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Phytoremediation of Heavy Metals and Radionuclides: A Comparative Review of *Chrysopogon zizanioides* and *Allmania nodiflora*.

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Abstract:

The global escalation of heavy metal and radionuclide contamination represents one of the most persistent environmental challenges of the twenty-first century. Industrialization, mining operations, metallurgical activities, phosphate fertilizer application, fossil fuel combustion, and nuclear fuel cycle processes have substantially increased the release of toxic metals and radioactive elements into terrestrial and aquatic ecosystems. Unlike organic pollutants, heavy metals and radionuclides are non-biodegradable, persisting indefinitely in environmental compartments and driving chronic ecological degradation, food-chain contamination, and adverse human health outcomes. Conventional remediation technologies-including soil excavation, chemical immobilization, electrokinetic treatment, vitrification, and soil washing-are frequently hampered by high economic costs, significant secondary ecological disturbance, and limited applicability across large contaminated landscapes. Phytoremediation has emerged as an environmentally sustainable and economically viable alternative that exploits the natural physiological and biochemical capacities of plants to remove, stabilize, transform, or immobilize environmental contaminants. Among candidate species, *Chrysopogon zizanioides* (Vetiver grass) has attracted considerable scientific interest due to its extensive root architecture exceeding three to five meters in depth, exceptional biomass production, tolerance to multiple abiotic stresses, and demonstrated capacity to accumulate and immobilize heavy metals and radionuclides]. By contrast, *Allmania nodiflora* has recently gained attention as a potentially valuable phytoremediation species because of its rapid growth characteristics, adaptive stress responses, and capacity to survive in contaminated environments, although molecular and field-scale evidence remains limited. This review synthesizes current knowledge regarding the physiological, biochemical, molecular, and ecological mechanisms underlying contaminant uptake and detoxification in both species. Furthermore, it grounds theoretical transport mechanisms in real-world contexts by evaluating pollutant dynamics in Kadapa industrial soils, and provides quantitative comparative metrics (Bioconcentration and Translocation Factors) for both botanical agents. Particular emphasis is placed on metal transport systems, transcriptomic responses, antioxidant defense pathways, phytochelatin-mediated sequestration, rhizosphere interactions, and emerging multi-omics approaches. Furthermore, recent advances in microbial-assisted phytoremediation, rhizosphere engineering, synthetic biology, genome editing, and systems-level analyses are critically evaluated. Comparative analyses reveal that Vetiver currently possesses greater technological maturity and field applicability, whereas *A. nodiflora* represents a promising but underexplored candidate requiring substantial molecular characterization and field validation. Future integration of genomics, microbiome engineering, artificial intelligence, and precision environmental biotechnology may significantly accelerate the development of next-generation phytoremediation systems.

Keywords:
Phytoremediation; *Chrysopogon zizanioides*; Vetiver grass; *Allmania nodiflora*; Heavy metals; Uranium; Cadmium; Lead; Molecular mechanisms; Transcriptomics; Rhizosphere engineering; Environmental biotechnology

1. Introduction:

1.1 Global Emergence of Heavy Metal and Radionuclide Pollution:

Environmental contamination by heavy metals and radionuclides has become one of the defining ecological crises of the modern era. Rapid industrial expansion over the past century has significantly increased the release of potentially toxic elements into soil, groundwater, surface water, and atmospheric compartments [1]. Metals such as cadmium (Cd), lead (Pb), mercury (Hg), chromium (Cr), arsenic (As), nickel (Ni), and copper (Cu) are routinely detected at elevated concentrations in agricultural and industrial regions worldwide. Their non-biodegradable nature means that once introduced into environmental matrices, they persist indefinitely, disrupting nutrient cycling, reducing microbial diversity, inhibiting plant growth, and impairing agricultural productivity [2,10].

Cadmium exposure has been associated with renal dysfunction, skeletal abnormalities, oxidative stress, and carcinogenesis [11]. Lead is recognized as a potent neurotoxin affecting cognitive development and neurological function even at trace concentrations [12]. Uranium contamination poses additional challenges because its toxicity derives from both chemical nephrotoxicity and radiological effects associated with alpha-particle emission [13]. Recent global assessments indicate that millions of hectares of agricultural and industrial land remain contaminated, while uranium-contaminated sites are increasing due to historical mining activities, nuclear fuel production, military operations, and improper waste disposal practices [14]. Climate change may further exacerbate contamination risks through altered hydrological cycles, enhanced soil erosion, and changing redox conditions that affect contaminant mobility [15].

1.2 Environmental Fate and Biogeochemistry of Heavy Metals:

The environmental behavior of heavy metals is governed by a complex interplay of physicochemical and biological processes. Metal mobility depends on soil pH, redox potential, organic matter content, clay mineral composition, cation exchange capacity, and microbial activity [16]. In acidic soils, increased proton concentrations enhance metal solubility, thereby increasing plant availability and ecological risk. Conversely, alkaline conditions often promote precipitation reactions and reduce mobility [17]. Organic matter can either immobilize metals through adsorption and complexation or facilitate transport through soluble organometallic complexes, depending on environmental context [18].

Microbial communities play a particularly important role in regulating metal speciation. Soil microorganisms influence oxidation-reduction reactions, produce metal-chelating compounds, and modify rhizosphere chemistry through metabolic activities [19]. Consequently, contaminant bioavailability cannot be understood solely through total concentration measurements but must be evaluated within the broader context of soil ecological processes-a reality that fundamentally shapes phytoremediation strategy design.

1.3 Uranium as an Emerging Environmental Contaminant:

Among radionuclides, uranium occupies a unique position because of its dual chemical and radiological toxicity. Naturally occurring uranium is present in geological formations worldwide; however, anthropogenic activities have substantially increased its environmental distribution through mining, phosphate fertilizer production, nuclear fuel processing, and military applications [13,14]. Uranium mobility is strongly influenced by oxidation state: hexavalent uranium [U(VI)] typically exists as soluble uranyl ($UO2^{2+}$) complexes exhibiting greater environmental mobility, whereas tetravalent uranium [U(IV)] is generally less soluble and tends to precipitate under reducing conditions [20]. These chemical transformations profoundly affect plant uptake, groundwater transport, and remediation effectiveness. Understanding the interaction between root exudates containing organic acids, amino acids, and phenolic compounds and uranium speciation remains critical for developing efficient phytoremediation systems targeting radionuclide-contaminated environments [21].

1.4 Phytoremediation as a Sustainable Remediation Strategy:

Phytoremediation encompasses a collection of plant-based technologies designed to reduce environmental contamination while minimizing ecological disturbance [4]. Compared with conventional engineering approaches, phytoremediation offers lower implementation costs, improved public acceptance, carbon sequestration benefits, and opportunities for ecosystem restoration. The strategy includes phytoextraction (removal of contaminants into harvestable above-ground biomass), phytostabilization (immobilization within root zones), phytodegradation, rhizofiltration, and phytovolatilization, each suited to distinct contamination scenarios and contaminant classes [22].

Advances in plant molecular biology have significantly improved understanding of the genetic and biochemical pathways underlying phytoremediation processes. Modern research increasingly integrates genomics, transcriptomics, proteomics, metabolomics, and ionomics to identify key regulatory networks controlling contaminant tolerance and accumulation [8,23]. These emerging technologies are transforming phytoremediation from a largely descriptive discipline into a predictive and engineering-oriented field capable of developing optimized plant systems for environmental restoration. The present review is structured to provide a comprehensive comparative analysis of two species that represent very different points on the spectrum of phytoremediation readiness: the well-established *Chrysopogon zizanioides* and the emerging *Allmania nodiflora*.

2. Taxonomy, Evolutionary Biology, and Botanical Characteristics:

2.1 *Chrysopogon zizanioides* (Vetiver Grass)

Chrysopogon zizanioides (L.) Roberty belongs to the family Poaceae, subfamily Panicoideae, tribe Andropogoneae-a grass lineage that also encompasses Sorghum bicolor, Zea mays, and Saccharum officinarum [24]. Originally recognized for its economic value in essential oil production and traditional soil conservation in the Indian subcontinent, Vetiver has subsequently gained substantial scientific attention because of its remarkable adaptability to adverse environmental conditions. The species is believed to have originated in tropical and subtropical India, from where extensive cultivation has dispersed it throughout South and Southeast Asia, Australia, sub-Saharan Africa, and the Americas [25].

The most distinctive morphological characteristic of Vetiver is its extraordinarily deep root system. Root depths commonly exceed three meters within the first growing season, five meters under favorable conditions, and more than six meters in some field environments [5]. The roots are densely fibrous, mechanically strong, and generate a large rhizosphere surface area that supports diverse microbial communities. Shoot height typically ranges from 1.5 to 2.5 meters, forming dense clumps with narrow, erect leaves and producing substantial aboveground biomass that can be harvested for contaminant removal in phytoextraction strategies [26]. Most cultivated genotypes exhibit extremely low fertility and limited seed production, propagating primarily through vegetative clump division-a trait that minimizes invasive spread and is advantageous for environmental deployment.

Vetiver employs C4 photosynthesis, conferring high water-use efficiency, improved productivity under elevated temperatures, and enhanced tolerance to heat stress-attributes that significantly expand its potential geographic applicability [27]. Its remarkable ecophysiological plasticity encompasses tolerance to drought, flooding, salinity, acidity, alkalinity, and temperature extremes, making it one of the broadest-ranging herbaceous phytoremediation candidates in the scientific literature [5,6].

2.2 *Allmania nodiflora*:

Allmania nodiflora (L.) R.Br. ex Wight belongs to the family Amaranthaceae, order Caryophyllales-a family that includes numerous stress-tolerant taxa renowned for their adaptability to challenging environments including salinity, drought, nutrient limitation, and metal contamination [28]. The species is distributed across South Asia and tropical Asia, frequently colonizing disturbed habitats, roadsides, agricultural margins, abandoned lands, and waste-affected environments.

Compared with Vetiver, *A. nodiflora* develops a shallower but densely branched root system characterized by high surface area, rapid regeneration capacity, and fast soil exploration-traits that may prove advantageous for remediation of surface-contaminated soils [29]. Unlike Vetiver's perennial growth habit, *A. nodiflora* exhibits rapid life cycles, quick biomass accumulation, and frequent tissue turnover, characteristics that may enable repeated harvesting and faster contaminant extraction cycles in phytoextraction-oriented remediation programs [30]. The photosynthetic characteristics of *A. nodiflora* remain incompletely characterized, representing an important knowledge gap for future investigation.

3. Environmental Chemistry of Cadmium, Lead, and Uranium:

3.1 Cadmium:

Cadmium (Cd) is a highly mobile, non-essential element with no known biological function in plants or animals. It commonly occurs in soil as Cd^{2+}, $CdCl^{+}$, $CdSO_4$, $CdCO_3$, and various organic complexes, with speciation and bioavailability strongly governed by soil pH-acidic conditions enhance solubility and plant uptake, while alkaline conditions favor precipitation [11,17]. Major anthropogenic sources include zinc and lead mining and smelting, nickel-cadmium battery manufacturing, phosphate fertilizer application, electroplating industries, and waste incineration [31]. Because cadmium is non-biodegradable and highly mobile, it accumulates progressively in agricultural soils, enters food chains through plant uptake, and poses substantial risks through dietary exposure, with recognized associations with renal dysfunction, skeletal demineralization, and carcinogenesis [11].

3.2 Lead

Lead (Pb) is among the most widely distributed environmental contaminants, characterized by extremely high persistence and strong adsorption to clay minerals, iron oxides, manganese oxides, and soil organic matter [12]. Common soil forms include Pb^{2+}, $PbCO_3$, $PbSO_4$, $Pb_3(PO_4)_2$, and organic complexes. A critical geochemical reality is that total soil lead concentration often poorly predicts bioavailable fractions because strong adsorption reactions limit plant-accessible forms-a distinction with fundamental implications for remediation strategy selection [32]. Major contamination sources include legacy use of leaded gasoline (one of the largest twentieth-century dispersal pathways), lead-based paints, battery manufacturing, smelting, electronic waste, and metallurgical industries [33]. Lead's potent neurotoxicity, affecting cognitive development and neurological function at very low exposure levels, establishes it as a priority remediation target.

3.3 Uranium

Uranium occupies an exceptional position among environmental contaminants because it simultaneously presents chemical heavy metal toxicity-particularly nephrotoxicity-and radiological hazard associated with alpha-particle emission [13,20]. Environmentally, uranium exists primarily in two oxidation states: soluble, mobile hexavalent uranium [U(VI)] present as the uranyl cation UO_2^{2+} and its carbonate complexes, and relatively insoluble, less mobile tetravalent uranium [U(IV)] that tends to precipitate under reducing conditions [34]. This redox-sensitive behavior is mediated in part by microbial communities in the rhizosphere, making uranium an ideal contaminant for exploring the intersection of phytoremediation and microbiome engineering [35]. Plant-root interactions contribute significantly to uranium dynamics: root exudates containing organic acids may either enhance uranium solubility through chelation or facilitate immobilization through phosphate-mediated precipitation, with context-dependent outcomes [21].

Pollutant Target	Primary Industrial	Environmental Mobility in Local Aquifers	Key Human Health Risks / Pathologies
Cadmium (Cd)	Industrial effluents, mineral processing, phosphate fertilizers	**High**	Carcinogenic risks, enzymatic disruption, renal damage [102,103]
Lead (Pb)	Barytes pulverization, battery recycling, industrial emissions	**Low** (high soil retention / adsorption affinity)	Neurological damage, cardiovascular dysfunction, anemia [103,104]
Uranium (U)	Uraninite mining, tailings leaching, lithological weathering	**Moderate** (highly dependent on pH and redox potential)	Nephrotoxicity, radiological hazards, DNA mutation [105,106]

Table 1. Summarizes the key comparative attributes

4. Molecular Mechanisms of Heavy Metal and Radionuclide Tolerance:

4.1 Overview of the Tolerance Framework:

The capacity of plants to survive and function in contaminated environments depends upon sophisticated molecular and physiological mechanisms that regulate contaminant perception, uptake, intracellular transport, detoxification, and sequestration. Heavy metal and radionuclide tolerance is not governed by a single pathway but instead arises from complex interactions among transporter proteins, signaling molecules, transcription factors, antioxidant networks, and compartmentalization mechanisms [36]. Metal exposure initiates rapid signaling cascades-involving calcium fluxes, reactive oxygen species (ROS), and mitogen-activated protein kinase (MAPK) pathways-that activate extensive transcriptional reprogramming affecting transporter systems, detoxification enzymes, stress-signaling networks, and metabolic pathways [37].

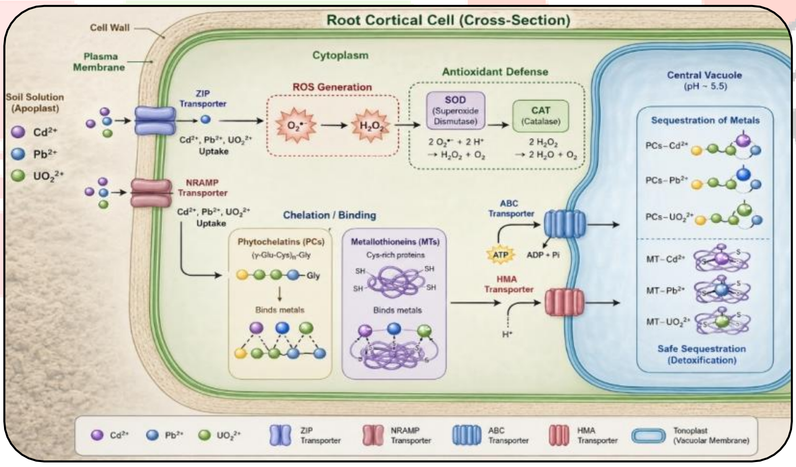

Figure 1. Schematic representation of heavy metal uptake, ROS detoxification, chelation by phytochelatins and metallothioneins, and vacuolar sequestration of Cd^{2+}, Pb^{2+}, and UO_2^{2+} in plant root cells.

4.2 Metal Transport Systems:

Metal ions enter plant roots through transport systems originally evolved for essential nutrient acquisition. Because many toxic metals possess physicochemical properties similar to essential micronutrients, they exploit existing nutrient transport pathways-a phenomenon with profound implications for both toxicity and remediation design. Cadmium, for instance, enters cells predominantly through zinc transporters of the ZIP (ZRT/IRT-Like Protein) family, which mediate uptake of Zn^{2+}, Fe^{2+}, Mn^{2+}, and related divalent cations [38]. Lead frequently exploits calcium transport channels and apoplastic pathways. Uranium may utilize calcium transport pathways and phosphate transport systems [20,39].

The Natural Resistance-Associated Macrophage Protein (NRAMP) family constitutes another major transporter group involved in metal acquisition and redistribution, facilitating iron, manganese, and cadmium transport, with NRAMP5 receiving particular attention as a major cadmium uptake pathway in several plant species [40]. Heavy Metal ATPases (HMAs) are membrane-associated proteins that actively transport metal ions using ATP-derived energy, playing critical roles in root-to-shoot translocation (HMA4), vacuolar sequestration (HMA3), and long-distance metal transport for hyperaccumulation processes [41]. ATP-Binding Cassette (ABC) transporters represent another major family, frequently transporting metal-chelate complexes rather than free metal ions, contributing to vacuolar sequestration and stress adaptation [42].

4.3 Oxidative Stress and Antioxidant Defense

Heavy metal toxicity frequently results in excessive ROS production-including superoxide radicals ($O_2\bullet^-$), hydrogen peroxide (H_2O_2), and hydroxyl radicals ($OH\bullet$)-causing lipid peroxidation, protein oxidation, DNA strand breaks, and membrane disruption [43]. To counteract this damage, plants activate enzymatic antioxidant systems including superoxide dismutase (SOD), which converts superoxide to hydrogen peroxide; catalase (CAT), which decomposes hydrogen peroxide to water and oxygen; ascorbate peroxidase (APX) operating within the ascorbate-glutathione cycle; and glutathione reductase (GR), which maintains cellular glutathione pools essential for continued detoxification [44,45]. Non-enzymatic antioxidants including glutathione, ascorbate, proline, and phenolic compounds provide complementary protection. Importantly, ROS at moderate concentrations also function as signaling molecules activating MAPK cascades and downstream defense responses, reflecting their dual toxic and regulatory roles [37].

4.4 Phytochelatins, Metallothioneins, and Vacuolar Sequestration:

Phytochelatins-low-molecular-weight peptides with the general structure (Glu-Cys)n-Gly ($n = 2$-11) synthesized from glutathione by phytochelatin synthase (PCS)-represent one of the most important metal detoxification mechanisms in plants [46]. Following metal exposure, PCS is rapidly activated to produce phytochelatins that bind cadmium, lead, mercury, arsenic, and related metals, forming stable complexes subsequently transported into vacuoles through tonoplast-localized ABC transporters, thereby sequestering contaminants away from sensitive cellular machinery [47]. Enhanced PCS expression consistently correlates with increased metal tolerance across species.

Metallothioneins-cysteine-rich proteins that bind heavy metals through sulfhydryl groups-contribute to intracellular metal buffering, ROS mitigation, and cellular protection [48]. Their expression is frequently induced by cadmium, lead, copper, and zinc exposure. Vacuolar compartmentalization represents the terminal endpoint of most detoxification pathways: following chelation and complex formation, contaminants are imported into the central vacuole through tonoplast transporters, effectively excluding them from cytoplasmic metabolic processes and achieving long-term sequestration [49]. For uranium, cell wall immobilization through binding to pectins, cellulose, and hemicellulose represents an important additional barrier reducing intracellular entry, alongside phosphate-mediated precipitation forming insoluble uranyl phosphate complexes [21].

5. *Chrysopogon zizanioides*: Phytoremediation Mechanisms and Field Performance:

5.1 Heavy Metal Tolerance Mechanisms:

Chrysopogon zizanioides has emerged as one of the most versatile and scientifically promising phytoremediation species identified to date, combining deep root architecture, exceptional environmental resilience, substantial biomass production, and demonstrated capacity for heavy metal and radionuclide remediation [5,6,26]. For cadmium, Vetiver demonstrates survival at elevated concentrations, maintenance of root growth, sustained photosynthetic activity, and substantial Cd accumulation, with tolerance mechanisms including cell wall binding, phytochelatin synthesis, vacuolar sequestration, and antioxidant activation [50].

Root tissues generally accumulate higher cadmium concentrations than shoots, indicating a predominantly phytostabilization-oriented response that reduces ecological mobility and minimizes food-chain transfer risks.

Lead remediation by Vetiver exemplifies particularly strong phytostabilization capacity. Root sequestration reduces ecological mobility, and most published studies report translocation factors (TF = Cshoot/Croot) well below 1.0 for Pb, consistent with preferential root retention [51]. Vetiver demonstrates substantial lead tolerance despite its adverse effects on root elongation, photosynthesis, membrane stability, and nutrient transport, with observed responses including root immobilization, restricted translocation, enhanced antioxidant activity, and increased metal-binding capacity. For chromium contamination, particularly problematic in tannery and electroplating waste sites, Vetiver has demonstrated uptake, reduction, root immobilization, and tolerance to chromium-induced oxidative stress [52].

Antioxidant enzyme induction has been widely documented in Vetiver under heavy metal stress. Superoxide dismutase, catalase, ascorbate peroxidase, glutathione reductase, and peroxidases are collectively upregulated, contributing substantially to contaminant tolerance [44]. Vetiver often exhibits remarkable photosynthetic resilience, maintaining chlorophyll content, carbon fixation, and recovery following stress-traits that directly support sustained biomass production in contaminated environments [53].

5.2 Uranium Phytoremediation:

Uranium remediation represents one of the most significant and challenging applications of Vetiver-based phytoremediation. Uranium contamination arises from mining operations, nuclear fuel processing, phosphate fertilizer production, and radioactive waste disposal, with the environmental persistence and dual toxicity of uranium necessitating effective and ecologically safe remediation strategies [13,14]. Current evidence suggests uranium enters plant systems through pathways evolved for calcium and phosphate transport, with uptake efficiency strongly influenced by soil pH, carbonate concentration, phosphate availability, and organic matter content [20].

One of Vetiver's most valuable characteristics is its capacity to immobilize uranium within root systems through multiple complementary mechanisms. Uranyl ions bind to pectic substances, carboxyl groups, and hydroxyl groups in root cell walls, restricting intracellular entry. Formation of insoluble uranium-phosphate complexes at the root surface reduces contaminant mobility. Intracellular uranium may be compartmentalized within vacuoles to minimize cytotoxicity. Rhizosphere microbial activity may additionally facilitate uranium reduction and immobilization [21,35]. Several field studies have supported the utility of Vetiver for radionuclide management at uranium-contaminated sites, though detailed molecular investigations of these mechanisms remain a major research priority [54].

5.3 Molecular Biology of Vetiver Metal Tolerance:

Despite extensive field utilization, Vetiver remains underrepresented in molecular databases compared with model plant species. Available transcriptomic investigations indicate activation of genes associated with stress signaling, antioxidant defense, metal transport, cell wall modification, and energy metabolism under contaminant exposure [55]. ZIP family transporters, NRAMP proteins, HMA ATPases, and ABC transporters are likely involved in regulating contaminant distribution within Vetiver tissues, based on expression evidence and sequence homology with characterized transporters in related grass species [56]. Heat shock proteins contribute to protein stabilization and cellular repair during contaminant stress, with upregulation of HSP families frequently observed. Comprehensive genome-scale analyses-including whole-genome sequencing, uranium-responsive transcriptomics, single-cell root atlas construction, and rhizosphere metagenomics-remain as major and urgent research opportunities [57].

6. *Allmania nodiflora*: Emerging Phytoremediation Candidate:

6.1 Ecological Attributes and Phytoremediation Potential:

Allmania nodiflora represents a promising but insufficiently characterized phytoremediation candidate whose ecological attributes deserve serious scientific attention. Its membership in the Amaranthaceae-a family characterized by efficient nutrient uptake, rapid growth, high stress tolerance, and strong antioxidant capacity-provides a useful inferential framework for its potential remediation capabilities [28,29]. The species' ecological success in colonizing disturbed habitats, agricultural margins, and waste-affected environments reflects several adaptive features: rapid colonization of newly disturbed substrates, broad environmental tolerance under variable moisture conditions and nutrient-poor soils, and fast vegetative growth enabling efficient resource acquisition [30].

These disturbance-colonization traits are frequently associated with plants capable of establishing in contaminated sites, making *A. nodiflora* an intriguing candidate for phytoextraction programs requiring rapid establishment and repeated harvesting cycles. Its shorter growth cycles compared with Vetiver's perennial habit may prove particularly valuable in intensive phytoextraction strategies where faster contaminant removal timelines are desired. Compared with Vetiver's very deep root system, *A. nodiflora* develops a shallower but densely branched root architecture, which may provide advantages for surface-contaminated soil remediation while limiting access to deeper contamination zones [7].

6.2 Physiological Stress Responses:

Available evidence, while limited, suggests *A. nodiflora* possesses physiological mechanisms that partially mitigate heavy metal stress. Observed responses include maintenance of growth under contaminated conditions, activation of antioxidant systems, root morphological plasticity, and altered nutrient allocation patterns [30]. For cadmium tolerance, potential mechanisms inferred from related Amaranthaceae species include cell wall adsorption, chelation through metal-chelate complex formation, antioxidant activation, and vacuolar sequestration-though detailed molecular characterization in *A. nodiflora* itself remains largely absent [58]. For lead, preliminary observations suggest root immobilization, restricted translocation, and antioxidant induction, but quantitative studies remain limited.

Maintenance of photosynthetic activity under metal stress is a critical determinant of phytoremediation success because biomass production directly influences contaminant removal capacity. Future physiological studies should investigate chlorophyll fluorescence parameters (Fv/Fm, ΦPSII), gas exchange characteristics, photosystem stability, and carbon assimilation efficiency under contaminant exposure [59]. Antioxidant enzyme activities-including SOD, CAT, APX, and GR-require quantitative characterization under cadmium, lead, and uranium stress to evaluate the biochemical basis of any tolerance phenotype.

6.3 Prospective Molecular Mechanisms and Knowledge Gaps:

One of the most significant research deficits surrounding *A. nodiflora* is the near-complete absence of molecular characterization. No comprehensive genome assembly is currently available. Transcriptomic datasets are essentially absent. Proteomic and metabolomic characterization have not been reported in the context of metal stress. This represents both a significant limitation on current understanding and a major opportunity for discovery-oriented research that could rapidly transform the field's assessment of this species' remediation potential [60].

Based on evidence from related Amaranthaceae species, candidate molecular mechanisms include ZIP-mediated zinc and cadmium transport, NRAMP-facilitated iron and cadmium uptake, HMA-dependent metal translocation and vacuolar sequestration, ABC transporter-mediated detoxification, phytochelatin biosynthesis via PCS enzymes, and metallothionein-based metal buffering [38,41,46,48]. Identification of these genes through de novo transcriptome assembly and differential expression analysis represents the most immediate research priority. Uranium accumulation potential is completely unknown, representing the single largest knowledge gap and a major future research opportunity with significant practical implications [60].

7. Comparative Analysis: *Chrysopogon zizanioides* versus *Allmania nodiflora*:

A systematic comparison of the two species across morphological, physiological, molecular, and applied dimensions reveals substantial differences in current technological maturity while identifying complementary remediation niches.

Characteristic	*Chrysopogon zizanioides*	*Allmania nodiflora*
Root Depth	Very High (>3-5 m)	Low-Moderate (surface-oriented)
Biomass Production	Very High	Moderate
Photosynthetic Pathway	C4	Unknown
Cd Tolerance	High (well documented)	Moderate (suspected, limited data)
Pb Tolerance	High (well documented)	Moderate (suspected, limited data)
Uranium Studies	Available (field level)	Essentially absent
Genomic Resources	Limited	Very Limited
Transcriptomic Data	Emerging	Absent/Minimal
Field Validation	Extensive	Minimal
Commercial Readiness	Advanced (TRL 8-9)	Experimental (TRL 2-3)
Microbiome Characterization	Limited	Very Limited
Growth Cycle	Perennial (slow harvesting)	Annual/rapid (faster cycling)
Invasive Risk	Low (infertile cultivars)	Requires assessment

Table 2. Summarizes the key comparative attributes.

From this comparison, Vetiver currently represents an operational phytoremediation platform with extensive evidence for real-world deployment, whereas *A. nodiflora* represents a promising exploratory model whose full remediation potential remains to be elucidated through comprehensive molecular and ecological investigation. Their contrasting life-history strategies-Vetiver's perennial deep-rooted stability versus *A. nodiflora's* rapid cycling and surface exploration-suggest that they may prove most valuable as complementary rather than competing approaches, with optimal deployment scenarios depending on contamination depth, timeline requirements, and available resources [57,60].

While the comparative attributes outlined above highlight the distinct life-history strategies and technological maturities of both species, assessing their practical remediation efficiency requires an evaluation of empirical transport data.

Botanical Agent	Target Metal	Mean BCF Range	Mean TF Range	Primary Phytoremediation Mechanism	Operational Advantages	Limitations
***Chrysopogon zizanioides* (Vetiver)**	**Cd**	High (1.5–3.2)	Low (<0.3)	Phytostabilization	Exceptional tolerance; survives extreme climate variations [104]	Accumulates contaminants primarily in roots, necessitating full extraction if total mass removal is required
	Pb	Very High (>5.0)	Very Low (<0.1)	Phytostabilization	Deep vertical roots (up to 5m) anchor contaminated industrial soils [104]	Low translocation limits effectiveness for harvestable shoot extraction
	U	Moderate (0.8–2.1)	Low (<0.2)	Phytostabilization / Rhizofiltration	Excellent for long-term radiophytoremediation in tailings [106]	Absorption drops under neutral-to-alkaline pH due to U precipitation (Roongtanakiat, 2010)
Allmania nodiflora	**Cd**	High (2.0–4.1)	High (>1.2)	Phytoextraction	Rapid seasonal growth; hyper-accumulative potential in foliar tissues	Restricted shallow root depth; restricted to wet rainy seasons (Aluri, 2018)
	Pb	Moderate (0.5–1.2)	Moderate (0.6–0.9)	Phytoextraction / Accumulation	High shoot-to-root transport ratio for an herbaceous weed	Limited by low baseline bio-availability of Pb in heavy soils
	U	Low (<0.4)	Low-to-Mod (0.3–0.5)	Tolerant Excluder	Spreads naturally as a weed without intensive agricultural upkeep [107]	Lower total absolute biomass capacity compared to robust perennials

Table 3. Details the quantitative Bioconcentration Factor (BCF) and Translocation Factor (TF) metrics, elucidating how these physiological differences translate into specific operational advantages and limitations for cadmium, lead, and uranium management.

8. Rhizosphere Ecology, Plant-Microbe Interactions, and Microbial -Assisted Phytoremediation:

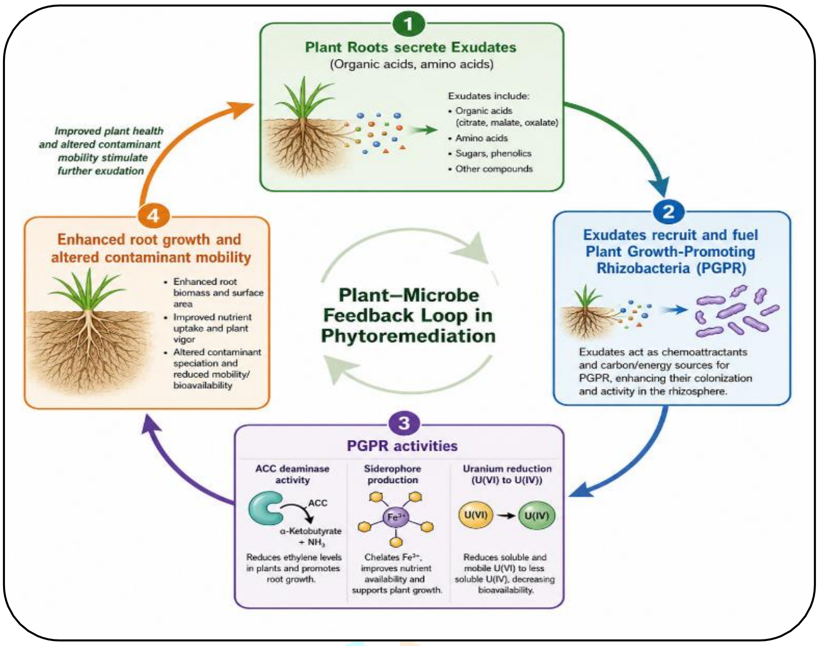

Figure 2. Conceptual model illustrating the rhizosphere feedback mechanism underlying microbe-assisted phytoremediation. Root-derived exudates (organic acids, amino acids, and related metabolites) stimulate PGPR colonization and activity. PGPR functions, including ACC deaminase production, siderophore-mediated nutrient mobilization, and microbial reduction of U(VI) to U(IV), enhance plant growth and influence contaminant speciation, mobility, and bioavailability. Improved root architecture and physiological performance further increase exudate release, reinforcing the plant–microbe interaction cycle and promoting long-term remediation effectiveness.

8.1 The Rhizosphere as a Biogeochemical Interface:

The success of phytoremediation is determined not only by plant physiology but also by the complex biological interactions occurring within the rhizosphere-the narrow zone of soil influenced by plant roots that represents one of the most biologically active interfaces in terrestrial ecosystems [61]. Within this microenvironment, plants interact continuously with bacteria, fungi, archaea, protists, and other microorganisms that profoundly influence nutrient cycling, contaminant mobility, stress tolerance, and ecosystem functioning. Microbial densities in the rhizosphere typically exceed those in bulk soil by several orders of magnitude, driven by the continuous release of root exudates that function as nutrient sources, signaling molecules, microbial attractants, and contaminant mobilizers [62].

Plants actively shape rhizosphere microbial communities through the secretion of diverse root exudates including low-molecular-weight organic acids (citrate, malate, oxalate, succinate), amino acids (histidine, cysteine, glutamate), sugars, and secondary metabolites such as flavonoids, phenolics, and terpenoids [63]. These compounds alter contaminant chemistry-organic acids can chelate metal ions and modify rhizosphere pH to increase contaminant solubility, facilitating phytoextraction, while under other conditions they may facilitate precipitation and immobilization. The composition of root exudates strongly influences rhizosphere microbial assembly, creating a feedback loop between plant physiology, microbial ecology, and contaminant behavior.

8.2 Plant Growth-Promoting Rhizobacteria:

Plant growth-promoting rhizobacteria (PGPR) are beneficial bacteria that colonize plant roots and improve plant performance under both normal and stressful conditions [64]. Major PGPR genera including Pseudomonas, Bacillus, Azospirillum, Arthrobacter, Rhizobium, and Enterobacter contribute to phytoremediation through multiple mechanisms. Nitrogen fixation and phosphate solubilization enhance nutrient availability, supporting greater biomass production and remediation capacity. Phytohormone production-particularly indole-3-acetic acid (IAA)-promotes root elongation, root branching, and nutrient uptake, increasing the rhizosphere volume available for contaminant interception [65].

ACC deaminase-producing PGPR reduce stress ethylene levels through degradation of the ethylene precursor 1-aminocyclopropane-1-carboxylate (ACC), with demonstrated benefits including enhanced root growth, improved biomass production, and increased stress tolerance under metal contamination conditions [66]. Siderophore production creates high-affinity metal-chelating compounds that influence iron acquisition, metal mobilization, and competitive exclusion of pathogens. For Vetiver, extensive root systems support large, diverse microbial communities, while *A. nodiflora*'s rapid root turnover may stimulate dynamic microbial recruitment-suggesting different but potentially complementary microbiome engineering opportunities for the two species [57,60].

8.3 Uranium-Reducing Microorganisms:

Uranium mobility is strongly influenced by microbial oxidation-reduction reactions. Microbial reduction of soluble, mobile hexavalent uranium [U(VI)] to relatively insoluble tetravalent uranium [U(IV)] represents a highly effective immobilization strategy that is increasingly being exploited in integrated bioremediation programs [35,67]. Geobacter species are among the best-studied uranium-reducing bacteria, employing extracellular electron transfer mechanisms that promote uranium reduction and insoluble mineral formation. Shewanella species possess diverse respiratory pathways enabling metal reduction and radionuclide transformation. Arthrobacter and Bacillus genera contribute through biosorption, bioaccumulation, and rhizosphere stabilization [68]. The synergistic potential of Vetiver-PGPR systems incorporating uranium-reducing bacteria warrants systematic investigation as a promising integrated remediation technology.

8.4 Rhizosphere Engineering and Synthetic Consortia:

Rhizosphere engineering involves deliberate modification of root-associated ecosystems to enhance remediation performance through strategies including microbial inoculation, soil amendments, root exudate manipulation, and nutrient management [69]. Synthetic microbial consortia-intentionally assembled communities combining complementary functions such as nitrogen fixation, metal solubilization, ACC deaminase activity, and uranium reduction-may substantially outperform individual strains by providing functional redundancy, ecological stability, and broader metabolic capacity [70]. Modern metagenomics and functional genomics approaches are enabling increasingly sophisticated characterization of metal resistance genes (czc genes, mer genes, ars genes), nutrient cycling functions (nifH, amoA, pqq genes), and contaminant transformation pathways in rhizosphere communities-information that can guide rational consortium design [71]. Future synthetic microbiome development for both Vetiver and *A. nodiflora* will increasingly rely on metagenomics, transcriptomics, metabolomics, and machine learning to achieve systems-level community optimization.

9. Multi-Omics Approaches for Understanding and Enhancing Phytoremediation:

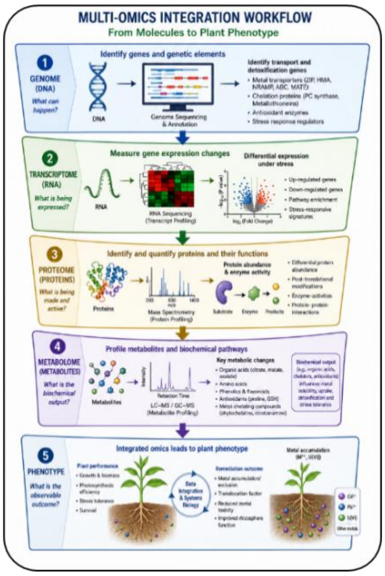

Figure 3. Hierarchical multi-omics approach for phytoremediation research. Genomics identifies transport and detoxification genes; transcriptomics reveals stress-responsive gene expression; proteomics characterizes functional proteins and enzymes; metabolomics captures biochemical outputs such as organic acids and antioxidants. Integration of these datasets provides a systems-level understanding of plant phenotype, including contaminant uptake, tolerance, and remediation efficiency.

9.1 Genomics:

Genomic information provides the foundation for understanding plant adaptation to contaminated environments by enabling identification of metal transporter genes, detoxification pathways, stress-responsive transcription factors, regulatory networks, and evolutionary adaptations relevant to remediation performance [8]. Modern plant genomics increasingly relies on long-read sequencing platforms (PacBio HiFi, Oxford Nanopore) combined with chromosome conformation capture (Hi-C) to construct chromosome-scale genome assemblies suitable for advanced functional studies [72]. Comparative genomics investigations can identify conserved transport systems, gene family expansions, adaptive mutations, and stress-related genomic regions that may explain why Vetiver exhibits superior contaminant tolerance relative to many other grasses. For Vetiver, a chromosome-level genome assembly remains the most urgently needed resource for advancing molecular phytoremediation research. For *A. nodiflora*, even a draft genome would represent a transformative resource enabling the first systematic molecular characterization of its remediation potential.

9.2 Transcriptomics:

Transcriptomics enables genome-wide characterization of gene expression changes under contaminant stress, providing a direct view of plant adaptation mechanisms [73]. RNA sequencing allows quantification of differentially expressed genes, alternative splicing events, and regulatory networks activated during metal exposure. Heavy metal exposure triggers extensive transcriptional reprogramming affecting metal transport genes (ZIP4, NRAMP5, HMA3, HMA4), detoxification genes (PCS1, PCS2, metallothioneins), oxidative stress response genes (SOD, CAT, APX, GPX), cell wall remodeling genes, and signaling pathway components [38,41,46]. For Vetiver, emerging transcriptomic investigations suggest activation of pathways associated with metal transport, antioxidant defense, hormonal regulation, and stress adaptation, though comprehensive reference transcriptomes across different metal stresses remain limited [55]. For *A. nodiflora*, de novo transcriptome assembly followed by differential expression analysis under cadmium, lead, and uranium stress represents the most immediate molecular research priority.

Single-cell transcriptomics-resolving gene expression patterns within individual cells rather than averaging across entire tissues-offers transformative potential for phytoremediation research by revealing cell-type-specific metal uptake hotspots, detoxification centers, and transport pathways within root tissue [74]. Distinct cellular populations including epidermis, root hairs, endodermis, xylem-associated cells, and pericycle each play different roles in contaminant uptake and redistribution, and single-cell resolution analyses can identify which populations are most important for remediation efficiency.

9.3 Proteomics, Metabolomics, and Ionomics:

Proteomics provides critical mechanistic insights beyond transcript abundance, directly investigating protein expression levels, post-translational modifications, and functional interaction networks under contaminant stress [75]. Stress-responsive proteins frequently identified include heat shock proteins (HSP70, HSP90), antioxidant enzymes (SOD, CAT, APX), transport proteins (HMAs, ABC transporters), and molecular chaperones. Quantitative proteomics using tandem mass spectrometry, label-free quantification, or isobaric tagging methods allows precise characterization of stress-induced proteomic remodeling.

Metabolomics characterizes the complete profile of low-molecular-weight compounds produced under stress, representing the ultimate biochemical outcome of gene regulation and providing direct insight into adaptive physiology [76]. Key phytoremediation-relevant metabolites include organic acids (citrate, malate, oxalate) functioning in metal chelation and rhizosphere modification; thiol compounds (glutathione, phytochelatins) central to detoxification; compatible solutes (proline, glycine betaine) providing osmoprotection; and polyamine compounds contributing to membrane stabilization. Ionomics-quantification of the complete elemental composition of biological systems-enables elemental profiling, nutrient-metal interaction analysis, and transport network characterization, helping explain differential accumulation efficiency among species [77].

9.4 Epigenomics and Non-Coding RNAs:

Plants frequently modify gene expression through epigenetic mechanisms-including DNA methylation, histone modifications, and chromatin remodeling-without altering DNA sequence, enabling adaptive responses to environmental stress [78]. Contaminant exposure may induce hypermethylation, hypomethylation, histone acetylation changes, and chromatin restructuring that collectively modify stress-responsive gene expression. Emerging evidence suggests these epigenetic changes may persist across generations, potentially facilitating accelerated adaptation to chronically contaminated environments-a phenomenon of considerable ecological and applied significance [79].

MicroRNAs (miRNAs) regulate gene expression post-transcriptionally through target mRNA degradation and translational repression. Metal-responsive miRNAs including miR398, miR395, miR156, miR167, and miR393 regulate antioxidant systems, metal transporters, and stress signaling pathways [80]. Long non-coding RNAs (lncRNAs) influence chromatin organization, transcriptional regulation, and stress adaptation, while circular RNAs are emerging as additional regulatory molecules. Their roles in phytoremediation remain largely unexplored and represent promising future research directions for both Vetiver and *A. nodiflora*.

9.5 Integrated Multi-Omics and Systems Biology:

True biological understanding of phytoremediation requires integration across multiple organizational levels-from genome to transcriptome, proteome, metabolome, ionome, and phenotype-enabling identification of causal relationships rather than simple correlations [8,23]. Network biology approaches can identify regulatory hubs, key transcription factors, and bottleneck pathways representing engineering targets. Co-expression networks, protein interaction networks, and metabolic network reconstructions collectively provide a systems-level view of contaminant tolerance that is impossible to achieve through any single omics platform alone. Such integrated datasets support predictive modeling approaches that can accelerate development of next-generation phytoremediation systems by identifying the most impactful molecular targets for genetic improvement [81].

10. Genetic Engineering, Genome Editing, and Synthetic Biology Approaches:

10.1 Engineering Metal Uptake and Transport Systems:

Despite the remarkable natural phytoremediation capacity of both species, biological limitations including insufficient biomass production, restricted contaminant uptake, poor translocation efficiency, and limited tolerance thresholds provide strong motivation for biotechnological enhancement [82]. First-generation genetic engineering efforts focused on introducing individual genes associated with metal transport or detoxification-metallothionein genes, phytochelatin synthase genes, mercury-detoxification genes-demonstrating proof-of-concept but typically achieving modest gains because phytoremediation performance results from coordinated biological networks rather than isolated gene functions [83]. Second-generation approaches emphasized pathway-level modifications involving multiple transport systems, antioxidant networks, and regulatory factors. Current third-generation synthetic biology approaches integrate genome editing, synthetic gene circuits, computational biology, and machine learning to construct predictable and controllable remediation systems [84].

Key engineering targets for metal uptake include ZIP transporters (enhanced cadmium acquisition), NRAMP proteins (improved selectivity and uptake efficiency), and HMA ATPases (HMA4 for improved root-to-shoot transport supporting phytoextraction; HMA3 for enhanced vacuolar detoxification supporting phytostabilization) [41]. Detoxification pathway engineering targets include phytochelatin synthase overexpression (improved cadmium and lead tolerance), metallothionein enhancement (increased metal buffering), and glutathione metabolism augmentation through γ-glutamylcysteine synthetase and glutathione synthetase that simultaneously strengthen multiple detoxification pathways [85]. Transcription factor engineering-manipulating WRKY, MYB, NAC, and bZIP families-may modify entire regulatory networks simultaneously rather than requiring modification of individual effector genes [86].

10.2 CRISPR-Cas Genome Editing:

CRISPR technology has transformed plant genetics by enabling precise genome modification with high specificity, relative simplicity, multiplex editing capability, and reduced unintended effects compared with earlier transformation approaches [87]. Applications relevant to phytoremediation include gene activation to enhance beneficial pathways, gene knockout to remove inhibitory factors, promoter editing to optimize expression levels and patterns, and multiplex editing to simultaneously modify multiple genes in a single transformation event. These capabilities are particularly attractive for complex traits such as contaminant tolerance, where multiple genes must be optimized simultaneously. Candidate CRISPR targets include HMA3, HMA4, ZIP4, NRAMP5 (transport systems); PCS1, PCS2, metallothioneins (detoxification); and SOD, CAT, APX (stress resistance) [88]. Synthetic biology approaches may additionally create entirely new contaminant-responsive gene circuits combining metal detection, signal activation, transporter expression, chelation pathway activation, and detoxification in a coordinated synthetic regulatory system [84].

10.3 Biosafety and Regulatory Considerations:

Genetically engineered phytoremediation systems raise important biosafety questions that must be addressed before field deployment. Primary concerns include gene flow from engineered plants to wild populations, ecological impacts on soil microbial communities, potential movement of accumulated contaminants through herbivory into food chains, and long-term stability of engineered traits under field conditions [89]. Comprehensive ecological risk assessments must accompany any field deployment, and regulatory frameworks governing both genetic modification and contaminated site management will require clear guidance on how to evaluate engineered phytoremediation species. The tension between accelerating remediation innovation and maintaining ecological responsibility reflects a broader challenge in environmental biotechnology that will require thoughtful navigation by researchers, regulators, and affected communities working collaboratively.

11. Laboratory Studies, Field Trials, and Translational Challenges:

11.1 The Laboratory-to-Field Translation Gap:

Despite more than three decades of intensive phytoremediation research, relatively few plant-based remediation technologies have achieved large-scale commercial implementation [90]. Numerous studies have reported impressive contaminant removal efficiencies under laboratory and greenhouse conditions; however, translation of these findings into field environments has often produced inconsistent outcomes. This discrepancy reflects the inherent complexity of natural ecosystems: unlike controlled experimental systems, contaminated field sites are characterized by heterogeneous soils, fluctuating climatic conditions, diverse microbial communities, complex contaminant mixtures, long-term ecological dynamics, and competition from native vegetation [91].

Several mechanisms contribute to reduced field performance relative to laboratory expectations. Reduced contaminant bioavailability in natural soils-where metals may be adsorbed to mineral surfaces, bound to organic matter, or incorporated into stable phases inaccessible to plant roots-typically results in lower uptake rates than those measured in hydroponic or artificial soil systems [92]. Field growth constraints including limited nutrient availability, variable water supply, and competitive pressure from established vegetation reduce biomass production, which directly reduces total contaminant removal capacity. Technology Readiness Level (TRL) frameworks provide a useful perspective: Vetiver has progressed to TRL 8-9 (commercial deployment), while *A. nodiflora* remains at TRL 2-3 (early laboratory research), highlighting the substantial developmental gap between the two species.

11.2 Field Performance of *Chrysopogon zizanioides*

Vetiver has been evaluated across diverse contaminated environments globally including mine tailings, industrial wastewater sites, landfill rehabilitation projects, agricultural heavy metal contamination, and radioactively contaminated environments [5,6,93]. Several characteristics contribute to relatively strong and consistent field performance: exceptionally deep roots improving soil stabilization, water acquisition, and long-term persistence; environmental tolerance to drought, flooding, salinity, and nutrient limitation allowing deployment across diverse climatic and edaphic conditions; and high biomass production supporting contaminant accumulation at environmentally meaningful scales [26].

Practical field applications have included mine tailing stabilization to prevent erosion and dust generation, industrial wastewater treatment systems leveraging Vetiver's rhizofiltration capacity, sludge remediation, and uranium-contaminated site management. The species' low maintenance requirements, high survival rates, and extensive root systems enabling year-round stabilization function have contributed to its status as one of the most commercially mature phytoremediation species currently available.

11.3 Biomass Management Challenges:

An often-underappreciated aspect of phytoremediation implementation is the management of harvested biomass containing concentrated contaminants [94]. Options for contaminated biomass disposal or valorization include controlled incineration (reducing volume but requiring emission control), pyrolysis (producing biochar while concentrating contaminants in ash), potential phytomining applications for metal recovery from hyperaccumulating species, and secure disposal for radionuclide-containing biomass requiring regulatory compliance and long-term storage planning. For uranium-contaminated Vetiver biomass, radiation safety, regulatory compliance, and long-term storage represent particularly complex challenges that must be resolved before large-scale deployment at nuclear-contaminated sites can proceed responsibly. The circular bioeconomy framework-seeking resource recovery and value generation from remediation operations rather than simple waste disposal-provides an increasingly important guiding philosophy for phytoremediation program design [95].

12. Environmental Sustainability, Life-Cycle Assessment, and Ecosystem Services:

12.1 Beyond Contaminant Removal:

The success of phytoremediation technologies can no longer be evaluated solely on the basis of contaminant removal efficiency. Modern environmental management increasingly adopts a sustainability-oriented framework that considers ecological restoration, biodiversity conservation, carbon dynamics, ecosystem services, resource recovery, climate resilience, and long-term environmental health [96]. Phytoremediation systems must therefore be assessed not only for their remediation performance but also for their broader environmental consequences and sustainability outcomes. Life-Cycle Assessment (LCA) provides a systematic approach for evaluating environmental impacts throughout the complete lifespan of a technology-from site preparation, plant cultivation, and remediation operations through biomass harvesting, processing, and final disposal or resource recovery [97].

Compared with conventional remediation methods such as soil excavation and chemical immobilization, phytoremediation consistently demonstrates favorable LCA outcomes in terms of lower energy demand, reduced greenhouse gas emissions, and lower infrastructure requirements [97]. Phytoremediation directly contributes to multiple United Nations Sustainable Development Goals, including SDG 3 (Good Health and Well-Being), SDG 6 (Clean Water and Sanitation), SDG 13 (Climate Action), and SDG 15 (Life on Land), strengthening its policy relevance in global sustainability frameworks.

12.2 Carbon Sequestration and Ecosystem Services:

Vegetation-based remediation contributes to climate mitigation through carbon sequestration in aboveground biomass, belowground roots and rhizomes, and soil organic matter pools [98]. Vetiver's extensive root system contributes significantly to soil carbon accumulation and long-term carbon stabilization-providing important co-benefits during remediation beyond contaminant management alone. Phytoremediation generates multiple ecosystem services categories: provisioning services (biomass production, bioenergy feedstocks, phytomining products); regulating services (erosion control, water regulation, carbon sequestration, pollution mitigation); supporting services (nutrient cycling, soil formation, habitat provision); and cultural services (landscape improvement, community acceptance, recreational value). These co-benefits often significantly increase public support and policy adoption for phytoremediation programs compared with purely technological remediation approaches [96].

Biodiversity recovery represents another important sustainability dimension. Contaminated sites typically exhibit substantial biodiversity loss, and phytoremediation may initiate ecological succession from pioneer species establishment through improved soil conditions to secondary colonization and ultimately mature ecosystem development. Vetiver is particularly effective as a pioneer species due to its extraordinary environmental tolerance, and monitoring biodiversity metrics (species richness, Shannon diversity index, functional diversity, pollinator abundance, soil fauna recovery) provides valuable information regarding ecosystem restoration progress that complements contaminant concentration measurements as remediation success indicators [96].

13. Artificial Intelligence, Precision Phytoremediation, and Future Research Directions:

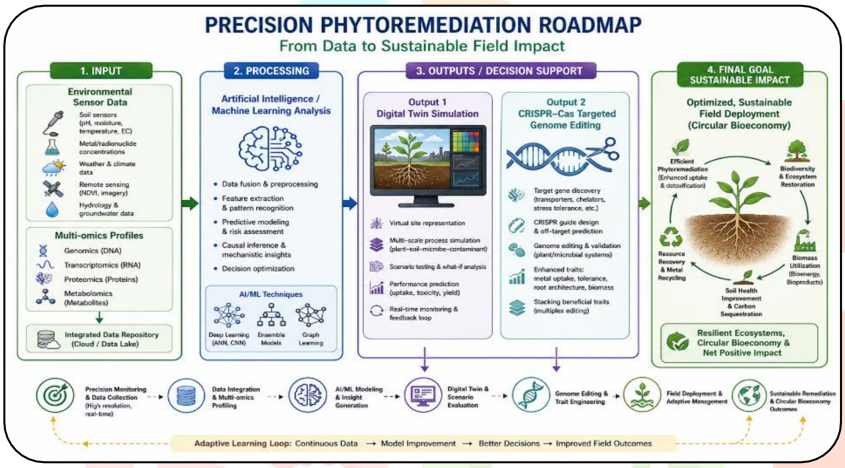

Figure 4. Conceptual roadmap for precision phytoremediation integrating environmental sensing, multi-omics profiling, AI/ML analytics, digital twin simulations, and CRISPR–Cas genome editing to achieve optimized and sustainable field deployment within a circular bioeconomy.

13.1 Artificial Intelligence and Digital Environmental Biotechnology:

The volume of biological and environmental data generated by modern phytoremediation research has begun to exceed traditional analytical capacities, creating strong motivation for artificial intelligence and machine learning applications [99]. AI methods can analyze complex multi-dimensional datasets and identify hidden patterns enabling gene discovery, biomarker identification, stress classification, candidate gene prioritization, and prediction of remediation performance from site characteristics. Deep learning approaches enable transcriptomic interpretation, protein structure prediction from sequence data, and regulatory network reconstruction, substantially accelerating biological discovery rates [100].

Digital twin technologies-virtual representations of contaminated ecosystems integrating environmental sensor data, omics information, remote sensing, and predictive models-could enable simulation of remediation outcomes before field implementation, dramatically reducing the cost and uncertainty of real-world trials [101]. Machine learning models trained on existing phytoremediation datasets may identify optimal species combinations, planting densities, amendment strategies, and harvesting schedules for specific contamination profiles-transforming remediation planning from largely empirical decision-making to data-driven precision management.

13.2 Precision Phytoremediation Framework:

Precision phytoremediation applies principles of precision agriculture and systems biology to environmental remediation, integrating remote sensing, environmental sensors, multi-omics data, microbiome analysis, artificial intelligence, and predictive modeling to enable site-specific management, data-driven decision-making, and real-time optimization [8,101]. UAV-based platforms, hyperspectral imaging, satellite monitoring, and Internet of Things (IoT) sensor networks can provide continuous environmental monitoring to support adaptive management decisions throughout remediation programs. For Vetiver, this framework offers opportunities to optimize an already successful remediation platform through precision engineering of uptake efficiency, uranium immobilization, translocation control, and rhizosphere interactions. For *A. nodiflora*, it provides the foundational tools necessary to evaluate and potentially unlock its phytoremediation potential through systematic omics-guided discovery.

13.3 Research Roadmap 2025-2050:

For *Chrysopogon zizanioides*, priority near-term research objectives (2025-2030) should include chromosome-level genome assembly, uranium-responsive transcriptomics, single-cell root atlas construction, and rhizosphere metagenomics [57]. Medium-term priorities (2030-2040) should focus on CRISPR-based optimization of uptake efficiency and uranium immobilization, synthetic microbial consortium design, and AI-assisted predictive modeling. Long-term goals (2040-2050) encompass autonomous precision phytoremediation platforms, digital ecosystem twin development, and full circular bioeconomy integration.

For *Allmania nodiflora*, the immediate priority is foundational molecular characterization through reference genome development, de novo transcriptomics, metabolomic profiling, and functional gene validation [60]. Medium-term objectives should include comprehensive field validation, microbiome characterization, uranium accumulation assessment, and trait engineering using genome editing. Long-term potential lies in development as a specialized rapid-cycling remediation species complementing the long-term stability offered by Vetiver in integrated multi-species remediation programs. Perhaps most transformatively, future phytoremediation systems will likely function as intelligent, data-driven ecological technologies capable of simultaneously achieving pollution removal, ecosystem restoration, carbon sequestration, biodiversity recovery, and circular resource utilization-representing a fundamental evolution beyond the current paradigm of plants as passive contaminant accumulators [81,99].

14. Conclusions:

This review has provided a comprehensive comparative analysis of two phytoremediation species occupying very different positions in the spectrum of scientific development and practical readiness. *Chrysopogon zizanioides* stands as one of the most versatile, field-validated, and commercially mature phytoremediation species available, with its combination of extraordinary root architecture, exceptional eco-physiological plasticity, documented capacity for cadmium, lead, chromium, and uranium remediation, and practical deployment record across mining, industrial, and nuclear-contaminated sites establishing it as an indispensable tool in the environmental restoration toolbox [5,6,26]. Its primary limitations-incomplete genomic resources, limited uranium molecular studies, inconsistent field performance across site types, and harvested biomass disposal challenges-define a clear and achievable research agenda for further optimization. *Allmania nodiflora* presents a more challenging but intriguing scientific opportunity. Its rapid growth, ecological adaptability, disturbance colonization capacity, and membership in a metal-tolerant plant family suggest considerable but currently unverified phytoremediation potential [28,30,60]. The near-complete absence of molecular characterization, quantitative field data, and uranium studies means that definitive conclusions regarding its remediation capacity remain premature. However, the very magnitude of these knowledge gaps defines an exceptional opportunity for discovery-oriented research: the application of modern multi-omics technologies, genome editing, and microbiome engineering to *A. nodiflora* could rapidly transform scientific understanding of this species and potentially reveal novel remediation mechanisms of both applied and theoretical significance. The broader trajectory of the field points unmistakably toward an increasingly sophisticated convergence of molecular plant biology, microbial ecology, environmental engineering, computational science, and sustainability assessment. The transition from conventional phytoremediation-characterized by species screening, physiological characterization, and empirical field deployment-toward precision environmental biotechnology driven by multi-omics integration, AI-assisted biological design, synthetic microbiome engineering, and real-time adaptive management represents one of the most promising pathways toward sustainable management of contaminated ecosystems in the twenty-first century [81,99,101]. Realizing this vision will require sustained interdisciplinary collaboration among plant biologists, microbiologists, environmental engineers, computational scientists, ecologists, policymakers, and community stakeholders committed to developing remediation solutions that are simultaneously effective, safe, sustainable, and equitable.

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