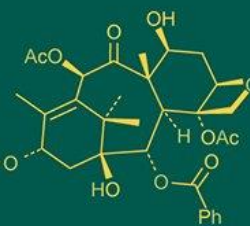
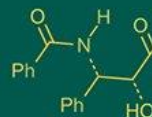


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A review on manipulating gut microbiota for insect pest control

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Abstract

The insect gut harbours a taxonomically diverse assemblage of bacteria, fungi and archaea that shape host nutrition, immunity and detoxification capacity, and this dependency has opened an alternative axis for pest suppression that does not rely solely on the insect's own genome. Rather than targeting the pest directly, manipulation of its resident microbiota offers routes to compromise nutrient acquisition, potentiate the action of existing biopesticides, deliver RNA interference constructs through paratransgenesis, or dismantle the detoxification pathways that make certain populations resistant to insecticides. Evidence accumulated across Lepidoptera, Diptera, Coleoptera and social Hymenoptera shows that gut bacterial communities are neither uniformly beneficial nor uniformly exploitable; their contribution to host fitness and to susceptibility varies with diet, developmental stage and the specific bacterial taxa present, and this context dependency has produced a literature in which effect sizes, and occasionally the direction of an effect, differ sharply between otherwise comparable studies. This review draws together mechanistic work on symbiont-mediated *Bacillus thuringiensis* synergy, symbiont-based RNA interference delivery and microbiota-linked insecticide detoxification, and sets these against the ecological and regulatory obstacles that have so far kept most applications at proof-of-concept stage. The analysis argues that progress now depends less on discovering further correlations between a gut bacterium and a pest phenotype, and more on establishing causal, reproducible, field-relevant mechanisms able to survive the transition from gnotobiotic insect rearing to open agricultural systems.

Keywords: Insect gut microbiota, paratransgenesis, *Bacillus thuringiensis* synergy, symbiont-mediated RNA interference, insecticide detoxification, biological pest control

Introduction

Every phytophagous or blood-feeding insect carries within its alimentary canal a community of microorganisms whose collective metabolic capacity often exceeds that encoded by the host genome itself. Dillon and Dillon (2004) ^[12] were among the first to frame this relationship in explicitly functional terms, arguing that gut bacteria in insects are rarely passive passengers and instead participate in digestion, nitrogen recycling and defence against pathogens. The decade that followed produced a shift from taxonomic cataloguing toward mechanistic dissection, a shift captured well by Engel and Moran (2013) ^[14], who showed that gut community composition in insects ranges from near-axenic in some Lepidoptera to densely colonised and host-specific in termites, aphids and bees. This structural diversity matters for pest management because it determines how tractable a given insect's microbiota is as an intervention target; a pest whose gut community is simple, horizontally acquired and dispensable for basic development is a very different proposition from one whose microbiota is vertically transmitted, obligate and tightly co-evolved with the host.

The rationale for manipulating gut microbiota as a pest control strategy rests on three overlapping premises. First, several gut bacteria have been shown to be necessary, not merely correlated, with the mortality caused by existing biopesticides such as *Bacillus thuringiensis*, so removing or altering them changes the efficacy of a tool already in wide agricultural use. Second, the gut lumen is an accessible entry point for foreign genetic material, and bacteria resident there can in principle be engineered to secrete double-stranded RNA or toxic peptides directly into the pest, an approach generally termed paratransgenesis and reviewed conceptually by Berasategui *et al.*, (2016) ^[2].

Third, gut bacteria are increasingly implicated in the very detoxification pathways that pests use to survive insecticide exposure, meaning that in some systems the microbiota is not a delivery vehicle for control but the resistance mechanism itself, a possibility documented for the diamondback moth by Xia *et al.*, (2018) ^[22].

None of these premises has translated cleanly from laboratory demonstration to field deployment, and the reasons are instructive rather than incidental. Gut communities are dynamic across instar, diet and geography, so a bacterial association discovered in one laboratory colony may be attenuated, absent or reversed in a field population reared on a different host plant. Douglas (2015) ^[13] made the broader point that resident microorganisms in insects should be understood as facultative contributors to a phenotype rather than fixed components of it, an argument with direct consequences for anyone hoping to exploit a single bacterium as a universal control lever. This review works through the main mechanistic routes by which gut microbiota manipulation has been proposed to control insect pests, weighs the comparative evidence for and against generalisability of each route, and identifies where the field's current gaps lie before setting out research priorities that would move the area from correlative description toward field-ready application.

Gut Bacteria as Modulators of *Bacillus thuringiensis* Efficacy

The clearest causal demonstration that gut bacteria influence pest susceptibility to an existing biopesticide came from work on the gypsy moth and cabbage looper, in which Broderick *et al.*, (2006) ^[4] showed that larvae rendered nearly germ-free by antibiotic treatment survived *Bacillus thuringiensis* challenge far better than larvae with an intact gut flora, and that reintroducing *Enterobacter* species restored susceptibility. The proposed mechanism was that Cry toxin damage to the midgut epithelium allows gut bacteria to breach into the haemocoel, where they trigger a lethal septicaemia that compounds the direct toxic action of the crystal protein rather than acting as a mere bystander effect. This finding reframed *Bt* mortality as a two-stage process, toxin-induced epithelial injury followed by bacteria-driven systemic infection, and the reframing had immediate practical weight because it implied that antibiotic residues, or naturally depauperate gut floras in field populations, could blunt the efficacy of a widely used biopesticide independent of any resistance allele in the insect genome.

Subsequent work complicated rather than confirmed this picture. Broderick *et al.*, (2009) ^[5] extended the antibiotic-suppression experiment across a wider range of Lepidoptera and found that the degree to which gut bacteria contributed to *Bt*-induced mortality varied substantially by species, with some larvae showing the expected loss of susceptibility under germ-free conditions and others showing little change at all. This variation argues against a single universal mechanism and instead suggests that the septicaemic route documented in gypsy moth is one of several pathways to Cry toxin lethality, with its relative importance depending on gut pH, peritrophic membrane integrity and the specific toxin receptor profile of the species in question. Where the mechanism does operate, it opens a genuinely novel management lever, because a formulation that pairs *Bt* with a compatible *Enterobacter* or related Enterobacteriaceae

inoculant could in theory restore or enhance efficacy in populations where natural gut flora has been depleted by prior antibiotic exposure, fungicide drift or unusually clean rearing diets.

The agronomic implication is double edged. If gut bacteria are required for full *Bt* potency in a given pest, then any agricultural practice that suppresses those bacteria, whether deliberate antibiotic use in integrated programmes or incidental exposure to bactericidal seed treatments, risks quietly eroding the performance of a biopesticide that growers assume is acting independently of the insect's microbial condition. Conversely, the same dependency is exploitable, because supplementing formulations with the right enteric bacterium, rather than reformulating the toxin itself, offers a comparatively cheap route to potentiation. What the literature has not yet delivered is a predictive framework for which lepidopteran pests fall into the septicaemia-dependent category and which do not, and without that framework the practical recommendation remains species specific rather than general.

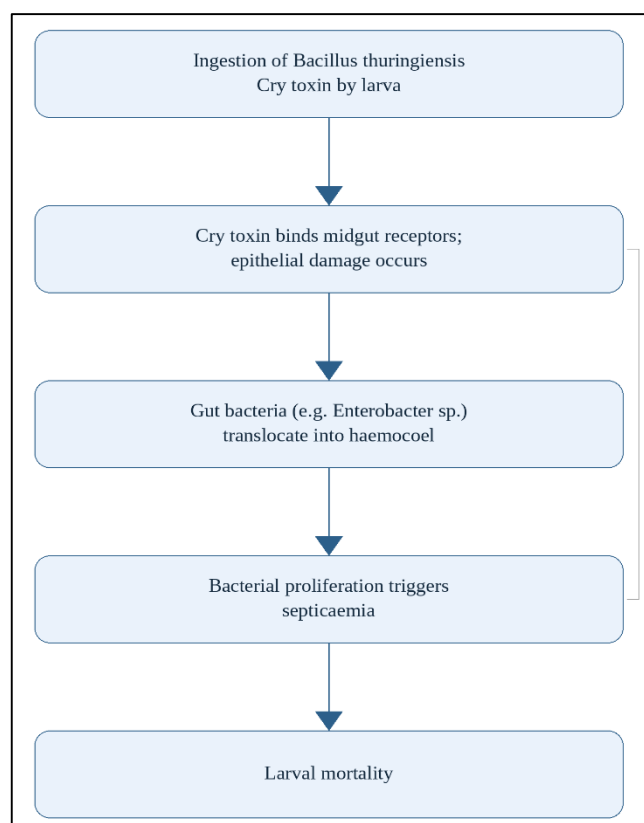


Fig 1: Proposed pathway by which gut bacteria contribute to *Bacillus thuringiensis*-induced mortality in susceptible Lepidoptera, integrating findings on Cry toxin-induced midgut epithelial damage, bacterial translocation into the haemocoel and resultant septicaemia.

Paratransgenesis and Symbiont-Mediated RNA Interference

Where the *Bt* synergy literature treats gut bacteria as passive contributors to an existing toxin's action, paratransgenesis treats them as active delivery vehicles that can be engineered to produce the toxic or gene-silencing agent themselves. The clearest proof of concept for disease vector control came from Wang *et al.*, (2017) ^[17], who engineered a symbiotic bacterium of *Anopheles* mosquitoes to secrete anti-*Plasmodium* effector molecules, achieving substantial reductions in oocyst infection intensity when the modified

bacterium was allowed to establish in the mosquito midgut. Although this system targets a pathogen rather than the insect itself, it demonstrates the essential engineering logic that underlies paratransgenic pest control more broadly, namely that a bacterium already tolerated by the host immune system can be repurposed as a stable, self-amplifying production platform for a molecule the insect would never encounter naturally.

Applying the same logic to gene silencing rather than pathogen blockade, Whitten *et al.*, (2016) ^[20] engineered a bacterial symbiont to produce double-stranded RNA against an essential insect gene and showed that colonisation of the gut by this modified bacterium was sufficient to trigger systemic RNA interference and elevated mortality in the host insect, circumventing the well-known problem of dsRNA degradation that plagues topical or dietary RNAi delivery in many pest species. Whitten and Dyson (2017) ^[21], reviewing this and related work, argued that symbiont-based delivery solves the stability problem inherent to naked dsRNA by continuously replenishing the silencing trigger from within a colonised niche, rather than relying on a single bolus dose that gut nucleases can degrade before it reaches target tissue. This continuous-production feature is arguably the single largest technical advantage paratransgenic RNAi holds over spray-applied or plant-incorporated dsRNA strategies, particularly for pests whose

gut environment is unusually hostile to exogenous nucleic acid.

The constraint that has kept paratransgenic RNAi largely within laboratory and semi-field trials is not the molecular biology, which is by now well rehearsed, but the ecology of establishment. A bacterium must not only be engineered successfully; it must also outcompete or coexist with the resident community, persist across moults and, ideally, transmit vertically or spread horizontally within a target population to be cost effective at field scale. Bourtzis *et al.*, (2016) ^[3], writing on symbiont-based approaches for mosquito and tsetse management, made the point that regulatory and containment questions around releasing genetically modified bacteria into open agricultural or public health settings remain substantially less resolved than the corresponding questions for genetically modified insects themselves, since a modified symbiont can in principle move between host individuals or even between species in ways a transgenic insect line typically cannot. This asymmetry between technical readiness and regulatory readiness is a recurring theme across the paratransgenesis literature and helps explain why the approach remains concentrated in vector-control programmes with strong public-health justification rather than in row-crop agriculture, where the cost-benefit calculus for accepting a novel release is less forgiving.

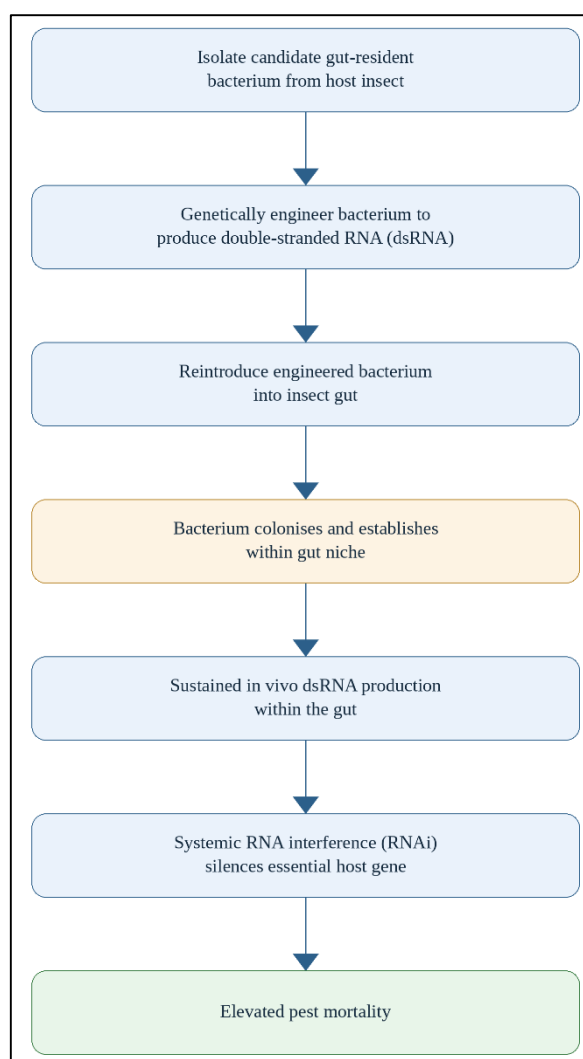


Fig 2: Generalised workflow for paratransgenic delivery of RNA interference constructs through an engineered gut symbiont, from isolation and transformation of the candidate bacterium through gut colonisation, sustained double-stranded RNA production and systemic gene silencing in the host insect.

Gut Microbiota-Mediated Insecticide Resistance and Detoxification

A separate strand of research inverts the control logic entirely by treating the gut microbiota not as a tool for suppression but as a mechanism the pest itself exploits to survive chemical control. Kikuchi *et al.*, (2012) ^[15] demonstrated that the bean bug *Riptortus pedestris* can acquire an organophosphate-degrading strain of *Burkholderia* from the soil and that this acquisition confers resistance to fenitrothion within a single generation, a striking example of resistance evolving through environmental symbiont acquisition rather than through mutation in the insect's own detoxification genes. Because this route to resistance bypasses the usual genetic assumptions built into resistance monitoring programmes, it raises the uncomfortable possibility that some populations scored as susceptible by genotyping at known resistance loci could nonetheless survive field rates of an insecticide if they happen to carry the right degrading bacterium, a possibility that standard genetic resistance surveillance is not designed to detect.

Comparable microbiota-linked resistance has since been reported in agricultural pests of direct crop relevance. Xia *et al.*, (2018) ^[22] found that gut bacterial communities in field populations of the diamondback moth, *Plutella xylostella*, differed measurably between insecticide-resistant and susceptible strains, and that manipulating the gut community through antibiotic treatment altered the insect's tolerance to chlorpyrifos, implicating specific bacterial taxa in xenobiotic breakdown within the host gut itself. Cheng *et al.*, (2017) ^[7] extended this logic to the oriental fruit fly, *Bactrocera dorsalis*, showing that a dominant gut symbiont enhanced host resistance to trichlorphon, and that this enhancement tracked with the abundance of the symbiont across populations sampled from different agricultural regions rather than with any single resistance allele. Together these studies suggest that microbiota-linked resistance is not confined to a single insect order or a single class of insecticide, but recurs wherever a gut bacterium happens to possess, or can acquire, catabolic capacity toward the compound in question.

The management consequence of this body of work is that gut microbiota manipulation cuts both ways within the same pest system. If a resident bacterium degrades an insecticide, then disrupting that bacterium, whether through a compatible antibiotic seed treatment, a bacteriophage targeted at the resistant strain or simply rotation to a chemical class the microbiota cannot metabolise, becomes a resistance management tool in its own right, distinct from rotating the insecticide's mode of action alone. Equally, any programme that intends to use gut bacteria constructively, for example through a paratransgenic delivery strain, needs to first establish whether the target pest's existing microbiota already includes detoxifying taxa that would blunt or interfere with the introduced construct's persistence, since colonisation resistance within an already-occupied gut niche is a well-documented obstacle to establishing a novel bacterial strain.

Divergence across Insect Taxa: Reconciling Conflicting Evidence

A reader moving from the Lepidoptera-focused *Bt* synergy literature to the Coleoptera-and Diptera-focused resistance literature could be forgiven for concluding that gut

microbiota research in entomology has produced a fragmented rather than a cumulative picture, and in one sense this conclusion is fair. Chandler *et al.*, (2011) ^[6], surveying gut bacterial communities across a broad panel of *Drosophila* species, found substantial interspecific variation in community composition even among closely related hosts sharing similar diets, which argues against extrapolating a mechanism discovered in one species directly onto a taxonomically adjacent pest without independent verification. This variability is not a methodological artefact so much as a biological reality; gut communities in most insects are acquired largely from diet and environment rather than transmitted with high fidelity from parent to offspring, so geography, host plant and rearing history can each reshape the community independently of the insect's taxonomic identity.

Bark and wood-boring beetles illustrate how far this divergence can run. Adams *et al.*, (2013) ^[1] showed that the gut and gallery-associated bacterial community of the mountain pine beetle is enriched for genes involved in terpene metabolism, a capacity plausibly linked to the insect's ability to detoxify the resinous defensive compounds of its conifer hosts, while Xu *et al.*, (2015) ^[23] found that gut-associated bacteria of the related bark beetle *Dendroctonus valens* participate directly in the production of verbenone, a compound that itself regulates beetle aggregation behaviour. Neither of these mechanisms maps onto the septicemia-based *Bt* synergy described for Lepidoptera or the organophosphate degradation described for the bean bug; instead they describe host-plant detoxification and semiochemical production, underscoring that the functional role gut bacteria play is dictated as much by the ecological niche of the insect, wood boring versus foliage feeding versus phloem feeding, as by any shared feature of insect gut physiology.

Even within a single well-studied host, contradictory results appear when experimental conditions differ. Where germ-free rearing sharply reduces *Bt* susceptibility in gypsy moth larvae, comparable manipulations in other Lepidoptera tested by Broderick *et al.*, (2009) ^[5] produced negligible change, and the honey bee literature reviewed by Raymann and Moran (2018) ^[16] likewise shows that core gut symbionts protective against certain pathogens and pesticide stressors are not interchangeable with the facultative, diet-acquired bacteria dominant in most agricultural pest species. Reconciling these discrepancies requires treating gut microbiota function as a property of the specific host-symbiont-diet combination under study rather than as a generalisable trait of a bacterial taxon, and reviewers who instead extrapolate a single mechanism across unrelated taxa risk overstating how close the field actually is to a broadly applicable control technology.

Translational Gaps: Ecological, Methodological and Regulatory Constraints

Much of the mechanistic evidence reviewed above derives from gnotobiotic or antibiotic-suppressed insects reared under controlled laboratory diets, conditions that isolate a causal relationship cleanly but simplify away the community complexity a real field population encounters. Coon *et al.*, (2014) ^[9] demonstrated that mosquito larvae reared axenically fail to develop past early instars unless bacteria are reintroduced, illustrating how thoroughly laboratory gnotobiotic systems can depart from field

physiology; a manipulation that looks decisive in an axenic assay may behave quite differently once competing bacterial taxa, host plant chemistry and temperature fluctuation are added back into the system. This gap between mechanistic clarity and ecological realism is arguably the single largest obstacle standing between the mechanisms catalogued in this review and any field-deployable product.

A second constraint is methodological rather than ecological, and concerns how gut communities are characterised in the first place. Much of the foundational literature, including Engel and Moran (2013) ^[14] and Dillon and Dillon (2004) ^[12], predates the routine use of high-throughput amplicon sequencing at the depth now considered standard, so community composition in older studies was often described from culturable isolates alone, a method known to undersample fastidious or obligately anaerobic taxa. More recent studies benefit from deeper sequencing but still rarely combine compositional data with functional validation, meaning that an association between a bacterial taxon's relative abundance and a pest phenotype is frequently reported without the reciprocal gnotobiotic or knockout experiment needed to establish causation, a gap explicitly acknowledged by Douglas (2015) ^[13] when

arguing that correlation between microbiota composition and host phenotype should not be mistaken for mechanism. Regulatory uncertainty compounds both problems. Bourtzis *et al.*, (2016) ^[3] noted that symbiont-based approaches for insect population management fall into a regulatory grey zone in many jurisdictions, neither clearly covered by frameworks built for chemical pesticides nor by those built for genetically modified whole organisms, and this ambiguity slows the transition of even mechanistically well-supported approaches, such as paratransgenic RNAi, from contained trial to open release. Crotti *et al.*, (2012) ^[10] made a related point specifically about agricultural rather than vector-control applications, arguing that symbiont-based biocontrol products face an additional commercial hurdle because formulation, storage stability and the need to maintain live bacterial viability through the supply chain are considerably harder logistical problems than those faced by conventional chemical or even *Bt*-based sprayable products. Taken together, these ecological, methodological and regulatory gaps explain why a literature rich in mechanistic insight has produced comparatively few field-ready technologies to date.

Table 1: Representative insect-symbiont systems relevant to gut microbiota-based pest control strategies

Insect host	Order	Symbiont	Mechanism	References
Gypsy moth (<i>Lymantria dispar</i>)	Lepidoptera	<i>Enterobacter</i> sp.	Required for full <i>Bt</i> -induced septicaemic mortality	Broderick <i>et al.</i> , (2006) ^[4]
Multiple Lepidoptera (comparative panel)	Lepidoptera	Native gut Enterobacteriaceae	Contribution to <i>Bt</i> mortality highly species dependent	Broderick <i>et al.</i> , (2009) ^[5]
Bean bug (<i>Riptortus pedestris</i>)	Hemiptera	<i>Burkholderia</i> sp.	Environmentally acquired organophosphate degradation confers resistance	Kikuchi <i>et al.</i> , (2012) ^[15]
Diamondback moth (<i>Plutella xylostella</i>)	Lepidoptera	Shifted gut community	Community shift linked to chlorpyrifos tolerance	Xia <i>et al.</i> , (2018) ^[22]
Oriental fruit fly (<i>Bactrocera dorsalis</i>)	Diptera	Dominant gut symbiont	Symbiont abundance enhances trichlorfon resistance	Cheng <i>et al.</i> , (2017) ^[7]
<i>Anopheles</i> mosquito	Diptera	Engineered symbiotic bacterium	Secreted effectors reduce <i>Plasmodium</i> oocyst intensity	Wang <i>et al.</i> , (2017) ^[17]
Generic Lepidoptera/Coleoptera pest models	Multiple	Engineered dsRNA-producing symbiont	Symbiont-delivered RNAi triggers systemic gene silencing	Whitten <i>et al.</i> , (2016) ^[20]
Mountain pine beetle (<i>Dendroctonus ponderosae</i>)	Coleoptera	Gut/gallery bacterial community	Community enriched for terpene-metabolism genes aiding host detoxification	Adams <i>et al.</i> , (2013) ^[1]
Red turpentine beetle (<i>Dendroctonus valens</i>)	Coleoptera	Gut-associated bacteria	Bacterial contribution to verbenone production influencing aggregation	Xu <i>et al.</i> , (2015) ^[23]
<i>Anopheles stephensi</i>	Diptera	<i>Wickerhamomyces anomalus</i> (yeast)	Midgut and reproductive tract colonisation exploited for paratransgenesis	Ricci <i>et al.</i> , (2011) ^[17]
Tsetse fly (<i>Glossina</i> spp.)	Diptera	Obligate/facultative endosymbionts	Symbiont presence required for immune system maturation in larvae	Weiss <i>et al.</i> , (2011) ^[18]
Western corn rootworm (<i>Diabrotica virgifera virgifera</i>)	Coleoptera	Gut bacterial community	Facilitates adaptation to crop rotation and novel host tissue	Chu <i>et al.</i> , (2013) ^[8]
Honey bee (<i>Apis mellifera</i>)	Hymenoptera	Core gut symbiont community	Protective role against pathogens and pesticide-associated stress	Raymann and Moran (2018) ^[16]

Table 2: Comparative outcomes of gut bacteria suppression on *Bacillus thuringiensis* susceptibility across Lepidoptera and related taxa

Species	Suppression method	Effect on <i>Bt</i> susceptibility	Proposed basis	References
Gypsy moth (<i>Lymantria dispar</i>)	Antibiotic treatment	Marked reduction in mortality	Loss of septicemia-inducing gut bacteria	Broderick <i>et al.</i> , (2006) ^[4]
Gypsy moth (<i>Lymantria dispar</i>)	Reintroduction of <i>Enterobacter</i>	Susceptibility restored	Re-establishment of translocating gut bacteria	Broderick <i>et al.</i> , (2006) ^[4]
Cabbage looper (<i>Trichoplusia ni</i>)	Antibiotic treatment	Partial reduction in mortality	Contribution of gut bacteria present but smaller in magnitude	Broderick <i>et al.</i> , (2009) ^[5]
Fall webworm (comparative panel species)	Antibiotic treatment	Minimal change observed	Cry toxin acting largely independent of gut bacteria in this species	Broderick <i>et al.</i> , (2009) ^[5]
Beet armyworm (comparative panel species)	Antibiotic treatment	Intermediate reduction in mortality	Mixed contribution of direct toxicity and bacterial translocation	Broderick <i>et al.</i> , (2009) ^[5]
Additional Lepidoptera surveyed by panel	Antibiotic treatment	Species-dependent, ranging from strong to negligible	Variation attributed to differing midgut pH and epithelial repair capacity	Broderick <i>et al.</i> , (2009) ^[4]
General Lepidoptera (background context)	Not applicable, descriptive	Not applicable	Baseline gut bacterial density and composition established as highly variable across species	Dillon and Dillon (2004) ^[12]
Cross-order comparison (background context)	Not applicable, descriptive	Not applicable	Structural diversity of gut communities across insect orders framed as a determinant of susceptibility variation	Engel and Moran (2013) ^[14]

Conclusion

Gut microbiota manipulation has moved, over roughly two decades, from an interesting biological footnote to a genuine third axis of insect pest management alongside conventional chemistry and transgenic host resistance. What the accumulated evidence supports is narrower than what the early enthusiasm for the field sometimes implied. Bacteria clearly modulate the efficacy of an established biopesticide in some Lepidoptera, clearly enable delivery of gene-silencing constructs when engineered and successfully established, and clearly underlie resistance to certain insecticides in specific pest populations, but none of these mechanisms yet generalises cleanly across taxa, and the same bacterial trait that suppresses one pest can protect another.

The most productive next phase for the field is unlikely to come from further single-species discovery work, however mechanistically elegant, and more likely to come from deliberately comparative studies that test whether a given mechanism travels between related pests, from semi-field trials that expose engineered or supplemented strains to the competitive and environmental pressures a laboratory colony never experiences, and from a regulatory conversation that has so far lagged well behind the molecular biology. Framed this way, gut microbiota manipulation is not a single technology awaiting deployment but a family of related strategies, each demanding its own evidence base, its own delivery logistics and its own risk assessment before it can take a place in an integrated pest management programme rather than remaining a compelling laboratory result.

References

- Adams AS, Aylward FO, Adams SM, Erbilgin N, Aukema BH, Currie CR, *et al.* Mountain pine beetles colonizing historical and naive host trees are associated with a bacterial community highly enriched in genes contributing to terpene metabolism. *Applied and Environmental Microbiology*. 2013;79(11):3468-3475.
- Berasategui A, Shukla S, Salem H, Kaltenpoth M. Potential applications of insect symbionts in biotechnology. *Applied Microbiology and Biotechnology*. 2016;100(4):1567-1577.
- Bourtzis K, Lees RS, Hendrichs J, Vreysen MJB. More than one rabbit out of the hat: Radiation, transgenic and symbiont-based approaches for sustainable management of mosquito and tsetse fly populations. *Acta Tropica*. 2016;157:115-130.
- Broderick NA, Raffa KF, Handelsman J. Midgut bacteria required for *Bacillus thuringiensis* insecticidal activity. *Proceedings of the National Academy of Sciences*. 2006;103(41):15196-15199.
- Broderick NA, Robinson CJ, McMahon MD, Holt J, Handelsman J, Raffa KF. Contributions of gut bacteria to *Bacillus thuringiensis*-induced mortality vary across a range of Lepidoptera. *BMC Biology*. 2009;7:11.
- Chandler JA, Lang JM, Bhatnagar S, Eisen JA, Kopp A. Bacterial communities of diverse *Drosophila* species: Ecological context of a host-microbe model system. *PLOS Genetics*. 2011;7(9):e1002272.
- Cheng D, Guo Z, Riegler M, Xi Z, Liang G, Xu Y. Gut symbiont enhances insecticide resistance in a significant pest, the oriental fruit fly *Bactrocera dorsalis* (Hendel). *Microbiome*. 2017;5:13.
- Chu CC, Spencer JL, Curzi MJ, Zavala JA, Seufferheld MJ. Gut bacteria facilitate adaptation to crop rotation in the western corn rootworm. *Proceedings of the National Academy of Sciences*. 2013;110(29):11917-11922.
- Coon KL, Vogel KJ, Brown MR, Strand MR. Mosquitoes rely on their gut microbiota for development. *Molecular Ecology*. 2014;23(11):2727-2739.
- Crotti E, Balloi A, Hamdi C, Sansonno L, Marzorati M, Gonella E, *et al.* Microbial symbionts: A resource for the management of insect-related problems. *Microbial Biotechnology*. 2012;5(3):307-317.
- Dennison NJ, Jupatanakul N, Dimopoulos G. The mosquito microbiota influences vector competence for human pathogens. *Current Opinion in Insect Science*. 2014;3:6-13.
- Dillon RJ, Dillon VM. The gut bacteria of insects: Nonpathogenic interactions. *Annual Review of Entomology*. 2004;49:71-92.
- Douglas AE. Multiorganismal insects: Diversity and function of resident microorganisms. *Annual Review of Entomology*. 2015;60:17-34.

14. Engel P, Moran NA. The gut microbiota of insects: Diversity in structure and function. *FEMS Microbiology Reviews*. 2013;37(5):699-735.
15. Kikuchi Y, Hayatsu M, Hosokawa T, Nagayama A, Tago K, Fukatsu T. Symbiont-mediated insecticide resistance. *Proceedings of the National Academy of Sciences*. 2012;109(22):8618-8622.
16. Raymann K, Moran NA. The role of the gut microbiome in health and disease of adult honey bee workers. *Current Opinion in Insect Science*. 2018;26:97-104.
17. Ricci I, Damiani C, Scuppa P, Mosca M, Crotti E, Rossi P, *et al.* The yeast *Wickerhamomyces anomalus* (*Pichia anomala*) inhabits the midgut and reproductive system of the Asian malaria vector *Anopheles stephensi*. *Environmental Microbiology*. 2011;13(4):911-921.
18. Weiss BL, Wang J, Aksoy S. Tsetse immune system maturation requires the presence of obligate symbionts in larvae. *PLOS Biology*. 2011;9(5):e1000619.
19. Wang S, Dos-Santos ALA, Huang W, Liu KC, Oshaghi MA, Wei G, *et al.* Driving mosquito refractoriness to *Plasmodium falciparum* with engineered symbiotic bacteria. *Science*. 2017;357(6358):1399-1402.
20. Whitten MMA, Facey PD, Del Sol R, Fernandez-Martinez LT, Evans MC, Mitchell JJ, *et al.* Symbiont-mediated RNA interference in insects. *Proceedings of the Royal Society B*. 2016;283(1825):20160042.
21. Whitten MMA, Dyson PJ. Gene delivery via symbiotic bacteria for RNAi-based pest control. *Current Opinion in Insect Science*. 2017;22:84-90.
22. Xia X, Sun B, Gurr GM, Vasseur L, Xue M, You M. Gut microbiota mediate insecticide resistance in the diamondback moth, *Plutella xylostella* (L.). *Frontiers in Microbiology*. 2018;9:25.
23. Xu L, Lou Q, Cheng C, Lu M, Sun J. Gut-associated bacteria of *Dendroctonus valens* and their involvement in verbenone production. *Microbial Ecology*. 2015;70(4):1012-1023.