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Review

From Phytoalexins to Environmental Regulators: An Evolving Understanding of the Role of Coumarins in Regulating Quorum Sensing and Shaping the Soil Microbiome

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Abstract

Quorum sensing (QS) governs microbial virulence, symbiosis, and critical ecosystem processes, such as rhizosphere nitrogen mineralization, positioning QS as both an attractive agricultural target and a potential point of ecological trade-off. This review synthesizes current evidence on coumarins, plant-derived secondary metabolites, that have evolved from being viewed as classical phytoalexins to being recognized as regulators of QS-mediated interaction in the plant-soil system. We synthesize current evidence on the multifaceted mechanisms of coumarin action, from direct antimicrobial effects to selective interference with bacterial QS systems and virulence. Key studies demonstrate that coumarins can suppress phytopathogens while sparing beneficial bacteria, thereby actively editing rhizosphere community composition. However, coumarin effects are profoundly context-dependent, with outcomes ranging from selective microbiome modulation to broad suppression or unintended pathogen enrichment - depending on concentration, plant host and native community structure. Beyond community assembly, coumarin-mediated QS disruption may have functional consequences for QS controlled ecosystem processes such as nutrient cycling. Revealing a potential ecological trade-off between pathogen defense and resource acquisition, this warrants further investigation. Coumarins are versatile compounds that plants use for sensing, communicating with, and actively shaping their microbial environments. Developing the ability to use them precisely and in an environmentally friendly manner represents a promising avenue for sustainable agriculture.

Keywords: quorum sensing; quorum quenching; coumarins; *Ralstonia solanacearum*; type III secretion system; rhizosphere microbiome; context-dependent effects

Introduction

Modern agriculture, even with advances in sustainable practices, grapples with persistent environmental challenges, including emerging microbial diseases, declining soil fertility, and loss of biodiversity. This necessitates a shift towards optimizing agrochemical use and harnessing the power of agricultural microbiology. A particularly promising avenue is targeted management of plant and soil microbiomes to enhance the resilience of agroecosystems. This approach encompasses the development of synthetic microbial consortia and novel delivery methods for beneficial microorganisms and their metabolites (Monica et al., 2025).

Quorum sensing (QS) is a fundamental regulatory mechanism of density-dependent intercellular communication in bacteria, mediated by diffusible chemical signals. First discovered in the 1970s (Nealson et al., 1979) and later termed in the 1990s (Fuqua et al., 1994). QS orchestrates collective behaviors such as virulence, biofilm formation, and symbiosis. Crucially, this cell-to-cell communication system represents a novel and attractive target for microbial control, distinct from

conventional antibiotics. This has led to the "quorum quenching" strategy - interfering with QS signals to disarm pathogens without exerting lethal pressure, thereby potentially mitigating the rise of resistance (Zhu et al., 2023).

In agriculture, QS-targeting strategies have primarily focused on using QQ-active microbes (e.g., *Bacillus* spp. producing AiiA-like lactonases) or designing synthetic anti-QS consortia (Rosa et al., 2024). However, these approaches and much of the underlying QS biology are based on reductionist studies of pure cultures. A critical and understudied area is the ecological role of QS and its manipulation in complex soil and rhizosphere microbiomes (Zhang et al., 2026). Key unanswered questions include the taxonomic diversity of QS-active microorganisms in soils, the specifics of QS regulation in soil-dwelling fungi and bacteria, and the impact of QS modulators on the structure and function of these intricate microbial communities.

Low-molecular-weight quorum sensing inhibitors (QSIs) are produced by a remarkable diversity of life forms, from prokaryotes and fungi to higher plants and mammals (Kalia, 2013). Among these, plants stand out as a particularly rich source of structurally diverse QS-modulating compounds (Viswanathan et al., 2015). This chemical arsenal is believed to play a crucial role in plant-microbe interactions.

Released into the soil via root exudates and plant litter, these phytometabolites exert a profound influence on rhizosphere communities. QS itself governs a plethora of key ecological traits in bacteria and fungi, including biofilm formation, antibiotic production, motility, and stress survival. While these mechanisms are well-characterized in pure cultures, a critical knowledge gap persists. In natural soils, these processes are embedded within complex, cross-kingdom networks involving a vast diversity of culturable and unculturable microorganisms. The ecological consequences of QS modulation in such a context remain largely speculative.

Therefore, bridging this gap requires a model system that connects molecular QS interference with community-level outcomes. Coumarins emerge as appropriate model compounds for such an ecological inquiry. Coumarins are a large family of lactone derivatives of cinnamic acid, comprising over 1300 identified molecules that include simple coumarins, hydroxy-, furano-, and pyranocoumarins (Hoult et al., 1996). They are widely distributed in the plant kingdom. These plant-derived secondary metabolites possess well-documented QS-modulating activity and are naturally and continuously introduced into the soil environment. Studying coumarins offers a unique window into how plants naturally shape their microbial surroundings through chemical interference.

The aim of this review is to analyze current evidence on the impact of coumarins on soil microorganisms and QS-related interkingdom interaction. We will systematically examine the consequences of this interaction at two critical levels: (1) induction of systemic resistance in host plants and (2) modulation of the structure and functional activity of rhizosphere and soil microbial communities. This synthesis positions coumarins as not merely phytoanticipins but as pivotal ecological regulators within the soil-microbiome-plant continuum.

1. The Phenomenon of Quorum Sensing in Microbial World

1.1. Quorum Sensing in Bacteria

The QS phenomenon in bacteria is mediated by a wide range of chemical signals - autoinducers (AIs). The main classes of bacterial AIs include N-acylhomoserine lactones (AHLs), autoinducing peptides (AIPs), furanosyl derivatives (type AI-2), gamma-butyrolactones (GBLs), alkylquinolones (e.g., PQS in *Pseudomonas* spp.) and diffuse signaling factors (DSFs) (Majdura et al., 2023, Coolahan et al., 2025) (Table 1).

Table 1. Interkingdom quorum sensing (QS) communication: bacterial, fungal, and plant participants in QS signal exchange.

QS communication participant	AI-class	Producers	Regulated processes	Relationship with plants	References
Symbiotic and pathogenic bacteria					
<i>Bacillus</i> spp.	AHL (3-oxo-C12-HSL)	No	Degradation of AHL (lactonase AiiA); detoxification; attenuation of pathogen virulence	Biocontrol (e.g. against <i>Erwinia carotovora</i>)	Dong et al., 2000; Barbey et al., 2013
<i>Bacillus licheniformis</i>	ComX pheromones	Yes		Inhibitory potential against the crop pathogen <i>Aspergillus flavus</i>	Esmailishirazifard et al., 2018
<i>Rhodococcus erythropolis</i>	AHL	Not specified	AHL degradation (lactonase activity)	Biocontrol (protection of potatoes from <i>Pectobacterium</i>), root colonization	Dong et al., 2000; Barbey et al., 2013
<i>Ensifer meliloti</i> (and <i>Ensifer</i> sp. NGR234)	AHL (3-oxo-C14-HSL)	Yes (symbiont)	Nitrogen fixation, suppression of AHL signals	Nitrogen-fixing symbiont of legumes; priming defense against aphids (<i>Rhopalosiphum padi</i>)	Krysciak et al., 2011; Mathesius et al., 2003; Wehner et al., 2021
<i>Pseudomonas putida</i>	AHL (C6-, C8-HSL)	Yes	AHL hydrolysis and production	Rhizobacterium (PGPR); induction of tomato defense against <i>Alternaria alternata</i>	Schuegger et al. 2006
<i>Azospirillum brasilense</i>	AHL (C4-, C12-HSL)	No (most), but there are LuxR solo receptors	AHL degradation, perception of external AHL (LuxR solo)	PGPR; plant growth promotion; root colonization; potential biocontrol	Fukami et al., 2018; Patel et al., 2013; Cassán et al., 2016; Vial et al., 2006; Gualpa et al., 2019

QS communication participant	AI-class	Producers	Regulated processes	Relationship with plants	References
<i>Serratia liquefaciens</i> MG1	AHL (C6-, C8-HSL)	Yes	QS-dependent virulence/interaction	Model organism; induction of tomato defense against <i>Alternaria alternata</i>	Schuhegger et al., 2006; Gantner et al., 2006
<i>Serratia plymuthica</i> HRO-C48	AHL (C4-, C6- 3-oxo-C6-HSL)	Yes	Induction of chitinase and antifungal volatile synthesis	Biocontrol of wilt (<i>Verticillium dahliae</i>) in rapeseed	Müller et al., 2009
<i>Rhizobium radiobacter</i> F4	AHL (short- and medium-chain)	Yes	Root colonization, growth stimulation, stress resistance	Endophytic PGPR bacterium; closely associated with the plant	Glaeser et al., 2015; Sharma et al., 2008; Alabid et al., 2020
<i>Acidovorax radicis</i> N35	AHL (OH-C10-HSL)	Yes	Root colonization, modulation of plant response (priming vs. defense)	PGPR; beneficial interaction with barley mediated by AHL	Li et al., 2011; Han et al., 2016
Bacterial plant pathogens					
<i>Erwinia carotovora</i> (<i>Pectobacterium</i>)	AHL	Yes	Virulence	Pathogen causing soft rot	Pöllumaa et al. 2012; Petrova et al. 2023
<i>Pectobacterium</i> spp.	AHL	Yes	Virulence	Pathogen causing soft rot	Barbey et al., 2013
<i>Burkholderia glumae</i>	AHL (C8-HSL, TofI/TofR system)	Yes	Synthesis of toxoflavin	Rice pathogen	Chung et al., 2011
<i>Pseudomonas syringae</i> pv. tomato (Pst)	Not specified (but responds to AHL)	Yes	Virulence	Pathogen of tomato and <i>Arabidopsis</i> ; susceptible to AHL-induced resistance (ISR)	Shrestha et al., 2020; Schikora et al., 2011

QS communication participant	AI-class	Producers	Regulated processes	Relationship with plants	References
<i>Agrobacterium</i> spp.	AHL	Yes	Virulence/symbiosis, degradation of own AHL	Plant pathogen/symbiont	Zhang et al., 2002
Key recipients of AHL (Plants)					
<i>Medicago truncatula</i>	AHL (3-oxo-C14-HSL, 3-oxo-C16:1-HSL)	No (perceives)	Induction of auxin-sensitive proteins and flavonoid synthesis; secretion of QS mimics	Model legume: early response to symbiont and pathogen signals	Mathesius et al., 2003
<i>Solanum lycopersicum</i>	AHL (C6-, C8-HSL)	No (perceives)	Induction of salicylic acid and defense genes (<i>PR1a</i> , chitinase); systemic resistance	Priming protection against fungal pathogen (<i>Alternaria alternata</i>)	Schuhegger et al., 2006
<i>Arabidopsis thaliana</i>	AHL (C4-, C6-, C8-, C12-, C14-HSL)	No (perceives)	Stimulation of root growth (GCR1/GPA1), priming of defense (MAPK cascade, oxylipins, SA), induction of detoxification enzymes	Model plant; complex response dependent on AHL chain length; receptor for hydrophobic AHL identified	von Rad et al., 2008; Shrestha et al., 2020; Liu et al., 2012
Barley (<i>Hordeum vulgare</i>), wheat (<i>Triticum aestivum</i>)	AHL (C6-, 3-oxo-C14-HSL)	No (perceives)	Growth stimulation, hormonal imbalance, priming protection against powdery mildew and aphids	Genetic variation of crops in response to AHL: successful field trials	Shrestha et al., 2019; Moshynets et al., 2019
Rapeseed (<i>Brassica napus</i>)	AHL (C4-, C6- 3-oxo-C6-HSL)	No (perceives)	Induction of systemic stability	Protection against <i>Verticillium dahliae</i> is mediated by AHL from <i>S. plymuthica</i>	Müller et al., 2009
Chickpeas (<i>Cicer arietinum</i>)	AHL (C4-HSL)	No (perceives)	Growth promotion, stress tolerance, Fusarium resistance	Positive response to applied AHL	Gupta et al., 2019

QS communication participant	AI-class	Producers	Regulated processes	Relationship with plants	References
Fungi					
<i>Histoplasma capsulatum</i> (Chemotopye II)	Density-dependent phenotypic switch (QS-like)	Yes (α -(1,3)-glucan synthesis)	Hyphae-to-yeast switching; biosynthesis of virulent α -(1,3)-glucan; masking of β -glucans from the dectin-1 receptor	A human and animal pathogen (histoplasmosis). A soil saprophyte that develops into a parasitic yeast form.	Kügler et al., 2000; Sprague et al., 2006; Rappleye et al., 2007; Brown et al., 2001; Marcos et al., 2016
<i>Histoplasma capsulatum</i> (Chemotopye I)	Density-dependent phenotypic switch (QS-like)	None or weak (absent α -(1,3)-glucan)	Hyphae $\rightarrow$ yeast switch; virulence is partly mediated by the <i>AGS1</i> gene	A human and animal pathogen	Edwards et al., 2011; Marcos et al., 2016
<i>Aspergillus fumigatus</i>	Farnesol	Yes	Inhibition of hyphae formation, blocking the conidia $\rightarrow$ hyphae transition; influence on the localization of CWI pathway proteins (AfRho1p, AfRho3p)	Soil saprotroph	Dichtl et al., 2010
<i>Aspergillus nidulans</i>	Farnesol	Yes	Induction of apoptosis through disruption of mitochondria, caspase, and ROS	Demonstration of the interspecies effect of farnesol as a communication molecule	Semighini et al., 2006; Fairn et al., 2007
<i>Aspergillus nidulans</i>	γ -Heptalactone	Yes	Penicillin production	Antagonistic interaction between microbes	Williams et al., 2012
<i>Aspergillus terreus</i>	Butyrolactone I	Yes	Secondary metabolism		Schimmel et al., 1998
<i>Saccharomyces cerevisiae</i>	Farnesol (exogenous)	No (perceives)	Induction of apoptosis through disruption of mitochondria, caspase, and ROS	Demonstration of the interspecies effect of farnesol as a communication molecule.	Fairn et al., 2007

QS communication participant	AI-class	Producers	Regulated processes	Relationship with plants	References
<i>Candida albicans</i>	Farnesol	Yes	Inhibition of hyphae formation (intraspecific QS); inhibition of QS in <i>P. aeruginosa</i> (interspecific interaction)	An example of antagonistic interaction between microbes	Cugini et al., 2007; Chung et al., 2010
Various fungi	Ambuic acid	Yes	Inhibition of QS in Gram-positive bacteria	An example of antagonistic interaction between microbes	Nakayama et al., 2009

It has been shown that some antimicrobial metabolites, such as *Bacillus subtilis* surfactin or 2,4-DAPG, can function as antimicrobial agents themselves by regulating the expression of their biosynthetic genes (Wei et al., 2023, Markelova et al., 2025). This interplay between virulence, antibiotic production and QS makes bacterial communication systems an important target for intervention.

1.2. Quorum Sensing in Fungi

The QS phenomenon is also widespread in fungi and regulates key adaptation processes. The first fungal AIs discovered were farnesol, tyrosol, and phenylethanol in the pathogen *Candida albicans* (Hornby et al., 2001). Subsequently, a wide range of signaling molecules was identified, including oxylipins, peptide pheromones, alcohols (tryptophol, farnesol, etc.), acetaldehydes, and volatiles (Padder et al., 2018, Mehmood et al., 2019). Fungal QS controls physiological functions, such as morphogenesis, spore germination, biosynthesis of secondary metabolites, and secretion of hydrolytic enzymes (Barriuso et al., 2018). Density-dependent regulation has been described for representatives of various taxa, including phytopathogenic *Fusarium oxysporum* (Vitale et al., 2019), *Aspergillus flavus* (Williams et al., 2012), opportunistic *Cryptococcus neoformans* (Lee et al., 2007) and saprotrophic *Neurospora crassa* (Roca et al., 2005), *Penicillium sclerotiorum* (Raina et al., 2010) species, which emphasizes the versatility and ecological significance of this mechanism in the fungal kingdom (Table 1).

2. Plants and QS-Related Molecules

QS signaling molecules are not limited to intra- and interspecific microbial communication. They are also important mediators in the microbe-plant dialogue (Table 1). The first evidence for this was obtained in the work of Mathesius et al. (2003). They showed that AHLs from pathogenic bacteria induce significant changes in the proteome of *Medicago truncatula* roots. These changes affect flavonoid and hormone metabolism, as well as the response to oxidative stress. Further research revealed the dual, structured nature of this influence. Short-chain AHLs (e.g., C6-AHLs) can stimulate root growth and branching by acting as a symbiotic recognition factor (Krumwiede et al., 2020). Long-chain AHLs (e.g., C12-AHLs) that are characteristic of many pathogens often trigger a priming mechanism in plants, a prepared systemic immune response (PSIR). Treatment with these molecules increases plant resistance to subsequent infection, for example by *Pseudomonas syringae*. This correlates with the induction of immune response genes such as *WRKY* and *GST6* (Krumwiede et al., 2020).

Thus, plants have evolved to “eavesdrop” bacterial QS communication, using AI as signals to trigger adaptive responses (Rebolleda-Gómez et al., 2019). The functional significance of QS eavesdropping extends beyond the plant's immediate physiological responses. QS signals also coordinate collective bacterial behaviors that shape the rhizosphere environment itself. DeAngelis et al. (2008) demonstrated that in the rhizospheres of *Avena fatua* L., QS controls the production of extracellular enzymes (chitinases, proteases) that drive nitrogen mineralization from organic matter (DeAngelis et al., 2008). Among 533 bacterial isolates, 24% possessed both AHL production and QS-regulated enzyme activity; disruption of QS abolished enzyme production in seven of the eight tested strains. Thus, QS is not merely a communication system that plants monitor - it is an ecological control point governing nutrient cycling and organic matter decomposition in the rhizosphere. This realization re-frames the plant's chemical response to QS signals.

If plants can detect bacterial QS activity (Mathesius et al., 2003), and if this activity regulates critical ecosystem functions (DeAngelis et al., 2008), then plants may have evolved not only to respond to QS but to intervene in it. This logic provides the conceptual foundation for understanding plant-derived QS inhibitors, particularly coumarins, not as incidental antimicrobials, but as intentional tools for rhizosphere engineering.

3. Coumarin as a Plant Metabolite Regulating Interactions in the “Soil-Plant” System

If bacterial autoinducers serve as signals that plants eavesdrop on, then the response from higher plants is the active secretion of low-molecular compounds into the rhizosphere, which are capable of modulating microbial communication.

One of the key classes of regulatory compounds are coumarins - phenolic secondary metabolites widely distributed in plants, especially in families such as Umbelliferae and Rutaceae (Gutiérrez-Mellado et al., 1996). In addition to their known function in protecting against abiotic stress and herbivores, they play a central role in managing microbial communities in the rhizosphere by interfering with QS systems.

The structural diversity of natural coumarins (simple coumarins, furanocoumarins and pyranocoumarin) determines the range of their biological activities. Simple hydroxy and methoxy derivatives, such as umbelliferone, scopoletin, esculetin and fraxetin are the most common when it comes to interactions with soil microorganisms.

For a long time, their accumulation in root tissues and release into the rhizosphere was considered primarily as part of the antimicrobial response to the invasion of phytopathogens – viruses, bacteria, fungi and oomycetes (Masuda et al., 1998; Dutsadee et al., 2008; Abou Zeid et al., 2008). However, modern data suggest a more complex and selective role for coumarins. They function not simply as broad-spectrum antibiotics, but as signaling molecules that finely regulate the plant's dialogue with the complex soil microbiome. This is supported by the fact that the accumulation of specific coumarins is induced not only by pathogens but also by beneficial rhizobacteria, such as *Pseudomonas fluorescens* (Van de Mortel et al., 2012) и *Paenibacillus polymyxa* (Zhou et al., 2016).

This fact indicates their involvement in establishing mutually beneficial interactions. In an early study predating the molecular characterization of quorum sensing, Shimizu et al. (2005) demonstrated that a non-pathogenic isolate of *Fusarium oxysporum* 101-2 (NPF) induced resistance in morning glory (*Pharbitis nil*) cuttings against pathogenic *F. oxysporum* f. sp. *batatas* O-17 (PF). This induced resistance was accompanied by the rapid activation of phenylalanine ammonia-lyase (PAL) and the accelerated accumulation of the coumarins scopoletin and scopolin in plant tissues. Strikingly, while the non-pathogenic strain consistently induced coumarin synthesis, the pathogenic strain at high inoculum density (10^8 bud-cells/ml) suppressed coumarin accumulation, suggesting that successful pathogens have evolved mechanisms to actively inhibit this protective phenylpropanoid response. The ability of plants to recognize beneficial microorganisms and specifically modify the rhizosphere environment for them is a clear manifestation of this interaction. A striking example is the induction of a specific signaling cascade (MYB72/BGLU42) in response to colonization by beneficial pseudomonads, leading to the secretion of scopoletin, which suppresses pathogens but does not affect inducers (Stringlis et al., 2018). This demonstrates that plants do not passively “eavesdrop” on QS, but actively use their metabolites (coumarins) to create favorable conditions for desired microorganisms.

Thus, plant-secreted coumarins act as ecological regulators: they can suppress the virulence of pathogens by disrupting their coordinated behavior, while simultaneously not hindering and possibly even supporting colonization by beneficial symbionts.

4. Mechanisms of Influence of Coumarins on Soil Microorganisms: From Direct Antimicrobial Action to Community Management Through QS

The influence of coumarins on soil microorganisms is realized at several levels: from direct toxicity, which is characteristic of many phytoalexins, to fine-tuning population dynamics and community composition through modulation of quorum sensing systems. Considering these levels allows us to move from the classical concept of coumarin as antimicrobial agents to a modern paradigm of its role as an ecophysiological regulator.

4.1. Direct Antimicrobial Action of Coumarins

The direct inhibitory effect of coumarins in vitro on a wide range of phytopathogens (fungi, oomycetes, and bacteria) is well documented. For example, scopoletin inhibits the growth of *Botrytis cinerea*, *Alternaria alternata*, and *Pseudomonas syringae* (Stringlis et al., 2019), and furanocoumarins such as psoralen and bergapten exhibit antibacterial activity (Abdul Hamid et al., 2022). Minimum inhibitory concentrations for various coumarins can reach submicromolar values (Kayser et al., 1999), which testifies to the effectiveness of this defense mechanism.

4.2. Coumarins as Quorum Sensing Inhibitors in Phytopathogens

A more specific and ecologically significant mechanism of coumarin action is QS inhibition, which disrupts the coordinated expression of virulence factors without cell death, reducing selective pressure for resistance. The first evidence that coumarins (umbelliferone, esculetin, daphnetin) can suppress the virulence of *R. solanacearum* was obtained by Yang and Chen. They demonstrated a reduction in the expression of the *fliC/fliA* motility genes and a decrease in colonization of tobacco roots. However, molecular targets remained unknown and the effect was interpreted in terms of "antivirulent" activity (Yang et al., 2016; Chen et al., 2016).

In the next work, Yang et al. (2017) revealed the mechanism. Umbelliferone inhibits both signaling cascades leading to T3SS activation - HrpG-HrpB and PrhG-HrpB. This results in decreased expression of six of the ten key T3SS effectors, while leaving T2SS unaffected. The selectivity of the action indicates the involvement of specific regulatory nodes, rather than general metabolic toxicity. Umbelliferone also inhibits biofilm formation, which is a QS-dependent collective behavior.

But why is the suppression of T3SS and biofilms so critical? The answer is provided by a metagenomic study by Zhang et al. (2026). In the infected rhizosphere, *R. solanacearum*, through its QS systems (eight different pathways), actively suppresses the QS genes of beneficial bacteria and simplifies the microbial network. In this context, the T3SS is not simply a tool for delivering effectors, but a key element of ecological dominance. The pathogen does not attack the plant in isolation. It first restructures the microbial community to suit its needs. By disarming the T3SS and disrupting QS-controlled collective behaviors, coumarins may simultaneously attenuate direct virulence and prevent pathogen-mediated disruption of the protective rhizosphere microbiome.

By disrupting QS communication, coumarins create the preconditions for a profound restructuring of the rhizosphere microbial community. The molecular basis for this effect has been confirmed using bioreporter systems. Coumarins such as bergamottin are able to suppress the production of autoinducers AI-1 and AI-2 in *Vibrio harveyi* (Lee et al., 2014), while for *Pseudomonas aeruginosa* and *Chromobacterium violaceum* the ability of hydroxylated coumarin derivatives to inhibit QS-controlled violacein production was established (D'Almeida et al., 2017). It is important to note that coumarins can selectively influence different QS pathways, without affecting, for example, the expression of the *luxS* synthase gene (AI-2), but suppressing the work of downstream regulons (for example, *lsrA*) (Lee et al., 2014).

4.3. The Influence of Coumarins on the Formation and Functioning of the Rhizosphere Microbial Community

However, in vivo the significance of the direct toxic effect is often limited to the concentrations achieved in the rhizosphere, indicating the leading role of more selective signaling mechanisms.

Key evidence for the selective, controlling effects of coumarins on the microbiome comes from experiments on *Arabidopsis thaliana*. It was shown that root colonization by the beneficial rhizobacteria *Pseudomonas simiae* WCS417 induces plant transcription factor MYB72, which activates biosynthesis and excretion of coumarin scopoletin (Stringlis et al., 2018). Scopoletin exhibits selective antimicrobial activity: it effectively suppresses soil fungal pathogens *Fusarium oxysporum* and *Verticillium dahliae*, but is tolerant to the pseudomonad strains that induce it. Metagenomic analysis revealed that the rhizosphere microbiome composition of scopoletin-producing mutants (F6'H1) was

significantly different from that of the wild type. This demonstrates that a specific coumarin secreted in response to a specific microbial signal acts as a selective factor shaping the composition of the microbial community favoring beneficial symbionts. The impact of coumarins on soil communities is context-dependent and varies with methodology. While some studies demonstrate clear selective effects, others report more nuanced outcomes.

Similar context-dependent outcomes were reported by Yang et al. (2023) in annual ryegrass. At 200 mg/kg, coumarin did not reduce bacterial diversity but significantly shifted community composition, enriching both beneficial bacteria and opportunistic pathogens. This dual outcome: stimulation of symbionts alongside proliferation of pathogens, underscores that coumarin effects are not inherently selective or suppressive; rather, the ecological outcome emerges from the interplay of concentration, plant species, and the native microbial community (Yang et al., 2023).

For instance, in a long-term microcosm experiment aimed at stimulating PCB degradation, coumarin (2 mmol/kg) did not alter the overall microbial community structure assessed by PLFA profiling nor enhance biodegradation (Luo et al., 2007). This suggests that at certain concentrations and in established communities, coumarins may exert subtle functional modulation (e.g., on QS pathways) without causing major taxonomic shifts detectable by broad profiling methods.

In contrast, other microcosm studies report a significant broad-spectrum suppressive effect. The application of coumarin at agriculturally relevant doses (100-150 mg/kg) selectively inhibits weed growth more than wheat and measurably reduces total microbial biomass and genetic diversity of both bacteria and fungi (Niro et al., 2016). Similarly, PLFA analysis has shown that coumarins can significantly decrease total microbial, bacterial and fungal biomass, indicating a potent non-selective pressure that can "reset" the microbial community structure (Li et al., 2013). This duality - specific induction versus broad suppression - highlights that the ecological outcome depends on concentration, soil properties and initial community state (Xiao et al., 2017).

The case of *R. solanacearum* illustrates how these context-dependent effects translate into ecological outcomes. At physiologically relevant concentrations, coumarins such as umbelliferone selectively disarm the pathogen by suppressing its T3SS and QS-regulated collective behaviors (Yang et al., 2016). Direct evidence for pathogen-driven QS restructuring comes from a metagenomic study comparing the rhizosphere microbiomes of healthy tobacco and *R. solanacearum*-infected plants (Zhang et al., 2026). The QS pathway was the most significantly enriched among the 50,960 differentially abundant genes. Overall, QS gene abundance was negatively correlated with *Ralstonia* density ($R^2 = 0.52$), indicating suppression of community quorum sensing as pathogen populations increased. Taxonomic attribution revealed why: while QS genes from most bacteria were depleted, *Ralstonia*'s contribution to QS pathways increased from 2.3% in healthy rhizospheres to 10.4% in diseased ones. Across seven QS subsystems (AI-1, GABA, PapR, NprX, Phr, cCF10, DSF), pathogen-attributed genes were significantly enriched. These findings demonstrate that *R. solanacearum* actively restructures the rhizosphere QS network during infection, suppressing beneficial bacterial communication while enhancing its own QS systems.

Thus, coumarin operates at the intersection of direct virulence inhibition and ecosystem-level intervention: it does not simply kill or weaken pathogens but restores the microbial network integrity that pathogens subvert during infection. This makes coumarin one of the rare classes of plant metabolites that functions as both an anti-virulent agent and a microbiome editor.

4.4. Functional Consequences: Interference with Quorum-Dependent Processes

The ecological significance of coumarin-induced shifts in communities lies in their functional consequences. Key soil processes such as biofilm formation and exoenzyme secretion for organic matter decomposition are controlled by QS, and coumarin inhibition of QS can have far-reaching effects (DeAngelis et al., 2008). Coumarins like scopoletin and esculetin inhibit biofilm formation by pathogens (e.g., *R. solanacearum*) and provide a competitive advantage to non-virulent microorganisms (Pruteanu et al., 2020). Suppressing QS signaling in the soil has also been shown to slow down the mineralization of organic matter (Strickland et al., 2013). By secreting coumarins,

plants not only shape their own microbiome, but also locally modulate carbon and nutrient cycling in the rhizosphere.

5. Challenges and Opportunities for Coumarin-Based Agricultural Strategies

5.1. Ecological Benefit vs. Agronomic Liability

Current agricultural approaches to disrupting quorum sensing fall into two distinct categories, each with inherent strengths and limitations. Microbial quorum quenching relies on live biocontrol agents - typically *Bacillus* or *Rhodococcus* strains expressing AHL-lactonases or other quorum-quenching enzymes. These agents have demonstrated efficacy against soft rot pathogens (*Pectobacterium*, *Erwinia*) under controlled conditions (Table 1). Their advantages include self-propagation, multifunctionality (some strains also produce antimicrobial agents or promote plant growth), and regulatory familiarity as biopesticides. However, living agents face persistent challenges such as inconsistent establishment in competitive rhizosphere environments, loss of quorum-sensing gene expression in situ, sensitivity to soil physicochemical conditions and short shelf life.

Molecular quorum quenching employs low-molecular-weight QS inhibitors, including plant-derived compounds such as coumarins, flavonoids, and furanones. Coumarins offer a distinct profile: (i) natural origin and biodegradability - they are already present in agroecosystems; (ii) multi-target action - they simultaneously interfere with QS, T3SS, and biofilm formation (Yang et al., 2016); (iii) potential selectivity - differential activity against pathogens vs. beneficial taxa (Stringlis et al., 2018), and (iv) chemical tractability - synthetic analogues can be developed. Yet, molecular approaches face their own challenges, most notably environmental persistence - or rather, lack thereof.

A major obstacle to the use of coumarins is their extremely rapid degradation in soil. The half-life (DT₅₀) of the coumarin can be less than one day, with 90% dissipation within 2–3 days under aerobic conditions (Gamiz et al., 2020). This instability is primarily mediated by microbial metabolism, with sorption to soil organic matter ($K_d \sim 1.04$ L/kg) playing a secondary and reversible role. This presents a paradox. From an ecotoxicological perspective, rapid degradation is highly desirable, as coumarins do not persist or bioaccumulate and do not contaminate groundwater, making them "green" by design. However, from an agronomic perspective, a half-life of less than 24 hours means that a single application provides only a transient window for quorum sensing interference, which is insufficient for sustained protection against chronic pathogens or reshaping of established microbial communities.

5.2. Critical Knowledge Gaps

Despite compelling mechanistic evidence in vitro and in model systems, several gaps must be addressed before coumarin-based strategies can be deployed in production agriculture. 1. Dose-response in soil. What concentrations of specific coumarins are actually achieved in the rhizosphere under natural exudation? How do these compare to effective concentrations determined in vitro? The current disconnect between laboratory MIC/QSI values and environmental concentrations is a major barrier to rational formulation design.

2. Non-target effects on beneficial QS functions. QS regulates not only virulence but also symbiotic nitrogen fixation, mycorrhizal establishment, and organic matter decomposition (DeAngelis et al., 2008). Do coumarins, at environmentally relevant concentrations, disrupt these beneficial processes? The trade-off between pathogen suppression and nutrient mineralization remains entirely unexplored.

3. Spectrum of activity across coumarin structural classes. Most studies have focused on a few compounds (umbelliferone, scopoletin, esculetin). How do structural variations (hydroxylation patterns, prenylation, glycosylation) affect QSI potency, selectivity, and environmental fate? A systematic structure-activity-ecotoxicity relationship is urgently needed.

4. Efficacy under realistic field conditions. To date, nearly all evidence for coumarin-mediated QS inhibition and microbiome editing comes from axenic systems, gnotobiotic plants, or laboratory microcosms. Field trials with naturally assembled soil communities, variable weather, and competing microbial processes are the essential next step.

6. Conclusion

Coumarins possess a unique combination of properties - natural origin, ecological relevance, multi-target anti-virulent activity, and demonstrated ability to edit rhizosphere microbial communities - that distinguish them from both live QS agents and synthetic QSI inhibitors. The metagenomic data for *Ralstonia*'s "QS takeover" - increasing its contribution to QS genes from 2.3% to 10.4%, while overall community QS potential decreases (Zhang et al., 2026) - redefines bacterial wilt as not just an infection, but suppression of cooperative interactions in the microbial community. Coumarins, by disarming the pathogen's QS and virulence cascades (Yang et al., 2016), may act as counter-coups, restoring the pre-infection functional network.

Their rapid environmental degradation, although agronomically challenging, is environmentally responsible and can be addressed through structural optimization, and integrated application strategies. The question is no longer whether coumarins can function as agricultural QSI modulators. Mechanistic evidence is compelling, and the question is how to translate this mechanism into reliable, cost-effective, and regulatory acceptable products. This requires convergent research at the intersection of natural product chemistry, soil microbiology, and agriculture.

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