High throughput phenotyping to accelerate crop breeding in cassava

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Crop phenomics research integrates agronomy, life sciences, information science, math and engineering sciences, and combines high-performance computing and artificial intelligence technology to explore multifarious phenotypic information of crop growth in a complex environment, of which the ultimate goal is to construct an effective technical system able to phenotype crops in a high-throughput, multi-dimensional, big-data, intelligent and automatically measuring manner, and create a tool comprehensively integrating big data achieved from a multi-modality, multi-scale, phenotypic = genotypic + environmental condition, in order to develop new methods of mining genes associated with important agronomic traits, and propose new intelligent solutions for precision breeding.

Cassava is an important crop in Africa, Asia, Latin America, and the Caribbean. Cassava can be produced adequately in drought conditions making it the ideal food security crop in marginal environments. Although cassava can tolerate drought stress, it can be genetically improved to enhance productivity in such environments. Drought adaptation studies in over three decades in cassava have identified relevant mechanisms which have been explored in conventional breeding. Drought is a quantitative trait and its multigenic nature makes it very challenging to effectively manipulate and combine genes in breeding for rapid genetic gain and selection process. Cassava has a long growth cycle of 12–18 months which invariably contributes to a long breeding scheme for the crop.

Modern breeding using advances in genomics and improved genotyping, is facilitating the dissection and genetic analysis of complex traits including drought tolerance, thus helping to better elucidate and understand the genetic basis of such traits. A beneficial goal of new innovative breeding strategies is to shorten the breeding cycle using minimized, efficient or fast phenotyping protocols. While high throughput genotyping has been achieved, this is rarely the case for phenotyping for drought adaptation. Some of the storage root phenotyping in cassava are often done very late in the evaluation cycle making selection process very slow. This paper highlights some modified traits suitable for early-growth phase phenotyping that may be used to reduce drought phenotyping cycle in cassava. Such modified traits can significantly complement the high throughput genotyping procedures to fast track breeding of improved drought tolerant varieties. The need for metabolite profiling, improved phenomics to take advantage of next generation sequencing technologies and high throughput phenotyping are basic steps for future direction to improve genetic gain and maximize speed for drought tolerance breeding.

In cassava for disease monitoring (CMD) and drought phenotypic study, standardising ground level data with drone camera images to identify the physiological traits for phenotyping the germplasm or breeding population in an easy, economical and with short time. Identification of suitable progenies for specific breeding objective is easy and short time we can do it, without involving huge labour and economically.

HTP platforms

Varying the scale of phenotyping platforms from proximal to remote sensing allows for precise and consistent monitoring of single leaves/plant organs, individual plants, field plots and full fields as required (Fig.1). These platforms include, but are not limited to, environmental sensor networks, autonomous ground vehicles/ rovers, phenomobiles/ tractors/ buggies, phenotyping towers, field scanning platforms, unmanned aerial vehicles (UAVs), aircraft, zeppelins and satellites.

HTP to accelerate crop breeding and monitor disease

HTP techniques in crop breeding are generally used to screen for architectural traits and early detection of desirable genotypes. HTP allows for accurate, automated, and repeatable measurements for traits such as seedling vigour, flower counts, biomass and grain yield, height, leaf erectness, and canopy structure. HTP can also be applied for screening physiological traits, including photosynthesis, transpiration, disease and stress tolerance. Accurate and early season detection of plant diseases are key to reducing crop yield losses. Plant disease

diagnosis traditionally relies on symptom recognition through visual observation and ratings. HTP, specifically methods such as RGB imaging, 3D scanning, thermal and near-infrared sensing, multi-spectral and hyperspectral sensing, and fluorescence imaging have successfully been used to identify, quantify and monitor plant diseases. A variety of sensors technologies have been used for different plant pathogen systems. Careful consideration and understanding of appropriate sensors and HTP timepoints for field traits of interest is critical for manageable data collection and analysis.

Sensing technologies for HTP (RGB/stereo RGB)

Suitable for use under natural illumination outdoors, RGB cameras are key optical sensors for non-invasive field pheno-typing. Providing high-resolution data with fast acquisition rates, RGB cameras allow for rapid and objective assessment of plant growth, architecture and disease screening. The use of single RGB images for effective field phenotyping however is limited by inherent size distortions in the 2D image plane caused by areas of the plant or field plot being closer to the camera than others. 3D information generated by stereo RGB imaging can increase the precision of phenotypic data. For example, a recent study in grapevine used stereo RGB imaging to calculate fruit to leaf ratios and assess the growth habits of new breeding lines compared to known cultivars

HTP infrastructure for data analysis/big data management

Effective use of HTP requires data management strategies for handling raw data, metadata, derived data, derived data provenance, and standardized processing workflows. To guide crop breeding decisions, reducing the sheer volume and dimensionality of plant sensor data with high spatial, temporal and spectral resolution will require advanced methods of data management, analysis, and interpretation. Public and private efforts to utilize big data analytics and machine learning capabilities to improve crop performance are dependent on successful integration of multiple layers of data, including pedigrees, sequence data, genotypes and phenotypes.

Leveraging field HTP with environmental sensors and geographic information system (GIS)

Environmental conditions throughout a growing season, including temperature, rainfall, radiation intensity, soil moisture, relative humidity and day length are all key contributors to predicting crop yield and disease tolerance. Accurate environmental characterization can be achieved using geographic information system (GIS) for crop monitoring. GIS allows users to search and link traits to spatial data by combining geographic data to generate maps and reports, enabling users to collect, manage, and interpret location-based information. The sources of such crop data include satellite imagery, aerial photos, maps, ground surveys, and global positioning systems (GPS).

Robust computational models for crop yield and disease traits require the incorporation of genotypic, phenotypic, environmental and crop management data. The concept of 'envirotyping' encompasses the measurement of all environmental factors that affect plant growth and production at the resolution of field plots and individual plants. Ensuring that envirotypic data are collected concurrently with specific genotypic and phenotypic data effectively inform crop modeling and phenotype prediction. Guiding current crop improvement and breeding strategies, reliable estimates of early season phenotypic traits and robust crop models could dramatically reduce the experiment duration, number of plots and locations needed for crop improvement trials. For example, ML and algorithms for predicting late-season pheno-types such as total biomass from early season phenotypes could be used to rapidly make multiple rounds of line selections within one growing season.

Conclusions and prospects

With the rapid advancement of robust and high quality genetic and genomic technologies, the functional analysis of crop genomes is currently limited by the quality and speed of high throughput phenotyping.

Perpetual advances in genomics and HTP creates multiple layers of valuable information that can be exploited to rapidly advance crop breeding and monitoring of diseases. In recent years, major contributions from government and private organizations have been invested in the creation and use of HTP tools to speed the development and deployment of phenotyping and breeding technologies to benefit researchers and farmers. Projects funded by the Department of Energy (terraref.org) and organizations such as the Bill & Melinda Gates Foundation aim to use HTP to increase the productivity and resilience of crops that can reduce hunger and poverty and make communities economically stronger and more stable. International and U.S.-based organizations and universities are employing cutting-edge technologies to sequence and analyze crop genomes, along with capturing millions of pheno-typic observations across growing seasons and acclerating

High Throughput Phenotyping – Accelerate Crop Breeding
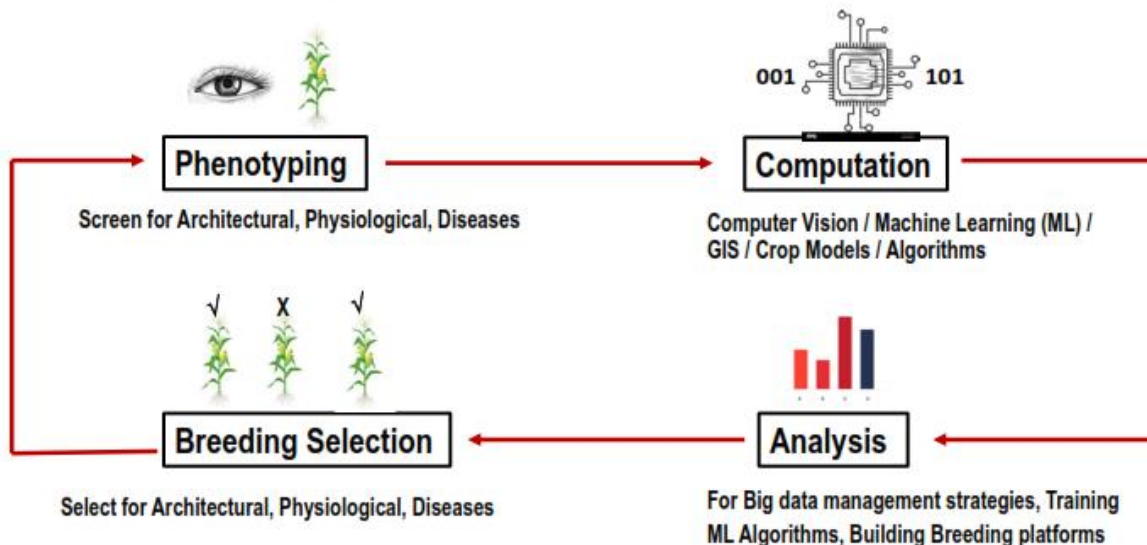
crop breeding efforts by connecting those phenotypes to genotypes.

Integrating heterogeneous information from reliable, automated, multifunctional, and high - throughput phenotyping platforms will require the continued development of novel technologies, with more effort dedicated towards developing low cost and high performance HTP technologies. With multi-functional phenotyping platforms obtaining large quantities of sensor data and images, data-storage, management and analysis will continue to be a challenge for crop HTP. Data volume is dependent on the resolution of the sensors /imagers and the numbers of acquired readings. To further promote the application of HTP in crop improvement programs, less expensive and more accessible data analysis infrastructures will need to be developed.