



Editorial

Leveraging Genetic Diversity for Abiotic Stress Tolerance

Andrés J. Cortés 

Facultad de Ciencias Agrarias—Departamento de Ciencias Forestales, Universidad Nacional de Colombia—Sede Medellín, Medellín 050034, Colombia; ancortesv@unal.edu.co

Climate-change-driven abiotic stresses, once regarded as episodic constraints for major staple crops, are now main selective forces driving the agronomic and evolutionary trajectories of plants [1]. Increasing climatic variability has been manifested in the last decade as recurrent and extreme droughts [2], heatwaves [3], and cold fronts [4–7], which together are pushing crops and natural populations toward the limits of their plastic [8] and adaptive capacity [9]. Plant breeding and management efforts have buffered some of these challenges [10,11], yet they have often relied on relatively narrow genetic bases and a reductionist set of productive [12] and eco-physiological functional traits [13]. Since this standing variation is insufficient to cope with the rapid pace of environmental change [14,15], an urgent expansion in the repertoire of nature-based solutions is demanded. In particular, boosting abiotic stress tolerance would benefit by expanding the classical recurrent trait improvement cycle and germplasm mobilization approaches to encompass a high-throughput exploration and introgression of hidden allelic variation [16], as well as genetic forecasting of the adaptive [17] and conservation potentials [18–21]. For that, modern and more integrated molecular, ecological, computational, and trait discovery and screening approaches must be envisioned [22]. In order to help bridge this gap, this second edition of the Special Issue “Abiotic Stress Tolerance and Genetic Diversity in Plants” has assembled nine contributions, spanning a rich variety of scales, from gene networks to population-level studies. This compilation reinforces the fact that abiotic stress tolerance is a complex, multi-dimensional, polygenic, and environmentally dependent abstractable property [23], rather than a simple predefined phenotype encoded by few deterministic genes with major effects. While abiotic stresses impact plant productivity and survival under climate change, genetic and omic platforms are converging to reshape strategies for breeding more resilient crops and maintaining species ecosystem services.

1. Molecular and Transcriptomic Bases of Abiotic Stress Responses

Understanding how plants perceive, process, and respond to abiotic stress at the molecular level remains a central challenge for advancing climate-resilient agriculture and conservation strategies [24]. Rapid progress in transcriptomics, comparative genomics, and systems biology has enabled a shift from single-gene studies to family- and network-based assessments, revealing the complex regulatory architectures that underlie stress adaptation [9,25]. These approaches are capable of uncovering cryptic functional variation within wild relatives [26], locally adapted germplasm [27,28], and polyploid genomes [29]—sources of innovation that, until very recently, have been systematically deployed into breeding and conservation programs. As discussed below, gene family evolution, functional validation, and temporal expression dynamics help to determine how transcriptional regulation shapes plant responses to environmental pressures [30–32].



Received: 23 April 2026

Accepted: 26 April 2026

Published: 11 May 2026

Copyright: © 2026 by the author.

Licensee MDPI, Basel, Switzerland.

This article is an open access article distributed under the terms and

conditions of the [Creative Commons](#)

[Attribution \(CC BY\)](#) license.

As a first case study that goes beyond primary gene pools, the contribution by Wong et al. [33] investigates cold tolerance response mechanisms by comparing cultivated alfalfa (*Medicago sativa*) with its wild relative *Medicago falcata*. The authors expose seedlings of both species to low-temperature treatment (4 °C) as well as to control conditions, and analyze leaf tissues at defined time points using RNA-seq, differential gene expression, and transcription factor enrichment analyses. The results show that *M. falcata* exhibits a broader transcriptional response with significantly more differentially expressed genes (DEGs) and enrichment in key regulatory families such as bHLH, ARR-B, and AP2/ERF [34–39]. The authors conclude that wild germplasm harbors a richer regulatory network for stress response than its cultivated counterparts, suggesting that domestication has eroded the diversity of stress-responsive pathways. It also illustrates how comparative transcriptomics uncover functionally relevant regulatory variation, reinforcing the importance of integrating wild genetic resources aimed at enhancing resilience.

Similarly, but this time looking into locally adapted germplasm, O'Rourke and Graham [40] provide a compelling example of how stress-resilient crop provenances can harbor novel adaptive mechanisms that are not predictable from model species. Focusing on soybean (*Glycine max*), the authors investigate the function of three iron deficiency response genes—FIT, HY5, and PYE—in the iron-deficit-tolerant Swedish line Fiskeby III (PI 438471), using virus-induced gene silencing combined with RNA-seq analyses under iron-sufficient and iron-deficient conditions. Strikingly, while silencing FIT and HY5 alters broader stress-responsive transcriptional networks, it does not compromise iron deficiency tolerance, demonstrating that this genotype relies on alternative, previously uncharacterized, genetic pathways to cope with iron scarcity. These findings challenge the widespread assumption that stress tolerance mechanisms are conserved across species, and highlight the limitations of extrapolating from model organisms such as *Arabidopsis thaliana*. Instead, the study encourages exploring crop-specific and locally adapted germplasm to uncover hidden sources of genetic diversity for stress resilience.

In a more temporal expression context, Khunsanit and collaborators [41] leverage time-series transcriptomics and network-based approaches to dissect the molecular basis of salinity tolerance in rice (*Oryza sativa*), focusing on the salt-tolerant Thai variety 'Jao Khao'. Using 36 RNA-seq libraries sampled across six time points (0–48 h) under 160 mM NaCl, the authors construct a two-state weighted gene co-expression network that enables the identification of 1950 highly variable genes and 111 key hub genes associated with the salt stress response. These hub genes were enriched in pathways related to energy metabolism, photosynthetic light reactions, ATP synthesis, and transport processes, with early upregulation during the initial phases of salt stress, a pattern further validated by qRT-PCR for key genes such as RuBisCo and ATP synthase. The study demonstrates that rapid metabolic reprogramming, particularly the management of cellular energy balance, is transversal to stress adaptation. It also demonstrates how merging integrative transcriptomic and systems biology frameworks across the temporal continuum uncover functionally relevant candidate gene targets to harness abiotic stress responses in crops.

Finally, Zhao and collaborators [42] offer a comprehensive genome-wide characterization of the *FCS-like zinc finger (FLZ)* gene family, implied in stress responses as well as plant development and senescence, across three *Brassica* species, identifying 113 genes and revealing their expansion largely driven by whole-genome duplication events, well-studied events in *Brassica* genome evolution. Through integrative phylogenomic, collinearity, and expression analyses, combined with protein–protein interaction assays, the study demonstrates that a subset of these genes (i.e., seven out of 15 tested) shows significant responsiveness to abiotic stresses, while many FLZ proteins interact with central energy-sensing kinases (SnRK1), highlighting a conserved regulatory module linking stress signaling and metabolic control.

Overall, these studies offer a genome-wide functional exploration of stress-responsive genetic mechanisms in plants, highlighting how integrated approaches can uncover candidate genes linked to abiotic stress resilience [43,44]. The works combine high-throughput genomic screening and expression profiling under stress conditions, which enables authors to identify key gene families exhibiting differential regulation and potential roles in adaptive responses [45–47], while also revealing patterns of gene duplication and structural diversification responsible for functional innovation [48]. The studies move beyond descriptive genomics after linking molecular signatures and expression profiles to stress-related pathways, thereby contributing to a more mechanistic understanding of how plants perceive and respond to climate pressures, even at local scales [49,50]. They also exemplify how modern bioinformatics and molecular biology tools can reveal previously hidden layers of genetic diversity, both at the population and the polyploid genomic levels, offering promising targets for molecular breeding and the customization of climate-resilient populations [51]. Ultimately, these studies reinforce the value of integrating genomic, functional, and evolutionary analyses to unlock adaptive potential in plants [52].

2. Transitioning from Functional Bases to Targeted Gene Editing

Based on the molecular and transcriptomic understanding outlined above, the natural next step is to functionally validate and bioengineer the causal variants that are responsible for abiotic stress responses [53]. While genome-wide expression and comparative evolutionary analyses of major gene families have been key in identifying candidate genes and regulatory networks [54], they are often limited in terms of determining how specific alleles, isoforms, or regulatory elements translate into phenotypic resilience. Recent advances in functional genomics are beginning to bridge this gap by combining fine-scale molecular characterization with experimental validation across heterologous systems and genome editing platforms. These approaches not only disclose previously overlooked layers of variation—such as alternative splicing or regulatory sequence diversity—but also enable their direct manipulation for plant improvement. That said, the following studies illustrate how moving from gene discovery to mechanistic validation and targeted intervention enable a first approach to utilizing cryptic adaptive potential, accelerating the deployment of stress-resilient traits, and reinforcing the convergence of molecular biology, biotechnology, and breeding in the face of escalating abiotic challenges [55].

Illustrating the first scenario, Imran et al. [56] study functional variation in the sodium transporter *OsHKT1;1* for salt tolerance in rice (*Oryza sativa*). The authors test two splicing variants across three heterologous systems (i.e., plant cells, yeast, and *Xenopus oocytes*) using subcellular localization, ion flux measurements, and gene expression analyses. The team demonstrate that splicing variants differ in ion selectivity and transport efficiency, offering a cryptic source of variation for crop improvement. After all, not only gene presence, but also alternative splicing contributes to plasticity, expanding the functional repertoire of key transporters involved in ion homeostasis.

Meanwhile, at the frontiers of gene editing, Fan and collaborators [57] reviewed CRISPR/Cas-based genome editing [58,59] in alfalfa (*Medicago sativa*), a key forage crop with historically underexploited genomic resources. The work summarizes how merging conventional breeding with emerging genomic, transcriptomic, and functional studies enable identifying candidate genes and pathways associated with traits such as nutrient use efficiency and freezing tolerance, among other abiotic stress responses. The synthesis prospects multiplex gene editing, regulatory region targeting, and trait engineering strategies to boost these candidate targets. The authors claim that while genome editing enables precise manipulation of stress-related genes, challenges remain in transformation efficiency and the complexity of polygenic traits. They conclude that genome editing with a systems-level understanding would enhance abiotic stress tolerance [60–62].

The convergence of molecular biology, genomics, and biotechnology fast-track plant improvement, particularly under relatively simple Mendelian genetic architectures underlying abiotic stress responses [63,64]. However, these efforts, while useful at identifying and manipulating individual target functional variants [65], demand an understanding of how such molecular bases perform across more complex polygenetic and environmentally conditioned scenarios [66,67]. In other words, while functional validation and genome editing provide unprecedented precision to customize stress-responsive pathways [68], their ultimate impact will depend on integrating these advances within frameworks that explicitly account for genotype-by-environment interactions [69,70] and phenotypic plasticity [71], as discussed in the next section. In this sense, a catalog of functionally characterized and gene-edited alleles represents only one component to achieve resilience in plants, since the former must be contextualized within diverse environmentally conditioned responses [72–75] and broader phylogenetic backgrounds [76–78]. Bridging this gap requires moving beyond controlled model systems toward strategies that harness both bioengineered variation and naturally occurring adaptive diversity for pre-breeding [79] and conservation initiatives [80].

3. Plastic and Adaptive Responses for Climate-Resilient Breeding

The previous works exemplify how the evolutionary diversification across hidden layers of genetic redundancy and functional specialization can harbor adaptive potential to cope with environmental stressors, providing a repertoire of candidate genes for molecular breeding. Additionally, while advances in functional genomics and genome editing are rapidly improving our ability to identify and manipulate some of these variants, their ultimate value depends on how effectively these efforts can be translated into reliable and deployable plant populations under current environmental variability. In this context, phenotypic plasticity forecasting [17,81] and pre-breeding efforts to mobilize alleles from locally adapted germplasm to elite backgrounds [82] are required to handle the intrinsic genotype-by-environment interaction that more deterministic molecular models often overlook. Rather than viewing environmental-dependent responses as a limitation, emerging frameworks now recognize plastic clines as genetically controlled [83], selectable traits that can be harnessed to enhance resilience across heterogeneous and shifting climates [84]. At the same time, stress-adapted populations thriving in extreme or marginal environments provide access to cryptic allelic variation that is largely absent from elite breeding gene pools [85]. The following studies illustrate how integrating genotype-by-environment interactions and pre-breeding-oriented approaches can bridge the gap between functional discovery and application, ultimately enabling the development of plant populations and varieties able to cope with increasing abiotic pressures.

In an first effort to understand the genomic bases of phenotypic plasticity, Arenas and Cortés [86] re-studied drought-induced phenotypic plasticity in barley (*Hordeum vulgare*) using a diversity panel of 1277 genotypes evaluated under contrasting water regimes (i.e., well-watered vs. drought conditions). Using five plasticity indices and four genome-wide association study (GWAS) models, the authors identified 239 significant SNPs, including 27 within coding regions. Notably, many loci exhibited context-dependent antagonistic pleiotropy, where allelic effects differed across environments. Therefore, the study was able to conclude that plasticity is genetically controlled and environment-dependent, challenging traditional breeding strategies that assume stable allele effects. The work moves beyond single-locality mapping to explicitly model genotype-by-environment interactions, offering a conceptual and methodological framework for integrating phenotypic plasticity into genomic prediction and breeding strategies. Once these contrasting genetic responses are understood, they can be utilized to unlock hidden adaptive potential for crop improvement under increasingly variable water availability [87].

Meanwhile, the work by Yin et al. [88] advances the deployment of cryptic genetic diversity within a pre-breeding framework by demonstrating how salt-stress-adapted germplasm can be harnessed for crop improvement through molecular breeding. Focusing on rice, the authors identify and functionally validate two jacalin-related lectin genes—*OsJRL45* and *OsJRL40*—derived from the stress-resilient “Sea Rice 86” genotype, showing that their marker-assisted introgression significantly enhances salt tolerance. Because this study integrates gene expression analyses under salinity stress with breeding-oriented validation, it bridges the gap between gene discovery and downstream applications, highlighting lectin-mediated pathways as key components of stress response networks. Importantly, this work exemplifies how underutilized germplasm pre-adapted to or extreme environments harbors adaptive alleles absent from conventional breeding gene pools and how modern genomic tools can accelerate their deployment. In doing so, the study reinforces the importance of coupling functional genomics with marker-assisted selection to unlock hidden reservoirs of abiotic stress tolerance, providing a practical roadmap for developing resilient crop varieties in the face of increasing soil salinization.

Together, these two studies highlight the fact that climate-resilient breeding not only requires identifying exotic superior genotypes and alleles [89] and reconstructing the molecular mechanism responsible for that superiority [90], but also urge an understanding of how those networks are reshaped across environmental contexts [91,92] and genetic backgrounds [93,94]. Once phenotypic plasticity, genotype-by-environment interactions, and stress-adapted germplasm are explicitly incorporated into breeding pipelines, it would be possible to transcend beyond single-trait plant improvement strategies toward more predictive frameworks of the adaptive potential. These same principles spread beyond crops, as the identification and mobilization of context-dependent adaptive variation help sustain resilience in natural populations under rapid environmental change.

4. Leveraging Abiotic Stress Tolerance in Natural Populations

Moving beyond crop breeding applications, which tend to occupy a major focus in the abiotic stress tolerance literature, the same conceptual and methodological workflows used to study and harness cryptic adaptive variation and its environmental dependency can be extended to natural populations facing rapid environmental change. As climate pressures intensify, conservation [95], restoration [96], and assisted migration [97] and gene flow [98,99] efforts increasingly rely on identifying and mobilizing adaptive variation already present in wild and marginal plant populations. In this context, integrating genomics, transcriptomics, and *in situ* ecological data offers a powerful avenue to uncover how non-model and perennial species respond to abiotic stress across their range.

In a first effort in this line, Li et al. [100] examine cold tolerance in a mangrove species (*Kandelia obovata*) by comparing a reference cold-sensitive population and its transplanted counterpart to higher-latitude environments, revealing adaptive responses in a coastal woody plant under novel climatic conditions. The authors perform RNA-seq, differential expression analysis, SNP identification, and transcription factor prediction to identify DEGs under chilling stress. Their analyses reveal the enrichment of pathways related to phenylpropanoid biosynthesis, carbohydrate metabolism, and plant hormone signaling, alongside the differential regulation of key transcription factor families such as NAC, MYB, WRKY, and ERF [101–104], all of which are central to stress signaling networks. The work highlights that both genetic and post-transcriptional mechanisms underlie cold adaptation. Integrating experimental *in situ* population surveys with transcriptomic and functional analyses enables an understanding of how perennial species rely on regulatory strategies to expand their ecological niche, complementing the genomic basis of stress tolerance in non-model systems and reinforcing the importance of leveraging ecologically relevant germplasm for conservation and restoration under shifting temperature regimes.

Natural populations offer not only reservoirs of biodiversity, but also repositories of adaptive potential shaped by local environmental pressures [55]. Merging multi-omics screenings [105] with ecological and geographic metadata allows for the identification and mobilization of standing adaptive variation as part of conservation, restoration, and assisted adaptation strategies [106]. All compiled efforts (Table 1) deepen our understanding of the evolutionary genomic basis of local adaptation, while providing applied tools for conserving the genetic diversity that underlies abiotic stress tolerance, maintaining ecosystem resilience, and guiding targeted interventions under shifting climatic regimes.

Table 1. Synthesis of the nine contributing studies to the Special Issue “Abiotic Stress Tolerance and Genetic Diversity in Plants” in its second edition. The table is ordered as per the narrative. Abbreviations: DEGs stand for differentially expressed genes, others are already declared within the table.

Species Group	Study Goal	Sampling	Omics Technologies	Key Findings	Reference
Cultivated alfalfa (<i>Medicago sativa</i>) & its wild relative (<i>Medicago falcata</i>)	Assess cold tolerance mechanisms in cultivated and wild seedlings	Expression screening 24 h and 120 h after low-temperature (4 °C)	RNA-seq	Wild <i>M. falcata</i> has broader transcriptional response with more DEGs	Wong et al. [33]
Soybean (<i>Glycine max</i>)	Validate three iron deficiency response genes (i.e., FIT, HY5 and PYE)	Iron-deficit-tolerant Swedish line Fiskeby III (PI 438471)	Virus-induced gene silencing and RNA-seq	Silencing FIT and HY5 does not compromise iron deficiency tolerance	O’Rourke and Graham [40]
Rice (<i>Oryza sativa</i>)	Dissect the molecular bases of salinity tolerance in rice	Salt-tolerant Thai variety ‘Jao Khao’	RNA-seq libraries sampled across six time points (0–48 h)	A total of 1950 variable and 111 hub genes linked with the salt tolerance	Khunsanit et al. [41]
Chinese kale (<i>Brassica oleracea</i> L. var. <i>alboglabra</i>)	Characterize abiotic stress response of FCS-like zinc finger (FLZ) genes	Chinese kale (<i>B. oleracea</i>), cabbage (<i>B. rapa</i>) and black mustard (<i>B. nigra</i>)	Phylogenomic, expression analyses, and protein–protein assays	FLZ proteins interact with central energy-sensing kinases (SnRK1)	Zhao et al. [42]
Rice (<i>Oryza sativa</i>)	Study variation in the sodium transporter <i>OsHKT1;1</i> for salt tolerance	Two splicing variants across three heterologous systems	Subcellular localization and expression analyses	Splicing variants differ in ion selectivity and transport efficiency	Imran et al. [56]
Alfalfa (<i>Medicago sativa</i>)	Review CRISPR/Cas in alfalfa for abiotic stress tolerance	Literature review	Genomics and transcriptomics	Systems-level genome editing benefits abiotic stress tolerance	Fan et al. [57]
Barley (<i>Hordeum vulgare</i>)	Reconstruct the genomic bases of plasticity to drought stress	Genotypes (1277) evaluated under well-watered vs. drought conditions	Five plasticity indices and four genome-wide association study (GWAS)	Drought stress plasticity is genetically and environment-dependent	Arenas and Cortés [86]
Rice (<i>Oryza sativa</i>)	Validate two genes (<i>OsJRL45</i> and <i>OsJRL40</i>) for salt stress tolerance	Salt stress-adapted “Sea Rice 86” and recombinant inbred lines (RILs)	RT-qPCR, yeast two-hybrid and bimolecular fluorescence	Marker-assisted introgression in RILs enhances salt tolerance	Yin et al. [88]
Mangrove (<i>Kandelia obovata</i>)	Examine cold tolerance in a cold-sensitive mangrove species	Cold-sensitive population transplanted to higher-latitude climates	RNA-seq	Genetic and post-transcriptional mechanisms underlie cold adaptation	Li et al. [100]

5. Perspectives

Taken together, the contributed studies on abiotic stress tolerance in plants reveal that the field is advancing rapidly in technical capacity but still grappling with conceptual, translational [107], and cross-disciplinary challenges [108,109]. A major persistent gap is the scale mismatch between molecular network discovery and ecological deployment. While transcriptomic experimental studies with moderate sample sizes provide high-resolution temporal snapshots of molecular stress responses, they capture only a fraction of the environmental variability experienced in the field. On the other hand, observational population-level analyses on hundreds and thousands of genotypes disclose complex genotype-by-environment interactions that are difficult to reconcile with epigenetic screening under controlled conditions. Bridging these scales together under the same lens would require experimental designs that integrate controlled setups with field-based validation [110] across environmental gradients [111,112] (Figure 1).

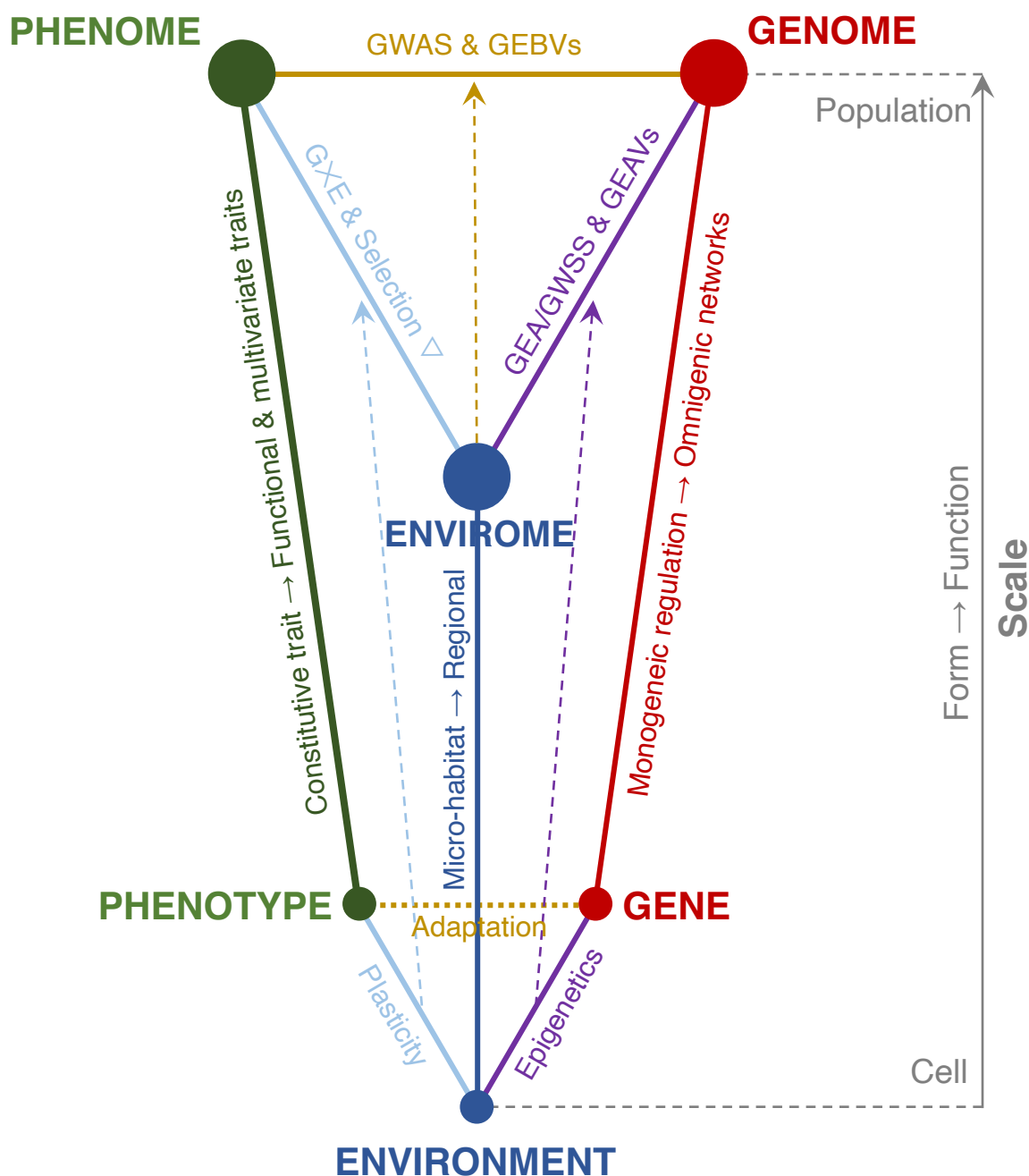


Figure 1. Conceptual framework depicting a tridimensional plant breeding triangle projected across spatial scales to leverage genetic diversity for abiotic stress tolerance under climate change. The diagram

links the environment in which the plant experiences abiotic stress, the phenotypic variation that shapes tolerance, and the corresponding standing genetic variation enabling such plant responses. Together, these axes contextualize how environment–genotype–phenotype relationships interplay across spatial scales. The vertical dimension represents biological spatial organization, spanning from micro-habitats to regional climatic gradients for the environmental axis, from cellular monogenic processes to population-level polygenic dynamics for the genetic axis, and from a single constitutive trait to multivariate functional traits for the phenotypic axis. For instance, (i) the abstraction of the environment is no longer a discretization into few localities and climatic variables, but instead is currently acknowledging its continuum nature across space and environmental layers (i.e., envirome) through the enviromics paradigm. Similarly, (ii) at the molecular level, the transition from a monogenic understating to omnigenic regulatory networks implies that abiotic stress responses are now being recognized as governed by complex, interconnected gene systems rather than single major-effect loci, yet identifying some of the latter are still necessary for more targeted gene editing and biotechnological applications. The more complex poly/omnigenic level can jointly be attributed to coding variation, regulatory elements, and epigenetic modifications, as well as post-transcriptional processes such as alternative splicing, all of which account for the missing heritability of the more monogenic models. These molecular interactions collectively define the functional genome, which interacts with environmental stresses and the envirome to regulate a cascade of transcriptional and metabolic responses with implications on the tolerant phenotype. Finally, moving upward in scale, (iii) the phenomic axis depicts a continuum from constitutive traits to complex multivariate phenotypes that integrate developmental, physiological, and morphological functional responses. Such phenomic responses are shaped by phenotypic plasticity and genotype-by-environment ($G \times E$) interactions, with the first mediating short-term acclimation through transgenerational epigenic inheritance and the second contributing to long-term adaptive potential, all of which serve as conceptual processes linking phenotype and environment (i.e., plasticity), phenotype and genotype (i.e., adaptation), and genotype and environment (i.e., epigenic responses). The framework also invites incorporating technical approaches and models borrowed from the plant breeding and eco-evolutionary disciplines capable of helping integrate all three axes. Specifically, analytical techniques such as genome-wide association studies (GWASs), genome–environment associations (GEAs), genome-wide selection scans (GWSSs), and genomic prediction and its corresponding genomic estimated breeding (GEBVs) and adaptive (GEAVs) values, enable the genomic architecture of stress tolerance (i.e., GWAS as a bridge between the phenotypic and genomic axes) and polygenic adaptation (i.e., GEA, GWSS and GEAVs as a link between the environmental and genomic axes) to be dissected and utilized to forecast climate change responses (i.e., GEBVs and GEAVs, respectively linking the phenotypic and environmental axes with the genetic axis). The cutting-edge integration of these approaches not only allow allelic variants and genomic regions associated with both functional trait performance and environmental adaptation to be identified, but also facilitate their deployment into pre-breeding and conservation programs. In parallel, the environmental filtering of functional phenotypes through natural and artificial selection can be assessed respectively using selection gradient and $G \times E$ analyses, unifying the phenomic and environmental dimensions. Last, the bidirectional feedback among phenotype, genotype, and environment reinforces the fact that adaptive responses to abiotic stresses are not solely a function of genetic determinants, but also of context-dependent expression and ecological interactions. This reflects the shift to a systems-level multi-dimensional understanding of abiotic stress tolerance, advocating for the integration of multi-omics data (e.g., genomics, transcriptomics, phenomics, and enviromics) with theoretical developments from the ecological, evolutionary, and plant breeding fields. More importantly, by bridging scales (from genes to ecosystems) and processes (from molecular function to population adaptation), the roadmap offers a valuable guideline to harness cryptic genetic diversity for abiotic stress tolerance under rapid climate change in both crops and natural plant populations.

A second challenge lies in the fragmentation of multi-omics data. While individual studies employ transcriptomics, GWASs, or functional assays, few integrate these layers into cohesive predictive models. For example, candidate SNPs derived from GWAS models are not always directly linked to expression profiles or metabolic pathways, limiting their interpretability [113,114]. Similarly, so far, efforts to utilize transcriptomic signatures into predictive breeding frameworks are scarce. This dichotomy translates into a conceptual tension between reductionist and systems-level functional studies, which together would provide mechanistic clarity at the level of individual gene families and metabolic pathways, and population genomics assessments, capable of revealing highly polygenic environmental-dependent architectures. Reconciling these paradigms requires moving toward omnigenic reconstructions and network-based functional validation [115], where multiple genes and pathways are accounted for simultaneously. Merging multi-omics [116] and environmental data, across spatial, temporal and evolutionary scales [117,118], is now being assisted by machine learning and systems biology workflows [119–122].

Meanwhile, the compiled studies report a persistent underutilization of secondary gene pools, wild resources, and marginal populations, which are the ones more likely to harbor allelic variation useful for abiotic stress tolerance after thousands of years of co-evolution with local pressures. The richness of adaptive variation outside elite germplasm remains unattractable for most pre-breeding programs, not to mention conservation and reforestation efforts, most likely due to difficulties in assessing and accessing the adapted variants and divergent complex epistatic fitness architectures that preclude their direct trade-off-free use [123]. Therefore, approaches such as genomic-guided introgression and assisted gene flow must be scaled up to fully exploit these resources, together with translational societal efforts to increase adoption [107] and communitarian involvement [124].

Additionally, although genome editing has transformative potential, its scalation to complex traits remains limited. At the moment, while editing single genes is feasible, manipulating entire polygenic architectures is still a bottleneck. Future efforts must therefore focus on multiplex editing and regulatory network bioengineering [125], potentially targeting transcription factor hubs. Last, acknowledging that plasticity is not only environmentally modulated but also genetically controlled [126] is reshaping it as a breeding target, enabling plant improvement to utilize plastic and adaptive responses [87] as part of the nascent enviromics paradigm [127–136], enhancing resilience under variable climates.

6. Conclusions

This Special Issue reinforces the fact that abiotic stress tolerance is governed by complex regulatory networks across highly polygenic and environmentally dependent architectures, which cannot be fully captured through single-layer or reductionist approaches. Instead, boosting plant resilience would require integrating cryptic genetic variation, transcriptional regulation, alternative splicing patterns, and genotype-by-environment interaction across spatial and temporal scales. Moving forward, a key priority would be to integrate multi-omics datasets—including genomics, transcriptomics, phenomics, and environmental covariates—into more unified, predictive frameworks capable of linking causal variants to system-level phenotypes under heterogeneous, and even simultaneous, abiotic stresses. Achieving this integration will require advances in network inference and machine learning, and particularly joint experimental designs that explicitly couple controlled functional assays with population-level validation across environmental gradients. Scaling the utilization of exotic germplasm through genomic-enabled introgression, multi-target genetic editing, and assisted gene flow will help mobilizing standing adaptation from the wild. Abiotic stress resilience can no longer be harnessed through discrete gene targets, but requires rethinking it as interconnected omnigenic regulatory networks embedded within evolving populations and ecosystems.

Funding: The working time of the Guest Editor for the second edition of the Special Issue “Abiotic Stress Tolerance and Genetic Diversity in Plants” has been kindly sponsored by the Swedish Research Council (VR’s grants 2016-00418/2022-04411) and the Royal Swedish Academy of Sciences (KVA’s grant BS2017-003).

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: All contributing articles to the Special Issue “Abiotic Stress Tolerance and Genetic Diversity in Plants”, second edition, are available here <https://www.mdpi.com/si/ijms/9Y8E57B7V3> as accessed on 24 April 2026.

Acknowledgments: This second edition of the Special Issue on “Abiotic Stress Tolerance and Genetic Diversity in Plants” would not have been possible without the interest and effort of all authors and reviewers.

Conflicts of Interest: The author declare no conflicts of interest.

References

- Hultgren, A.; Carleton, T.; Delgado, M.; Gergel, D.R.; Greenstone, M.; Houser, T.; Hsiang, S.; Jina, A.; Kopp, R.E.; Malevich, S.B.; et al. Impacts of climate change on global agriculture accounting for adaptation. *Nature* **2025**, *642*, 644–652. [\[CrossRef\]](#)
- Merchuk-Ovnat, L.; Silberman, R.; Laiba, E.; Maurer, A.; Pillen, K.; Faigenboim, A.; Fridman, E. Genome scan identifies flowering-independent effects of barley HsDry2.2 locus on yield traits under water deficit. *J. Exp. Bot.* **2018**, *69*, 1765–1779. [\[CrossRef\]](#) [\[PubMed\]](#)
- Leon-Garcia, I.V.; Lasso, E. High heat tolerance in plants from the Andean highlands: Implications for paramos in a warmer world. *PLoS ONE* **2019**, *14*, e0224218. [\[CrossRef\]](#)
- Gottfried, M.; Pauli, H.; Futschik, A.; Akhalkatsi, M.; Barančok, P.; Benito Alonso, J.L.; Coldea, G.; Dick, J.; Erschbamer, B.; Fernández Calzado, M.A.R.; et al. Continent-wide response of mountain vegetation to climate change. *Nat. Clim. Change* **2012**, *2*, 111–115. [\[CrossRef\]](#)
- Rumpf, S.B.; Hulber, K.; Klöner, G.; Moser, D.; Schutz, M.; Wessely, J.; Willner, W.; Zimmermann, N.E.; Dullinger, S. Range dynamics of mountain plants decrease with elevation. *Proc. Natl. Acad. Sci. USA* **2018**, *115*, 1848–1853. [\[CrossRef\]](#)
- Fragata, I.; Lopes-Cunha, M.; Barbaro, M.; Kellen, B.; Lima, M.; Santos, M.A.; Faria, G.S.; Santos, M.; Matos, M.; Simoes, P. How much can history constrain adaptive evolution? A real-time evolutionary approach of inversion polymorphisms in *Drosophila subobscura*. *J. Evol. Biol.* **2014**, *27*, 2727–2738. [\[CrossRef\]](#)
- Chala, D.; Brochmann, C.; Psomas, A.; Ehrich, D.; Gizaw, A.; Masao, C.A.; Bakkestuen, V.; Zimmermann, N.E. Good-bye to tropical alpine plant giants under warmer climates? Loss of range and genetic diversity in *Lobelia rhynchopetalum*. *Ecol. Evol.* **2016**, *6*, 8931–8941. [\[CrossRef\]](#)
- Valladares, F.; Matesanz, S.; Guilhaumon, F.; Araujo, M.B.; Balaguer, L.; Benito-Garzon, M.; Cornwell, W.; Gianoli, E.; van Kleunen, M.; Naya, D.E.; et al. The effects of phenotypic plasticity and local adaptation on forecasts of species range shifts under climate change. *Ecol. Lett.* **2014**, *17*, 1351–1364. [\[CrossRef\]](#)
- Gutaker, R.M.; Purugganan, M.D. Adaptation and the Geographic Spread of Crop Species. *Annu. Rev. Plant Biol.* **2023**, *75*, 679–706. [\[CrossRef\]](#)
- Varshney, R.K.; Barmukh, R.; Roorkiwal, M.; Qi, Y.; Kholova, J.; Tuberosa, R.; Reynolds, M.P.; Tardieu, F.; Siddique, K.H.M. Breeding custom-designed crops for improved drought adaptation. *Adv. Genet.* **2021**, *2*, e202100017. [\[CrossRef\]](#)
- Migicovsky, Z. Genomic resources for crop wild relatives are critical for perennial fruit breeding and conservation. *Am. J. Bot.* **2025**, *112*, e70068. [\[CrossRef\]](#)
- Gomez-Fernandez, A. Reconstructing the evolutionary history of herbaceous crops through trait-based ecology. *Am. J. Bot.* **2025**, *112*, e70107. [\[CrossRef\]](#)
- Branch, H.A. The sleeping giant needs coffee: Overlooked areas for integrating plant ecophysiology and evolutionary biology. *Am. J. Bot.* **2026**, *113*, e70164. [\[CrossRef\]](#) [\[PubMed\]](#)
- Cortinovis, G.; Di Vittori, V.; Bellucci, E.; Bitocchi, E.; Papa, R. Adaptation to novel environments during crop diversification. *Curr. Opin. Plant Biol.* **2020**, *56*, 203–217. [\[CrossRef\]](#)
- Kristensen, T.N.; Ketola, T.; Kronholm, I. Adaptation to environmental stress at different timescales. *Ann. N. Y. Acad. Sci.* **2018**, *1476*, 5–22. [\[CrossRef\]](#)
- Cortés, A.J. Abiotic Stress Tolerance Boosted by Genetic Diversity in Plants. *Int. J. Mol. Sci.* **2024**, *25*, 5367. [\[CrossRef\]](#)

17. Razgour, O.; Forester, B.; Taggart, J.B.; Bekaert, M.; Juste, J.; Ibanez, C.; Puechmaille, S.J.; Novella-Fernandez, R.; Alberdi, A.; Manel, S. Considering adaptive genetic variation in climate change vulnerability assessment reduces species range loss projections. *Proc. Natl. Acad. Sci. USA* **2019**, *116*, 10418–10423. [\[CrossRef\]](#)
18. Ibáñez, I.; Primack, R.B.; Miller-Rushing, A.J.; Ellwood, E.; Higuchi, H.; Lee, S.D.; Kobori, H.; Silander, J.A. Forecasting phenology under global warming. *Philos. Trans. R. Soc. B Biol. Sci.* **2010**, *365*, 3247–3260.
19. Cotto, O.; Wessely, J.; Georges, D.; Klonner, G.; Schmid, M.; Dullinger, S.; Thuiller, W.; Guillaume, F. A dynamic eco-evolutionary model predicts slow response of alpine plants to climate warming. *Nat. Commun.* **2017**, *8*, 15399. [\[CrossRef\]](#) [\[PubMed\]](#)
20. Jay, F.; Manel, S.; Alvarez, N.; Durand, E.Y.; Thuiller, W.; Holderegger, R.; Taberlet, P.; François, O. Forecasting changes in population genetic structure of alpine plants in response to global warming. *Mol. Ecol.* **2012**, *21*, 2354–2368. [\[CrossRef\]](#) [\[PubMed\]](#)
21. Botkin, D.B.; Saxe, H.; Araújo, M.B.; Betts, R.; Bradshaw, R.H.W.; Cedhagen, T.; Chesson, P.; Dawson, T.P.; Etterson, J.R.; Faith, D.P.; et al. Forecasting the Effects of Global Warming on Biodiversity. *BioScience* **2007**, *57*, 227–236. [\[CrossRef\]](#)
22. Cortés, A.J.; López-Hernández, F.; Blair, M.W. Crop Modeling for Future Climate Change Adaptation. In *Digital Agriculture: A Solution for Sustainable Food and Nutritional Security*; Priyadarshan, P.M., Jain, S.M., Suprasanna, P., Al-Khayri, J.M., Eds.; Springer International Publishing: Cham, Switzerland, 2024; pp. 625–639.
23. Barghi, N.; Hermisson, J.; Schlötterer, C. Polygenic adaptation: A unifying framework to understand positive selection. *Nat. Rev. Genet.* **2020**, *21*, 769–781. [\[CrossRef\]](#)
24. Peng, B.; Guan, K.; Tang, J.; Ainsworth, E.A.; Asseng, S.; Bernacchi, C.J.; Cooper, M.; Delucia, E.H.; Elliott, J.W.; Ewert, F.; et al. Towards a multiscale crop modelling framework for climate change adaptation assessment. *Nat. Plants* **2020**, *6*, 338–348. [\[CrossRef\]](#)
25. Benitez-Alfonso, Y.; Soanes, B.K.; Zimba, S.; Sinanaj, B.; German, L.; Sharma, V.; Bohra, A.; Kolesnikova, A.; Dunn, J.A.; Martin, A.C.; et al. Enhancing climate change resilience in agricultural crops. *Curr. Biol.* **2023**, *33*, R1246–R1261. [\[CrossRef\]](#) [\[PubMed\]](#)
26. Cortés, A.J.; Cornille, A.; Yockteng, R. Evolutionary Genetics of Crop-Wild Complexes. *Genes* **2022**, *13*, 1. [\[CrossRef\]](#)
27. Weigel, D.; Nordborg, M. Population Genomics for Understanding Adaptation in Wild Plant Species. *Annu. Rev. Genet.* **2015**, *49*, 315–338. [\[CrossRef\]](#) [\[PubMed\]](#)
28. Castaneda-Alvarez, N.P.; Khoury, C.K.; Achicanoy, H.A.; Bernau, V.; Dempewolf, H.; Eastwood, R.J.; Guarino, L.; Harker, R.H.; Jarvis, A.; Maxted, N.; et al. Global conservation priorities for crop wild relatives. *Nat. Plants* **2016**, *2*, 16022. [\[CrossRef\]](#)
29. Cortés, A.J.; Barnaby, J.Y. Editorial: Harnessing genebanks: High-throughput phenotyping and genotyping of crop wild relatives and landraces. *Front. Plant Sci.* **2023**, *14*, 1149469. [\[CrossRef\]](#) [\[PubMed\]](#)
30. Parmesan, C.; Hanley, M.E. Plants and climate change: Complexities and surprises. *Ann. Bot.* **2015**, *116*, 849–864. [\[CrossRef\]](#)
31. Alsos, I.G.; Ehrich, D.; Thuiller, W.; Eidesen, P.B.; Tribsch, A.; Schönschetter, P.; Lagaye, C.; Taberlet, P.; Brochmann, C. Genetic consequences of climate change for northern plants. *Proc. R. Soc. B Biol. Sci.* **2012**, *279*, 2042–2051. [\[CrossRef\]](#) [\[PubMed\]](#)
32. Jump, A.S.; Penuelas, J. Running to stand still: Adaptation and the response of plants to rapid climate change. *Ecol. Lett.* **2005**, *8*, 1010–1020. [\[CrossRef\]](#) [\[PubMed\]](#)
33. Wang, Q.; Wu, J.; Di, G.; Zhao, Q.; Gao, C.; Zhang, D.; Wang, J.; Shen, Z.; Han, W. Identification of Cold Tolerance Transcriptional Regulatory Genes in Seedlings of *Medicago sativa* L. and *Medicago falcata* L. *Int. J. Mol. Sci.* **2024**, *25*, 10345. [\[CrossRef\]](#)
34. Mizoi, J.; Shinozakib, K.; Yamaguchi-Shinozaki, K. AP2/ERF family transcription factors in plant abiotic stress responses. *Biochim. Et Biophys. Acta* **2012**, *1819*, 86–96. [\[CrossRef\]](#) [\[PubMed\]](#)
35. Yang, C.-Y.; Hsu, F.-C.; Li, J.-P.; Wang, N.-N.; Shih, M.-C. The AP2/ERF transcription factor AtERF73/HRE1 modulates ethylene responses during hypoxia in *Arabidopsis*. *Plant Physiol.* **2011**, *156*, 202–212. [\[CrossRef\]](#)
36. Qi, W.; Sun, F.; Wang, Q.; Chen, M.; Huang, Y.; Feng, Y.; Luo, X.; Yang, J. Rice ethylene-response AP2/ERF factor OsEATB restricts internode elongation by down-regulating a gibberellin biosynthetic gene. *Plant Physiol.* **2011**, *157*, 216–228. [\[CrossRef\]](#)
37. Yu, Z.X.; Li, J.X.; Yang, C.Q.; Hu, W.L.; Wang, L.J.; Chen, X.Y. The Jasmonate-Responsive AP2/ERF Transcription Factors *AaERF1* and *AaERF2* Positively Regulate Artemisinin Biosynthesis in *Artemisia annua* L. *Mol. Plant* **2011**, *5*, 353–365. [\[CrossRef\]](#) [\[PubMed\]](#)
38. Zhuang, J.; Xiong, A.S.; Peng, R.H.; Gao, F.; Zhu, B.; Zhang, J.A.; Fu, X.Y.; Jin, X.F.; Chen, J.M.; Zhang, Z.; et al. Analysis of Brassica rapa ESTs: Gene discovery and expression patterns of AP2/ERF family genes. *Mol. Biol. Rep.* **2010**, *37*, 2485–2492. [\[CrossRef\]](#)
39. Licausi, F.; Giorgi, F.M.; Zenoni, S.; Osti, F.; Pezzotti, M.; Perata, P. Genomic and transcriptomic analysis of the AP2/ERF superfamily in *Vitis vinifera*. *BMC Genom.* **2010**, *11*, 719. [\[CrossRef\]](#)
40. O'Rourke, J.A.; Graham, M.A. Investigating the Role of Known Arabidopsis Iron Genes in a Stress Resilient Soybean Line. *Int. J. Mol. Sci.* **2024**, *25*, 11480. [\[CrossRef\]](#)
41. Khunsanit, P.; Plaimas, K.; Chadchawan, S.; Buaboocha, T. Profiling of Key Hub Genes Using a Two-State Weighted Gene Co-Expression Network of 'Jao Khao' Rice under Soil Salinity Stress Based on Time-Series Transcriptome Data. *Int. J. Mol. Sci.* **2024**, *25*, 11086. [\[CrossRef\]](#) [\[PubMed\]](#)
42. Zhao, Y.; Chen, S.; Qin, M.; Shui, K.; Li, R.; Yang, B.; Liu, J.; Chen, Z. Genome-Wide Identification of FCS-Like Zinc Finger (FLZ) Family Genes in Three Brassica Plant Species and Functional Characterization of *BolFLZs* in Chinese Kale Under Abiotic Stresses. *Int. J. Mol. Sci.* **2024**, *25*, 12907. [\[CrossRef\]](#)

43. López-Hernández, F.; Roda, F.; Cortés, A.J. Machine Learning and Pangenomics: Revolutionizing Plant Breeding for a Sustainable Future. In *Plant Breeding 2050*; Priyadarshan, P.M., Ortiz, R., Eds.; Springer: Singapore, 2025; pp. 509–523.
44. Reichstein, M.; Bahn, M.; Mahecha, M.D.; Kattge, J.; Baldocchi, D.D. Linking plant and ecosystem functional biogeography. *Proc. Natl. Acad. Sci. USA* **2014**, *111*, 13697–13702. [[CrossRef](#)]
45. Zhao, X.; Han, X.; Lu, X.; Yang, H.; Wang, Z.Y.; Chai, M. Genome-Wide Identification and Characterization of the Msr Gene Family in Alfalfa under Abiotic Stress. *Int. J. Mol. Sci.* **2023**, *24*, 9638. [[CrossRef](#)]
46. Wang, H.; Yu, J.; Zhu, B.; Gu, L.; Wang, H.; Du, X.; Zeng, T.; Tang, H. The SbbHLH041-SbEXPA11 Module Enhances Cadmium Accumulation and Rescues Biomass by Increasing Photosynthetic Efficiency in Sorghum. *Int. J. Mol. Sci.* **2023**, *24*, 13061. [[CrossRef](#)]
47. Huang, X.; Qiu, X.; Wang, Y.; Abubakar, A.S.; Chen, P.; Chen, J.; Chen, K.; Yu, C.; Wang, X.; Gao, G.; et al. Genome-Wide Investigation of the NAC Transcription Factor Family in *Apocynum venetum* Revealed Their Synergistic Roles in Abiotic Stress Response and Trehalose Metabolism. *Int. J. Mol. Sci.* **2023**, *24*, 4578. [[CrossRef](#)]
48. López-Hernández, F.; Cortés, A.J. Transcriptomic Signatures of Somaclonal Variation. In *Plant Transcriptomics and Epitranscriptomics*; Springer: Singapore, 2026; pp. 135–153.
49. Lembrechts, J.J.; Lenoir, J. Microclimatic conditions anywhere at any time! *Glob. Change Biol.* **2020**, *26*, 337–339. [[CrossRef](#)] [[PubMed](#)]
50. Abdelaziz, M.; Anderson, J.T.; Rochford, M.E.; Bemmels, J.B.; Jameel, M.I.; Denney, D.A. Small spaces, big impacts: Contributions of micro-environmental variation to population persistence under climate change. *AoB Plants* **2020**, *12*, plaa005. [[CrossRef](#)]
51. Du, H.; Liang, Z.; Cortés, A.J. Editorial: Evolution of crop genomes and epigenomes, volume II. *Front. Plant Sci.* **2025**, *16*, 1623554. [[CrossRef](#)]
52. Cortés, A.J. Unlocking genebanks for climate adaptation. *Nat. Clim. Change* **2025**, *15*, 590–592. [[CrossRef](#)]
53. Myburg, A.A.; Hussey, S.G.; Wang, J.P.; Street, N.R.; Mizrahi, E. Systems and Synthetic Biology of Forest Trees: A Bioengineering Paradigm for Woody Biomass Feedstocks. *Front. Plant Sci.* **2019**, *10*, 775. [[CrossRef](#)] [[PubMed](#)]
54. Ma, Y.; Zhong, M.; Li, J.; Jiang, Y.; Zhou, X.; Justice Ijeoma, C.; Tang, X.; Chen, S.; Cao, S. Genome Identification and Evolutionary Analysis of LBD Genes and Response to Environmental Factors in *Phoebe bournei*. *Int. J. Mol. Sci.* **2023**, *24*, 12581. [[CrossRef](#)]
55. Bohra, A.; Kilian, B.; Sivasankar, S.; Caccamo, M.; Mba, C.; McCouch, S.R.; Varshney, R.K. Reap the crop wild relatives for breeding future crops. *Trends Biotechnol.* **2021**, *40*, 412–431. [[CrossRef](#)]
56. Imran, S.; Ono, S.; Horie, R.; Katsuhara, M.; Horie, T. Chloride-Transporting OsHKT1;1 Splice Variants and Their Expression Profiles Under Salinity Stress in Rice. *Int. J. Mol. Sci.* **2026**, *27*, 1178. [[CrossRef](#)]
57. Fan, S.; Jia, L.; Wu, J.; Zhao, Y. Harnessing the Potential of CRISPR/Cas in Targeted Alfalfa Improvement for Stress Resilience. *Int. J. Mol. Sci.* **2025**, *26*, 3311. [[CrossRef](#)] [[PubMed](#)]
58. Doudna, J.A.; Charpentier, E. Genome editing. The new frontier of genome engineering with CRISPR-Cas9. *Science* **2014**, *346*, 1258096. [[CrossRef](#)] [[PubMed](#)]
59. Rodríguez-Leal, D.; Lemmon, Z.H.; Man, J.; Bartlett, M.E.; Lippman, Z.B. Engineering Quantitative Trait Variation for Crop Improvement by Genome Editing. *Cell* **2017**, *171*, 470–480.e478. [[CrossRef](#)] [[PubMed](#)]
60. Barrero, L.S.; Willmann, M.R.; Craft, E.J.; Akther, K.M.; Harrington, S.E.; Garzon-Martinez, G.A.; Glahn, R.P.; Piñeros, M.A.; McCouch, S.R. Identifying genes associated with abiotic stress tolerance suitable for CRISPR/Cas9 editing in upland rice cultivars adapted to acid soils. *Plant Direct* **2022**, *6*, e469. [[CrossRef](#)]
61. Li, R.; Liu, C.; Zhao, R.; Wang, L.; Chen, L.; Yu, W.; Zhang, S.; Sheng, J.; Shen, L. CRISPR/Cas9-Mediated *SINPR1* mutagenesis reduces tomato plant drought tolerance. *BMC Plant Biol.* **2019**, *19*, 38. [[CrossRef](#)]
62. Wang, L.; Chen, L.; Li, R.; Zhao, R.; Yang, M.; Sheng, J.; Shen, L. Reduced Drought Tolerance by CRISPR/Cas9-Mediated SIMAPK3 Mutagenesis in Tomato Plants. *J. Agric. Food Chem.* **2017**, *65*, 8674–8682. [[CrossRef](#)]
63. Robinson, J.M.; Hodgson, R.; Krauss, S.L.; Liddicoat, C.; Malik, A.A.; Martin, B.C.; Mohr, J.J.; Moreno-Mateos, D.; Munoz-Rojas, M.; Peddle, S.D.; et al. Opportunities and challenges for microbiomics in ecosystem restoration. *Trends Ecol. Evol.* **2023**, *38*, 1189–1202. [[CrossRef](#)]
64. Park, D.S.; Willis, C.G.; Xi, Z.; Kartesz, J.T.; Davis, C.C.; Worthington, S. Machine Learning Predicts Large Scale Declines in Native Plant Phylogenetic Diversity. *New Phytol.* **2020**, *227*, 1544–1556. [[CrossRef](#)]
65. Guo, H.; Nie, C.Y.; Li, Z.; Kang, J.; Wang, X.L.; Cui, Y.N. Physiological and Transcriptional Analyses Provide Insight into Maintaining Ion Homeostasis of Sweet Sorghum under Salt Stress. *Int. J. Mol. Sci.* **2023**, *24*, 11045. [[CrossRef](#)] [[PubMed](#)]
66. Wirojsirasak, W.; Songsri, P.; Jongrunklang, N.; Tangphatsornruang, S.; Klomsa-Ard, P.; Ukoskit, K. A Large-Scale Candidate-Gene Association Mapping for Drought Tolerance and Agronomic Traits in Sugarcane. *Int. J. Mol. Sci.* **2023**, *24*, 12801. [[CrossRef](#)]
67. Ravelombola, W.; Dong, L.; Barickman, T.C.; Xiong, H.; Manley, A.; Cason, J.; Pham, H.; Zia, B.; Mou, B.; Shi, A. Genetic Architecture of Salt Tolerance in Cowpea (*Vigna unguiculata* (L.) Walp.) at Seedling Stage Using a Whole Genome Resequencing Approach. *Int. J. Mol. Sci.* **2023**, *24*, 15281. [[CrossRef](#)]

68. Brautigam, K.; Vining, K.J.; Lafon-Placette, C.; Fossdal, C.G.; Mirouze, M.; Marcos, J.G.; Fluch, S.; Fraga, M.F.; Guevara, M.A.; Abarca, D.; et al. Epigenetic regulation of adaptive responses of forest tree species to the environment. *Ecol. Evol.* **2013**, *3*, 399–415. [\[CrossRef\]](#)
69. Parra-Londono, S.; López-Hernández, F.; Montoya, G.; Henao-Rojas, J.C.; Ossa-Ossa, G.A.; Cortés, A.J. Merging Phenotypic Stability Analysis and Genomic Prediction for Multi-Environment Breeding in *Capsicum* spp. *Agronomy* **2025**, *15*, 2690. [\[CrossRef\]](#)
70. López-Hernández, F.; Burbano-Erazo, E.; León-Pacheco, R.I.; Cordero-Cordero, C.C.; Villanueva-Mejía, D.F.; Tofiño-Rivera, A.P.; Cortés, A.J. Multi-Environment Genome-Wide Association Studies of Yield Traits in Common Bean (*Phaseolus vulgaris* L.) × Tepary Bean (*P. acutifolius* A. Gray) Interspecific Advanced Lines in Humid and Dry Colombian Caribbean Subregions. *Agronomy* **2023**, *13*, 1396. [\[CrossRef\]](#)
71. Arnold, P.A.; Kruuk, L.E.B.; Nicotra, A.B. How to analyse plant phenotypic plasticity in response to a changing climate. *New Phytol.* **2019**, *222*, 1235–1241. [\[CrossRef\]](#)
72. Tognetti, R. Adaptation to climate change of dioecious plants: Does gender balance matter? *Tree Physiol.* **2012**, *32*, 1321–1324. [\[CrossRef\]](#)
73. Chuine, I. Why does phenology drive species distribution? *Philos. Trans. R. Soc. Lond. B Biol. Sci.* **2010**, *365*, 3149–3160. [\[CrossRef\]](#) [\[PubMed\]](#)
74. Valladares, F.; Niinemets, U. Shade Tolerance, a Key Plant Feature of Complex Nature and Consequences. *Annu. Rev. Ecol. Evol. Syst.* **2008**, *39*, 237–257. [\[CrossRef\]](#)
75. Franks, S.J.; Weis, A.E. A change in climate causes rapid evolution of multiple life-history traits and their interactions in an annual plant. *J. Evol. Biol.* **2008**, *21*, 1321–1334. [\[CrossRef\]](#)
76. Bai, X.; Qiao, P.; Liu, H.; Shang, Y.; Guo, J.; Dai, K. Genome-wide identification of the E-class gene family in wheat: Evolution, expression, and interaction. *Front. Plant Sci.* **2024**, *15*, 1419437. [\[CrossRef\]](#)
77. Jezkova, T.; Wiens, J.J. Rates of change in climatic niches in plant and animal populations are much slower than projected climate change. *Proc. Biol. Sci.* **2016**, *283*, 20162104. [\[CrossRef\]](#)
78. Franks, S.J.; Weis, A.E. Climate change alters reproductive isolation and potential gene flow in an annual plant. *Evol. Appl.* **2009**, *2*, 481–488. [\[CrossRef\]](#)
79. Bedoya-Londoño, S.; Cañas-Gutiérrez, G.P.; Cortés, A.J. Breeding Without Breeding: Enabling Indirect Selection Schemes for Tropical Tree Improvement. In *Genomics Based Approaches for Tropical Tree Improvement and Conservation*; Springer: Singapore, 2025; pp. 19–42.
80. Arenas, S.; Cortés, A.J.; Jaramillo-Correa, J.P. Toward a Genomic-Enabled Selection in Natural Tree Populations for Long-Term Management and Conservation. In *Genomics Based Approaches for Tropical Tree Improvement and Conservation*; Springer: Singapore, 2025; pp. 243–278.
81. Lachmuth, S.; Capblancq, T.; Keller, S.; Fitzpatrick, M. Assessing uncertainty in genomic offset forecasts from landscape genomic models (and implications for restoration and assisted migration). *Front. Ecol. Evol.* **2023**, *11*, 1155783. [\[CrossRef\]](#)
82. López-Hernández, F.; Villanueva-Mejía, D.F.; Tofiño-Rivera, A.P.; Cortés, A.J. Genomic prediction of adaptation in common bean (*Phaseolus vulgaris* L.) × Tepary bean (*P. acutifolius* A. Gray) hybrids. *Int. J. Mol. Sci.* **2025**, *26*, 7370. [\[CrossRef\]](#)
83. Arenas, S.; Djabali, Y.; Rincen, R.; Cubry, P.; Martin, M.L.; Blein-Nicolas, M.; Laplace, L.; Schneider, H.; Grondin, A. Modeling plant phenotypic plasticity and its underlying genetic architecture: A comparative study. *J. Exp. Bot.* **2025**, *76*, 2239–2251. [\[CrossRef\]](#) [\[PubMed\]](#)
84. Reyer, C.P.; Leuzinger, S.; Rammig, A.; Wolf, A.; Bartholomeus, R.P.; Bonfante, A.; de Lorenzi, F.; Dury, M.; Gloning, P.; Abou Jaoude, R.; et al. A plant's perspective of extremes: Terrestrial plant responses to changing climatic variability. *Glob. Change Biol.* **2013**, *19*, 75–89. [\[CrossRef\]](#)
85. Bedoya-Canas, L.E.; López-Hernández, F.; Cortés, A.J. Climate change adaptation of high-elevation *Polylepis* forests. *Forests* **2024**, *15*, 811. [\[CrossRef\]](#)
86. Arenas, S.; Cortés, A.J. Unveiling the Genomic Architecture of Phenotypic Plasticity Using Multiple GWAS Approaches Under Contrasting Conditions of Water Availability: A Model for Barley. *Int. J. Mol. Sci.* **2026**, *27*, 652. [\[CrossRef\]](#)
87. Campbell, Q.; Castañeda-Álvarez, N.; Domingo, R.; Bishop-von Wettberg, E.; Runck, B.; Nandkangré, H.; Halpin-McCormick, A.; Fumia, N.; Neyhart, J.; Kilian, B.; et al. Prioritizing parents from global genebanks to breed climate-resilient crops. *Nat. Clim. Change* **2025**, *15*, 673–681. [\[CrossRef\]](#)
88. Yin, X.; Gao, Q.; Wang, F.; Liu, W.; Luo, Y.; Zhong, S.; Feng, J.; Bai, R.; Chen, L.; Dai, X.; et al. Marker-Assisted Selection of Jacalin-Related Lectin Genes *OsJRL45* and *OsJRL40* Derived from Sea Rice 86 Enhances Salt Tolerance in Rice. *Int. J. Mol. Sci.* **2024**, *25*, 10912. [\[CrossRef\]](#)
89. McCouch, S. Diversifying Selection in Plant Breeding. *PLoS Biol.* **2004**, *2*, 1507–1512. [\[CrossRef\]](#) [\[PubMed\]](#)
90. Lasky, J.R.; Josephs, E.B.; Morris, G.P. Genotype-environment associations to reveal the molecular basis of environmental adaptation. *Plant Cell* **2023**, *35*, 125–138. [\[CrossRef\]](#) [\[PubMed\]](#)

91. López-Hernández, F.; Rosero-Alpala, M.G.; Rosero, A.; Cortés, A.J. Projected Shifts in Colombian Sweet Potato Germplasm Under Climate Change. *Horticulturae* **2025**, *11*, 1080. [\[CrossRef\]](#)
92. Juma, I.; Valencia, J.B.; Cortés, A.J. Predicting Suitable Regions for Avocado (*Persea americana* Mill.) Tree Cultivation in Tanzania. *Horticulturae* **2025**, *12*, 24. [\[CrossRef\]](#)
93. Cañas-Gutierrez, G.P.; López-Hernandez, F.; Cortés, A.J. Whole Genome Resequencing of 205 Avocado Trees Unveils the Genomic Patterns of Racial Divergence in the Americas. *Int. J. Mol. Sci.* **2025**, *26*, 10353. [\[CrossRef\]](#)
94. Cortés, A.J.; Hussein, J.M.; Juma, I. Genomic Diversity of Avocado in the Morogoro Region and Southern Highlands of Tanzania. *Int. J. Mol. Sci.* **2026**, *27*, 3083. [\[CrossRef\]](#) [\[PubMed\]](#)
95. Ramírez-Gil, J.G.; López-Hernandez, F.; Conejo-Rodriguez, D.F.; Henao-Rojas, J.C.; Quiroga-Benavides, K.E.; Cortés, A.J.; Chacón-Sanchez, M.I. GermVersity: A free and user-friendly interface to enhance the visualization and analysis of genebank data. *PLoS ONE* **2026**, *21*, e0340826. [\[CrossRef\]](#)
96. Breed, M.F.; Harrison, P.A.; Blyth, C.; Byrne, M.; Gaget, V.; Gellie, N.J.C.; Groom, S.V.C.; Hodgson, R.; Mills, J.G.; Prowse, T.A.A.; et al. The potential of genomics for restoring ecosystems and biodiversity. *Nat. Rev. Genet.* **2019**, *20*, 615–628. [\[CrossRef\]](#) [\[PubMed\]](#)
97. Aitken, S.N.; Yeaman, S.; Holliday, J.A.; Wang, T.; Curtis-McLane, S. Adaptation, migration or extirpation: Climate change outcomes for tree populations. *Evol. Appl.* **2008**, *1*, 95–111. [\[CrossRef\]](#) [\[PubMed\]](#)
98. Aitken, S.N.; Whitlock, M.C. Assisted Gene Flow to Facilitate Local Adaptation to Climate Change. *Annu. Rev. Ecol. Evol. Syst.* **2013**, *44*, 367–388. [\[CrossRef\]](#)
99. Aitken, S.N.; Bemmels, J.B. Time to get moving: Assisted gene flow of forest trees. *Evol. Appl.* **2016**, *9*, 271–290. [\[CrossRef\]](#)
100. Li, H.; Sun, Z.; Li, W.; Yin, X.; Xu, X.; Zhang, X.; Yan, X.; Wang, X.; Li, Y.; Ma, A. Research on Cold Resistance of *Kandelia obovata* Transplanted to Zhoushan Area at the mRNA Level. *Int. J. Mol. Sci.* **2025**, *27*, 429. [\[CrossRef\]](#)
101. Fick, A.; Swart, V.; Bombarely, A.; van den Berg, N. Comparative transcriptional analysis of *Persea americana* MYB, WRKY and AP2/ERF transcription factors following *Phytophthora cinnamomi* infection. *Mol. Plant Pathol.* **2024**, *25*, e13453. [\[CrossRef\]](#)
102. Seo, P.J.; Lee, S.B.; Suh, M.C.; Park, M.-J.; Go, Y.S.; Park, C.-M. The MYB96 Transcription Factor Regulates Cuticular Wax Biosynthesis under Drought Conditions in *Arabidopsis*. *Plant Cell Online* **2011**, *23*, 1138–1152. [\[CrossRef\]](#)
103. Galbiati, M.; Matus, J.; Francia, P.; Rusconi, F.; Cañón, P.; Medina, C.; Conti, L.; Cominelli, E.; Tonelli, C.; Arce-Johnson, P. The grapevine guard cell-related *VvMYB60* transcription factor is involved in the regulation of stomatal activity and is differentially expressed in response to ABA and osmotic stress. *BMC Plant Biol.* **2011**, *11*, 142. [\[CrossRef\]](#) [\[PubMed\]](#)
104. Mellway, R.D.; Tran, L.T.; Prouse, M.B.; Campbell, M.M.; Constabel, C.P. The Wound-, Pathogen-, and Ultraviolet B-Responsive MYB134 Gene Encodes an R2R3 MYB Transcription Factor That Regulates Proanthocyanidin Synthesis in Poplar. *Plant Physiol.* **2009**, *150*, 924–941. [\[CrossRef\]](#)
105. Cortés, A.J. Omics Technologies in Molecular Biology. *Int. J. Mol. Sci.* **2026**, *27*, 3349. [\[CrossRef\]](#)
106. Cortés, A.J.; Castillejo, M.Á.; Yockteng, R. ‘Omics’ Approaches for Crop Improvement. *Agronomy* **2023**, *13*, 1401. [\[CrossRef\]](#)
107. Kholova, J.; Urban, M.O.; Bavorova, M.; Ceccarelli, S.; Cosmas, L.; Desczka, S.; Grando, S.; Lensink, R.; Nchanji, E.; Pavlik, J.; et al. Promoting new crop cultivars in low-income countries requires a transdisciplinary approach. *Nat. Plants* **2024**, *10*, 1610–1613. [\[CrossRef\]](#)
108. McCouch, S.; Navabi, K.; Abberton, M.; Anglin, N.L.; Barbieri, R.L.; Baum, M.; Bett, K.; Booker, H.; Brown, G.L.; Bryan, G.J.; et al. Mobilizing crop biodiversity. *Mol. Plant* **2020**, *13*, 1341–1344. [\[CrossRef\]](#)
109. Spindel, J.E.; McCouch, S.R. When more is better: How data sharing would accelerate genomic selection of crop plants. *New Phytol.* **2016**, *212*, 814–826. [\[CrossRef\]](#)
110. Khaipho-Burch, M.; Cooper, M.; Crossa, J.; Leon, N.d.; Holland, J.; Lewis, R.; McCouch, S.; Murray, S.C.; Rabbi, I.; Ronald, P.; et al. Scale up trials to validate modified crops’ benefits. *Nature* **2023**, *621*, 470–473. [\[CrossRef\]](#) [\[PubMed\]](#)
111. VanWallendael, A.; Lowry, D.B.; Hamilton, J.A. One hundred years into the study of ecotypes, new advances are being made through large-scale field experiments in perennial plant systems. *Curr. Opin. Plant Biol.* **2022**, *66*, 102152. [\[CrossRef\]](#) [\[PubMed\]](#)
112. Barrett, R.D.H.; Hoekstra, H.E. Molecular spandrels: Tests of adaptation at the genetic level. *Nat. Rev. Genet.* **2011**, *12*, 767–780. [\[CrossRef\]](#)
113. Manolio, T.A.; Collins, F.S.; Cox, N.J.; Goldstein, D.B.; Hindorff, L.A.; Hunter, D.J.; McCarthy, M.I.; Ramos, E.M.; Cardon, L.R.; Chakravarti, A.; et al. Finding the missing heritability of complex diseases. *Nature* **2009**, *461*, 747–753. [\[CrossRef\]](#)
114. Maher, B. The case of the missing heritability. *Nature* **2008**, *456*, 18–21. [\[CrossRef\]](#)
115. Boyle, E.A.; Li, Y.I.; Pritchard, J.K. An Expanded View of Complex Traits: From Polygenic to Omnigenic. *Cell* **2017**, *169*, 1177–1186. [\[CrossRef\]](#)
116. Zavafer, A.; Bates, H.; Mancilla, C.; Ralph, P.J. Phenomics: Conceptualization and importance for plant physiology. *Trends Plant Sci.* **2023**, *28*, 1004–1013. [\[CrossRef\]](#) [\[PubMed\]](#)
117. Feng, J.; Dan, X.; Cui, Y.; Gong, Y.; Peng, M.; Sang, Y.; Ingvarsson, P.K.; Wang, J. Integrating evolutionary genomics of forest trees to inform future tree breeding amid rapid climate change. *Plant Commun.* **2024**, *5*, 101044. [\[CrossRef\]](#) [\[PubMed\]](#)
118. Jaramillo, C.; Rueda, M.J.; Mora, G. Cenozoic plant diversity in the neotropics. *Science* **2006**, *311*, 1893–1896. [\[CrossRef\]](#)

119. Varshney, R.K. The Plant Genome special issue: Advances in genomic selection and application of machine learning in genomic prediction for crop improvement. *Plant Genome* **2021**, *14*, e20178. [[CrossRef](#)]
120. Schrider, D.R.; Kern, A.D. Supervised Machine Learning for Population Genetics: A New Paradigm. *Trends Genet.* **2018**, *34*, 301–312. [[CrossRef](#)]
121. Libbrecht, M.W.; Noble, W.S. Machine learning applications in genetics and genomics. *Nat. Rev. Genet.* **2015**, *16*, 321–332. [[CrossRef](#)]
122. Ma, C.; Zhang, H.H.; Wang, X. Machine learning for Big Data analytics in plants. *Trends Plant Sci.* **2014**, *19*, 798–808. [[CrossRef](#)]
123. Monyak, T.; Morris, G.P. Epistatic fitness landscapes emerge from parallel adaptive walks in breeding network metapopulations. *bioRxiv* **2026**. [[CrossRef](#)]
124. Peláez, D.; Aguilar, P.A.; Mercado, M.; López-Hernández, F.; Guzmán, M.; Burbano-Erazo, E.; Denning-James, K.; Medina, C.I.; Blair, M.W.; De Vega, J.J.; et al. Genotype selection, and seed uniformity and multiplication to ensure common bean (*Phaseolus vulgaris* L.) var. Liborino. *Agronomy* **2022**, *12*, 2285. [[CrossRef](#)]
125. Lemmon, Z.H.; Reem, N.T.; Dalrymple, J.; Soyk, S.; Swartwood, K.E.; Rodriguez-Leal, D.; Eck, J.V.; Lippman, Z.B. Rapid improvement of domestication traits in an orphan crop by genome editing. *Nat. Plants* **2018**, *4*, 766–770. [[CrossRef](#)]
126. Laitinen, R.A.E. Importance of phenotypic plasticity in crop resilience. *J. Exp. Bot.* **2024**, *75*, 670–673. [[CrossRef](#)]
127. Callister, A.N.; Costa-Neto, G.; Bradshaw, B.P.; Elms, S.; Crossa, J.; Brawner, J.T. Enviromic prediction enables the characterization and mapping of *Eucalyptus globulus* Labill breeding zones. *Tree Genet. Genomes* **2024**, *20*, 3. [[CrossRef](#)]
128. Heinemann, A.B.; Costa-Neto, G.; Fritsche-Neto, R.; da Matta, D.H.; Fernandes, I.K. Enviromic prediction is useful to define the limits of climate adaptation: A case study of common bean in Brazil. *Field Crops Res.* **2022**, *286*, 108628. [[CrossRef](#)]
129. Resende, R.T.; Piepho, H.P.; Rosa, G.J.M.; Silva-Junior, O.B.; Silva, F.F.e.; Resende, M.D.V.d.; Grattapaglia, D. Enviromics in breeding: Applications and perspectives on envirotypic-assisted selection. *Theor. Appl. Genet.* **2021**, *134*, 95–112. [[CrossRef](#)] [[PubMed](#)]
130. Costa-Neto, G.; Fritsche-Neto, R. Enviromics: Bridging different sources of data, building one framework. *Crop Breed. Appl. Biotechnol.* **2021**, *21*, e393521S393512. [[CrossRef](#)]
131. Crossa, J.; Fritsche-Neto, R.; Montesinos-Lopez, O.A.; Costa-Neto, G.; Dreisigacker, S.; Montesinos-Lopez, A.; Bentley, A.R. The Modern Plant Breeding Triangle: Optimizing the Use of Genomics, Phenomics, and Enviromics Data. *Front. Plant Sci.* **2021**, *12*, 651480. [[CrossRef](#)]
132. Cooper, M.; Messina, C.D. Can We Harness “Enviromics” to Accelerate Crop Improvement by Integrating Breeding and Agronomy? *Front. Plant Sci.* **2021**, *12*, 735143. [[CrossRef](#)]
133. Costa-Neto, G.; Crossa, J.; Fritsche-Neto, R. Enviromic assembly increases accuracy and reduces costs of the genomic prediction for yield plasticity. *bioRxiv* **2021**. [[CrossRef](#)]
134. Costa-Neto, G.; Crossa, J.; Fritsche-Neto, R. Enviromic Assembly Increases Accuracy and Reduces Costs of the Genomic Prediction for Yield Plasticity in Maize. *Front. Plant Sci.* **2021**, *12*, 717552. [[CrossRef](#)]
135. Costa-Neto, G.; Galli, G.; Carvalho, H.F.; Crossa, J.; Fritsche-Neto, R.; de Koning, D.J. *EnvRtype*: A software to interplay enviromics and quantitative genomics in agriculture. *G3* **2021**, *11*, jkab040. [[CrossRef](#)] [[PubMed](#)]
136. Costa-Neto, G.; Fritsche-Neto, R.; Crossa, J. Nonlinear kernels, dominance, and envirotyping data increase the accuracy of genome-based prediction in multi-environment trials. *Heredity* **2020**, *126*, 92–106. [[CrossRef](#)] [[PubMed](#)]

Disclaimer/Publisher’s Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.