



FEED THE FUTURE

The U.S. Government's Global Hunger and Food Security Initiative

Feed the Future Public-Private Partnership Technical Forum DISCUSSION PAPER: GENOMICS/CROP AND ANIMAL IMPROVEMENT

Session Purpose: *This session will focus on coordination of newly developed sequencing technologies, bioinformatics, and genomic tools to significantly accelerate progress on breeding and genetic engineering research in crop and animal improvement and nutrition in Feed the Future countries.*

Session Deliverable: *Identify potential public-private partnership opportunities related to trait evaluation, cataloging genomic information, and/or the creation of platforms for data sharing in genomics or other areas of new technology research to address climate change, nutrition, and disease resistance.*

Context/Rationale:

Given global population and middle-class growth rates, changing climate conditions and limits on agricultural land, scientific innovation and technology in agriculture and nutrition are needed to improve global food security. Partnerships between private companies and publicly funded research organizations are a way of getting the technological advances in agriculture to benefit poor farmers and consumers in developing countries. The aim is to use complementary assets of both partners to maximum advantage and create a win-win situation for industry and farmers. Newly developed sequencing technologies and bioinformatic and genomic tools offer the possibility to analyze genetic variation at an unprecedented level of precision. This discussion paper lays out two potential public-private partnership focus areas: crop improvement for climate and disease resistance, and sustainable intensification of the four major agro-ecosystems outlined in the Feed the Future Research Strategy.

Potential Partnership Focus Area:

Crop improvement for climate resilience and disease resistance: Partnerships could be developed to advance the identification, evaluation, or enhancement of traits that contribute to climate resilience (e.g., heat and drought tolerance, nitrogen-use efficiency, higher yields), to include advanced approaches such as genome mapping, transgenics, and marker-assisted breeding.

Example projects:

- Develop a comprehensive catalog of DNA sequence variation at the whole-genome level for 1000 wheat lines to accelerate the discovery and incorporation of valuable genes into wheat varieties using modern genetic technologies. (See Appendix for more detail).
- Develop platforms for data and information generation and sharing in genomics, trait mapping for climate change, and disease-resistant traits.
- Improve the availability of plant and animal breeding and genomic information: Private-sector partners could donate technology to the public sector and select priority projects to support more fully. Partnerships could also promote public access to enabling key technologies, such as improved transformation methods.

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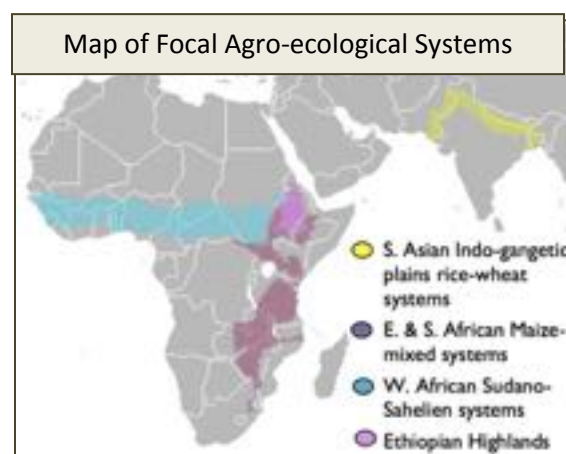
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- Expand plant breeding and genetic engineering joint efforts to improve water-use efficiency, nutrient-use efficiency, and heat and drought tolerance in crops, especially for species and markets which generally receive lower levels of investment.
- Expand animal breeding and genomic selection efforts to improve drought tolerance, disease resistance and improve yield gaps in major livestock species.

Crop improvement through sustainable intensification (conservation agriculture, mechanization, post-harvest storage) of the four major agro-ecosystems outlined in the FTF research strategy: Agro-ecosystem development aims to improve rural livelihoods and increase food security and sustainable natural resource management. Farmers will need a diverse portfolio of improved crop varieties, suited to a range of agro-ecosystems and farming practices, resilient to climate change. Fundamentally, this effort would require integrating component technologies, such as small-scale machinery, post-harvest storage, and animal or crop improvement with management practices to enhance yields. The result would diversify cropping systems (to include animals) and improve incomes while encouraging the sustainable use of resources, both natural (water, soil, energy) and human (labor). Many of these component technologies could be developed by private partners. The four major agro-ecosystems are the South Asian Indo-gangetic Plains rice and wheat systems, the East and South African maize-mixed systems, the West African Sudano-Sahelian systems, and the Ethiopian Highlands.

Example projects:

- Evaluate germplasm suited to conservation agriculture systems (e.g. varieties that work well under zero/low till systems).
- Partner to develop equipment suited to small-scale mechanization for resource-poor farmers.
- Partner to develop integrated post-harvest storage solutions that can be scaled up by small farmers. For example maize dryers that reduce aflatoxin contamination.



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Key Questions for Discussion

- What is the potential role of private-sector organizations in genomics, such as in sequencing, bioinformatics, data generation, and training?
- How can the U.S. Government leverage private-sector efforts and how can the private sector leverage U.S. government efforts in genomics, such as in the 1000 wheat genomes idea?
- How might data and enabling technologies be made publicly available? What are the mechanisms and constraints?
- What role might the private sector play in improving food security through sustainable agriculture intensification in South Asia or Africa, e.g., germplasm improvement for no-till systems, tool development for small-scale farmers or post-harvest solutions for small-scale farmers?

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APPENDIX

Example Partnership - A “1000 Wheat Genomes Partnership” -- A comprehensive analysis of genetic variation for wheat improvement in developing countries

Wheat is an important agricultural commodity and the second most abundant staple crop grown worldwide, supplying more than 20% of the calories in the human diet and an important major source of protein in developing countries. Development of new wheat varieties in a timely manner with improved nutritional qualities, adapted to harsh climatic conditions, resistant to diseases and insects is one of the major challenges of modern wheat breeding efforts. To reduce the time from trait discovery to new wheat varieties requires a more broad utilization of new genomics tools and resources in breeding. The complete catalog of DNA sequence variation in the wheat genome combined with large-scale phenotyping (trait analysis) can enable the association of small changes in DNA sequence at the whole-genome level to genetic variation in important agronomic traits. A comprehensive analysis of genetic variation in wheat could build a stronger foundation for integrated breeding worldwide and provide the tools for analyzing complex traits using the methods of molecular biology, breeding and biotechnology. This would help address one of the major challenges of modern wheat breeding efforts -- the timely development of new wheat varieties with improved nutritional qualities, adapted to harsh climatic conditions, resistant to diseases and insects. At the same time, this will also be useful to characterize and enhance diversity of cultivars, as over-reliance on any one elevates the risks posed by pests and disease.

A “1000 wheat genomes partnership” would focus on re-sequencing a diverse collection of wheat cultivars, land races, and wild relatives important for breeding programs of Feed the Future countries (e.g., Bangladesh, Ethiopia, Ghana, Kenya, Rwanda, Tanzania, and Uganda). Selection of these wheat lines could be performed in collaboration with international partners (e.g., ICARDA - Syria; CIMMYT – Mexico; USDA-ARS National Small Grains Germplasm Collection - USA) and the research/breeding community. Bioinformatic analysis of sequence data generated could be performed in collaboration with private breeding companies.

Next steps could include:

- 1) Initiate a “1000 wheat genomes partnership” to empower breeders/researchers to accelerate the discovery and incorporation of valuable genes into wheat varieties using modern genetic technologies. This could be accomplished by establishing an international collaborative network and partnership between private and public wheat research/breeding programs.
- 2) Generate a comprehensive catalog of genomic sequence variation in 1000 wheat lines selected from international and national wheat breeding and genetics programs. The selection of lines for sequencing could be performed by the international community, focusing on lines relevant to FTF wheat breeding programs.
- 3) Develop the bioinformatic infrastructure for sequence data storage, analysis, and dissemination. Integrate data with the publicly accessible databases and research programs.
- 4) Develop an educational framework for training wheat researchers and breeders from developing countries in next-generation breeding strategies that use whole genome DNA sequence information, state of the art genomic technologies, and bioinformatic and statistical tools for wheat improvement. Trainees could have an opportunity to spend time in private and public participating research groups.

Existing efforts:

Multiple private and public partners are involved in the USDA NIFA-funded Triticeae (wheat and barley) Coordinated Agricultural Project (TCAP) and the wheat SNP project, which are generating large amounts of genotypic and phenotypic data for a diverse collection of wheat lines. The wheat SNP project in the

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United States closely collaborates with CSIRO, the Department of Primary Industries (Australia) and CIMMYT (Mexico) on the genotyping and development of high-density genetic maps. These resources could facilitate the selection of FTF-relevant lines for re-sequencing and creating a resource for detecting associations between genetic variation and variation in important agronomic traits. Australian collaborators have already sequenced 10 wheat cultivars with the expected public release of whole genome sequence data by spring 2012. This sequence data could be used to test the bioinformatic approaches for the analysis of genetic variation at the whole genome level. CIMMYT is already collaborating with the USDA TCAP and wheat SNP project on genotyping wheat cultivars and integrating their data with the activities of Mexico's SeeD program. TCAP could develop the bioinformatic infrastructure for genotyping data storage and dissemination that could be used by the "1000 wheat genomes partnership."

USDA-Agricultural Research Service wheat researchers are developing genetic resources, genomics, and genetic improvement with public (TCAP, NSF) and private partners in the United States. USDA-ARS wheat researchers are partnering with the global wheat program (CIMMYT and ICARDA) to genotype disease resistant and superior end-use quality germplasm and elite breeding lines adapted throughout the world. ARS is also providing wheat disease expertise and bioinformatics capacity (GrainGenes) to these international programs.

The International Wheat Genome Sequencing Consortium (IWGSC) recently released the draft genome assembly of individual chromosomal arms of wheat (<http://urgi.versailles.inra.fr/Species/Wheat/Sequence-Repository>). The reference will be upgraded using the data generated by the IWGSC in ensuing years. The availability of reference sequences for aligning reads generated from new accessions is critical for successful re-sequencing projects.

The physical locations of genes within the wheat genome can be inferred using new ultra high-density genetic maps, including hundreds of thousands of molecular markers developed (or being developed) by the USDA wheat SNP project and TCAP. The same projects have already developed new tools for analyzing genomic variation. These 'targeted sequence capture' technologies enable high value targets (genes and regulatory elements) in the wheat genome to be prioritized for analysis.

Additional phenotypic and genotypic data are being generated by several national wheat research/breeding projects funded recently in UK, Canada, France (BreedWheat) and USA (TCAP). ARS can provide genotyping, bioinformatics, and genomics expertise. These projects, in addition to performing genotyping, are also generating a large amount of phenotypic data that would increase the utility of sequence information that would be generated by a "1000 wheat genomes partnership."

<i>Purpose/Brief description</i>	<i>Organization (and partners when applicable)</i>	<i>Amount (1,000's) of dollars</i>	<i>Year(s)</i>	<i>Point of Contact</i>
Triticeae Coordinated Agricultural Project (TCAP) for barley and wheat improvement	USDA NIFA, ARS, private sector	250	4	Jorge Dubcovsky
Wheat SNP discovery project	USDA NIFA, ARS, private sector	150	2	Eduard Akhunov
Innovation Center for Advanced Plant Design: Plants for the Heartland	Kansas Bioscience Authorities	50	4	Eduard Akhunov
Development of wheat exon capture assay	Biogemma (France)	50	1	n/a
Coordination with related plant genome,	USDA, USAID,	n/a	Ongoing	Program

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genetics and breeding research programs/projects	NSF, BMGF			Leaders
USDA-ARS Wheat Research (regional genotyping labs, crop genome databases, National Small Grains Repository, genomics research program)	USDA, NIFA, USAID, private sector	n/a	Ongoing	David Marshall, Kay Simmons

Examples of similar partnerships:

- Collaboration between the USDA NIFA wheat SNP project and Pioneer Hi-Bred (USA), Monsanto (USA), Syngenta and KWS (Germany) on the analysis of wheat genetic variation. These private companies made the results of their genotyping experiments publicly available, which made a significant contribution to the USDA NIFA-funded public effort.
- Public-private initiative to develop wheat varieties with durable resistance to Ug99 stem rust has been led by USDA-ARS in partnership with 28 U.S. Universities, 7 multinational companies, CIMMYT, ICARDA, the Borlaug Global Rust Initiative and the Durable Rust Resistance in Wheat Project at Cornell University. This public-private cooperative is contributing genetic resources, genomics and genetics tools to Eastern Africa partners.