

'Omics' Approaches for Crop Improvement

Andrés J. Cortés ^{1,*†‡} , María Ángeles Castillejo ^{2,*†}  and Roxana Yockteng ^{3,4,*†}

- ¹ Corporación Colombiana de Investigación Agropecuaria—AGROSAVIA, C.I. La Selva, Km 7 vía Rionegro—Las Palmas, Rionegro 054048, Colombia
- ² Agroforestry and Plant Biochemistry, Proteomics and Systems Biology—Department of Biochemistry and Molecular Biology, University of Cordoba, CO-CeiA3, 14014 Cordoba, Spain
- ³ Corporación Colombiana de Investigación Agropecuaria—AGROSAVIA, C.I. Tibaitatá, Km 14 vía Mosquera, Mosquera 250047, Colombia
- ⁴ Institut de Systématique, Evolution, Biodiversité—UMR-CNRS 7205, National Museum of Natural History, 75005 Paris, France
- * Correspondence: acortes@agrosavia.co (A.J.C.); bb2casam@uco.es (M.Á.C.); ryockteng@agrosavia.co (R.Y.)
- † All authors contributed equally and share first authorship; their names are sorted alphabetically.
- ‡ Secondary address: Facultad de Ciencias Agrarias—Departamento de Ciencias Forestales, Universidad Nacional de Colombia—Sede Medellín, Medellín 050034, Colombia.

1. Introduction

The growing human population and climate change are imposing unprecedented challenges on the global food supply [1]. To cope with these pressures, crop improvement demands enhancing important agronomical traits beyond yield, such as adaptation, resistance, and nutritional value, by pivoting direct and indirect selection approaches [2]. The development of next-generation high-throughput screening technologies, referred to as 'omics', promises to speed up plant trait improvement [3] while producing more sustainable crops.

Large-scale techniques, such as genomics, transcriptomics, proteomics, metabolomics, and phenomics, have already provided large datasets for that purpose. Meanwhile, modern bioinformatic and machine-learning approaches are helping us to process this heterogeneous hyper-dimensional data [4] while ultimately understanding the mechanisms behind agronomic features within the contemporary plant breeding triangle (i.e., genomics vs. phenomics vs. enviromics) [5]. 'Omics' datasets are also being generated to study macro-scale interactions and deepen our knowledge of crop behavior across the microbial [6] and environmental [7,8] continua. However, despite these massive technological and computational developments [4], systemic efforts to integrate 'omics' studies to understand biochemical pathways and cellular networks of crop systems are in their infancy [9], especially in orphan species [10].

Therefore, this Special Issue envisions offering updated emergent views on large-scale 'omics'-based approaches. Specifically, the compilation explores the conceptual framework of the 'omics' paradigm [11], the practical uses of multiple 'omics' technologies, and their integration through trans-disciplinary bioinformatics as tools to improve qualitative and quantitative traits in a diverse panel of crop species.

2. Genomic-Enabled Crop Traceability and Improvement

Genomics is speeding up multiple steps in the breeding scheme (Table 1). For instance, in the downstream extreme of the breeding pipeline, Campuzano-Duque et al. [12] demonstrated the utility of high-throughput single nucleotide polymorphism (SNP) genotyping using SNP arrays to trace varietal purity of single plant selections (SPS). The authors successfully assessed the relationships and ancestry of plant selections from three inbred origins (one original variety and two additional multi-lines) of forage oat (*Avena sativa*), and prioritized SNP candidates to ensure the genetic purity of these varieties. Meanwhile, in a



Citation: Cortés, A.J.; Castillejo, M.Á.; Yockteng, R. 'Omics' Approaches for Crop Improvement. *Agronomy* **2023**, *13*, 1401. <https://doi.org/10.3390/agronomy13051401>

Received: 12 May 2023
Revised: 17 May 2023
Accepted: 18 May 2023
Published: 19 May 2023



Copyright: © 2023 by the authors. 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 (<https://creativecommons.org/licenses/by/4.0/>).

more upstream introgression-breeding step, Pandit et al. [13] exemplified genomic-assisted selection within backcrossing schemes. The team pyramided three quantitative trait loci (QTLs) for submergence tolerance and grain yield in the rice (*Oryza sativa*) ‘Maudamani’ variety background, sourcing pyramided lines as novel cultivars or potential ‘bridge’ donors for further backcrossed generations.

Table 1. Collection of 10 studies in the Special Issue ‘Omics Approaches for Crop Improvement’.

Plant Species	‘Omics’	Research Goal	Sampling	Key Finding	Reference
Review					
Papaya (<i>Carica papaya</i>)	Transversal to ‘omics’ and systems biology	Review omics and bioinformatics advances for Papaya	Diverse cultivars and germplasm	‘Omics’ improved ripening, tolerance, and fruit quality	Zainal-Abidin et al. [11]
Genomics					
Forage Oat (<i>Avena sativa</i>)	iSelect 6K Bead-Chip	Evaluate the purity and relationships of SPS	AV-25 original, and AV25-T and AV25-S multi-lines	SNPs are a suitable tool to ensure genetic purity of oats	Campuzano-Duque et al. [12]
Rice (<i>Oryza sativa</i>)	Sub1, OsSPL14, and GW5 QTLs for tolerance and yield	Pyramid QTLs for submergence tolerance and yield	‘Maudamani’ variety background	Pyramided lines are useful as cultivars and as donors	Pandit et al. [13]
Transcriptomics					
Cacao (<i>Theobroma cacao</i>)	Phylogenetic, gene structure, and in silico expression	Report and characterize <i>tcGASA</i> genes in cacao	Cacao reference genome	<i>tcGASA</i> genes are target for resistant cacao varieties	Abdullah et al. [14]
Malvaceae family: Cacao, cotton, and jute fiber	Phylogenetic, synteny, and in silico expression	Characterize <i>MGT</i> genes in the Malvaceae family	<i>T. cacao</i> , <i>Gossypium hirsutum</i> , and <i>Corchorus capsularis</i>	<i>MGTs</i> interact with lipid/cell wall and photo-protection	Heidari et al. [15]
Rice (<i>Oryza sativa</i>)	In-house micro-array and mGCN	Unveil the mechanism of drought tolerance in <i>ABP57</i>	Drought-tolerant transgenic <i>Abp57</i> -OE line	MAPK, IAA and SA co-determine tolerance response	Abdullah-Zawa wi et al. [16]
Proteomics					
Faba bean (<i>Vicia faba</i>)	2DE, MAL-DI-TOF/TOF, and zymography	Test leaf proteome effects to <i>Botrytis fabae</i> fungus	‘Baraca’ susceptible genotype, and resistant BPL710	Chloroplast PSII protein repair cycle linked to resistance	Castillejo et al. [17]
Tomato (<i>Solanum lycopersicum</i>)	TMT, HPLC, MS	Identify the effects of EFI vs. TSI on roots’ protein level	Seedlings from the pure tomato cultivar ‘Ouxiu-201’	EFI induces 513 DAPs adapted responses in roots	Wang et al. [18]
Phenomics					
Bean (<i>Phaseolus vulgaris</i>) × Tepary (<i>P. acutifolius</i>)	Multi-locality trials	Assess abiotic tolerance in inter-specific crosses	Interspecific backcross (86) between beans and Tepary	Interspecific backcrosses pyramid polygenic tolerance	Burbano-Erazo et al. [19]
Peanut (<i>Arachis hypogaea</i>)	HTP	Assess morphological variation in a CSSL	A total of 26 lines from a CSSL population	Chromosome segment from CWR sources variation	Gimode et al. [20]

Table is sorted bottom-up by ‘omics’ and species. ABP: auxin-binding protein, CSSL: chromosome segment substitution line, CWR: crop wild relatives, DAPs: differentially accumulated proteins, 2DE: two-dimensional gel electrophoresis, EFI: Ebb-and-flow sub-irrigation, GASA: gibberellic acid-stimulated *Arabidopsis*, HPLC: high-performance liquid chromatography, HTP: high-throughput phenotyping, IAA: indole-3-acetic acid, MALDI-TOF/TOF: matrix-assisted laser desorption/ionization-time of flight, MAPK: mitogen-activated protein kinase, mGCN: modular gene co-expression network, MGT: magnesium (Mg) transporter, MS: mass-spectrometry, OE: overexpressed, SA: salicylic acid, SPS: single plant selections, TMT: tandem mass tag, TSI: top sprinkle irrigation.

3. Transcriptomic-Based Characterization and Validation

Studies at the genomic-transcriptomic interface prove insightful for gene-oriented phylogenetics [21], structural mapping [22], and functional characterizations [23]. In this regard, two studies from this Special Issue merged genome-based gene family screening with in silico expression analyses. First, Abdullah et al. [14] characterized *tcGASA* paralogous in cacao (*Theobroma cacao*) and identified targets to customize fungi-resistant varieties. Similarly, Heidari et al. [15] described *MGT* (O-6-Methylguanine-DNA Methyltransferase) genes also in cacao, and they expanded the search to orthologous in two other species of the Malvaceae family with economic importance, cotton (*Gossypium hirsutum*), and jute fiber (*Corchorus capsularis*). In silico expression analysis enabled the authors to pinpoint that *MGT* targets the network as part of the lipid/cell wall metabolism and photoprotection pathways. Both studies demonstrate how well consolidated genomic and transcriptomic resources can be combined in silico to source *ad hoc* gene and allelic mining.

Transcriptomic screenings are equally informative of functional gene validation and tissue/environment-conditioned expression profiling. For instance, in rice, Abdullah-Zawawi et al. [16] used in-house microarray technology to determine the subjacent regulatory machinery of drought tolerance in an *Abp57*-overexpressing transgenic line. The team recovered the MAPK, IAA, and SA pathways as co-determinants of the stress response. This way, transcriptomic resources offer detailed mechanistic understating underlying agronomical relevant phenotypes.

4. Proteomics Meets Orphan Species

Proteomics is a powerful tool that allows the identification of proteins that can be used as markers in breeding programs. The development of new methodologies, and genomics and transcriptomics databases has provided a rapid advance in plant proteomics in recent decades, including orphan species. The gel-free based techniques (shotgun or LC-MSMS), DDA (data dependent acquisition), and DIA (data-independent acquisition), and targeted strategies are the most frequently chosen methods.

Identifying proteins and derived prototypic peptides throughout shotgun proteomics has already lit up feasible paths to improve or select tolerant individuals to abiotic stresses, such as drought [24] and heavy metal toxicity [25]. By using a DIA strategy, a panel of peptides and proteins has been proposed as putative markers of resistance to *Peyronellaea pinodes* in peas [26]. However, classical gel-based proteomics techniques, such as 2DE, remain the method of choice in many experiments. Castillejo et al. [17] explored the proteomic consequences of biotic stresses using 2DE-MALDI/TOF MSMS analysis combined with protease activity assays. The authors evaluated leaf proteome responses to *Botrytis fabae* necrotrophic fungus in susceptible and resistant Faba bean (*Vicia faba*) genotypes, finding a predominant role in the chloroplast PSII protein repair cycle. More interestingly, these studies reinforce that proteomics advancements are already permeating orphan species [10], even in the forestry sector [3].

Meanwhile, in a slightly more studied crop system (*Solanum lycopersicum*), Wang et al. [18] traced the effects of ebb-and-flow sub-irrigation (EFI) at roots' protein level as compared to top sprinkle irrigation (TSI). The team identified 513 differentially accumulated proteins between treatments. Overall, these two studies are promising for un-leashing plant improvements via proteomics. We are looking forward to similar developments in proteomics and also in metabolomics on non-model crop species [27].

Meanwhile, a more challenging research gap remains open in the long term, regardless the crop species. An unanswered question until now is how upstream genomic, transcriptomic, proteomic, and metabolomic layers collide and jointly interact across climates and through time to finally shape downstream multi-dimensional phenomic expression in the field.

5. Phenomics Leverage Crop Wild Gene pools

A long-standing research gap in phenomic screening is its factual implementation in crop wild gene pools [28], which typically exhibit more environmentally dependent trait segregation [29,30]. Fortunately, in this collection, two studies have harnessed crop-wild diversity through phenomics. First, Gimode et al. [20] studied the morphological consequences of a chromosome segment in peanuts (*Arachis hypogaea*) inherited from a wild relative. The authors demonstrated that this chromosome segment sources valuable trait variation from the exotic gene pool into the cultivated background. This work is also outstanding because it sidesteps the main bottlenecks of interspecific crossing, which are recurrent species incompatibility [31] and polygenic variation [32]. To do so, the study relied on a panel of chromosome segment substitution lines (CSSL) that narrowed the introgression to discrete chromosome segments, which are easier to be retained within the recurrent parental species while conferring the desired phenotypic novelty (by definition, it would be highly desirable that the substituted chromosome segment matched a single haplotype block with strong internal linkage disequilibrium (LD) to avoid spurious recombination events that may jeopardize its integrity and phenotypic determinism).

Another crop-wild innovation was the one by Burbano-Erazo et al. [19], who utilized multi-locality phenomics trials to characterize heat and drought tolerance in 86 interspecific backcross lines between the common bean (*Phaseolus vulgaris*) × the Tepary bean (*P. acutifolius*). The team managed to unlock interspecific adaptive variation, despite the natural incompatibility, throughout ‘bridge’ genotypes (those with comparatively lower incompatibility), and eventually delivered candidate introgressed lines capable of pyramiding polygenic abiotic tolerance. Other studies have also aimed to break interspecific barriers between the two species [33], genomically characterize the hybridization, and re-discover naturally occurring ecological adaptive variation for drought and heat stresses [34].

Overall, throughout this Special Issue, the works by Pandit et al. [13], Gimode et al. [20], and Burbano-Erazo et al. [19], respectively illustrated in rice, peanuts, and beans, the feasibility and power to update classical introgression breeding [35] with modern ‘omics’ approaches, such as genomics and phenomics. This integration enables guiding more rapidly and with better precision the pyramiding of exotic variation into elite commercial backgrounds. Alternatives to utilize interspecific genomic variability include grafting [36]. This ancient horticultural technique capable of physically merging two distinct species can be optimized for desirable trait variation using genomics [37], transcriptomics [38,39], phenomics, epigenomics [40,41], and beyond [42–44]. These promising examples amalgamate species diversity via introgression breeding and grafting, and update it to last-generation high-throughput standards. They corroborate the utility of ‘omics’ technologies for crop improvement without denying more classical, yet still very timing, schemes.

So far, the ultimate consequence of the bottom-up genomic, transcriptomic, proteomic, and metabolomic continuum is the phenotype. However, additional phenotypic modulation may be conferred by the emerging layers of the enviromics [7,8], epigenomics [45], and soil metagenomics [6] fields, as we envision in the next section.

6. Perspectives

Despite the effort of this Special Issue in compiling a diverse array of ‘omics’ sub-disciplines for crop improvement (Figure 1), high-throughput screening technologies have also permeated other promising fields that do not necessarily exhibit prominence in the present collection. For instance, as introduced in the previous section, scaling phenomics across the environmental continuum gradient would offer a more accurate prediction of the $G \times E$ interaction as part of the nascent enviromics framework [7,8], which ultimately merges [46] multi-environment phenomics screening [47] with genomic-based prediction [5,48,49]. Similarly, embracing an epigenomic footprint profiling [45] could also mechanistically disentangle a great proportion of crop phenotypic variance in reaction norms and plasticity gradients [50] naturally seen across climates [51,52].

SYNTHESIZED 'OMICS' APPROACHES FOR CROP IMPROVEMENT

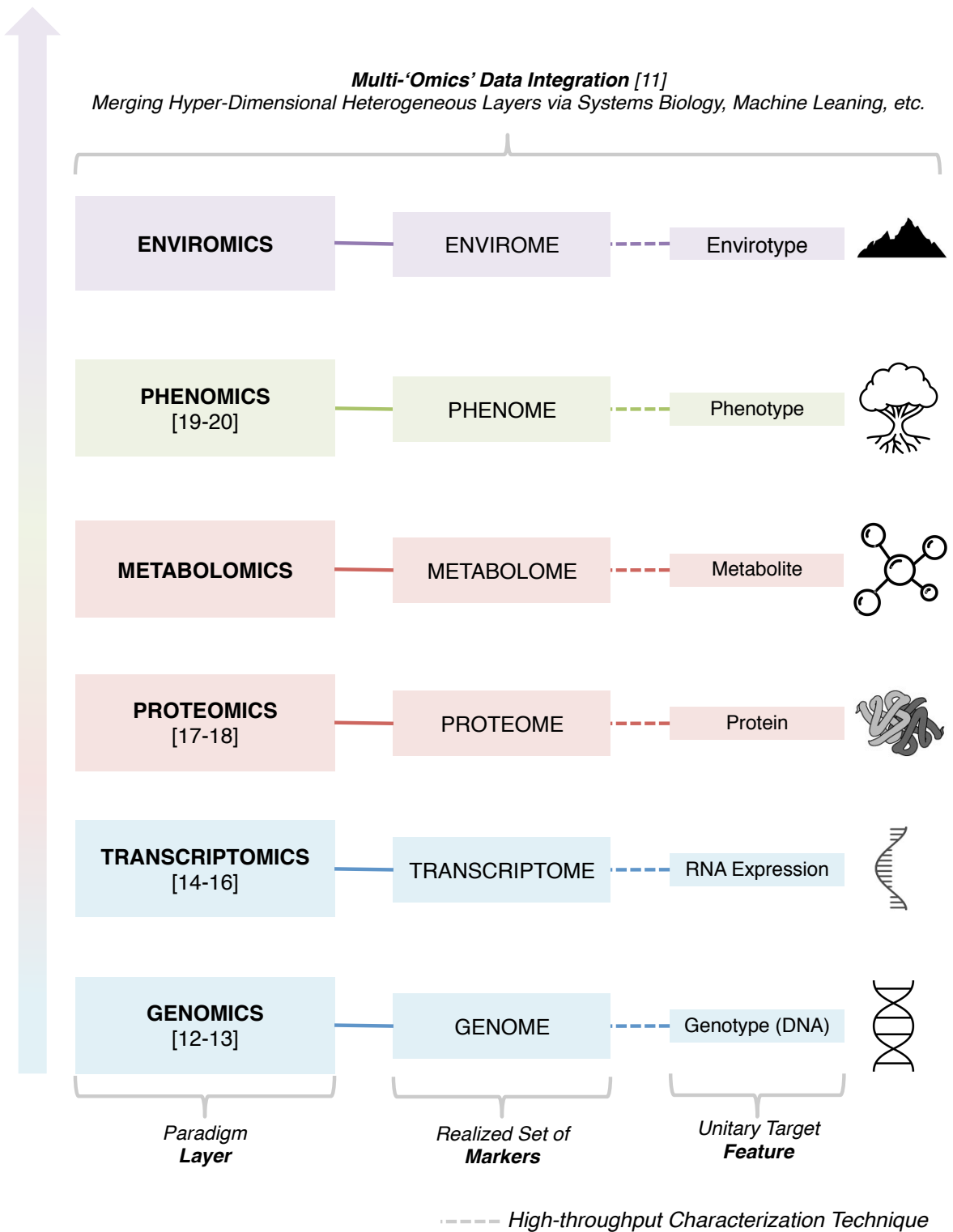


Figure 1. Synthesized 'Omics' Approaches for Crop Improvement. References from this Special Issue are indicated under Paradigm Layer within square brackets.

At another level, soil metagenomics on ‘environmental’ DNA [6] is boosting the retrieval of synergistic microorganisms for agriculture, given a growing sustainability requirement [53]. Backward ‘omics’ tools are also improving our understanding of crops’ evolution [54,55] and their cultural heritage [56] by updating archeological records [57] with genomics [58] and phylogenomics [59,60] into modern paleogenomics [61,62].

While heterogeneous ‘omics’ data piles up across sub-disciplines, effective trans-disciplinary data merging and bioinformatics processing demands revolutionizing open-source record access [63,64], novel statistical algorithms [65], and unprecedented computational resources [66–68]. Speed breeding [69,70] through ‘omics’-enabled [48,49,71], systems biology [9,72], and machine learning [4,73] predictions exemplify the promises of fast-forward customized crop breeding [2,74] by bridging the curse of dimensionality inherent from multi-‘omics’ data [10,75,76], while matching the modern seed delivery requirements [77]. This trend of analytical innovation may proceed further into the inflection point of the artificial general intelligence (AGI) hypothesis [78], eventually enabling human-unguided ‘omics’-based plant improvement at an unforeseen pace.

Author Contributions: A.J.C., M.Á.C. and R.Y. conceived this Special Issue and together processed submissions. All authors have read and agreed to the published version of the manuscript.

Funding: A.J.C. received support from the British Council’s Newton Fund during the execution of this Special Issue through grant 527023146. He was thanks Vetenskapsrådet (VR, 2016-00418/2022-04411) and Kungliga Vetenskapsakademien (KVA, BS2017-0036).

Data Availability Statement: Raw datasets were made available by each of the ten published articles [11–20] from the Special Issue on “Omics Approaches for Crop Improvement” (https://www.mdpi.com/journal/agronomy/special_issues/crop_omics_genetic (revised 18 May 2023)).

Acknowledgments: A.J.C., M.Á.C. and R.Y., in their role as guest editors, thank the interest and determination of all authors, reviewers, and topic editors. Otherwise, this compilation on “Omics Approaches for Crop Improvement” would not have been possible. Agronomy’s editorial team, editor-in-chief, and section assistant managing editor are as well thanked for encouraging and enabling A.J.C., M.Á.C. and R.Y. to host this Special Issue.

Conflicts of Interest: The authors declare no conflict of interest.

References

- McCouch, S. Feeding the future. *Nature* **2013**, *499*, 23–24. [[CrossRef](#)] [[PubMed](#)]
- Varshney, R.K.; Bohra, A.; Roorkiwal, M.; Barmukh, R.; Cowling, W.A.; Chitiki, A.; Lam, H.-M.; Hickey, L.T.; Croser, J.S.; Bayer, P.E.; et al. Fast-forward breeding for a food-secure world. *Trends Genet.* **2021**, *37*, 1124–1136. [[CrossRef](#)] [[PubMed](#)]
- Castillejo, M.A.; Pascual, J.; Jorrín-Novó, J.V.; Balbuena, T.S. Proteomics research in forest trees: A 2012–2022 update. *Front. Plant Sci.* **2023**, *14*, 1130665. [[CrossRef](#)] [[PubMed](#)]
- Libbrecht, M.W.; Noble, W.S. Machine learning applications in genetics and genomics. *Nat. Rev. Genet.* **2015**, *16*, 321–332. [[CrossRef](#)]
- 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](#)]
- Zhang, L.; Chen, F.; Zeng, Z.; Xu, M.; Sun, F.; Yang, L.; Bi, X.; Lin, Y.; Gao, Y.; Hao, H.; et al. Advances in Metagenomics and Its Application in Environmental Microorganisms. *Front. Microbiol.* **2021**, *12*, 3847. [[CrossRef](#)]
- Resende, R.T.; Piepho, H.-P.; Rosa, G.J.M.; Silva-Junior, O.B.; e Silva, F.F.; de Resende, M.D.V.; Grattapaglia, D. Enviromics in breeding: Applications and perspectives on envirotypic-assisted selection. *Theor. Appl. Genet.* **2021**, *134*, 95–112. [[CrossRef](#)]
- Costa-Neto, G.; Fritsche-Neto, R. Enviromics: Bridging different sources of data, building one framework. *Crop Breed. Appl. Biotechnol.* **2021**, *21*, e393521S12. [[CrossRef](#)]
- Escandón, M.; Castillejo, M.; Jorrín-Novó, J.V.; Rey, M.-D. Molecular Research on Stress Responses in *Quercus* spp.: From Classical Biochemistry to Systems Biology through Omics Analysis. *Forests* **2021**, *12*, 364. [[CrossRef](#)]
- Maldonado-Alconada, A.M.; Castillejo, M.; Rey, M.-D.; Labella-Ortega, M.; Tienda-Parrilla, M.; Hernández-Lao, T.; Honrubia-Gómez, I.; Ramírez-García, J.; Guerrero-Sanchez, V.M.; López-Hidalgo, C.; et al. Multiomics Molecular Research into the Recalcitrant and Orphan *Quercus ilex* Tree Species: Why, What for, and How. *Int. J. Mol. Sci.* **2022**, *23*, 9980. [[CrossRef](#)]
- Zainal-Abidin, R.-A.; Ruhaizat-Ooi, I.-H.; Harun, S. A Review of Omics Technologies and Bioinformatics to Accelerate Improvement of Papaya Traits. *Agronomy* **2021**, *11*, 1356. [[CrossRef](#)]

12. Campuzano-Duque, L.F.; Bejarano-Garavito, D.; Castillo-Sierra, J.; Torres-Cuesta, D.R.; Cortés, A.J.; Blair, M.W. SNP Genotyping for Purity Assessment of a Forage Oat (*Avena sativa* L.) Variety from Colombia. *Agronomy* **2022**, *12*, 1710. [\[CrossRef\]](#)
13. Pandit, E.; Pawar, S.; Barik, S.R.; Mohanty, S.P.; Meher, J.; Pradhan, S.K. Marker-Assisted Backcross Breeding for Improvement of Submergence Tolerance and Grain Yield in the Popular Rice Variety 'Maudamani'. *Agronomy* **2021**, *11*, 1263. [\[CrossRef\]](#)
14. Abdullah; Faraji, S.; Mehmood, F.; Malik, H.M.T.; Ahmed, I.; Heidari, P.; Poczai, P. The GASA Gene Family in Cacao (*Theobroma cacao*, Malvaceae): Genome Wide Identification and Expression Analysis. *Agronomy* **2021**, *11*, 1425. [\[CrossRef\]](#)
15. Heidari, P.; Abdullah; Faraji, S.; Poczai, P. Magnesium transporter Gene Family: Genome-Wide Identification and Characterization in *Theobroma cacao*, *Cochlosoma capsularis*, and *Gossypium hirsutum* of Family Malvaceae. *Agronomy* **2021**, *11*, 1651. [\[CrossRef\]](#)
16. Abdullah-Zawawi, M.-R.; Tan, L.-W.; Ab Rahman, Z.; Ismail, I.; Zainal, Z. An Integration of Transcriptomic Data and Modular Gene Co-Expression Network Analysis Uncovers Drought Stress-Related Hub Genes in Transgenic Rice Overexpressing *OsAbp57*. *Agronomy* **2022**, *12*, 1959. [\[CrossRef\]](#)
17. Castillejo, M.Á.; Villegas-Fernández, Á.M.; Hernández-Lao, T.; Rubiales, D. Photosystem II Repair Cycle in Faba Bean May Play a Role in Its Resistance to *Botrytis fabae* Infection. *Agronomy* **2021**, *11*, 2247. [\[CrossRef\]](#)
18. Wang, K.; Ali, M.M.; Guo, T.; Su, S.; Chen, X.; Xu, J.; Chen, F. TMT-Based Quantitative Proteomic Analysis Reveals the Response of Tomato (*Solanum lycopersicum* L.) Seedlings to Ebb-and-Flow Subirrigation. *Agronomy* **2022**, *12*, 1880. [\[CrossRef\]](#)
19. Burbano-Erazo, E.; León-Pacheco, R.I.; Cordero-Cordero, C.C.; López-Hernández, F.; Cortés, A.J.; Tofiño-Rivera, A.P. Multi-Environment Yield Components in Advanced Common Bean (*Phaseolus vulgaris* L.) × Tepary Bean (*P. acutifolius* A. Gray) Interspecific Lines for Heat and Drought Tolerance. *Agronomy* **2021**, *11*, 1978. [\[CrossRef\]](#)
20. Gimode, D.; Chu, Y.; Holbrook, C.C.; Fonceka, D.; Porter, W.; Dobrev, I.; Teare, B.; Ruiz-Guzman, H.; Hays, D.; Ozias-Akins, P. High-Throughput Canopy and Belowground Phenotyping of a Set of Peanut CSSLs Detects Lines with Increased Pod Weight and Foliar Disease Tolerance. *Agronomy* **2023**, *13*, 1223. [\[CrossRef\]](#)
21. André, T.; Sass, C.; Yockteng, R.; Wendt, T.; Palma-Silva, C.; Specht, C.D. Deep genetic structure of a ground-herb along contrasting environments of seasonally dry understories in Amazonia and Cerrado as revealed from targeted genomic sequencing. *Bot. J. Linn. Soc.* **2021**, *199*, 196–209. [\[CrossRef\]](#)
22. Osorio-Guarín, J.A.; Berdugo-Cely, J.A.; Coronado-Silva, R.A.; Baez, E.; Jaimes, Y.; Yockteng, R. Genome-Wide Association Study Reveals Novel Candidate Genes Associated with Productivity and Disease Resistance to *Moniliophthora* spp. in Cacao (*Theobroma cacao* L.). *G3 Genes Genomes Genet.* **2020**, *10*, 1713–1725. [\[CrossRef\]](#) [\[PubMed\]](#)
23. López-Hernández, F.; Cortés, A.J. Whole Transcriptome Sequencing Unveils the Genomic Determinants of Putative Somaclonal Variation in Mint (*Mentha* L.). *Int. J. Mol. Sci.* **2022**, *23*, 5291. [\[CrossRef\]](#) [\[PubMed\]](#)
24. San-Eufrasio, B.; Bigatton, E.D.; Guerrero-Sánchez, V.M.; Chaturvedi, P.; Jorrín-Novó, J.V.; Rey, M.-D.; Castillejo, M. Proteomics Data Analysis for the Identification of Proteins and Derived Proteotypic Peptides of Potential Use as Putative Drought Tolerance Markers for *Quercus ilex*. *Int. J. Mol. Sci.* **2021**, *22*, 3191. [\[CrossRef\]](#) [\[PubMed\]](#)
25. Salas-Moreno, M.; Castillejo, M.; Rodríguez-Cavallero, E.; Marrugo-Negrete, J.; Méndez-Cuadro, D.; Jorrín-Novó, J. Proteomic Changes in *Paspalum fasciculatum* Leaves Exposed to Cd Stress. *Plants* **2022**, *11*, 2455. [\[CrossRef\]](#)
26. Castillejo, M.Á.; Fondevilla-Aparicio, S.; Fuentes-Almagro, C.; Rubiales, D. Quantitative Analysis of Target Peptides Related to Resistance Against Ascochyta Blight (*Peyronellaea pinodes*) in Pea. *J. Proteome Res.* **2020**, *19*, 1000–1012. [\[CrossRef\]](#)
27. Tienda-Parrilla, M.; López-Hidalgo, C.; Guerrero-Sánchez, V.M.; Infantes-González, Á.; Valderrama-Fernández, R.; Castillejo, M.; Jorrín-Novó, J.V.; Rey, M.-D. Untargeted MS-Based Metabolomics Analysis of the Responses to Drought Stress in *Quercus ilex* L. Leaf Seedlings and the Identification of Putative Compounds Related to Tolerance. *Forests* **2022**, *13*, 551. [\[CrossRef\]](#)
28. 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. [\[CrossRef\]](#)
29. Cortés, A.J.; Cornille, A.; Yockteng, R. Evolutionary Genetics of Crop-Wild Complexes. *Genes* **2022**, *13*, 1. [\[CrossRef\]](#)
30. Beebe, S.E.; Rao, I.M.; Cajiao, C.; Grajales, M. Selection for Drought Resistance in Common Bean Also Improves Yield in Phosphorus Limited and Favorable Environments. *Crop Sci.* **2008**, *48*, 582–592. [\[CrossRef\]](#)
31. Coyne, C.J.; Kumar, S.; von Wettberg, E.J.; Marques, E.; Berger, J.D.; Redden, R.J.; Ellis, T.N.; Brus, J.; Zablatzka, L.; Smýkal, P. Potential and limits of exploitation of crop wild relatives for pea, lentil, and chickpea improvement. *Legum. Sci.* **2020**, *2*, e36. [\[CrossRef\]](#)
32. Barghi, N.; Hermisson, J.; Schlötterer, C. Polygenic adaptation: A unifying framework to understand positive selection. *Nat. Rev. Genet.* **2020**, *21*, 769–781. [\[CrossRef\]](#)
33. Munoz, L.C.; Blair, M.W.; Duque, M.C.; Tohme, J.; Roca, W. Introgression in Common Bean × Tepary Bean Interspecific Congruity-Backcross Lines as Measured by AFLP Markers. *Crop Sci.* **2004**, *44*, 637–645. [\[CrossRef\]](#)
34. Buitrago-Bitar, M.A.; Cortés, A.J.; López-Hernández, F.; Londoño-Cañedo, J.M.; Muñoz-Florez, J.E.; Muñoz, L.C.; Blair, M.W. Allelic Diversity at Abiotic Stress Responsive Genes in Relationship to Ecological Drought Indices for Cultivated Tepary Bean, *Phaseolus acutifolius* A. Gray, and Its Wild Relatives. *Genes* **2021**, *12*, 556. [\[CrossRef\]](#)
35. Migicovsky, Z.; Myles, S. Exploiting Wild Relatives for Genomics-assisted Breeding of Perennial Crops. *Front. Plant Sci.* **2017**, *8*, 460. [\[CrossRef\]](#)
36. Warschefsky, E.J.; Klein, L.L.; Frank, M.H.; Chitwood, D.H.; Londo, J.P.; von Wettberg, E.J.B.; Miller, A.J. Rootstocks: Diversity, Domestication, and Impacts on Shoot Phenotypes. *Trends Plant Sci.* **2016**, *21*, 418–437. [\[CrossRef\]](#)
37. Loupit, G.; Cookson, S.J. Identifying Molecular Markers of Successful Graft Union Formation and Compatibility. *Front. Plant Sci.* **2020**, *11*, 610352. [\[CrossRef\]](#)

38. Gautier, A.T.; Chambaud, C.; Brocard, L.; Ollat, N.; A Gambetta, G.; Delrot, S.; Cookson, S.J. Merging genotypes: Graft union formation and scion–rootstock interactions. *J. Exp. Bot.* **2019**, *70*, 747–755. [\[CrossRef\]](#)
39. Guillaumie, S.; Decroocq, S.; Ollat, N.; Delrot, S.; Gomès, E.; Cookson, S.J. Dissecting the control of shoot development in grapevine: Genetics and genomics identify potential regulators. *BMC Plant Biol.* **2020**, *20*, 70. [\[CrossRef\]](#)
40. Kapazoglou, A.; Tani, E.; Avramidou, E.V.; Abraham, E.M.; Gerakari, M.; Megariti, S.; Doupis, G.; Doulis, A.G. Epigenetic Changes and Transcriptional Reprogramming Upon Woody Plant Grafting for Crop Sustainability in a Changing Environment. *Front. Plant Sci.* **2021**, *11*, 613004. [\[CrossRef\]](#)
41. Tsaballa, A.; Xanthopoulou, A.; Madesis, P.; Tsaftaris, A.; Nianiou-Obeidat, I. Vegetable Grafting From a Molecular Point of View: The Involvement of Epigenetics in Rootstock-Scion Interactions. *Front. Plant Sci.* **2021**, *11*, 621999. [\[CrossRef\]](#) [\[PubMed\]](#)
42. Albacete, A.; Martínez-Andújar, C.; Martínez-Pérez, A.; Thompson, A.; Dodd, I.C.; Pérez-Alfocea, F. Unravelling rootstockxscion interactions to improve food security. *J. Exp. Bot.* **2015**, *66*, 2211–2226. [\[CrossRef\]](#) [\[PubMed\]](#)
43. Goldschmidt, E.E. Plant grafting: New mechanisms, evolutionary implications. *Front. Plant Sci.* **2014**, *5*, 727. [\[CrossRef\]](#) [\[PubMed\]](#)
44. Wang, J.; Jiang, L.; Wu, R. Plant grafting: How genetic exchange promotes vascular reconnection. *New Phytol.* **2017**, *214*, 56–65. [\[CrossRef\]](#) [\[PubMed\]](#)
45. Mehrmohamadi, M.; Sepehri, M.H.; Nazer, N.; Norouzi, M.R. A Comparative Overview of Epigenomic Profiling Methods. *Front. Cell Dev. Biol.* **2021**, *9*, 714687. [\[CrossRef\]](#)
46. Cooper, M.; Messina, C.D. Can We Harness “Enviromics” to Accelerate Crop Improvement by Integrating Breeding and Agronomy? *Front. Plant Sci.* **2021**, *12*, 735143. [\[CrossRef\]](#)
47. 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. [\[CrossRef\]](#)
48. Desta, Z.A.; Ortiz, R. Genomic selection: Genome-wide prediction in plant improvement. *Trends Plant Sci.* **2014**, *19*, 592–601. [\[CrossRef\]](#)
49. Crossa, J.; Pérez-Rodríguez, P.; Cuevas, J.; Montesinos-López, O.; Jarquín, D.; de los Campos, G.; Burgueño, J.; González-Camacho, J.M.; Pérez-Elizalde, S.; Beyene, Y.; et al. Genomic Selection in Plant Breeding: Methods, Models, and Perspectives. *Trends Plant Sci.* **2017**, *22*, 961–975. [\[CrossRef\]](#)
50. 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. [\[CrossRef\]](#)
51. Cortés, A.J.; López-Hernández, F.; Blair, M.W. Genome–Environment Associations, an Innovative Tool for Studying Heritable Evolutionary Adaptation in Orphan Crops and Wild Relatives. *Front. Genet.* **2022**, *13*, 1562. [\[CrossRef\]](#)
52. Hancock, A.M.; Brachi, B.; Faure, N.; Horton, M.W.; Jarymowycz, L.B.; Sperone, F.G.; Toomajian, C.; Roux, F.; Bergelson, J. Adaptation to Climate Across the *Arabidopsis thaliana* Genome. *Science* **2011**, *334*, 83–86. [\[CrossRef\]](#)
53. Nwachukwu, B.C.; Babalola, O.O. Metagenomics: A Tool for Exploring Key Microbiome With the Potentials for Improving Sustainable Agriculture. *Front. Sustain. Food Syst.* **2022**, *6*, 886987. [\[CrossRef\]](#)
54. Meyer, R.S.; Purugganan, M.D. Evolution of crop species: Genetics of domestication and diversification. *Nat. Rev. Genet.* **2013**, *14*, 840–852. [\[CrossRef\]](#)
55. Cortés, A.J.; Skeen, P.; Blair, M.W.; Chacón-Sánchez, M.I. Does the Genomic Landscape of Species Divergence in Phaseolus Beans Coerce Parallel Signatures of Adaptation and Domestication? *Front. Plant Sci.* **2018**, *9*, 1816. [\[CrossRef\]](#)
56. Przelomska, N.A.S.; Armstrong, C.G.; Kistler, L. Ancient Plant DNA as a Window Into the Cultural Heritage and Biodiversity of Our Food System. *Front. Ecol. Evol.* **2020**, *8*, 74. [\[CrossRef\]](#)
57. Purugganan, M.D.; Fuller, D.Q. Archaeological data reveal slow rates of evolution during plant domestication. *Evolution* **2011**, *65*, 171–183. [\[CrossRef\]](#)
58. Purugganan, M.D.; Jackson, S.A. Advancing crop genomics from lab to field. *Nat. Genet.* **2021**, *53*, 595–601. [\[CrossRef\]](#)
59. Wang, M.; Zhang, L.; Zhang, Z.; Li, M.; Wang, D.; Zhang, X.; Xi, Z.; Keefover-Ring, K.; Smart, L.B.; DiFazio, S.P.; et al. Phylogenomics of the genus *Populus* reveals extensive interspecific gene flow and balancing selection. *New Phytol.* **2020**, *225*, 1370–1382. [\[CrossRef\]](#)
60. Cheng, L.; Li, M.; Han, Q.; Qiao, Z.; Hao, Y.; Balbuena, T.S.; Zhao, Y. Phylogenomics Resolves the Phylogeny of Theaceae by Using Low-Copy and Multi-Copy Nuclear Gene Markers and Uncovers a Fast Radiation Event Contributing to Tea Plants Diversity. *Biology* **2022**, *11*, 1007. [\[CrossRef\]](#)
61. Barrera-Redondo, J.; Piñero, D.; Eguiarte, L.E. Genomic, Transcriptomic and Epigenomic Tools to Study the Domestication of Plants and Animals: A Field Guide for Beginners. *Front. Genet.* **2020**, *11*, 742. [\[CrossRef\]](#) [\[PubMed\]](#)
62. Swarts, K.; Gutaker, R.M.; Benz, B.; Blake, M.; Bukowski, R.; Holland, J.; Kruse-Peebles, M.; Lepak, N.; Prim, L.; Romay, M.C.; et al. Genomic estimation of complex traits reveals ancient maize adaptation to temperate North America. *Science* **2017**, *357*, 512–515. [\[CrossRef\]](#)
63. McCouch, S.R.; Wright, M.H.; Tung, C.-W.; Maron, L.G.; McNally, K.L.; Fitzgerald, M.; Singh, N.; DeClerck, G.; Agosto-Perez, F.; Korniliev, P.; et al. Open access resources for genome-wide association mapping in rice. *Nat. Commun.* **2016**, *7*, 10532. [\[CrossRef\]](#) [\[PubMed\]](#)
64. 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. [\[CrossRef\]](#) [\[PubMed\]](#)
65. Cortés, A.J.; López-Hernández, F. Harnessing Crop Wild Diversity for Climate Change Adaptation. *Genes* **2021**, *12*, 783. [\[CrossRef\]](#)
66. Wang, P.; Schumacher, A.M.; Shiu, S.-H. Computational prediction of plant metabolic pathways. *Curr. Opin. Plant Biol.* **2022**, *66*, 102171. [\[CrossRef\]](#)

67. Tirnaz, S.; Zandberg, J.; Thomas, W.J.W.; Marsh, J.; Edwards, D.; Batley, J. Application of crop wild relatives in modern breeding: An overview of resources, experimental and computational methodologies. *Front. Plant Sci.* **2022**, *13*, 1008904. [\[CrossRef\]](#)
68. Montesinos-López, O.A.; Vallejo, F.J.M.; Crossa, J.; Gianola, D.; Hernández-Suárez, C.M.; Montesinos-López, A.; Juliana, P.; Singh, R. A Benchmarking Between Deep Learning, Support Vector Machine and Bayesian Threshold Best Linear Unbiased Prediction for Predicting Ordinal Traits in Plant Breeding. *G3 Genes Genomes Genet.* **2019**, *9*, 601–618. [\[CrossRef\]](#)
69. 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. [\[CrossRef\]](#)
70. 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.* **2022**, *40*, 412–431. [\[CrossRef\]](#)
71. Arenas, S.; Cortés, A.J.; Mastretta-Yanes, A.; Jaramillo-Correa, J.P. Evaluating the accuracy of genomic prediction for the management and conservation of relictual natural tree populations. *Tree Genet. Genomes* **2021**, *17*, 12. [\[CrossRef\]](#)
72. Myburg, A.A.; Hussey, S.; 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. [\[CrossRef\]](#)
73. Schrider, D.R.; Kern, A.D. Supervised Machine Learning for Population Genetics: A New Paradigm. *Trends Genet.* **2018**, *34*, 301–312. [\[CrossRef\]](#)
74. Grattapaglia, D.; Silva-Junior, O.B.; Resende, R.T.; Cappa, E.P.; Müller, B.S.F.; Tan, B.; Isik, F.; Ratcliffe, B.; El-Kassaby, Y.A. Quantitative Genetics and Genomics Converge to Accelerate Forest Tree Breeding. *Front. Plant Sci.* **2018**, *9*, 1693. [\[CrossRef\]](#)
75. Guerrero-Sánchez, V.M.; López-Hidalgo, C.; Rey, M.-D.; Castillejo, M.Á.; Jorrín-Novó, J.V.; Escandón, M. Multiomic Data Integration in the Analysis of Drought-Responsive Mechanisms in *Quercus ilex* Seedlings. *Plants* **2022**, *11*, 3067. [\[CrossRef\]](#)
76. López-Hidalgo, C.; Guerrero-Sánchez, V.M.; Gómez-Gálvez, I.; Sánchez-Lucas, R.; Castillejo-Sánchez, M.A.; Alconada, A.M.M.; Valledor, L.; Jorrín-Novó, J.V. A Multi-Omics Analysis Pipeline for the Metabolic Pathway Reconstruction in the Orphan Species *Quercus ilex*. *Front. Plant Sci.* **2018**, *9*, 935. [\[CrossRef\]](#)
77. 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. [\[CrossRef\]](#)
78. Khan, M.H.U.; Wang, S.; Wang, J.; Ahmar, S.; Saeed, S.; Khan, S.U.; Xu, X.; Chen, H.; Bhat, J.A.; Feng, X. Applications of Artificial Intelligence in Climate-Resilient Smart-Crop Breeding. *Int. J. Mol. Sci.* **2022**, *23*, 11156. [\[CrossRef\]](#)

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.