



Review Article

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ARTIFICIAL INTELLIGENCE-ASSISTED PRECISION HOMOEOPATHY: A GLOBAL RESEARCH FRAMEWORK FOR INDIVIDUALISED PRESCRIBING, BIOMARKER INTEGRATION AND N-OF-1 EVIDENCE GENERATION

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ABSTRACT

Background: Homoeopathy has historically emphasized individualisation, totality of symptoms and selection of the similimum rather than treatment based solely on diagnostic labels. Contemporary biomedical research, however, increasingly demands reproducible phenotyping, objective outcome measurement, transparent reporting and biologically testable hypotheses. The future of homoeopathic research therefore requires methodologies capable of preserving individualised prescribing while introducing rigorous tools from modern clinical science.

Objective: To examine how artificial intelligence (AI), structured clinical phenotyping, biomarker research, systems biology and N-of-1 trial methodology could be integrated into a contemporary research architecture for individualised homoeopathy.

Methodology: A narrative, literature-informed review was undertaken using published literature on clinical research in homoeopathy, high-dilution/basic research, artificial intelligence in medicine, precision medicine, N-of-1 methodology and international research-reporting standards. Global policy developments concerning evidence generation, safety, regulation, innovation and digital health in traditional, complementary and integrative medicine were also considered. The proposed framework was designed to remain compatible with individualised homoeopathic prescribing while improving reproducibility and scientific transparency.

Results: The current evidence base demonstrates a heterogeneous research landscape. Randomised trials and meta-analyses of individualised homoeopathy have produced findings that remain methodologically contested, with risk of bias and inconsistency limiting definitive conclusions. Basic research has reported physicochemical phenomena, including nanoparticulate findings in some highly diluted preparations, but such observations cannot by themselves establish clinical efficacy. Modern precision-medicine and AI methodologies offer an opportunity to transform the research question from a purely disease-centred model into a multidimensional investigation of patient phenotype, treatment selection, biological response and longitudinal outcome. A five-layer research architecture is proposed: structured digital case phenotyping; AI-assisted repertorial decision support; biomarker and systems-biology profiling; personalised N-of-1 evaluation; and federated real-world evidence generation.

Conclusion: The next phase of homoeopathic research should not depend on either uncritical acceptance or categorical dismissal. It should generate falsifiable, transparent and reproducible evidence while preserving the central research characteristic of individualised prescribing. AI should function as decision support rather than an autonomous prescriber. Biomarkers should be used to investigate patient stratification and response rather than to retrospectively justify treatment. N-of-1 methodology may provide an important bridge between individualisation and experimental rigor. This framework could position homoeopathic research within the broader global movement toward evidence-based, personalised and data-driven healthcare.

Keywords: Homoeopathy; Individualisation; Artificial Intelligence; Precision Medicine; N-of-1 Trial; Biomarkers; Systems Biology; Repertorization; Digital Health; Translational Research

INTRODUCTION

The central methodological challenge in homoeopathic research is also one of its defining clinical characteristics: individualisation.

In conventional therapeutic research, the intervention is commonly standardised before recruitment. A diagnostic category is identified, patients are allocated to a predefined intervention, and the effect of that intervention is subsequently measured. Individualised homoeopathy operates differently. The prescription is generated from the patient's complete symptom picture, including characteristic symptoms, modalities, concomitants, generals and other clinically relevant individual features. Consequently, the intervention may differ between two patients who share the same biomedical diagnosis.

This creates a fundamental research problem. The more faithfully a study attempts to reproduce individualised prescribing, the more difficult it becomes to standardise the intervention. Conversely, the more rigidly a prescription is standardised, the greater the possibility that the research design no longer represents authentic individualised homoeopathic practice.

The August 2026 issue of The Homoeopathic Heritage explicitly points toward a new direction involving precision medicine, systems biology, network pharmacology, metabolomics, transcriptomics, AI-assisted repertorization, biomarker-guided selection and rigorous whole-system clinical research. It further argues that future research should examine not only whether homoeopathy works, but also how it may work, for whom it may work best, and under which clinical circumstances [1].

The global research environment is also moving toward evidence-based and data-enabled approaches to traditional, complementary and integrative medicine. The World Health Organization Global Traditional Medicine Strategy 2025-2034 identifies research and evidence, safety and regulation, health-system integration, and innovation and technology as strategic priorities [2].

Therefore, the question for modern homoeopathic research is no longer simply whether classical principles can be repeated in conventional trial formats. A more scientifically productive question is: Can individualised homoeopathy be investigated using the tools of precision medicine without destroying the individualisation that defines the intervention? The present paper proposes that this is possible, but only through a deliberate methodological architecture.

AIM AND OBJECTIVES

Aim: To propose a scientifically rigorous research framework integrating artificial intelligence, structured individualised phenotyping, biomarker investigation and N-of-1 methodology for contemporary homoeopathic research.

- To examine the methodological limitations and opportunities within the existing homoeopathic evidence base.
- To evaluate the potential role of artificial intelligence in structured case analysis and repertorial decision support.
- To propose methods for integrating biomarkers, metabolomics, transcriptomics and systems-biology measures without replacing individualised clinical assessment.
- To describe an N-of-1 research model suitable for investigating individualised homoeopathic interventions.
- To establish a reproducible research pipeline that can generate individual-level as well as population-level evidence.
- To propose safeguards concerning algorithmic bias, privacy, informed consent, clinical accountability and responsible use of AI.

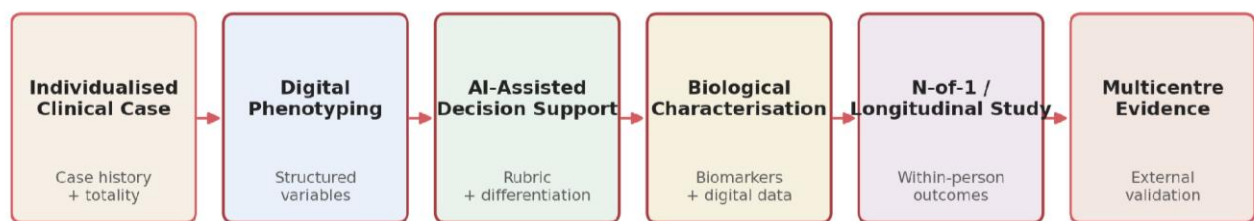
CURRENT STATE OF HOMOEOPATHIC RESEARCH

The modern evidence base for homoeopathy contains several distinct streams: clinical trials, observational studies, individual case reports, basic laboratory research, physicochemical investigations and methodological studies.

The clinical literature is heterogeneous. A systematic review and meta-analysis of randomised placebo-controlled trials of individualised homoeopathic treatment identified 32 eligible RCTs. The pooled evidence suggested a favourable direction for individualised treatment, but risk-of-bias concerns and study heterogeneity limited the strength of inference [3].

Other systematic reviews have also shown that interpretation depends strongly on study quality, comparator characteristics and whether the investigated intervention is individualised or protocolised [4,5]. A major implication follows: the existence of positive studies is not equivalent to proof of efficacy, and the existence of negative or inconclusive studies is not equivalent to proof of ineffectiveness under every clinical model.

The appropriate response is methodological improvement. The August 2026 issue provides a useful example in its prospective single-arm observational study of acute pharyngitis, which used a defined assessment tool, explicit eligibility criteria, scheduled follow-up and a transparent statement that larger controlled studies are needed [6].



Core principle: preserve individualisation while increasing transparency, measurement and reproducibility

Figure 1. Proposed translational pathway from an individualised case to multicentre evidence generation.

FROM CLASSICAL INDIVIDUALISATION TO DIGITAL PHENOTYPING

The classical homoeopathic case contains a large quantity of information. A comprehensive consultation may include the chief complaint, location, sensation and modalities, concomitants, physical generals, mental and emotional characteristics, sleep, appetite and thirst, thermal preferences, environmental sensitivities, past history, family history, laboratory findings and treatment response. Much of this information is unstructured.

A contemporary research system could convert the narrative case into a structured individual phenotype vector. The objective would not be to reduce the patient to a score, but to create a machine-readable representation that remains traceable to the original clinical narrative.

Domain	Examples of variables
Demographic	Age, sex, occupation, geography
Disease phenotype	Diagnosis, duration, severity, complications

Domain	Examples of variables
Symptom phenotype	Location, sensation, modalities, concomitants
General phenotype	Thermal state, appetite, thirst, sleep, energy
Psychosocial phenotype	Stressors, emotional state, coping patterns
Environmental phenotype	Climate, pollutants, allergens, occupational exposures
Laboratory phenotype	CBC, inflammatory markers, metabolic markers
Imaging phenotype	Radiological features where relevant
Treatment phenotype	Previous medication, response, adverse effects
Homoeopathic phenotype	Rubrics, repertorial hierarchy, remedy differentiation

ARTIFICIAL INTELLIGENCE-ASSISTED REPERTORIZATION

Artificial intelligence has already begun transforming medicine through pattern recognition, prediction, workflow support and analysis of large datasets. Contemporary guidance increasingly frames AI as clinician support rather than autonomous replacement, while emphasising the need to address bias, privacy, security, explainability and accountability [7,8].

In homoeopathic research, AI could be investigated in five specific roles.

- 1. Symptom Structuring:** Natural-language processing could identify symptom, location, sensation, modality, concomitant, temporal pattern, causative factor and intensity from clinical narratives.
- 2. Rubric Mapping:** AI could suggest candidate repertory rubrics from the clinical narrative. The system should display candidate rubrics and confidence rather than silently converting a narrative into a prescription.
- 3. Remedy Differentiation:** The system could compare candidate remedies across characteristic symptoms, modalities, generals, mental symptoms and materia-medica references.
- 4. Longitudinal Learning:** A patient response record could be analysed over time, linking initial phenotype, prescription, follow-up phenotype, treatment changes and outcomes.
- 5. Research Signal Detection:** Large datasets could be analysed for recurring patient-phenotype/remedy/outcome associations. Such associations should initially be treated as hypotheses, not established therapeutic facts.

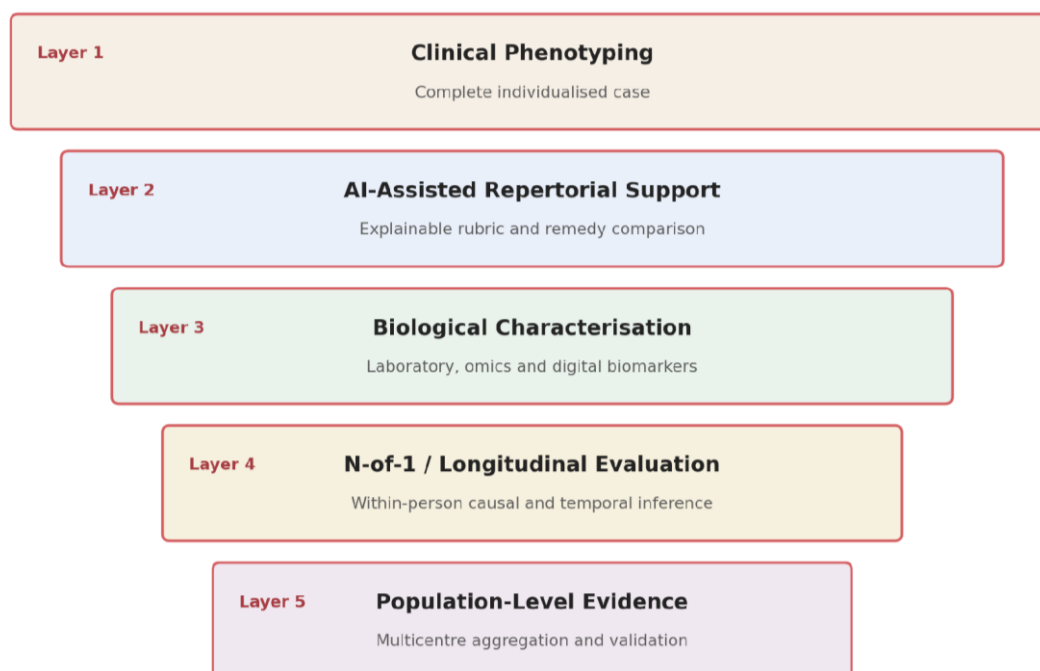


Figure 2. Five-layer architecture for precision homoeopathic research.

BIOMARKER INTEGRATION: FROM CLINICAL PHENOTYPE TO BIOLOGICAL PHENOTYPE

One major limitation of traditional clinical research is the separation between subjective clinical observations and biological measurements. A modern research programme can investigate both simultaneously, provided biomarkers are treated as research variables rather than retrospective proof of efficacy.

Possible biomarker domains include inflammatory markers, immune-cell profiles, metabolic markers, transcriptomic signatures, metabolomic signatures, microbiome features and digital biomarkers such as sleep, activity and heart-rate patterns.

The scientific question should therefore be: Does a reproducible biological phenotype correlate with treatment response, and can such a phenotype help explain heterogeneity among individuals? This is more testable than asking whether a biomarker proves that a particular remedy works.

BASIC RESEARCH AND THE PHYSICOCHEMICAL QUESTION

One of the most controversial areas of homoeopathic science concerns highly diluted preparations. Research has reported physicochemical findings in some high-potency preparations. Chikramane and colleagues reported nanoparticles of starting materials in extreme dilutions using transmission electron microscopy, electron diffraction and elemental analysis [9]. Subsequent research has investigated physicochemical changes associated with the preparation process, including trituration and succussion [10].

However, detection of physicochemical differences does not demonstrate clinical efficacy. A robust translational pathway should therefore separate three questions: whether a preparation can be analytically characterised reproducibly; whether a characterised preparation produces

reproducible biological effects under blinded experimental conditions; and whether those effects are related to measurable clinical outcomes.

PROPOSED PRECISION HOMOEOPATHY RESEARCH ARCHITECTURE

Layer 1: Individual Clinical Phenotyping: The physician conducts a complete individualised case, producing a structured patient phenotype.

Layer 2: AI-Assisted Clinical Decision Support: AI processes the structured phenotype and assists with rubric extraction, repertorial cross-checking, remedy differentiation and missing-data detection. The algorithm does not independently prescribe.

Layer 3: Biological Characterisation: When ethically and clinically justified, laboratory, omics and digital measures are collected to investigate biological heterogeneity.

Layer 4: Individual-Level Experimental Evaluation: N-of-1 methodology is used where repeated within-person assessment is appropriate.

Layer 5: Population-Level Evidence Generation: Individual-level findings are aggregated through multicentre datasets to test reproducibility and external validity.

N-OF-1 MODEL FOR INDIVIDUALISED HOMOEOPATHY

N-of-1 research is attractive for individualised medicine because repeated periods within the same patient may support inference about whether outcome changes are temporally associated with an intervention while accounting for between-person variability. The CENT reporting framework provides specific recommendations for individual and series of N-of-1 trials [11].

Patient selection should use predefined diagnostic and clinical criteria. Baseline assessment should capture symptom severity, functional status, quality of life, medication use and objective measures when appropriate. The intervention should then be documented in sufficient detail to allow replication of the decision process, while the exact repeated-period structure must be tailored to disease characteristics, reversibility, carry-over and ethical considerations.

For conditions in which repeated treatment withdrawal would be unsafe or scientifically inappropriate, alternative within-person designs should be considered rather than forcing an A-B-A-B structure.

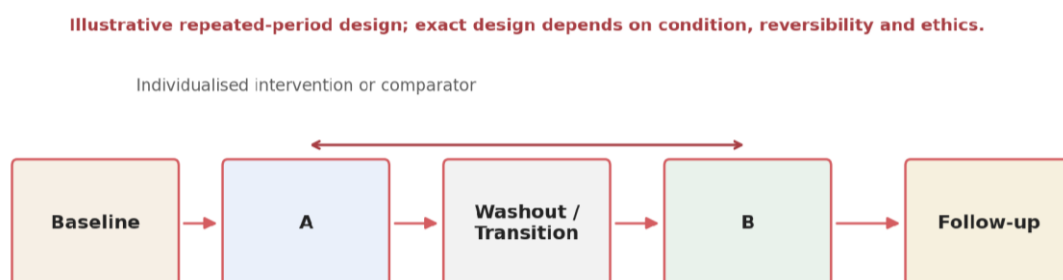


Figure 3. Conceptual repeated-period N-of-1 structure. Exact design should be disease-specific and ethically justified.

PROPOSED AI-ENABLED RESEARCH PIPELINE

A future multicentre programme could follow the sequence below:

- Patient consultation -> structured digital case -> phenotype extraction.
- AI-assisted rubric identification -> repertorial analysis -> physician remedy differentiation.
- Individualised prescription -> clinical and biomarker monitoring.
- N-of-1 or longitudinal evaluation -> outcome database.
- Population-level machine-learning analysis -> hypothesis generation -> prospective controlled validation.

The central principle is: AI may accelerate reasoning and improve documentation; it must not manufacture evidence.

Current research gap	Proposed advancement	Expected scientific benefit
Unstructured case narratives	Digital phenotyping	Reproducible case representation
Variable repertorization	AI-assisted reproducible decision support	Improved transparency
Subjective outcomes alone	Clinical + objective outcomes	Stronger outcome validity
Limited biological correlation	Biomarker profiling	Mechanistic hypothesis generation
Population-average trial designs	N-of-1 trials	Individual-level inference
Isolated case reports	Federated real-world database	Pattern detection
Retrospective hypothesis generation	Prospective validation	Reduced confirmation bias
Opaque AI models	Explainable algorithms	Auditability
Small institutional datasets	Multi-centre collaboration	External validity
Fragmented basic research	Standardised physicochemical protocols	Reproducibility

RESEARCH REPORTING STANDARDS

Future homoeopathic research should align its reporting practices with internationally recognised methodological guidance. Randomised trials should use CONSORT 2025, which supersedes CONSORT 2010 and provides a 30-item checklist plus a participant-flow diagram [12]. Trial protocols should follow SPIRIT 2025, which provides 34 minimum protocol items and incorporates open-science, patient-involvement, data-sharing and monitoring elements [13]. Observational studies should be reported according to STROBE [14]. Systematic reviews should follow PRISMA 2020 [15]. N-of-1 studies should incorporate the CENT reporting extension [11].

Homoeopathic manuscripts should additionally describe case-taking procedure, repertory used, repertorization strategy, remedy-selection rationale, potency, dosage, repetition, criteria for changing the prescription, concomitant conventional treatment, follow-up schedule and outcome instruments. This level of documentation would improve reproducibility without requiring that all cases be prescribed identically.

ETHICAL AND GOVERNANCE CONSIDERATIONS

Algorithmic bias: AI models trained on one geographical population, institution or prescribing school may reproduce the biases of the training dataset. Independent external validation is essential.

Explainability: A clinically useful model should show why a candidate rubric or remedy was suggested rather than returning an opaque probability score.

Privacy: Digital case-taking may contain highly sensitive health and psychological information; governance should include consent, de-identification, secure storage and controlled access.

Human accountability: AI should be treated as decision support, not autonomous treatment. Clinical responsibility remains with the appropriately trained physician.

Avoidance of circular validation: A model that learns historical prescribing patterns and then reproduces those same patterns cannot by itself validate the underlying therapeutic claims. External benchmarks and prospective validation are required.

PROPOSED MULTICENTRE RESEARCH PROGRAMME

Phase I - Data Standardisation: Participating centres establish a common electronic case-record format covering demographics, diagnosis, symptom phenotype, generals, repertorial data, remedy, potency, repetition, follow-up and objective outcomes.

Phase II - Retrospective AI Development: Historical de-identified cases are used to develop symptom extraction, rubric-mapping, remedy-differentiation and outcome-prediction tools. No clinical decision should initially depend on the model.

Phase III - Prospective Validation: New patients are enrolled prospectively. AI suggestions are recorded and evaluated against expert decisions, with attention to agreement, reproducibility, explainability, calibration and error patterns.

Phase IV - Clinical Outcome Studies: Validated decision-support tools are evaluated in pragmatic clinical research. At this stage the AI system becomes a research intervention rather than merely a technical experiment.

Proposed outcome matrix: Digital case-taking - completeness of phenotype capture, with time required as a secondary measure; AI repertorization - agreement with an expert panel, with reproducibility as a secondary measure; biomarker studies - biological change from baseline, with correlation to clinical response; N-of-1 studies - prespecified clinical outcomes, with quality of life as a secondary measure; cohort studies - longitudinal response, with exacerbation or medication use; multicentre studies - external validity, with centre-to-centre heterogeneity; AI validation - predictive performance, with bias and explainability.

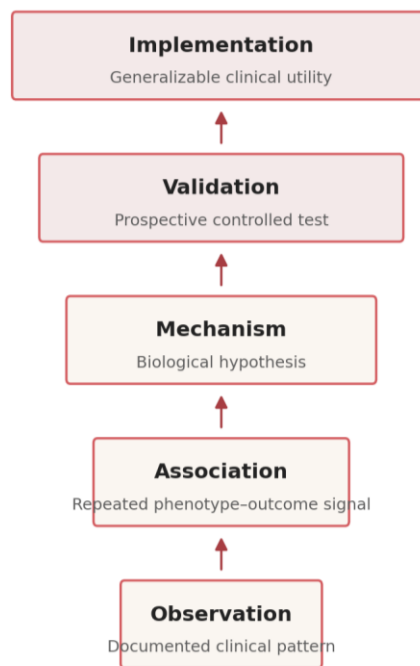


Figure 4. Evidence-maturity ladder from clinical observation to validated clinical utility.

DISCUSSION

The proposed framework represents a shift from conventional disease-centred research toward a multi-dimensional individual-centred research model. Its principal strength is conceptual compatibility with the defining principle of individualisation. Instead of forcing every patient with the same diagnosis into a single treatment protocol, the research dataset preserves patient-level heterogeneity.

However, individualisation cannot become a methodological exemption. A prescription should not become scientifically untestable simply because it is individualised. The challenge is therefore to operationalise individualisation without trivialising it.

Three separations are particularly important. First, clinical individualisation must be separated from research bias: a physician may individualise treatment, but the research process must document exactly how this occurred. Second, biological findings must be separated from clinical

claims: a laboratory observation may generate a mechanism hypothesis but cannot by itself establish efficacy in humans. Third, AI prediction must be separated from clinical validation: an algorithm may detect an association, whereas only appropriately designed prospective studies can establish clinical usefulness.

These distinctions are important because the homoeopathic evidence base has substantial heterogeneity in study designs, interventions and methodological quality [3-5]. The appropriate response is methodological escalation rather than defensive advocacy or dismissal.

CAN “PRECISION HOMOEOPATHY” BECOME A SCIENTIFIC DISCIPLINE?

The term precision homoeopathy should currently be regarded as a proposed research construct rather than an established biomedical category. For research purposes, it can be defined as an individualised therapeutic model that combines detailed clinical phenotyping with reproducible prescription documentation, objective outcome measurement and, where justified, biological and digital biomarkers to investigate heterogeneity of treatment response.

Under this definition, precision homoeopathy does not mean that a biomarker determines the remedy. Instead, clinical individualisation, biological characterisation and longitudinal measurement form the research unit. Modern precision medicine is fundamentally concerned with patient-level information to improve prediction, prevention and treatment. This provides a useful conceptual bridge for contemporary homoeopathic research [7].

LIMITATIONS OF THE PROPOSED FRAMEWORK

- This paper is a conceptual research framework rather than a clinical trial and therefore has not itself prospectively validated the proposed architecture.
- The availability, cost and standardisation of advanced biomarkers will vary among centres.
- AI models may amplify biases present in historical homoeopathic records.
- The reproducibility of individualised prescribing remains a significant methodological challenge.
- Physicochemical findings in highly diluted preparations remain insufficient to establish clinical efficacy.
- N-of-1 methods are not appropriate for every disease, particularly when withdrawal is unsafe or effects are delayed or irreversible.
- The proposed term “precision homoeopathy” should not be interpreted as a claim that homoeopathy has already achieved the evidentiary standards of precision medicine.

FUTURE RESEARCH DIRECTIONS

- International digital case registry with de-identified, harmonised data.

- Common data model and research dictionary for symptoms, rubrics, modalities, generals, remedies, potency, repetition and outcomes.
- AI repertorization benchmark using blinded expert assessment.
- Prospective biomarker-homoeopathy studies with predefined biological endpoints.
- Multicentre N-of-1 research network for conditions suitable for repeated measurement.
- Translational laboratory-to-clinic studies with predefined mechanistic and clinical endpoints.
- Independent external validation of AI models across countries and prescribing traditions.
- Open research practices, including preregistration of protocols and analytic plans where feasible.

CONCLUSION

The next major advancement in homoeopathic research may not be the discovery of another remedy indication. It may be the development of a better research architecture.

Artificial intelligence can help convert complex narratives into structured clinical phenotypes. Biomarker research can investigate biological heterogeneity. N-of-1 methodology can connect individualised treatment with experimental design. Multicentre databases can convert isolated clinical experiences into analyzable real-world evidence. None of these tools should be used as a substitute for evidence; the opportunity lies in connecting them.

A future homoeopathic study could therefore follow a sequence: individualised case -> structured phenotype -> transparent prescription -> objective measurement -> biomarker investigation -> N-of-1 evaluation -> multicentre aggregation -> prospective validation.

Such a framework respects the historical principle of individualisation while responding to contemporary demands for reproducibility, transparency and methodological rigor. The World Health Organization Global Traditional Medicine Strategy 2025-2034 places evidence generation, safety, regulation, health-system integration, and innovation and technology at the centre of its global agenda [2]. This creates an unusually relevant environment for a new generation of homoeopathic research.

The critical objective should therefore not be to prove a predetermined conclusion. It should be to build a research system capable of producing a scientifically defensible answer.

DECLARATIONS

Ethical Approval: Not required, as this manuscript is a narrative review and conceptual research framework and does not involve recruitment of human participants or collection of new patient data.

Informed Consent: Not applicable.

Source of Funding: None declared.

Conflict of Interest: None declared.

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Data Availability: Not applicable. No original patient-level dataset was generated for this manuscript.

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