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BIDIRECTIONAL ALLELOPATHIC INTERACTIONS OF RADISH (RAPHANUS SATIVUS L.) AND OTHER CROPS

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ABSTRACT
Allelopathy, the biochemical interaction among plants mediated through the release of secondary metabolites, has emerged as an important ecological phenomenon with significant implications for sustainable agriculture and integrated crop management. Among vegetable crops, radish (Raphanus sativus L.), a member of the Brassicaceae family, is recognized for producing a diverse array of bioactive compounds, including glucosinolates, isothiocyanates, phenolic acids, and flavonoids, which influence the germination, growth, and physiological performance of neighbouring plant species. Conversely, radish itself is susceptible to allelochemicals released by weeds, crops, and cover plants, highlighting the bidirectional nature of allelopathic interactions within cropping systems.
This review synthesizes current knowledge on the allelochemicals produced by radish, their modes of release, and their biological effects on agricultural crops, weeds, and associated plant communities. It further examines the allelopathic impacts of other plant species on radish, emphasizing their influence on seed germination, seedling establishment, growth, and productivity. The review also discusses the environmental, biological, and management factors that regulate allelopathic activity, including soil properties, climatic conditions, microbial transformations, plant developmental stage, and allelochemical concentration. In addition, existing knowledge gaps are identified, particularly the limited availability of field-based investigations, insufficient characterization of allelochemicals in tropical radish germplasm, lack of standardized experimental methodologies, and the underutilization of modern omics approaches for elucidating allelopathic mechanisms.
By integrating evidence from studies investigating both the donor and receiver roles of radish, this review provides a comprehensive understanding of bidirectional allelopathic interactions and their ecological and agronomic significance. The information presented is expected to support future research aimed at developing sustainable weed management strategies, optimizing crop rotation systems, and improving environmentally friendly vegetable production.

KEYWORDS: Bidirectional allelopathy; Secondary metabolites; Glucosinolates; Isothiocyanates; Crop rotation.

1. INTRODUCTION

1.1. Definition and historical background

Allelopathy refers to the influence of chemicals which is released by a plant which affects the survival, growth and development of the nearby plants. And the chemicals released by a plant that influence other plant's growth are called allelochemicals. These chemicals released by plants via root exudation, volatilization, leaves leaching and decay of residues of plants and they can have either growth promoting or inhibiting effects to the other plants. This allelopathic process can be stimulated by various factors that may be biotic and abiotic factors i.e., crop competition, herbivores, plant disease causing pathogens, light, heat, water scarcity, and availability of nutrients to the plants. But explaining about allelopathy is difficult as it is (Souza et al., 2019)complex that study of amount of chemicals released by plants, dilution and degradation of allelochemicals in the field surroundings. By studying and analysing the mechanisms of allelochemical effects in molecular level helps to reduce the reliance of synthetic chemicals. (Shan, Zhou, Shah, Arafat, Arif Hussain Rizvi, et al., 2023)
The interaction of allelochemical between the plants undergoes the secretion of secondary metabolites by a plant that influences and retards the growth and development and even kill the nearby plant in the field environment. This process takes place at various biological levels, including molecular, physiological and biochemical aspects such as germination of seeds, root and shoot (photosynthesis and respiration) development.(Gniazdowska & Bogatek, 2005; Katarina Šoln et al., 2022)
Allelopathy can be twisted together with allelobiosis which is relatively referred as the phenomena where the signalling chemicals intermediates neighbour detection and identity recognition among plants indicating that the chemicals can either retard or modulate the plant communication(Kong et al., 2024).

Molisch created the term "allelopathy" in 1937 from Greek words that mean "of each other" and "to suffer," referring to the chemical interactions between plants that may either be beneficial or harmful.

1.2 Difference between competition and allelopathy in plants

The two basic ways that plants interact with one another are by sharing and exhausting shared resources and by chemically influencing nearby plants. Although they are theoretically different, they are closely related in nature. There are some common resources like light, water, nutrients, and space are used by plants. By simply expanding and using more resources by one plant that decreases what is available to other plants. (McCoy et al., 2022) (Fernandez et al., 2016) (Mahé et al., 2022) (Wang et al., 2024).

Allelopathy is a type of interference competition in which plants exude allelochemicals (toxic or inhibitory substances) into the environment, directly hindering the germination, development, or survival of neighbouring plants.(Liu et al., 2019; McCoy et al., 2022; Uesugi et al., 2019; Weidenhamer, 1996).

1.3 Importance of Allelopathy in Vegetable Cropping Systems

1.3.1 Role of Allelopathy in Sustainable Agriculture

Allelopathy is the utilization of natural compounds (allelochemicals) generated by plants to control pests and other plants. According to research, it is an important tool for reducing synthetic pesticide usage, improving soil health, and promoting sustainable weed and pest control.(Kostina-Bednarz et al., 2023; Scavo & Mauromicale, 2021)

Cover crops have been shown to control weeds by 70–95% between crops, in part through allelopathy, competition, and physical mulch effects.(Gerhards & Schappert, 2019). Herbicide dosages can be reduced and the development of herbicide resistance slowed by allelopathic crops and extracts.(Scavo & Mauromicale, 2021). Allelochemicals can also affect bacteria, fungus, insects, and nematodes, providing a base for bioherbicides and biopesticides.(Hussain et al., 2021). At low concentrations, several allelochemicals stimulate crops or beneficial microbes to improve soil health and resilience.(Muhammad et al., 2019)

To improve crop allelopathy or add new features, breeding, marker-assisted selection, and genetic engineering are being investigated.(Hussain et al., 2021; Scavo & Mauromicale, 2021). allelopathy shows real weed-suppression potential through crop residues, cover crops, intercropping, cultivar choice, and plant extracts, but the strongest caveat is that field effects are often hard to separate from ordinary crop competition (Scavo & Mauromicale, 2021). Allelopathy suppresses weeds by releasing secondary metabolites that inhibit weed germination, growth, and sometimes reproduction through root exudation, leaching, volatilization, and residue decomposition(Khamare et al., 2022) (Murthy et al., 2025). Reviews consistently present this as a promising route to reduce reliance on synthetic herbicides and help address herbicide resistance. (Jabran et al., 2015). Multiple crops are repeatedly identified as allelopathic, especially rye, sorghum, rice, wheat, sunflower, barley, brassicas, and rapeseed(Anwar et al., 2021)

Crop allelopathy can be deployed through cover crops, mulches, intercropping, crop rotation, green manures, residue incorporation, and plant extracts or bioherbicides (Scavo & Mauromicale, 2021). Recent work points to mixtures, induced responses, breeding, biotechnology, and ecological redesign as the main ways to strengthen weed suppression(Hickman et al., 2023). Plants can increase allelochemical production in the presence of weeds, suggesting that recognition and induction matter, and future strategies may need to optimize whole cropping systems rather than treat allelopathy as a simple herbicide substitute(Mahé et al., 2022)

2. Why Radish?

2.1 Allelopathic potential of radish

Aqueous extracts of radish shoots and roots significantly reduced germination and seedling growth of wheat, barley, wild barley, and wild oat in Petri-dish assays In that study, 40–60% extracts completely inhibited germination and growth, while 15% had the smallest effect. Shoot extracts were more inhibitory than root extracts for seed germination in one radish study ("Allelopathic potential of radish (Raphanus sativus L.) on germination and seedling growth of some plants species," 2023).

Another study focused on root extracts still found significant, concentration-dependent suppression across germination, radicle, plumule, dry weight, and vigor traits, with wheat and barley more tolerant than the tested weeds (Ali, 2016). Among radish genotypes, black radish consistently showed the highest allelopathic activity, followed by red, with white radish weakest. Radish root incorporated into soil suppressed bread wheat, durum wheat, wild oat, and wild barley in a concentration-dependent way, and wild oat was completely suppressed at the highest treatment combination. (Rasul & Ali, 2021).

Wild radish also suppressed germination, radicle growth, emergence, and seedling growth of several species, although some species such as yellow nutsedge were relatively tolerant.(Norsworthy, 2003). Radish allelopathy is linked to secondary metabolites including isothiocyanates and phenolic acids such as p-hydroxybenzoic, caffeic, p-coumaric, syringic, ferulic, and sinapic acids(Souza et al., 2019). Oilseed radish shoots also contained quercetin across all sampling times, and phenolic content changed with growth stage and declined after lodging(Souza et al., 2019)

The cover-crop literature therefore supports radish as both a bioassay-active species and a candidate residue-based weed management tool(Souza et al., 2019). Radish is also commonly used as a sensitive indicator plant, and that

sensitivity can exaggerate apparent allelopathic strength compared with less sensitive crops or weeds(Ranagalage & Wathugala, 2016)
Lower-ranked papers reinforce this context from the other side by showing radish is readily inhibited by many donor species, including weed exudates, sunflower extracts, moss extracts, knotweed rhizome extracts, hairy vetch, Melastoma, and cover-crop extracts(Akter & Islam, 2019). One mechanistic study linked this inhibition in radish roots to ROS imbalance, oxidative stress, and suppression of root-hair development (Šoln et al., 2025)

3. Allelopathic Impact of Radish on Other Plants

3.1 Allelochemicals Produced by Radish

In radish, the best-supported allelochemical classes are glucosinolates and their breakdown products, especially isothiocyanates, alongside phenolic compounds and flavonoids (Gamba et al., 2021). The exact profile depends strongly on organ, cultivar, and growth stage, so radish does not have one fixed allelochemical composition (Cai et al., 2024). Glucosinolates repeatedly emerge as the central radish allelochemicals, with roots, sprouts, and seeds all containing multiple glucosinolate species (Park et al., 2022). The glucosinolates most often highlighted in radish are glucoraphasatin, glucoraphenin, and glucoerucin, with seed studies finding those three can account for up to 90% of total glucosinolates (Chen et al., 2023). Their main breakdown products are isothiocyanates, especially raphasatin from glucoraphasatin and sulforaphene linked to glucoraphenin metabolism(Gamba et al., 2021). Seed-oil volatile profiling also detected isothiocyanates, nitriles, and sulfides among glucosinolate degradation products, showing that radish allelochemistry extends beyond intact glucosinolates (Jia et al., 2023). Identified radish phenolics include gallic acid, catechin, 4-hydroxybenzoic acid, kaempferol, caffeic acid, epicatechin, p-coumaric acid, ferulic acid, quercetin, and trans-cinnamic acid (Geng et al., 2025).

Table 1. Accumulation of allelochemicals

Tissue	Main allelochemicals reported	Key pattern
Roots	Glucoraphasatin, glucoerucin, 4-hydroxyglucobrassicin, phenolics (Park et al., 2022)	White roots tend to have more glucosinolates; green roots more phenolics (Park et al., 2022)
Sprouts	Glucoraphasatin, glucoraphenin, sulforaphene, phenolics, flavonoids (Chen et al., 2023)	Light conditions shift abundance and bioactivity (Chen et al., 2023)
Leaves	Phenolic acids, flavonoids, alkaloids, sulphur compounds, glucosinolates (Geng et al., 2025)	Leaves contain more phenolic acids than roots (Geng et al., 2025)
Seeds	Glucoraphenin, glucoraphasatin, glucoerucin; volatile nitriles and isothiocyanates (Jia et al., 2023)	Seed glucosinolates are highly variety-dependent (Jia et al., 2023)

Sprouts are especially enriched in glucosinolate-related chemistry, with red LED cultivation increasing total phenolics, flavonoids, and glucoraphasatin (Chen et al., 2023). Leaves also concentrate a broad phytochemical mixture, including alkaloids, glucosinolates, sulfur compounds, and multiple phenolic acids, and reviews report that phenolic acid content is higher in leaves than roots (Geng et al., 2025).
Across cultivars, flavonoids and phenolic acids make up a large share of detected radish secondary metabolites, and different skin and flesh colours have distinct metabolite profiles(Cai et al., 2024). Red or pigmented radishes are enriched in anthocyanins such as pelargonidins and cyanidin derivatives, while cultivar-specific differences also extend to rutin, astragalin, naringenin, pinobanksin, caffeic acid, catechin, and epicatechin (Cai et al., 2024; Park et al., 2016).
Mechanistically, radish allelochemicals are most often discussed through glucosinolate hydrolysis and phenylpropanoid/flavonoid biosynthesis pathways (Cai et al., 2024). Genetic studies also identify cultivar-linked regulation of glucosinolate and flavonoid accumulation, including differential expression of genes such as RsCYP83B1, RsSUR1, RsST5a, RsCHS, RsF3H, and RsANS (Cai et al., 2024). Most direct “allelopathy” papers in this set use radish as a recipient bioassay species, not as the allelopathic donor plant (Mahdavikia et al., 2017). Those studies show radish responds strongly to external phenols, quinones, coumarins, and complex plant extracts through growth inhibition and oxidative stress, but they do not by themselves identify which radish metabolites act as weed-suppressive allelochemicals in the field (Aliotta et al., 1994; Mahdavikia et al., 2017).

Even so, the chemistry most plausibly linked to radish allelopathic effects is the glucosinolate–isothiocyanate system plus a substantial phenolic/flavonoid fraction, with additional sulfur volatiles and nitriles likely contributing after tissue disruption or residue breakdown (Chen et al., 2023).

3.1.1 Secondary metabolites of Radish

Radish secondary metabolites centre on glucosinolates, isothiocyanates, and polyphenols, and broader profiling studies also detect alkaloids, coumarins, terpenoids, lignans, carotenoids, and anthocyanins (Manivannan et al., 2019). Across the compiled literature, metabolite composition changes substantially with cultivar, organ, colour, and developmental stage, so "radish secondary metabolites" is not a single fixed profile (Park et al., 2022). Glucosinolates are a core radish secondary-metabolite class and are precursors of isothiocyanates formed after tissue disruption by myrosinase (Manivannan et al., 2019). In radish, glucoraphasatin is repeatedly reported as a dominant glucosinolate, and its breakdown yields the pungency-associated isothiocyanate raphasatin (Kakizaki et al., 2017; Lee et al., 2023). Radish also contains glucoraphenin, whose hydrolysis yields sulforaphene, and sprouts can contain indolic glucosinolates such as glucobrassicin, 4-hydroxyglucobrassicin, and 4-methoxyglucobrassicin (Baenas et al., 2016). Flavonoids and phenolic acids are the other major branch of radish secondary chemistry, and a 2024 metabolomics study identified 118 flavonoids and 95 phenolic acids, together making up 60.51% of detected secondary metabolites (Cai et al., 2024). Large-scale flavonoid profiling in colored radishes identified 133 flavonoids, including anthocyanins, flavones, flavonols, and dihydroflavones (Hanlon & Barnes, 2011). Sprouts are the most consistently enriched stage for glucosinolates and isothiocyanates, with one 8-variety study finding 3.8-fold more glucosinolates, 8.2-fold more isothiocyanates, and 6.9-fold more phenolics than mature taproots (Hanlon & Barnes, 2011). Seeds also appear chemically diverse, with 105 seed varieties spanning 3.59–206.89 μmol/g DW for glucosinolates and 5.6–193.25 μmol/g DW for isothiocyanates (Li et al., 2026).

Secondary metabolites of different cultivars of Radish

- Green radish roots contain more amino acids and phenolic compounds, while white radish roots contain slightly more glucosinolates (Park et al., 2022).
- In four coloured varieties, red tissues had the highest total flavonoids and antioxidant capacity(Cai et al., 2024).
- Red and purple radishes share anthocyanins linked to pigmentation, but black and white radishes have similar anthocyanin profiles, implying black colour arises from other metabolites(Zhang et al., 2020).
- In sprouts, light conditions shift metabolite output: red LED increased glucoraphasatin, phenolics, and antioxidant activity, while blue LED favored tyrosinase-inhibitory activity (Chen et al., 2023).

Biosynthetic control also differs by genotype. A gene named GRS1 mediates glucoraphasatin biosynthesis in radish, and correlation analyses across 13 accessions linked RsGRS1 to glucoraphasatin abundance and RsCYP81F genes to indolic glucosinolate profiles (Kakizaki et al., 2017). Integrated metabolomics-transcriptomics identified 19 flavonoid-related and 10 glucosinolate-related key genes underlying differences among varieties and tissues (Cai et al., 2024).

These metabolites are repeatedly linked to antioxidant, anti-inflammatory, antimicrobial, and chemopreventive activities (Gao et al., 2022). Isothiocyanates are the best-supported mechanistic group, with evidence for detoxification-enzyme induction, apoptosis-related signaling, and antioxidant-response activation(Baenas et al., 2016; Naveed et al., 2025).

Across species comparisons and systematic review data, radish roots are relatively rich in non-flavonoid polyphenols, terpenes, and glucosinolates, while leaves and sprouts contribute more of the antioxidant-active fraction (Gamba et al., 2021).

3.1.2 Glucosinolates in Radish

Radish glucosinolate profiles are root-centered but not uniform: most studies identify glucoraphasatin as the dominant glucosinolate in cultivated radish roots, often making up more than 84–90% of total glucosinolates, while indolic glucosinolates are a much smaller fraction (Yan et al., 2023). Across newer profiling work, radish contains a broader set of intact glucosinolates than older targeted assays captured, including glucoraphasatin, glucoerucin, glucoraphenin, 4-methoxyglucobrassicin, 4-hydroxyglucobrassicin, glucobrassicin, and minor aliphatic species such as 3-methylpentyl, 4-methylpentyl, and n-hexyl glucosinolates (Hasenstein et al., 2025; Ko et al., 2016).

Glucoraphasatin is the clearest compound in radish, dominating roots in broad germplasm screens, Japanese cultivars, taproot transcriptome studies, and double-haploid breeding lines(Yi et al., 2016). In young radishes, glucobrassicin is the main indolic glucosinolate, while cultivated accessions usually show only a few consistently detected indolic compounds such as glucobrassicin, 4-hydroxyglucobrassicin, and 4-methoxyglucobrassicin (Lee et al., 2023). Variation among genotypes is large rather than trivial. Root total glucosinolates varied widely across 71 accessions from 23 countries, Japanese cultivars differed markedly in 4MTB-GSL content, and recent sprout comparisons also found large cultivar-to-cultivar differences in total glucosinolates and glucoraphasatin abundance (Ishida et al., 2012).

Tissue and organ strongly shape the profile. In cultivated radish, roots usually hold more glucoraphasatin than leaves, skins tend to contain higher glucosinolate levels than flesh, and seeds shift toward glucoraphenin as the dominant glucosinolate (Kim et al., 2013; Ko et al., 2016). Wild radish shows a different organ pattern: fruits are

especially glucosinolate-rich and dominated by glucoraphenin, leaves are enriched in glucobrassicin and 4-hydroxyglucobrassicin, and roots still center on glucoraphasatin (Maldini et al., 2017). Season and development also matter. In white radish grown in the field, root and shoot glucosinolate concentrations fell during autumn growth, root concentration tended to decline in spring, and inflorescences reached the highest concentrations when present (Jeon et al., 2022). A separate dynamic profiling study found taproot glucosinolate content could peak at 232.46 μmol/g DW at 42 days after germination, while leaf glucosinolate content declined over the same vegetative period (Yan et al., 2023).

3.1.3 Isothiocyanates in Radish

Radish isothiocyanates are formed when glucosinolates meet myrosinase after tissue damage or digestion, yielding isothiocyanates alongside other possible hydrolysis products (Endo et al., 2023). In radish, the two headline compounds are sulforaphene and raphasatin, mainly derived from glucoraphenin and glucoraphasatin, respectively(Baenas et al., 2016). Sulforaphene is the best-supported radish isothiocyanate in seeds and sprouts, and several studies describe it as a major or dominant radish ITC(Yamaguchi et al., 2024). Raphasatin is also a major radish ITC, especially in sprouts, and is a major contributor to radish pungency and bioactivity (Scholl et al., 2011).

Purple radish sprouts gave the highest sulforaphene among six cultivars, peaking after 2 days of germination

- Raphasatin induced quinone reductase and several phase I/II detoxification enzymes more strongly than its degradation products (Lim et al., 2016).
- Sulforaphene showed hepatoprotective effects in mice similar to sulforaphane (Yamaguchi et al., 2024)
- Radish-derived sulforaphene showed broad antimicrobial activity, including strong effects against multidrug-resistant H. pylori and MRSA (Lim et al., 2016).
- Purified sulforaphene inhibited multiple cancer cell lines and induced apoptosis in A549 lung cancer cells (Lim et al., 2020).

3.1.4 Phenolic compounds in Radish

In crucifer comparisons, the main radish-associated phenolics fall within glycosylated quercetin, kaempferol, and isorhamnetin derivatives plus hydroxycinnamic acids such as ferulic, sinapic, caffeic, and p-coumaric acids (Li et al., 2018). Colored radishes add a large anthocyanin fraction, especially cyanidin- and pelargonidin-based compounds (Koley et al., 2017). In one purple genotype, 66 phenolics were putatively identified, including 28 anthocyanins and 23 flavonols, and anthocyanins accounted for 80–90% of phenolics in root tissues (Koley et al., 2017).

Leaves repeatedly show the richest conventional phenolic profile. In red radish, leaves contained about 695 mg GAE/100 g d.m. total phenolics versus lower root values, and flavonoids were about fourfold higher in leaves (Goyeneche et al., 2015). Detailed leaf analyses found abundant flavonols as the dominant class, contributing 70–83% of total leaf phenolics across four cultivars (Kajszczak et al., 2024).

Roots contain both free and bound phenolics, but with a narrower profile than leaves. Reported root compounds include rutin, vanillic, pyrogallol, gallic, coumaric, caffeic, and trans-ferulic acids, with vanillic acid prominent in the bound fraction (Goyeneche et al., 2015).

4. Allelopathic Impact of Other Plants on Radish

4.1 Weed Allelopathy Against Radish

Aqueous root exudates from five weeds inhibited radish across germination, growth, biomass, and pigment traits, with Vernonia patula the most suppressive and Spilanthes acmella next, while radish was more sensitive than cucumber in the same assay (Lopes et al., 2022). In a separate laboratory study, oilseed radish germination responded to water extracts from 20 weed species, with allelopathic pressure ranking from relatively weak for field mustard and ragweed to strongest for white Mary and thistles (Tsytsiura & Inna, 2021). Common chickweed also altered radish performance: its aqueous extracts lowered radish germination overall, but effects on seedling growth varied by extract form and cultivar, including stimulation in some cultivars and consistent inhibition in ‘Półdługa’ (Zandi et al., 2018). Two exotic weeds, Ageratum houstonianum and Chromolaena odorata, were likewise reported to exert strong derogative effects on radish along with other crops (Pertin et al., 2018).

Japanese and Bohemian knotweed provide the clearest mechanistic evidence for how other plants suppress radish: 10% rhizome extracts shortened radish roots by up to 70%, and the whole extracts were more inhibitory than resveratrol, epicatechin, emodin, or their mixture alone (Serniak, 2016). In glasshouse soil assays with individual knotweed compounds, germination and shoot size were unchanged, but resveratrol, emodin, and epicatechin still significantly shortened radish roots, suggesting root-specific phytotoxicity and multi-compound action (Serniak, 2016). Knotweed extracts also disrupted radish at the cellular level by increasing oxidative stress, lipid peroxidation, protease activity, and ultrastructural damage in root-cap and meristem cells(K. Šoln et al., 2022). Newer transcriptomic work extends this mechanism: Fallopia extracts reduced root biomass by up to 70%, downregulated genes for root hair formation, and disturbed ROS homeostasis through changes in glutathione, cysteine, ascorbate, and antioxidant-cycle genes (Šoln et al., 2025).

Table 2. plants affect radish germination and seedling growth across the supplied studies.

Donor plant or group	Main effect on radish	Key qualifier
Weed root exudates	Broad inhibition of germination, growth, biomass, pigments (Akter & Islam, 2019).	Radish more sensitive than cucumber (Akter & Islam, 2019).
Fallopia extracts	Strong root inhibition and oxidative damage (K. Šoln et al., 2022; Šoln et al., 2023).	Whole extracts outperform single phenols (K. Šoln et al., 2022; Šoln et al., 2023).
Southeast Asian species	Several species strongly suppress radish germination and growth (Hong et al., 2003).	Effects differ by plant part (Hong et al., 2003).
Moss extracts	Effects can be positive, negative, or neutral (Matić et al., 2024).	Higher doses more often inhibitory (Matić et al., 2024).
Photinia extracts	Concentration-dependent inhibition of radish germination (Bayhun & Yilmazer, 2025).	Flower extracts stronger than leaves (Bayhun & Yilmazer, 2025).

4.2 Crop Residue allelopathical effect on Radish

Sorghum residue mixed into soil inhibited radish at higher concentrations, while low concentrations promoted germination and growth traits in a pot study (Babiker & Mutwali, 2019). Rhazya residue showed the same pattern: low soil incorporation stimulated early radish dry weight, but increasing residue rates inhibited growth, root:shoot ratio, and dry weight across stages (Abad, 2019). Grass mulch extracts had the strongest negative effect on radish germination and shoot and root development among several organic mulches (Jodaugienė et al., 2018).

Crop-residue allelopathy is relevant to crop rotation and mulching, but direct radish-after-previous-crop evidence is still thin. The sorghum-radish study explicitly noted that field studies are still needed to evaluate residue effects in rotation and preceding-crop settings (Babiker & Mutwali, 2019). Broader rotational-crop work found that root leachates and aboveground residue leachates can either suppress or stimulate growth, reflecting different allelochemicals among crop species (Elsekran & Üstüner, 2024).

Residues also act through the soil environment, not just direct phytotoxicity. Soil microorganisms can offset or reshape residue-derived allelopathic effects over time, with microbe-by-residue interactions showing early inhibition but later weak promotion in one residue system (Xiao et al., 2020).

4.3 Cover crop allelopathy affecting on radish and radish emergence

Direct evidence on radish shows that cover-crop or plant extracts often suppress radicle elongation, germination, or emergence, but low concentrations can be neutral or stimulatory and field evidence is thinner than lab evidence (Price et al., 2008). Cover crop extracts from twelve species all inhibited radish radicle elongation relative to water in an extract-agar bioassay, and the magnitude varied strongly among species, cultivars, and even within cultivars (Price et al., 2008). In a broader cover-crop literature review, laboratory studies commonly found allelopathic effects of cover crops on row-crop germination, but only one field study showed a clear allelopathic effect in the field (Koehler-Cole et al., 2020). Responses are consistently concentration-dependent. Brassicaceae cover-crop extracts were species- and concentration-dependent against ragweed, with radish and white mustard inhibiting only at concentrations of at least 7.5% (Šćepanović et al., 2021). In radish bioassays used as a model plant, high-concentration extracts inhibited germination while 1–10% extracts sometimes improved germination speed or seedling elongation (Fecowicz et al., 2020; Khan, 2021).

4.4 Autotoxicity in Radish by Continuous radish cropping

Autotoxicity in radish under continuous radish cropping is not directly demonstrated in the supplied papers, but continuous-cropping obstacles are widely defined as abnormal growth after repeated cultivation of the same or related crop, and autotoxicity is repeatedly identified as one important mechanism within that syndrome (F. Wang et al., 2023).

Most species-specific evidence in this set comes from other crops rather than radish itself. Rehmannia, Angelica, Atractylodes, Coix, cucumber, melon, potato, tobacco, and Panax all show continuous-cropping or replant problems linked to autotoxic compounds or root exudates (Li et al., 2012; M. Wang et al., 2023).

Across the autotoxicity literature, the dominant candidate compounds are secondary metabolites, especially phenolic acids and related aromatics, along with aldehydes, terpenoids, alkaloids, coumarins, quinones,

phthalates, and some fatty-acid–derived compounds (Bu et al., 2023). A recurring mechanistic theme is oxidative stress in roots. Angelica autotoxic allelochemicals increased reactive oxygen species in root tips, melon root exudate stress caused ROS accumulation and lipid peroxidation, and Panax autotoxicity impaired photosynthesis while altering antioxidant systems (Xin et al., 2019). That pattern aligns with radish toxicology studies, where U, Cd+U, Cs, As, and PVC stress all increased ROS-related damage, MDA, antioxidant responses, or root cell death (Wen et al., 2025).

Autotoxicity in continuous cropping is not only a plant-chemistry problem; it is tightly linked to rhizosphere change. Continuous cropping altered soil biochemical properties and reduced bacterial and fungal diversity in Atractylodes, shifted potato root-exudate metabolism and favored less beneficial microflora after 4 or more years, and tobacco replant problems were linked to autotoxin accumulation plus microbial dysfunction (M. Wang et al., 2023; Xing et al., 2024).

5. Factors affecting allelopathy in radish

In radish, allelopathic activity changes mainly with genotype, plant part, extract concentration, target species, and assay context. Environmental stress, soil processes, and oxidative-stress responses further modify whether effects are inhibitory, neutral, or occasionally stimulatory (Shan, Zhou, Shah, Arafat, Rizvi, et al., 2023).

Radish genotype or cultivar changes allelopathic strength. Black and red radish were more allelopathic than white radish, and the bioassay differences tracked genetic diversity among the three radish types (Rasul & Ali, 2021).

Plant part is another major factor. In radish donor studies, stem extracts could be most inhibitory in one system, while root extracts were strongest in another, showing that tissue ranking depends on the receiving species and cultivar tested (Sisek et al., 2019).

Extract chemical composition matters because radish allelopathy is attributed to secondary metabolites such as p-hydroxybenzoic acid and isothiocyanates, and GC-MS studies detected multiple candidate bioactive compounds rather than a single universal toxin (Rasul & Ali, 2021).

Allelopathic effects on or from radish are consistently concentration-dependent. Higher concentrations increased inhibition in radish extracts against target weeds, in weed or tree extracts tested on radish, and in radish bioassays more generally (Qadeer et al., 2025; Rasul & Ali, 2021). Low concentrations can instead be neutral or stimulatory, as seen with Filipendula extracts, some moss extracts, Allium fistulosum below 10 g/L for some traits, and Quercus extracts that stimulated antioxidant activity at lower doses (Fecowicz et al., 2020).

Environmental and management conditions alter allelopathic expression by changing the type and amount of released compounds. Biotic triggers include competition, herbivory, and pathogens, while abiotic triggers include light, temperature, drought, CO2, and nutrient deficiency (Shan, Zhou, Shah, Arafat, Rizvi, et al., 2023).

A recurring mechanism is oxidative stress. Impatiens extract and 2-MNQ inhibited radish while activating antioxidant defenses and causing lipid and protein damage, Fallopia extracts disturbed ROS homeostasis and downregulated root-hair pathways, and Allium extract changed POD, CAT, and MDA responses in radish seedlings (Domijan et al., 2025).

5.1 Environmental factors affecting Allelopathy

Abiotic stressors including temperature, nutrient deficiency, drought, UV radiation, and salinity stimulate allelochemical biosynthesis in donor plants by activating phenylalanine ammonia-lyase and jasmonate signaling pathways (Trezzi et al., 2016). Changes in soil pH and conductivity directly induce plants to produce higher concentrations of phenolic allelochemicals (Shan, Zhou, Shah, Arafat, Rizvi, et al., 2023).

5.2 Soil pH effects on activity of Allelopathy

Soil pH governs allelochemical behaviour in soil by controlling adsorption, desorption, and degradation rates, which together determine the concentration of allelochemicals available in soil water for plant uptake (Kobayashi, 2004). Allelopathy in soil is further complicated by interactions among soil texture, organic matter, moisture, and microbial communities, all of which are themselves influenced by pH (Kobayashi, 2004). In radish bioassays, extract pH did not account for the observed allelopathic effects. Studies using aqueous leaf extracts of Piper mikanianum and Schinus molle on radish germination and growth confirmed that pH and osmotic potential were measured but did not drive the inhibitory outcomes (Borella et al., 2012; Borella et al., 2011). Similarly, Solanum americanum fruit extracts exerted allelopathic effects on radish seeds independent of extract pH and osmotic potential (Borella et al., 2011).

Invasive-species root extracts can shift soil pH itself: Rhus typhina root extracts significantly increased soil pH with rising extract concentration, reaching an 11.5% change at 10 $mg \cdot mL^{-1}$, and this pH shift was identified as a major driver of altered soil microbial activity (Qu et al., 2021).

5.3 Temperature effects on activity of Allelopathy

Temperature acts as a key driver of allelopathic activity by modulating allelochemical production in donor plants (Shan, Zhou, Shah, Arafat, Rizvi, et al., 2023).

Elevated temperature increases receiver-plant sensitivity to allelochemicals. (-)-Catechin exhibited concentration-dependent inhibition of radicle and hypocotyl elongation in recipient plants, and this inhibition was significantly

more pronounced at 30 °C than at 25 °C (Sheng et al., 2026). Transcriptomic analysis revealed that elevated temperature increased oxidative damage and stress responses in recipient plant tissues, thereby enhancing sensitivity to allelopathic effects rather than increasing the intrinsic allelopathic potency of the compound (Sheng et al., 2026).

- Radish seed germination is maximized at 20–25 °C, with reductions at suboptimal or supraoptimal temperatures (Toscano et al., 2025).
- Adverse effects of salt stress on radish germination progressively increase as temperature moves away from the optimum (Toscano et al., 2025).
- Warming enhanced sensitivity of Picea schrenkiana seedlings to autotoxic compounds, paralleling the temperature-sensitivity pattern seen with catechin (Sheng et al., 2026).

5.4 Microbial Degradation of Allelochemicals

Soil microorganisms play a dual role in allelopathy, both degrading toxic allelochemicals and transforming harmless precursors into phytotoxic compounds (Xiao et al., 2020). Microbial degradation of allelochemicals depends on chemical nature of the compound, soil texture, aeration, temperature, soil organic matter, and pH, as well as the specific microbial species involved (Scavo et al., 2019). Seasonal variation in microbial populations influences allelochemical availability, meaning allelopathic effects fluctuate temporally (Scavo et al., 2019).

- Pseudomonas putida catabolizes juglone in soil, preventing phytotoxic accumulation beneath walnut trees (Jilani et al., 2008).
- Acinetobacter calcoaceticus converts BOA to AZOB, a more inhibitory derivative (Jilani et al., 2008).
- Pseudomonas species transform (-)-catechin into protocatechuic acid, which exhibits higher phytotoxicity than the parent compound (Wang et al., 2013).

6. Research Gaps and Future Perspectives

6.1 Knowledge gaps in allelopathy

Future radish allelopathy research must transition from in vitro bioassays to field-validated, multi-disciplinary applications, while addressing critical gaps in genetic characterization, allelochemical identification, and environmental persistence (Bamal et al., 2024; Scavo & Mauromicale, 2021).

Table 3. Evidence Coverage Across Radish Allelopathy

Sub-topic	In vitro Bioassays	Field Validation	Genetic Basis	Allelochemical ID
Radish as donor	8	GAP	2	4
Radish as receiver	10	GAP	GAP	3
Mechanism of action	4	GAP	GAP	2

The most striking gap is the complete absence of field validation; despite extensive in vitro evidence demonstrating allelopathic inhibition, no studies confirm these effects under natural soil conditions for radish (Inderjit et al., 2005).This persists because experimental frameworks rarely integrate bioassay, chemical analysis, and field trials within a single study (Hickman et al., 2023). Crude extract synergism is frequently invoked without proof to explain why combined extract effects exceed those of isolated compounds (Duke & Zeng, 2010).

- Bioassays using Rosa blanda and Ageratum houstonianum extracts inhibit radish germination but do not identify the specific allelochemicals responsible (Możdżeń et al., 2021).
- GC-MS analysis of radish stem extracts reveals bioactive compounds, but the exact chemicals driving allelopathy remain unconfirmed ("Effects of Aqueous Extracts Obtained from Two Radish Cultivars (Raphanus sativus L. and Raphanus sativus L. var. radikula) Using Liquid Nitrogen Is Germination of Barnyard Grass (Echinochloa crus-galli) and Allelopathic Effect on Seedling Growth," 2022).
- The assumption that allelochemicals must be highly water soluble biases extraction methods, potentially missing the most effective lipophilic compounds (Duke & Zeng, 2010).

6.2 Future Research Directions

Translating radish allelopathy into agricultural tools requires integrating genomic, metabolomic, and field-based approaches (Aci et al., 2022; Hickman et al., 2023). Genetic technologies like CRISPR/Cas9 and QTL mapping could identify allelopathic traits for transfer into elite crop cultivars, though this remains unexplored in radish(Aci et al., 2022). Holistic metabolomic techniques would allow identification of specialized metabolites and their biosynthetic pathways, enabling targeted breeding for weed suppression (Aci et al., 2022).

Mechanistic and Transitional gaps

Molecular mechanisms underlying radish allelopathy are poorly understood, though recent transcriptomic studies on receiver plants reveal oxidative stress and root hair inhibition as primary pathways (Šoln et al., 2025). Fallopia extracts downregulate root hair formation genes and induce ROS imbalance in radish seedlings, providing a mechanistic framework for allelopathic damage (Šoln et al., 2025). However, the molecular target sites of allelochemicals in sensitive species and the enzymes involved in their production remain largely unknown (Inderjit et al., 2005).

- Allelopathy research suffers from poor scientific quality, often equating phytotoxic presence with ecological function without field proof (Inderjit et al., 2005).
- No commercial crop cultivars are currently sold with allelopathic properties as a primary trait (Duke & Zeng, 2010).
- Interdisciplinary studies combining chemistry, physiology, soil science, and genetics are rarely conducted (Hickman et al., 2023).

Advancing radish allelopathy from bioassay observations to agricultural application requires multi-disciplinary frameworks that track allelopathic interactions from in vitro through glasshouse to field settings, identify specific allelochemicals, and elucidate their molecular mechanisms in target species (Hickman et al., 2023; Inderjit et al., 2005).

6.3 Omics and AI application in allelopathy

Multi-omics approaches are beginning to elucidate the molecular mechanisms of allelopathy in radish, while artificial intelligence applications remain largely unexplored in this specific crop (Šoln et al., 2025).

Transcriptomic analysis of radish seedlings treated with Fallopia rhizome extracts revealed downregulation of genes associated with root hair formation, resulting in decreased or completely blocked root hair development (Šoln et al., 2025). Treated radish roots exhibited disturbed homeostasis of reactive oxygen species, indicated by increased proline, total glutathione, and total cysteine alongside decreased total ascorbate (Šoln et al., 2025). The extracts induced several genes associated with the glutathione-ascorbate cycle, including glutathione peroxidases, ascorbate peroxidase, dehydroascorbate reductase, and catalase (Šoln et al., 2025). Fallopia × bohemica extract caused more severe transcriptomic and morphological changes in radish seedlings than F. japonica extract (Šoln et al., 2025).

Combined transcriptomic and metabolomic analyses of Cyclachaena xanthiifolia allelopathy identified disruptions in the antioxidant system, primary metabolic pathways, and phytohormone signalling in recipient mustard plants (Yang et al., 2025). The ABA signalling pathway appears to play a dominant role, with allelochemical stimulation increasing ABA levels and antagonizing gibberellin signalling to inhibit seed germination (Yang et al., 2025). GC-MS metabolomics identified fatty acids, terpenes, esters, alkanes, and aldehydes as compounds with allelopathic potential (Yang et al., 2025).

The supplied literature contains no direct evidence of artificial intelligence, machine learning, or deep learning applications specifically targeting allelopathy in radish. Current computational approaches in the identified studies rely on standard bioinformatics tools such as KEGG and GO enrichment analyses for pathway mapping (Yang et al., 2025).

7. CONCLUSION

Allelopathy plays a significant role in shaping plant–plant interactions and has emerged as an important component of sustainable agricultural systems. As a member of the Brassicaceae family, radish (Raphanus sativus L.) possesses considerable allelopathic potential owing to its diverse secondary metabolites, particularly glucosinolates, isothiocyanates, phenolic compounds, and flavonoids. These allelochemicals can influence the germination, growth, and physiological performance of neighboring crops and weed species, highlighting the potential of radish as a natural tool for weed suppression and ecological crop management.

At the same time, radish is also affected by allelochemicals released from neighboring plants, weeds, crop residues, and cover crops, demonstrating that allelopathy is a bidirectional process in which radish functions as both a donor and a receiver of allelochemicals. The intensity and outcome of these interactions are influenced by several factors, including allelochemical concentration, plant developmental stage, soil properties, environmental conditions, and microbial activity. Understanding these factors is essential for predicting allelopathic responses under field conditions and for integrating allelopathy into sustainable crop production systems.

Despite increasing research on radish allelopathy, several knowledge gaps remain. Most studies have been conducted under controlled laboratory conditions, while long-term field investigations are comparatively scarce. Furthermore, there is limited information on tropical radish germplasm, varietal differences in allelochemical production, the molecular mechanisms underlying allelopathic interactions, and the role of soil microbial communities in regulating these processes. Future research should emphasize multidisciplinary approaches combining field validation with metabolomics, transcriptomics, and microbiome analyses to better understand the ecological significance of radish allelopathy. Standardized experimental methodologies and quantitative

assessments of allelochemicals will further improve the comparability and practical application of research findings.

Overall, a comprehensive understanding of the bidirectional allelopathic interactions involving radish will contribute to the development of environmentally sustainable weed management strategies, optimized crop rotation and intercropping systems, and resilient vegetable production practices. Such knowledge will support the efficient utilization of radish as both a productive vegetable crop and a biologically active component of sustainable agroecosystems.

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