

# Enviromics crosstalk between internal and external plant environments for enhanced adaptation and *de novo* domestication

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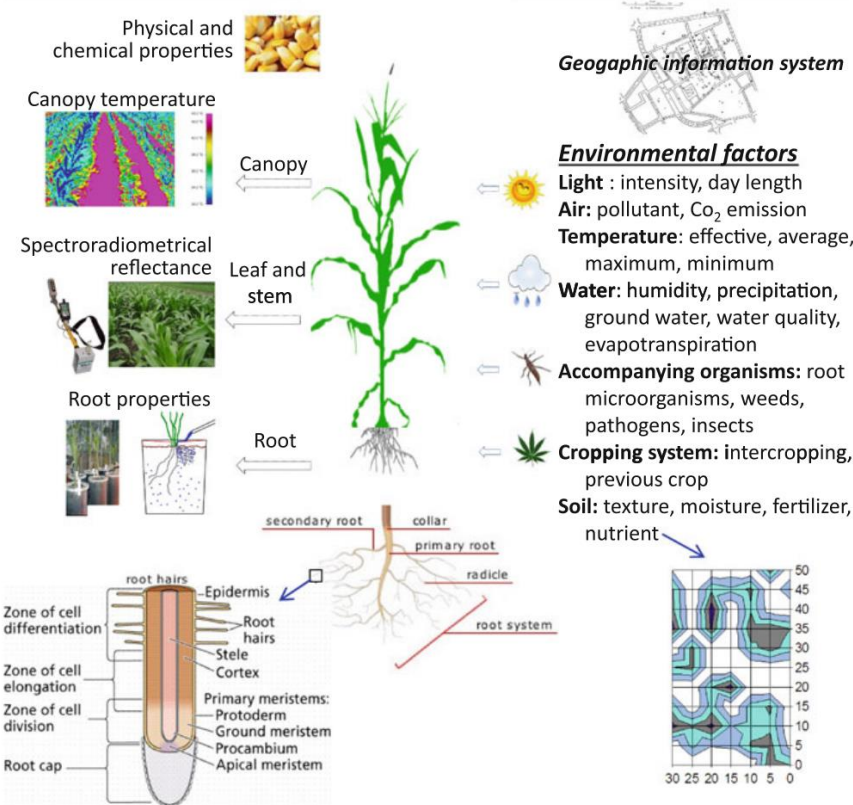
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# Introduction

## The "Black Box" of Environment



Xu, Y., 2012. *Molecular Breeding* 29:833–854

### Genotype-environment interaction (GEI): the unseen driver

Plant phenotype arises from genotype, environment, and genotype-environment interactions (GEI). Traditionally, the environment was treated as static "background noise," leaving the mechanisms linking environmental signals to phenotypic outcomes largely uncharacterized.

Environment-related research has predominantly focused on external environments, largely overlooking the interaction between **internal and external environments**.

#### Limit 1: Genomic breeding constraints

Genomic-assisted breeding is limited by poorly characterized environments. Without quantifying environmental factors, marker-based predictions cannot account for field variability, reducing breeding efficiency.

#### Limit 2: "Black Box" GEI models

Classical statistical models treat the environment as a single variable rather than interacting cues, preventing mechanistic insights and predictive capacity under novel climates.

#### Limit 3: Wild germplasm utilization

*De novo* domestication of resilient wild species is hindered by limited knowledge of their environmental sensing and adaptation mechanisms.

**Our core mission:** Break through the bottleneck by deciphering the environmental "black box". We aim to develop a mechanistic framework that decodes GEI, enabling precise, data-driven plant improvement strategies for sustainable agriculture.



# The multi-scale environmental continuum

## External enviromics ( $E_{\text{external}}$ ): the macro perspective

This branch employs remote sensing (satellites) to monitor landscape-scale environmental variables, including climate, soil, and biotic factors.

AI models like GEFFormer leverage these datasets for crop performance prediction, though they provide a top-down view without direct insights into internal plant responses.

## Internal enviromics ( $E_{\text{internal}}$ ): the micro perspective

This discipline employs electrochemical microsensors and genetically encoded biosensors to quantify cellular-level metabolic fluxes, pH shifts, and gene expression.

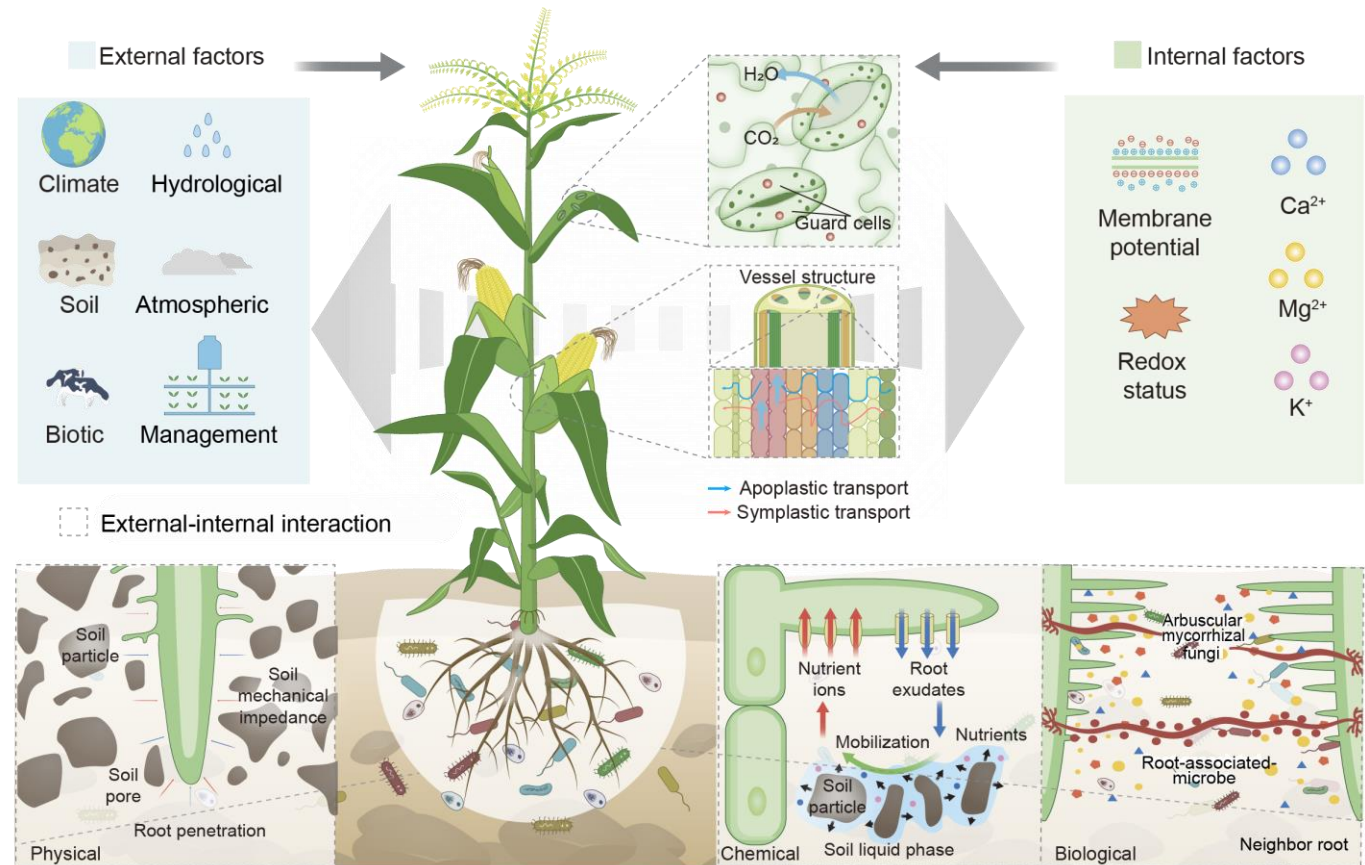
By capturing physiological responses to external cues, Internal Enviromics mechanistically links environmental signals to phenotypic outcomes for precise crop improvement.

$$\text{Classic model: } P = G + E + G \times E$$

$$\text{Refined model: } E = E_{\text{internal}} + E_{\text{external}} + E_{\text{internal}} \times E_{\text{external}}$$

## What is enviromics?

Enviromics is defined as the study of multi-scale environmental factors controlling plant growth. This framework integrates internal ( $E_{\text{internal}}$ ) and external ( $E_{\text{external}}$ ) environments into a unified framework for understanding plant-environment interactions.







# Internal envirotyping for predictive crop improvement

## Why is internal envirotyping valuable?

It represents a paradigm shift in crop science, moving beyond surface-level observations to decode the plant's internal state. This approach provides a deeper, more actionable understanding of plant responses to environmental stressors, enabling smarter and faster crop improvement.

### Beyond single genetic marker analysis

Genetic analysis with internal parameters (e.g., xylem Na<sup>+</sup> concentration) captures the integrated output of polygenic networks, providing more robust and biologically relevant predictors of plant performance across diverse environments compared to single genetic marker analysis.

### Causal insight

Unlike traditional measurements that merely record stress symptoms, envirotyping deciphers traits into quantifiable variables, revealing causal drivers behind plant responses. This mechanistic understanding enables targeted interventions at specific physiological bottlenecks (e.g., nutrient transport).

### Technological advancements

Microprobe advances (electrochemical sensors, NMT, nanowire sensors) enable real-time, non-destructive field envirotyping, revolutionizing large-scale phenotyping.

## Transforming crop improvement: from reactive to proactive

By integrating systems-level biomarkers, mechanistic insights, and advanced measurement technologies, internal envirotyping enables breeders to translate complex biological data into actionable strategies, accelerating the development of climate-resilient, high-yielding crops and bridging fundamental plant science with agricultural impact.



# Comparative value: internal environment ( $E_{\text{internal}}$ )-based analysis versus traditional marker-based analysis

## Traditional marker-based mapping

This traditional gene-locus approach neglects environmental factors and is constrained by complex genetic interaction networks, making causal relationships difficult to disentangle. Marker-assisted selection based on such single-gene markers often performs inconsistently across environments, as external conditions and genetic background noise obscure phenotypic effects.

**Key Limitation:** Reliance on static genetic markers rather than dynamic physiological responses reduces robustness in real-world agricultural settings.

## Internal environment ( $E_{\text{internal}}$ )-based analysis

$E_{\text{internal}}$  captures the integrated physiological state of plants (e.g., salinity tolerance, nutrient balance) as a direct determinant of performance. Unlike traditional genetic marker analysis, genetic analysis incorporating internal environmental parameters ( $E_{\text{internal}}$ ) inherently reflects dynamic responses to environmental fluctuations and genetic background variation.

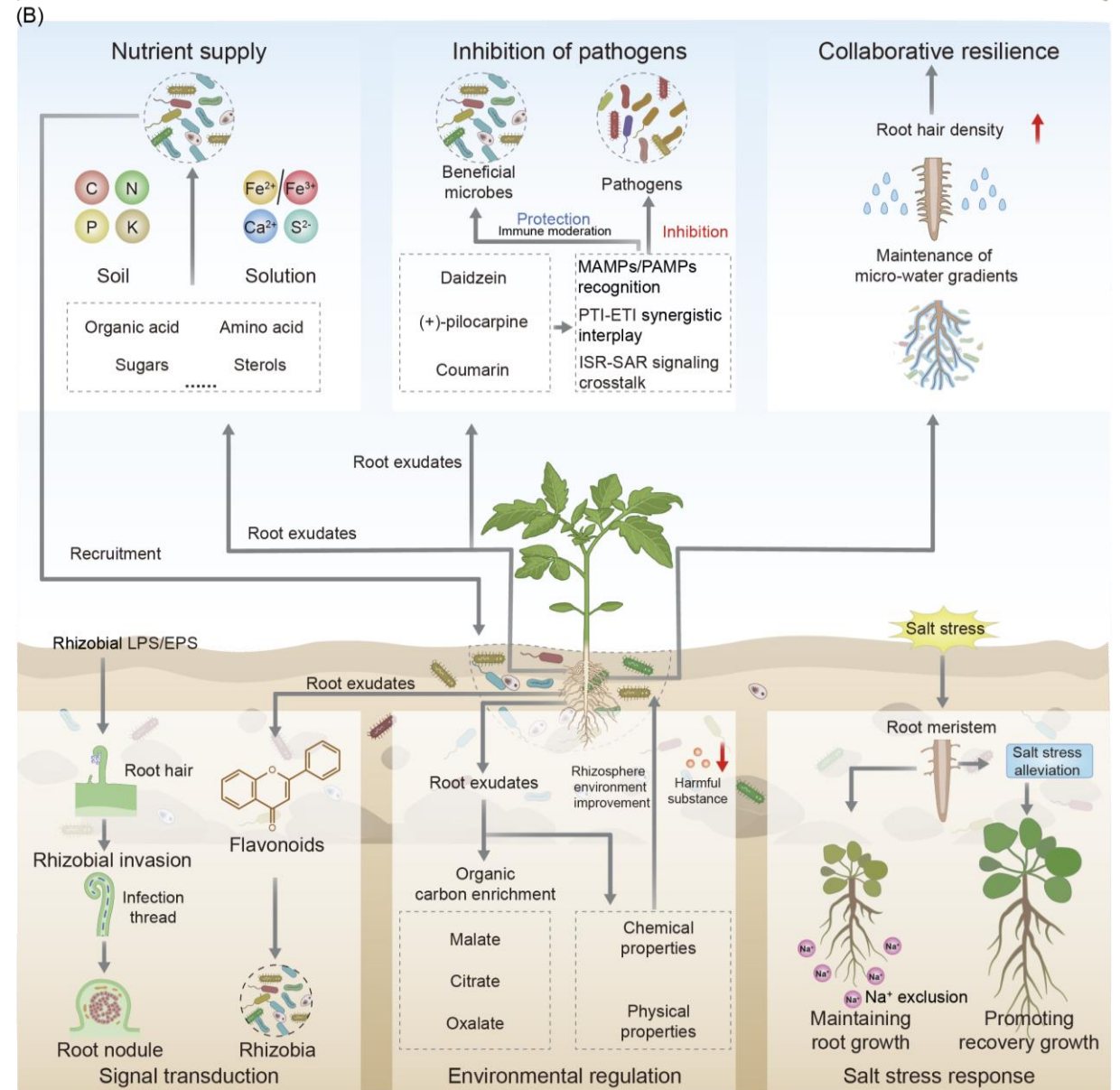
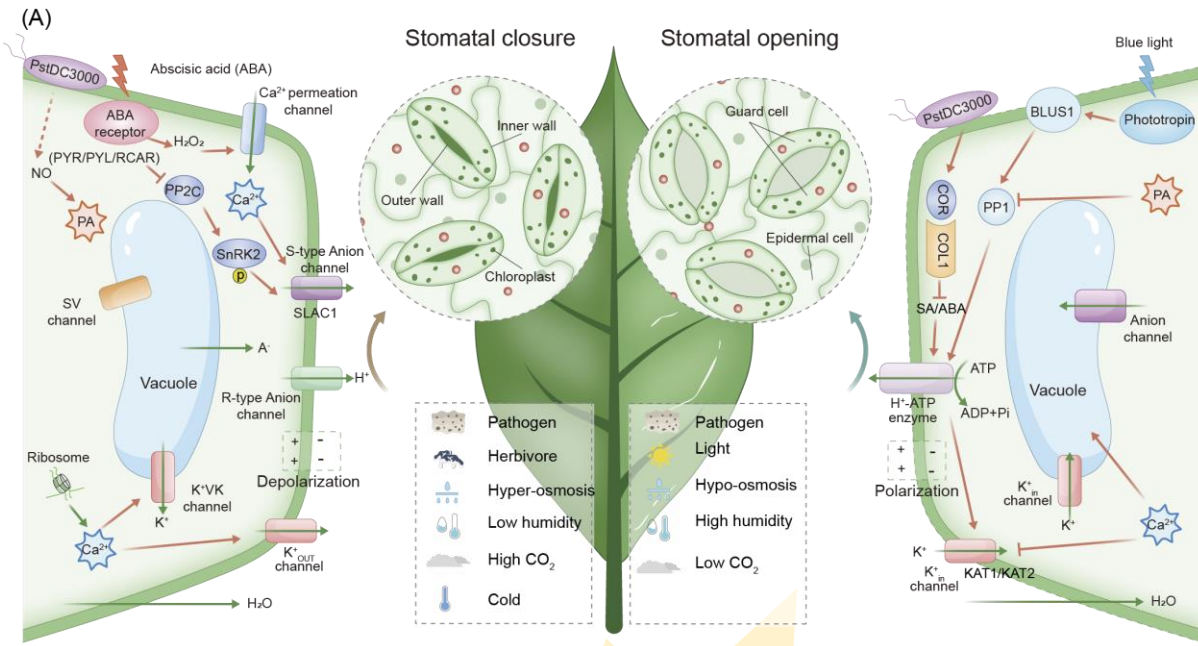
**Key Advantage:** It provides a functional, holistic readout of plant health that reflects real-world adaptability without requiring specific gene identification.

## Strategic conclusion for breeding programs

Integrating genomics with internal and external environmental phenotyping of plants, replacing static genetic marker analysis with dynamic functional indicator analysis, thereby identifying resilient varieties that perform stably across multiple environments.



# Mechanisms of interaction: interface compartments



## Key interface roles:

Stomata: Regulate gas ( $\text{CO}_2/\text{O}_2$ ) & water vapor exchange.

Roots: Sense soil gradients & recruit beneficial microbes.

**Plant stomatal movement and rhizosphere interaction regulatory network.**

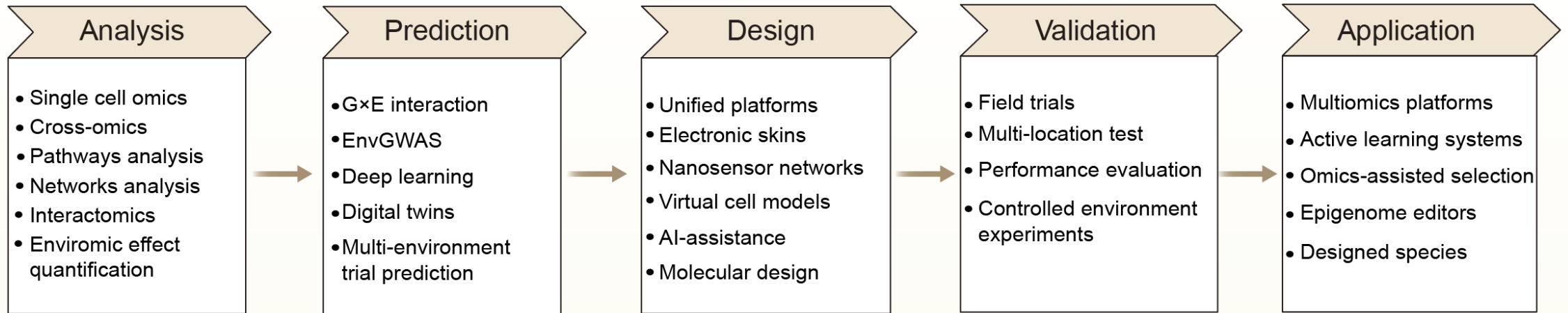


# Five-stage workflow for *de novo* domestication

## An integrated paradigm for predictive design

Envirotyping integrates multi-omics and machine learning to accelerate *de novo* domestication of climate-resilient crops from wild germplasm.

### Technical flowchart



## Future outlook: accelerating evolution for a changing planet

This predictive design paradigm transforms traditional domestication into a data-driven workflow. By integrating environmental intelligence with synthetic biology, we can engineer crop resilience directionally to safeguard food security.



# de novo domestication & future outlook

## Internal as a key intermediate layer

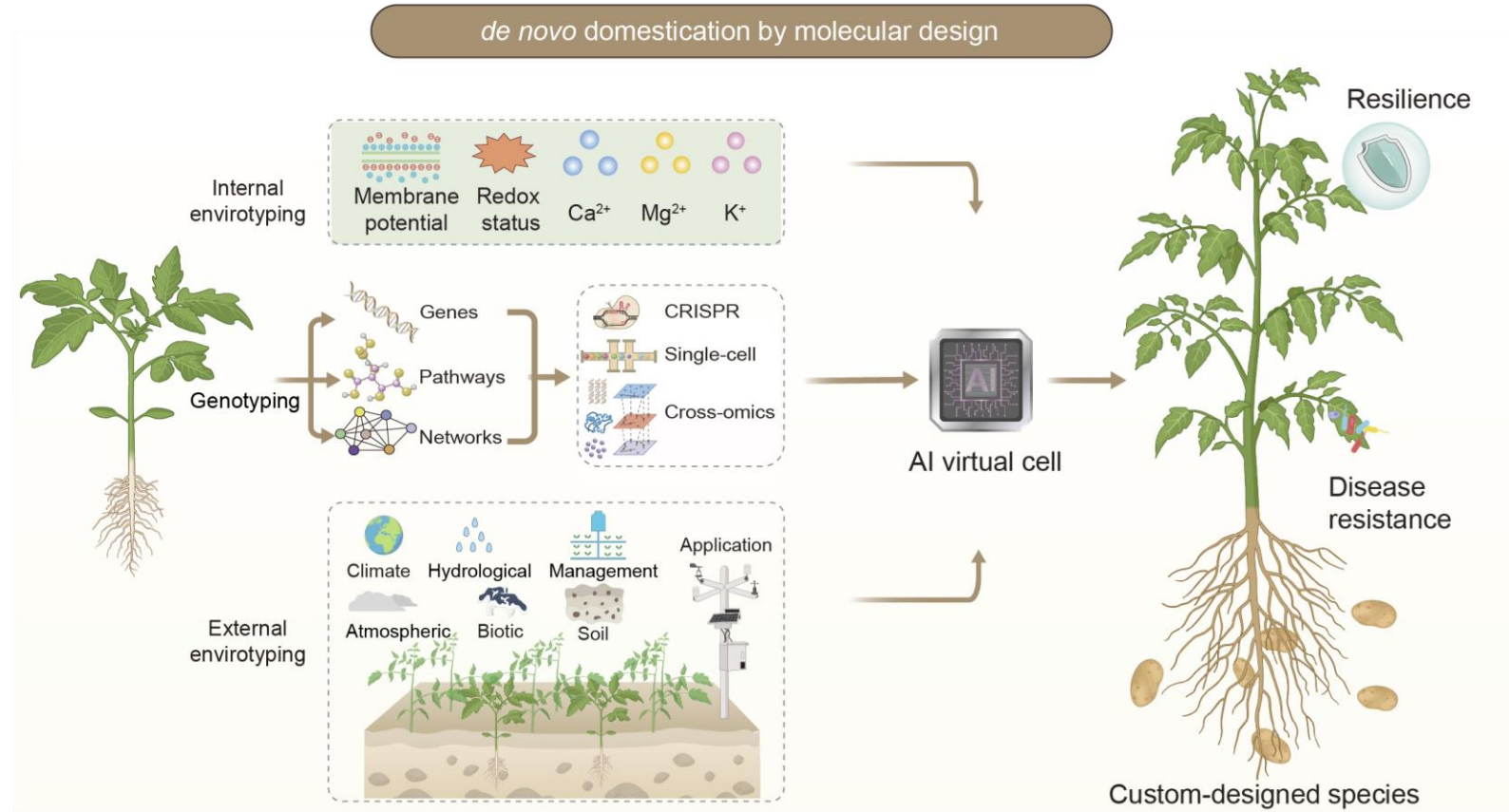
Internal physiological parameter-based analysis outperforms single-locus marker analysis in connecting genotype to phenotype, offering more robust predictability.

## Technology-driven paradigm shift

Real-time internal envirotyping is shifting plant science from descriptive approaches to predictive engineering for precise trait optimization.

## de novo domestication workflow

This five-step framework accelerates *de novo* domestication by engineering wild species' environmental responses into climate-adaptive crops.



These insights redefine crop improvement by centering the internal environment, embracing technological innovations, and applying structured domestication, thereby empowering the development of high-yielding, climate-resilient crops for the 21st century.



# Challenges and future directions

## Technological bottleneck

Non-invasive internal sensing technology is still in its infancy. Current tools lack the precision needed for real-time, in vivo monitoring of subtle internal environmental fluctuations within organisms.

## Data integration

Integrating massive enviromics and other omics datasets into accurate predictive models is a major computational challenge. Heterogeneous data formats and scales create significant barriers to holistic analysis.

## Standardization

A global lack of standardized envirotyping protocols hinders cross-study validation and reproducibility. Establishing shared data frameworks is essential for building a unified knowledge base.

## 1. Unified standards

Develop universal envirotyping protocols and establish a shared global database. This will enable seamless cross-regional data sharing and accelerate collaborative breakthroughs.

## 2. Sensor innovation

Advance next-generation microprobe sensor arrays for high-resolution, non-invasive monitoring. Breakthroughs in miniaturization and sensitivity are key to capturing dynamic internal signals.

## 3. Mechanism elucidation

Unravel cross-scale signal integration pathways. Linking micro-environmental stimuli to phenotypic responses will unlock predictive capabilities for complex biological systems.

## 4. Global networks

Foster international research consortia to pool expertise and resources. Collaborative networks are vital for addressing global environmental challenges and scaling research impact.



# Summary

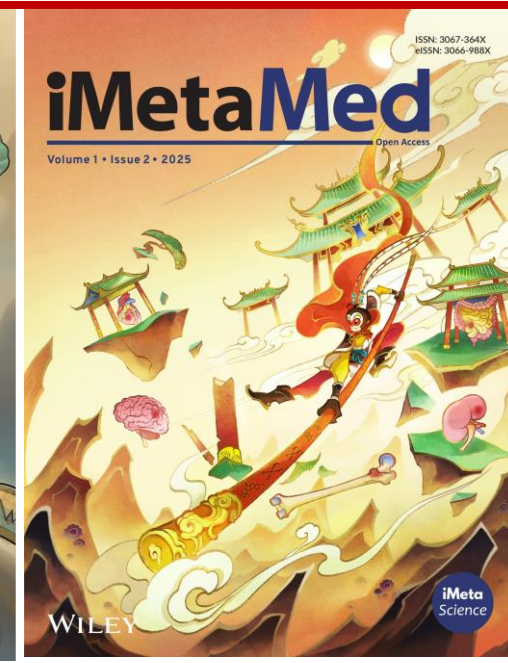
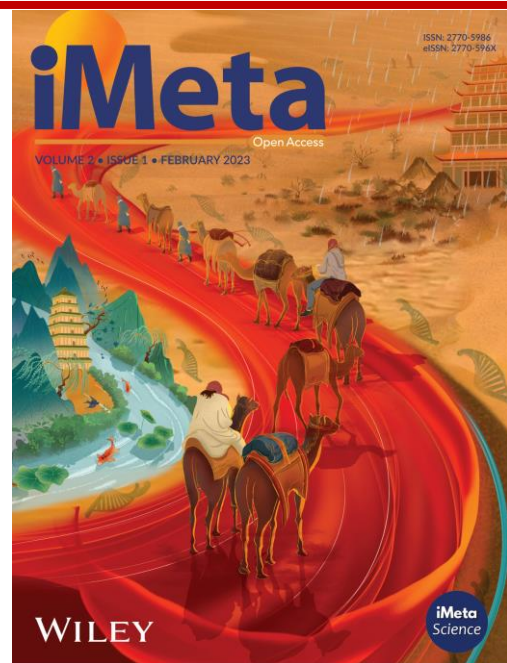
- ❑ We propose a multi-scale environmental continuum framework that deciphers the environmental black box into measurable internal ( $E_{\text{internal}}$ ) and external ( $E_{\text{external}}$ ) domains.
- ❑ We emphasize that internal enviromics serves as a critical bridge connecting genotype and phenotype, with enviromics-based analysis providing more robust parameters than traditional genetic marker analysis.
- ❑ We present a five-stage workflow for the predictive design of *de novo* domestication, integrating envirotyping, multi-omics, and precision breeding.
- ❑ Ultimately, the evolution from multi-omics parsing to targeted *de novo* design will enable the precise engineering of crop adaptation, securing global food security.

By merging enviromics with synthetic biology, this research translates environmental complexity into actionable strategies to accelerate *de novo* domestication of climate-resilient crops.

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