Biotechnology Challenges in Conservation: Microbiome Engineering in Honey Bees

The honey bee (*Apis mellifera*) exists in both managed and free-living colonies. They are important pollinators in agricultural and natural landscapes alike (Dainese et al. 2019). In agriculture, it is one of the world's most widespread and intensively managed forms of livestock, maintained for honey, wax and above all their role in food production as pollinators. In the wild, honey bees nest in natural cavities, such as in hollow trees, rocky crevices and sometimes in houses and buildings. These wild populations, along with other pollinators provide pollination 'services' but are also vital for maintaining the genetic diversity of the *Apis mellifera,* including the conservation of local subspecies and genotypes.

Unlike some of its wild relatives and other wild pollinators, the managed honey bee is not threatened with extinction. Its conservation significance therefore lies not in species survival, but in its profound ecological and economic impacts – and in the way it intersects with, and influences, wild environments.

Honey bees occupy landscapes from farmland and hedgerows to semi-natural habitats, often overlapping with thousands of wild bee species and other pollinators. These pollinators face severe pressures from habitat loss, food scarcity, pesticides and disease. Honey bees, both wild and domesticated, act as mobile reservoirs of pathogens and competitors for floral resources. As such, they function as ecological conduits: what affects honey bees does not remained confined to managed hives or wild colonies but can spill over into wider ecosystems.[1]

Against this backdrop, genetic engineering is promoted as a tool to safeguard managed honey bee colonies. Proposed approaches include RNA interference (RNAi) sprays, vaccines, CRISPR editing and most advanced, engineered gut symbionts (paratransgenesis).[2] By targeting honey bee microbiome, these interventions propose to influence bee health, development, physiology and behaviour, and in some cases to mitigate pesticide exposure. But releasing genetically engineered feeds or microbes into honey bee systems cannot be treated as an isolated husbandry measure.[3] Because honey bees are deeply embedded in wild pollinator communities and plant networks, interventions in their biology risk cascading into broader ecological systems.

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[1] Keller, A., et al., *(More than) Hitchhikers through the network: the shared microbiome of bees and flowers.* Current Opinion in Insect Science. **44**: p. 8-15; Lignon, V., et al., *The floral interface: a playground for interactions between insect pollinators, microbes, and plants.* Environment and Agriculture, 2023. **52**(2)

[2] Kwong, W. and N. Moran, *Gut microbial communities of social bees.* Nature reviews microbiology, 2016. **14**: p. 374–384.

[3] Boëte, C., *Gene drives, species complexes, and the risks of collateral damage.* PNAS, 2025. **122**(45).

A technical reality check

Microbiome engineering is often described as a "Trojan Horse" approach: modifying gut bacteria to deliver molecules toxic to ecoparasite mite *Varroa destructor* or the intracellular parasite *Nosema ceranae.*[4] While laboratory studies have demonstrated proof of concept, no field releases have yet been authorised.

Key technical challenges include:

Microbiome complexity: The honey bee gut community is diverse, variable with age, season, diet[5], pesticide exposure[6] and landscape context (urban versus rural)[7]. Engineered strains must integrate without disrupting this balance. Comparative field studies demonstrate that environmental context (natural vs anthropised landscapes) significantly affects microbiome composition, implying lab or simplified conditions overlook key ecological drivers.[8] Likewise, honey bee microbiome research underscores the influence of host behaviour, environment and social context on microbial community outcomes, noting that laboratory studies alone cannot fully capture these dynamics.[9] Together, this complexity undermines the feasibility of a "one-size-fits-all" approach and helps explain why laboratory successes might fail to translate to real-world colonies.

Spread and host range: While some gut bacteria (e.g. *Snodgrassella*) are largely host-specialised, transmission within colonies and apiaries is virtually certain,[10] and spillover to wild bees or other insects cannot be ruled out. Shared flowers provide a direct pathway into wild ecosystems; and act as a hub for microorganisms as an interface between insects and microbes.[11] While biocontainment tools such as kill switches, auxotrophies and xenobiology safeguards are under development, reviews underline that no containment

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[4] Huang, Q., et al., *Engineered gut symbiont inhibits microsporidian parasite and improves honey bee survival.* Proc Natl Acad Sci USA, 2023. **120**(25): p. E2220922120; Leonard, S., et al., *Engineered symbionts activate honey bee immunity and limit pathogens.* Science, 2020. **367**(6477): p. 573-576.

[5] Ellegaard, K. and P. Engel, *Genomic diversity landscape of the honey bee gut microbiota.* Nature communications, 2019. **10**(446).

[6] Kwong, W. and N. Moran, *Gut microbial communities of social bees.* Nature reviews microbiology, 2016. **14**: p. 374–384.

[7] Rüstemoğlu, M., *Next Generation Sequencing of Bee Gut Microbiota in Urban and Rural Environments.* DIversity, 2023(9): p. 1016; Soares, K., et al., *Comparing the impact of landscape on the gut microbiome of Apis mellifera in Atlantic Forest and Caatinga Biomes.* Scientific Reports, 2025. **15**(5293).

[8] Gorrochategui-Ortega, J., et al., *A short exposure to a semi-natural habitat alleviates the honey bee hive microbial imbalance caused by agricultural stress.* Scientific Reports, 2022. **12**(18832).

[9] Nguyen, P. and S. Rehan, *Integrating behaviour and microbiomes into considerations of bee health.* Canadian Science Publishing, 2026. **69**.

[10] Kwong, W. and N. Moran, *Gut microbial communities of social bees.* Nature reviews microbiology, 2016. **14**: p. 374–384.

[11] Lignon, V., et al., *The floral interface: a playground for interactions between insect pollinators, microbes, and plants.* New Zealand Journal of Zoology, 2024. **52**(2): p. 218-237.

system is entirely fail-proof.[12]

Resistance: As with chemical pesticides, repeated use could select and drive resistance in pests and pathogens, eroding long-term effectiveness. Unlike chemicals, engineered microbes may persist and evolve independently once released into the environment.

Ecological considerations

Honey bees forage across farmland, grasslands and protected areas. They share floral resources with wild pollinators and act as vectors of pathogens and microbes. Any engineered change in their biology has the potential to spill over into wider ecosystems.

Research shows that bees and flowers share a common microbiome, with flowers acting as hubs of microbial exchange that shape chemistry, scent and pollinator visitation.[13] Synthetic biology application risks disrupting floral microbiomes, altering plant-pollinator interactions and enabling horizontal transfer of engineered traits. Such changes could facilitate the spread of pathogens and exacerbate disease in wild pollinator communities.

Governance and transboundary issues

Bees do not recognise national borders. They forage across agricultural landscapes and conservation areas, drift between apiaries and are traded internationally. This creates two interlinked governance challenges:

Physical transboundary spread. Bees carrying genetically modified microbes may cross national frontiers, meaning that a release in one country or territory could affect pollinators, plants and ecosystems in another. Such transboundary movement raises questions of liability, notification and consent under existing biosafety and environmental governance frameworks.

Regulatory boundary-crossing. Microbiome engineering blurs established regulatory categories, such as “contained use” verses “deliberate release,” “veterinary product” versus “pesticide.” Existing legal frameworks were not designed for self-disseminating organisms, and potentially self-propagating organisms, leaving significant gaps in regulatory oversight.

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[12] Kim, D. and J. Lee, *Genetic Biocontainment Systems for the Safe Use of Engineered Microorganisms.* Biotechnology and bioprocess Engineering, 2020. **E**(25): p. 974–984

[13] Adler, L., et al., *Floral traits affecting the transmission of beneficial and pathogenic pollinator-associated microbes.* Current Opinion in Insect Science, 2021. **44**: p. 1-7.

The 2025 Ad Hoc Technical Expert Group (AHTEG) on Risk Assessment[14] confirms that microorganisms fall within the scope of the Cartagena Protocol on Biosafety as products of modern biotechnology. However, the report also identifies substantial technical challenges and regulatory challenges specific to microorganisms. Living modified microorganisms may cause adverse effects on biodiversity and ecosystems, and may also have indirect effects on human health. The AHTEG reported that microorganisms raise multiple challenges for the current Protocol and that additional guidance is therefore required. The AHTEG reported:

> Challenges could relate to microbial biology, microbial ecology, persistence, the genetic modification, the availability of data, monitoring and surveillance, containment and risk management, and little experience with the environmental release of living modified microorganisms.[15]

These characteristics pose fundamental recognised by Parties to the Cartegena Protocol, which have called for the development of additional guidance, as well as by the expert group, which agreed such organisms raise novel risks and uncertainties that are not adequately addressed by current risk assessment methodologies. [16] The inherent capacity of microorganisms to persist, evolve and cross national borders further amplifies these concerns and underscores the need for heightened caution.

In response, discussions are underway to develop new guidance for consideration and possible adoption at the Conference of the Parties in Armenia in 2026. Any such guidance must be firmly grounded in the precautionary principle and explicitly acknowledge the profound uncertainties and knowledge gaps that currently prevent comprehensive and reliable risk assessments. These challenges are compounded by issues of consent and control, given the self-propagating and potentially self-spreading nature of microorganisms, which can undermine assumptions of key regulatory assumptions regarding containment and reversibility.

Patenting the honey bee microbiome: equity, access, and conservation implications

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[14] Convention on Biological Diversity, *Report of the Ad Hoc Technical Expert Group on Risk Assessment*, in *Ad Hoc Technical Expert Group on Risk Assessment, 8–11 July 2025 Agenda item 5 Adoption of the report*, CBD/CP/RA/AHTEG/2025/1/3, Editor. July 2026, CBD: Montreal Canada.

[15] *Ibid*..

[16] Brewer, A., D. George, and E. Frow, *Emerging governance considerations for the deployment of genetically engineered microbes.* Current Opinion in Microbiology, 2026. **89**.

Recent patents on engineered microbial populations native to the honey bee microbiome,[17] including applications and granted patents covering the use of genetically modified gut bacteria to induce RNA interference in bees, signal a significant expansion of intellectual property claims into living pollinator systems. While framed as tools for bee health, such patents effectively extend proprietary control over biological functions of *Apis mellifera* itself, raising profound questions about ownership, dependency, and access in beekeeping and conservation contexts.

The enclosure of bee-associated microbiomes through patents risks creating cost and dependency burdens for Indigenous people and community beekeepers, increasing exposure to patent infringement liability, and displacing traditional, low-input, and locally adapted health practices. As voiced repeatedly within the beekeeping community, including at international fora such as Apimondia, the patenting of bees or their essential biological processes challenges ethical norms around the treatment of shared species and undermines the principle that pollinators constitute a common ecological heritage rather than a proprietary technology platform.

Beyond equity concerns, the prospect of patented “GMOs in nature” risks eroding public trust in conservation and pollinator protection efforts, particularly where technologies are developed within academic–corporate pipelines but deployed across shared landscapes. Transparent and independent risk assessments, open-access research pathways, meaningful participation of Indigenous Peoples and Local Communities, and governance frameworks that explicitly limit enclosure and prioritise ecosystem stewardship must therefore be foundational, not optional, if such interventions are to align with conservation objectives rather than intensify existing power asymmetries.

Microbiome engineering relies on proprietary vectors, payloads and biocontainment systems. This concentration of intellectual property risks shaping pricing and access for hobbyist, Indigenous, and community beekeepers and restricting public-sector research[18], echoing patterns already seen in RNAi crop-protection patents.[19]

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[17] Moran, N., J. Barrick, and S. Leonard, *Engineered microbial population*, Patent # 20230026506 in *https://patents.justia.com/inventor/nancy-moran*. 2022: USA; Moran, N., J. Barrick, and S. Leonard, *Engineered microbial population*, Patent # 11382989 in *https://patents.justia.com/inventor/nancy-moran*. 2018: USA; Moran, N., J. Barrick, and S. Leonard, *Engineered microbial population*. Patent # 20190015528 2018: USA.

[18] Saukschmya T and Chugh A (2010) **Intellectual property rights in synthetic biology: an anti-thesis to open access to research?**
https://pubmed.ncbi.nlm.nih.gov/22132050

[19] Germing, K., et al., *Crop protection by RNA interference: a review of recent approaches, current state of developments and use as of 2013.* Environmental Sciences Europe, 2025. **37**(15).

Without strong safeguards, the prospect of “GMOs in nature” risks eroding public trust and undermining broader conservation efforts. Transparent, robust and reliable risk assessments,[20] independent trials, meaningful participation of Indigenous Peoples and local communities, and governance systems that prioritise equity and ecosystem stewardship must be foundational elements, not afterthoughts, if such technologies are to align with conservation objectives.

Alternatives grounded in conservation practice

Microbiome engineering is still experimental and primarily oriented toward productivity approach rather than biodiversity protection. For managed bees, the priority is not new technological fixes but a reassessment of how the beekeeping industry operates. Hive densities should reflect ecological carrying capacity, especially in biodiversity hotspots and urban environments. Public funding would be better directed toward habitat restoration, forage diversity and support for wild pollinators rather than expanding honey production. Low-intensity, diversified beekeeping can play a role, but only when balanced within broader conservation goals.

For wild-bee conservation, the most effective measures are already well established: restoring habitat quantity and quality, reducing pesticide risks and improving landscape connectivity. These actions, embedded in EU pollinator initiative (2018)[21] now known as the “A new deal for pollinators” (2023)[22] should remain the primary focus of agri-environment support.

Lessons for conservation policy

Managed honey bees are a largely hidden form of intensive livestock, often maintained at densities that strain ecosystems. Treating them as conservation symbols obscures their role in the transmission of pathogens within shared landscapes.

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[20] EFSA (European Food Safety Authority), *Outcome of the public consultation on the draft Scientific Opinion on the evaluation of existing guidelines for their adequacy for the microbial characterisation and environmental risk assessment of micro-organisms obtained through synthetic biology. EFSA supporting publication 2020: EN-1934. 90 pp.*; EFSA Scientific Committee, *Evaluation of existing guidelines for their adequacy for the food and feed risk assessment of microorganisms obtained through synthetic biology.* EFSA Journal, 2022. **20**(8): p. e07479.

[21] European Commission. *COMMUNICATION FROM THE COMMISSION TO THE EUROPEAN PARLIAMENT, THE COUNCIL, THE EUROPEAN ECONOMIC AND SOCIAL COMMITTEE AND THE COMMITTEE OF THE REGIONS EU Pollinators Initiative*, C. final, Editor. 2018.

[22] European Commission, *REPORT FROM THE COMMISSION TO THE EUROPEAN PARLIAMENT, THE COUNCIL, THE EUROPEAN ECONOMIC AND SOCIAL COMMITTEE AND THE COMMITTEE OF THE REGIONS. Progress in the implementation of the EU Pollinators Initiative*, C. final, Editor. 2021. https://eur-lex.europa.eu/legal-content/EN/TXT/?uri=COM%3A2023%3A35%3AFIN

Growing evidence highlights the unsustainability of this model. In Southern California, managed honey bees have been shown to remove up to 80% of available pollen in a single day, severely depleting floral resources for more than 700 wild bee species.[23] Globally, introduced honey bees are frequently implicated in reduced pollination services to native plants and shifts toward invasive species proliferation.[24]

Protecting biodiversity requires refocusing conservation efforts on wild pollinators and ecosystems, while evaluating managed honey bee practices, including emerging technologies, through a lens of ecological responsibility and precaution.

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[23] Travis, D., et al., *Pollen exploitation by non-native, feral honey bees: Potential consequences for interspecific competition.* Insect Conservation and Diversity, 2025: p. 1-11.

[24] Iwasaki JM and Hogendoorn K (2022) https://pmc.ncbi.nlm.nih.gov/articles/PMC9387436