



HOW CAN WE FOSTER CROP IMPROVEMENT?

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ABSTRACT

In this paper, the current scenario and challenges that crop improvement faces in response to the increasing world demand for food and biofuels is described. The fact that the rate of improvement in crop performance has plummeted in a number of important crops is discussed. To revert this situation, in my opinion, a truly interdisciplinary approach should be applied to the breeding process, making use of the vast amount of knowledge recently generated in the areas of genomics, ecophysiology, statistics, bioinformatics, etc.. Moreover, a special emphasis should be put on phenotyping which -in my opinion- is the new bottleneck, considering the increasingly fast pace and continuously decreasing costs of genotypic data generation. In the meanwhile, a challenge needs to be faced on how to organize, compile and parse phenotypic data while making them available to the broad scientific community. In conclusion, an unprecedented opportunity for a quantum leap in crop improvement rests before us; now, a concerted effort needs to be done to truly integrate the massive amount of knowledge generated into better crops for the world.

RESUMEN

En el presente trabajo se describe el escenario actual y los desafíos a los que se enfrenta el mejoramiento de cultivos en respuesta a la creciente demanda mundial de alimentos y biocombustibles. Se discute el hecho de que la tasa anual de incremento del rendimiento se ha estancado en los últimos años en algunos de los cultivos más importantes. Para revertir esta situación, en mi opinión, debería aplicarse un verdadero enfoque multidisciplinario al proceso de mejoramiento genético, haciendo uso de los vastos conocimientos generados recientemente en las áreas de genómica, ecofisiología, estadística, bioinformática, entre otras. Además, debería ponerse especial énfasis en la caracterización fenotípica -en mi opinión el nuevo “cuello de botella”- a la luz de la reducción creciente del costo y de la velocidad de generación de datos genotípicos. Mientras tanto, deberá enfrentarse el desafío de compilar y ordenar los datos fenotípicos para su utilización por parte de la comunidad científica. En conclusión, actualmente existen las condiciones para que se produzca un salto cualitativo en el mejoramiento de cultivos; para ello es esencial hacer un esfuerzo concertado y plasmar la gran cantidad de conocimientos generados en mejores cultivos para el mundo.

The fascinating history of crop improvement started with crop domestication, more than 10,000 years ago. Since then, humans have achieved steady increases in crop yield, pest and disease resistance, and quality. Moreover, some breakthroughs as the Green Revolution in the XXth century, greatly influenced the life and fate of millions of human beings. Today, crop improvement has become a key factor for guaranteeing world food security. Aside from the necessary moral debates about the world's food distribution inequity and the use of food products for biofuels, it is unquestionable that world demand for food and biofuels is growing, and will continue to do so, even under the most conservative mid- and long-term prospects (DEXIA, 2010). Therefore, breeders today face the challenge of having to develop ever higher yielding cultivars for increasingly unstable environments, while improving quality and tolerance to biotic and abiotic stresses. Also, agricultural inputs are becoming scarce and/or more expensive, which poses the need for more input-efficient crops. In particular, environmental sustainability must be guaranteed to attain stable crop production and territorial development in the long term.

Over thousands of years since crop domestication, artificial phenotypic selection was the main force leading to the fixation of a number of traits that shape the most distinctive features of modern crops, such as indehiscence of fruits or seeds, ease of threshing, tolerance to high plant density growth, etc. Unlike the empirical nature of this process, modern breeding methodologies were developed starting in the XXth century, which were based on knowledge of statistics and the genetic structure of plant populations. Since then, great progress has been achieved in crop yield, adaptation, resistance to pests and diseases, quality and stability. In the last few years, however, the rate of improvement in crop performance has plummeted in a number of important crops such as wheat and rice (Conforti, 2011). As a result of many years of breeding, several favorable traits, especially those with simple genetic control, have been fixed in elite populations, or they can be easily bred. The challenge now is how to deal more effectively with complex traits such as yield and tolerance to abiotic stress, and how to increase genetic variability for these traits while maintaining agronomic performance.

Indeed, a first approach to tackle the previously mentioned challenge could be to increase the accuracy of phenotyping. Let's apply an example to illustrate the present case. Increasing yield in bread wheat is undoubtedly a paramount objective of every wheat breeding program in the world. We know that yield is controlled by many genes, with a great environmental influence that causes significant genotype x environment interactions. What would happen if we could dissect yield into its physiological components? The concept is far from being new, but a number of recent investigations have provided new insights into the physiological mechanisms responsible for the trait, and on how to perform high throughput determination of relevant variables (see, for example, Reynolds et al., 2012; Abbate et al., 2012; Foulkes et al., 2012). Andrade et al. (2009) have provided other examples of how crop physiology has aided in the elucidation of the genetic control of key traits and their interaction with the environment. Besides crop physiology, modern statistical models, experimental designs and analysis tools undoubtedly have a substantial impact on the quality of field data generation for selection of elite materials, estimation of genetic parameters, phenotyping of mapping populations, etc.

Most remarkably, crop improvement of complex traits can benefit from the true scientific and technological revolution that has taken place over the last 5-10 years in the plant sciences, particularly in the genomics field. With ~40 plant genomes sequenced to date, among which several important crop species are included (CoGePedia, <http://www.genomeevolution.org>), and a myriad of bioinformatics, reverse genetics, epigenetics, gene targeting and molecular marker tools available or being developed, one can only envision the potential, unimaginable outcomes of such vast body of information and knowledge when put to the service of crop improvement.

Still, the effects of such "genomics revolution" are, in some crops, materializing less evidently than initially expected. One of the reasons for this, in my opinion, lies on the fact that the pace of genomic data generation largely exceeds that of the other disciplines, and that a truly interdisciplinary approach directed to crop breeding is often lacking. We are now having easier and easier access to information on candidate genes, massive SNP discovery, whole genome selection tools, association

mapping panels, etc, even in minor crops....but we need to make ends meet! No such thing will happen without high quality phenotyping. Current emphasis is being put on phenotyping platforms that allow high-throughput analysis, and although a most valuable tool, the core of success remains in the collaborative, interdisciplinary work. For instance, and to name only some of the key players in this endeavor, breeders know the target, envision the ideotype, deal with the genetic structure of the material under study, can provide insights into the strategy for reaching the target at the fastest pace.... physiologists can provide the rationale for which phenotypic variables to determine and the best way to do it, genomicists can use comparative genomics, transcriptomics, proteomics, etc., to find suitable candidate genes/markers to track...statisticians and bioinformaticians can deal with the way data are generated, collected, and managed effectively. It is clear (and several scientific teams have already put this into practice) that a strong interdisciplinary effort is needed to continue to improve crops as the world needs.

In my opinion, high quality phenotyping is becoming the new bottleneck, as genotyping costs continue to drop. The dramatically fast pace of genomic data generation needs to be accompanied by a similar trend in phenotypic data generation, and a particular emphasis will be needed in figuring out how to organize, compile and parse phenotypic data while making them available to the broad scientific community, as it has been done with genomic data. This is challenging, however, because there is no “common language” in phenotypic data, as it is the case of genomic data. This might change in the near future, as we are starting to see the emergence of such databases and tools, like the Human Phenotype-Genotype Integrator at NCBI (<http://www.ncbi.nlm.nih.gov/gap/PheGenI>).

In conclusion, an unprecedented opportunity for yet another quantum leap in crop improvement rests before us. Now, we need to make a concerted effort to truly integrate the massive amount of knowledge generated into better crops for the world.

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