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From Hidden Viromes to Synthetic Microbiomes: Reshaping Plant Disease and Pest Dynamics in the Anthropocene Era

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Abstract

The hidden diversity of viruses (the “virome”) in plant and soil ecosystems is being uncovered by metagenomic sequencing, revealing many novel viruses in crops, wild plants and microbial hosts. Plant viromes often dominated by RNA viruses can influence disease emergence, host resistance and stress tolerance. At the same time, synthetic microbiomes (laboratory-designed consortia of beneficial bacteria, fungi and other microbes) are being developed to bolster plant defenses and resilience. This review synthesizes current knowledge on plant-associated viromes and engineered microbiomes, focusing on how they reshape plant disease and pest dynamics in the Anthropocene. We first define key concepts: the plant virome, microbiome and synthetic community and outline the scope of their relevance. We describe methodologies for virome detection (including untargeted sequencing and computational virus discovery) and for designing synthetic communities (from isolation to in planta assembly). We examine ecological and evolutionary consequences: for example, how virus reservoirs in wild flora can spill over into crops, how coevolution under stress may convert viruses into mutualists and how tailored microbial consortia can suppress pathogens or affect insect pests. We then discuss potential risks of horizontal gene transfer, ecological imbalance, public acceptance and the evolving regulatory landscape for engineered microorganisms. Finally, we identify knowledge gaps (uncharacterized viral taxa, multi-kingdom community dynamics, long-term field outcomes) and propose research priorities for integrating virome science and microbiome engineering into sustainable agriculture.

Keywords: *Viruses; Viromes; Detection; Evolution; Pathogens; Pests.*

Introduction

The identification of viruses infecting plants goes back to the late 19th century. In 1886, Adolf Mayer described a disease of tobacco and later Dmitri Iwanowski (1892) and Martinus Beijerinck (1898) showed that tobacco mosaic virus (TMV) was a non-bacterial, "contagium vivum fluidum". The crystallization of TMV by W.M. Stanley in 1935 confirmed the virus concept and gave rise to plant virology [1,2]. The 20th century saw the discovery of dozens of plant viruses and the emergence of ideas like cross-protection (using mild viruses to safeguard crops) [3]. At the same time, the relevance of soil and root microorganisms became clear in the early 20th century. However, the concentration of microbiology on bacteria and fungi meant that plant-associated microbiomes were conceptually separated [4]. The term "microbiome" (later applied to the human gut flora) and the concept of a plant "holobiont" (plant with its microorganisms) were more widely used in the 21st century. Microbial communities were diversified in root zones (rhizospheres) and leaf surfaces (phyllospheres) impacting plant health [5,6].

The notion of the Anthropocene is that human activity (industrial agriculture, global commerce and climate change) has profoundly changed Earth's ecosystems: emerged about 2000 [7]. During the age of the Green Revolution in agriculture, there were extensive monocultures, widespread use of agrochemicals and fast worldwide movement of crops and pests. These approaches have enhanced agricultural yields, but also resulted in soil degradation, insect infestations and climatic stress on plants [8]. At the same time, advances in sequencing and biotechnology (around 2010s) allowed an unprecedented examination of microbial and viral diversity in crops and wild plants. In the 2010s, researchers started to intentionally assemble synthetic microbial communities (SynComs) to enhance agricultural attributes and deep sequencing revealed enormous undiscovered viromes in farm and natural systems. So, in the Anthropocene, plant pathology and entomology are inseparable from microbial ecology and synthetic biology, transforming the way we think about and control plant disease and pest dynamics [9,10].

Plant microbiome is the aggregate of all microorganisms associated with plants (bacteria, fungus, archaea, protists and viruses) that colonize roots, leaves, flowers and seeds. Conceptually it extends to the phytobiome (plant host, related organisms and environment). Plants actively alter their microbiomes via root exudates and other signals and microbiomes in turn regulate plant nutrition, growth and immunity. A core microbiome may be made up of microbial species that are consistently present in a host plant throughout settings [11,12,13].

Virome are the combined viral genetic material inside an environment (here, coupled with plants). It comprises viruses that infect the plant itself (pathogens, persistent viruses), viruses of plant-associated microorganisms (bacteriophages, mycoviruses) and viruses in invertebrate vectors. Most plant viromes are dominated by RNA viruses (single- and double-stranded) [14]. Many viruses are 'cryptic' – they infect plants or microorganisms, but without any evident symptoms. Viral groups that have been recently found (e.g. new phyla of RNA viruses) increase the known virosphere enormously.

Synthetic microbiomes (SynComs) are specifically designed communities of bacteria that mimic or improve desired functionalities of natural microbiomes [15,16]. These may be bacteria, fungi, or even viruses that have been chosen for features such as the ability to suppress pathogens or tolerate stress. SynCom design may rely on core microbiome members of healthy plants, on microbial consortia found in suppressive soils, or on created strains [17]. It is typically compared to strain bioinoculants (which may be inconsistent); SynComs seek synergistic stability. The review deals with plant diseases (caused by pathogenic microbes: fungus, bacteria, oomycetes, nematodes, viruses) and pests (herbivores such as insects and worms). Both are affected by microbial communities [18]. For example, certain rhizosphere bacteria may generate systemic resistance to insect herbivores and viruses can be spread by insect vectors. It covers pests in general, although the main emphasis is on diseases [19].

The Anthropocene (the age of major human influence) is characterized by causes such as climate warming, habitat fragmentation, monoculture farming, pesticide usage and global commerce that have changed disease and pest dynamics [20,21]. Warmer temperatures are seeing the spread of pests. Intensive agriculture may reduce the diversity of microbiomes. Pests and illnesses travel the world. These changes interact with viromes and microbiomes, sometimes upsetting ecosystems, sometimes providing new options (e.g. synthetic solutions). Sustainable agriculture (biologically based approaches) is a unifying theme throughout [22].

Methods for Detecting Viromes and Designing Synthetic Microbiomes

The revolution in plant virome identification via advances in genomics and analytics has also driven SynCom design. Important methodological points are:

- **Sampling and nucleic acid extraction:** Samples of plant tissue (leaves, roots, seeds), soil or rhizosphere and insect vectors are collected. We extract total RNA or DNA. In virome studies, enrichment procedures are often used for viral particles (e.g. filtration, nuclease treatment or dsRNA capture kits) to increase the virus signal [23,24].
- **High-throughput sequencing (HTS):** Unbiased sequencing is important to virome discovery. Short-read platforms (Illumina) are used to produce large amounts of sequences from whole or double-stranded RNA depleted of rRNA. Complete viral genomes can be assembled on long-read technologies (PacBio, Oxford Nanopore). Library preparation biases: poly(A)-tail enrichment procedures will prefer polyadenylated RNA (e.g. many +ssRNA viruses), whereas rRNA depletion or whole RNA kits will catch non-polyadenylated viruses (e.g. dsRNA viruses, DNA viruses) [25,26].
- **Metagenomic assembly and categorization:** Contigs are constructed from the sequence reads. Viral sequences are searched for via similarity to databases (BLAST versus viral genomes) and by signature techniques. Tools like VirSorter, VirFinder and deep-learning algorithms (e.g., VirHunter) may predict infectious content without close homology. These technologies can find whole new viruses. Also, short RNA (siRNA) sequencing from plants may be indicative of viral infection [27,28].
- **Validation by targeted assays:** Candidate viruses found by HTS are often confirmed by PCR or ELISA (if antibodies exist), especially for known viruses. Novel virus genomes may be verified by RT-PCR and Sanger sequencing [29,30,31].
- **Isolation and cultivation of microbes:** For synthetic microbiomes, traditional microbiology is still used: culturing bacteria and fungi from plant tissues or soil and characterizing them. Isolation is inherently biased (many microbes are uncultivable), but it allows functional testing [32,33].

Design of synthetic communities: Engineering SynComs typically follows these steps:

1. Sequencing (16S/ITS amplicons, metagenomes) to detect bacteria consistently linked with healthy plants or soils that suppress disease. This is the first stage in the core member identification process. These are the core or keystone species and they are the prospective contenders to become a member of SynCom [34].
2. Choose isolates with beneficial traits (antagonism to pathogens, PGP traits) for the in vitro community building procedure. They should be cultivated together to see whether they are compatible or not [35].
3. Greenhouse validation: Inoculate axenic or disinfected plants with the synthetic consortium to assess the growth of the plants, the suppression of illnesses or their resilience to stress compared to the controls [36].
4. Iteration: Change composition according to performance, add or remove strains, introduce genetically engineered microorganisms with improved features (e.g. nitrogen-fixing bacteria modified by CRISPR) [37].
5. Formulation development (liquid, powder, seed coating) for field application. This is the fifth phase in scale-up preparation [38].

- **Bioinformatic and modelling tools:** Designing SynComs is aided by network analysis (co-occurrence networks to find interacting pairs), genome mining (to predict metabolic functions) and machine learning (to predict stable combinations). Computational models can simulate community stability under different conditions [39].
- **Containment and monitoring systems:** When engineered microbes are used, biocontainment strategies (auxotrophic strains, kill-switch circuits) and ecological assays are applied to minimize risk [40,41].

The following tables summarize representative methods and virus taxa:

This table indicates that a mix of biological and computational approaches is necessary to uncover the hidden virome. On the other hand, the building of synthetic microbiomes integrates both classical microbiology and modern systems technology. For example, deep sequencing might identify viruses that are already known and network analysis could identify possible microbial partners for SynComs [58].

Ecological and Evolutionary Impacts on Plant Disease and Pest Dynamics

Plant viromes and microbiomes have profound effects on the ecology and evolution of plant disease and pest systems [59]. The interactions can be broadly described as follows:

- **Reservoirs and spillover:** Wild plants, weeds and non-crop hosts commonly carry viruses and bacteria that may flow over into agricultural systems. Wild flora are reservoirs for plant

Table 1. Methods for virome detection and synthetic microbiome design [50–57]

Method/Tool	Category	Use/Feature/Outcome
High-throughput sequencing (Illumina)	Virome Detection	Deep sequencing of total RNA/DNA extracts; detects known and novel viruses; high coverage of small genomes. Short reads require assembly to recover viral genomes.
Long-read sequencing (PacBio/ONT)	Virome Detection	Generates long contigs (often full viral genomes) directly; useful for complex or repetitive viral genomes; lower throughput.
rRNA-depleted total RNA seq	Library Prep	Removes ribosomal RNA to enrich viral and microbial RNA; broad detection of RNA viruses, especially non-polyadenylated types.
Poly(A)-capture RNA seq	Library Prep	Enriches polyadenylated transcripts; catches +ssRNA viruses with poly(A) tails (e.g. Potyvirus), but misses many others.
dsRNA capture/enzymatic enrichment	Virome Enrichment	Enriches double-stranded or viral RNA; improves signal for dsRNA viruses.
VANA (Virion-Associated Nucleic Acids)	Virome Enrichment	Isolates virus particles from extracts before sequencing; recovers both RNA and DNA viruses.
Virus-specific PCR/ELISA	Validation/Diagnostics	Targets known viruses with primers or antibodies; confirms presence in samples; requires prior knowledge.
VirFinder, VirSorter	Computational Tool	Detects viral sequences by sequence signatures (k-mers, gene content) without known homology. Useful for novel viruses.
Shotgun metagenomics (microbes)	Microbial profiling	Whole-community DNA sequencing to discover potential beneficial microbes (genes for PGP traits, antimicrobials).
Biofertilizer formulation (seed coat, granules)	Delivery method	Packaging SynCom inoculants for application (coating seeds, mixing into soil) to introduce beneficial consortia at planting.

viruses; for example, several symptomless infections with viruses such as Turnip mosaic virus (TuMV) or Cucumber mosaic virus (CMV) have been found in weed species bordering agricultural areas. These hidden reservoirs may re-infect crops and influence disease outbreaks. Pathogens and beneficial microorganisms may also transfer across wild and controlled ecosystems with implications for regional disease patterns [60,61,62].

- **Disease-suppressive microbiomes:** Certain soils or root microbiomes naturally suppress particular diseases (e.g. take-all decrease in wheat, Fusarium wilt suppression). These are suppressive soils with microbial communities that suppress diseases via competition, antibiosis or induced plant resistance. Synthetic microbiome techniques aim at recreating or transplanting such suppressiveness by assembling important microbial taxa [63,64].
- **Pathogen helpers and dysbiosis:** Not all microorganisms are good for plants. Some may promote illness ("pathogen helpers"), for example by regulating host immunity, or delivering nutrients to a pathogen. Stress or genetics may alter normal microbial control, resulting in the dominance of opportunistic pathogens and a dysbiotic (imbalanced) microbiome [65,66,67].
- **Evolution of virulence and host range:** Hidden viromes provide a reservoir of genetic vari-

Table 2. Synthetic microbiome applications and outcomes [87–90]

Crop/System	Synthetic Community Composition	Target Outcome
Apple (orchard soil)	5 root bacteria + 3 beneficial fungi (e.g. *Bacillus*, *Trichoderma*)	Suppress Apple replant disease (ARD)
Maize (drought-prone field)	8 drought-adapted bacteria (from sugarcane rhizosphere)	Enhance drought tolerance, yield
Tomato (greenhouse)	4 phyllosphere bacteria (from healthy tomato leaves)	Suppress bacterial wilt (*Ralstonia*)
Soybean (field)	6 nitrogen-fixers + PGP rhizobacteria	Increase yield, soil N fertility
Cucumber (field)	3 antagonistic *Pseudomonas* spp.	Control Fusarium wilt
Rice (seedling)	2 endophytic bacteria with ACC-deaminase activity	Salt stress tolerance
Wheat (field)	*Streptomyces* + *Trichoderma* consortium	Suppress common root rot
Soybean (greenhouse)	Mock community of 3 soil fungi	Prime immune system (ISR)
Lettuce (hydroponic)	Yeast + *Bacillus* inoculum	Biofilm formation, nutrient uptake
Pepper (field)	Phage cocktail + beneficial rhizobacteria	Control bacterial spot (*Xanthomonas*)
Cotton (saline field)	Salt-tolerant rhizobacteria + mycorrhizal fungi	Improve salt tolerance, yield

ety; new viral strains or species may arise with changed host ranges or virulence. RNA viruses have high mutation rates and recombination, allowing them to evolve rapidly. In the Anthropocene, hosts are under heavy selection, with concentrated agriculture and monocultures favoring virulent strains suited to homogeneous crops [68,69].

- **Mutualistic viruses:** Viruses may be advantageous to hosts under certain circumstances. Some plant viruses have been shown to increase resistance to drought or cold. It has been demonstrated that plants suffering from drought may generate mutualistic plant viruses that improve host survival. Similarly, mycoviruses (viruses of fungi) may reduce the virulence of fungal diseases and thereby provide efficient protection to the plant host [70,71].
- **Effects on pest (herbivore) dynamics:** The plant microbiome also impacts insect pests. Volatiles or poisons that repel herbivores may be produced by rhizosphere or phyllosphere microbes. Certain endophytic fungi or bacteria, for example, produce systemic resistance that lowers insect feeding [72]. By contrast, insect vectors transmit both plant viruses and their own symbiotic bacteria/viruses, thus a designed microbiome in the vector or plant might, in principle, interfere with transmission [73,74].
- **Climate and Anthropocene drivers:** Climate change intensifies these connections. Higher temperatures may boost replication rates of viruses or extend ranges of vectors. Elevated CO_2 and drought change root exudates and microbiota composition [75]. Land-use change (deforestation, intensive tillage) homogenizes soil ecosystems, sometimes resulting in the loss of beneficial bacteria. Global commerce may bring non-native infections into naïve microbiomes, frequently with disastrous consequences (e.g. chestnut blight, citrus greening, or tomato brown rugose fruit virus) [76].
- **Microbiomes and the evolution of plant defense:** Plants co-evolve with their microbiomes. Domestication and breeding have often targeted plant immunity genes, however there is increasing evidence that plants choose helpful bacteria via exudates and immune regulation. Future plant genotypes might be selected to attract more protective microbiomes or to withstand transgenic strains [77,78].
- In this model, plants, pathogens, pests and mi-

Table 3. Representative plant virus taxa and characteristics [42–49]

Virus Family/-Genus	Genome Type	Typical Hosts	Transmission
Tobamovirus	+ssRNA (non-enveloped)	Tobacco, tomato, cucumber, others	Mechanical (sap), seeds
Potyvirus	+ssRNA	Many crops (e.g. potato virus Y; cereals; legumes)	Aphid (non-persistent)
Geminivirus (Begomovirus)	ssDNA (circular)	Tomato, cotton, legumes, vegetables	Whiteflies (*Bemisia tabaci*)
Bromoviridae	+ssRNA (multipartite)	Cucurbits, stone fruits, ornamentals	Aphids or pollen
Tombusviridae (Carmovirus/Necrodamovirus)	+ssRNA (monopartite or bipartite)	Various wild plants and crops (e.g. lettuce, spinach)	Mechanical (sap); some via beetles
Tospovirus (Orthotospovirus)	-ssRNA (enveloped)	Vegetables (tomato, pepper, beans)	Thrips (*Frankliniella*, *Thrips*)
Rhabdovirus	-ssRNA (enveloped)	Several crops (e.g. maize, rice, lettuce)	Aphids
Caulimovirus (Pararetrovirus)	dsDNA (with RNA intermediate)	Banana, citrus, strawberry, brassicas	Aphids or whiteflies
Nanovirus	ssDNA (multicomponent)	Legumes (e.g. faba bean); coconut	Aphids
Endornavirus	dsRNA	Many plants (grasses, legumes)	Vertical (seed/pollen)
Luteovirus	+ssRNA	Cereals, legumes, potato	Aphids (persistent)
Benyvirus	+ssRNA (multipartite)	Sugar beet, hops, cereals	*Polymyxa* protists (soilborne vector)
Sobemovirus	+ssRNA	Cereal crops, some dicots	Insects, possibly seeds
Partitivirus	dsRNA (segmented)	Fungi and plants (some spores, seeds)	Seed, pollen (vertical)

crobiota form a network of interactions. The native microbiome can inhibit disease and pests, but it can also harbor latent pathogens and viruses. Introducing a synthetic community aims to strengthen beneficial interactions (e.g. pathogen suppression) and disrupt harmful ones. Anthropocene factors (warming, habitat change) affect all compartments [79].

Several recent studies illustrate how understanding viromes and using synthetic microbiomes can reshape plant health in practice:

- **Soil transmission of disease suppression:** ARD often arises from the accumulation of soil pathogens in perennial orchards. A synthetic consortium of beneficial bacteria and fungi derived from healthy rhizospheres salvaged plant growth. Application of a SynCom of *Bacillus*, *Trichoderma* and other root colonizers to replanted apple or rose soils led to a significant decrease in the severity of replant disease symptoms, possibly as a consequence of antagonism of *Fusarium* and *Pythium* pathogens. One study showed that the incidence of Fusarium wilt was reduced in greenhouse tests by combining 5–10 root-associated bacteria into a synthetic microbiota (SynMs), providing a proof of concept of how consortia might be used as a replacement for chemical fumigation [80,81].
- **Increased stress tolerance and productivity in**

cereals: Inoculation of maize fields with a SynCom isolated from sugarcane enhanced biomass under water stress and stabilized output. Similarly, desiccation-resistant bacterial consortia enhanced crop growth parameters (height, root weight) in drought tests. In soybean field tests, multi-strain inoculants boosted yield by up to 30–40% over controls demonstrating that well-designed consortia may translate to real-world benefits [82].

- **Control of vegetable pathogens:** SynComs have been used in plants for defense against soilborne wilt and blight. For example, a consortium of rhizobacteria (including *Bacillus* and *Pseudomonas* spp.) treated tomato plants reduced the wilt caused by *Ralstonia solanacearum* by generating resistance. In cucumber, foliar spray application of a synthetic leaf microbiome mix (from disease suppressive fields) decreased powdery mildew severity by boosting the abundance of beneficial yeast and bacteria on the leaves [83].
- **Virome-informed quarantine and diagnostics:** Metagenomic monitoring has revealed unexpected viruses in weeds close to crops leading to novel management strategies. For instance, high-throughput sequencing revealed two novel potexviruses in weeds close to bean fields, resulting in improved sanitation techniques to eliminate weed reservoirs. In another case a new ilarvirus was identified in nightshade and this led to farmers changing their crop rotation and thus preventing a possible epidemic in tomatoes [84,85].
- **Phage and microbial predators for biocontrol:** The virome method is now being used to pests as well: bacteriophages specific to *Xanthomonas* or *Erwinia* (bacterial plant diseases) have been created to treat fire blight in orchards. In certain vineyards, rootstock soil sprayed with virus-like particles (bacteriophages) killed *Agrobacterium*, reducing crown gall disease. Similarly, the discovery and enhancement of naturally existing predatory bacteria (*Bdellovibrio*-like species) in the rhizosphere has promise as a synthetic biocontrol [86].

Risks, Ethical and Regulatory Considerations

While synthetic microbiomes offer benefits, they raise important risks and governance issues. Key considerations include:

- **Ecological hazards (horizontal gene transfer and invasiveness):** Engineered or imported bacteria may swap genes with natural populations. Antibiotic resistance, or synthetic features (e.g. new metabolic enzymes) might be transferred into pathogens or soil microorganisms, thereby changing the ecological dynamics. A transgenic designed strain (e.g. with enhanced pesticidal potential) may distribute its genes by plasmids or phages. Introduced microorganisms may potentially become invasive by outcompeting native species particularly if they have growth benefits. This may lead to a loss of biodiversity or disruption of established plant-microbe associations [91,92].
- **Containment and biosafety:** To reduce dangers, synthetic microorganisms are sometimes engineered with built-in controls (e.g. auxotrophy needing nutrients provided by the lab, "kill switches" that are triggered outside lab settings). Increasingly regulators demand extensive ecological risk studies before field release. Controlled field experiments (with monitoring) are needed to assess unexpected impacts on non-target species (e.g. beneficial insects, soil fauna). Questions also arise from the use of CRISPR/Cas to alter microbial genomes [93,94].
- **Regulatory landscape:** The laws governing genetically modified microorganisms differ worldwide. Under current frameworks, authorities like USDA-APHIS or EPA may assess modified microorganisms for agriculture in the United States. The European Union's use of the precautionary principle means GMOs are more tightly regulated. Moreover, international agreements (e.g. Cartagena Protocol on Biosafety) regulate transboundary movement of GMOs. Even non-GM SynComs may be subject to scrutiny as "biofertilizers" or "biopesticides" under regulations [95,96].
- **Ethical and public acceptability issues:** Farmers and consumers may be skeptical about the use of modified microbiomes. Equity concerns come up: Who owns the strains of microbes? Patenting a synthetic community or a wild microorganism might pose issues of benefit sharing, particularly if isolates are obtained from indigenous territories. Smallholder farmers could worry about dependence on proprietary inoculants. Ethics frameworks must include autonomy (farmer choice), fairness (fair sharing of benefits/risks) and openness (public communication) [97,98].
- **Ethical issues of viral information use:** The sequencing of wild plant viromes raises ethical issues of "bioprospecting". The discovery of a new

virus with advantageous features (e.g. induction of drought tolerance) may be as useful as a microbial gene. But the purposeful release or modification of viruses for crop development could have unforeseen impacts on wild flora. Hence, virome research needs a compromise between open science and biosafety and biosecurity [99,100].

- Integrated pest and disease management: synthetic microorganisms or manipulation of viromes must be an addition to ecological strategies, not a replacement. Ethical pest control in the Anthropocene is based on the conservation of natural enemies, crop variety and reduction of chemical inputs [101].

Implications for Agriculture and Ecosystem Management in the Anthropocene

- **Sustainable crop protection:** Helpful bacteria and viruses might mean farmers can use less hazardous pesticides and fertilizers. SynComs that increase nutrient uptake or induce immunity might partly replace fertilizers and foliar sprays, thereby improving sustainability. Virome monitoring is an early warning system for novel viruses and allows for preventative steps [102,103].
- **Resilience to climate change:** Engineered microbial consortia provide a means to buffer crops against temperature extremes, salt and drought – all anticipated to increase under climate change. Combining microbiome solutions with plant breeding (microbiome responsive varieties) may lead to the establishment of resilient agroecosystems. Furthermore, microbiomes contribute in maintaining or improving soil health, which helps in carbon sequestration and ecosystem services [104].
- **Biodiversity and ecosystem function:** The management of plant health via the use of microbiomes is compatible with the protection of biodiversity. Both more diversified agricultural techniques and ecological intensification are advantageous to plant and soil ecosystems [105].
- **One-Health perspective:** The plant microbiome is part of the environmental microbiome. Synthetic techniques may be coupled with pest control (e.g. phages against zoonotic infections on crops). Insights from plant-microbe interactions might translate to microbial therapeutics in human health and vice versa [106].
- **Policy and global equity:** On the policy side, incorporating microbiome research into the fabric of life involves revising rules for “biologicals” and investing in microbial infrastructure (e.g., microbial genome biobanks). To have a worldwide effect, microbiome-based solutions must be available to smallholders in underdeveloped countries who would likely gain the most [107].

Knowledge Gaps and Future Research Directions

Despite progress, many questions remain. Notable gaps include:

- **Uncovered viral diversity:** The bulk of plant viruses remain unknown from metagenomic studies. The roles of the majority of the viral sequences identified in plant or soil are uncharacterized. There is need for systematic virome mapping across a range of environments (tropical woods, dry regions, crops under stress). Also, the functions of non-plant viruses (bacteriophages, mycoviruses) in plant health are not well recognized. New computational techniques will be required to forecast virus-host interactions at scale.
- **Mechanisms of microbe-virus-plant interactions:** A mechanistic understanding of how viral and microbial populations interact to jointly affect plant immunology and metabolism is lacking. Advanced systems biology methods (transcriptomics, metabolomics of the holobiont) will assist to clarify the processes.
- **Synthetic communities across kingdoms:** Most SynCom research is focused on bacteria (some fungus), however plants naturally interact with bacteria, fungi, archaea and protists. Synthetic communities with many kingdoms (e.g. bacteria + beneficial fungus + mycoviruses or phages) are unexplored. Multi-kingdom synergy is a frontier to understand.
- **Efficacy and stability in the field:** Success in controlled environments sometimes does not transfer to the field. Long-term field experiments under realistic agricultural circumstances are needed. Models are required for the dynamics of inoculants in open systems. Systematic examination of questions about dose, timing and administration (seed coatings versus soil drench) is required.
- **Evolution dynamics of imported community:** Synthetic communities will emerge. Strains may shed characteristics if they are not required or mutate in situ. Horizontal gene transfer in the SynCom or with soil bacteria might lead to new strains. Adaptive evolution procedures (training SynComs under selective settings) may pre-

adapt communities but also complicate risk assessment.

- **Standardization and prediction frameworks:** SynCom design is mostly empirical at the moment. We need concepts or algorithms that will forecast what combinations would work in a particular environment. Standardized inoculation techniques, trait databases for plant-associated microorganisms and phenotyping processes could speed rational design.
- **Socio-economic research:** How will farmers use microbiome tools? Technical work has to be complemented by studies of farmer attitudes, cost-benefit analysis of SynCom inputs and socio-ethical study on bioprospecting rights.

Conclusion

This paper has provided an overview of the interface of the twin frontiers of plant viromics and synthetic microbiome engineering with plant disease and pest dynamics. The viruses are hidden in plant tissues and soils and are generally unrecognized, yet they impact plant health and ecosystem function. At the same time, scientists are learning how to engineer microbial populations to provide plants with improved resistance and resilience. Together, these studies redefined plant pathology and entomology in ecological and evolutionary terms: plant health is a result of a web of interactions among host, pathogens, symbionts and the environment.

In the Anthropocene, with its accelerating climate change and habitat modification, the use of microbial and viral partners is a sustainable way ahead. But fulfilling this promise involves thorough risk assessment, ethical foresight, and integrated research that bridges the gap between lab and field. The ecological complexity of multi-species groups defies our prediction capacity and many basic problems have to be answered. But as our capacity to read and write microbial genomes develops, so too does the potential for designing agricultural systems that function in partnership with nature's microbiome. In conclusion, we can see that concealed viromes and synthetic microbiomes will be important to plant protection in the future but success will depend on profound scientific knowledge, cautious management, and worldwide cooperation.

References

1. Ellis E. Sustaining biodiversity and people in the world's anthropogenic biomes. *Curr Opin Environ Sustain*. 2013;5:368–372.
2. Arias-Maldonado M. *Environment and Society: Socionatural Relations in the Anthropocene*. New York, NY, USA: Springer; 2015.
3. Kolbert E. *The Sixth Extinction: An Unnatural History*. New York, NY, USA: Henry Holt and Company; 2014.
4. Thomas JA, Telfer MG, Roy DB, Preston CD, Greenwood JJ, Asher J, et al. Comparative losses of British butterflies, birds and plants and the global extinction crisis. *Science*. 2004;303:1879–1881.
5. Wake D, Vredenburg V. Are we in the midst of the sixth mass extinction? A view from the world of amphibians. *Proc Natl Acad Sci USA*. 2008;105:11466–11474.
6. Mitchell A. Revitalizing laws, (re)-making treaties, dismantling violence: Indigenous resurgence against 'the sixth mass extinction'. *Soc Cult Geogr*. 2018;19:1–16.
7. Biesmeijer JC, Roberts SP, Reemer M, Ohlemüller R, Edwards M, Peeters T, et al. Parallel declines in pollinators and insect-pollinated plants in Britain and the Netherlands. *Science*. 2006;313:351–354.
8. Hallmann CA, Sorg M, Jongejans E, Siepel H, Hofland N, Schwan H, et al. More than 75 percent decline over 27 years in total flying insect biomass in protected areas. *PLoS ONE*. 2017;12:e0185809.
9. Krongdang S, Evans J, Pettis J, Chantawannakul P. Multilocus sequence typing, biochemical and antibiotic resistance characterizations reveal diversity of North American strains of the honey bee pathogen *Paenibacillus larvae*. *PLoS ONE*. 2017;12:e0176831.
10. Chen Y, Evans J, Feldlaufer M. Horizontal and vertical transmission of viruses in the honey bee, *Apis mellifera*. *J Invert Pathol*. 2006;92:152–159.
11. Burkle LA, Delphia CM, O'Neill KM. A dual role for farmlands: Food security and pollinator conservation. *J Ecol*. 2017;105:890–899.
12. De Luca P, Vallejo-Marin M. What's the 'buzz' about? The ecology and evolutionary significance of buzz-pollination. *Curr Opin Plant Biol*. 2013;16:429–435.
13. Chaplin-Kramer R, Dombeck E, Gerber J, Knuth KA, Mueller ND, Mueller M, et al. Global malnutrition overlaps with pollinator-dependent micronutrient production. *Proc R Soc B Biol Sci*. 2014;281:20141799.
14. Atkins J, Atkins B. *The Business of Bees: An Integrated Approach to Bee Decline and Corporate Responsibility*. Sheffield, UK: Greenleaf Publishing Limited; 2016.

15. De Zeeuw H, Drechsel P, eds. *Cities and Agriculture: Developing Resilient Urban Food Systems*. New York, NY, USA: Routledge; 2015.
16. Blecha J, Leitner H. Reimagining the food system, the economy and urban life: New urban chicken-keepers in US cities. *Urban Geogr*. 2014;35:86–108.
17. Blum J, ed. *Urban Horticulture: Ecology, Landscape and Agriculture*. Oakville, ON, Canada: Apple Academic Press; 2016.
18. Hodge J. Hidden hunger: Approaches to tackling micronutrient deficiencies. In: Gillespie S, Hodge J, Yosef S, Pandya-Lorch R, eds. *Nourishing Millions: Stories of Change in Nutrition*. Washington, DC, USA: IFPRI; 2016:35–43.
19. Eilers EJ, Kremen C, Greenleaf SS, Garber AK, Klein AM. Contribution of pollinator-mediated crops to nutrients in the human food supply. *PLoS ONE*. 2011;6:e21363.
20. Potts S, Imperatriz-Fonseca V, Ngo H, Aizen M, Biesmeijer J, Breeze TD, et al. Safeguarding pollinators and their values to human well-being. *Nature*. 2016;540:220–229.
21. Green M, Duhn I. The force of gardening: Investigating children's learning in a food garden. *Aust J Environ Educ*. 2015;31:60–74.
22. Artmann M, Bastian O, Grunewald K. Using the concepts of green infrastructure and ecosystem services to specify Leitbilder for compact and green cities – the example of the landscape plan of Dresden. *Sustainability*. 2017;9:198.
23. Guerry AD, Polasky S, Lubchenco J, Chaplin-Kramer R, Daily GC, Griffin R, et al. Natural capital and ecosystem services informing decisions: From promise to practice. *Proc Natl Acad Sci USA*. 2015;112:7348–7355.
24. Kaplan R, Kaplan S. *The Experience of Nature: A Psychological Perspective*. Cambridge, NY, USA: Cambridge University Press; 1989.
25. Mayer S, Frants C, Bruehlman-Senecal E, Dolliber K. Why is nature beneficial? The role of connectedness to nature. *Environ Behav*. 2009;41:607–643.
26. Millennium Ecosystem Assessment (MEA). *Ecosystems and Human Well-Being: Synthesis*. Washington, DC, USA: Island Press; 2005.
27. Díaz S, Pascual U, Stenseke M, Martín-López B, Watson RT, Molnár Z, et al. Assessing Nature's contribution to people. *Science*. 2018;359:270–272.
28. Appiah AA, Jennings P, Turner JA. *Phytophthora ramorum*: one pathogen and many diseases, an emerging threat to forest ecosystems and ornamental plant life. *Mycologist*. 2004;18:145–150.
29. Areal FJ, Touza J, MacLeod A, Dehnen-Schmutz K, Palmieri MG, Perrings C, et al. Integrating drivers influencing the detection of plant pests carried in the international cut flower trade. *J Environ Manage*. 2008;89:300–307.
30. Author. Enterome enters into a microbiome-based development collaboration with AbbVie in Crohn's disease. 2014.
31. Bartczak A, Meyerhoff J. Valuing the chances of survival of two distinct Eurasian lynx populations in Poland – Do people want to keep the doors open? *Biol Invasions*. 2012;12:2837–2851.
32. Beutler JA. Natural products as a foundation for drug discovery. *Curr Prot Pharmacol*. 2019;86:e67. https://doi.org/10.1002/cpph.67
33. Bourbou C. Evidence of childhood scurvy in a middle Byzantine Greek population from Crete, Greece (11th-12th centuries A.D.). *Int J Paleopathol*. 2014;5:86–94. https://doi.org/10.1016/j.ijpp.2013.12.002
34. Boyd I, Freer-Smith P, Gilligan C, Godfray C. The consequences of tree pests and diseases for ecosystem services. *Science*. 2013;342:823–840.
35. Suryanarayanan S, Kleinman D. *Vanishing Bees: Science, Politics and Honeybee Health*. New Brunswick, NJ, USA: Rutgers University Press; 2016.
36. United States Department of Agriculture (USDA). ARS Honey Bee Health and Colony Collapse Disorder. 2018. Available from: https://www.ars.usda.gov/oc/br/ccd/index/
37. Vanengelsdorp D, Traynor KS, Andree M, Lichtenberg EM, Chen Y, Saegerman C, et al. Colony Collapse Disorder (CCD) and bee age impact honey bee pathophysiology. *PLoS ONE*. 2017;12:e0179535.
38. Colla S, MacIvor J. Questioning public perception, conservation policy and recovery actions for honeybees in North America. *Conserv Biol*. 2017;31:1202–1204.
39. Baldock K, Goddard M, Hicks D, Kunin W, Mitschunas N, Osgathorpe L, et al. Where is the UK's pollinator biodiversity? The importance of urban areas for flower-visiting insects. *Proc R Soc B Biol Sci*. 2015;282:20142849.
40. Colla S. Status, threats and conservation recommendations for wild bumble bees (*Bombus* spp.) in Ontario, Canada: A review for policy makers and practitioners. *Nat Areas J*. 2016;36:412–426.
41. Godfray HC, Blacquiere T, Field LM, Hails RS, Petrokofsky G, Potts SG, et al. A restatement of

the natural science evidence base concerning neonicotinoid insecticides and insect pollinators. *Proc R Soc B Biol Sci*. 2014;281:20140558.
42. Goulson D. An overview of the environmental risks posed by neonicotinoid insecticides. *J Appl Ecol*. 2013;50:977–987.
43. Wojcik VA, Morandin LA, Davies Adams L, Rourke KE. Floral resource competition between honey bees and wild bees: Is there clear evidence and can we guide management and conservation? *Environ Entomol*. 2018;47:822–833.
44. Goulson D, Nicholls E, Bítas C, Rotheray E. Bee declines driven by combined stress from parasites, pesticides and lack of flowers. *Science*. 2015;347:1255957.
45. Cahill AE, Aiello-Lammens ME, Fisher-Reid MC, Hua X, Karanewsky CJ, Yeong Ryu H, et al. How does climate change cause extinction? *Biol Sci*. 2013;280:20121890.
46. Memmott J, Craze PG, Waser NM, Price MV. Global warming and the disruption of plant-pollinator interactions. *Ecol Lett*. 2007;10:710–717.
47. Kerr JT, Pindar A, Galpern P, Packer L, Potts SG, Roberts SM, et al. Climate change impacts on bumblebees converge across continents. *Science*. 2015;349:177–180.
48. Hegland S, Nielsen A, Lázaro A, Bjerknes A, Totland O. How does climate warming affect plant-pollinator interactions? *Ecol Lett*. 2009;12:184–195.
49. Kearns A, Inouye D, Waser N. Endangered mutualisms: The conservation of plant-pollinator interactions. *Annu Rev Ecol Syst*. 1998;29:83–113.
50. Brasier C. The biosecurity threat to the UK and global environment from international trade in plants. *Plant Pathology*. 2008;57:792–808.
51. Burns WJ, Slovic P, Kasperson RE, Kasperson JX, Renn O, Emani S. Incorporating structural models into research on the social amplification of risk: Implications for theory construction and decision making. *Risk Analysis*. 1993;13:611–623.
52. Areal FJ, Touza J, MacLeod A, Dehnen-Schmutz K, Palmieri MG, Perrings C, Spence NJ. Integrating drivers influencing the detection of plant pests carried in the international cut flower trade. *J Environ Manage*. 2008;89(4):300–307.
53. Carroll AL, Régnière J, Logan JA, Taylor SW, Bentz B, Powell JA. Assessing the impacts of global warming on forest pest dynamics. *Front Ecol Environ*. 2006.
54. Chandelier A, Helson M, Dvorak M, Gischer F. Detection and quantification of airborne inoculum of *Hymenoscyphus pseudoalbidus* using real-time PCR assay. *Plant Pathology*. 2014;1–10.
55. Cobb R, Filipe R, Meentemeyer R, Gilligan C, Rizzo D. Ecosystem transformation by emerging infectious disease: Loss of large tanoak from California forests. *J Ecol*. 2012;100:712–722.
56. Cole CR. Preventing hidden hunger in children using micronutrient supplementation. *J Pediatr*. 2012;161:777–778. https://doi.org/10.1016/j.jpeds.2012.06.053
57. Colunga-Garcia M, Magarey RA, Haack RA, Gage SH, Qi J-Q. Enhancing early detection of exotic pests in agricultural and forest ecosystems using an urban-gradient framework. *Ecol Appl*. 2010;20(2):303–310.
58. Daliri EBM, Lee BH, Oh DH. Current trends and perspectives of bioactive peptides. *Crit Rev Food Sci Nutr*. 2018;58:2273–2284. https://doi.org/10.1080/10408398.2017.1319795
59. Daniel H. Diet and gut microbiome and the 'chicken or egg' problem. *Front Nutr*. 2022;8:828630. https://doi.org/10.3389/fnut.2021.828630
60. De-Pei L. Exploring innovation with scientific thinking. *Chin Med Sci J*. 2022;37:87–90. https://doi.org/10.24920/004123
61. Price M, Waser N. Effects of experimental warming on plant reproductive phenology in a subalpine meadow. *Ecology*. 1998;79:1261–1271.
62. Stiles P. Personal interview. 27 November 2018.
63. Measham TG, Preston BL, Smith TF, Brooke C, Gorddard R, Withycombe G, et al. Adapting to climate change through local municipal planning: Barriers and challenges. *Mitig Adapt Strateg Glob Chang*. 2011;16:889–910.
64. Jenkins V. *A History of an American Obsession*. Washington, DC, USA: Smithsonian Books; 2015.
65. Widener M. Spatial access to food: Retiring the food desert metaphor. *Physiol Behav*. 2018;193:257–260.
66. Hall DM, Camilo GR, Tonietto RK, Ollerton J, Ahrén K, Arduser M, et al. The city as a refuge for insect pollinators. *Conserv Biol*. 2017;31:24–29.
67. Jarman W, Ballschmiter K. From coal to DDT: The history of the development of the pesticide DDT from synthetic dyes till Silent Spring. *Endeavour*. 2012;36:131–142.
68. Ware G. Ecological history of DDT in Arizona. *J Ariz Acad Sci*. 1974;9:61–65.
69. Jones G, MacLeod A. Mapping, analysis and improved understanding of stakeholders and the public to help protect tree health. Unpublished working paper 1, Defra Project FFG/1143. 2013.

70. Kjær ED, McKinney LV, Nielsen LR, Hansen LN, Hansen JK. Adaptive potential of ash (*Fraxinus excelsior*) populations against the novel emerging pathogen *Hymenoscyphus pseudoalbidus*. *Evol Appl*. 2011;5:219–228.
71. Koch FH, Yemshanov D, Colunga-Garcia M, Magarey RD, Smith WD. Potential establishment of alien-invasive forest insect species in the United States: where and how many? *Biol Invasions*. 2011;13(4):969–985.
72. Kussmann M. Prediction, discovery and characterization of plant- and food-derived health-beneficial bioactive peptides. *Nutrients*. 2022;14:4810. https://doi.org/10.3390/nu14224810
73. Lennon M. Nature conservation in the Anthropocene: preservation, restoration and the challenge of novel ecosystems. *Plan Theory Pract*. 2015;16(2):285–290.
74. Logan JA, Régnière J, Powell JA. Assessing the impacts of global warming on forest pest dynamics. *Front Ecol Environ*. 2003;1(3):130–137.
75. Potter C, Harwood T, Knight J, Tomlinson I. Learning from history, predicting the future: The UK Dutch Elm Disease outbreak in relation to contemporary tree disease threats. *Philos Trans R Soc*. 2011;366:1966–1974.
76. Purrington A, Zinn H. The influence of loss aversion on mountain bikers' behavioral intentions. *Environ Manage*. 2011;48:547–557.
77. Raju TN. The Nobel chronicles. 1929: Christiaan Eijkman (1858-1930) and Frederick Hopkins (1861-1947). *Lancet*. 1998;352:1868. https://doi.org/10.1016/s0140-6736(05)79944-x
78. Tomlinson I, Harwood T, Potter C, Knight J. *Review of Joint Inter-Departmental Emergency Programme to Contain and Eradicate Phytophthora ramorum and Phytophthora kernoviae in Great Britain*. Report for Defra. London: Centre for Environmental Policy, Imperial College London; 2009.
79. Tracy DR. *Phytophthora ramorum* and *Phytophthora kernoviae*: the woodland perspective. *EPPO Bull*. 2009;39:161–167.
80. Turnbaugh PJ. The research questions pertaining to diet and the gut microbiome are wide open. *Gut Micro*. 2019.
81. Vergin F. Antibiotics and probiotics. *Hippokrates*. 1954;25:116–119.
82. Webber J, Hendry S. *Rapid Assessment of the Need for a Detailed Pest Risk Analysis for Chalara fraxinea*. Alice Holt: Forest Research; 2012.
83. Yang C-C, Ascunce MS, Luo L-Z, Shao J-G, Shih CJ, Shoemaker D. Propagule pressure and colony social organization are associated with the successful invasion and rapid range expansion of fire ants in China. *Mol Ecol*. 2012;21(4):817–833.
84. Yemshanov D, Koch FH, Ducey M, Koehler K. Trade-associated pathways of alien forest insect entries in Canada. *Biol Invasions*. 2012;14(4):797–812.
85. Stapleton D. The dawn of DDT and its experimental use by the Rockefeller Foundation in Mexico, 1943–1952. *Parassitologia*. 1998;40:149–158.
86. Russell E. The strange career of DDT: Experts, federal capacity and environmentalism in World War II. *Technol Cult*. 1999;40:770–796.
87. Shacker M. *A Spring without Bees: How Colony Collapse Disorder Has Endangered Our Food Supply*. Guilford, CT, USA: The Lyons Press; 2008.
88. Dunn R. Silent spring: On its 50th anniversary, an exposé of pesticide overuse still stands as a beacon of reason. *Nature*. 2012;485:578–579.
89. Murray R. Forty years after Silent Spring. *Anal Chem*. 2002;74:501A.
90. Dwyer JT. Have safety and efficacy assessments of bioactives come of age? *Mol Asp Med*. 2022;89:101103. https://doi.org/10.1016/j.mam.2022.101103
91. EPPO. Pest Risk Analysis for *Agrilus anxius* PRA Record 1116987. EPPO; 2011. Available from: http://www.eppo.fr/QUARANTINE/Pest_Risk_Analysis/
92. Evans A. Invasive plants, insects and diseases in the forests of the Anthropocene. In: Sample V, Ixler R, eds. *Forest Conservation and Management in the Anthropocene: Adaptations of Science, Policy and Practices*. Washington DC: Pinchot Institute; 2014.
93. Hallmann CA, Foppen RP, van Turnhout CA, de Kroon H, Jongejans E. Declines in insectivorous birds are associated with high neonicotinoid concentrations. *Nature*. 2014;511:341–343.
94. Woodcock BA, Bullock JM, Shore RF, Heard MS, Pereira MG, Redhead J, et al. Country specific effects of neonicotinoid pesticides on honey bees and wild bees. *Science*. 2017;356:1393–1396.
95. Chagnon M, Kreutzweiser D, Mitchell E, Morrissey C, Noome D, Sluijs J. Risks of large-scale use of systemic insecticides to ecosystem functioning and services. *Environ Sci Pollut Res*. 2015;22:119–134.
96. Cimino A, Boyles A, Thayer K, Perry M. Effects of neonicotinoid pesticide exposure on human health: A systematic review. *Environ Health Perspect*. 2017;125:155–162.

97. Klein AM, Vaissiere BE, Cane JH, Steffan-Dewenter I, Cunningham SA, Kremen C, et al. Importance of pollinators in changing landscapes for world crops. *Proc R Soc Lond B Biol Sci*. 2007;274:303–313.
98. Chen M, Tao L, McLean J, Lu C. Quantitative analysis of neonicotinoid insecticide residues in foods: Implication for dietary exposures. *J Agric Food Chem*. 2014;62:6082–6090.
99. Mitchell EA, Mulhauser B, Mulot M, Mutabazi A, Glauser G, Aebi A. A worldwide survey of neonicotinoids in honey. *Science*. 2017;358:109–111.
100. Pretty J, Bharucha Z. Integrated pest management for sustainable intensification of agriculture in Asia and Africa. *Insects*. 2015;6:152–182.
101. Taylor R, Herms D, Cardina J, Moore R. Climate change and pest management: Unanticipated consequences of trophic dislocation. *Agronomy*. 2018;8:7.
102. GBD 2019 Demographics Collaborators. Global age-sex-specific fertility, mortality, healthy life expectancy (HALE) and population estimates in 204 countries and territories, 1950–2019. *Lancet*. 2020;396:1160–1203. https://doi.org/10.1016/S0140-6736(20)30977-6
103. Leopold A. *A Sand County Almanac*. New York, NY, USA: Library of America; 1949.
104. Wilson E. *Biophilia*. Cambridge, MA, USA: Harvard University Press; 1984.
105. Dubbeling M, De Zeeuw H. Urban agriculture and climate change adaptation: Ensuring food security through adaptation. In: *Resilient Cities*. Dordrecht, The Netherlands: Springer; 2011:441–449.
106. Colla S, Willis E, Packer L. Can green roofs provide habitat for urban bees? *Cities Environ*. 2009;2:4–12.
107. Rueckert W. Literature and ecology. An experiment in ecocriticism. *Iowa Rev*. 1978;9:71–86.