

From Genomes to Hives: 'Omics Perspectives on Eusocial Evolution and the Ecology of Bees

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As one of the most important global pollinators for a large diversity of flowering plants, bees and related species (i.e. insects of the clade Apoidea; Fig. 1) sustain entire ecosystems and contribute to up to one-third of the global food supply (Khalifa et al. 2021). Beyond agriculturally important species, such as honey bees and bumblebees, many species play a key role in ecosystem functions and span a wide range of social organization. As habitat loss, climate change, and other anthropogenic pressures increasingly threaten bee populations worldwide, there is a growing need to understand both the large-scale evolutionary patterns that shape bee diversity and the finer-scale molecular and ecological processes that underlie their behavior.

Bees comprise a highly diverse clade with over 20,000 species, which has coevolved with flowering plants for over 100 million years. To date, only around 0.7% of the described bee species have had their genome sequenced. The past two decades have nevertheless witnessed a steady growth in genetic resources, bringing an increasing number of both wild and managed bee species into focus for evolutionary and ecological research.

Obtaining answers for the plethora of questions on bee ecology and evolution has relied enormously on recent 'omics advances. The insights from these efforts are synthesized in a recent Review article published in *Genome Biology and Evolution* by Dova Brenman-Suttner (Fig. 2) and Amro Zayed from York University in Canada (Brenman-Suttner and Zayed 2026). Zayed explains that “these are very exciting times to summarize some of the major insights into bee biology that we have gained by applying genomic tools,” adding that

“two decades ago, we only had the honey bee genome and genomic applications were fairly narrow, but now we are seeing genomics used to answer a wide range of questions on an ever increasing number of bee species.”

A key line of research that has benefitted from the expanding array of applications is the study of the evolution of eusociality. Defined as a social system with reproductive division of labor and cooperative brood care (Wilson 1971), eusociality has arisen repeatedly throughout insect evolution—at least 11 times independently in Hymenoptera and four times in bees alone—and is associated with different underlying gene regulatory mechanisms. Zayed explains that genomic approaches provide new ways to test hypotheses on the drivers of this social system, stating that “recent studies emphasize the roles of alternative splicing and other types of regulatory RNA in creating complex networks that underpin social behaviors such as caste differentiation, behavioral plasticity and immune responses.”

Brenman-Suttner and Zayed (2026) provide examples of how genomics has advanced this field. In the honey bee (*Apis mellifera*), alternative gene splicing and certain types of RNA—including long noncoding, micro-RNA and circular-RNAs—regulate reproductive division of labor (Chen and Shi 2020; Zheng et al. 2023). Comparative genomics also further our understanding of phenotypic evolution in bees. For example, comparisons of genomes from multiple sweat bee species (Halictidae) with different social phenotypes (social vs. solitary) suggest that the transition toward eusociality requires enhanced regulation of gene expression and is shared between lineages exhibiting social behavior (Jones et al. 2023).

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Fig. 1. Collection of bee species (Superfamily: Apoidea). On the left is *Apis mellifera* (Apidae; top left) or “honey bee,” the first bee and the third insect to have its genome sequenced. This species showcases division of labor among morphological castes regulated by alternative splicing and certain types of RNA (queen and workers shown in bottom left; Chen and Shi 2020; Zheng et al 2023). In the center, *Lasioglossum* spp. (Halictidae; female top, male bottom), or “sweat bees”; these span a range of social phenotypes, from solitary to eusocial. Comparative genomics show that regulation on gene expression underpins the transition to eusociality (Jones et al 2023). On the right, a male (top right) and female (bottom right) representatives of the genus *Bombus* (Apidae; bumblebees) are shown. Several species in this group have been used to detect recent anthropogenic-driven shifts in foraging behavior and community structure using museomics (Kolter et al 2023). All photos were provided by Amro Zayed.

Beyond social evolution, bees’ key role as pollinators has also driven the application of ‘omics tools to ecological questions. Ongoing habitat loss and climate change have increased the anthropogenic pressure that threatens multiple bee species. According to Zayed, environmental ‘omics, based on DNA collected from environmental samples or pollen metabarcoding ‘provide a rapid way to assess interactions between bees and their mutualists, such as the plant species that they forage on, or the microbiomes that support their metabolism and immunity, and how these interactions shape overall bee health’. These environmental ‘omics approaches include museomics, which leverage historical DNA of bees and pollen stored in museum collections. For example, Kolter et al. (2023) sequenced DNA from pollen preserved in the Zoological Museum of Hamburg to reveal shifts toward more generalist foraging behavior, accompanied by changes in pollination and community networks, over the past 50 years across multiple endangered bumble bee species (*Bombus* spp.) in Germany.

The emergence of different ‘omics tools is reshaping how we study bees, from the mechanisms of social evolution to bees’ responses to rapidly increasing environmental and anthropogenic pressures. According to Zayed, the quick pace of technological development suggests that researchers may not need to prioritize either of these two fields. He states that “understanding the ‘hows’ and

‘whys’ of eusocial evolution is one of the holy grails of biology, and that understanding bee health and conservation is important for maintaining ecosystem services and our food security.” Combining studies on eusocial evolution and ecology of bees holds great power to inform us on the past, present, and future of these vital ecosystem engineers.

Want to learn more? Check out these other articles on bee ‘omics recently published in *SMBE* journals:

- David C. Prince, Anders Wirén, Timothy J. Huggins, David H. Collins, Tamas Dalmay, Andrew F. G. Bourke, Molecular Basis of Eusocial Complexity: The Case of Worker Reproductivity in Bees, *Genome Biology and Evolution*, Volume 16, Issue 12, December 2024, evae269, <https://doi.org/10.1093/gbe/evae269>.
- Beryl M. Jones, Andrew E. Webb, Scott M. Geib, Sheina Sim, Rena M. Schweizer, Michael G. Branstetter, Jay D. Evans, Sarah D. Kocher, Repeated Shifts in Sociality Are Associated With Fine-tuning of Highly Conserved and Lineage-Specific Enhancers in a Socially Flexible Bee, *Molecular Biology and Evolution*, Volume 41, Issue 11, November 2024, msae229, <https://doi.org/10.1093/molbev/msae229>.
- Lianfei Cao, Zhijun Dai, Hongwei Tan, Huoqing Zheng, Yun Wang, Jie Chen, Haiou Kuang, Rebecca A. Chong, Minjin Han, Fuliang Hu, Wei Sun, Cheng Sun, Ze



Fig. 2. GBE author spotlight: Dova Brenman-Suttner. Dova Brenman-Suttner is currently completing her PhD in Biology at York University in Dr. Amro Zayed's lab. She uses population genomics and bio-informatic tools to study how social behavior evolves at the genomic level. Her work focuses on bees with varying degrees of sociality, including the advanced eusocial honey bee *Apis mellifera* and the facultatively incipiently social small carpenter bee *Ceratina calcarata*. She examines patterns of genetic differentiation and selection associated with social behavior, and studies how mutation and recombination vary with queen age in honey bees.

Zhang, Population Structure, Demographic History, and Adaptation of Giant Honeybees in China Revealed by Population Genomic Data, *Genome Biology and Evolution*, Volume 15, Issue 3, March 2023, evad025, <https://doi.org/10.1093/gbe/evad025>.

- Thibault Leroy, Pierre Faux, Benjamin Basso, Sonia Eynard, David Wragg, Alain Vignal, Inferring Long-Term and Short-Term Determinants of Genetic Diversity in Honey Bees: Beekeeping Impact and Conservation Strategies, *Molecular Biology and Evolution*, Volume 41, Issue 12, December 2024, msae249, <https://doi.org/10.1093/molbev/msae249>.

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