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Original Paper

Microbial Community and Ecological Network Responses to Spartina alterniflora Invasion in Coastal Wetlands: A Mini-Review with Bibliometric Insights

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Abstract

Spartina alterniflora invasion has become one of the most intensively studied plant-invasion processes in coastal wetlands because its effects extend beyond aboveground vegetation change to soil microbial communities, microbial interaction networks, and biogeochemical cycling. This mini-review synthesizes a Web of Science dataset of 209 records retrieved with a search strategy linking S. alterniflora, microbial communities or networks, and invasion-related terms. A CiteSpace-compatible bibliometric analysis showed that the literature expanded markedly after 2020, with publication output peaking in 2025 within the exported dataset. The keyword structure was centered on S. alterniflora, salt marsh, coastal wetland, plant invasion, microbial community, bacterial community, carbon, and nitrogen, indicating a field that now connects invasion ecology with microbial network ecology and ecosystem-function research. Evidence from chronosequence, rhizosphere, mangrove, and salt-marsh studies shows that S. alterniflora invasion often restructures bacterial and fungal communities through changes in organic matter, salinity, pH, hydrology, and plant-derived substrates. Network studies suggest a context-dependent reorganization rather than a uniform increase or decrease in complexity: bulk-soil fungal or mixed microbial networks often become simpler or less stable, whereas rhizosphere, host-associated bacterial, and arbuscular mycorrhizal fungal subnetworks may become more modular or more densely connected. Functionally, these microbial changes are linked to denitrification, N2O emissions, sulfur cycling, decomposition, soil organic carbon dynamics, and carbon-cycling functional genes. Future studies should combine standardized network inference, multi-omics, manipulative experiments, and restoration monitoring to move from correlation-based network description toward causal understanding of belowground invasion mechanisms.

Keywords

Spartina Alterniflora, Plant Invasion, Microbial Community, Co-Occurrence Network, Citespace, Coastal Wetland, Soil Microbiome, Carbon And Nitrogen Cycling

1. Introduction

The invasion of *Spartina alterniflora* in coastal wetlands has reshaped many salt-marsh, mangrove, and estuarine ecosystems, especially along the coast of China. Unlike many terrestrial invasions, this species modifies strongly coupled plant-soil-water systems: it changes sediment trapping, soil organic matter inputs, redox conditions, salinity gradients, and nutrient cycling (Cao, Cui, Sun, Zhang, Zheng, & Jiang, 2021). These changes create new belowground habitats, and microbial communities respond rapidly because they mediate decomposition, carbon stabilization, nitrogen transformation, greenhouse-gas production, and plant-soil feedbacks.

Early studies on *S. alterniflora* invasion mainly emphasized vegetation replacement, soil carbon and nitrogen pools, and wetland biogeochemistry. More recent work has shifted toward microbiome composition, microbial assembly, and co-occurrence networks. This shift is important because microbial diversity alone cannot explain whether invaded soils become more functionally connected, more modular, more vulnerable to disturbance, or more dependent on rare taxa. Co-occurrence networks are not direct maps of biological interaction, but they provide a useful ecological lens for detecting how taxa covary across environmental gradients and how potential keystone taxa or modules reorganize after invasion.

This mini-review connects two levels of evidence. First, it summarizes the research landscape using a CiteSpace-based bibliometric analysis of the Web of Science export used in this study. Second, it synthesizes core ecological findings on microbial community composition, co-occurrence networks, assembly processes, and ecosystem functions under *S. alterniflora* invasion. The central argument is that *S. alterniflora* invasion should be interpreted as a belowground network and function problem, not only as a shift in dominant plant cover (Chen & Wen, 2021).

2. Bibliometric Profile of the Research Field

Annual publication output increased from 6 records in 2015 to 24 in 2020, 29 in 2022, 36 in 2024, and 40 in 2025. This trajectory indicates that microbial and network perspectives became a visible hotspot after the first wave of work on invasion-driven changes in soil carbon, nitrogen, and microbial composition.

Keyword analysis revealed the thematic core of the field. The highest-frequency normalized keywords were *Spartina alterniflora* (97 records), salt marsh (66), diversity (56), coastal wetland (54), plant invasion (51), nitrogen (40), microbial community (39), *S. alterniflora* invasion (37), bacterial community (36), invasion (36), and carbon (35).The strongest co-occurrence links connected *S. alterniflora* with salt marsh, invasion, coastal wetland, diversity, nitrogen, microbial community, and bacterial community.

3. Microbial Community Responses to *S. alterniflora* Invasion

In a coastal wetland of eastern China, Yang et al. (2016) found that short-term invasion increased microbial biomass carbon and total PLFA abundance relative to bare flats and native plant communities, suggesting that higher plant productivity and substrate inputs can stimulate belowground microbial pools.

In a mangrove nature reserve, Liu et al. (2017) found that cordgrass invasion increased bacterial richness, particularly through rare and conditionally rare taxa, and altered predicted community function. At a continental scale, Gao et al. (2022) reported that *S. alterniflora* invasion reshuffled the soil microbiome of blue carbon ecosystems across 2451 km of Chinese coastlines, increasing bacterial richness but promoting biotic homogenization and weakening microbial network complexity and stability. In contrast, a recent Yellow River Delta study reported that *S. alterniflora* invasion reduced bacterial alpha-diversity while strongly shifting bacterial and fungal beta-diversity (Zhang et al., 2024).

Yang et al. (2019) demonstrated significant changes in soil fungal abundance, richness, and diversity along a chronosequence of *S. alterniflora* invasion in a Yellow Sea coastal wetland. Zhang et al. (2021) found that invasion reduced fungal richness and phylogenetic diversity in the Yellow River Delta, homogenized fungal communities, increased the proportion of saprophytic fungi, and inhibited pathogenic fungi.

Several environmental filters repeatedly emerge. Soil pH and salinity were identified by Zhang et al. (2021) as important drivers of fungal community structure. Inundation frequency and water content strongly shaped bacterial community composition and assembly in *S. alterniflora* wetlands (Gao et al., 2021). Seasonality also matters: Zhang et al. (2023) found that bacterial and fungal diversity in invaded coastal salt marshes was lowest in spring and increased in summer and autumn with higher organic carbon and nitrogen availability.

4. Microbial Network Reorganization and Community Assembly

The current evidence is best summarized as ecological reorganization rather than a universal increase or decrease in network complexity. Bulk-soil fungal or mixed microbial networks often become simpler, more homogenized, or less stable after invasion, especially when invaded stands are compared with nearby native *Suaeda salsa* or mudflat controls. By contrast, host-associated, rhizosphere, or arbuscular mycorrhizal fungal networks may become more modular or densely connected, suggesting that *S. alterniflora* can create a strongly filtered microbial neighborhood around its own roots.

Table 1. Representative Network-focused Studies on *S. alterniflora* Invasion

Study	**Compartment and design**	**Network focus**	**Main interpretation**
Zhang et al. (2021)	Yellow River Delta salt marsh; bulk soil under native *Suaeda salsa* versus invaded *S. alterniflora*	Fungal ITS2 co-occurrence network; links and modularity	Invasion reduced fungal richness and phylogenetic diversity, homogenized communities, increased saprotrophs, and simplified fungal networks.
Chen and Wen (2021)	Subtropical mangrove sediments; mangrove, ecotone, cordgrass, and mudflat habitats	Archaeal and bacterial 16S networks; centrality, modularity, natural connectivity, Zi-Pi keystone roles	Bacterial networks were more complex than archaeal networks, and low-abundance taxa often occupied keystone positions.
Gao et al. (2021)	Zhangjiang estuary mesocosm; *S. alterniflora* soils along an inundation-frequency gradient	Bacterial co-occurrence and assembly under hydrological filtering	Soil water content was a decisive driver, increasing inundation reduced bacterial network complexity, and deterministic assembly dominated.
Gao et al. (2022)	Continental-scale Chinese coast; six soil depths across 2451 km	Soil bacterial microbiome and ecological network complexity/stability	Invasion increased bacterial richness but promoted biotic homogenization, reduced network complexity and stability, and weakened microbe-carbon coupling.
Zhang et al. (2024)	Yellow River Delta; bulk soil from invaded stands versus adjacent *Suaeda salsa*	Bacterial and fungal networks; nodes, links, cohesion, natural connectivity	Invasion reduced bacterial alpha-diversity and weakened bacterial and fungal inter-species relationships.

This table helps reconcile the main controversy in the field. Zhang et al. (2021), Gao et al. (2022), and Zhang et al. (2024) support the view that invasion can simplify or destabilize bulk-soil networks. Network responses also differ among microbial domains (Gao, Li, Zhong, Shen, Chen, Li et al., 2019).

Chen and Wen (2021) analyzed archaeal and bacterial communities in subtropical mangrove sediments under *S. alterniflora* invasion and found that bacterial networks were more complex than archaeal networks. They also showed that keystone taxa were often low-abundance conditionally rare taxa.

Assembly processes provide a complementary view of network change. In mangrove sediments, Chen and Wen (2021) found that overall archaeal and bacterial assembly was predominantly stochastic, with stronger stochasticity for bacteria than archaea. By contrast, Gao et al. (2021) found that deterministic processes dominated bacterial assembly along an inundation-frequency gradient in *S. alterniflora* salt marshes, with soil water content acting as a key driver.

5. Biogeochemical and Functional Consequences

Microbial restructuring under *S. alterniflora* invasion has direct implications for wetland carbon and nitrogen cycling. Gao et al. (2019) showed that invasion altered bacterial communities and enhanced soil N2O emissions by stimulating denitrification in mangrove wetland soils.Related work in Jiuduansha wetland also linked *S. alterniflora* invasion to bacterial communities and greenhouse-gas emissions, indicating that microbial pathways can mediate ecosystem-scale atmospheric feedbacks.

Carbon cycling is equally important but more complex (Gao, Peng, Zhang, Li, Fan, Tripathi et al., 2021). Invasion often increases plant biomass, litter input, and soil organic carbon, yet microbial responses may either stabilize or accelerate carbon turnover depending on substrate quality, redox conditions, and decomposer guilds. Zhang et al. (2021) reported a higher proportion of saprophytic fungi in invaded soils, suggesting enhanced organic matter decomposition potential.More recent work during the cold season showed that invasion reduced microbial biomass carbon and the diversity of carbon-cycling functional genes (Zhang et al., 2025). These findings argue against treating *S. alterniflora* invasion as simply beneficial or harmful for blue carbon. Its net effect depends on how plant-derived inputs, microbial functional genes, decomposition, and physical sediment stabilization interact.

The newer network-focused literature also points to sulfur and functional-gene coupling as emerging mechanisms. Liu et al. (2025) further connected dense microbial and functional-gene co-occurrence networks in mangrove systems with nitrogen-removal and microbial carbon-fixation functions.

6. Management Relevance and Future Research

Management of *S. alterniflora* invasion is no longer only a matter of removing aboveground biomass. Eradication, mowing, herbicide treatment, mangrove restoration, and hydrological manipulation can all alter microbial habitats and microbial functions. Gong et al. (2025) showed that different eradication strategies reduced *S. alterniflora* but also changed bacterial communities, macrobenthos, and sediment physicochemical properties. These studies imply that restoration assessment should include microbial indicators, especially network complexity, functional-gene diversity, nitrification and denitrification potential, and carbon-cycling traits.

Several priorities emerge from the bibliometric and narrative synthesis. First, network analyses need methodological standardization. Different sequencing depths, taxonomic resolutions, correlation methods, filtering thresholds, and compositional corrections can produce different networks from the same ecological system. Second, studies should distinguish bacteria, fungi, archaea, protists, and cross-kingdom networks rather than treating the "microbial community" as a single unit. Third, chronosequence designs should be combined with repeated seasonal sampling because invasion age and seasonality can produce different signals (Gao, Li, Shi, Yang, Gao, Fan et al., 2022). Fourth, field experiments should manipulate salinity, inundation, litter input, and restoration treatments to test causal pathways. Finally, researchers should connect microbial network modules to measured functions, such as N2O flux, methane production, sulfur cycling, enzyme activity, organic carbon stabilization, and functional-gene expression.

Table 2. Methodological Choices Affecting Microbial Network Interpretation

Methodological choice	How it varies in the corpus	Why it matters
Taxonomic unit	Networks are built from OTUs, ASVs, or genus-level taxa.	Node number, centrality, and keystone assignment change with taxonomic resolution.
Prevalence and abundance filtering	Studies retain taxa using different occurrence and abundance thresholds.	Filtering can strongly change nodes, edges, hub taxa, and apparent complexity.
Association rule	Most studies use Spearman correlations, but thresholds vary from approximately 0.6 to 0.8 and correction strategies differ.	Edge density and positive/negative link balance are not directly comparable across studies.
Stability metric	Stability may be measured as natural connectivity, robustness to node removal, cohesion, modularity, or other indices.	A reported increase in modularity and a decrease in robustness can both be true because they measure different properties.
Functional interpretation	Some studies rely on predicted functions, whereas others include functional genes, qPCR, isotopes, or process measurements.	Predicted functions are useful for hypothesis generation but weaker than measured genes, transcripts, enzymes, or fluxes.

Methodological choice	How it varies in the corpus	Why it matters
Sampling frame	One-time bulk-soil comparisons dominate, but some studies include depth profiles, warming experiments, hydrological gradients, or rhizosphere-root contrasts.	Inconsistencies may reflect compartment, depth, season, and scale rather than a true disagreement about invasion effects.

7. Conclusions

The current literature shows that *S. alterniflora* invasion consistently affects coastal wetland microbiomes, but its effects are context-dependent rather than uniform. Bacterial and fungal communities respond to invasion age, plant identity, salinity, pH, hydrology, soil depth, and seasonality. Network studies reveal that invasion can simplify fungal or mixed microbial networks in bulk soil, alter bacterial and archaeal network complexity, shift keystone roles toward rare taxa, and change the balance between deterministic and stochastic assembly. At the same time, host-associated bacterial and AMF subnetworks may become more modular or densely connected under *S. alterniflora*, suggesting that invasion reorganizes microbial associations across compartments rather than pushing the whole microbiome in one direction. Functionally, these microbial changes are linked to denitrification, N2O emissions, sulfur cycling, decomposition, carbon-cycling genes, and soil organic carbon dynamics.

The bibliometric evidence confirms that this research area has grown rapidly since 2020 and has moved from descriptive microbial community surveys toward microbial network ecology and ecosystem-function analysis. Future work should use standardized, experimentally grounded, and multi-omic approaches to test how microbial interactions mediate the ecological consequences of *S. alterniflora* invasion. For management, the key message is clear: successful control or restoration should be evaluated not only by plant removal or vegetation recovery, but also by whether microbial networks and microbial functions recover toward desired wetland conditions.

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