

# Field high-throughput phenotyping: the new crop breeding frontier

José Luis Araus<sup>1</sup> and Jill E. Cairns<sup>2</sup>

<sup>1</sup> Department of Plant Biology, Unit of Plant Physiology, University of Barcelona, 08028 Barcelona, Spain

<sup>2</sup> CIMMYT Southern Africa Regional Office, Harare, Zimbabwe

**Constraints in field phenotyping capability limit our ability to dissect the genetics of quantitative traits, particularly those related to yield and stress tolerance (e.g., yield potential as well as increased drought, heat tolerance, and nutrient efficiency, etc.). The development of effective field-based high-throughput phenotyping platforms (HTPPs) remains a bottleneck for future breeding advances. However, progress in sensors, aeronautics, and high-performance computing are paving the way. Here, we review recent advances in field HTPPs, which should combine at an affordable cost, high capacity for data recording, scoring and processing, and non-invasive remote sensing methods, together with automated environmental data collection. Laboratory analyses of key plant parts may complement direct phenotyping under field conditions. Improvements in user-friendly data management together with a more powerful interpretation of results should increase the use of field HTPPs, therefore increasing the efficiency of crop genetic improvement to meet the needs of future generations.**

## Why is phenotyping so important in the breeding pipeline?

Crop production must double by 2050 to meet the predicted production demands of the global population [1]. However, achieving this goal will be a significant challenge for plant breeders because crop yields would have to increase at a rate of 2.4% per year, yet the average rate of increase is only 1.3%, with yields stagnating in up to 40% of land under cereal production [2,3]. Extensive breeding and agronomic efforts over the past 50 years have been responsible for tripling cereal yields [4]. Continuing advances in the techniques available to breeders offer the potential to increase the rate of genetic improvement [5]. Attempts to exploit new molecular tools to their full potential (Figure 1), particularly the ability to dissect the genetics of quantitative traits such as yield and stress tolerance [6–10], are limited by our ability to phenotype. However,

plant breeders and farmers have been making selections based on phenotypes long before the discovery of DNA and molecular markers. The development of improved varieties relies on the ability to identify the best genetic variation for advancement. Breeding is essentially a numbers game: the more crosses and environments used for selection, the greater the probability of identifying superior variation. Plant breeders want to be able to phenotype large numbers of lines rapidly and accurately identify the best progeny. To meet future needs there is a need to increase breeding efficiency. Advances in high-throughput genotyping have provided fast and inexpensive genomic information. Low cost, high-throughput genotyping has paved the way for the development of large mapping populations and diversity panels of thousands of recombinant inbred lines for phenotyping [11]. Although molecular breeding strategies, such as marker-assisted recurrent selection (MARS) and genomic selection, place greater focus on selections based on genotypic information, they still require phenotypic data [12]. In genomic selection, phenotypes are not used for selection but are used to train a prediction model [13]; whereas in MARS, a single phenotyping cycle is used to identify markers for subsequent selection through generations. Similarly, phenotyping is necessary to identify promising events in transgenic studies [14,15]. Given that molecular breeding populations can include up to 5000 lines, the ability to accurately characterize all lines simultaneously is challenging [11]. Advances in phenotyping are likely to be essential to capitalize on developments in conventional, molecular, and transgenic breeding and ensure genetic improvement of crops for future food security.

## High-throughput phenotyping

In recent years, there has been increased interest in high-throughput phenotyping platforms (HTPPs) [16,17]. Most HTPPs, both those run by the big transnational seed companies and the most advanced public plant research institutions around the world, such as the Australian Plant Phenomics Facility (<http://www.plantphenomics.org.au/>), the European Plant Phenotyping Network (<http://www.plant-phenotyping-network.eu/eppn/structure>), and the USDA ([http://www.nifa.usda.gov/nea/plants/pdfs/whitepaper\\_finalUSDA.pdf](http://www.nifa.usda.gov/nea/plants/pdfs/whitepaper_finalUSDA.pdf)), ([http://www.wheatgenetics.org/downloads/Projects/HTP\\_ProjectNarrative\\_20130219.pdf](http://www.wheatgenetics.org/downloads/Projects/HTP_ProjectNarrative_20130219.pdf)) are fully automated facilities in greenhouses or growth chambers with robotics, precise environmental control, and remote sensing techniques to assess plant growth and performance. However, low-cost HTPP approaches are now

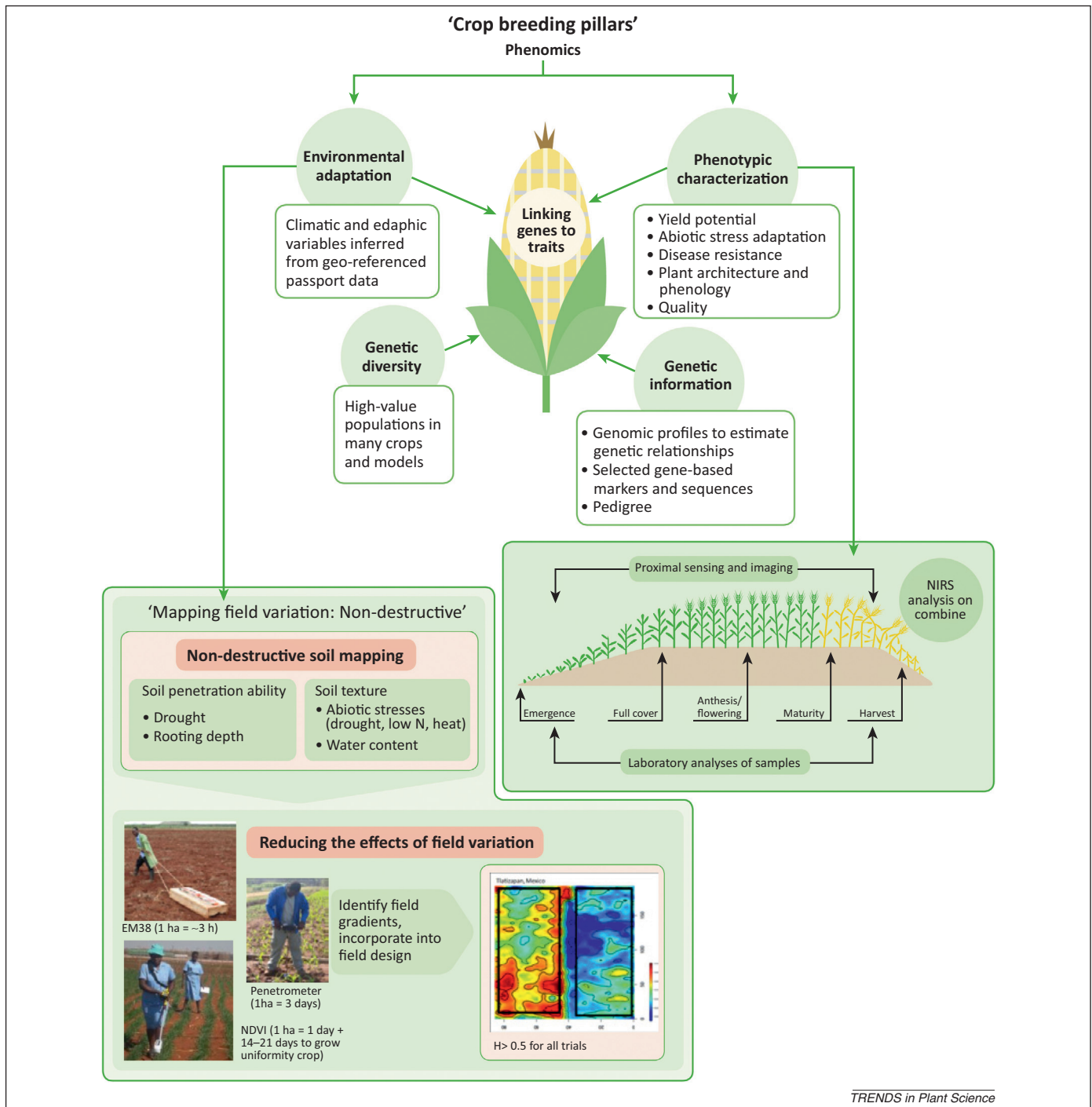
Corresponding author: Araus, J.L. ([jaraus@ub.edu](mailto:jaraus@ub.edu)).

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**Figure 1. (Upper)** The four pillars of the crop breeding pipeline (environmental adaptation, phenotypic characterization, genetic diversity, and genetic information) and the implications of phenotyping. The importance of phenotyping is highlighted by its involvement in two of these pillars. **(Lower left)** Mapping field variability in a non-destructive manner implies the use of different methodological alternatives and its further integration. **(Lower right)** Diagram of the main categories of phenotyping techniques deployed over the life cycle of an annual seed crop. Types of data acquisition include: proximal sensing and imaging at frequent intervals, laboratory analyses of samples taken at specific intervals, and near-infrared spectroscopy (NIRS) of seed for oil or protein content during combine harvesting. Redrawn from [20].

starting to be developed [18]. In this review, we examine the need for high-throughput field phenotyping, the current technical developments, and the factors that limit its implementation, together with the future avenues that will pave the way for its wide adoption in practical breeding.

### Field phenotyping

Although HTPPs enable detailed, non-invasive information to be captured throughout the plant life cycle in a

carefully controlled environment, quantitative trait loci and candidate genes identified within controlled environments have generally not translated into gains in grain yield in the field [19–21]. Field conditions are notoriously heterogeneous and the inability to control environmental factors makes results difficult to interpret. However, results from controlled environments are far removed from the situation plants will experience in the field and, therefore, are difficult to extrapolate to the field. The problems

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