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## SASHA (ALEXANDER) S. MIKHEYEV

**Education** PhD, *University of Texas, Austin*, Integrative Biology, 2009  
MA, *University of Florida, Tallahassee*, Biology, 2002  
B.A., *Cornell University*, Neurobiology and Behavior, 2000

**Appointments** *Australian National University, Research School of Biology*

Senior Lecturer. 2018–.  
Group Leader (Future Fellow). 2017–.  
Associate Dean (International). 2019–.

*Okinawa Institute of Science and Technology*

Associate Professor (adjunct). 2017–.  
Associate Professor. 2015–2017.  
Assistant Professor. 2012–2015.  
Independent New Investigator. 2009–2012.

**Academic awards** *Future Fellowship (level 2)*, Australian Research Council, 2016–2020.  
*Postdoctoral fellowship in biological informatics (declined)*, U.S. National Science Foundation, 2009.  
*George H. Mitchell Award for Excellence in Graduate Research*, University of Texas, 2008, (the university's top graduate research award).  
*George Eickwort Award*, North American Section of the International Union for the Study of Social Insects, 2007, (for “exceptional research and scholarly activity by students in the field of social insect biology”).

**Editor** *Journal of Tropical Ecology*, Editor-in-Chief. 2019–.  
*Myrmecological News*, Subject Editor. 2013–.  
*PeerJ*, Academic Editor. 2015–.

**Research Grants & Fellowships** *Grants*  
*Australian National University*, Vice-Chancellor's Teaching Enhancement Grant, “Teaching quantitative skills to biologists using an interactive virtual environment”. AU\$ 9,989. 2019 (Project Lead, Co-applicants: Robert Lanfear, Teresa Neeman, Dan Noble and Eric Stone).  
*Ministry of Education, Culture, Sports, Science & Technology in Japan*, KAKENHI Fund for the Promotion of Joint International Research, “Using machine vision to understand causes and consequences of collective behavior in a honey bee society”. ¥13,130,000. 2016.

- Australian Research Council*, Discovery Project, “Resolving the role of DNA methylation in insect social evolution”. AU\$ 380,000. 2018 (Co-investigator with Luke Holman).
- Ministry of Education, Culture, Sports, Science & Technology in Japan*, KAKENHI Grant-in-Aid for Scientific Research (B), “Origins, spread and evolution of novel honey bee parasites and diseases”. ¥16,900,000. 2018.
- Ministry of Education, Culture, Sports, Science & Technology in Japan*, KAKENHI Young Scientist (A), “Genetic control of honeybee dance”. ¥16,640,000. 2016.
- Ministry of Education, Culture, Sports, Science & Technology in Japan*, KAKENHI (S), “Royal Epigenetics: Molecular basis of the extended longevity of reproductives in social insects”. ¥212,940,000. 2013 (co-PI with Kenji Matsuura (lead), Iuchi Yoshihito and Masaki Kamakura).
- Ministry of Education, Culture, Sports, Science & Technology in Japan*, KAKENHI Young Scientist (B), “Study of sex determination mechanisms in *Wasmannia auropunctata*”. ¥1,430,000. 2013.
- United States National Science Foundation*, Division Of Environmental Biology, “Phylogenetic research on the origin and evolution of agriculture in ants”. \$444,988.00. 2010 (Co-Pi with Ted Schultz (Principal Investigator), Charles Mitter, Ulrich Mueller and Natasha Mehdiabadi).

### *Fellowships*

- Australian Research Council*, Future Fellowship, “The origins, global spread and evolution of novel honey bee parasites”. AU\$ 809,000. 2018.
- Fulbright Foundation*, Fellowship to Cameroon and Gabon, “Impact of an invasive ant on mainland Africa”. 2005–2006.
- Environmental Protection Agency*, STAR pre-doctoral fellowship, “Worldwide traffic, impact and the evolutionary trajectory of invasive populations in the little fire ant *Wasmannia auropunctata*”. 2004–2005.

### Teaching *Australian National University*

- Ecology (BIOL2131), lecturer, 2019. (undergrad).
- Evolution (BIOL2114), lecturer, 2017 – 2019. (undergrad).

### *Okinawa Institute of Science and Technology Graduate University*

- Biology (Bo2), sole instructor, 2012 – 2015. (grad).
- Quantitative Evolutionary Comparative Biology Workshop, organizer, 2011, 2012. (grad).

### *University of Maryland University College*

- Introductory Biology Lab (BIOL 102), sole instructor, 2010. (undergrad).
- Introductory Biology (BIOL 101), sole instructor, 2010. (undergrad).

### Southwestern University

Genetics and Evolution (BIO50-122), sole instructor, 2007. (undergrad).

#### Students *Supervisor*

Carmen Emborski (PhD), “Transgenerational effects of ancestral dietary modifications: investigations of progeny response consistency and modes of transmission,” 2018

Claire Morandin (PhD), “To be or not to be a Queen – Caste-specific gene expression patterns in ants,” 2015

#### *External Examiner*

Thomas Dejaco (PhD, University of Innsbruck), “Integrative species delimitation in the alpine jumping-bristletail genus *Machilis latreille*, 1832,” 2014

#### *Honours/Masters Committee Member*

Holly Sargent (Honours, supervisor: Craig Moritz), “Genetic erosion of island marsupial populations,” 2018

Somasundhari Shanmuganadam (Masters, supervisors: Benjamin Schwessinger /Robyn Hall), “Uncovering the Hare microbiome,” 2019

#### Presentations *Invited Departmental Presentations*

“TBD.” Viikki Lectures, University of Helsinki, Helsinki, Finland, 2020.

“Coevolution while you wait: the arms race between honey bees and ectoparasitic *Varroa* mites.” Melbourne University School of BioSciences Seminar Series, Melbourne, Australia, 2019.

“Using historical collections to understand the evolutionary response of bees to an emergent parasite.” Macquarie University, Sydney, Australia, 2016.

“Evolutionary response by wild honey bees to *Varroa*.” Plymouth University, Plymouth, United Kingdom, 2016.

“Evolutionary response by wild honey bees to *Varroa*.” Plymouth University, Plymouth, United Kingdom, 2016.

“Evolutionary response by wild honey bees to *Varroa*.” Institute of Science and Technology, Vienna, Austria, 2016.

“Evolutionary response by wild honey bees to *Varroa*.” Max Planck Institute for Evolutionary Biology, Plön, Germany, 2016.

“Evolutionary response by wild honey bees to *Varroa*.” Texas A&M University, College Station, Texas, United States, 2016.

“Whole-genome re-sequencing of museum specimens reveals resilience to disease in a feral population of European honey bees.” Academia Sinica, Taipei, Taiwan, 2016.

“Using historical collection to understand feral honey bee evolution.” United States Department of Agriculture, Carl Hayden Bee Research Center, Tucson, Arizona, United States, 2015.

- “Using population genomics to look at selection and evolution in social insects.” University of Pennsylvania, Philadelphia, Pennsylvania, United States, 2015.
- “When subspecies collide: What can genome-wide signatures of hybridisation tell us about speciation?.” Australian National University, Species delimitation in the age of genomics Workshop, Canberra, Australia, 2015.
- “Museum samples reveal population genomic changes associated with a rapid evolutionary response by wild honey bees *Apis mellifera* to a novel parasite.” Australian National University, Species delimitation in the age of genomics Workshop, National University of Singapore Biology Colloquium, 2015.
- “Working with ancient DNA: tools and insights.” Kazan’ Federal University, Kazan’, Russian Federation, 2014.
- “Working with degraded DNA: laboratory and bioinformatic approaches.” CSIRO, Canberra, Australia, 2014.
- “Whole genome re-sequencing of museum specimens reveals resilience to disease in a feral population of European honey bees.” Australian National University, Canberra, Australia, 2014.
- “Molecular signatures of ancient mutualistic coevolution in attine ants and their fungal cultivars.” Experimental Evolution Discussion Group, Wageningen University, Wageningen, Netherlands, 2014.
- “Whole genome re-sequencing of museum specimens reveals resilience to disease in a feral population of European honey bees.” University of Southern California, Los Angeles, California, United States, 2014.
- “Whole genome re-sequencing of museum specimens reveals resilience to disease in a feral population of European honey bees.” University of Southern California, Los Angeles, California, United States, 2014.
- “Working with degraded DNA: laboratory and bioinformatic approaches.” University of Southern California, Los Angeles, California, United States, 2014.
- “Development and applications of techniques to work with degraded DNA.” Kazan’ Federal University, Kazan’, Russian Federation, 2013.
- “Using museum collections to understand how honey bees have survived a disease pandemic.” School of Life Sciences, Arizona State University, Tempe, Arizona, 2013.
- “Using museum collections to understand how honey bees have survived a disease pandemic.” School of Life Sciences, Arizona State University, Tempe, Arizona, 2013.
- “Using museum collections to understand how honey bees have survived a disease pandemic.” Integrative Biology, University of Texas, Austin, Texas, United States, 2013.
- “Using museum collections to understand how honey bees have survived a disease pandemic.” Neurobiology and Behavior, Cornell University, Ithaca, New York, United States, 2013.
- “Using museum collections to understand how honey bees have survived a disease pandemic.” CAS-MPG Partner Institute for Computational Biology, Shanghai, China, 2012.
- “Evolutionary fate of horizontally acquired genes in bdelloid rotifers.” Ehwa Womans University, Seoul, Korea, 2013.

- “The role of adaptation and mutualistic interactions in the invasion of an African rainforest by the little fire ant *Wasmannia auropunctata*.” Rice University, Houston, Texas, United States, 2008.
- “The spread of an invasive ant in African lowland rainforest: effects of environment and genetics.” University of Hawaii, Hilo, Hawaii, United States, 2008.
- “Coevolution at the phylogenetic vs. population-genetic scales in the attine ant-fungal cultivar symbiosis.” Wageningen University, Wageningen, Netherlands, 2007.

#### *Invited Conference and Workshop Talks*

- “Staying alive: Genetic confirmation that the Lord Howe stick insect is not extinct.” *Genomics and collections: adaptation to macroevolution*, Canberra, Australia, 2017.
- “When subspecies collide: What can genome-wide signatures of hybridisation tell us about speciation?.” *Australian National University, Species delimitation in the age of genomics Workshop*, Canberra, Australia, 2015.

#### *Oral Conference Presentations*

- “Staying alive: Genetic confirmation that the Lord Howe stick insect is not extinct.” *Entomological Society of America*, Boulder, Colorado, United States, 2018.
- “Using historical collections to understand the evolutionary response of bees to an emergent parasite.” *Society for Molecular Biology and Evolution*, Austin, Texas, United States, 2016.
- “Transcriptional profiling of attine ant fungal symbionts.” *British Mycological Society*, Alicante, Spain, 2012.
- “Invasion of lowland rainforest by their little fire ant *Wasmannia auropunctata*.” *Department and Graduate Institute of Entomology, National Taiwan University*, Taipei, Taiwan, 2011.

#### *Poster Conference Presentations*

- “RAD-tagging and low-coverage shotgun phylogenetics with degraded DNA from non-destructively sampled museum specimens.” *Illumina*, Phuket, Thailand, 2013.

#### *Local Talks*

- “Molecular signatures of ancient mutualistic coevolution in attine ants and their fungal cultivars.” *OIST-NTU Invasive Ant Symposium, Okinawa Institute of Science and Technology*, Okinawa, Japan, 2014.
- “Ecology and evolution: the next synthesis.” *Sydney Brenner commemorative symposium, Okinawa Institute of Science and Technology*, Okinawa, Japan, 2011.

### Journal Articles

63. Barua, A and **AS Mikheyev** (2019). “Many options, few solutions: over 60 million years snakes converged on a few optimal venom formulations”. *Molecular Biology and Evolution*. I.F.: 10.2
62. Emborski, C and **AS Mikheyev** (2019). “Ancestral diet transgenerationally influences offspring in a parent-of-origin and sex-specific manner”. *Philosophical Transactions of the Royal Society B* **374**(1768), 20180181. CITATIONS: 3
61. Holman, L, H Helanterä, K Trontti, and **AS Mikheyev** (2019). “Comparative transcriptomics of social insect queen pheromones”. *Nature Communications* **10**(1), 1593. I.F.: 12.4
60. Jovanovic, N and **AS Mikheyev** (2019). “Interactive web-based visualization and sharing of phylogenetic trees using phylogeny.IO”. *Nucleic Acids Research* **47**(W1), W266–W269. I.F.: 11.6 CITATIONS: 1
59. Morandin, C, VP Brendel, L Sundström, H Helanterä, and **AS Mikheyev** (2019). “Changes in gene DNA methylation and expression networks accompany caste specialization and age-related physiological changes in a social insect”. *Molecular ecology* **28**(8), 1975–1993. I.F.: 6.1
58. Smith, CC, JN Weber, **AS Mikheyev**, F Roces, M Bollazzi, K Kellner, JN Seal, and UG Mueller (2019). “Landscape genomics of an obligate mutualism: Concordant and discordant population structures between the leafcutter ant *Atta texana* and its two main fungal symbiont types”. *Molecular Ecology*. I.F.: 6.1
57. Techer, MA, RV Rane, ML Grau, JMK Roberts, ST Sullivan, I Liachko, AK Childers, JD Evans, and **AS Mikheyev** (2019). “Genomic analyses of sibling honey bee ectoparasitic mite species show divergent strategies of adaptation”. *Communications Biology* **in press**. CITATIONS: 2
56. Wallberg, A, I Bunikis, OV Pettersson, M-B Mosbech, AK Childers, JD Evans, **AS Mikheyev**, HM Robertson, GE Robinson, and MT Webster (2019). “A hybrid de novo genome assembly of the honeybee, *Apis mellifera*, with chromosome-length scaffolds”. *BMC Genomics* **20**(1), 275. I.F.: 3.7 CITATIONS: 5
55. Warner, MR, **AS Mikheyev**, and TA Linksvayer (2019). “Transcriptomic basis and evolution of the ant nurse-larval social interactome”. *PLoS Genetics* **15**(5), e1008156. I.F.: 5.5 CITATIONS: 1
54. Warner, MR, L Qiu, MJ Holmes, **AS Mikheyev**, and TA Linksvayer (2019). “Convergent eusocial evolution is based on a shared reproductive groundplan plus lineage-specific plastic genes”. *Nature Communications* **10**(1), 2651. I.F.: 12.4 CITATIONS: 4

53. Aird, S, N da Silva, L Qiu, A Villar-Briones, V Saddi, PM de Campos Telles, M Grau, and **AS Mikheyev** (2017a). “Coralsnake venomomics: analyses of venom gland transcriptomes and proteomes of six Brazilian taxa”. *Toxins* **9**(6), 187. *I.F.*: 3.3 [CITATIONS: 21](#)
52. Aird, SD, J Arora, A Barua, L Qiu, K Terada, and **AS Mikheyev** (2017b). “Population genomic analysis of a pitviper reveals microevolutionary forces underlying venom chemistry”. *Genome Biology and Evolution* **9**(10), 2640–2649. *I.F.*: 3.9 [CITATIONS: 23](#)
51. **AS Mikheyev**, A Zwick, MJL Magrath, ML Grau, L Qiu, YN Su, and D Yeates (2017). “Museum genomics confirms that the Lord Howe Island stick insect survived extinction”. *Current Biology* **27**(20), 3157–3161. e4. *I.F.*: 9.3 [CITATIONS: 11](#)
50. Carlson, AL, HD Ishak, J Kurian, **AS Mikheyev**, I Gifford, and UG Mueller (2017). “Nuclear populations of the multinucleate fungus of leafcutter ants can be dekarotized and recombined to manipulate growth of nutritive hyphal nodules harvested by the ants”. *Mycologia* **109**(5), 832–846. *I.F.*: 2.8 [CITATIONS: 3](#)
49. Gospocic, J, EJ Shields, KM Glastad, Y Lin, CA Penick, H Yan, **AS Mikheyev**, TA Linksvayer, BA Garcia, SL Berger, J Liebig, D Reinberg, and R Bonasio (2017). “The neuropeptide corazonin controls social behavior and caste identity in ants”. *Cell* **170**(4), 748–759. e12. [CITATIONS: 47](#)
48. Morandin, C, **AS Mikheyev**, JS Pedersen, and H Helanterä (2017). “Evolutionary constraints shape caste-specific gene expression across 15 ant species”. *Evolution* **71**(5), 1273–1284. *I.F.*: 3.8 [CITATIONS: 7](#)
47. Mueller, UG, HD Ishak, SM Bruschi, CC Smith, JJ Herman, SE Solomon, **AS Mikheyev**, C Rabeling, JJ Scott, M Cooper, A Rodrigues, A Ortiz, CRF Brandão, JE Lattke, FC Pagnocca, SA Rehner, TR Schultz, HL Vasconcelos, RMM Adams, M Bollazzi, RM Clark, AG Himler, JS LaPolla, IR Leal, RA Johnson, F Roces, J Sosa-Calvo, R Wirth, and M Bacci Jr (2017). “Biogeography of mutualistic fungi cultivated by leafcutter ants”. *Molecular Ecology* **26**(24), 6921–6937. *I.F.*: 6.1 [CITATIONS: 12](#)
46. Okada, Y, Y Watanabe, MMY Tin, K Tsuji, and **AS Mikheyev** (2017). “Social dominance alters nutrition-related gene expression immediately: Transcriptomic evidence from a monomorphic queenless ant”. *Molecular Ecology* **26**(11), 2922–2938. *I.F.*: 6.1 [CITATIONS: 19](#)
45. Warner, MR, **AS Mikheyev**, and TA Linksvayer (2017). “Genomic signature of kin selection in an ant with obligately sterile workers”. *Molecular Biology and Evolution* **34**(7), 1780–1787. *I.F.*: 10.2 [CITATIONS: 26](#)
44. Aird, S, A Villar Briones, M Roy, and **AS Mikheyev** (2016). “Polyamines as snake toxins and their probable pharmacological functions in envenomation”. *Toxins* **8**(10), 279. *I.F.*: 3.3 [CITATIONS: 3](#)

43. Helmkamp, M, **AS Mikheyev**, Y Kang, J Fewell, and J Gadau (2016). “Gene expression and variation in social aggression by queens of the harvester ant *Pogonomyrmex californicus*”. *Molecular ecology* **25**(15), 3716–3730. *I.F.*: 6.1 **CITATIONS: 7**
42. Mitaka, Y, K Kobayashi, **AS Mikheyev**, MMY Tin, Y Watanabe, and K Matsuura (2016). “Caste-specific and sex-specific expression of chemoreceptor genes in a termite”. *PLoS One* **11**(1), e0146125. *I.F.*: 2.8 **CITATIONS: 15**
41. Morandin, C, MMY Tin, S Abril, C Gómez, L Pontieri, M Schiøtt, L Sundström, K Tsuji, JS Pedersen, H Helanterä, and **AS Mikheyev** (2016). “Comparative transcriptomics reveals the conserved building blocks involved in parallel evolution of diverse phenotypic traits in ants”. *Genome Biology* **17**(1), 43. *I.F.*: 13.2 **CITATIONS: 51**
40. Morozova, I, P Flegontov, **AS Mikheyev**, S Bruskin, H Asgharian, P Ponomarenko, V Klyuchnikov, GP ArunKumar, E Prokhortchouk, Y Gankin, E Rogaev, Y Nikolsky, A Baranova, E Elhaik, and TV Tatarinova (2016). “Toward high-resolution population genomics using archaeological samples”. *DNA Research* **23**(4), 295–310. *I.F.*: 5.4 **CITATIONS: 16**
39. Reyes-Bermudez, A, A Villar-Briones, C Ramirez-Portilla, M Hidaka, and **AS Mikheyev** (2016). “Developmental progression in the coral *Acropora digitifera* is controlled by differential expression of distinct regulatory gene networks”. *Genome Biology and Evolution* **8**(3), 851–870. *I.F.*: 3.9 **CITATIONS: 10**
38. Yeates, DK, A Zwick, and **AS Mikheyev** (2016). “Museums are biobanks: unlocking the genetic potential of the three billion specimens in the world’s biological collections”. *Current Opinion in Insect Science* **18**, 83–88. *I.F.*: 4.2 **CITATIONS: 23**
37. Aird, SD, S Aggarwal, A Villar-Briones, MMY Tin, K Terada, and **AS Mikheyev** (2015). “Snake venoms are integrated systems, but abundant venom proteins evolve more rapidly”. *BMC Genomics* **16**(1), 647. *I.F.*: 3.7 **CITATIONS: 31**
36. **AS Mikheyev** and TA Linksvayer (2015). “Genes associated with ant social behavior show distinct transcriptional and evolutionary patterns”. *Elife* **4**, e04775. *I.F.*: 7.6 **CITATIONS: 54**
35. **AS Mikheyev**, MMY Tin, J Arora, and TD Seeley (2015). “Museum samples reveal rapid evolution by wild honey bees exposed to a novel parasite”. *Nature communications* **6**, 7991. *I.F.*: 12.4 **CITATIONS: 36**
34. Fischer, G, FL Azorsa, FH Garcia, **AS Mikheyev**, and EP Economo (2015). “Two new phragmotic ant species from Africa: morphology and next-generation sequencing solve a caste association problem in the genus *Carebara* Westwood”. *ZooKeys* **525**, 77-105(525, 77-105), 77–105. *I.F.*: 1.1 **CITATIONS: 15**
33. Miyakawa, MO and **AS Mikheyev** (2015a). “Males are here to stay: fertilization enhances viable egg production by clonal queens of the little fire ant (*Wasmannia auropunctata*)”. *The Science of Nature* **102**(102 (3-4), 15), 15. **CITATIONS: 3**



32. Miyakawa, MO and **AS Mikheyev** (2015b). “QTL mapping of sex determination loci supports an ancient pathway in ants and honey bees”. *PLoS Genetics* **11**(11), e1005656. *I.F.*: 5.5 [CITATIONS: 12](#)
31. Parmesan, C, A Williams-Anderson, M Moskwik, **AS Mikheyev**, and MC Singer (2015). “Endangered Quino checkerspot butterfly and climate change: Short-term success but long-term vulnerability?” *Journal of Insect Conservation* **19**(2), 185–204. *I.F.*: 1.6 [CITATIONS: 19](#)
30. Smith, CR, S Helms Cahan, C Kemena, SG Brady, W Yang, E Bornberg-Bauer, T Eriksson, J Gadau, M Helmkampf, D Gotzek, M Miyakawa, and AV Suarez **AS Mikheyev** (2015). “How do genomes create novel phenotypes? Insights from the loss of the worker caste in ant social parasites”. *Molecular Biology and Evolution* **32**(11), 2919–2931. *I.F.*: 10.2 [CITATIONS: 29](#)
29. Tin, MMY, FE Rheindt, E Cros, and **AS Mikheyev** (2015). “Degenerate adaptor sequences for detecting PCR duplicates in reduced representation sequencing data improve genotype calling accuracy”. *Molecular Ecology Resources* **15**(2), 329–336. *I.F.*: 7.1 [CITATIONS: 37](#)
28. **AS Mikheyev** and MMY Tin (2014). “A first look at the Oxford Nanopore MinION sequencer”. *Molecular Ecology Resources* **14**(6), 1097–1102. *I.F.*: 7.1 [CITATIONS: 268](#)
27. Gusev, O, Y Suetsugu, R Cornette, T Kawashima, MD Logacheva, AS Kondrashov, AA Penin, R Hatanaka, S Kikuta, S Shimura, H Kanamori, Y Katayose, T Matsumoto, E Shagimardanova, D Alexeev, V Govorun, J Wisecaver, **AS Mikheyev**, R Koyanagi, M Fujie, T Nishiyama, S Shigenobu, TF Shibata, V Golygina, M Hasebe, T Okuda, N Satoh, and T Kikawada (2014). “Comparative genome sequencing reveals genomic signature of extreme desiccation tolerance in the anhydrobiotic midge”. *Nature Communications* **5**, 4784(5, 4784), 4784. *I.F.*: 12.4 [CITATIONS: 63](#)
26. Tin, MMY, EP Economo, and **AS Mikheyev** (2014). “Sequencing degraded DNA from non-destructively sampled museum specimens for RAD-tagging and low-coverage shotgun phylogenetics”. *PloS one* **9**(5), e96793. *I.F.*: 2.8 [CITATIONS: 73](#)
25. Aird, SD, Y Watanabe, A Villar-Briones, MC Roy, K Terada, and **AS Mikheyev** (2013). “Quantitative high-throughput profiling of snake venom gland transcriptomes and proteomes (*Ovophis okinavensis* and *Protobothrops flavoviridis*)”. *BMC Genomics* **14**(1), 790. *I.F.*: 3.7 [CITATIONS: 100](#)
24. **AS Mikheyev**, CS McBride, UG Mueller, C Parmesan, MR Smee, C Stefanescu, B Wee, and MC Singer (2013). “Host-associated genomic differentiation in congeneric butterflies: now you see it, now you do not”. *Molecular Ecology* **22**(18), 4753–4766. *I.F.*: 6.1 [CITATIONS: 10](#)
23. Smee, MR, Y Pauchet, P Wilkinson, B Wee, MC Singer, DJ Hodgson, and **AS Mikheyev** (2013). “Microsatellites for the marsh fritillary butterfly: de novo transcriptome sequencing, and a comparison with amplified fragment length polymorphism (AFLP) markers”. *PloS One* **8**(1), e54721. *I.F.*: 2.8 [CITATIONS: 10](#)

22. Mueller, UG, **AS Mikheyev**, E Hong, R Sen, DL Warren, SE Solomon, HD Ishak, M Cooper, JL Miller, KA Shaffer, and TE Juenger (2011a). "Evolution of cold-tolerant fungal symbionts permits winter fungiculture by leafcutter ants at the northern frontier of a tropical ant–fungus symbiosis". *Proceedings of the National Academy of Sciences of the United States of America* **108**(10), 4053–4056. CITATIONS: 63
21. Mueller, UG, **AS Mikheyev**, SE Solomon, and M Cooper (2011b). "Frontier mutualism: co-evolutionary patterns at the northern range limit of the leaf-cutter ant–fungus symbiosis". *Proceedings of the Royal Society B: Biological Sciences* **278**(1721), 3050–3059. I.F.: 4.8 CITATIONS: 35
20. **AS Mikheyev**, UG Mueller, and P Abbot (2010). "Comparative dating of attine ant and lepiotaceous cultivar phylogenies reveals coevolutionary synchrony and discord". *The American Naturalist* **175**(6), E126–E133. I.F.: 0.5 CITATIONS: 68
19. **AS Mikheyev**, T Vo, B Wee, MC Singer, and C Parmesan (2010). "Rapid microsatellite isolation from a butterfly by de novo transcriptome sequencing: performance and a comparison with AFLP-derived distances". *PLoS One* **5**(6), e11212. I.F.: 2.8 CITATIONS: 52
18. Dunham, AE and **AS Mikheyev** (2010). "Influence of an invasive ant on grazing and detrital communities and nutrient fluxes in a tropical forest". *Diversity and Distributions* **16**(1), 33–42. I.F.: 4.6 CITATIONS: 26
17. Foucaud, J, J Orivel, A Loiseau, JHC Delabie, H Jourdan, D Konghouleux, M Vonshak, M Tindo, J-L Mercier, D Fresneau, J-B Mikissa, T McGlynn, **AS Mikheyev**, J Oettler, and A Estoup (2010). "Worldwide invasion by the little fire ant: routes of introduction and eco-evolutionary pathways". *Evolutionary Applications* **3**(4), 363–374. I.F.: 4.7 CITATIONS: 65
16. **AS Mikheyev**, S Bresson, and P Conant (2009). "Single-queen introductions characterize regional and local invasions by the facultatively clonal little fire ant *Wasmannia auropunctata*". *Molecular Ecology* **18**(14), 2937–2944. I.F.: 6.1 CITATIONS: 38
15. Vo, TL, UG Mueller, and **AS Mikheyev** (2009). "Free-living fungal symbionts (Lepiotaceae) of fungus-growing ants (Attini: Formicidae)". *Mycologia* **101**(2), 206–210. I.F.: 2.8 CITATIONS: 66
14. **AS Mikheyev** (2008). "History, genetics and pathology of a leaf-cutting ant introduction: a case study of the Guadeloupe invasion". *Biological Invasions* **10**(4), 467–473. I.F.: 3.1 CITATIONS: 24
13. **AS Mikheyev**, L Tchingnoumba, A Henderson, and A Alonso (2008). "Effect of propagule pressure on the establishment and spread of the little fire ant *Wasmannia auropunctata* in a Gabonese oilfield". *Diversity and Distributions* **14**(2), 301–306. I.F.: 4.6 CITATIONS: 34

12. **AS Mikheyev**, T Vo, and UG Mueller (2008). "Phylogeography of post-Pleistocene population expansion in a fungus-gardening ant and its microbial mutualists". *Molecular Ecology* **17**(20), 4480–4488. *I.F.*: 6.1 [CITATIONS: 59](#)
11. **AS Mikheyev** and UG Mueller (2007). "Genetic relationships between native and introduced populations of the little fire ant *Wasmannia auropunctata*". *Diversity and Distributions* **13**(5), 573–579. *I.F.*: 4.6 [CITATIONS: 29](#)
10. **AS Mikheyev**, UG Mueller, and JJ Boomsma (2007). "Population genetic signatures of diffuse co-evolution between leaf-cutting ants and their cultivar fungi". *Molecular Ecology* **16**(1), 209–216. *I.F.*: 6.1 [CITATIONS: 87](#)
9. Jr, J Martins, SE Solomon, **AS Mikheyev**, UG Mueller, A Ortiz, and M Bacci Jr (2007). "Nuclear mitochondrial-like sequences in ants: evidence from *Atta cephalotes* (Formicidae: Attini)". *Insect molecular biology* **16**(6), 777–784. *I.F.*: 2.5 [CITATIONS: 52](#)
8. **AS Mikheyev**, UG Mueller, and P Abbot (2006). "Cryptic sex and many-to-one coevolution in the fungus-growing ant symbiosis". *Proceedings of the National Academy of Sciences of the United States of America* **103**(28), 10702–10706. [CITATIONS: 140](#)
7. Solomon, SE and **AS Mikheyev** (2005). "The ant (Hymenoptera: Formicidae) fauna of Cocos Island, Costa Rica". *Florida Entomologist* **88**(4), 415–424. *I.F.*: 1.1 [CITATIONS: 20](#)
6. **AS Mikheyev** (2004). "Male accessory gland size and the evolutionary transition from single to multiple mating in the fungus-gardening ants". *Journal of Insect Science* **4**(1), 37. *I.F.*: 1.3 [CITATIONS: 27](#)
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1. Bozek, K, L Hebert, **AS Mikheyev**, and GJ Stephens (2018). “Towards dense object tracking in a 2D honeybee hive”. In: *2018 IEEE/CVF Conference on Computer Vision and Pattern Recognition*, pp. 4185–4193. DOI: [10.1109/CVPR.2018.00440](https://doi.org/10.1109/CVPR.2018.00440). CITATIONS: 3

### Commentary

1. **AS Mikheyev** and UG Mueller (2006). “Invasive species: customs intercepts reveal what makes a good ant stowaway”. *Current Biology* **16**(4), R129–R131. I.F.: 9.3 CITATIONS: 6

Service **Associate Dean (International), Joint Colleges of Science, Health and Medicine, Australian National University**

Indian Institute of Technology Madras Joint Degree Program steering committee. 2019–.

### Professional Organizations

Australian Entomological Society, Education Committee member. 2018–.

### Reviewer

**Journals:** Applied Sciences, Bioinformatics, Biology Letters, BMC Biology, BMC Evolutionary Biology, BMC Genomics, Current Opinion in Insect Science, Ecological Research, Ecology, Ecology and Evolution, Ecology Letters, Insectes Sociaux, Journal of Animal Ecology, Journal of Evolutionary Biology, Journal of Visualized Experiments, Molecular Biology and Evolution, Molecular Ecology, Molecular Ecology Resources, Nature Ecology & Evolution, Philosophical Transactions of the Royal Society B: Biological Sciences, PLoS Computational Biology (Guest Editor), PLoS Genetics, Proceedings of the Royal Society B: Biological Sciences, Scientific Data, Scientific Reports, Toxins.

**Granting Agencies:** Australian Research Council, Deutsche Forschungsgemeinschaft, U.S. National Science Foundation.

Outreach **TV Interview**

SBS News. [Commenting on the use of neonicotinoid pesticides](#). 2019-05-08

### Public talk

Japan Institute, ANU College of Asia & the Pacific. OBJECTively - Connecting Australia and Japan: objects, cultural stories, people, [Coversations: bee parasitic mites](#). 2019-03-08