



## Review

# LiDAR: An important tool for next-generation phenotyping technology of high potential for plant phenomics?



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## ABSTRACT

Plant phenomics, the link between plant genomics and environment, recently is explosively highlighted. As its basis, a large variety of phenotyping approaches have been developed, but meanwhile, the related technical demands have gone ahead into the levels of high-throughput, field and comprehensive phenotyping. This reality-lagging-behind situation suggests that it is time to envisage the next-generation techniques of plant phenotyping. From the perspective of noninvasive measurement of phenotypic traits, the state-of-the-art remote sensing technology of light detection and ranging (LiDAR) shows the potential. In fact, researchers are calling for more incorporations of LiDAR into phenotyping facilities. At the same time, it has also been realized that the currently-available LiDAR forms cannot effectively support the development of the next-generation techniques of plant phenotyping. In order to bridge this technical gap, the theoretically more-powerful LiDAR variant forms now in research and development, such as high-density, full-waveform and hyperspectral LiDAR, were previewed. Their supposed advanced capacities mean a higher possibility of pushing forward plant phenotyping into a new stage. Overall, with LiDAR determined as a key technical constituent, this study pointed out a novel way for developing the next-generation plant phenotyping techniques, which will be helpful for biologists and agronomists to investigate plant phenomes.

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## 1. Introduction

As a novel discipline in the field of biology, even regarded as its “next challenge” (Houle et al., 2010), phenomics has obtained more and more attention within these years. Comparable to other “-omics” such as genomics (Cabrera-Bosquet et al., 2012) and proteomics (Boggess et al., 2013) established for biology understanding, phenomics refers to the systematic study of phenomes (physical and biochemical traits of organisms) and concerns how to efficiently measure and analyze various phenotypic traits at different levels of organization (Houle et al., 2010). With phenomes taken as the *in vitro* indicators of the results of genomes sequencing and environment responding, phenomics can “close the gene-to-genotype loop” (Furbank and Tester, 2011). Thereby, phenomics is of numerous implications for various biological studies and applications, such as metabolic engineering (Schilling et al., 1999), human genomics (Freimer and Sabatti, 2003) and pharmaceutical research (Zbuk and Eng, 2006).

Currently, plant phenomics is a thriving branch of phenomics, and it is also of considerable implications for practical applications such as crop cultivation (Eberius and Lima-Guerra, 2009), livestock production (Boggess et al., 2013) and cultivar breeding (Araus and Cairns, 2014). In a boarder sense, its study facilitates meeting the future challenges imposed by climate change, population growth and resource reduction (Walter et al., 2012). However, our ability of characterizing phenomes lags far behind our ability of characterizing genomes (Houle et al., 2010), and the achievements made in genomics in recent decades are yet to be matched by a vigorous progress of phenomics (Deery et al., 2014). As reviewed by Yang et al. (2013), evaluation of rice phenotypic traits now is manually-performed, subjective, inefficient, destructive and error-prone, in contrast to the robustness of the concurrent genetic techniques. These analyses suggest that considerable efforts are necessitated for the task of exploring new technologies capable of effectively supporting phenomics.

### 1.1. Phenotyping – the basis of plant phenomics

Phenomics is rooted in phenomes or phenotypic traits, collectively referred to as phenotypes, which for any organism is the composite of its observable characteristics such as morphology, behavior and physiological properties. Gathering phenotypes, terminologically referred to as phenotyping (Fiorani and Schurr, 2013), serves as the basis of implementing phenomics. However, phenotyping for quantitative traits has attracted relatively insufficient attention until recently (Araus et al., 2008), and plant phenotyping remains the weak point in practical phenomic applications such as crop breeding (Cabrera-Bosquet et al., 2012). As summarized by Houle et al. (2010), the question ‘why not measure it all?’ for plant genomes has been affirmatively answered. Now, it is time to answer the same question for phenotypes. After all, for most biologists, the characteristics of organisms of greater interest are phenotypes rather than genotypes. Consequently, developing the techniques of high-performance phenotyping, sometimes termed as precision phenotyping (Cabrera-Bosquet et al., 2012), is

deemed as the fundamental option for advancing the field of phenomics.

In fact, the demand of efficient phenotyping techniques has been posed in numerous domains. In most cases, phenotypes are the most powerful predictors of important biological outcomes, such as fitness, disease and mortality (Houle et al., 2010). Molecular biologists and breeders realized that advancing molecular techniques may only be useful in breeding if the gathering of quantitative traits is based on reliable phenotyping (Araus et al., 2008). It is even expected that high-performance phenotyping and genomic selection of complex traits can revolutionize the breeding process by accelerating the generation-advance (Cabrera-Bosquet et al., 2012). For livestock production, the last piece of its puzzle is “the demand for high-dimensional phenotypic data or deeply phenotyped populations in the animal sciences” (Boggess et al., 2013). Based on these analyses, it can be learnt that phenotyping is intuitively considered as the first option for propelling the whole field of phenomics.

Specifically for plants, phenotypic variation, theoretically, is yielded through “a complex web of interactions between genotypes and environment ( $G \times E$ )” (Dhondt et al., 2013). The  $G \times E$  webs influence both the developmental program and growth of plants and plant functioning, which can be characterized using the structural- and physiological-type phenotypic traits of plants, respectively (Dhondt et al., 2013). In other words, precision phenotyping can help to find out which component in the phenotype set has predictive power over something in the field, and acquiring detailed phenotypic data allows the  $G \times E$  interactions to be exposed. As reviewed in Tuberosa (2012), accurate phenotyping facilitates identifying the quantitative trait loci, which can govern yield across different water regimes; but for a more effective transition of the results from the drought-related studies to improved cultivars, the difficulty of implementing accurate phenotyping is a widely-recognized obstacle. Thus, phenotyping techniques capable of revealing plant responses to environmental challenges for both *in-lab* and *field* experiment conditions are required (Fiorani and Schurr, 2013). In a more general sense, as the technical basis of plant phenomics, the methods of precision phenotyping are intensively and extensively demanded.

### 1.2. Literature review of plant phenotyping techniques

Since the concept of plant phenomics became popular in the late 1990s (e.g. Schilling et al., 1999), a number of plant phenotyping techniques aimed at different phenotypic traits have been proposed, validated and evaluated during the last 15 years. Several organizations have been founded, including such as Australian Plant Phenomics Facility (APPF, Australia) (<http://www.plantphenomics.org.au>), Jülich Plant Phenotyping Center (JPPC, Germany) ([http://www.fz-juelich.de/ibg/ibg-2/DE/Organisation/JPPC/JPPC\\_node.html](http://www.fz-juelich.de/ibg/ibg-2/DE/Organisation/JPPC/JPPC_node.html)) and Phenopsis and Phenodyn (INRA, France) (<http://bioweb.supagro.inra.fr/phenopsis>). Multiple plant phenomics platforms have been constructed, including such as LemnaTec (Rajendran et al., 2009) and PhenoMobile (Deery et al., 2014) for measurement of plant phenotypes in both *lab* and *field*. The

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