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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.

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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

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