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CIMMYT's Seeds of Discovery Initiative: Harnessing Biodiversity for Food Security and Sustainable Development

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A visionary investment by Mexico's Secretariat of Agriculture, Livestock, Rural Development, Fisheries and Food (SAGARPA) has enabled the Seeds of Discovery (SeeD) initiative to assemble a platform of technologies to facilitate the effective use of genetic resources in breeding to address challenges of climate change and evolving consumer demands to ensuring universal food security. The platform consists of 1) high-density genotypic data and extensive phenotypic data characterizing maize and wheat germplasm bank accessions, 2) software tools to enable bioinformatics analyses of these and relevant germplasm bank data, and 3) maize and wheat lines incorporating novel diversity for priority traits from exotic germplasm into breeder-preferred, elite genetic backgrounds. Each of these platform components was co-developed with partners bringing unique expertise and resources to the project. Sustained impact, and equitable access to the platform and the maize and wheat genetic resources it describes, are pursued via multi-pronged capacity development and proactive intellectual property strategies described herein. After describing the SeeD initiative and some of its products, we conclude by sharing comments and insights from eminent scientists and partners who attended a special session on 'Harnessing Biodiversity for Food Security and Sustainable Development' during the 1st International Agrobiodiversity Congress (IAC), in New Delhi, November 2016.

Introduction

Humankind will soon face unprecedented challenges to ensuring its food security. Recent estimates by the United Nations (2017) project that global population will reach 9.8 billion by 2050, and 11.2 billion by 2100, and the world community is committed to ensuring that every person has access to a sufficient, nutritious diet (United Nations, 2015). Of course, the food for our growing population must be produced sustainably, to ensure the wellbeing of future generations. Making agriculture sustainable will require that we reverse trends that today are common in too many of our production areas, including depletion of aquifers, inefficient use of fertilizers, and degradation of soil health. Finally, the added challenges from changing climate, particularly rising temperatures and associated increasing frequency of extreme weather events (IPCC, 2014), make the goal of ensuring sustainable food security more daunting.

Although several actions will be crucial for meeting future food demand (Godfray *et al*., 2010), including reducing the current 30-40 percent global rates of food waste, sustainably enhancing agricultural productivity must be prioritized. Numerous examples have shown the value of crop biodiversity for developing improved varieties (Pimentel *et al*., 1997; Fig. 1). Similarly, and perhaps critically, genetic resources or biodiversity of crop plants will be valuable for the development of varieties that thrive in the emerging environments of the future.

Paradoxically, plant breeders are often reluctant to use wild relatives or unimproved collections of crop plants in their variety development programs. This reluctance is first because it is generally difficult to identify genetic resources that contain outstanding alleles for genes of interest, like searching for a needle in a haystack. Secondly, unimproved crop plants that contain such outstanding alleles also generally contain many undesired alleles for traits that the breeders have worked long and hard to improve in their elite lines. The International Maize and Wheat Improvement Center (CIMMYT) and the Mexican Government established the Seeds of Discovery (SeeD) initiative to address these

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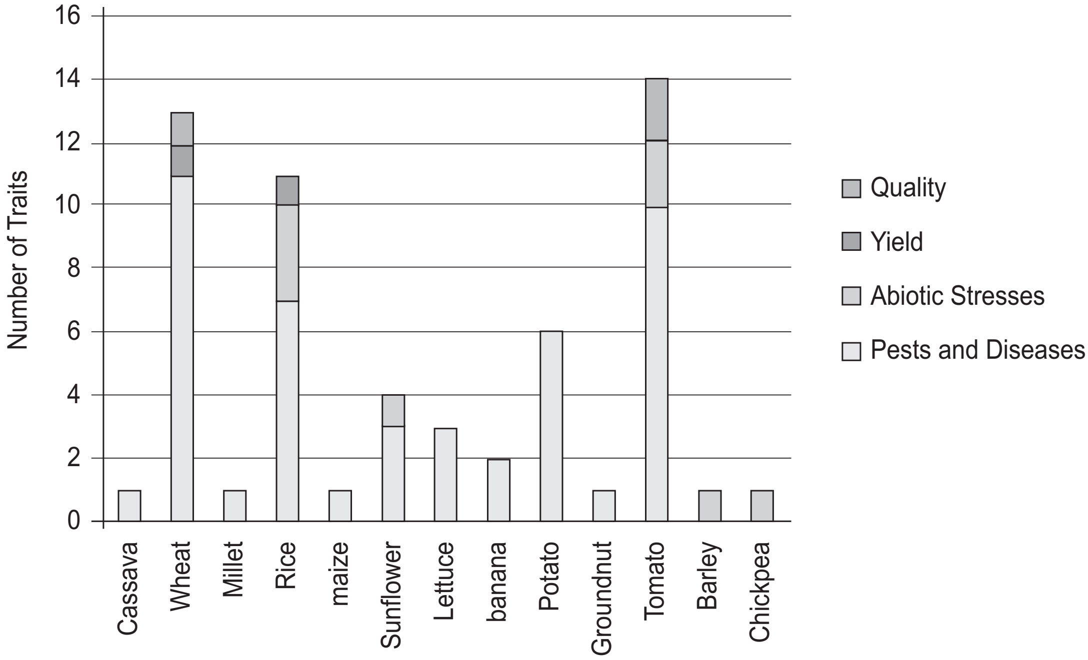

Fig. 1. Use of crop wild relatives in the past 20 years in released cultivars for 13 crops of international importance. Adapted from Hajjar and Hodgkin (2007)

important constraints to the use of maize and wheat biodiversity. The SeeD initiative aims to assemble a platform of technologies that facilitate the effective use of genetic resources to accelerate the development of improved crop varieties in breeding to address challenges of climate change and evolving needs of farmers and consumers.

This manuscript describes the SeeD initiative as a model that can inform other initiatives with similar objectives for other crops. Specifically, we will describe the SeeD strategy to enable more effective and equitable use of maize and wheat biodiversity, present selected results, and share feedback received from diverse partners and stakeholders.

Methods

Impact Pathway

The goal of the SeeD initiative is to enhance the use of novel genetic diversity held in germplasm banks to accelerate the development of maize and wheat varieties that meet the demands and contribute to food security of a growing population in a changing climate. SeeD develops products that when used by researchers will result in varieties grown by farmers to produce the food consumed by all. The SeeD initiative has five main components, described in this section.

- Genotyping, which produces data describing the genetic composition of germplasm bank collections;
- Phenotyping, which produces data describing the attributes of germplasm bank collections;
- Informatics, which produces software tools to capture, analyze and interpret the data;
- Pre-breeding, which produces improved wheat and maize germplasm, incorporating novel diversity from germplasm bank collections; and
- Capacity development, which produces public information, and provides training through various mechanisms including workshops and thesis projects for students.

The main users of SeeD's products are plant breeders, researchers, academics, and students. The beneficiaries of the SeeD initiative, however, include farmers, consumers, food and feed industry, advocates of equitable use of biodiversity, advocates of increased sustainability of farming systems, supporters of agricultural development, and society at large.

To achieve greater and equitable positive impacts in the shortest possible time, SeeD has applied "social network analysis" (Borgatti *et al*., 2013) to study the Mexican maize and wheat breeding and genetic resources conservation systems. Using this approach, it has been possible to identify and collaborate with key players with greatest influence on the dissemination of knowledge and germplasm.

Genotyping

A cost-efficient genotyping service laboratory was established at CIMMYT headquarters and is available to SeeD partners. The laboratory uses the DArTSeq next generation sequencing technology (DArT, 2017), with which genotyping of CIMMYT's and some partner maize and wheat collections is underway. This platform produces several hundred thousand markers, both single nucleotide polymorphism (SNP) and presence absence variance (PAV) markers, for each genotype sequenced. This density of markers is ideal for studies of diversity, selection imprints, or to identify target genomic regions associated with traits of interest. About 28,000 maize and 60,000 wheat accessions in CIMMYT's germplasm bank have been sequenced, as have about 30,000 accessions from ICARDA's wheat and wild relatives collection.

Phenotyping

Phenotyping of wheat and maize germplasm bank accessions and pre-breeding lines seeks to identify useful donor alleles for traits prioritized by breeding programs (Table 1). The characterization of these prioritized traits is done mostly by SeeD partners who grow collaborative trials or nurseries; for example, a network of scientists in Mexico, India and Kenya are involved in the exploration of the wheat germplasm for resistance to yellow rust, stem rust, powdery-mildew and leaf spot diseases.

Informatics

Several partners have contributed to the suite of data storage, data management and data analysis tools assembled by the SeeD initiave (Fig. 2). The large volumes of genotypic and phenotypic data generated and

Table 1. Partial list of important breeding traits that have been evaluated by SeeD partners for various sub-sets of wheat or maize germplasm bank accession and pre-breeding lines

Wheat	Maize
Grain yield	Grain yield
Drought tolerance	Drought tolerance
Heat tolerance	Heat tolerance
Low soil phosphorus tolerance	Low soil nitrogen tolerance
Tan spot resistance	Tar spot complex resistance
Karnal bunt resistance	Turcicum blight resistance
Spot blotch resistance	Stalk rot resistance
Powdery mildew resistance	Ear rot resistance
Yellow rust resistance	Cercospora leaf spot resistance
Zinc concentration in grain	Carotenoid concentrations in grain
Iron concentration in grain	Root lodging resistance
Grain quality traits	Stem lodging resistance
Phenology	Phenology

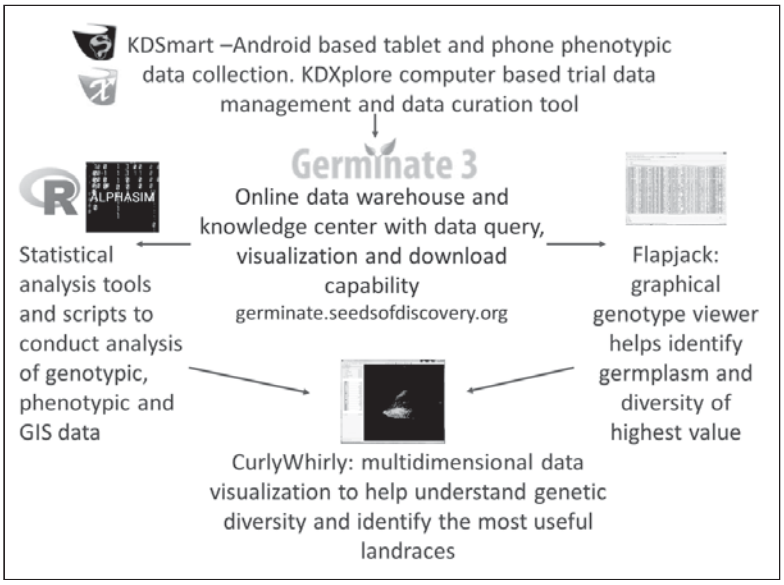

Fig. 2. Informatics components being assembled into a molecular atlas. KDSmart and DKXplore are co-developed with Diversity Arrays Technology (DArT, Pvt) and are useful for field collection, and data management and curation, respectively. Germinate is a data warehouse developed by the James Hutton Institute (JHI), while Flapjack and CurlyWhirly are genotypic data visualization tools co-developed with the JHI. R and AlphaSim are data analysis packages used to conduct the combined analysis of genotypic, phenotypic, GIS and other data. Figure credit: Sarah Hearne.

used in this platform exceed the capacities of common data spreadsheets, and necessitated the development or adaptation of specialized databases and software tools. In addition, the electronic collection and real-time curation of experimental data are important time-saving, cost-saving and error-reducing steps for which specialized tools were developed. All of these software tools are freely available (www.seedsofdiscovery.org). Work is ongoing to develop user-friendly interfaces that facilitate the use of this suite of tools. As a whole, these data and tools, referred to as a molecular atlas, can help a plant scientist to identify which accessions in the germplasm bank are most useful in breeding for a trait of interest. This suite of tools is analogous to a satellite navigation system that integrates diverse data – from maps, satellite imaging, user feedback, service providers, etc. – to assist the driver of a car to navigate efficiently from her current location to an unknown desired destination.

Pre-breeding

Wheat pre-breeding lines (PBLs) are developed using a three-way topcross strategy in which an exotic germplasm bank accession is crossed to an elite line, and the resulting F1 is crossed to a second elite line. The resulting populations are first advanced in bulk, and later by individual head selections with evaluation for grain yield and yield components under drought and heat at Obregon, Mexico, and mild selection for rust resistance and agronomic traits at El Batan or Toluca, Mexico. The resulting PBLs are shared with interested partners who evaluate them for biotic stresses (yellow rust, stem rust, powdery mildew and leaf spot diseases) and agronomic performance.

The maize pre-breeding strategy consists of identifying promising germplasm bank accessions for priority traits, especially drought and heat tolerance, and tar spot disease complex or maize lethal necrosis. The accessions are crossed with elite CIMMYT Maize lines (CMLs), and line development is either from these F1s or from back-cross populations using the elite line as recurrent parent. Line development then proceeds with selection for the primary trait plus general agronomic performance, and includes selection for combining ability by evaluating testcross hybrids of the experimental lines crossed to elite testers.

Capacity Development and Open Access for Equity in the Use of Genetic Resources

SeeD pursues sustained impact and equitable access to its genetic resources utilization platform and the maize and wheat genetic resources it describes, via multifaceted capacity development and proactive intellectual property strategies. Capacity development, including graduate student thesis projects, technical workshops, visiting scientist projects, and publically available software tools is essential to ensure that the current and next generations of researchers are able and keen to use SeeD's products. Capacity development is a cornerstone of SeeD's strategy to achieve equity in the use and benefit sharing from use of genetic resources. Empowering scientists from a broad range of public and private organizations to apply cutting-edge technologies and tools in the use of genetic resources to benefit their diverse range of client farmers and consumers, will increase equity in the access to and benefit from agrobiodiversity.

A proactive intellectual property strategy ensures that the data and tools developed by SeeD are freely accessible to all under a "one-click" agreement that prevents users from seeking intellectual property that would restrict others from using them. This policy forms a second cornerstone of SeeD's strategy in pursuit of equitable access and benefit sharing from genetic resources. The strategy seeks to facilitate widespread sharing of SeeD outputs and the benefits arising from their use by addressing two main objectives: 1) stimulate the innovative use of genetic resources in a pre-competitive and equitable environment, and 2) equitably share the benefits arising from the use of wheat and maize genetic resources with researchers, farmers and with the original germplasm custodians.

Results and Discussion

The SeeD initiative has produced a large number of products and services including germplasm, data, informatics tools, technical workshops, and publications; many of these are viewable in an on-line products catalogue (www.seedsofdiscovery.org). More than twenty international, refereed journal publications on methods or bioinformatics (Faux *et al*., 2016; Shaw *et al*., 2017; Swarts *et al*., 2014), wheat diversity and genetics (Crossa *et al*., 2016; Li *et al*., 2015 and 2016; Lopes *et al*., 2015; Saint Pierre *et al*., 2016; Sehgal *et al*., 2015; Singh *et al*., 2016), and maize diversity and genetics (Brandenburg *et al*., 2017; Chen *et al*., 2016; Figueroa *et al*., 2013a and 2013b; Gorjanc *et al*., 2016; Hellin *et al*., 2014; Hickey *et al*., 2014; Romero *et al*., 2017) are beginning to document the knowledge gained from SeeD collaborative work.

Partnerships have been crucial to every component of SeeD, for example, as described below by Dr. Anthony Hall of the Earlham Institute in the United Kingdom:

"Huge advances have been made over the last few years in our understanding of the wheat genome (IWGSC *et al*., 2014; Clavijo *et al*., 2017). Fortunately, these advances have been paralleled by huge investments by UK funding agencies, specifically the BBSRC (Biotechnology and Biological Sciences Research Council), which recently invested £35M in a cross-UK-institute program, "Designing Future Wheat". The SeeD initiative offers open access to genotype and phenotype data describing germplasm bank accessions, which are also publically available. These data are critical material as the global wheat research community moves from a single reference genome to exploring population scale genome diversity and developing tools capable of identifying genes playing major roles controlling important traits (Borrill *et al*., 2015). Within the SeeD initiative, a role of the Earlham Institute is to integrate new genomics technologies. By adding new genomic approaches, the global wheat research community can use SeeD material to ask fundamental and applied biological questions; for example: what genes have been selected during domestication and adaption to specific agricultural mega-environments? How much genetic variation exists for important genes within germplasm collections? Which allelic combinations deliver robust and sustainable yield under changing climate? In addition to these important questions, practically we can generate imputation methods to add more depth to existing genotypes (IWGSC et al., 2015), and we can also identify candidate genes and markers underlying the important traits brought into elite material from the SeeD initiative's diverse material (Gardiner *et al*., 2016)."

Characterization of Wheat Genetic Resources

Nearly 100,000 wheat accessions from CIMMYT's germplasm bank have been evaluated in field trials and laboratory tests for different traits. This includes phenotypic evaluation of 70,000 accessions for heat and/or drought, 20,000 for grain quality traits, 10,000 for disease resistances, and 2,000 for phosphorus use efficiency. As expected, the accessions exhibited huge variability and encompass potential trait donors for drought tolerance, heat tolerance, grain quality, nutritional traits (e.g. zinc and iron content in grain), disease resistances and yield-related traits.

The genotyping and phenotyping efforts enabled various and ongoing bioinformatics analyses to understand and mobilize valuable diversity into breeding programs; for example, diversity analyses (Sehgal *et al*., 2015; Lopes *et al*., 2015) and the development of a wheat genetic map for use in further research (Li *et al*. 2015). Another study identified rare and potentially valuable allelic variations among more than 8,000 Mexican wheat landraces (Vikram *et al*., 2016). SeeD scientists subsequently formulated a unique strategy for selecting core sets of germplasm bank accessions. The approach incorporates genotypic and phenotypic variability and can capture up to 89% of rare allelic variation. This approach is the only published method that captures so much rare allelic variation (Vikram *et al*., 2016; Singh *et al*., 2016). Core sets of wheat germplasm bank accessions are available to the global wheat research community:

1. Mexican bread wheat landrace core set: 1,100 accessions selected to represent the approximately 10,000 Mexican wheat landraces held at CIMMYT. These landraces are descendants of wheat varieties brought to Mexico by the Spaniards during the colonial period. The core set was developed using 20,000 DArTSeq markers as genotypic data, combined with phenotypic data for several traits including days to heading, days to maturity, plant height, grain yield under heat, drought and irrigated conditions, and grain quality measures (Vikram *et al*., 2016).
2. Iranian wheat landrace core set: 249 accessions selected to represent the approximately 2,000 Iranian wheat landraces available from CIMMYT's germplasm bank. The core set was formed as described above for the Mexican bread wheat landrace core set.

Wheat and Maize Pre-breeding Germplasm

Wheat pre-breeding efforts have focused on developing drought and heat tolerant lines for use in wheat improvement. An array of pre-breeding germplasm, including about 15,000 pre-breeding lines (PBLs), has been developed, and partners in India, Mexico, Iran and Pakistan have evaluated about 2,000 PBLs for traits of interest to them (yellow rust, crown and root rot, powdery mildew, leaf spot diseases). The large-scale, multi-location characterization of diverse PBLs developed from a broad array of germplasm bank accessions, is identifying valuable germplasm for current and future wheat improvement. Several wheat pre-breeding products are available from SeeD to the global wheat research community:

1. Wheat Drought Tolerant Pre-breeding Lines: These are wheat pre-breeding lines derived from top-crosses using one germplasm bank accession, crossed to an elite line, and then crossed to a second elite line. The accessions were selected as promising sources for use in breeding for drought tolerance, while the elite lines were recommended as the best available lines by CIMMYT wheat breeders. The experimental lines were selected based on field trials under drought stress and well-irrigated conditions in Mexico, with mild selection to eliminate material susceptible to yellow rust or with serious agronomic weaknesses.
2. Pre-breeding Wheat Heat Tolerant Pre-breeding Lines: These are wheat pre-breeding lines derived from top-crosses using one germplasm bank accession, crossed to an elite line, and then crossed to a second elite line. The lines were selected based on field trial results under heat stress and well-irrigated conditions in Mexico, with mild selection to eliminate material susceptible to yellow rust or with serious agronomic weaknesses.

Wheat Pre-breeding Lines with High Grain Yield: These are wheat pre-breeding lines derived from top-crosses using one germplasm bank accession, crossed to an elite line, and then crossed to a second elite line. The experimental lines were selected based on field trials under well-irrigated conditions in Mexico, with mild selection to eliminate material susceptible to yellow rust or with serious agronomic weaknesses. The lines may be useful in breeding for improved grain yield following further testing to confirm their performance in additional environments.

Maize pre-breeding efforts have focused on drought and/or heat tolerance, resistance to tar spot complex (TSC) disease, and more recently also on resistance to maize lethal necrosis (MLN). A small effort has also been invested to increase anthocyanin content of grain (for its nutritional value). The initial work on TSC identified two landraces in the germplasm bank that have subsequently been evaluated by smallholder farmers in the Mexican State of Oaxaca. The farmers are now using these landraces directly and in farmer-participatory improvement projects to enhance the TSC resistance of their landraces that are susceptible to this disease. Some of the maize pre-breeding products that are or will soon be available to the maize research and breeding community are described below (Terence Molnar and Sarah Hearne, personal communication, 2017).

1. Drought tolerant landraces: Germplasm bank landrace accessions that are promising for use in research and pre-breeding for drought tolerance at flowering and grain fill stages of the crop life cycle. Adaptation-based, e.g. lowland tropical or highland, panels have been developed comprising 500, 250, 100 and 50 landrace accessions that maximize and maintain representativeness of the diversity of the landrace collection.
2. Drought tolerant semi-inbred lines: Early generation lines developed through backcross breeding, which have demonstrated enhanced levels of drought tolerance at flowering and grainfill stages of crop growth. Drought tolerant landrace accessions were used as donors, and elite CIMMYT Maize Lines (CMLs) were used as recurrent parents.
3. Tar spot disease complex (TSC) tolerant semi-inbred lines: Early-generation lines developed through backcross breeding with demonstrated levels of TSC tolerance. Landrace accessions with useful levels of disease tolerance were used as donors, and elite CMLs were used as recurrent parents.
4. Heat tolerant landraces: Germplasm bank landrace accessions that are promising for use in research and pre-breeding for heat tolerance at flowering and grain fill stages of the crop life cycle. Adaptation-based, e.g. lowland tropical or highland, panels have been developed comprising 1000, 500, 250, 100 and 50 landrace accessions that maximize and maintain representativeness of the diversity of the landrace collection.
5. Maize blue kernel inbred lines: Lines developed through backcross breeding that have grain with enhanced levels of anthocyanin content. Landrace accessions with useful and stable levels of anthocyanin content were used as donors, and elite CMLs were used as recurrent parents.

Capacity Development for Equity in Access and Benefits from Genetic Resources

By the time of the 1st International Agrobiodiversity Congress (IAC), in November 2016, 238 researchers, faculty and students had participated in SeeD workshops, 13 bachelor, 8 MSc and 13 PhD students were enrolled or had graduated conducting research projects with SeeD, 5 Mexican scientists were working with SeeD scientists on specific projects of their choice, and researchers from 75% of the most important breeding organizations in Mexico had participated in capacity development activities facilitated by SeeD. These numbers continue to grow and provide evidence of demand for SeeD products that can lead to impact in farmers' fields and consumers' homes. Two PhD and one MSc student shared some of their experiences and learnings from working with the SeeD project during the "Harnessing biodiversity for food security and sustainable development" session of the IAC in New Delhi.

Ankita Suhalia, a doctoral student in botany and crop sciences at Punjab Agricultural University, spoke about her experience as a student within the SeeD initiative:

"My research work aims to dissect drought tolerant and salinity tolerant genotypes from Mexican landraces. This opportunity led to my personal as well as professional growth.

The conference proved to be a memorable and meaningful experience. The conference events were very useful in developing my skills and leadership abilities as a biological scientist. During the "Harnessing biodiversity for food security and sustainable development" session, I had my first time opportunity to speak in front of eminent scientists and subject leaders from national as well as international institutes. The talks by eminent scientists of the field regarding networking were also interesting and the speakers provided good material that I could share with the rest of the students back home about the importance of germplasm in wheat. It was very helpful for me in understanding the importance and quick use of germplasm for wheat improvement. The conference provided rare opportunities for me to get in touch with esteemed scientists and fellow students from other countries. During the sessions, I also had the chance to meet many people who have contributed much to the field and it was inspiring seeing so many like-minded biologists working to make the exploration of germplasm in detailed manner. Furthermore, attending the conference helped me build relationships with other biologists and students for future collaborations.""

Cynthia Ortiz attended the IAC, where she presented a poster and spoke about her experience as a master's degree student with Mexico's Center for Research and Advanced Studies (CINVESTAV) and SeeD:

"My master's research project focused on yellow rust disease, caused by Puccinia striiformis, which is one of the most devastating diseases of wheat, causing significant grain yield losses globally. The aim of my research was to identify genomic regions associated with yellow rust resistance in wheat bi-parental mapping population. The populations were genotyped using the DArTSeq technology, and genomic regions were identified that can be used to improve popular but susceptible wheat varieties using marker assisted breeding. Genomics assisted approaches offer promise for fast-track breeding in wheat to enhance yellow rust resistance and thereby grain yield.

This presentation was part of my continuing education and professional development, as well as an opportunity to share and disseminate the types of research and projects carried out at CIMMYT.""

Laura Bouvet, a postgraduate researcher in crop sciences from the University of Cambridge, UK, spoke about and presented her experience as an intern in capacity development with SeeD:

"Equitable access to genetic diversity and breeding material is at the core of SeeD. This project has been successful in reaching a significant number of scientists at different stages in their professional career. In addition to technical workshops and postgraduate student thesis projects, the initiative is exploring the option of an online training platform in genetic diversity, to reach a higher number of individuals. My role as an intern was to develop the structure of such a training platform and generate educational and promotional material. This included a video explaining the DArTSeq genotyping method used in SeeD, as part of a module on genotypic data, and a video showcasing the benefits of the training platform to different stakeholders.

Working closely with SeeD scientists and across CIMMYT departments, I learnt about the multi-disciplinary and collaborative nature of a large-scale project such as SeeD, two aspects that underlie many crop science projects nowadays. Furthermore, contributing to the capacity building strategy of the project has given me valuable insight into its increasingly important role in agricultural science.""

Part of the SeeD strategy is to invite scientists to apply for visiting scientist opportunities, during which they work with SeeD scientists to apply the tools and products of SeeD to benefit their own programs. A total of 20 such projects have been initiated. In 2016, SeeD received 11 proposals from Mexican scientists interested to work on such projects, of which five were funded. Topics were characterization of yellow rust resistance of Mexican wheat accessions; genomic characterization of maize accessions in the University of Guadalajara germplasm bank; development and validation of bioinformatics models to select germplasm bank accessions based on allele frequency; genetic resources for forage maize for highland Mexico; and, analysis of pigmented maize landraces. Nine applications were received in 2017, including two on popcorn, one on nutritional quality of maize, one on heterotic patterns for maize, one on Karnal bunt resistance in wheat, and two on diversity and genomics of coffee. The proposals for work on coffee were funded by a special grant from the Mexican Government to the Mexican coffee research institution, which was keen to implement a project similar to SeeD for coffee.

Comments about SeeD from Eminent Scientists and Partners

Several distinguished crop scientists and representatives from international agricultural research funding agencies

Table 2. Comments from participants in the 'Harnessing biodiversity for food security and sustainable development' session of the 1st International Agrobiodiversity Congress, New Delhi, 6-9 November 2016. NB: These comments were recovered from notes taken by the authors during this event, and the authors regret any inaccuracy we may have committed in capturing the intended messages from these participants.

Dr. BS Dhillon, Vice Chancellor, Punjab Agricultural University, Ludhiana	The green revolution had impact due to a number of factors, but the basis was germplasm strength. Germplasm is like a dowry. Elite × elite crosses have strength worldwide, including India, USA and other countries, but considering climate change, change in cropping/farming patterns and other emerging needs, we should look beyond elite germplasm i.e. exotic × elite crosses (pre-breeding).
Dr. RK Singh, Former Country Representative, International Rice Research Institute	Climate change is prominent in Eastern India and this is the reason we need more genetic variation in farmers fields. Broadening of the cultivated wheat gene pool through pre-breeding is urgently required. As an example, "Sahbhagi dhan" rice variety came from a similar approach and has had significant impact in rain-fed regions of Eastern India.
Dr. Steve Visscher, Biotechnology and Biological Sciences Research Council (BBSRC), UK	There is need for partnership with NARS in target ecosystems. It is important for SeeD scientists to convince the donors of how investment will have impact in farmers' fields. Three challenges for the SeeD project are: 1) Convey the work of SeeD in layman words; 2) what are the impacts of SeeD on breeding programs, and 3) what are the real potential and practical impacts of SeeD. Overall, SeeD should channel its investments for impact at farmer field level.
Ms. Lisa Wilson, United States Agency for International Development (USAID), USA	To work with USAID, remember what our mandates are... and SeeD addresses plenty of them. There is need and opportunity to increase partnerships in low andmiddle income countries for a wider impact of the SeeD project; for example, Bangladesh and also in African countries.
Pawan Kumar Agrawal, Indian Council of Agricultural Research (ICAR) representative	Clarity is required about "how to deliver impact at the farmer field level".
Dr. NN Singh, Secretary, Trust for Advancement in Agricultural Sciences	Appreciated the wheat pre breeding efforts ongoing in the SeeD-Wheat project. System change is dynamic and demand is changing. A bottom up approach is required to address this. Collection of the on-farm diversity and close association of farmers with breeders in wheat pre-breeding should be impactful. Large scale involvement of rural youth and women is instrumental in the process.
Dr. Kuldeep Singh, Director, National Bureau of Plant Genetic Resources (NBPGR), India	Breeders too often state that "Biotech is taking money from breeding." On the contrary, biotech is helping the use GeneBank germplasm for wheat prebreeding For example, wheat landrace core formulation by NBPGR as well as Mexican wheat landrace core development in SeeD were done using high density genomics.
Dr. Ravi Singh, Distinguished Scientist, wheat breeder, CIMMYT	"In breeding, when you bring something good, you also bring bad things. Need to understand the genes underlying the traits. Learn the genetics, then mine them carefully to avoid one step forward, two steps back."
Dr. Nagendra Kumar Singh, National Professor, National Research Centre for Plant Biotechnology, India	It is important to break unwanted linkage of gene(s)/QTL(s)/traits with desirable ones prior to prebreeding. As an example in rice, an unholy linkage between drought QTL (qDTY 1.1) and green revolution gene (sd1) has been broken, and semi-dwarf genotypes developed that are being utilized in broadening the genetic base. Similar efforts need to be followed in wheat prebreeding, and genomics approaches can help in this efficiently.
Dr. Sanjaya Rajaram, 2014 World Food Prize laureate	"The program was very well presented, including integration of students. Is there a role for old cytogenetics tools in bringing diversity – translocations?" He suggested to utilize cytogenetics tools and to incorporate "red grain × white grain" crosses in the SeeD wheat prebreeding work to widen the gene pool.
Dr. Gurdev Kush, 1996 World Food Prize laureate	"My only regret is that if I were 30 years younger I would be able to use these technologies." He suggested to utilize all possible technologies in an intelligible fashion for developing prebreeding germplasm. His remarkable contribution in rice i.e. "IR64" was developed through a similar approach.

offered insights, suggestions and comments about the SeeD initiative during the discussion session at the IAC in New Delhi (Table 2). Two scientists mentioned climate change, and the need for agrobiodiversity and pre-breeding to meet the challenges it will present. Four breeders reminded the audience of the large challenges when using exotic (e.g. germplasm bank accessions) material in breeding programs, and of the value of using genetic tools, as in SeeD, to accelerate this process. The 1996 World Food Laureate, Dr. G. Kush lamented that such technologies as used in SeeD were not available to him when he was active as a breeder. Finally, two donor agency representatives reminded us of the need to always show value or return to investments, especially in farmers' fields; and indicated that SeeD addresses many of their priorities, and that there are opportunities to increase partnerships in low and mid-income countries for a wider impact of SeeD.

Conclusion

The SeeD initiative offers an innovative model for enhancing the efficiency and equity of use of genetic resources. This model can be adopted and improved for other crops, as indeed is now happening for coffee in Mexico. Many of the tools and much of the data produced by SeeD can be used for scientific discovery and be applied across many crops. The strategies of the SeeD initiative, outlined herein, are designed to increase not only the use of agrobiodiversity to address challenges to food security, e.g. from climate change, but also to foster equity in the access to and benefits from crop agrobiodiversity. While it is too soon to attempt measuring impacts of SeeD, preliminary outcomes are encouraging, including that large numbers of students and scientists are using the products of SeeD. The observation by a representative of a major international agricultural research funding organization, that there are opportunities to increase impacts of SeeD to benefit low and mid-income countries, raises hopes that resources will be secured to do so.

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