BMC Genomics. 11, 228, 2010. [\[JCR\]](#) [\[WOS\]](#)
120. (Kuo CH), Ochman H*. [The extinction dynamics of bacterial pseudogenes](#). PLoS Genetics. 6(8), e1001050, 2010. [\[JCR\]](#) [\[WOS\]](#)
121. (Kuo CH), Ochman H*. [Deletional bias across the three domains of life](#). Genome Biology and Evolution. 2009, 145-152, 2009. [\[JCR\]](#) [\[WOS\]](#)
122. (Kuo CH), Ochman H*. [Inferring clocks when lacking rocks: the variable rates of molecular evolution in bacteria](#). Biology Direct. 4, 35, 2009. [\[JCR\]](#) [\[WOS\]](#)
123. (Kuo CH), Moran NA, Ochman H*. [The consequences of genetic drift for bacterial genome complexity](#). Genome Research. 19(8), 1450-1454, 2009. [\[JCR\]](#) [\[WOS\]](#)
124. (Kuo CH), Ochman H*. [The fate of new bacterial genes](#). FEMS Microbiology Reviews. 33(1), 38-43, 2009. [\[JCR\]](#) [\[WOS\]](#)

125. (Kuo CH)*, Kissinger JC. [Consistent and contrasting properties of lineage-specific genes in the apicomplexan parasites Plasmodium and Theileria](#). BMC Evolutionary Biology. 8, 108, 2008. [[JCR](#)] [[WOS](#)]
126. (Kuo CH)*, Avise JC. [Does organismal pedigree impact the magnitude of topological congruence among gene trees for unlinked loci?](#). Genetica. 132(3), 219-225, 2008. [[JCR](#)] [[WOS](#)]
127. (Kuo CH)*, Wares JP, Kissinger JC. [The Apicomplexan whole-genome phylogeny: an analysis of incongruence among gene trees](#). Molecular Biology and Evolution. 25(12), 2689-2698, 2008. [[JCR](#)] [[WOS](#)]
128. (Kuo CH)*, Corby-Harris V, Promislow DE. [The unavoidable costs and unexpected benefits of parasitism: population and metapopulation models of parasite-mediated competition](#). Journal of Theoretical Biology. 250(2), 244-256, 2008. [[JCR](#)] [[WOS](#)]
129. (Kuo CH)*, Janzen FJ. [Longevity, overlapping generations, and conservation of turtle populations](#). Turtle and Tortoise Newsletter. 11, 18-23, 2007. [[JCR](#)]
130. (Kuo CH)*, Avise JC. [Phylogeographic breaks in low-dispersal species: the emergence of concordance across gene trees](#). Genetica. 124(2-3), 179-186, 2005. [[JCR](#)] [[WOS](#)]
131. (Kuo CH)*, Janzen FJ. [Genetic effects of a persistent bottleneck on a natural population of ornate box turtles \(Terrapene ornata\)](#). Conservation Genetics. 5, 425-437, 2004. [[JCR](#)] [[WOS](#)]
132. (Kuo CH)*, Janzen FJ. [BottleSim: a bottleneck simulation program for long-lived species with overlapping generations](#). Molecular Ecology Notes. 3, 669-673, 2003. [[JCR](#)] [[WOS](#)]