

Indigenous Intentional Epigenetics: A New Conceptual Framework for Understanding Pre-Columbian Plant Domestication and Adaptation

Perspective Article

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Submitted to: Frontiers in Plant Science

Section: Ethnobotany | Article Type: Perspective

Date: June 2026

Author Note: This article was developed by an independent researcher and practitioner without formal university affiliation. The author is a certified agricultural technician (Técnico Agrícola, Escola Agrícola Dona Sebastiana de Barros, São Manuel, São Paulo, Brazil) with extensive applied experience in participatory seed selection in semi-arid Bahia, Brazil. The absence of academic affiliation does not diminish the validity of the conceptual framework proposed, which is grounded in peer-reviewed genomic and epigenomic literature. The author declares no conflict of interest. No funding was received for this work.

Abstract

The domestication of crops by pre-Columbian indigenous populations in the Americas has traditionally been framed as a process of phenotypic selection driven by random genetic mutations. However, recent genomic and epigenomic data challenge this paradigm. This perspective article proposes a new conceptual framework:

Indigenous Intentional Epigenetics (IIE). We argue that indigenous agricultural practices—such as continuous selection under environmental stress, clonal propagation, and regional adaptation during long-distance migrations—constituted a systematic and intentional manipulation of plant epigenomes across millennia. Using cassava (*Manihot esculenta* Crantz) as a primary genomic model, and potato (*Solanum tuberosum*) as an architectural model (Andean terrace systems), we synthesize recent findings on selective sweeps, DNA methylation patterns, differential epiallele inheritance, and haplotype-resolved methylomes to demonstrate that indigenous populations functioned as sophisticated applied epigeneticists. They intuitively understood that controlled environmental stress induces heritable phenotypic plasticity, effectively utilizing ecological gradients to encode adaptive memory into the plant epigenome across generations. Recognizing IIE not only rewrites the history of agricultural science by restoring the intellectual authorship of indigenous bio-engineers, but also offers a critical paradigm for developing climate-resilient agricultural systems in the Global South. We propose that contemporary participatory seed selection practices—such as Foundational Seed Reproduction (Reprodução de Sementes Fundacionais; RFS)—represent a scientifically grounded operationalization of ancestral IIE principles.

Keywords: epigenetics; plant domestication; indigenous knowledge; cassava; participatory breeding; DNA methylation; Andean terraces; food sovereignty; pre-Columbian agriculture; climate resilience

1. Introduction: Rethinking the Cognitive Status of Indigenous Agricultural Science

The dominant narrative in agricultural history has long positioned pre-Columbian indigenous populations as passive beneficiaries of random genetic mutation — discoverers of domestication by chance rather than practitioners of systematic biological science [1]. Within this Eurocentric framework, the extraordinary complexity and diversity of American crop varieties is attributed to millennia of unconscious selection, driven by survival necessity rather than deliberate scientific inquiry.

This narrative is increasingly contradicted by molecular evidence. The transformation of cassava (

Manihot esculenta Crantz) from a cyanogenic wild plant into a staple crop feeding over 800 million people globally required not merely the reduction of toxic glucosides, but the coordinated modification of complex, polygenic traits across radically distinct biomes — from the Amazon basin to the semi-arid Northeast Brazil to the subtropical Atlantic Forest [2,3]. The achievement is not consistent with random, passive selection.

Similarly, the Andean terrace system of Moray (Cusco, Peru) — an archaeological site comprising concentric circular terraces with a thermal gradient of approximately 15°C between the lowest and highest rings — presents an architectural configuration that cannot be adequately explained by food production alone. The structure's low yield capacity, its precise thermal engineering, and its proximity to major Inca administrative centers suggest a deliberate experimental function [4,5].

Recent advances in genomics and epigenomics provide the molecular framework necessary to re-evaluate these achievements. We propose the concept of

Indigenous Intentional Epigenetics (IIE): the systematic, multigenerational practice of observing, selecting, and propagating plants under controlled environmental stress, driven by an empirical understanding — not articulated in molecular terms but functionally equivalent — that stress-induced phenotypic changes can be fixed, amplified, and transmitted across generations.

This Perspective article synthesizes evidence from three convergent domains: (1) genomic analyses of cassava domestication revealing directional selective sweeps and structured epigenetic variation; (2) architectural and ecological analysis of Andean terrace systems as environmental gradient laboratories; and (3) modern epigenomic principles of DNA methylation inheritance and transgenerational stress memory. We further propose that IIE is not merely of historical interest, but constitutes a living framework with direct applications to climate-resilient agriculture in tropical regions.

2. The Four Principles of Indigenous Intentional Epigenetics

The IIE framework is built upon four interconnected principles, each of which aligns an observable indigenous agricultural practice with a documented epigenetic mechanism:

2.1 Systematic Observation of Phenotypic Plasticity

Indigenous agriculturists possessed a profound empirical understanding of phenotypic plasticity — the capacity of a single genotype to produce multiple phenotypes in response to environmental variation. Ethnobotanical records and modern analyses of indigenous crop lexicons document that pre-Columbian populations maintained detailed nomenclature systems for plant behavioral variation under different soil conditions, moisture regimes, altitudes, and seasonal stressors [6,7].

This observational precision is not incidental. It represents a longitudinal, multi-generational knowledge base functionally equivalent to what modern plant science calls quantitative trait characterization. By identifying individuals that exhibited superior adaptive responses — rather than simply superior yield — indigenous breeders were, in effect, selecting for epigenetic robustness.

2.2 Directed Selection for Adaptive Responses

Selection was highly directional, not stochastic. Genomic evidence from comprehensive genotyping of Brazilian cassava germplasm has identified significant selective sweeps — genomic regions of dramatically reduced variation resulting from strong positive selection pressure — in genes associated with cyanogenesis reduction and stress response pathways [8]. These sweeps are inconsistent with random genetic drift and indicate intentional, sustained selection over many generations.

More critically, this selection operated at the epigenome level. Continuous selection under consistent environmental stress conditions preferentially propagates epialleles — allele variants differing in DNA methylation state rather than nucleotide sequence — that confer adaptive advantages. Modern epigenomic theory predicts exactly this outcome when directional selection pressure is applied across multiple generations [9,10].

2.3 Clonal Fixation of Epigenetic Memory

Many of the most complex crops domesticated in the Americas — notably cassava and potato — are propagated clonally via vegetative organs (stem cuttings and tubers, respectively). Modern epigenomics confirms that clonal propagation is significantly more effective than sexual reproduction at preserving and stabilizing DNA methylation patterns across generations [11]. The maintenance of Polycomb-mediated histone modifications and RNA-directed DNA methylation (RdDM) pathways during mitotic rather than meiotic division ensures that stress-acquired epigenetic states are transmitted with high fidelity.

By selecting phenotypically superior individuals and propagating them clonally, indigenous farmers were effectively locking in adaptive epigenetic memory acquired during the plant's exposure to specific environmental stressors. This constitutes applied epigenetic stabilization — achieved without molecular instrumentation, but fully consistent with modern mechanistic principles.

2.4 Migratory Regional Adaptation and Epigenetic Diversification

As indigenous populations migrated across the South American continent — from the Amazonian basin of origin for cassava [2] to the semi-arid Caatinga of Northeast Brazil, the cerrado, and the subtropical South — they carried their crops through a succession of novel biomes. Each new environment imposed distinct abiotic stress signatures: different photoperiods, thermal regimes, soil microbiomes, water availability patterns, and UV radiation levels.

Modern epigenomics predicts that this sequence of environmental transitions would generate a cascade of locus-specific DNA methylation changes, creating distinct regional epigenotypes from a common genomic background. A recent study comparing DNA methylation profiles of two Brazilian cassava landraces (BRS Formosa and BRS Dourada) under water deficit conditions documented that 88% of identified methylation sites were unique to each variety [12], despite their common geographic origin in Northeast Brazil. This profound epigenetic divergence between varieties from the same region underscores how localized selection pressures create distinct epigenetic signatures — precisely the outcome predicted by the IIE framework.

3. Genomic and Epigenomic Evidence

3.1 Cassava as Primary Model

Cassava (*Manihot esculenta* Crantz) represents an ideal model system for the IIE framework given its well-characterized domestication history, its dependence on clonal propagation, and the recent availability of high-resolution genomic and epigenomic datasets.

The selective sweep analysis of Ogbonna et al. (2021) [8], based on comprehensive genotyping of Brazilian cassava germplasm, identified genomic signatures of intense, directional selection in genes associated with cyanogenesis and stress response. The specificity

of these sweeps — concentrated in functionally relevant gene families rather than randomly distributed across the genome — is inconsistent with neutral evolution and strongly suggests intentional, sustained selection pressure.

The methylation study by da Silva Filho et al. (2024) [12] provides direct evidence for structured epigenetic variation in cassava landraces. The finding that 88% of drought-responsive methylation sites are variety-specific, rather than shared, indicates that each landrace carries a unique epigenetic biography reflecting its particular history of selection and environmental exposure. This is precisely the molecular signature predicted by IIE: distinct environmental histories create distinct epigenetic identities, which are preserved across generations through clonal propagation.

Furthermore, research on African cassava landraces by Zhong et al. (2022) [13] demonstrated that nucleotide diversity at methylated loci is highly structured, indicating that epigenetic variation is not random noise but a stable, heritable component of the plant's adaptive repertoire. The structured nature of this variation — organized around functional genomic regions rather than distributed randomly — is consistent with selection acting on epigenetic states over extended time periods.

3.2 Andean Terrace Systems as Epigenetic Architecture

The Andean terrace system at Moray, Cusco, Peru, provides an architectural model for IIE in potato domestication. The site comprises three major sets of concentric circular terraces, the deepest reaching approximately 30 meters below the surrounding plain, creating a thermal gradient of approximately 15°C between the lowest and highest terraces [4].

Critically, the productive capacity of the Moray terraces is insufficient to explain their construction as a food production facility. The architectural investment required to build and maintain the structure is disproportionate to its agricultural output. The consistent thermal gradient, the proximity to Cusco (the Inca administrative capital), and the documented Inca practice of systematic seed exchange through state-controlled networks collectively suggest a deliberate experimental function: the controlled exposure of plant populations to defined environmental gradients to generate and select for altitude-specific adaptive traits.

A recent population genomic analysis of Andean potato varieties documented significant genomic differentiation correlated with altitude of origin, with distinct patterns of selection in genes associated with cold tolerance (CBF/COR family), heat stress response (HSP70/HSP90 family), and phenotypic plasticity (LEA proteins, ABA signaling) at different altitudinal zones [14]. This gene-by-altitude specificity is consistent with deliberate selection within a controlled gradient environment — the functional outcome predicted by IIE operating through the Moray system.

3.3 Transgenerational Stress Memory — Modern Mechanistic Basis

The IIE framework is grounded in well-established epigenetic mechanisms. Transgenerational epigenetic inheritance — the transmission of stress-induced epigenetic states to offspring not exposed to the original stress — has been documented in multiple plant species [15,16]. The primary mechanisms include:

- RNA-directed DNA methylation (RdDM): small interfering RNAs (siRNAs) guide de novo methylation of transposable elements and stress-responsive gene regions; this

methylation is maintained through mitotic and, under some conditions, meiotic cell divisions

- Polycomb Repressive Complex 2 (PRC2): catalyzes H3K27me3 histone modification, silencing developmental and stress-response genes; PRC2-mediated states can persist across generations in clonally propagated species
- Epiallele inheritance: stable allele variants differing only in DNA methylation state, not nucleotide sequence, have been documented to segregate in plant populations and confer heritable phenotypic differences [17]

The stability of these mechanisms across generations is particularly pronounced in clonally propagated species — precisely the category that includes cassava and potato, the two most significant crops in the IIE model. This mechanistic congruence is not coincidental: the crops for which indigenous epigenetic engineering achieved its most dramatic results are exactly those for which modern epigenomics predicts the highest efficiency of epigenetic memory transmission.

4. The Epistemological Dimension: From 'Primitive' to Applied Bio-engineers

Recognizing IIE requires a fundamental epistemological reorientation. It demands the abandonment of the colonial assumption that equates 'science' exclusively with Western, laboratory-based methodologies employing formal mathematical and molecular language.

Indigenous populations did not possess sequencing instruments, the vocabulary of molecular biology, or formal statistical frameworks. They possessed something functionally equivalent and, in terms of timescale, far more powerful: a rigorous empirical methodology based on multi-generational, longitudinal observation; systematic knowledge transmission through oral tradition, material culture (Andean quipus, for example), and community practice; and direct, non-mediated interaction with the living organisms under selection.

They operated at the level of the phenotype and the ecosystem — precisely the level at which epigenetic modifications manifest as observable biological differences. By intentionally imposing environmental stress to induce phenotypic change, and then fixing those changes through clonal propagation and selective reproduction, indigenous farmers were practicing applied epigenetics in the fullest sense of the term.

The epistemological importance of IIE extends beyond the correction of a historical misattribution. It establishes that sophisticated, systematic biological science is not the exclusive product of post-Enlightenment Western institutions. It is a universal human capacity that has been practiced — successfully, durably, and at planetary scale — by multiple indigenous civilizations, using the environmental and biological resources available to them.

This recognition does not romanticize or mystify indigenous knowledge. It does the opposite: it subjects it to rigorous molecular analysis and finds it consistent with contemporary mechanistic understanding. The result is not diminishment of modern science, but its expansion to include a category of practitioners it had systematically excluded.

5. Implications for Contemporary Climate-Resilient Agriculture

5.1 The Structural Fragility of Commercial F1 Hybrids

Modern commercial agriculture relies primarily on F1 hybrid varieties bred for maximum yield under high-input, controlled conditions. This breeding strategy, while effective at increasing productivity in stable environments, systematically reduces the epigenetic plasticity required to respond to unpredictable environmental stressors — precisely those associated with contemporary climate change, including the intensification of El Niño Southern Oscillation (ENSO) events, shifting precipitation regimes, and novel pathogen pressure [18].

The genetic and epigenetic uniformity of F1 hybrids constitutes both their commercial advantage and their structural vulnerability. When the controlled conditions for which they are optimized are disrupted, they lack the adaptive repertoire — encoded in epigenetic diversity — that landrace varieties carry as a legacy of their history of selection under adversity.

5.2 Dehybridization as Epigenetic Restoration

When F1 hybrids are replanted across successive generations (F2 and beyond), they undergo genetic segregation and what modern epigenomics identifies as an epigenetic reset — a partial return toward ancestral methylation states through the reactivation of silenced transposable elements and developmental regulators [19]. Commercial seed industries characterize this process as vigor loss. The IIE framework reframes it as adaptive restoration: the recovery of epigenetic plasticity that was systematically suppressed by industrial breeding.

This reframing has direct practical implications. The deliberate management of dehybridization under controlled stress conditions — rather than its avoidance — may constitute a pathway to recovering the epigenetic adaptive capacity present in ancestral landraces.

5.3 Foundational Seed Reproduction as Contemporary IIE

The IIE framework can be operationalized today through participatory breeding approaches that mirror ancestral practice. Foundational Seed Reproduction (Reprodução de Sementes Fundacionais; RFS) — a methodology developed in the context of Brazilian crioulo variety conservation — involves the systematic exposure of locally adapted landrace populations to controlled environmental stressors and the selection of the most resilient individuals across multiple generations [20].

From the IIE perspective, RFS is not a novel methodology. It is a scientifically grounded re-implementation of the same principles that indigenous bio-engineers applied across millennia. The contemporary contribution is not the invention of the method but its molecular documentation: the ability to verify, through DNA methylation sequencing using portable nanopore platforms, that the epigenetic changes predicted by IIE are occurring and are being transmitted across generations in the predicted manner.

This molecular verification creates a bridge between ancestral practice and contemporary science that benefits both: indigenous and smallholder agricultural communities gain scientific validation for traditional practices that have often been dismissed as folklore; and the scientific community gains access to millennia of applied epigenetic experimentation encoded in the diversity of surviving landrace varieties.

5.4 Implications for Seed Sovereignty and Intellectual Property

The IIE framework has significant implications for the ongoing global debate over plant intellectual property. If indigenous agricultural practices constitute a form of applied

epigenetics — a systematic, intentional manipulation of plant biological information — then the products of those practices (landrace varieties and their epigenetic signatures) represent intellectual creations, not merely natural objects available for appropriation.

Current intellectual property frameworks in agriculture — dominated by utility patents and plant breeders' rights — are designed around genetic sequence novelty and are fundamentally incapable of capturing or protecting epigenetic innovation. The IIE framework suggests the need for new legal and scientific instruments capable of recognizing, documenting, and protecting the epigenetic intellectual heritage embodied in indigenous and smallholder-maintained crop varieties.

6. Limitations and Future Research Directions

The IIE framework as presented here is a conceptual synthesis rather than a report of primary experimental data. Several of its central propositions — including the claim that Moray functioned as a deliberate epigenetic selection facility, and the claim that specific methylation signatures in cassava landraces reflect intentional ancestral selection rather than random epigenetic drift — require direct experimental verification.

Key research directions include: (1) large-scale DNA methylation profiling of Brazilian cassava landraces stratified by geographic origin, historical migration route, and ethnographic records of selection practice, to test whether epigenetic structure correlates with documented indigenous agricultural history; (2) experimental replication of altitude-gradient selection in potato and cassava populations under controlled conditions, with longitudinal tracking of methylation state changes across multiple generations; (3) ancient DNA methylation analysis of archaeobotanical seed samples from pre-Columbian contexts, to directly assess the epigenetic state of domesticated crops prior to European contact; and (4) collaborative research with indigenous knowledge holders to document selection criteria and practices that may encode epigenetic principles without molecular vocabulary.

These research directions are not merely of historical interest. The identification of epigenetic variants associated with climate resilience in indigenous landrace populations — variants generated by millennia of selection under real environmental stress — represents a potentially invaluable resource for contemporary crop adaptation programs, entirely complementary to, and arguably more durable than, approaches based on transgenic modification.

7. Conclusion

The concept of Indigenous Intentional Epigenetics provides a scientifically grounded framework for understanding the profound achievements of pre-Columbian agriculturists. Genomic and epigenomic data increasingly confirm that the domestication and diversification of crops like cassava were not the products of passive, accidental selection, but of systematic, intentional manipulation of plant biological memory across millennia and ecosystems.

Acknowledging IIE requires — and enables — a necessary decolonization of agricultural science. It restores the intellectual agency of indigenous populations, recognizing them not as fortunate beneficiaries of natural processes, but as the original applied epigeneticists of the Americas: practitioners of a science whose principles are now being

confirmed, with molecular precision, by the very instruments they did not need to achieve their results.

This recognition carries an urgent practical dimension. The landrace varieties maintained by indigenous and smallholder agricultural communities across the Global South are not merely genetic repositories. They are epigenetic archives — repositories of stress-adaptation information accumulated across thousands of years of intentional, systematic biological experimentation. Their loss to genetic erosion represents not merely a reduction in biodiversity, but the permanent destruction of an irreplaceable body of applied epigenetic knowledge.

Preserving, documenting, and building upon this knowledge — through frameworks like IIE and practices like RFS, supported by accessible molecular tools such as portable nanopore sequencing — is among the most scientifically and ethically significant contributions that contemporary plant biology can make to the global challenge of food security in a changing climate.

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Supplementary Material

Table S1. Correspondence Between IIE Principles and Modern Epigenetic Mechanisms

IIE Principle	Indigenous Practice	Epigenetic Mechanism	Key Evidence
Systematic Observation	Multi-generational phenotype tracking; crop variety nomenclature systems	Phenotypic plasticity driven by differential gene expression via methylation	Ethno-botanical lexicons; quantitative trait diversity in landraces
Directed Selection	Continuous selection under stress; rejection of low-performing individuals	Selective sweep of stress-responsive epialleles; enrichment of adaptive DMRs	Ogbonna et al. (2021) [8]; Li et al. (2018) [14]
Clonal Fixation	Vegetative propagation of superior individuals via cuttings and tubers	Mitotic maintenance of DNA methylation; preservation of H3K27me3 states	Ong-Abdullah et al. (2015) [11]; Zhong et al. (2022) [13]
Migratory Adaptation	Long-distance crop dispersal through trade networks and migration routes	Locus-specific methylation changes induced by novel environmental stressors; creation of regional epiallelic variants	da Silva Filho et al. (2024) [12]; Wibowo et al. (2016) [15]

Table S2. Summary of Key Genomic Evidence Supporting IIE Framework

Study	Crop	Method	Finding Relevant to IIE
Ogbonna et al. (2021)	Cassava (Brazil)	SNP genotyping — 5,458 accessions	Selective sweeps in stress-response and cyanogenesis genes — inconsistent with neutral evolution
da Silva Filho et al. (2024)	Cassava (NE Brazil)	Whole genome bisulfite sequencing	88% of drought-responsive methylation sites are variety-specific — structured epigenetic diversity reflecting distinct selection histories
Zhong et al. (2022)	Cassava (Africa)	Haplotype-resolved methylome	Methylated loci show structured nucleotide diversity — epigenetic variation is heritable and non-random
Li et al. (2018)	Potato (Andes)	WGS — 201 accessions	609 genes under selection; altitude-correlated gene expression patterns in stress-response families
Wibowo et al. (2016)	Arabidopsis (model)	Bisulfite sequencing	Transgenerational inheritance of stress-induced methylation confirmed — mechanistic basis for IIE