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Review

Horticultural Salinity-Stress Phenotyping and Tolerance Inference: A Critical Evidence Map and Validation Framework for AI-Related Claims

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Highlights

What are the main findings?

- Horticultural salinity-stress tolerance depends on crop-specific ion homeostasis, osmotic adjustment, ROS control, photosynthetic protection and production-system context.
- Only a small AI/sensing/phenotyping subset directly addresses salinity; current AI evidence is strongest as a phenotyping and validation layer, not as autonomous management proof.

What are the implications of the main findings?

- Validation ladders, leakage controls, biological metadata and reporting checklists should align AI claims with physiological, biochemical and omics evidence.
- Field-ready and commercially defensible claims require external validation, stress-confusion testing, economic feasibility assessment and prospective decision trials.

Abstract

Salinity stress constrains horticultural production in protected cultivation, hydroponics, coastal agriculture and reclaimed-water irrigation. This critical narrative review and evidence map synthesizes a DOI-verified core corpus of 160 peer-reviewed journal articles to ask how artificial intelligence (AI) can support, rather than overstate, salinity-stress inference in horticultural crops. The evidence base is uneven: 22 retained records were AI-, sensing- or phenotyping-relevant, six treated ML, deep learning, edge intelligence or agentic AI as a central method, and four directly tested salinity- or water-stress AI/sensor phenotyping in a crop-relevant system. Among the six explicit-AI records, none externally validated a salinity-specific AI model; one distinguished salinity from drought, and none reported a prospective AI-guided intervention trial. Accordingly, this article is framed as a validation and reporting framework, not as a quantitative meta-analysis of model or intervention efficacy. Across the broader corpus, evidence for salinity tolerance centres on osmotic limitation, Na+ and Cl^- toxicity, K^+ retention, ROS regulation, photosynthetic protection, hormonal signalling, root hydraulics, rhizosphere processes and metabolic reprogramming. The review links these mechanisms to measurable traits and to claim-specific AI validation requirements. We propose a mechanism-to-AI map, a validation ladder, an intervention maturity framework and a reporting checklist. The conclusion is deliberately conservative: AI can improve salinity research when it is constrained by rigorous metadata,

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physiological grounding, external validation, stress-confusion testing and explicit uncertainty, but current evidence is insufficient to support autonomous, economically validated or field-ready AI-based salinity management.

Keywords: artificial intelligence; salinity stress; horticultural crops; high-throughput phenotyping; machine learning; multi-omics; external validation; evidence synthesis; rootstock; biostimulants

1. Introduction

Soil salinization and irrigation-water salinization remain persistent constraints on high-value horticultural production, particularly in protected cultivation, hydroponic systems, grafted orchards, reclaimed-water irrigation and coastal or arid-zone fields. Existing reviews have summarized salinity physiology, high-throughput phenotyping, machine learning for plant-stress detection, multi-omics integration and agronomic innovation in greenhouse systems [1–12]. The unresolved question is narrower: which AI-related claims are justified by the current horticultural salinity evidence, and which remain measurement, validation or future-standard claims rather than management-ready conclusions?

Salt stress is sequential, organ-specific and production-system-dependent. Early osmotic limitation restricts water status, stomatal conductance, leaf expansion and root hydraulic adjustment; later ionic stress reflects Na^+ and Cl^- accumulation, K^+ competition, Ca^{2+} signalling disruption, membrane injury and oxidative imbalance. These phases interact with energy costs, developmental stage, cultivar, rootstock, substrate and greenhouse technology level, so a single composite salt-stress score is usually too coarse to support mechanistic interpretation [1,2,4,6,11,12].

The horticultural literature is broad but fragmented. Studies on tomato, cucumber, lettuce, citrus, grapevine, pepper, melon, watermelon, eggplant, strawberry and potato report growth suppression, ion imbalance, oxidative damage, reduced fluorescence, altered osmolyte profiles and partial rescue through grafting, microbial inoculants, biostimulants, nanoparticles or signal molecules. However, doses, substrates, cultivars, rootstock combinations, stress duration, developmental stage, sampled tissue and production targets differ widely enough that success in a single crop or greenhouse system rarely supports general salinity-management claims.

AI is relevant because this evidence base is heterogeneous, but heterogeneity alone does not make AI evidence mature. Machine learning, computer vision, hyperspectral sensing, chlorophyll fluorescence, UAV imagery, multi-omics integration and AI-assisted workflows can improve detection sensitivity, phenotyping scale, data linkage and auditability. They cannot, by architecture alone, transform treatment classification into mechanistic understanding, internal predictive accuracy into field usefulness, or single-system evidence into cross-crop transferability [7–10].

This review therefore addresses four explicit questions: what salinity mechanisms and crop contexts must anchor AI phenotypes; what portion of the current corpus provides direct AI/sensing evidence; what validation designs are required for detection, transfer, mechanism and decision claims; and what reporting standards would make future horticultural salinity AI studies reusable. The novelty is not another broad salinity-physiology review or a pooled model ranking, but a claim-calibration framework linking biological mechanism, evidence maturity and AI validation boundaries. Figure 1 presents a mechanism-to-AI framework linking salinity exposure and biological responses to measurable traits, sensing and AI inference, and claim-specific validation boundaries.

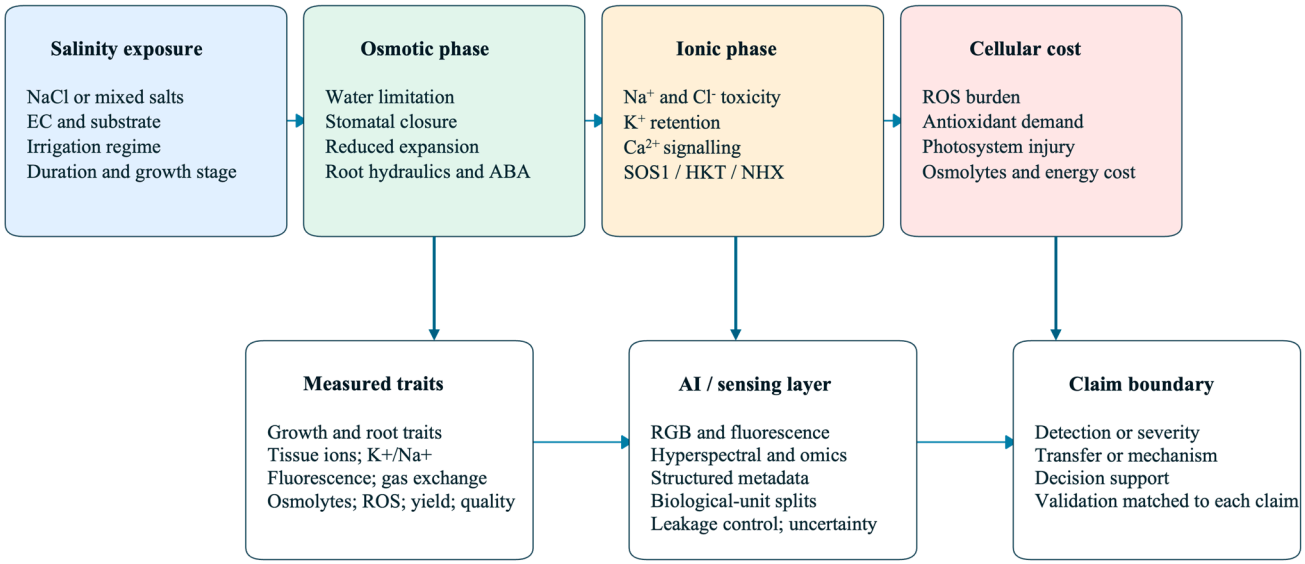

Figure 1. Mechanism-to-AI map for salinity-stress tolerance inference. This figure links osmotic limitation, Na^+/Cl^- toxicity, K^+ retention, ROS control, root hydraulics, stomatal regulation and energy cost to measurable phenotypes, sensor streams and AI validation boundaries.

2. Review Methodology and Evidence-Map Construction

This article uses a structured critical narrative review supported by an auditable evidence map. The design was chosen to calibrate claims across biologically heterogeneous studies, rather than to estimate pooled effects, study prevalence or comparative model performance. Quantitative pooling was avoided because the corpus varies sharply in crop, cultivar, rootstock, substrate, salt composition, dose, duration, endpoint, intervention timing, sampled organ, validation design and claim level. Pooling such studies would risk producing a false average across biologically non-equivalent experiments.

The structured database search was conducted in Web of Science, Scopus and PubMed up to 27 May 2026. Search blocks combined crop terms, salinity terms, physiological and biochemical response terms, multi-omics terms, sensing terms, machine-learning terms and AI-workflow terms. Google Scholar was used only after database retrieval for supplementary discovery and backward or forward citation chasing. Its ranked result set was neither treated as a bounded screening frame nor counted as a standalone source denominator. Any record first encountered through Google Scholar entered the same DOI/source verification and scope-anchoring procedure before consideration for the evidence map. Supplementary Information S1 reports the search date, 87 query expressions preserved in the source log, candidate-log categories, core-citation selection rationale, AI validation audit, study-level AI-subset evidence and operational definitions in Tables S1–S7. Database-specific syntax, searched fields, per-database hit counts, language restrictions and publication-type restrictions were not recorded contemporaneously and cannot be reconstructed without false precision. Supplementary Table S1 now reports each unavailable item explicitly, and Table S7 labels the 87 entries as preserved discovery phrases rather than database-executable search strings. Accordingly, this review does not claim PRISMA-level search reproducibility or exhaustive or bounded literature coverage.

To keep the 172-reference main bibliography manageable without oversized citation strings, the DOI-verified 160-paper core corpus is introduced once, in full, as an ordered citation-spine table. Table 1 is an audit device: it establishes first-appearance order for the core corpus, while later sections cite only the sources needed for a specific claim. Two additional contextual references were added during revision to address greenhouse species specificity and technology-context transferability [11,12].

Table 1. Ordered citation spine for the DOI-verified retained corpus. Contiguous reference ranges identify audit segments in the core corpus; later narrative sections use claim-specific citations. The supplementary study-level audit is provided in Supplementary Information S1, Tables S3–S6.

Corpus Segment	Evidence Use in Main Review	Detailed Coding
AI, phenotyping and validation-method support [13–34]	Defines sensor, imaging, ML, workflow and validation boundaries.	S1: AI subset and validation audit
Molecular, omics and mechanism evidence [35–64]	Links visible phenotypes to candidate regulatory, metabolic, genomic and rhizosphere mechanisms.	S1: omics and mechanism tags
Intervention evidence [65–96]	Maps rootstocks, grafting, biostimulants, microbial treatments, nanomaterials and signal molecules.	S1: intervention maturity coding
Crop-specific physiology and agronomy I [97–112]	Supports crop-specific response interpretation across lettuce, tomato, cucumber, grapevine and citrus.	S1: crop and endpoint tags
Crop-specific physiology and agronomy II [113–127]	Adds potato, grapevine, cucumber, melon, pepper and eggplant physiology or regulatory evidence.	S1: crop and endpoint tags
Crop-specific physiology and agronomy III [128–142]	Covers drought–salinity contrasts, rootstock studies, nanoparticles, hormones and cultivar variation.	S1: crop and intervention tags
Crop-specific physiology and agronomy IV [143–157]	Extends citrus, tomato, strawberry, eggplant, pepper, grapevine and microbial/field-context evidence.	S1: crop and mechanism tags
Crop-specific physiology and agronomy V [158–172]	Completes the retained corpus with compound stress, rootstock, genotype, salinity–drought and cultivar-response evidence.	S1: final corpus audit

The evidence map distinguishes direct from supporting evidence and avoids using supporting-method papers as proof of crop-specific salt tolerance. Direct evidence required a salinity, salt–alkali or closely related stress treatment applied to a horticultural crop, rootstock or crop-relevant system, with physiological, biochemical, ionomic, omics, microbial or agronomic endpoints. Supporting evidence comprised broader phenotyping, sensing, machine-learning and workflow papers that inform measurement or validation standards but do not, on their own, demonstrate crop-specific salinity tolerance.

The candidate log contained 542 unique DOI-bearing records. A curated core of 160 peer-reviewed journal articles was assembled to support the manuscript's biological, intervention, sensing and validation claims. The remaining 382 records remained in the candidate log but were not selected for core citation because they were outside the target crop/stress scope, provided indirect methodological support beyond the review boundary, overlapped with a more directly relevant source for a peripheral illustrative role, or had source/type ambiguity. The 69 records in the overlap category met the broad topic scope but were not selected to duplicate a peripheral illustration already supported by a retained source. This was a core-citation selection decision, not a systematic-review eligibility exclusion or a scientific-quality judgement. The category cannot establish that retained and nonselected records are scientifically equivalent or that contradictory evidence is absent. The 160-paper corpus is therefore a curated citation set, not an eligible-study denominator. These disposition counts document only the article's internal evidence-map

workflow and are not used to estimate field prevalence, study quality, intervention efficacy or model superiority. Of the 160 core records, 22 were assigned to the AI, phenotyping and validation-method segment. Figure 2 reports corpus construction and the associated audit trail.

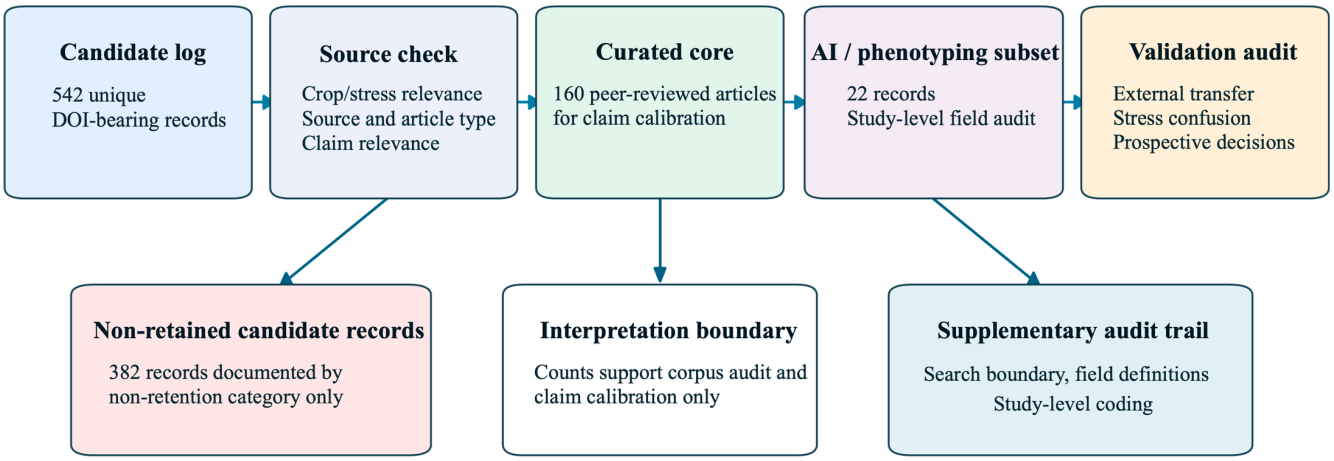

Figure 2. Evidence-map corpus construction and audit trail. The diagram documents how the DOI-bearing candidate log informed the curated core corpus and the AI/phenotyping validation audit. Counts describe the internal evidence-map workflow and are used only for claim calibration. The corresponding supplementary audit trail is provided in Supplementary Information S1 (Tables S1–S7).

Each retained study was tagged by crop group, stress composition where available, developmental context, experimental scale, evidence type, intervention class, data modality, validation design and claim level. Claim levels distinguished descriptive association, internal prediction, external validation, mechanistic triangulation and prospective decision testing. For the 22 AI-, sensing- or phenotyping-relevant records, Supplementary Information S1 provides study-level information in Table S4A–C, covering crop/system, data stream, model or sensor modality, prediction or phenotyping target, validation unit, external transfer, stress-confusion testing, prospective decision testing, performance metrics, data/code availability and claim level. For the remaining non-AI corpus, coding was limited to the biological and intervention evidence needed for narrative claim calibration, rather than full extraction of model-performance metrics.

Figure 3 summarizes the publication-year distribution, overlapping evidence tags, and main crop or methodological focus of the 160-paper core corpus.

The AI/phenotyping subset was audited separately because it carries the highest risk of evidence inflation. For denominator reconciliation, each of the 22 records was assigned one primary category according to the methodological role for which it is cited; secondary modalities remain listed in Supplementary Table S4A. The mutually exclusive primary categories are 14 image/fluorescence phenotyping records, five explicit ML/AI-method records, one remote/hyperspectral record, one agentic-workflow record and one non-AI physiological-support record. The 6/22 explicit ML/deep/agentic result is a nested analytical flag rather than a sixth category: it comprises the five explicit ML/AI-method records (refs. [21,24,27,29,34]) plus the agentic-workflow record (ref. [33]). Four records directly tested salinity- or water-stress AI/sensor phenotyping in a crop-relevant system; none of the six explicit-AI records externally validated a salinity-specific AI model; one record directly tested salt-versus-drought stress confusion; and none of the 22 records reported a prospective AI-guided intervention trial [13–34]. Table 2 therefore functions as a validation-risk audit, not as a ranking of model quality. These counts support a claim about evidence maturity, not model superiority.

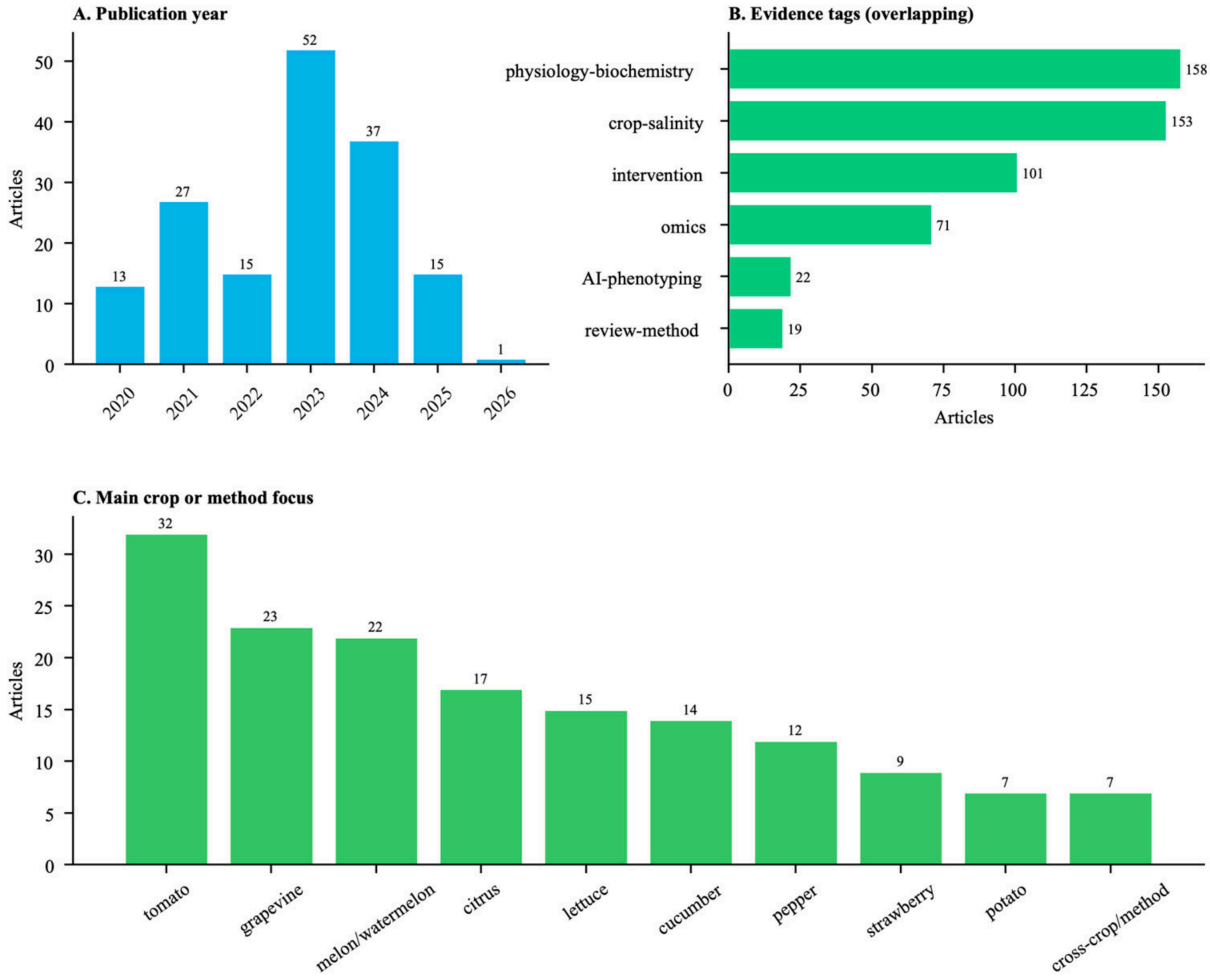

Figure 3. Evidence profile of the 160-paper core corpus. Evidence tags overlap because one article can contribute simultaneously to physiology, omics, intervention and AI-method evidence. Counts indicate evidence availability, not effect size or certainty.

Table 2. AI/phenotyping validation audit supporting the claim that decision-grade AI evidence remains scarce.

Audit Dimension	Operational Coding	Result	Interpretation	Qualifying/Reference Basis
AI/phenotyping-relevant subset	Core-corpus records in the AI, phenotyping and validation-method segment, including conventional non-AI physiological support used to define claim boundaries.	22/160	AI is important to the review question but is not the dominant direct evidence base.	Full subset in Supplementary Information S1, Tables S3 and S4A–S4C; representative sources: [19,21,24,29,33].
Explicit ML/deep/agentic AI	Machine learning, deep learning, edge intelligence, review-level AI analytics or multi-agent AI stated as central method or workflow.	6/22	Most AI-relevant records support measurement or workflow standards rather than full decision systems.	Qualifying records: [21,24,27,29,33,34].
Direct salinity AI/sensor phenotyping	Salinity- or water-stress treatment plus image, fluorescence, hyperspectral, sensor or ML phenotype endpoint in a crop or crop-relevant system; broad reviews excluded from the count.	4/22	Direct evidence exists but remains too sparse for broad management claims.	Qualifying examples: [19,21,24,31].

Table 2. *Cont.*

Audit Dimension	Operational Coding	Result	Interpretation	Qualifying/Reference Basis
External salinity-model validation	Test of a salinity-specific AI model on an independent dataset beyond the original experimental split and acquisition context.	0/6 explicit-AI records	No study met the strict external salinity-model definition; transfer and deployment claims remain unsupported.	No qualifying study identified.
Stress-confusion testing	Explicit salt-vs-drought or salt-vs-other-stress discrimination.	1/22	Most models do not yet show that salt stress is separated from visually or physiologically similar stresses.	Qualifying example: [21].
Prospective decision trial	AI-guided intervention tested prospectively against a management or experimental baseline.	0/22	No reviewed AI subset record supports autonomous intervention recommendation.	No eligible study identified.
Reusable benchmark metadata	Crop, genotype, stress composition, growth stage, imaging/sensor protocol and validation split sufficiently specified for transfer testing.	Heterogeneous	Benchmark-quality datasets and consistent metadata are needed before strong cross-study AI claims are credible.	Useful partial sources: [19,21,24,31,33].

3. Salinity Biology and Crop-Specific Evidence Signals

Salt stress produces interacting constraints rather than a single uniform response. The osmotic phase reduces water uptake, leaf expansion, stomatal conductance and carbon gain before large tissue Na^+ or Cl^- accumulation is necessarily detectable. The ionic phase reflects Na^+ and Cl^- accumulation, impaired K^+ retention, disrupted Ca^{2+} signalling, membrane leakage and progressive photosynthetic inhibition. Because these phases overlap in time and vary by organ, growth stage and crop architecture, mechanistic claims must remain crop-, organ- and stage-specific.

Most reviewed studies measured biomass, leaf area, root morphology, gas exchange, chlorophyll fluorescence, relative water content, membrane leakage, malondialdehyde, proline, soluble sugars, antioxidant enzymes, tissue ions and yield–quality traits [16,18,20,22,26,67,113,137,172]. These endpoints are informative but not interchangeable. Elevated proline may indicate osmotic adjustment, cellular injury or delayed development; antioxidant activity may indicate protection or a stronger oxidative challenge; and lower shoot Na+ may reflect exclusion, vacuolar sequestration, altered transpiration or reduced uptake by smaller plants.

Distinguishing genuine tolerance from injury or escape therefore requires complementary measurements. A defensible interpretation should connect growth or image signals with at least some combination of tissue Na^+ and Cl^-, K^+/Na^+ ratio, osmotic potential, stomatal conductance, chlorophyll fluorescence, ROS or antioxidant markers, root hydraulic traits, yield or quality, and recovery after stress removal. Without these convergent measurements, AI models risk learning treatment labels rather than salinity physiology.

Crop-specific biology determines which proxy traits are worth modelling. In leafy vegetables, canopy expansion and marketable biomass sit close to the production target itself. In grapevine and citrus, rootstock-mediated Na^+ or Cl^- exclusion, perennial ion accumulation and scion–rootstock compatibility are central [14,54,55,75,129,143,171]. In fruiting vegetables, early fluorescence, root-trait or omics signals become useful only when linked to later yield, quality, recovery or greenhouse-management context [11,12].

4. AI as a Measurement and Evidence-Integration Layer

AI enters salinity research through several distinct routes that should not be pooled indiscriminately: image-based phenotyping, optical sensing, fluorescence and hyperspectral measurement, omics analytics, remote sensing and integrated decision-support workflows. RGB and root images, thermal data, fluorescence, hyperspectral reflectance, transcriptomes, metabolomes, ionomes and microbiome profiles all generate useful signals, but each supports a different level of inference [19,24,27–29,33,34].

The main methodological danger is endpoint substitution. Images and spectral indices can be acquired cheaply and repeatedly, whereas yield, fruit quality, postharvest performance, tissue ion content, and recovery are slower and more costly to measure. A model that detects early stress is valuable only when its claim is explicitly limited to detection, or when the proxy traits it relies on are explicitly linked to agronomic outcomes [19,21,24,31].

Each data stream carries its own claim boundary. RGB or root images can reveal differences in growth or morphology, but not ion homeostasis. Fluorescence and hyperspectral data can support early detection under a clearly stated protocol, but not robust diagnosis across all compound stresses. Omics models can prioritize candidate pathways, but cannot establish causal regulation without perturbation experiments, independent validation, or convergent physiological evidence [36,37,46,57,72].

Standard computer-vision assumptions require particular caution in plant-stress biology. Repeated images or temporal observations from the same biological unit can create direct train–test leakage, as the study-level designs in refs. [19,21,24] illustrate. In ref. [21], five-fold cross-validation was applied to 240 temporal observations derived from 48 pots, but pot-grouped partitioning was not reported. In ref. [24], a random 80/20 partition and repeated 10-fold cross-validation were reported, but grouping by recombinant inbred line and repeated time point was not specified. Their performance estimates are therefore treated here as internally exploratory and potentially optimistic, not as deployment evidence. Technical replicates, tray or chamber effects, acquisition date, lighting background, preprocessing before partitioning and full-dataset feature selection create additional acquisition-context leakage risks emphasized in the sensing and phenotyping literature [27–29]. A rigorous study should therefore split by plant or genotype for internal biological claims and by experiment, date, sensor, site or production system for the corresponding transfer claim; workflow papers such as ref. [33] are used here only to support auditable task separation, not salinity-model validation.

Label quality is often the weaker link, not model architecture. In many datasets, "salt stress" denotes treatment assignment rather than a validated physiological state. Stronger labels would combine treatment metadata with leaf Na^+ or Cl^- content, K^+/Na^+ ratio, fluorescence decline, gas exchange, osmotic potential, yield penalty, or recovery time [19,21,24,31,119,171].

Modelling should begin with the intended claim. Early detection requires earlier time points and independent plants, with repeated observations kept within one split [19]. Stress diagnosis requires explicit comparison with biologically similar non-salt stresses [21], whereas genotype ranking requires validation on unseen genotypes or trials [24]. Mechanism claims require alignment with ions, ROS, hormones or omics, and intervention recommendation requires prospective testing against a decision baseline. Model complexity is secondary to validation design; workflow evidence [33] is treated as methodological support rather than crop-specific validation. Figure 4 translates this claim hierarchy into a validation ladder.

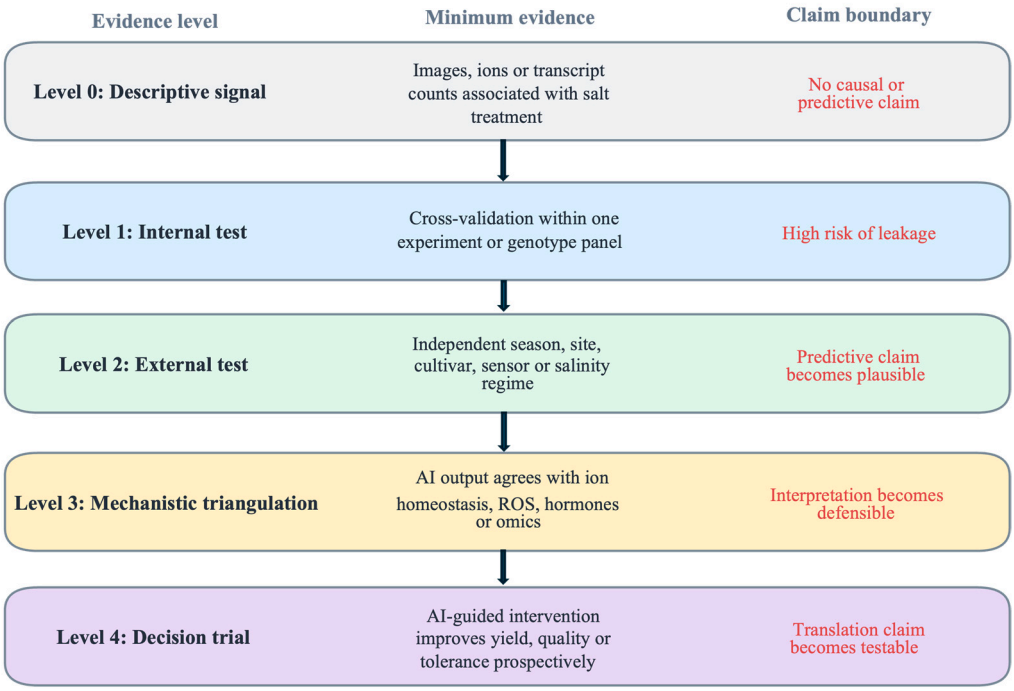

Figure 4. Validation ladder for AI claims in horticultural salinity research. Stronger biological and translational claims require external tests, mechanistic triangulation and prospective decision trials.

The validation ladder is a claim-control device. Level 0 and Level 1 studies remain useful when framed as descriptive or internal phenotyping evidence, as illustrated by the internal designs in refs. [21,24]. External-transfer, mechanistic and prospective decision levels are proposed requirements for stronger claims rather than observed properties of the current corpus. The goal is not to punish early studies but to prevent internal accuracy from being sold as deployment readiness.

5. Multi-Omics and Knowledge-Structured Inference

Multi-omics studies bridge visible phenotypes and cellular mechanisms by linking ion transport, osmoprotection, antioxidant regulation, photosynthesis, hormone pathways, cell-wall remodelling, aquaporins, transcription factors and rhizosphere processes [36–38,42,46–49,57,59,72,103,114,163]. They define the feature space that future AI systems should use, but they also expose the danger of naive feature selection.

The useful role for AI is not to discover tolerance de novo from sparse, high-dimensional matrices, but rather to organize candidate mechanisms, test whether features remain stable across genotypes or time points and render underlying assumptions visible. Omics-informed AI should rank pathways for confirmation, not replace physiological interpretation [34,36,37,46,57,62,72].

Small sample size relative to feature dimensionality remains a major risk. A transcriptome classifier may appear to separate treatment from control while having, in fact, learned batch structure, tissue age, or sampling time. Feature importance should therefore be checked across resampling schemes, normalization choices, genotypes, stress durations, and the biological direction of the effect [37,46,57,59,62,103,111,114].

Knowledge graphs and mechanism-constrained models are particularly promising because they encode prior relations among Na^+ exclusion, K^+ retention, ROS, ABA, ethylene, auxin, aquaporins, photosystem impairment, root architecture, and compatible solutes [34,36,46,57,72,91,147]. Even a simple graph linking crop, cultivar, dose, duration, tissue, intervention, response direction, and outcome quality would help surface contradictions rather than smoothing them away.

6. Intervention Evidence and Translational Maturity

The intervention literature is rich but uneven in maturity. Rootstocks and grafting offer the clearest translational logic because they are durable and already embedded in horticultural production, but they remain genotype-, scion-, site- and management-dependent [13,31,54,73,75,162]. Microbial inoculants are deployable but strongly conditioned by rhizosphere and substrate context [43,70,71,82]. Plant-derived biostimulants can improve selected endpoints, but responses vary with product, crop, cultivar and dose [41,84,88]. Nanomaterial studies report strong short-term responses, but the reviewed experiments provide limited evidence on dose transfer, environmental fate or regulatory readiness [44,53,74,85]. Signal molecules can also improve stress markers, but recovery dynamics and long-term performance remain incompletely tested [16,39,45,67,79].

AI should first triage existing evidence rather than recommend interventions autonomously. It can help identify where evidence for a given crop, stress type, endpoint, and intervention is dense enough to support synthesis, and where it remains confined to isolated case studies [27–29,33,34,50]. Figure 5 visualizes this uneven crop-by-intervention evidence density. Tomato, lettuce, citrus, grapevine, strawberry and melon do not have equal evidence maturity, so they should not receive equal translational confidence.

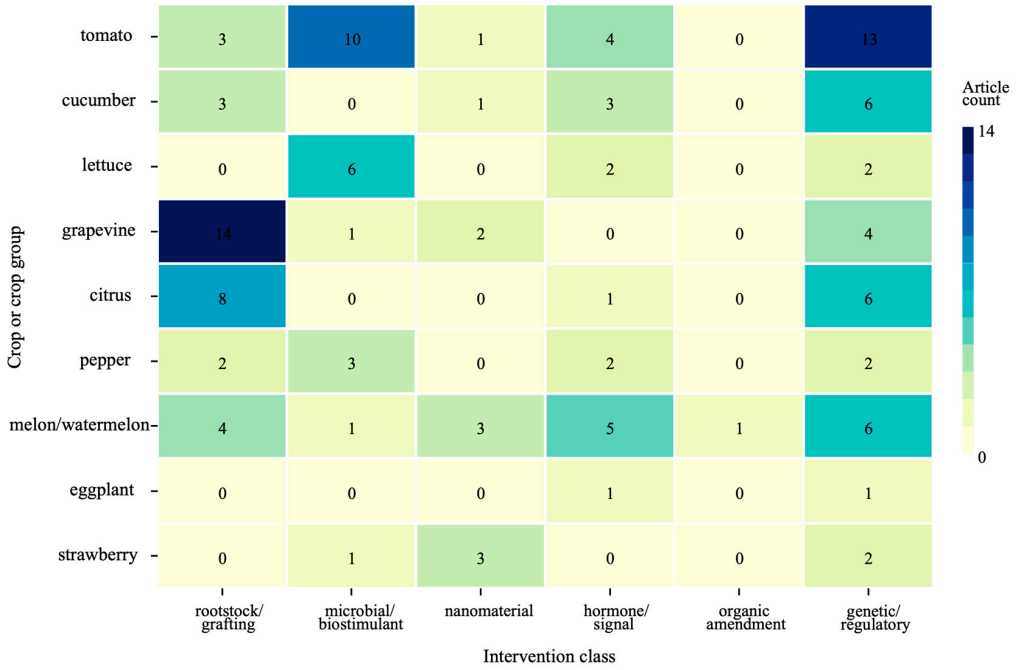

Figure 5. Crop-by-intervention evidence density in the reviewed literature. Counts indicate article co-occurrences in the evidence map; they do not indicate effect size, certainty or management readiness.

Rootstocks and grafting are not simply another input class: they can alter Na^+ and Cl^- transport, K^+/Na^+ balance, hydraulic function, root architecture, photosynthetic stability, and root-zone interactions. Their usefulness depends on scion–rootstock compatibility, stress duration, ion species, substrate, growth stage, and production target [55,83,86,95,96,131].

Biostimulants, microbial inoculants and nanomaterials introduce different sources of uncertainty. Protein hydrolysates and seaweed-derived biostimulants can improve selected physiological endpoints, but the evidence is often product-, cultivar-, dose- or duration-specific [41,84,88]. Microbial treatments, including *Bacillus* and mycorrhizal inoculants, show context-dependent benefits shaped by substrate and rhizosphere conditions [43,70,71,82]. Silicon- and selenium-based formulations modify antioxidant, ion-balance and photosynthetic responses, but transferability remains limited by short experi-

mental windows and incomplete dose assessment [74,81,138,140]. Metal-oxide nanoparticles, graphene oxide nanomaterials and hybrid lipid nanoparticles require separate toxicity and environmental-fate evaluation [44,53,85,92]. Biochar and related carbon amendments may alter yield and rhizosphere responses, but the evidence remains intervention- and production-system-specific [35,69].

Mechanistic maturity also differs among intervention classes. Rootstock effects should be interpreted through ion exclusion, vacuolar sequestration, K^+/Na^+ maintenance, aquaporin-mediated hydraulic conductance, hormonal signalling, photosynthetic stability and recovery after stress removal. Microbial and biostimulant effects require evidence for rhizosphere modification, nutrient uptake, oxidative regulation and persistence across substrates rather than short-term endpoint improvement alone.

For these interventions, AI is most useful when it models heterogeneity, failure cases, and dose–response relationships. A toxicity-aware response surface with explicit uncertainty boundaries is far more informative than a binary classifier that merely separates treated from untreated plants after the fact; negative results and cases of non-transfer are especially valuable for model calibration [27–29,33,34,50,53,138,140].

The next experimental step is response-surface design. AI can help select salinity doses, genotype–intervention combinations, scion–rootstock pairings and sampling times that avoid ceiling effects and reveal nonlinear windows. Table 3 translates the intervention evidence into maturity classes using five criteria: commercial embedding, mechanistic plausibility, durability across stress duration, transfer across genotype or production system, and unresolved safety or regulatory uncertainty. This would move the field beyond binary treatment–control studies toward designs that are more useful for growers and breeders [12,50,53,73,138,140,162].

Table 3. Translation maturity of major salinity-intervention classes and AI endpoints worth modelling.

Intervention Class	Translation Maturity	Strongest Evidence Signal	AI-Relevant Endpoint	Main Failure Mode
Rootstocks and grafting	Commercially embedded but genotype- and site-dependent.	Ion exclusion, hydraulic stability and durable scion–rootstock interactions [13,54,73,75,162].	Genotype-by-salinity response surfaces and yield–quality trade-offs.	Overgeneralizing from one scion–rootstock combination.
Microbial inoculants and biostimulants	Greenhouse promising; field establishment variable.	Root-zone modulation, antioxidant activation, nutrient uptake and partial yield rescue [36,43,70,77,84].	Treatment-response heterogeneity and failure-case prediction.	Substrate context and microbiome context determine transfer.
Nanomaterials	Mechanistically plausible but regulatory and dose–response maturity low.	Antioxidant defence, ion balance, photosynthetic protection and priming [44,53,74,85,138].	Toxicity-aware dose–response modelling.	Positive short-term physiology may not equal safe agronomic deployment.
Signal molecules and osmoprotectants	Experimental; timing- and concentration-sensitive.	ABA/ethylene/NO/H2S/melatonin/salicylic signalling and osmolyte balance [16,26,67,79,115].	Temporal response trajectories and recovery prediction.	Biochemical marker increases may encode injury rather than tolerance.
Genetic and regulatory approaches	Discovery-stage to breeding-candidate level.	Transporters, transcription factors, aquaporins, polyploidy and gene-editing candidates [15,61,64,89,160].	Candidate prioritization across omics and phenotypes.	Gene-level evidence often stops before agronomic validation.

Transferability should be treated as a set of separate tests rather than a single claim. Evidence may transfer from one cultivar to another, from one scion–rootstock combination to another, across related species, across seasons or sites, across sensors, or from low-tech

to high-tech greenhouse systems. A model or intervention can pass one transfer boundary while failing another.

7. Reporting Standards, Failure Modes and Research Priorities

The central reporting rule is straightforward: every AI claim should be paired with the weakest condition under which it has been tested. Internal cross-validation supports internal discrimination, not field-level generalization [21,24]. In refs. [21,24], grouping of repeated temporal observations by pot or recombinant inbred line was not reported, so leakage through non-independent observations cannot be excluded. Repeated images or measurements from the same plant, pot or genotype must remain within one partition [19]. Training a model to distinguish salt-treated from control plants does not, by itself, support discrimination from drought, heat, nutrient deficiency, hypoxia, alkalinity or disease; among the audited subset, only ref. [21] explicitly compared salt with drought.

Reporting standards should specify the salinity protocol, plant age, developmental stage, cultivar, rootstock, sampled organ, tissue position, sampling time, number of independent plants, biological replication, technical replication, experimental unit, imaging or sensor protocol, preprocessing steps, data-split strategy, leakage controls, class balance, external-test definition, uncertainty estimates and code or model availability where possible. Table 4 turns these requirements into a minimum reporting checklist. Omics studies should add accession, tissue and time point, normalization, batch correction, multiple-testing procedure and validation criteria [36,37,46,57,72].

Table 4. Minimum reporting checklist for AI-enabled salinity studies in horticultural crops.

Checklist Item	Minimum Reporting Expectation	Why it Matters	Reviewer Decision if Absent
Stress protocol	NaCl or mixed-salt composition, EC, duration, timing, substrate and irrigation context.	Defines the biological state being modelled.	Downgrade all generalization claims.
Biological metadata	Cultivar, rootstock, growth stage, tissue, replication and environmental conditions.	Prevents hidden biological and environmental confounding.	Require clarification or reanalysis.
Data split and leakage controls	Plant-level or experiment-level separation; no image/time-point leakage; external test if claiming transfer.	Separates memorization from prediction.	Reject broad AI performance claims.
Mechanistic alignment	At least one convergent physiological, biochemical, ionomic or omics layer for mechanism claims.	Prevents accuracy from being misread as understanding.	Restrict conclusion to detection.
Uncertainty and negative results	Confidence intervals, failure cases, stress confusions and boundary conditions.	Makes the model useful outside ideal conditions.	Treat as exploratory only.
Reproducibility	Code, model, raw/processed data or clear reason for restrictions.	Allows verification and reuse.	Flag as incomplete for decision-grade claims.

Data availability deserves particular attention. Study-level data or Supplementary Material was available in some audited records [19,21,24], but images, growth measurements, ion data, omics tables and environmental metadata were not consistently released as one integrated reusable dataset. Workflow and data-organization papers [33,34] support the need for structured provenance, but they are not counted as direct salinity-model evidence. Without standardized metadata, future AI systems risk reproducing narrow, study-specific validation patterns.

Auditable workflows can usefully separate planning, trait extraction, visualization, model checking and human review [33,34]. Figure 6 shows how this separation can be adapted to salinity phenotyping. Its value is not autonomous interpretation but structured accountability: requesting missing metadata, flagging leakage, comparing outputs against physiological priors and documenting uncertainty.

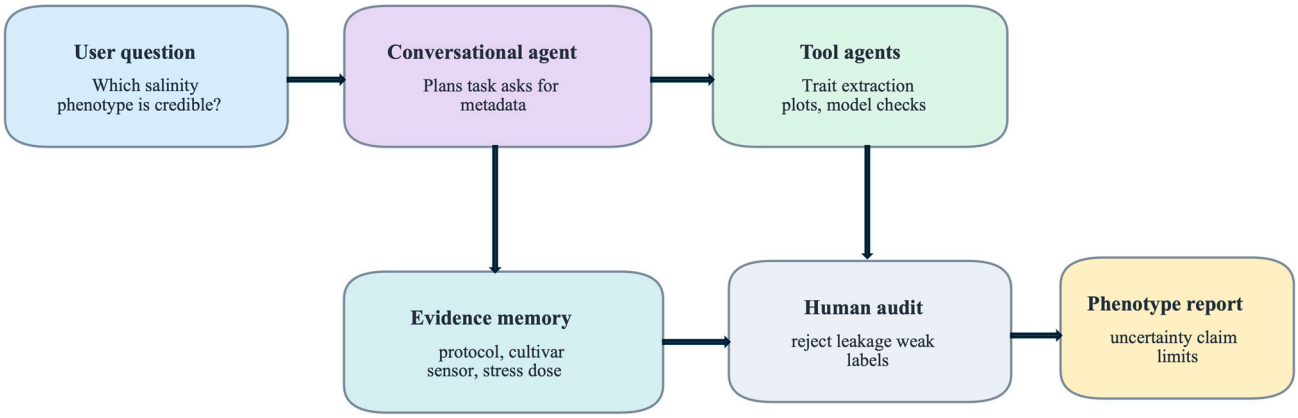

Figure 6. Proposed auditable AI workflow for salinity phenotyping. The workflow is redrawn as an original conceptual figure adapted from task-separated plant phenotyping architectures.

Commercial deployment requires evidence beyond biological detection and internal model accuracy. A deployable system must address sensor cost, camera or sensor mounting, calibration frequency, lighting variability, computational requirements, maintenance, data connectivity, compatibility with irrigation and fertigation infrastructure, grower usability, technical support and failure consequences.

False positives can trigger unnecessary leaching, fertigation changes or intervention costs, whereas false negatives can allow irreversible yield or quality losses. Deployment claims should therefore distinguish laboratory prototypes, advisory decision-support tools and autonomous commercial systems. None of the reviewed AI subset provides enough prospective, economic or regulatory evidence to support autonomous salinity management.

Six failure modes recur across the evidence map: data leakage, weak labels, stress confusion, intervention overgeneralization, field-transfer failure and premature commercialization. The AI validation risks are illustrated by the study-level evidence in refs. [19,21,24] and by the methodological workflow boundary in ref. [33]. Intervention overgeneralization and short experimental windows are separately supported by refs. [31,50,108,138,163,170]. These are not minor technical issues; they explain why internal accuracy or a short-term rescue effect cannot on its own be treated as decision-grade salinity evidence.

This review has six material limitations. First, the source log lacks database-specific syntax, searched fields, per-database hit counts, language and publication-type restrictions, and a bounded Google Scholar screening depth; therefore, this review cannot support a database-executable rerun, PRISMA-style search reproducibility or exhaustive literature-coverage claim. Second, evidence coding was conducted by one author, and no independent duplicate coding was performed. Third, treatment effects and model-performance estimates were not pooled, so model or intervention classes could not be ranked by average efficacy. Fourth, the 22-record AI, phenotyping and validation-method segment is small and methodologically heterogeneous. Fifth, none of the six explicit-AI records externally validated a salinity-specific AI model, and none of the 22 records conducted a prospective AI-guided decision trial. Sixth, the evidence cannot establish economic feasibility, field robustness, cultivar-to-cultivar transfer, cross-species applicability or autonomous salinity management.

Direct AI-specific salinity evidence remains a minority of the corpus. Many AI, sensing and workflow papers function as methodological support rather than direct evidence, so the frameworks proposed here should be read as standards for future evidence generation rather than proof that current systems have already reached decision-grade performance.

Initial evidence coding was performed by one author and then converted into the auditable operational categories in Supplementary Information S1. The coding supports claim calibration within this article and is not used for prevalence inference or pooled effect estimates. Nevertheless, source-verification notes, non-retention categories, preserved query expressions and the AI-subset matrix reduce, but do not eliminate, subjective judgement. Independent screening and evidence coding by a second author would be required before stronger prevalence or efficacy claims could be made.

The next phase of research should design studies around explicit claims: detection, severity estimation, genotype ranking, mechanism inference, intervention recommendation or commercial decision support. External tests should match the prediction claim and experimental unit, as the limitations of the internal designs in refs. [21,24] make clear; workflow evidence such as ref. [33] supplies audit structure rather than external validation. Mechanistic interpretation should be constrained by convergent physiological and omics evidence [36,37,57,72], while transfer across greenhouse technology levels requires explicit production-system context [12].

Factorial stress testing is urgently needed. Real horticultural systems combine salinity with heat, drought, high vapour-pressure deficit, nutrient imbalance, alkalinity, or pathogen pressure, and a single-factor NaCl model may fail precisely when saline irrigation coincides with heat or nutrient stress [21,31,32,98,108,138,159,163,170].

Experiments should also move toward dose–response and response-surface designs. AI can help select informative doses, prioritize sensors that predict later yield penalties, and identify genotype-by-intervention interactions—but only if failure cases and boundary conditions are consistently reported [50,53,73,138,140,162].

Cross-study learning requires shared metadata, including crop, cultivar, rootstock, growth stage, salt composition, electrical conductivity (EC), substrate, irrigation context, greenhouse technology level, sensor calibration, sampling time, endpoint definition and economic or management target. The audited sensing and modelling studies illustrate the need for stable experimental-unit and sensor metadata [19,21,24], and workflow evidence supports explicit provenance [33]. Crop, rootstock and production-system studies separately show why biological transfer metadata are necessary [11,12,54,119,171].

Review writing should be held to the same standard it asks of primary studies. Search terms, inclusion logic, evidence weighting, citation provenance, and figure licencing must all be transparent. The safest high-level claim is not that AI will solve salinity stress, but that it can improve how salinity evidence is measured, compared, and challenged.

8. Conclusions

The reviewed literature supports a cautious but constructive conclusion. Established biological evidence shows that horticultural salinity responses involve recurring processes, including osmotic limitation, ion homeostasis, K^+ retention, ROS control, photosynthetic protection, hormone signalling, root architecture, root hydraulics, microbiome shifts and metabolic reprogramming. Their relative importance differs by crop, cultivar, developmental stage, organ, rootstock and production system.

The limited AI subset supports a narrower conclusion. Current evidence does not justify claims that AI can independently manage salinity stress. Most AI/phenotyping studies remain at the level of descriptive phenotyping, internal prediction or workflow support. Among the six explicit-AI records, none externally validated a salinity-specific AI

model; only one explicitly distinguished salinity from drought. No prospective AI-guided decision trial was identified, and the evidence is insufficient for economic claims.

The defensible path forward is hybrid and claim-limited. AI should function as an inference-support layer embedded within salinity biology, not as a replacement for physiological reasoning. Claims regarding early detection, phenotype stratification, evidence triage and experiment prioritization are defensible when metadata, validation split and biological endpoints are transparent. Causal, management, cross-species or autonomous-control claims based on internal accuracy alone should remain outside the conclusions that the current evidence can support.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/horticulturae12080921/s1. Supplementary Information S1: Table S1. Review design and search-source record. Unavailable fields are reported as not preserved and were not reconstructed retrospectively; Table S2. Candidate-log disposition and core-citation selection rationale. Categories describe evidence-map construction, not formal eligibility exclusion or scientific quality; Table S3. AI/phenotyping validation audit. Counts are based on the 22-record AI-, sensing- or phenotyping-relevant subset; Table S4A. Study identity, modality and evidence role. Review/method papers are not treated as original model validations; Table S4B. Biological design and validation strategy. Grouping omissions in refs. [21,24] are retained as validation-risk findings; Table S4C. Target, metrics, availability and claim boundary. External validation refers only to an independent salinity-specific model test beyond the original split and acquisition context; Table S5. Minimum reporting checklist for reusable salinity AI/phenotyping studies. These are proposed reporting requirements, not evidence that current systems are deployment-ready; Table S6. Operational field definitions and inference boundaries. Definitions were applied to prevent internal validation, repeated measurements and review papers from being upgraded to external model evidence; Table S7. Discovery phrases preserved in the original source log (search date: 27 May 2026). These are the 87 phrases exactly as recorded. They are not database-specific executable search strings; database syntax, searched fields, language restrictions, publication-type restrictions and per-database hit counts were not preserved.

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Abbreviations

The following abbreviations are used in this manuscript:

ABA	Abscisic acid
AI	Artificial intelligence
CNN	Convolutional neural network
DEG	Differentially expressed gene

EC	Electrical conductivity
ML	Machine learning
NO	Nitric oxide
PGPB	Plant-growth-promoting bacteria
ROS	Reactive oxygen species
UAV	Unmanned aerial vehicle
XAI	Explainable artificial intelligence

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