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Editorial

Plants for Extreme and Changing Environments: Domestication, Evolution, Crop Breeding and Genetics 2.0

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1. Introduction

The contributions in this issue do not measure one common form of resilience. They address distinct questions: whether stress-responsive genes merit functional testing; whether an engineered metabolic change improves crop performance; how environment and developmental stage shape a physiological phenotype; whether chemical and elemental profiles distinguish taxa; and how breeding methods or underused species may expand future improvement. These are complementary but unequal forms of evidence. Treating them all as demonstrations of adaptation would obscure what each study actually establishes.

The editorial argument is that stress response, phenotypic differentiation, breeding efficiency and adaptation should not be used interchangeably. Each claim requires a defined outcome and an appropriate scale of validation. A candidate gene requires functional evidence; a sensor-derived trait must predict performance under relevant conditions; and a breeding method or candidate crop must ultimately contribute useful, stable variation. This perspective connects the papers while keeping their conclusions within the limits of their designs.

2. From Stress-Responsive Genes to Agronomic Evidence

Guo et al. identified 11 plant defensin (*MsPDF*) genes in *Medicago sativa* and reported stress-responsive expression under cold, drought and salinity [1]. Their analyses nominate *MsPDF* genes for functional study, but expression patterns and computational predictions do not establish effects on alfalfa performance. The key next test is whether perturbing selected genes changes growth, forage production or reproduction under relevant stress conditions.

Wu et al. tested a chimeric glycerol-3-phosphate dehydrogenase construct (*OEGD*) in rice and reported responses to drought, phosphorus deficiency, high temperature and cadmium, alongside changes in glycerol-3-phosphate, antioxidant activity, fatty-acid profiles and stress-associated pathways [2]. They also report improved growth and yield under adult-stage drought. This is more direct evidence of a genetic effect than expression-based candidate discovery, although its breeding value will depend on whether the yield response is reproducible across genetic backgrounds and field environments.

The distinction between these studies is instructive. A gene-family analysis identifies candidates; a genetic intervention tests effects under the conditions examined. Neither step alone establishes broad adaptation. The relevant question is whether the observed effect predicts a defined production outcome where the crop is intended to grow, a problem that links stress biology to phenotyping and selection [3,4].

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3. Phenotypes Depend on When and Where They Are Measured

Flores-Olave et al. show that canopy temperature in spring wheat varies with time of day, phenological stage and water regime; genotype rankings were less stable across measurement hours under rainfed conditions [5]. A single thermal reading could therefore rank genotypes differently from a stage- and time-defined assessment. Canopy temperature may inform selection only when its measurement conditions and predictive relation to the breeding objective are established in the target environment.

This finding has a broader methodological implication: increasing the volume of sensor data does not itself improve selection accuracy. The value of a phenotype depends on its repeatability and its relationship to a specified outcome. Genetic gain likewise depends on selection accuracy, usable variation and breeding-cycle design [4,6].

Mora-Poblete et al. used near-infrared spectroscopy and micro-X-ray fluorescence to characterize South American *Nothofagus* in an ex situ collection [7]. Elemental profiles discriminated taxa more accurately than near-infrared spectra, while combining the platforms added only a modest improvement. These results support multimodal characterization of living collections; they do not establish adaptive differentiation or climate tolerance. Replication in natural populations is needed to determine whether the taxonomic patterns extend beyond this collection.

4. Breeding Methods and Domestication Resources

Chen et al. review the use of anther culture to develop rice breeding lines in China [8]. The method can shorten the route to homozygous material, but genotype-dependent response, low green-plant regeneration and lower efficiency in indica rice remain constraints. Its value should therefore be judged by whether it increases the production of lines that meet breeding objectives, rather than by culture efficiency alone.

Dos Santos et al. assess Amazonian *Eugenia* species as potential fruit and biotechnological resources [9]. Their review identifies useful functional and genetic diversity, alongside barriers that include irregular fruiting, fruit perishability, recalcitrant seeds and incomplete germplasm characterization. These findings establish a case for further domestication research, not evidence that the species already perform as resilient crops. Propagation and comparative production trials are needed to evaluate that potential.

The reviews point to different routes for broadening crop improvement: refining an established method for generating breeding lines and evaluating a diverse, underused plant resource. In both cases, the decisive evidence lies downstream of the method or inventory, in the performance of selected material under intended production conditions.

5. What the Collection Leaves to Be Tested

The next experiments should follow the inferential gap specific to each contribution. For alfalfa, the stress-responsive candidates require functional tests linked to whole-plant performance. For rice, *OEGD* requires independent evaluation of its drought-yield effect across backgrounds and field environments. In wheat, thermal measurements should be assessed for their ability to predict the breeding target, not only to discriminate genotypes. *Nothofagus* profiles need replication beyond the ex situ collection, while anther culture and *Eugenia* require evidence that their respective methods and resources deliver useful breeding or production outcomes.

The evolutionary dimension is represented indirectly through taxonomic characterization and the appraisal of genetic resources; none of the contributions tests evolutionary change as a process. A useful next step would be to connect population-level heritable variation with stress performance and selection across generations.

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6. Conclusions

The six contributions do not establish one general measure of plant resilience. Instead, they show why adaptation claims must be matched to the kind of evidence available: stress-responsive expression, a genetic intervention, a context-sensitive phenotype, taxonomic differentiation, a breeding method or a prospective crop resource. Their value for adaptation will depend on whether these signals and resources can be linked to outcomes that matter in production or conservation settings. The collection's central contribution is therefore a framework for asking what each result demonstrates, what it leaves unresolved and what evidence would justify the next step.

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