The Hologenome Approach: Co-Engineering Crop Genomes and Their Core Microbiome for Bioprotection

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Background

Crop protection has long relied on host resistance breeding and external chemical/biological inputs. Both approaches are increasingly challenged by fast-evolving pathogens, pesticide restrictions, and climate stress. The **hologenome** concept reframes crops as **holobionts**: plants plus their co-evolved microbiome.

Why the Microbiome Matters

High-throughput sequencing repeatedly detects a conserved **core microbiome** enriched in disease-suppressive soils and elite cultivars. These microbes can: (i) prime immunity (ISR/SAR), (ii) disrupt pathogen quorum sensing, (iii) produce antimicrobials, (iv) improve nutrient mobilization, and (v) buffer drought/salinity stress.

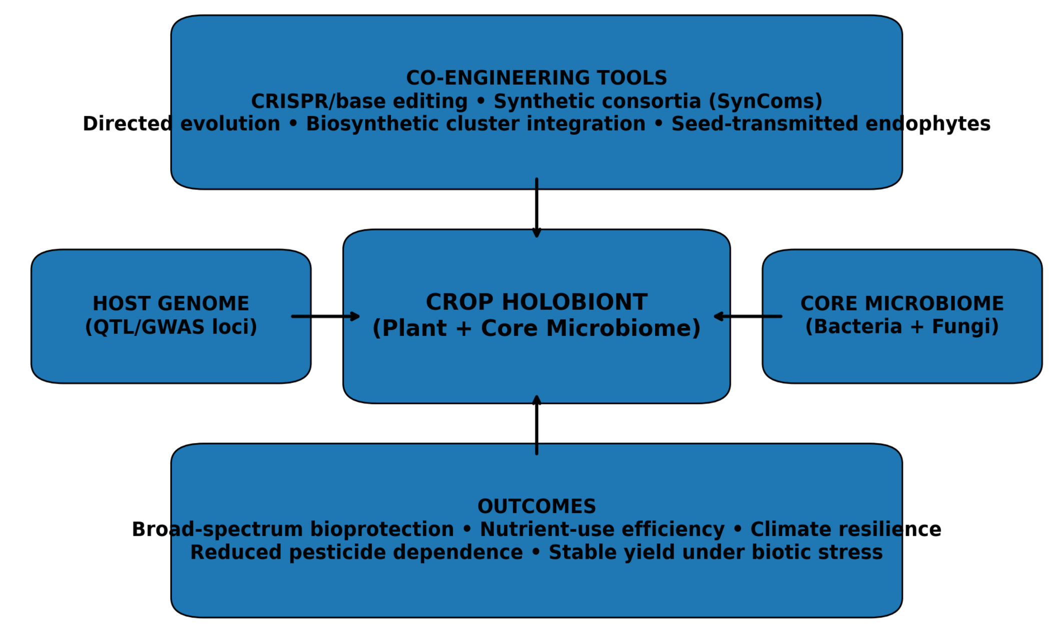
Objective

• Build a proactive, residue-free framework for bioprotection by **co-engineering** host loci that shape microbiome assembly and by deploying stabilised beneficial consortia across generations.

Core Microbiome: Who & What

Core taxa (examples)	Key functions
Pseudomonas, Bacillus	ISR priming, antimicrobials, competition
Paraburkholderia, Sphingomonas	Nutrient mobilization, stress mitigation, suppression
Trichoderma, Serendipita	Antagonism, immune priming, root growth
Mycorrhizal taxa	Nutrient uptake, drought tolerance, yield stability

Concept Diagram



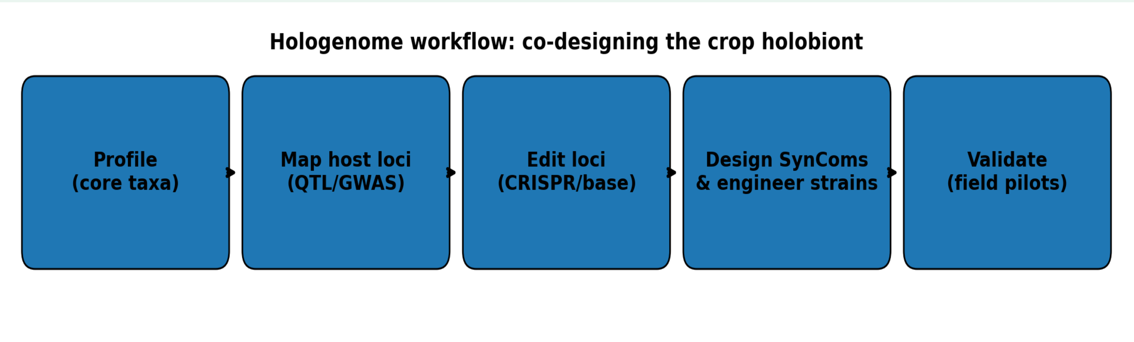
Host Genetic Control

Host genetic control of microbiome assembly is supported by GWAS/QTL studies across crops. Candidate loci influence **root exudate chemistry**, **cuticle composition**, **strigolactone signalling**, and suppression/activation of defence pathways that determine microbial recruitment and retention.

Editing & Reported Bioprotection

Genome editing (CRISPR-Cas9/base editing) can tune microbiome recruitment. Examples reported in the abstract include edited rice lines enriched for *Trichoderma*/*Pseudomonas* showing **~65–90%** reductions in *Magnaporthe oryzae* and *Xanthomonas oryzae* infections, and edited wheat recruiting *Paraburkholderia* associated with **up to ~80%** suppression of *Gaeumannomyces tritici*.

Workflow



Microbial Engineering

Beyond host editing, microbial engineering enables robust, heritable benefits: directed evolution, chromosomal integration of biosynthetic clusters, and **synthetic microbial consortia (SynComs)** can stabilise colonisation in the spermosphere and phyllosphere.

Seed-Transmitted Endophytes

Seed transmission of beneficial endophytes has been demonstrated in multiple plant species, effectively adding functional traits to the plant without changing the plant genome. This can deliver multi-gene protection and growth benefits while supporting residue-free IPM.

Translational Potential

Early field trials and commercial pilots reported in the abstract indicate microbiome-enhanced varieties can reduce fungicide/insecticide applications by **~70–100%** while maintaining or exceeding yield benchmarks. This approach delivers **polygenic**, environmentally responsive protection that single resistance genes often cannot provide alone.

Take-Home Points

• Treat the crop holobiont as a selectable unit.
• Combine host-locus tuning + SynCom design for durable bioprotection.
• Co-design improves pest/disease resistance, nutrient-use efficiency, and climate resilience.

Keywords

Zero-pollution plant protection; microbiome; Magnaporthe oryzae; Xanthomonas oryzae; synthetic microbiomes; hologenome approach.