

Concepts and Strategies in Plant Sciences
Series Editor: Chittaranjan Kole

Jianfeng Zhou
Henry T. Nguyen *Editors*

High-Throughput Crop Phenotyping

 Springer

Concepts and Strategies in Plant Sciences

Series Editor

Chittaranjan Kole, Raja Ramanna Fellow, Government of India,
ICAR-National Institute for Plant Biotechnology, Pusa, Delhi, India

This book series highlights the spectacular advances in the concepts, techniques and tools in various areas of plant science. Individual volumes may cover topics like genome editing, phenotyping, molecular pharming, bioremediation, miRNA, fast-track breeding, crop evolution, IPR and farmers' rights, to name just a few. The books will demonstrate how advanced strategies in plant science can be utilized to develop and improve agriculture, ecology and the environment. The series will be of interest to students, scientists and professionals working in the fields of plant genetics, genomics, breeding, biotechnology, and in the related disciplines of plant production, improvement and protection.

Interested in editing a volume? Please contact Prof. Chittaranjan Kole, Series Editor, at ckoleorg@gmail.com

More information about this series at <http://www.springer.com/series/16076>

Jianfeng Zhou · Henry T. Nguyen
Editors

High-Throughput Crop Phenotyping

 Springer

Editors

Jianfeng Zhou
University of Missouri
Columbia, MO, USA

Henry T. Nguyen
University of Missouri
Columbia, MO, USA

ISSN 2662-3188

ISSN 2662-3196 (electronic)

Concepts and Strategies in Plant Sciences

ISBN 978-3-030-73733-7

ISBN 978-3-030-73734-4 (eBook)

<https://doi.org/10.1007/978-3-030-73734-4>

© Springer Nature Switzerland AG 2021

This work is subject to copyright. All rights are reserved by the Publisher, whether the whole or part of the material is concerned, specifically the rights of translation, reprinting, reuse of illustrations, recitation, broadcasting, reproduction on microfilms or in any other physical way, and transmission or information storage and retrieval, electronic adaptation, computer software, or by similar or dissimilar methodology now known or hereafter developed.

The use of general descriptive names, registered names, trademarks, service marks, etc. in this publication does not imply, even in the absence of a specific statement, that such names are exempt from the relevant protective laws and regulations and therefore free for general use.

The publisher, the authors and the editors are safe to assume that the advice and information in this book are believed to be true and accurate at the date of publication. Neither the publisher nor the authors or the editors give a warranty, expressed or implied, with respect to the material contained herein or for any errors or omissions that may have been made. The publisher remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

This Springer imprint is published by the registered company Springer Nature Switzerland AG
The registered company address is: Gewerbestrasse 11, 6330 Cham, Switzerland

Preface

Global population is expected to reach 9.8 billion and food demand is expected to be 60% higher than it is today by 2050, which requires a double current yield increase rate to meet the demand. During the past 20 years, molecular profiling and sequencing technologies enabled major advances toward the large-scale characterization of crop genomes. However, the acquisition of crop phenotypic information has lagged behind to allow a better understanding of genotype-to-phenotype relationships and becomes one of the bottlenecks to crop improvement, genetics, and genomic selection (GS). Thanks to the advances in emerging technologies in sensors, machine vision, robotics, Unmanned Aerial Systems (UASs), crop traits (phenotypic data) are able to be acquired in a large-scale and high-throughput manner. Big data processing and analytic technologies (e.g., machine learning and deep learning) and high-performance computation systems are transforming the conventional crop breeding to the next-generation AI-based crop breeding.

This book presents state-of-the-art information on the important innovations of high-throughput crop phenotyping technology in quantifying crop traits of shoots and roots through various applications in field and controlled environments. The applications cover a large range of crops (including soybean, wheat, maize, grains, and potato), various measurements of crop phenotypes in different levels (crop organ, plot, and field), and for different purposes. Different novel technologies and the implementation of these technologies in high-throughput crop phenotyping are reviewed and discussed. The technologies include emerging sensors to measure different crop traits, automated data acquisition platforms for fast and large-scale data collection (e.g., autonomous ground and aerial vehicles, robotic systems), big data processing and analytics, and their integration. Each chapter of the book focuses on different aspects of the high-throughput phenotyping technology and the applications for specific crops. The book starts with a chapter (Chap. 1) that briefly explains the concept, content, and roles of the high-throughput crop phenotyping technology in crop breeding towards yield improvement using the breeder's equation. Chaps. 2 and 3 provide the applications of innovative field-based crop phenotyping systems using ground-based robot systems and a cable-suspended robot system. As one of the key components of image-based phenotyping systems,

Chap. 4 discusses novel methods for developing three-dimensional (3D) architecture of crop plants based on images or videos collected with field crop phenotyping systems. The following chapters (Chaps. 5–8) provide applications in crop breeding of wheat, rice, soybean, and potato, followed by the applications in a controlled environment (Chap. 9) and root phenotyping (Chap. 10). The final chapter (Chap. 11) discusses the challenges in adopting high-throughput crop phenotyping technology into crop breeding pipelines by considering of cost.

This book provides insights into high-throughput crop phenotyping technology from the different perspectives of leading researchers in multiple disciplines, including but not limited to Crop Breeding, Genetics, Engineering, Computer Science, and Data Science. The authors have extensive knowledge and practical experiences in their respective fields and are actively involved in the international community of crop phenotyping. We wish to acknowledge their expert contributions and great efforts in the preparation for the book chapters. Finally, we hope that this book will assist all readers who are working in or associated with the fields of high-throughput crop phenotyping.

Columbia, MO, USA

Jianfeng Zhou
Henry T. Nguyen

Contents

1	Solve the Breeder’s Equation Using High-Throughput Crop Phenotyping Technology	1
	Jianfeng Zhou and Henry T. Nguyen	
2	Field Robotic Systems for High-Throughput Plant Phenotyping: A Review and a Case Study	13
	Yin Bao, Jingyao Gai, Lirong Xiang, and Lie Tang	
3	Cable Suspended Large-Scale Field Phenotyping Facility for High-Throughput Phenotyping Research	39
	Geng (Frank) Bai and Yufeng Ge	
4	Structure from Motion and Mosaicking for High-Throughput Field-Scale Phenotyping	55
	Hadi AliAkbarpour, Ke Gao, Rumana Aktar, Steve Suddarth, and Kannappan Palaniappan	
5	Experiences of Applying Field-Based High-Throughput Phenotyping for Wheat Breeding	71
	Jared Crain, Xu Wang, Mark Lucas, and Jesse Poland	
6	High-Throughput Phenotyping (HTP) and Genetic Analysis Technologies Reveal the Genetic Architecture of Grain Crops	101
	Wanneng Yang, Xuehai Zhang, and Lingfeng Duan	
7	High-Throughput Phenotyping in Soybean	129
	Asheesh K. Singh, Arti Singh, Soumik Sarkar, Baskar Ganapathysubramanian, William Schapaugh, Fernando E. Miguez, Clayton N. Carley, Matthew E. Carroll, Mariana V. Chiozza, Kevin O. Chiteri, Kevin G. Falk, Sarah E. Jones, Talukder Z. Jubery, Seyed V. Mirnezami, Koushik Nagasubramanian, Kyle A. Parmley, Ashlyn M. Rairdin, Johnathon M. Shook, Liza Van der Laan, Therin J. Young, and Jiaoping Zhang	

8 High-Throughput Phenotyping in Potato Breeding 165
Jagesh Kumar Tiwari, Sushil S. Changan, Tanuja Buckseth,
Rajesh K. Singh, Brajesh Singh, Satish K. Luthra, Shashi Rawat,
and Manoj Kumar

**9 High-Throughput Crop Phenotyping Systems for Controlled
Environments** 183
Jianfeng Zhou, Jing Zhou, Heng Ye, and Henry T. Nguyen

**10 Phenotyping Root System Architecture, Anatomy,
and Physiology to Understand Soil Foraging** 209
Larry M. York

**11 Got All the Answers! What Were the Questions? Avoiding
the Risk of “Phenomics” Slipping into a Technology Spree** 223
Vincent Vadez, Jana Kholova, Grégoire Hummel,
and Uladzimir Zhokhavets

Index 243

Contributors

Rumana Aktar University of Missouri-Columbia, Columbia, USA

Hadi AliAkbarpour Transparent Sky, Edgewood, USA;
University of Missouri-Columbia, Columbia, USA

Geng (Frank) Bai Department of Biological Systems Engineering, University of
Nebraska-Lincoln, Nebraska, Lincoln, USA

Yin Bao Department of Biosystems Engineering, Auburn University, Auburn, AL,
USA

Tanuja Buckseth ICAR-Central Potato Research Institute, Shimla, Himachal
Pradesh, India

Clayton N. Carley Department of Agronomy, Iowa State University, Ames, IA,
USA

Matthew E. Carroll Department of Agronomy, Iowa State University, Ames, IA,
USA

Sushil S. Changan ICAR-Central Potato Research Institute, Shimla, Himachal
Pradesh, India

Mariana V. Chiozza Department of Agronomy, Iowa State University, Ames, IA,
USA

Kevin O. Chiteri Department of Agronomy, Iowa State University, Ames, IA, USA

Jared Crain Department Plant Pathology, Kansas State University, Throckmorton
Plant Sciences Center, Manhattan, KS, USA

Lingfeng Duan College of Engineering, Huazhong Agricultural University,
Wuhan, People's Republic of China

Kevin G. Falk Department of Agronomy, Iowa State University, Ames, IA, USA

Jingyao Gai Department of Agricultural and Biosystems Engineering, Iowa State
University, Ames, IA, USA

Baskar Ganapathysubramanian Department of Mechanical Engineering, Iowa State University, Ames, IA, USA

Ke Gao University of Missouri-Columbia, Columbia, USA

Yufeng Ge Department of Biological Systems Engineering, University of Nebraska-Lincoln, Nebraska, Lincoln, USA

Grégoire Hummel Phenospex, Heerlen, The Netherlands

Sarah E. Jones Department of Agronomy, Iowa State University, Ames, IA, USA

Talukder Z. Jubery Department of Agronomy, Iowa State University, Ames, IA, USA

Jana Kholova Crop Physiology Laboratory, ICRISAT, Patancheru, Telangana, India

Manoj Kumar ICAR-Central Potato Research Institute, Shimla, Himachal Pradesh, India

Mark Lucas Department Plant Pathology, Kansas State University, Throckmorton Plant Sciences Center, Manhattan, KS, USA

Satish K. Luthra ICAR-Central Potato Research Institute, Shimla, Himachal Pradesh, India

Fernando E. Miguez Department of Agronomy, Iowa State University, Ames, IA, USA

Seyed V. Mirnezami Department of Mechanical Engineering, Iowa State University, Ames, IA, USA

Koushik Nagasubramanian Department of Electrical Engineering, Iowa State University, Ames, IA, USA

Henry T. Nguyen Division of Plant Science and Technology, University of Missouri, Columbia, MO, USA

Kannappan Palaniappan University of Missouri-Columbia, Columbia, USA

Kyle A. Parmley Department of Agronomy, Iowa State University, Ames, IA, USA

Jesse Poland Department Plant Pathology, Kansas State University, Throckmorton Plant Sciences Center, Manhattan, KS, USA;
Wheat Genetics Resource Center, Kansas State University, Throckmorton Plant Sciences Center, Manhattan, KS, USA

Ashlyn M. Rairdin Department of Agronomy, Iowa State University, Ames, IA, USA

Shashi Rawat ICAR-Central Potato Research Institute, Shimla, Himachal Pradesh, India

Soumik Sarkar Department of Mechanical Engineering, Iowa State University, Ames, IA, USA

William Schapaugh Department of Agronomy, Kansas State University, Manhattan, KS, USA

Johnathon M. Shook Department of Agronomy, Iowa State University, Ames, IA, USA

Arti Singh Department of Agronomy, Iowa State University, Ames, IA, USA

Asheesh K. Singh Department of Agronomy, Iowa State University, Ames, IA, USA

Brajesh Singh ICAR-Central Potato Research Institute, Shimla, Himachal Pradesh, India

Rajesh K. Singh ICAR-Central Potato Research Institute, Shimla, Himachal Pradesh, India

Steve Suddarth Transparent Sky, Edgewood, USA

Lie Tang Department of Agricultural and Biosystems Engineering, Iowa State University, Ames, IA, USA

Jagesh Kumar Tiwari ICAR-Central Potato Research Institute, Shimla, Himachal Pradesh, India

Vincent Vadez Institut de Recherche pour le Développement (IRD), UMR DIADE, University of Montpellier, Montpellier, France

Liza Van der Laan Department of Agronomy, Iowa State University, Ames, IA, USA

Xu Wang Department Plant Pathology, Kansas State University, Throckmorton Plant Sciences Center, Manhattan, KS, USA

Lirong Xiang Department of Agricultural and Biosystems Engineering, Iowa State University, Ames, IA, USA

Wanneng Yang National Key Laboratory of Crop Genetic Improvement and National Center of Plant Gene Research, Huazhong Agricultural University, Wuhan, People's Republic of China

Heng Ye Division of Plant Science and Technology, University of Missouri, Columbia, MO, USA

Larry M. York Noble Research Institute, LLC, Ardmore, OK, USA

Therin J. Young Department of Mechanical Engineering, Iowa State University, Ames, IA, USA

Jiaoping Zhang Department of Agronomy, Iowa State University, Ames, IA, USA

Xuehai Zhang National Key Laboratory of Wheat and Maize Crops Science/College of Agronomy, Henan Agricultural University, Zhengzhou, People's Republic of China

Uladimir Zhokhavets Phenospex, Heerlen, The Netherlands

Jianfeng Zhou Division of Plant Science and Technology, University of Missouri, Columbia, MO, USA

Jing Zhou Division of Plant Science and Technology, University of Missouri, Columbia, MO, USA

Abbreviations

$\Delta^{13}\text{C}$	Carbon isotope discrimination
ΔG_{year}	Genetic gain per year
^{13}C	Isotope Carbon 13
2D	Two-dimensional
2-D	2 dimension
3D	Three-dimensional
3-D	3 dimension
AGV	Automatic guided vehicles
AI	Artificial Intelligence
API	Application programming interface
ATV	All-terrain vehicle
BC	Backcross population
BOVW	Bag of Visual Words
CCD	Charge-coupled device
CIMMYT	International Maize and Wheat Improvement Center
CMOS	Complementary metal-oxide-semiconductor
CNN	Convolutional neural networks
CO_2	Carbon dioxide
CPU	Central processing unit
CSS	Cable-suspended system
CT	Computed Tomography
DAE	Day after emerging
DEM	Digital Elevation Model
DH	Double haploid population
DIRT	Digital imaging of root traits
DL	Deep learning
DPS	Global positioning system
DR	Drought tolerance
EKF	Extended Kalman filter
ELM	Extreme Learning Machine
ELR	Extreme learning
EMS	Electromagnetic spectrum

EPV	Estimated processed value
EVI2	Enhanced vegetation index
FIP	Field Phenotyping Platform
F_m	Maximum fluorescence value
F_o	Minimum fluorescence value
FOV	Field of view
FPP	Field plant phenotyping
F_v	Variable fluorescence
G2P	Genotype-to-phenotype
GBS	Genotype-by-sequence
GBS	Genotyping-by-sequencing
GCPs	Ground control points
GEBV	Genomic estimated breeding values
gLAI	green Leaf Area Index
GNSS	Global navigation satellite system
GP	Genomic prediction
GPS	Global positioning system
GS	Genomic selection
GSD	Ground sample distance
GSR	Green super rice
GUIs	Graphic User Interfaces
GVPF	Green Vegetation Pixel Fraction
GWAS	Genome-Wide Association Study
HHIS	High-throughput hyperspectral imaging system
HLS	High-throughput leaf scoring
HPC	High-performance computing
HRPF	High-throughput rice phenotyping facility
HTP	High-throughput phenotyping
HTPP	High-throughput plant phenotyping
IAP	Inbred association panel
IAP	Integrated analysis platform
IDC	Iron deficiency chlorosis
ILs	Introgression lines
IMU	Inertial measurement unit
inGaAs	Indium gallium arsenide
IPK	Leibniz Institute of Plant Genetics and Crop Plant Research
IPPN	International plant phenotyping network
IR	Infrared
IRT	Infrared thermography
IRT	Infrared thermometer
K-NN	K-Nearest Neighbors
LAI	Leaf area index
LAN	Local area network
LAT	Laser ablation tomography
LD	Linkage disequilibrium

LDA	Linear Discriminant Analysis
LEADER	Leaf elemental accumulation for deep roots
LED	Light Emitting Diodes
LiDAR	Light detecting and ranging
LIF	Laser-induced Fluorescence
LQG	Linear-Quadratic-Gaussian
LQR	Linear Quadratic Regulator
LSTM	Long short-term memory
LWIR	Long-wave Infrared
MAE	Mean absolute error
MAGIC	Multiparent advanced generation intercross population
MAS	Marker-assisted selection
MED	Minimum Euclidean Distance
ML	Machine learning
MLP	Multilayer perceptrons
MLR	Multiple linear regression
MPC	Model predictive control
MRI	Magnetic resonance imaging
N	Nitrogen
NAM	Nested association mapping
NARS	National Agriculture Research Systems
NAS	Network-attached storage
NASA	National Aeronautics and Space Administration
NASA	The National Aeronautics and Space Administration
NDRE	Normalized Difference Red Edge
NDVI	Normalized difference vegetation index
NIL	Near isogenic lines
NIR	Near-infrared
NMPC	Nonlinear model predictive control
NPQ	Non-photochemical quenching
NSF	National Science Foundation
PAM	Pulse Amplitude Modulated
PAR	Photosynthetically active radiation
PCB	Printed circuit board
PET	Positron emission tomography
PH	Plant height
PheWAS	Phenome-wide association study
Pi	Phosphate
PID	Proportional-integral-derivative
PLS	Partial least squares
PLSR	Partial least squares regression
PNN	Probabilistic Neural Network
PTS	Plant-to-sensor
QDA	Quadratic Discriminant Analysis
QTL	Quantitative trait loci

RANSAC	Random sample consensus
R-CNN	Region-based convolutional neural networks
REST	Root Estimator for Shovelomics Traits
RF	Random Forest
RGB	Red, Green, Blue
RGB-D	RGB and depth
RH	Relative humidity
RIL	Recombinant inbred lines
RMSE	Root mean square error
RNN	Recurrent neural networks
ROAM	Random-open-parent association mapping
ROI	Region of interest
ROS	Robot Operating System
RSA	Root system architecture
RTK	Real-time kinematic
RTK-GPS	Real-time kinematic global positioning system
RUE	Radiation use efficiency
SAM	Shoot apical meristem
SAM	Spectral Angle Mapper
SCN	Soybean cyst nematode
SEA	Seed Evaluation Accelerator
SfM	Structure from Motion
SMO	Sequential Minimal Optimization
SNP	Single nucleotide polymorphism
STP	Sensor-to-plant
STR	Salt tolerant rate
SVM	Support Vector Machine
SVR	Support Vector regression
SWIR	short-wave infrared
T	Temperature
T_a	Air temperature
T_c	Canopy temperature
TEB	Timed elastic band
ToF	Time-of-flight
T_s	Soil temperature
UAS	Unmanned aerial systems
UAV	Unmanned Aerial Vehicle
UAVs	Unmanned aerial vehicles
UGV	Unmanned ground vehicle
UGVs	Unmanned ground vehicles
UTC	Coordinated universal time
UTM	Universal transverse mercator
UV	Ultraviolet
VI _s	Vegetation indices
VNIR	Visible near-infrared

VPD	Vapor pressure deficit
VREI2	Vogelmann red edge index 2
X-ray CT	X-ray computed tomography
XRF	X-ray fluorescence
YTS	Yield traits scorer

Chapter 1

Solve the Breeder's Equation Using High-Throughput Crop Phenotyping Technology



Jianfeng Zhou and Henry T. Nguyen

Abstract This chapter provides an overview of high-throughput crop phenotyping technology on its concept and significance under the context of crop production improvement. The roles of different components in the crop production equation ($P = G \times E \times M + \varepsilon$) toward crop yield, i.e., crop yield (P) is a function of crop genotype (G), environment (E) and management (M) is discussed. It is concluded that all components have a great impact on the agriculture yield. Studies suggest that the contribution of crop genetic improvement to yield improvement can be increased substantially upon the breakthroughs in high-efficient crop phenotyping technologies. The potential solutions to improve crop yield gain are discussed and guided by the genetic gain (breeder's) equation. In this chapter, the concept of high-throughput phenotyping technology is introduced and their potential contributions toward genetic improvement are discussed. This chapter also provides some background information for the high-throughput phenotyping technologies discussed in the following chapters.

Keywords Crop production · Interaction of genotype, environment and management · Genetic gain equation · High-throughput phenotyping

1.1 Crop Production

The world population is estimated to increase by 2 billion in the next 30 years, from 7.7 billion currently to 9.7 billion in 2050, although the growth speed is at a slower pace (UN DESA 2019). It is estimated that global crop production needs to double by 2050 to meet the projected demands from rising population, diet shifts, and increasing biofuels consumption (Alexandratos and Bruinsma 2012a; Hickey et al. 2019; Ray

J. Zhou (✉)

Division of Plant Science and Technology, University of Missouri, MO 65211 Columbia, USA
e-mail: zhoujianf@missouri.edu

H. T. Nguyen

Division of Plant Science and Technology, University of Missouri, MO 65211 Columbia, USA
e-mail: nguyenhenry@missouri.edu

© Springer Nature Switzerland AG 2021

J. Zhou et al. (eds.), *High-Throughput Crop Phenotyping*,
Concepts and Strategies in Plant Sciences,
https://doi.org/10.1007/978-3-030-73734-4_1

et al. 2013). However, the current yearly increases of crop production for maize (*Zea mays* L.) at 1.6%, rice (*Oryza sativa* L.) at 1.0%, wheat (*Triticum aestivum* L.) at 0.9%, and soybean [*Glycine max* (L.) Merr.] at 1.3% are insufficient to meet the projected demands of $\sim 2.4\%$ in 2050 (Alexandratos and Bruinsma 2012b; Ray et al. 2013). How to improve the production of the major crops has become an impressive pressure to the global research communities (Hatfield and Walthall 2015).

Crop production is very complicated and determined by many factors, such as crop genotypes (varieties), growing environments (e.g., weather, soil, microclimate, and location), and agronomic management strategies (e.g., seed treatment and placement, planting, fertilizer, and pest management). All the effects of different factors to crop production can be summarized using a crop production equation, i.e., crop production (P) is the function of the interactions of genotype (G), environment (E), and management (M), as shown in Eq. 1.1 (Beres et al. 2020; Hatfield and Walthall 2015).

$$P = G \times E \times M + \varepsilon \quad (1.1)$$

where, P = plant Phenotypes that refer to the observable physical properties of an organism, including yield; G = Genotype that refers to the genetic makeup of an organism; E = Environmental factors that affect plant growth, such as climate, soil quality, light, temperature, and water availability; and M = Management practices of plant and field, such as seed treatment, planting, pest management, nutrition management, and irrigation; ε is the total errors of the model. The equation suggests that crop yield can be increased with the improvement in crop genotypes through breeding programs, adoption of crops to environment, and improvement in field and crop management strategies (von Mogel 2013).

The natural environment is not possible to manage, but it has a great impact on crop production. Under climate change, environment is becoming unfavorable to plant growth, such as changes in CO₂ level, global temperature, degradation of soil quality, and extreme weather conditions (e.g., flood and drought). For example, according to the US National Aeronautics and Space Administration (NASA) weather simulation models, there is a predicted 30% increase in heavy precipitation events by the year 2030, which is expected to significantly increase the risk and frequency of flooding (Rosenzweig et al. 2002). Flooding damage to crops can be caused by extreme rainfall events, excess irrigation, or by rainfall that occurs after an irrigation event (Heatherly and Pringle III 1991). Environment will continue generating strong impacts on crop production negatively. According to a recent study (Aggarwal et al. 2019), it is found that global crop yields declines due to climate change starts as early as the 2020s, and yield losses are projected to increase with time, up to 50% by the 2080s. Therefore, there is a pressing need to develop climate-resilient crops and agronomic management strategies to suite for the dynamic environment.

Advances in agronomic management in crops and fields have a great positive impact on crop production. Some studies even suggest that the influence of management is more than the genotype does on the crop yield. For example, it is found that N

and water limit crop yield more than plant genetics (Sinclair and Rufty 2012). A study from Brisson et al. (2010) also suggested that wheat yield was significantly affected by the increased variability in climate during the growing season because of the heat stress during grain-filling and water stress during stem elongation and tillering. Affholder et al. (2013) found that poor soil fertility and weed infestation have more impact on agriculture production than other factors of environment and genotypes. In addition, research also shows that yield of corn and soybean is heavily affected by the planting date and planting depth (Baum et al. 2018; Hu and Wiatrak 2012). With continuous improvement in agronomic management with emerging technologies, using emerging technologies in precision agriculture, sensors, internet of things, big data and artificial intelligence, management will make a greater contribution in crop yield improvement.

Although the production of major commodity crops has been increasing over time due to the improved genetics, improved management, and environmental adaptations, their contributions of each factor are difficult to quantify due to the complicated interactions and the dynamic nature of environment and management practices. However, in a study, Fischer (2009) found that Australian wheat yield had a 1.3% total increase per year over the past 100 years. The author attributed 0.2% of the total increase to the environment, 0.5% to genetic improvement and the interaction of genotype with management, and 0.6% to management alone, which are equivalent to about 30% to genetic improvement, 15% to environment adoption, and 55% to management (Hillel and Rosenzweig 2013). In addition, Duvick (2005) argued that increases in maize yield in the past 50 years were due equally to breeding and improved management. Although the yield gain of the world's staple crops continues improving due to improvement in breeding technologies (Li et al. 2018), the yield increases also depend on the improved agronomic management to realize the potential of these breeding-based improvements in farmer's fields (Fischer and Connor 2018). The potential yield is defined as the yield of the best-adapted cultivar with currently the best agronomic management practices ensuring the absence of manageable abiotic and biotic stresses (Fischer 2015). However, the gap between potential yield and yield in farm yields can be substantial (Beres et al. 2020), for example, the farm yields of rice, wheat, and maize are about 80% of potential yields under irrigated conditions, and 50% or less under rainfed conditions (Lobell et al. 2009). Therefore, it is critical to consider the interaction effects of $G \times E \times M$ as the key to screening genotypes and closing yield gaps (Hatfield and Walthall 2015).

Field and crop management strategies have been improved significantly thanks to the advances in precision agriculture, sensing technologies, data processing, and analysis (Yost et al. 2019). However, there are practical constraints in management that are needed to be considered when maximizing the crop yield. Management strategies are heavily dependent on accumulative experiences from practices, but climate change makes it difficult to make proper decisions on management for the unpredictable environment, which brings significant challenges in crop management to maintain a stable and high yield production. In addition, although modern agriculture with advanced management has been successful in increasing food production, it has also caused extensive environmental damage. For example, increasing fertilizer

use has led to the degradation of water quality in many regions (Bennett et al. 2001; Matson et al. 1997). It is also evident that some irrigated lands have become heavily salinized, causing the worldwide loss of ~ 1.5 million hectares of arable land per year, along with an estimated \$11 billion losses in production (Wood et al. 2000). Up to $\sim 40\%$ of global croplands may also be experiencing some degree of soil erosion, reduced fertility, or overgrazing (Wood et al. 2000). Therefore, over-managed agricultural systems may not be beneficial for sustainable agricultural system in long run.

There are very limited natural resources that are available for farmers to make desired management practices to optimize crop production. For example, 92% of the soybean acreage in the United States is under rainfed dryland conditions (Irwin et al. 2017) where crop productivity is always threatened by unpredictable drought but irrigation is not an option. In addition, the management of crops under flooding conditions is always challenging. It was reported that the 2011 Mississippi River flood caused a loss of \$2 billion in crop damages when fewer than 6,500 acres of soybean were harvested in the southern counties of Illinois (Olson and Morton 2013). The situation was even worse in 2015, as more than half of the states' soybean crop was affected and the crop damage caused by the floods of 2019 was even severer than that of 2015. The crop yield loss due to the constraints in management may be compensated through the development of new crop varieties with flood or drought-resilient traits. The conventional breeding programs are transferring to more efficient modern breeding programs through integrating emerging technologies, especially the high-throughput phenotyping technology. It is believed by authors that the contributions of genetic improvement based on high-throughput phenotyping technology will increase crop yield gains significantly in the near future. In the following sections of this chapter, we will focus on how to improve the yield gain in breeding programs using high-throughput phenotyping technology.

1.2 Breeder's Equation for Crop Production

Crop yield can be improved through optimal management and breeding new crop varieties with improved traits. The improvement of crop yield and other traits due to artificial or genomic selection is quantified using the genetic gain equation (commonly known as 'breeder's equation') calculated using Eq. 1.2 (Eberhart 1970; Li et al. 2018).

$$\Delta G = \frac{ir\sigma_A}{L} \quad (1.2)$$

where ΔG is the genetic gain (yearly gain due to genetic factors), i is the selection intensity, r is the selection accuracy, σ_A is the square root of the additive genetic variance within the population, and L is the length of breeding cycle interval or

generation. The breeder's equation provides general guidance and useful framework for the design of breeding programs leading to the improvement of genetic gain. It can be seen from Eq. 1.2 that genetic gain is positively proportional to the parameters of selection intensity, selection accuracy and genetic variance. Selection intensity is determined by the selection rate, i.e., the proportion of the population selected from the total population (Xu et al. 2017). A larger population size allows a greater selection intensity and improves the probability of identifying progenies with desired traits, such as high yield potential and resilience to stresses. Therefore, the first way to improve the genetic gain is to increase the breeding population. The second favorable factor, the selection accuracy, refers to the accuracy of selection on breeding value. The selection accuracy is determined by heritability and can be increased by increasing the marker density. The advances in high-throughput sequencing technologies and genomic selection (GS) can remarkably improve the selection accuracy (Bhat et al. 2016; Crossa et al. 2017). In addition, the selection accuracy can be increased by increasing repeatability in the breeding population thus increases the selection response for the trait of interest (Araus et al. 2018). For the breeding programs with a fixed budget, it needs to balance between the population and replication to maximize the genetic gain.

In addition, genetic variance is also positive to the increase of genetic gain. Although the vast number of valuable germplasm collections in gene banks can be used as a source to acquire genetic variation, the contribution is limited by the time and resources required to precisely characterize the accessions at large scale, and identifying and transferring the useful alleles into adapted germplasm. Advanced tools are needed to identify more molecular markers that can reveal genetic variation (Xu et al. 2017) and accurately quantify genetic variations due to environment (Araus et al. 2018). In the equation, the length of breeding cycle interval or generation is directly reciprocal to genetic gain. Conventional breeding programs have a fixed timeline for the development of new varieties and it is hard to change the breeding cycles. However, in recent years, researchers are studying a method called 'speed breeding' or 'rapid breeding' to shorten the breeding cycle and accelerate breeding and research programs (Li et al. 2018; Watson et al. 2018). For example, speed breeding technology is potential to achieve up to six generations per year for spring wheat, durum wheat, barley, chickpea, and pea, and four generations for canola under normal glasshouse conditions (Watson et al. 2018). In addition, breeding cycle is also potentially to accelerate by improving the prediction accuracy and discovering more reliable secondary crop traits using emerging phenotyping tools (Araus et al. 2018).

In summary, there are many approaches to increase genetic gain of a breeding program by solving the breeder's equation (Cobb et al. 2019; Hickey et al. 2019; Pieruschka and Schurr 2019). To develop next-generation breeding programs, we should consider some critical factors closely related to genetic gains (Araus et al. 2018; Awada et al. 2018; Cobb et al. 2019; Li et al. 2018; Zhao et al. 2017). Some examples include: (a) how to increase the capacity for larger breeding population to enable higher selection intensity; (b) how to enhance selection accuracy using emerging technologies; (c) how to identify genetic variations; and (d) how to reduce the breeding cycles. While we continue advancing the molecular-based breeding

strategies using genomic technology, special efforts should be taken to eliminate the bottlenecks in current breeding programs, i.e., how to measure plant phenotypes efficiently and accurately for a large breeding population. Current breeding programs are limited by cost, time, human labor, land and other resources to efficiently scan a large population of progenies (Rebetzke et al. 2016), which limit the selection intensity, affect the genetic accuracy, and result in low genetic gain. Therefore, the development and application of low-cost, high-throughput phenotyping tools allow reallocation of resources to manage larger populations, enable an increase in selection intensity within a fixed budget.

1.3 High-Throughput Crop Phenotyping

The term “phenotype” as a counterpart concept to “genotypes” was created one century ago (Johannsen 1903, 1911), which has been used to describe a wide range of traits in plants, microbes, fungi and animals (Walter et al. 2015). Plant phenotype is the functional plant body that is formed during plant growth and development from the dynamic interaction between the genetic background (genotype) and the physical world in which plants develop (environment). The term ‘phenotyping’ began using in the 1960s (Walter et al. 2015) and later was referred to as the set of methodologies and protocols used to accurately measure plant growth, architecture, and composition at different scales (Fiorani and Schurr 2013). Traditionally, to select superior progenies or identify gene loci in the genome controlling a trait, usually, hundreds to thousands of plant phenotypes are measured by breeders using low-throughput laboratory assessments, visual observations, and manual tools. Traditional crop phenotyping methods are labor-intensive, time-consuming, subjective, and frequently destructive to plants (Chen et al. 2014; Furbank and Tester 2011). The lags in the advances of emerging technologies and low throughput in plant phenotyping have become a critical constraint to crop breeding and functional genomics studies (Deery et al. 2016).

High-throughput phenotyping (HTP) technologies emerged in the last decade thanks to the advances and reduced cost in sensor, computer vision, automation and advanced machine learning technologies. Crop HTP refers as the gathering of multi-dimensional phenotypic data at multiple levels from cell, organ, plant to population using emerging technologies (Lobos et al. 2017; Zhao et al. 2019). A comprehensive HTP system is consisted of supportive hardware (sensors and platforms) and computation component (data process and analytics). Widely used sensors in HTP technology are primarily non-contact and non-invasive sensors, such as digital cameras (e.g., visible, multispectral, hyperspectral Chlorophyll fluorescence and thermal cameras), three-dimensional depth sensors (LiDAR, time-of-flight camera) (see list of the cameras in Araus et al. 2018 and Zhao et al. 2019). Explorable research is testing and adopting some advanced imaging techniques that are widely used in medical applications, such as magnetic resonance imaging (MRI), positron emission tomography (PET), and computed tomography (CT), to HTP systems in the growth

chamber or greenhouse. The advances in sensor technology are primarily driven by the industry sector, while efforts have been made toward integrating them to crop HTP systems. In addition, supportive hardware also includes automation platforms for efficient data collection. Commonly used automation platforms include track-based automation systems (Zhou et al., 2018a; b), indoor and outdoor robotic systems (Awada et al. 2018; Chapman et al. 2014; Yang et al. 2020; Zhao et al. 2019), unmanned aerial system (UAS) (Yang et al. 2017), which are commercially available or developed by the research team for special need.

The more important component of an HTP system is data processing and analytic system. Current HTP systems, especially high-resolution imaging systems, are ready to collect high-dimensional data of crops of a large population. However, researchers will realize soon that they may be overwhelmed by the huge data that are beyond their ability to handle (Blumenthal et al. 2020; Yang et al. 2020; Zhao et al. 2019). Therefore, one of the urgent tasks for HTP system is to develop frameworks or pipelines for efficient data processing and analytics that can translate sensor data to important crop traits (Blumenthal et al. 2020; Hallowell et al. 2018; Zhou et al. 2018a). More efforts should be taken to develop and integrate emerging technologies such as cloud computing, edge computing, machine learning, deep learning and artificial intelligence (AI) into HTP systems. With the continuous efforts from the community, HTP technology can potentially be the key component to solve the breeder's equation and accelerate the process of breeding new crop varieties with advanced traits. The following examples demonstrate the potential applications of HTP technologies to breeding programs based on the breeder's equation:

- (1) Delivery efficient and objective measurements of crop traits. High-throughput phenotyping systems are able to phenotype breeding fields in a more efficient and cost-effective way, which allows an increase in the capacity of breeding programs to handle a larger breeding population and improve the selection intensity. For example, UAS-based HTP platforms are able to screen breeding fields within a short period (e.g., 30 min for a 5-acre field). The implements of spectrum reflectance, photogrammetry, and computer vision provide consistent criteria to estimate crop traits in multiple dimensions, such as plant height, plant temperature, chlorophyll content.
- (2) Identification of novel crop traits. Advanced sensors (e.g., hyperspectral and infrared cameras) capture crop information beyond human vision and sense. Advanced data analytics and AI models reveal hidden information from human and sensor data and have great potential in discovering novel crop traits. The novel traits can be used to describe crop performance at a specific growth stage (e.g., emerging, flowering or harvesting) or to profile crop dynamic responses to environments along growth seasons. Novel crop traits are able to provide additional information to quantify subtle genetic variations of different genotypes and potentially increase the genetic variance.
- (3) Integration of phenotypic data and genotypic data. HTP-based phenotypes could be integrated into genetic analysis, such as quantitative trait locus (QTL) mapping or genome-wide association study (GWAS) to identify key genetic

elements underlying or associated with the yield gain or stress tolerance. The genetic elements for favorable crop traits could be further incorporated into the current germplasm through marker-assisted selection (MAS) during breeding. The integration will allow accurate selection, reduce breeding cycles and increase the genetic gain.

- (4) Allow advanced models to integrate $G \times E \times M$. High-throughput phenotyping technology allows collecting big data of crops in a high spatiotemporal resolution and discovering novel crop traits, which will enable the integration with environment and management to reveal $G \times E \times M$ interactions. Advanced models based on machine learning and deep learning technologies will transform breeding program from **descriptive** phenotyping, to **predictive** phenotyping and **prescriptive** phenotyping that allow ‘manufacture’ crop traits based on needs.

In summary crop HTP technology provides a potential solution to the breeder’s equation to maximize the genetic gains by increasing the selection intensity and accuracy, improving the identification of genetic variations, and accelerating breeding cycles. Crop HTP technology uses an interdisciplinary and holistic approach to integrate research in agronomy, life sciences, information science, mathematics, and engineering sciences, and combines high-performance computing and artificial intelligence technology. Advanced data analytic methods (e.g., machine learning, deep learning) are used to analyze the multifarious phenotypic information of crops and develop predictive and prescriptive models to phenotype crops in a high-throughput, multi-dimensional, big-data, intelligent and automatically measuring manner. The big data of plant phenotypic data collected by plant HTP systems will be integrated with multi-scale genomic and environmental data to mining genes associated with important agronomic traits, and propose new intelligent solutions for precision breeding (Zhao et al. 2019). This book provides showcases HTP applications in the world-leading research programs and by the active researchers and scientists in the areas of crop breeding, genetics, agronomy, engineering, computers, and information technology. The following chapters will focus on the showcases (a) application of merging sensing technology (sensors), (b) introduction of HTP platforms (hardware), (c) approaches of data mining and analytics (big data and AI) and (d) development of HTP framework and pipeline in various crops. We hope this book provides the state-of-the-art of HTP technology and its applications in plant breeding and genetics and brings some case studies that can help researchers to develop and advance the HTP in their research projects.

References

- Alexandratos N, Bruinsma J (2012a) World agriculture toward 2030/2050, the 2012 revision. ESA Working Paper 12–03, June 2012. Food and Agriculture Organization of the United Nations (FAO), Rome. <https://www.fao.org/>.
- Alexandratos N, Bruinsma J (2012b). World agriculture toward 2030/2050: the 2012 revision