Editorial

'Omics' Approaches for Crop Improvement

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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 assessed the relationships and ancestry of plant selections from three inbreed 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 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 (*Carica papaya*)	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 (*Avena sativa*)	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 (*Oryza sativa*)	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 (*Theobroma cacao*)	Phylogenetic, gene structure, and in silico expression	Report and characterize *tcGASA* genes in cacao	Cacao reference genome	*tcGASA* 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 *MGT* genes in the Malvaceae family	*T. cacao*, *Gossypium hirsutum*, and *Corchorus capsularis*	MGTs interact with lipid/cell wall and photo-protection	Heidari et al. [15]
Rice (*Oryza sativa*)	In-house micro-array and mGCN	Unveil the mechanism of drought tolerance in *ABP57*	Drought-tolerant transgenic *Abp57*-OE line	MAPK, IAA and SA co-determine tolerance response	Abdullah-Zawawi et al. [16]
Proteomics					
Faba bean (*Vicia faba*)	2DE, MAL-DI-TOF/TOF, and zymography	Test leaf proteome effects to *Botrytis fabae* fungus	'Baraca' susceptible genotype, and resistant BPL710	Chloroplast PSII protein repair cycle linked to resistance	Castillejo et al. [17]
Tomato (*Solanum lycopersicum*)	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 (*Phaseolus vulgaris*) × Tepary (*P. acutifolius*)	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 (*Arachis hypogaea*)	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, HTTP: 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. The latter example adds to a robust list of studies that have aimed to break interspecific barriers between the two species [33], genomically characterize the nature of 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. Other alternatives to utilize and recombine 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. This way, 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' subdisciplines 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 × 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
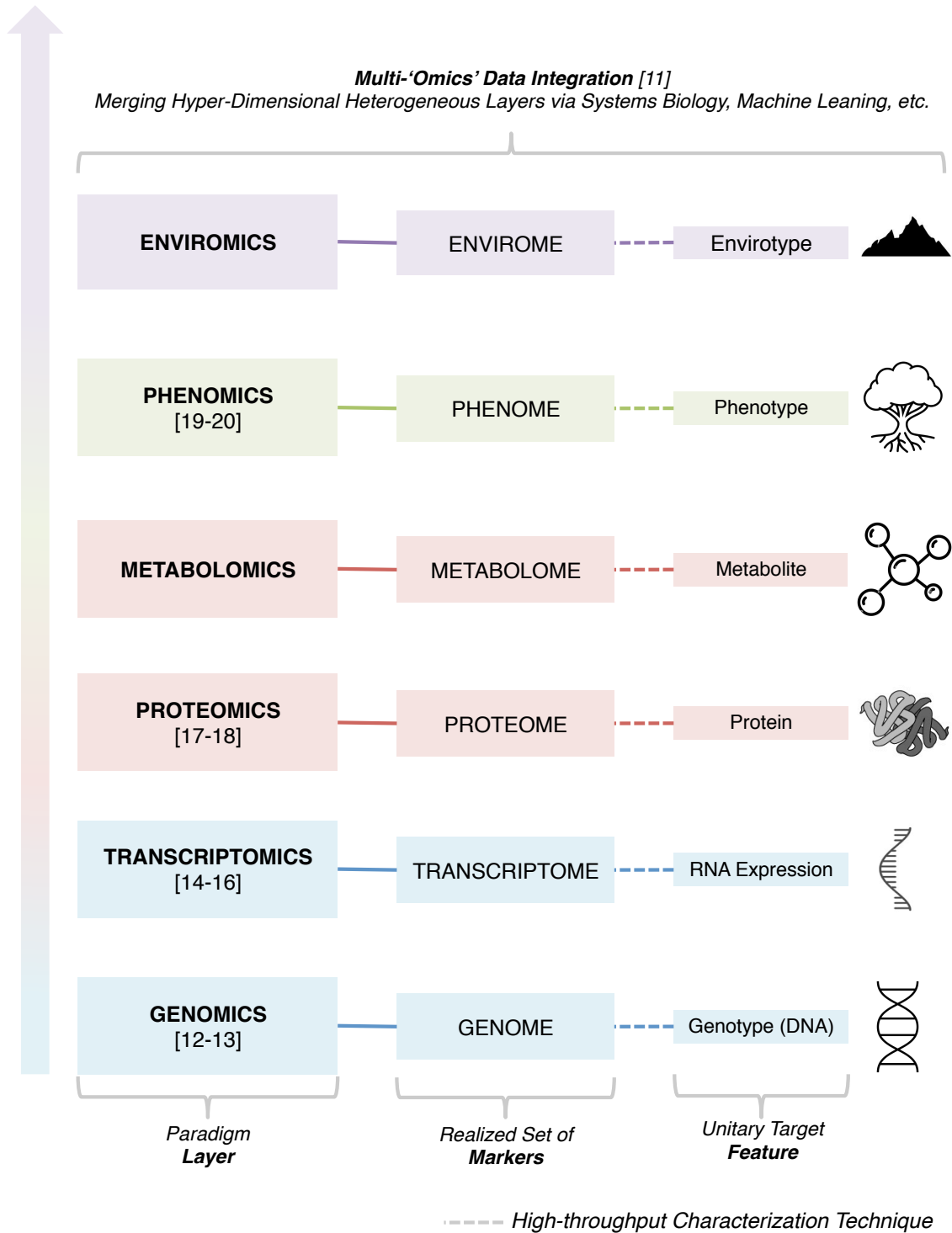
Figure 1. Synthesized 'Omics' Approaches for Crop Improvement.

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 transdisciplinary data merging and bioinformatics processing demands revolutionizing opensource 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.

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