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Breeding to Optimize Agriculture in a Changing World

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ABSTRACT

Breeding to Optimize Chinese Agriculture (OPTICHINA) was a three-year EU–China project launched in June of 2011. As designed, the project acted as a new strategic model to reinforce systematic cooperation on agricultural research between Europe and China. The OPTICHINA International Conference "Breeding to Optimize Agriculture in a Changing World" was held in Beijing, May 26–29, 2014. The conference included six thematic areas: (1) defining and protecting the yield potential of traits and genes; (2) high-throughput precision phenotyping in the field; (3) molecular technologies in modern breeding; (4) plant ideotype; (5) data analysis, data management, and bioinformatics; and (6) national challenges and opportunities for China. The 10 articles collected in this special issue represent key contributions and topics of this conference. This editorial provides a brief introduction to the OPTICHINA project, followed by the main scientific points of articles published in this special issue. Finally, outcomes from a brainstorming discussion at the end of the conference are summarized, representing the authors' opinions on trends in breeding for a changing world.

1. Introduction

The world is changing! The population continues to grow rapidly, and societal behavior (including consumption habits) is experiencing rapid evolution, particularly in developing countries. Demand for and pressure on resources (mainly land and water) continues to increase. Potential climate changes pose further and less-predictable challenges. According to the recent Declaration of the World Summit on Food Security (http://www.fao.org/wsfs/world-summit/en/), an increase of more than 70% food is needed by 2050 to meet the demands of the increasing population. It will be a great challenge to ensure food and nutrition security for an ever-increasing population based on limited resources under

a climate-change scenario. Crop management and breeding are the pillars of efforts to tackle the present and future challenges of food production.

China and the European Union (EU) face common challenges in the changing world. Both are dedicating great R&D efforts to agriculture, food security, and food safety, to increase food production and improve product quality in an environmentally sustainable manner. In view of the common challenges, a three-year EU-China project called "Breeding to Optimize Chinese Agriculture (OPTICHINA)" was launched in June of 2011 as a new strategy that may serve as a model to reinforce systematic cooperation on agricultural research between Europe and China. The project had five European partners: the University of Barcelona in Spain, Rothamsted Research Centre in the UK, the Max-Planck Institute in Germany, the John Innes Center in the UK, and the University of Lleida in Spain. The five Chinese partners were the Chinese Academy of Agricultural Sciences (CAAS), China Agricultural University (CAU), North Western Agricultural and Forestry

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University, Yunnan Academy of Agricultural Science, and Tianmin Henan Seed Company. Prof. Jose Luis Araus from the University of Barcelona acted as the project coordinator, together with Prof. Jiankang Wang, CAAS, appointed as the Chinese counterpart.

OPTICHINA was a three-year project jointly supported by the EU Seventh Framework and the Chinese Ministry of Science and Technology. The major objectives of the project were: (1) to link the agricultural research activities performed on one side by EU research programs and on the other side by China national research programs; and (2) to build on previously funded research collaborations between European and Chinese researchers involved in the project. To meet the project objectives, two workshops, four advanced courses, and more than 30 training fellowships were organized under the financial support of the European Commission and the Chinese Government.

The final OPTICHINA international conference "Breeding to Optimize Agriculture in a Changing World" was held in Beijing, May 26–29, 2014. Forty distinguished scientists from China, Europe, and elsewhere delivered talks on defining and protecting yield potential of traits and genes; high-throughput precision phenotyping in the field; molecular technologies in modern breeding; models of ideotype designs; data analysis, data management, and bioinformatics; and national challenges and opportunities in China. Fourteen OPTICHINA fellowship holders presented their work in a Young Scientist Forum.

2. Highlights of papers in the special issue

This special issue of The Crop Journal publishes key presentations and topics addressed at the OPTICHINA international conference. The 10 articles collected in this issue have been grouped in the following four areas.

2.1. Defining and Protecting Yield Potential

In their review article, Uphoff et al. [1] state that decades of rice breeding have been selecting for the best crop genetic endowments under suboptimal growing conditions. These conditions include crowding of plants that impedes their photosynthesis and growth, flooding of rice paddies that causes roots to degenerate and forgoes benefits derived from aerobic soil organisms, and overuse of agrochemicals that adversely affect these organisms as well as soil and human health [1]. Practices developed by the System of Rice Intensification (SRI) at Cornell University are being used in various combinations by as many as 10 million farmers on some 4 million hectares in over 50 countries. Based on their long-term research in India and Indonesia, Uphoff et al. argue that changes in crop and water management can improve the expression of genetic potential in rice plants, thereby creating more productive and robust phenotypes. More productive crops, with higher resistance to biotic and abiotic stresses and shorter crop cycles, are possible through modifications in the management of soil, water, and nutrients, reducing rather than increasing inputs. Breeding for density-neutral cultivars will enable more effective exploitation of available crop growth resources. Density-neutral cultivars can achieve high productivity under both ample and limited resources. In the meantime, lower densities can avoid crop failure due to overcrowding [1].

Knowledge of existing genetic diversity and its distribution in crop species is useful for germplasm conservation and selection for parents with diverse genetic background. Mengistu et al. [2] evaluated phenotypic variation in agro-morphological traits in Ethiopian durum wheat sampled from major wheat growing regions of the country. Their purpose was to determine the amount, extent, and distribution of genetic variation in durum wheat landraces according to their geographical (district) and ecological (altitude) origin. Phenotypic diversity for eight qualitative and three quantitative traits in 274 Ethiopian durum wheat accessions was analyzed. The accessions were clustered into three groups by district of origin and altitude class. The authors concluded that Ethiopian durum wheat landraces are diverse both within and among districts of origin and altitude classes. This wealth of genetic diversity is available to be exploited for durum wheat improvement for yield and for resistance to biotic and abiotic stresses, particularly terminal drought.

2.2. High-Throughput Precision Phenotyping in the Field

Wheat is the most widely cultivated cereal worldwide. *Puccinia striiformis* is the causal agent of yellow rust in grasses and infects a wide variety of cultivated cereals, including wheat, rye, barley, and triticale [3]. The use of wheat varieties resistant to the pathogen has historically ensured minimal losses. Vergara-Diaz et al. [3] analyzed vegetation indices derived from conventional red–green–blue (RGB) images of crop canopies under field conditions. The authors evaluated their accuracy in predicting grain yield and assessing disease severity in comparison with other field measurements including the normalized difference vegetation index (NDVI) of the canopy measured with a portable spectroradiometer, leaf chlorophyll content, stomatal conductance, and canopy temperature. From yield components and agronomic parameters in relation to grain yield and disease severity, the authors concluded that RGB-based indices are accurate predictors of grain yield and grain yield losses associated with yellow rust, with predictive ability far surpassing that of NDVI and the other approaches tested. The authors found that the presence of disease was correlated with reduction in number of grains per spike, grains per square meter, kernel weight, and harvest index. Grain yield losses in the presence of yellow rust were greater in later-heading varieties. The combination of RGB-based indices and days to heading together explained more than 70% of variation in grain yield and 63% of yield loss.

Rapid screening for individual genotypes with high yield and increased tolerance to abiotic and biotic stresses is of great importance to help meet the world's ever-increasing demand for food [4]. Duan et al. [4] review the potential of plant phenomics for understanding gene function and environmental responses, and its limitations due to labor cost and to the destructive and often subjective nature (associated for example with visual ranking) of conventional phenotypic measurements. These include the proper evaluation of

agronomical yield components, which are the main determinants of final yield. There has been progress in automating plant phenotyping, including automated counts of plant parts and whole adult plants. However, few studies have investigated automated rice panicle counting. Duan et al. present a novel method for the nonintrusive counting of panicle number in rice at the full heading stage. Using custom image analysis software to analyze color images of rice plants taken from multiple angles, the method was able to determine the panicle number of pot-grown rice plants in vivo in a non-intrusive manner. This approach is useful for predicting rice yield and screening candidate rice plants in breeding.

Improving water use efficiency (WUE) in crops is a primary aim for agricultural sustainability in semiarid areas. WUE is normally measured at the leaf level because portable equipment of leaf gas exchange rates facilitates the simultaneous measurement of photosynthesis and transpiration [5]. It is an open question whether measurement at the leaf level is able to represent WUE of the whole plant. Medrano et al. [5] collected and analyzed data from several experiments and identified different sources of environmentally induced leaf WUE variation. Their results show the importance of light environment as well as that of dark respiration (often neglected) to whole-plant carbon balance and in turn to whole-plant WUE. By evaluating the importance of the spatial and time variations of carbon and water balances at the leaf and plant levels, the authors identified two main components to fill the gap between leaf and whole plant water use efficiency (WUE). From their results, Medrano et al. conclude that conventional approaches for WUE evaluation among genotypes or treatments need to be revised to improve the applicability of WUE evaluation as a trait in breeding and crop management.

2.3. Molecular Technologies in Modern Breeding

Resistance to *Aspergillus flavus* infection and aflatoxin contamination in maize and peanut is a complex trait. Recent technological advances have provided the tools necessary to obtain and apply knowledge from metabolomic, proteomic, and transcriptomic studies in production breeding populations. Fountain et al. [6] review recent findings in the biochemistry of defense regulation with respect to environmental stress, reactive oxygen species (ROS), the intercellular communication between *A. flavus* and its host crops, and the current status of molecular breeding and marker discovery for resistance to *A. flavus* colonization and aflatoxin contamination in maize and peanut. The authors highlight recent advances in conventional and molecular breeding for aflatoxin resistance in maize and peanut, and the potential use of molecular markers in marker-assisted selection (MAS) in breeding programs. The authors finally propose that the role of host-derived ROS in stimulating aflatoxin production needs further study. The use of identified proteins, metabolites, and candidate genes as selectable biomarkers for use in MAS should be addressed. Using such markers, breeding programs can be optimized to select not only for aflatoxin resistance but also for associated abiotic stress tolerance.

Pea (*Pisum sativum* L.) is a valuable cool-season pulse crop grown worldwide for its seed and soil fertility benefits. As a leguminous crop, pea fixes its own nitrogen and could thus become an excellent bio-energy crop, especially in temperate regions [7]. An understanding of genetic diversity and population structure in diverse germplasm is a prerequisite for genetic dissection of complex characteristics and marker trait associations. Ahmad et al. [7] assessed the genetic diversity of 35 diverse pea accessions using 100 SSR markers, aiming to identify the population structure and preliminary marker trait associations. The accessions formed five major clusters. Based on the diversity of the accessions and information on SSR markers, the authors identified useful marker–trait associations that may facilitate oilseed pea breeding. This study is among the first to have performed association mapping in pea grown under field conditions and is the first to have done so for lipid content.

Compared with other crops, peanut is considered to be drought-tolerant [8]. During long evolution, plants have developed a delicate dynamic balance system for generation and scavenging of endogenous reactive oxygen species during normal development. As one of the key enzymes in the antioxidant protection system, superoxide dismutase (SOD) plays a crucial role in responding to drought-associated stresses. In peanut, Cu/Zn-SOD comprises a major proportion of SOD isozymes and is one of the most important antioxidant enzymes in leaves [8]. To identify the molecular mechanism of SOD activity and the *AhCSD2* gene in response to drought stress, Zhang et al. [8] obtained the full-length DNA sequence of the chloroplast Cu/Zn-SOD gene (*AhCSD2*) from 11 allotetraploid cultivars and five diploid wild species in peanut. Sequence alignment revealed the conservation and importance of chloroplast Cu/Zn-SOD in the evolution of plants. SOD and related genes provide valuable information on the mechanism of SOD response to drought and other environmental stresses.

2.4. Data Analysis, Data Management, and Bioinformatics

Faba bean (*Vicia faba* L.) is among the most important pulse crops produced in China and in many other countries including Ethiopia. To evaluate yield stability and the relative importance of stability parameters, Temesgen et al. [9] planted 16 faba bean varieties in 13 environments in Ethiopia during the main cropping season in three years and estimated genotype-by-environment (G × E) interaction and yield stability using 17 stability parameters. None of the varieties showed consistently superior performance across all environments, but one variety called EK01024-1-2 ranked in the top third in most test environments and was identified as the most stable, and also showed a seed size advantage over the standard varieties. EK01024-1-2 was released in 2013 as a new variety and renamed "Gora" for commercial production. Different stability parameters explained genotypic performance differently, and the authors accordingly concluded that the assessment of G × E interaction and yield stability should use several stability parameters simultaneously.

Genetics and breeding are closely linked! Information identified in genetic studies is important for gene fine mapping, map-based cloning, and efficient use of gene information in molecular breeding [10]. For many genetic studies, linkage analysis and map construction must be performed in genetically segregating populations derived from two inbred parental

lines. Based on the constructed linkage maps, genes for breeding-targeted traits can be located by quantitative trait locus (QTL) mapping approaches. Efficient genetic studies depend on large populations with high-quality genotypic and phenotypic data, and genetic analysis of large amounts of data requires extensive computing capabilities. Linkage analysis and QTL mapping are two closely related aspects of genetic studies, but conventionally have been handled by separate software packages. Meng et al. [10] describe an integrated software package called QTL IciMapping, capable of building high-density linkage maps and mapping quantitative trait loci in biparental genetic populations. The integration of the software provides a seamless pipeline from treatment of redundant markers to estimation of recombination frequency to construction of linkage maps and finally to mapping of QTL. The software, developed over the past ten years, is highly user-friendly and freely available. Its use greatly reduces the work of data format transformation from one computer software program to others.

3. Brainstorming Discussion on the Future of Plant Breeding

A brainstorming discussion was arranged toward the end of the OPTICHINA international conference. Chairmen of different sessions together with the conference organizers prepared in advance one question each for the seven conference sessions. The audience was asked to give their answers or suggestions, which were required to be critical, constructive, clear, and feasible. The question for Session 1 "Defining and Protecting Yield Potential – Traits and Genes" was "What are the major achievable approaches to increasing/maintaining yield potential?" The answers received for this question were:

- Close yield gap with agronomic changes, such as with conservation agriculture;
- Combine genomics with physiology; more effective breeding systems;
- Shorten time to cultivar delivery;
- Boost photosynthesis;
- Improve canopy architecture;
- Change photosynthesis pathways;
- Develope better root systems for resource capture;
- Understand temperature and radiation interaction;
- Keep raising sink strength for kernel number and kernel weight;
- Maintain harvest index;
- Open the respiration black box;
- Develop more efficient respiration pathways;
- Maintain/update biotic tolerance;
- Learn from past experience; and
- Understand the role of source versus sink in efforts to boost photosynthesis.

The question for Session 2 "High-Throughput Precision Phenotyping in the Field" was "What are the most important secondary traits that can be phenotyped with high-throughput precision that may also contribute to the improvement of yield?" The answers we received for this question were:

- Determine the priority target environments and context for given traits;
- Determine when and what phenotyping are useful based on greater heritability, lower price, and higher throughput;
- Adopt hyperspectral and other high throughput remote sensing techniques.

The question for Session 3 "Molecular Technologies in Modern Breeding" was "How can we go from the molecular lab to practical application in plant breeding?" The answers we received for this question were:

- MAS is still a "concept" in public breeding in China and elsewhere; bridge gap between "molies" and breeders;
- Develop cheaper molecular techniques based on cost per assay/marker;
- Develop breeders' chips packed with known key markers for which all breeders need to select.

The question for Session 4 "Ideal Plant Ideotype" was "The plant ideotype for high yield potential or high yield performance under drought conditions of plants (or any specific crop) should be like …" The answers we received for this question were:

- Learn from other similar species or even wild relatives;
- Take triticale as an example even if a bit shorter plant height is preferable ;
- Improved resource capture in both favorable and marginal environments;
- CO_2 resource is becoming more available — develop other resources to exploit this;
- Develop greater lodging tolerance to increase plant height, if plant height is limiting biomass accumulation;
- Need much-improved WUE at all scales under less water, higher temperature, and more-variable environments;
- Do we need leaf sheaths? Can we find something else to hold up leaves!

The question for Session 5 "Data Analysis, Data Management, and Bioinformatics" was "What should breeders do with the huge amount of phenotypic and genotypic data?" The only two answers we had for this question were:

- Pressure phenotypers to deliver data in an easily usable form;
- Develop user-friendly software — integrated, open, cloud-processed.

The question for Session 6 "National Challenges and Opportunities: the Case of China" was "How should China handle global change challenges?" The answers we received for this question were:

- Use simulation models to predict crop adaptation as climate changes;
- Adapt national policies to limit climate change drivers and effects — which are large, considering that China represents a quarter of the world population;
- WUE, WUE and WUE are the key problems;

- Tactical nitrogen management;
- For maize, adapt Chinese hybrids to greater plant density.

The last question "What will you say about the 3-yr OPTICHINA project as it concludes?" went to Session 7 "OPTICHINA Fellowship and Young Scientist Forum". The answers we received were:

- Great having Chinese students in European labs for students and hosts;
- Hosts learn what hard work means;
- Students learn different approaches to science from the "Chinese" view.

At the end of the brainstorm discussion, the participants enthusiastically acknowledged the success of the conference and of the OPTICHINA project.

4. Conclusions

Conventional breeding has proven to be successful. In recent decades, breeding has contributed a greater than 50% increase of the world's food crop production. However, in a changing world, an urgent issue is to accelerate plant breeding for increased yield potential and better adaptation to drought, heat, and other abiotic stresses together with the surge of new biotic challenges, so as to meet the future demand for agricultural production. The only viable way to solve the issue is to raise the productivity of existing farmland, but it is a great challenge to increase food production and improve product quality in an environmentally sustainable manner. To reach this goal, plant breeding requires intensive and integrated application of a wide range of sciences and technologies.

To meet the challenge, we must develop more productive, stable, and nutritious varieties of agricultural crops, which incorporate both high intrinsic yield potential and resilience to climatic and biotic constraints, while improving the efficiency of resource use. To ensure the success of future plant breeding, we must adopt a multidisciplinary approach combining the field expertise of breeders with advanced phenotyping based on a physiological understanding of the crop, molecular tools and approaches (such as MAS, transgenic, TILLING, omics, and genomewide selection) provided by biotechnology, and the support of advanced data analysis and management.

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