IUSSI NAS Newsletter 2025

Dear NAS Colleagues!

Do we ever stop in personal growth? Evidence suggests that we may think so, but do not (‘end of history illusion’: everyone thinks that a lot happened in the last 10 years, but now they’ve arrived at who they are and the next 10 years will be boring – but people think this no matter their age - DOI: 10.1126/science.1229294). I find this highly uplifting: it means we all have the chance, collectively and individually, to make progress. My perception is that many NAS members have taken on the responsibility of engaging the public in a better understanding of what science is and why we care about insects: see images below of my lab’s stand at the Arizona Insect Festival in 2025, including demonstrations on ant diversity as well as activities for kids around measuring things – it’s surprising how much joy many find in numbers when they are hands-on, such as from weighing a rock on my kitchen scale.

For the North American Section of the IUSSI, 2025 was a year of thinking about what we value, and how those values inform our practice. The IUSSI is a nonpartisan scientific society committed to advancing the study of social insects through rigorous, evidence-based research – which can only be advanced if we uphold values of truth and honesty, evidence and freedom. In March, we sent a letter to all members with some hopefully helpful facts and pointers to remind your congressional and other representatives of this – and of how much our current wealth and way of life depends on evidence-based science and these values. We also sent another letter in July with the reminder that merit-based science, as well as organizational success, depend on reducing barriers and minimizing bias – not to mention the fact that most of us want to live in a just, not just an efficient, world.

Your NAS IUSSI Executive Committee

President-elect: Matina Donaldson-Matasci, Harvey-Mudd

President: Chris Smith, Utah State

Past President: Anna Dornhaus, University of Arizona

Secretary: Mike Simone-Feinstrom, USDA-ARS

Clare Rittschof, University of Kentucky

Congratulations to Chris, who is our president for this year (2026), and Matina, who will be the NAS president next year (2027).

In other news, we have completed the transition to the new membership system, where you can set your membership to be auto-renewing: https://iussi.cyberbee.net/membershipx/

Our DEIJ Committee set up a website that allows members to share any resources, such as career-relevant websites or funding programs, or resources for outreach: https://www.beepboopstats.com/iussi-nas-deij/

We have expanded the social media committee, and our committee members are hard at work composing a new social media strategy and set of policies – watch this space. Our social media accounts are
https://bsky.app/profile/iussi-nas.bsky.social
https://www.instagram.com/iussi_nas/
https://www.facebook.com/groups/1609993625726965
https://x.com/IUSSI_NAS

We have a wonderful list of awardees as well, and reports from two of them, Paige Caine and Allina Win, about their wonderful work are included below (the others gave reports at the business meeting in November).

Best wishes for our future growth to all of us,
Anna Dornhaus, outgoing president

List of awardees
Mary Jane West-Eberhard Best Paper Award:
Ashley Y Kim, Ben Saavedra, Benjamin Smarr, James Nieh (2024) Exposure to constant artificial light alters honey bee sleep rhythms and disrupts sleep, Scientific Reports, Vol 114:25865

Robert L. and Louise B. Jeanne Social Wasp Research Grant:
Paige Caine, Mike Goodisman Lab, Georgia Tech, "The effect of social parasitism on genome evolution in social wasps"

Charles Michener Bee Research Grant:
Kathryn Naherny, Samuel Ramsey lab, University of Colorado, "Untangling the Microcosm of a Stingless Bee Nest: Using Host Traits to Understand the Interplay of Melittophiles and Peruvian Stingless Bees"

William L. and Ruth D. Nutting Termite Research Grant:
Elijah Carroll, Auburn University in the lab of Dr. Nobuaki Mizumoto. "Does sexual conflict in nest-site selection act as a barrier to hybridization in Cryptotermes termites?"

Tschinkel Ant Natural History Research Grant:
Allina Win, Arizona State University in the lab of Dr. Timothy Linksvayer. "A Comparative Study of Larval Fluid as a Novel Social Regulator of Queen Fecundity and Colony Sociogenesis"

George C. Eickwort Student Research Award:
Patrick Piekarski, Kronauer lab, Rockefeller University

Jeffery P. La Fage Student Award:
Joanne Tzu-Chia Chen, Chow-Yang Lee lab, UC Riverside, “Bridging Fundamental Discovery and Pest Management: Integrative Studies on Social Insects”

Turner-Collins Outreach Award–2 given in its inaugural year:
Dr. Duane M. Jackson
Dr. Hongmei Li-Byarlay

A Comparative Study of Larval Fluid as a Novel Social Regulator of Queen Fecundity and Colony Sociogenesis

Allina Win
School of Life Sciences, Arizona State University
(Linksvayer Lab)

Colonies of social insects function as highly integrated biological systems, in which the fitness of the whole depends on coordinated interactions among queens, workers, and brood. Queen fecundity, in particular, plays a central role in determining colony growth, persistence, and reproductive success. While queen egg-laying is often viewed as being governed primarily by intrinsic physiological processes, accumulating evidence suggests that other colony members, especially larvae may exert powerful bottom-up influences on queen reproduction. Understanding how such brood-derived regulation operates remains a key unresolved problem in ant natural history. This project investigates the role of larval-derived fluid as a social regulator of queen fecundity. Previous studies have shown that the presence of late-instar larvae can stimulate queen egg-laying, but the proximate source of this effect and the mechanisms by which it operates are poorly understood. In particular, it is unclear whether the effect depends on the physical presence of larvae or on specific larval secretions produced during development.

To address this question, while additional ant species are being collected and acclimated for laboratory rearing, I am beginning this work with the pharaoh ant (*Monomorium pharaonis*) by experimentally manipulating larval presence and larval-derived components in standardized laboratory colonies. Focusing on a molting-associated secretion released by late-instar larvae, I am testing whether larval fluid alone is sufficient to alter queen egg-laying rates and survival, independent of the larva itself. Queens are monitored longitudinally for reproductive output under controlled conditions, allowing direct comparison of fecundity across treatments. In parallel, behavioral observations are used to document how larvae release the fluid and how queens and workers interact with it, providing insight into whether its effects are mediated through direct consumption, worker handling, or indirect signaling. With such experimental manipulation with close behavioral and developmental observation, this work aims to clarify how brood actively shape queen reproductive physiology. More broadly, my study highlights larvae as dynamic participants in colony regulation rather than passive recipients of care, contributing to a deeper understanding of bottom-up processes in colony sociogenesis and the evolution of complex social systems.

Project Report: The effect of social parasitism on genome evolution in social wasps

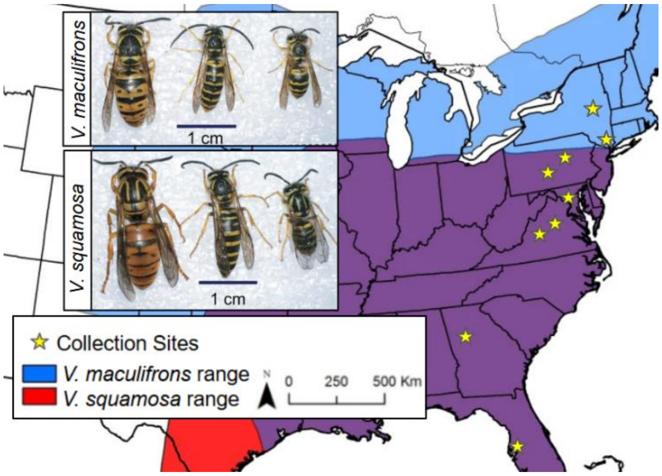

Figure 1.Range of Vespula maculifrons and V. squamosa in the United States, with collection sites highlighted by yellow stars.

Social parasites hijack the colonies of other social insects to jumpstart their own life cycle. The social wasp *Vespula squamosa* is a facultative social parasite of *V. maculifrons*. These two species overlap for much of their range, but also exist separately on the edges of their respective ranges (figure 1). Thus, these species provide a great opportunity to test hypotheses on the genome evolution of social parasites and hosts.

This study investigates the effects of social parasitism on genome evolution by studying the population genomics of *V. squamosa* and *V. maculifrons* across their ranges. The first goal of this study is to assess the selective pressures operating on genes in the parasite and host. The second goal is to evaluate effective population size and gene flow and determine how these factors impact selection.

We are making great progress on this project. We have collected 25 *V. maculifrons* samples ranging from Georgia to New York, and 19 *V. squamosa* samples ranging from Florida to Pennsylvania. Additionally, our sampling of the eastern United States also uncovered 4 *V. germanica*, 5 *V. flavopilosa*, 3 *V. alasecensis*, 1 *V. vidua*, and 1 *Dolichovespula arenaria.*

I sequenced the cytochrome B gene of the samples to confirm species identity and construct a phylogeny of the taxa. Our results suggest some population structuring (figure 2). We are proceeding with genome sequencing for the *V. maculifrons* and *V. squamosa* samples. I have extracted their genomic DNA, and performed quality control on these samples by measuring concentration and purity. These samples have been sent out for genome sequencing

Our next steps include genome assembly and analysis. Low quality reads will be trimmed, and sequences will be mapped to existing genomes. We will look for geographic clustering and population structure within species, assess gene flow, estimate effective population size, and calculate linkage disequilibrium. Finally, we will assess selective signatures, and compare these signatures within and outside overlapping regions. Ultimately, our research will provide insight into how social parasitism shapes the evolution of both parasite and host.

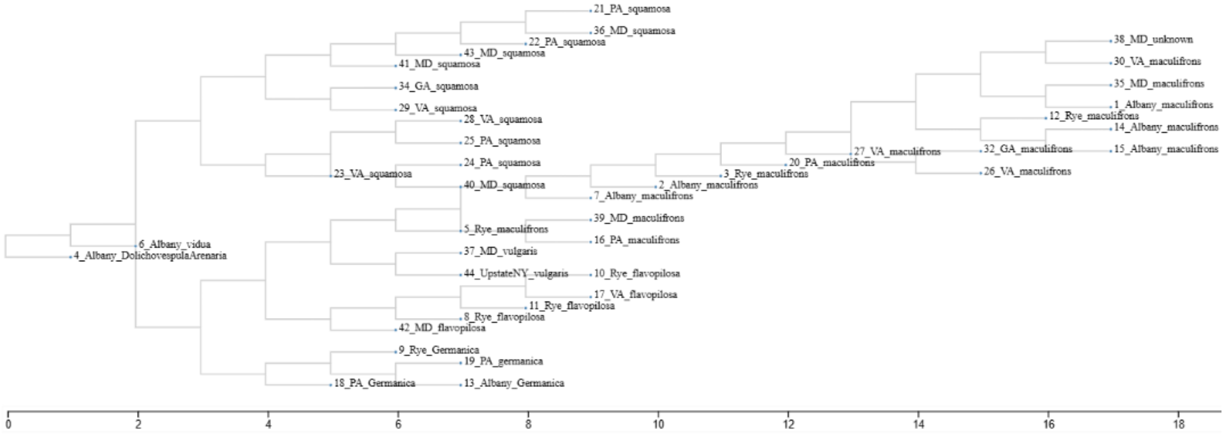

Figure 2. Phylogenetic tree showing cytochrome B sequences from all collected Vespula and Dolichovespula samples. Constructed with PHYLIP NJ