



Research Bottlenecks to Crop Productivity

Workshop Summary

Washington, D.C.
September 4-5, 2024

Executive Summary

The Research Bottlenecks to Crop Productivity workshop brought together researchers, industry partners and funders to explore opportunities for integrated, collaborative solutions for [pressing constraint on improving crop productivity](#). Discussions highlighted both specific scientific gaps and broader systemic needs that must be addressed to accelerate progress. **Key Takeaways**

- **Roots, hormone crosstalk, maintenance respiration and source-sink balance** remain critical but underexplored drivers of crop performance.
- **Systems-level integration**—linking genetics, physiology, environment and management—is essential for meaningful gains.
- **Modeling and AI/LLM tools** can unify bottleneck areas and enable prediction, hypothesis generation and decision support.
- **Phenotyping and data standards** are foundational gaps; consistent standard operating procedures (SOP), shared infrastructure and interoperable platforms are needed.
- **Using genetic diversity resources as part of cross-sector collaboration**, especially with industry, are key to translating discovery to impact.
- **Training** in modeling, phenomics and AI is needed to build future research capacity.

Funder Alignment

Funding organizations emphasized integrative science, tool development, climate resilience and translational pathways, indicating strong alignment with the needs participants identified and meaningful potential for future co-funding

Community-Driven Next Steps

Although the group did not converge on a singular program concept, participants expressed strong interest in practical, integrative experimentation. **FFAR invites participants to develop targeted, community-led proof-of-concept project proposals that:**

- Focus on one crop,
- Apply insights from multiple bottlenecks, and
- Target one shared outcome (e.g., stress resilience, yield stability, resource efficiency, etc.).

FFAR welcomes the opportunity to review these concepts and, where appropriate, work with participants to explore potential funding partners. This approach provides a low-risk, collaborative avenue to test ideas, surface challenges and build consensus to guide future, larger-scale programs.

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Introduction/Background

The Research Bottlenecks to Crop Productivity workshop convened experts from academia, industry and funding organizations to identify and address critical barriers limiting crop productivity. Despite significant advances in agricultural research, key knowledge gaps remain, particularly in areas such as root structure and function, hormone crosstalk, efficiency of maintenance respiration and source-sink balance. Scientists from major seed companies agreed on these gaps, and leading academics presented potential solutions in "[Addressing Research Bottlenecks to Crop Productivity](#)." The workshop aimed to prioritize these research gaps, foster collaboration and explore investment opportunities to enhance crop productivity through integrative and systems-based approaches.

Focus Group Summaries

Prior to convening in person, to help drive the agenda and foster rich discussion at the workshop, focus groups were organized around each of the five prioritized bottlenecks summarized below. These groups met virtually to: i) explore gaps and opportunities within the respective research space; ii) discuss the connection with the other topic areas as relevant; and iii) identify potential research avenues towards improving crop productivity through guided and open discussion. Scientists from both academia and industry comprised the focus groups. Summaries from each focus group session are below.

Hormone Crosstalk

This focus group emphasized the complexity of hormonal interactions and their critical role in crop productivity. The group discussed the need for interdisciplinary research, particularly in translating basic hormonal knowledge into breeding applications. Key gaps identified include leveraging the variation in hormone levels among elite materials and the difficulty in quantifying hormone flux. The group explored potential avenues for manipulating plant hormones to enhance stress resilience and productivity, but participants also acknowledged challenges related to unintended consequences of hormone manipulation, as well as regulatory environments associated with crop engineering. Discussions underscored the importance of integrating hormone signaling research with broader crop improvement models.

Respiration Efficiency

This focus group addressed the need for further research on maintenance respiration, a major yet understudied energy cost in crops. Genetic variation in respiration rates and its correlation with a changing climate – particularly rising nighttime temperatures – may increase costly plant respiration, negatively impacting yield. The group proposed screening

elite germplasm for variations in respiration efficiency, identifying genes associated with optimal respiration rates and leveraging AI for metabolic pathway analyses as research opportunities. Additionally, the group identified the role of plant hydration and soil water status in respiration processes as a connection across bottlenecks.

Root Structure and Function

The group discussed the role of roots in nutrient uptake, drought resilience and soil interactions. Key research gaps include the need for improved root phenotyping methods, understanding how root traits interact with soil microbiomes and linking single-trait studies to large-scale agricultural applications. The session emphasized the importance of public-private partnerships in the precompetitive space to accelerate root-based breeding solutions and integrating climate modeling with root phenotyping to optimize crop performance in future climate scenarios. The group also mentioned AI-based predictive modeling as a promising tool for analyzing root function across diverse environments, again highlighting the connection across bottlenecks.

Source-Sink Balance

This session explored in detail strategies for optimizing the balance between resource production (source) and utilization (sink) to enhance crop yields. The focus group discussed strengths and weaknesses in existing research and identified the need for better integration of functional and structural models with AI to improve data analysis. A significant discussion point was the impact of climate change on source-sink relationships, with recommendations to study high-yielding crops under different environmental conditions. The group emphasized as obstacles challenges such as siloed research efforts, limited long-term funding and the need for demand-driven research packages.

Integrated Biology and Modeling

Using integrative modeling to overcome research bottlenecks and improve crop productivity was the central theme within this focus group. AI, omics data and remote sensing could refine crop growth predictions and improve resilience. However, the challenge of modeling non-heritable, complex traits and ensuring multi-scale mechanistic models effectively translate scientific discoveries into actionable solutions remain crucial components to develop more comprehensive models. The group proposed strategies, such as improving statistical modeling and incorporating spatial connectivity into crop models, to enhance predictive accuracy and inform on-the-ground decisions.

Presenter Summaries

Overview of Research Bottlenecks

Dr. Matthew Reynolds (CIMMYT) – High-Level Overview of Research Bottlenecks:

Dr. Matthew Reynolds provided a comprehensive overview of critical bottlenecks to crop productivity, detailing modern advances in genomics, remote sensing and AI-based modeling and providing unprecedented opportunities to tackle these long-standing research gaps. Primary bottlenecks that remain underexplored offer an opportunity for high returns on research investment. Bottlenecks discussed include:

- **Roots:** Root systems are fundamental for water and nutrient uptake, drought resilience and symbiotic interactions within the soil microbiome. However, phenotyping methods for roots remain a major limitation, making it difficult to incorporate root traits into breeding programs effectively. Dr. Reynolds discussed emerging technologies such as canopy temperature proxies and deep-root imaging as potential solutions.
- **Hormone Crosstalk:** Hormones regulate nearly every aspect of plant growth, yet their interactions remain poorly understood in breeding programs. Dr. Reynolds highlighted the importance of integrating hormone research into crop models and breeding efforts, particularly in relation to stress responses and source-sink balance.
- **Maintenance Respiration:** A major energy drain on crops, maintenance respiration occurs continuously and impacts overall yield efficiency. Understanding genetic variation in respiration rates could provide new breeding targets to optimize energy efficiency. Additionally, the effects of rising nighttime temperatures on respiration demand more attention, as this phenomenon is reducing net carbon gain in crops.
- **Source-Sink Balance:** The ability of a plant to efficiently allocate energy from photosynthetic tissues (source) to grain or fruit production (sink) is a key determinant of yield. However, current breeding strategies have yet to fully optimize this balance. Enhancing sink strength through molecular approaches such as Trehalose 6-Phosphate (T6P) manipulation could lead to measurable yield gains.

Dr. Bingru Huang (Rutgers University) – Hormone Crosstalk: Dr. Huang provided a detailed analysis of how hormone crosstalk functions as a fundamental communication mechanism in plants. She discussed how hormones such as auxins, gibberellins and cytokinins interact to regulate growth, stress responses and productivity. Despite their importance, hormonal interactions remain poorly integrated into crop breeding programs. The need for real-time, non-destructive monitoring techniques to measure hormone flux in plants cannot be understated; by improving our understanding of these interactions,

researchers can develop more precise breeding strategies to enhance stress tolerance and optimize resource allocation in crops.

Dr. Cara Griffiths (Rothamsted Research) – Source-Sink Relationships: Dr. Griffiths explored the inefficiency of carbon allocation in many modern crops and its implications for productivity, explaining how the source (photosynthetic tissues) and sink (developing grains or fruits) must be optimally balanced to achieve higher yields. A key limitation of current breeding approaches is the inability to fully harness the plant’s potential to distribute carbohydrates efficiently. Dr. Griffiths presented promising research on manipulating Trehalose 6-Phosphate (T6P), a sugar signaling molecule, to enhance grain filling and productivity. Integrating source-sink balance into breeding programs could result in significant yield gains, particularly in staple crops like wheat.

Dr. Jonathan Lynch (Penn State, Retired) – Root Structure and Function: Dr. Lynch highlighted the critical role of root architecture in crop adaptation to challenging environments. While roots are fundamental to water and nutrient uptake, they remain one of the least studied plant structures due to difficulties in measurement and characterization. New phenotyping tools that allow researchers to assess root traits more efficiently, such as canopy temperature as a proxy for root performance, may prove crucial to mitigating this bottleneck. The importance of deep-rooted crops in improving drought tolerance and reducing fertilizer dependence is critical, necessitating greater investment in root-based breeding strategies to enhance the resilience of global agricultural systems.

Dr. Jeffrey Amthor (Independent Researcher) – Maintenance Respiration: Dr. Amthor addressed the significant but often overlooked role of maintenance respiration in determining crop yields. Respiration occurs continuously in plants and that inefficient energy use can lead to substantial yield losses. A key finding in his research is high nighttime temperatures can disproportionately increase respiration rates, reducing net carbon gain in crops. He proposed targeted breeding approaches to reduce maintenance respiration by identifying genetic traits associated with improved energy efficiency. Additionally, the potential for metabolic engineering to optimize energy use at the cellular level may be the next era of energy use optimization, offering new opportunities for improving crop performance under climate stress.

Dr. Charlie Messina (University of Florida) – Integrative Modeling: Dr. Messina described how integrative crop modeling can help overcome bottlenecks in agricultural research. The numerous advantages of multi-scale models that incorporate genetics, physiology and environmental interactions to predict crop performance have thus far been met with significant challenges. The need for AI-driven tools and remote sensing

technologies to enhance the precision of these models is vast. Dr. Messina also highlighted how modeling can bridge the gap between fundamental research and applied breeding by providing a framework to test different scenarios before field implementation. Greater collaboration between breeders, physiologists and data scientists to maximize the impact of modeling efforts in agricultural research is needed.

Industry Panel Summary

Industry representatives emphasized that delivering value to growers—through higher yield stability, improved stress resilience and better resource efficiency—is their primary measure of impact. While academia excels at generating foundational discoveries, panelists highlighted a substantial gap in the translational space between academic research and deployable products. Stronger public–private partnerships are essential to bridge this gap. For example, industry can contribute broader field-testing networks, richer datasets and translational expertise, while benefiting from early access to promising germplasm, trait concepts and insights emerging from academic research.

Participants emphasized that complex traits such as yield and drought tolerance can no longer be addressed through single-gene strategies. Progress requires systems-level approaches that integrate gene networks, pan-genomic information and environmental interactions. Modeling provides a shared platform for this work, enabling academia and industry to explore trait complexity, predict performance and reduce uncertainty. As single-gene targets become exhausted, digital tools like *in silico* gene discovery and digital twins can be especially valuable for complex trait manipulation, especially for long-cycle crops like cacao. Furthermore, hormone crosstalk research was highlighted as one example where academic insights from a bottleneck topic can directly inform development of plant growth regulators (PGR), though current phenotyping and regulatory constraints remain limiting factors. In closing, they cautioned that early intellectual property (IP) negotiations can slow collaboration and recommended focusing first on scientific innovation, with IP discussions occurring later in the process.

Finally, the panel emphasized the urgent need for workforce training, particularly in modeling, genomics, trait integration and the ability to link biological insights to economic outcomes. The panel cited programs like [FFAR Fellows](#) as valuable models for preparing the next generation of scientists to operate effectively across the academic–industry interface.

Funder Presentations Summary

Presenters included: The Advanced Research Projects Agency-Energy Division (ARPA-E), Biotechnology and Biological Sciences Research Council (BBSRC), The Bill and Melinda Gates Foundation (BMGF), National Institute of Food and Agriculture (NIFA), National Science Foundation (NSF), Novo Nordisk Foundation (NNF) and the United States Agency for International Development (USAID). Presentations reveal several commonalities across programs in both agricultural research and innovation. These shared themes are summarized below.

Integration of Basic and Translational Research

All funders emphasized the importance of both foundational science and its translation into real-world applications. While some maintained strong support for basic research, there is a clear and growing interest across all organizations in bridging research with practice, particularly through tool development, breeding and field deployment. Several funders also highlighted the importance of ensuring that innovations ultimately translate into accessible products, inputs and technologies that farmers can use.

Focus on Crop Productivity and Resource Efficiency

Enhancing agricultural productivity through genetic improvement, physiological optimization and resource-use efficiency is a central goal highlighted by all presenters. There was a shared emphasis on increasing yield potential while reducing inputs such as water, nutrients and energy. Certain funders emphasized ecosystem-level approaches—examining agroecosystem biology, circularity and regenerative production systems—to better understand how cropping systems respond to environmental change.

Climate Resilience and Sustainability

Each organization discussed the need for agriculture to adapt to and mitigate climate change. Improving crop tolerance to abiotic and biotic stresses, enhancing soil and water sustainability and reducing greenhouse gas (GHG) emissions are all common areas of interest. Within this context, the interaction between crops and their associated microbiomes was identified as an important but underexplored area of opportunity.

Innovation in Tools and Technologies

Tool development—such as sensors, phenotyping platforms, decision support tools and precision agriculture technologies—is a research area widely supported by funding organizations. Funders see these tools as enablers for both research and application, especially in monitoring, modeling and breeding. Investments in germplasm accessibility,

digital agriculture and genotype-to-phenotype data pipelines were highlighted as essential for strengthening predictive modeling and accelerating trait discovery.

Cross-Sector and Cross-Agency Collaboration

Presentations championed collaboration across government agencies, private sector partners and international organizations as a common strategy to leverage complementary strengths, reduce redundancy and address global agricultural challenges more effectively.

Emphasis on Education and Workforce Development

A recurring theme and crucial area of investment for future research opportunities was investment in the next generation of agricultural scientists, particularly through training and education programs. Most agencies stressed the importance of building a diverse, well-equipped workforce to sustain innovation in agriculture.

Commitment to Global and Equitable Impact

There is a shared commitment to ensuring that the benefits of agricultural innovation reach diverse and underserved communities, both domestically and internationally. Many existing programs aim to promote equitable access to technologies and food security solutions.

Breakout Discussions

Participants took part in a series of breakout sessions designed to translate research bottlenecks into actionable program ideas. Early discussions focused on identifying connections among bottleneck areas, followed by prioritization exercises within and across those domains. Later sessions refined potential program targets and explored practical program models. The breakout sessions were held in table groups organized to maximize the diversity of the participants (academic, funders, industry and by area of expertise). The insights that follow summarize the key themes and opportunities that emerged from these group discussions, by table.

Breakout Discussions Insights

Table 1 Key Takeaways

- Emphasized the necessity of public-private partnerships to align phenotyping methodologies.
- Recommended the development of agreed-upon phenotyping SOPs to ensure consistency across research efforts.
- Highlighted the role of ERA germplasm panels—commercial varieties released over time representing a history of breeding—in integrating historical data into new explorations of research bottlenecks for crop improvement.

Table 1 Expanded Findings

The table did not come to consensus on which bottlenecks topics should have priority, or which should be nested inside other priorities, but did agree an integrative modeling component will be important to organizing and integrating across the research topics.

The table's major theme was phenotyping. The table emphasized the importance of collaboration (public/private, project team/project team, controlled environments/field trials) with set standards for data collection methods.

- Industry partnership (public/private) is critical for the following reasons:
 - Early partnership and engagement, as research plans are being made, will help steer and speed the translation of basic knowledge and discoveries made under the program toward practical outcomes within global agricultural systems and the market.
 - The deep experience and skill within industry to execute high-quality field trials across diverse environments (e.g., across the agricultural target population of environments (TPE)) could be leveraged.
 - ERA germplasm panels are valuable sources of historic and current commercial hybrids/varieties; they are well-studied in terms of general agronomic and environmental responses and physiology, and there is precedence for ERA panels being shared and evaluated in public/private research trials.
 - A focus on student and post-doc internships and training could help facilitate partnership with industry and ensure all aspects of the field trials and data sharing are established under pre-aligned research agreements.
- Agreed-upon methods and phenotyping SOPs will be critical to interpreting, leveraging and integrating outputs across the individual project teams and priority research topics. This includes defining and agreeing on field trial appropriate proxy phenotypes for

detailed and hard-to-collect measurements typically taken in controlled environments (greenhouses, growth chambers and laboratories).

- A core set of instrumentation, phenotypes and metadata to be collected at all experiments should be defined before any experiments begin, particularly for field trials. This should include phenotypes relevant to and across all priority research topics.

A single, public resource will be foundational to sharing and integrating data and learnings effectively across the project teams and the scales of the research.

Table 2 Key Takeaways

- Identified root system architecture (RSA) adaptation as key to climate resilience.
- Highlighted opportunities for hormone-mediated root response studies to improve abiotic stress tolerance and promote deeper roots.
- Called for integrating soil microbiome interactions into breeding models to enhance sustainability.

Table 2 Expanded Findings

Agricultural systems need to be more resilient to environmental challenges. There is evidence from climate and crop models that crop yield is going to be negatively affected by environmental changes by 2050, leading to a strong decrease in yield. Therefore, new cultivars able to withstand biotic and abiotic stresses are required. These need to support interactions between crops and soils in agricultural rotations to allow improved water use efficiency, reduced use of synthetic fertilizers, reduced production of atmospheric emissions and enhanced contributions to carbon sequestration.

Given their central role in many biological functions in soil, consideration of root traits and their environmental plasticity (defined as their ability to contribute to the stability of production against a set of stresses) is essential. However, despite important advances in knowledge about crop roots over the past decade, major gaps remain, including:

- How crop Root System Architecture (RSA) is controlled by abiotic stress signals—often mediated by hormones—like aerial and soil temperature. While aerial heat stress impairs wheat growth at any developmental stage, RSA traits such as greater rooting depth appear to help reduce its effects.
- How much carbon/biomass should crops invest in their root systems to maximize resource capture and sustainability, yet minimize its impact on yield. In addition to RSA, anatomical scale traits like cortical aerenchyma can reduce root respiration, enabling crops to reinvest their carbon in roots or other organs.

- Despite growing recognition of the importance of the soil microbiome on crop RSA and vice versa, major gaps exist in our knowledge of the mechanisms integrating root and biotic signaling.

Table 3 Key Takeaways

- Stressed the importance of genetic variation and the need for multiple tools to study it, integrating functional/structural gene annotation with physiological modeling.
- Proposed a source-sink model integrating hormones, roots and respiration that could advance crop improvement, working from diversity panels to outcomes that translate across crops.
- Cross-sector collaboration and training programs are critical for enabling research-driven crop improvement and supporting long-term progress.

Table 3 Expanded Findings

The group agreed that genetics and genetic variation are core to crop improvement but not sufficient on their own. There is a clear need to incorporate both functional and structural annotation at the gene level. At a physiological level, there is a need to understand how inputs and stressors integrate to influence crop productivity. Plant hormone function could be a good starting point for understanding how plants integrate this “information” and respond, but all the bottleneck topics should be modeled together. Modeling is key to further integrating spatial and temporal effects, metabolic changes and Carbon:Nitrogen:Phosphorus stoichiometry that ultimately define crop productivity.

The group presented a pitch for integrating data on hormones, roots and respiration into a source-sink model for crop improvement. Source-sink research isn’t novel, but there are new opportunities to build on past accomplishments with new tools, systems approaches and iterative modeling. Ultimately, the bottleneck topics represent tools for understanding plant physiology and how it relates to crop productivity. The proposal included starting with diversity panels, identifying the gaps in current knowledge and using modeling to predict outcomes. The importance of translatability of outcomes from an initial crop to others was highlighted.

Beyond the research, the group shared that collaboration (e.g., public-private partnerships; interagency partnerships; NSF Technology, Innovation, and Partnerships program; International Wheat Yield Partnership) and training programs at various levels of education (e.g., industry internships, graduate traineeships, advanced technological education at community colleges) are key contributors to advancing our efforts towards research-driven crop improvement.

Table 4 Key Takeaways

- Shared, diverse genetic panels are a key enabler for coordinated bottleneck research.
- Phenotyping plus modeling is crucial for revealing trait–gene relationships.
- AI-enabled modeling and validation hubs offer strong translational potential for identifying and testing promising traits.

Table 4 Expanded Findings

The group aligned on the need to first define crops and Target Population of Environments (TPEs) of most relevance to public and private breeding objectives. Designing genetically diverse genome-wide association study (GWAS) panels of sequenced genotypes, including elite lines as well as outstanding, adapted genetic resources (e.g., pre-breeding material), while controlling major genes that may otherwise confound results (e.g., for height, cycle length) will be key. Collaboration among researchers to share germplasm panels and research platforms/infrastructure where feasible will drive efficiency and ensure that “bottlenecks” research is mutually complementary.

In addition to new research, the group emphasized measuring established, high-value traits, such as phenology, growth analysis and traits suited to high-throughput phenotyping, using tools like aerial spectral radiometry, including thermal imaging for canopy-scale traits, and laser-ablation tomography for vascular-architecture traits. These measurements help provide a consistent context for interpreting newly collected traits.

The development of AI-assisted simulation models that use context-specific wiring diagrams as the initial knowledge base to guide predictions, allows Deep Learning to, at a scale not otherwise feasible:

- Simulate potentially winning trait/marker combinations and selection criteria.
- Use pattern recognition to:
 - Identify key genomic regions, like useful linkage-blocks.
 - Pinpoint chromosome regions where “exotic” DNA adds value that could be enhanced through gene-editing and/or targeted exploration of genetic resources.
 - Indicate other potential research bottlenecks.

Testing prioritized model outputs at dedicated trait/gene validation hubs (e.g., the IWYP Hubs/SuperHub in the case of wheat) by crossing in a realistic breeding context for proof of concept for novel trait/haplotype constellations in elite backgrounds and multiple locations will allow for translation of new findings. This genetic and physiological dissection of validated translational research products will help deliver cost-effective technologies to breeders, guide further breeding strategies and refine models.

Table 5 Key Takeaways

- Emphasized the need for a modeling infrastructure that focuses on large language models (LLM) to build systems that can predict, revise and learn from data.
- Shifting from linear thinking (one gene-one pathway) to systems thinking is crucial to alleviating bottlenecks to crop productivity.
- Imperative to integrate modeling with crop management practices, moving beyond modeling to in-field application and study of connected complex traits.

Table 5 Expanded Findings

The group's overarching message was the need for integrative, adaptive models that bring together genetic data, phenomics and management practices to improve crop productivity. The group proposed forming an integrative modeling consortium of researchers within academia and industry that fosters innovation and shares data to bring together modeling components like AI tools (e.g., LLMs), genomics and phenomics. This approach aims to accelerate learning cycles, ensuring researchers and farmers can optimize practices even within the limited temporal windows they have to observe crop outcomes. The group explored the following key topics:

1. Modeling and System Thinking

- The group emphasized the need to shift from linear thinking (one gene → one pathway) to system-level thinking. This approach integrates multiple layers of biological data (e.g., genomes, phenotypes) and management practices (e.g., chemistries, plant growth regulators) to improve crop productivity.
- Integrative modeling was highlighted as essential. This involves iterative processes in which models predict, revise and learn from data, enabling more dynamic and responsive systems.
- Wire diagrams (simpler models) can serve as foundational tools but must evolve into next-level models that reflect complex systems and interactions.
- A new framework is needed for AI enabled crop improvement, akin to the integration of neuroscience and psychology in the field of neuropsychology, that seeks to predict emergence behavior from underlying genetic determinants.

2. LLMs and Gene-to-Phenotype Predictions

- By identifying new patterns in genomes (based on haplotypes), LLMs could be used for advanced annotations, enhanced gene network modeling, and the transition from structure to function promoting a more holistic view of plant biology.
- There is an opportunity to connect crop-level models with genomic selection to assist with genetic diversity selection, defining gene-editing targets and informing breeding decisions.

3. Training and Infrastructure

- The group recognized a need to train the next generation of plant scientists in new methodologies (modeling, AI, phenomics) with programs that can build upon open-source resources and encourage system-level thinking and modeling approaches.
- Phenomics (high-throughput plant trait analysis) was called out as a critical bottleneck and recommended investments in phenomics infrastructure that leverage or repurpose existing resources like those developed under ARPA-E.

Summary of Breakout Group Discussions

- **Systems-level integration is essential.** Across groups, participants emphasized the need to link genetics, physiology, modeling and management practices to better understand and improve crop productivity.
- **Modeling emerged as a central unifier.** From source-sink frameworks to AI-enabled simulations and large language models, groups consistently highlighted modeling as the backbone for connecting bottleneck areas, predicting outcomes and guiding decisions.
- **Phenotyping and data standards are critical bottlenecks.** Multiple tables stressed the need for consistent phenotyping SOPs, shared instrumentation and unified data platforms to ensure comparability and integration across research efforts.
- **Genetic diversity and root system insights remain foundational.** Participants identified leveraging diverse germplasm, annotating genetic variation and understanding RSA and soil interactions as key drivers of stress resilience and long-term productivity.
- **Collaboration and data sharing are necessary for impact.** Participants highlighted public-private partnerships, cross-institutional data access and shared research platforms as enabling more efficient research pipelines and stronger translational outcomes.
- **Training and workforce development are strategic priorities.** Groups pointed to the need for training programs—including internships and cross-disciplinary education—to build capacity in modeling, AI, phenomics and modern breeding approaches.

Conclusion

The Foundation for Food & Agriculture Research (FFAR) is committed to advancing innovative, interdisciplinary solutions that address critical challenges in agriculture. This workshop exemplified FFAR's mission by fostering collaboration among leading scientists, industry stakeholders and research funding organizations to tackle fundamental bottlenecks that limit crop productivity. The workshop not only identified urgent research priorities but also emphasized the necessity of strategic investment and translational science to bridge the gap between discovery and on-the-ground agricultural applications.

Improving crop productivity requires a holistic approach—one that integrates genetics, physiology and cutting-edge technologies such as AI-driven modeling and precision phenotyping—and partnerships with both public and private entities.

By prioritizing these efforts, a paradigm shift in crop genetic improvement that moves beyond incremental gains toward transformative breakthroughs that can withstand future agricultural pressures is possible. The findings from this workshop will serve as a foundation for future funding initiatives and research collaborations, ensuring that these bottlenecks are addressed with urgency and scientific rigor.

As a community-driven next step, FFAR invites participants to develop targeted, proof-of-concept proposals that focus on one crop, apply integrated insights from the major bottleneck areas and target a shared outcome (e.g., improved stress resilience, yield stability or resource-use efficiency). FFAR would welcome the opportunity to review such concepts and, where appropriate, explore potential funding partners to help advance them. This approach would allow the community to test integrative ideas, evaluate practical challenges and build consensus around priorities that enable the development of larger-scale programs.

Appendices

Appendix A – Acknowledgements & Participating Organizations

Thank you to CIMMYT and KWS for co-sponsoring this convening along with FFAR, and to the presenters, panelists, the planning committee and participants.

Agricultural Research and Consulting, LLC (ARAC)
Bayer Crop Science
Biotechnology and Biological Sciences Research Council (BBSRC)
Bill & Melinda Gates Agricultural Innovations (Gates Ag One)
Bill and Melinda Gates Foundation
Cornell University
Corteva Agriscience
Foundation for Food & Agriculture Research (FFAR)
Inari Agriculture, Inc.
International Maize and Wheat Improvement Center (CIMMYT)
KeyGene USA
KWS SAAT SE & Co. KGaA
Lancaster University
Mars
National Science Foundation (NSF)
National Institute of Agricultural Botany (NIAB)
Northern Arizona University
Novo Nordisk Foundation
United States Department of State, Office of Agricultural Policy
United States Department of State, Office of Global Food Security
Pennsylvania State University
Rothamsted Research
Rutgers University
Syngenta Group
Technological Institute of Sonora
United States Agency for International Development (USAID)
United States Department of Agriculture, Agricultural Research Service (USDA-ARS)
USDA, National Institute of Food and Agriculture (USDA-NIFA)
University of California, Davis
University of Florida
University of Lleida
University of Nottingham
University of Western Australia

Appendix B – Pre-Workshop Summary

Participants from FFAR and scientists from the public and private sectors held virtual focus groups on each of the five research bottlenecks topics to evaluate the strengths, weaknesses, opportunities and threats (SWOT) of each research area and propose potential projects/programs. One-page summaries of the focus groups are available on the following pages.

- Hormone Crosstalk
- Source-Sink Relationships
- Root Structure and Function
- Efficiency of Maintenance Respiration
- Integrated Biology and Modeling

Role of Hormone Crosstalk in Crop Productivity

Focus Group Summary

Strengths:

- Strong foundational knowledge
- Proofs of concept established for regulatory roles impacting yield and climate resilience in several crops.
- Genetic diversity among elite cultivars established.
- Several master/regulatory genes (e.g. CKX) already cloned (targets for gene editing).
- Research facilitated by use of exogenous application of hormone analogues and other chemicals

Weaknesses:

- Lack of investment in techniques for accurate and high-throughput measurement of hormone levels and dynamics.
- Spatial & dynamic nature of hormones makes them challenging to quantify in planta – need for more refined tools and models, such as biosensors and proxies.
- Complexity of Hormone Interactions at different development stages and environmental conditions

Opportunities:

- Leverage genetic diversity in crops & wild relatives through strategic hybridization.
- A large body of knowledge from research in controlled environments is ready for translation to crop scenarios.
- New technologies (e.g. deep sequencing /genome editing) allow gene discovery and engineering to increase phenotypic variation in elite material
- Integrate pharmacological tools with genetics to establish key mechanisms of action / develop crop management packages

Threats:

- Silos e.g. limited integration with crop modelling community
- Climate zone shifts – hormone interplay with crop climate migration – processes (root biology, senescence, flowering, and seed setting/filling for seed production) not deeply explored

Opportunities for investment and translational research on hormone crosstalk to improve crop productivity:

1. Develop a framework that highlights the key roles of hormones on agronomics

(e.g. harvest index, phenology, plasticity, acclimation) in different target environments.

Impact: Prioritize breeding, gene discovery and genome engineering targets to capitalize on technical advancements.

2. **Leverage existing genetic diversity** for favorable hormone expression (e.g. impacting seed set/filling, leaf/fruit senescence, stomatal conductance, root traits, stress response, etc.) among elite material and novel genetic resources.

Impact: Breeding for hormone-mediated responses to changing environments can fine-tune stress responses to extreme weather events.

3. **Improve throughput capacity of measuring hormone concentrations** and their proxies, such as those in a gaseous state like ethylene and/or its precursors, and their dynamic changes in specific tissues/organs and transport across tissues/organs.

Impact: Useful genetic diversity is more readily identified and applied in mainstream breeding and included for the first time in crop simulation models.

Role of Source-Sink Relationships in Crop Productivity

Focus Group Summary

Strengths:

- Well-established protocols for measuring SS traits.
- Measuring consequences of [source:sink](#) balance is relatively easy.
- Critical growth periods determining sink strength and when to boost source strength established in various crops, helping focus research.
- Cytokinin and ethylene are known to regulate grain set and abortion, respectively, connecting SS with the Hormone focus group.
- Promising targets already identified including fruiting efficiency; sink-driven boost to photosynthesis; modify timing of competing sinks.
- A tool to manipulate SS balance – T6P – has shown proof of concept.
- Expert collaboration and sharing of technologies is common.

Weaknesses:

- HTP phenotyping platforms needed for most sink traits.
- Research in controlled conditions not validated in the field.
- Investment in model species/crops limits broader application.
- Response of reproductive growth – determining sink strength – to extreme weather is poorly studied, despite its sensitivity.
- Need for proxy traits responsible for consequential traits.
- Unequal funding for sink vs. source research.
- Siloed approaches miss opportunities for holistic solutions.
- Capacity and expertise are waning.

Opportunities:

- 'Wiring Diagrams' of SS trait interactions in wheat (adaptable to any crop) provide a framework for AI-assisted breeding models, employing extant high-quality trait, gene-sequence, and metadata sets.
- Build on cytokinin and ethylene research in rice & wheat to optimize hormonal control of grain set and genes involved.
- Optimize development so fertility not competing with other sinks.
- Optimize vascular architecture to boost grain set and grain-fill rate.
- Include role of roots in determining [source:sink](#).
- Use Big Data to identify lines with robust grain set under stress.

Threats:

- Inbreeding & outbreeding crops show different mechanisms related to SS balance – due to evolutionary factors.
- Determinacy of reproductive structures varies among and within crops, adding another dimension of complexity to SS research.
- Limited and unsustainable funding linking discovery research to the breeding industry (via pre-breeding for example); translational research is generally "off-radar."
- Resources limited globally, restricting multilocation research including local germplasm, crucial to understand environmental cues.
- Marketing & pipe-dream research capturing more funding vs. demand-driven research.

Opportunities for investment and translational research on source-sink balance (SSB) to improve crop productivity, climate resilience and input use efficiency:

1. **Variation of Harvest Index (HI; a proxy for SSB).** Diverse, deep-sequenced elite lines used in GWAS to identify genetic bases of SSB; calculation of HI will also include estimates of below ground biomass using remote sensed proxies. Big data sets from decades of international breeding trials will also be analyzed to identify lines with stable yield despite environmental stress at grain set.
Impact: markers to improve HI mainstreamed; gene discovery to suggest editing and genetic resource targets; sources of robust grain-set under environmental stress.
2. **Identify trait sources that optimize investment** in reproductive structures (e.g. floret survival rates).
Impact: Optimized partitioning of carbon maximizes crop fertility and yield potential.
3. **Improve spike vascular architecture**, such as number and diameter of sieve tube elements in rachis/rachilla and discover genetic bases.
Impact: Increased grain set and grain filling rate.

Role of Root Structure and Function in Crop Productivity

Focus Group Summary

Strengths:

- Optimized root systems can substantially improve stress tolerance, resource-use-efficiency and crop yield.
- Breakthroughs in understanding root phenomes allow precise targeting of root-traits for drought tolerance, low N & P levels & mechanical impedance.
- Recent advances in genome sequencing have accelerated gene/SNP haplotypes for root traits.
- Remote sensing of root capacity permits breeding-scale throughput

Weaknesses:

- Most research is conducted in artificial environments on model species.
- Root systems are highly plastic and responsive to environment, questioning the relevance of research in controlled environments.
- Root architecture quantification beyond 20cm soil depth is scant.
- The true carbon cost of roots is uncertain, including the potential cost-benefits associated with plant-soil microbiology interactions.

Opportunities:

- Harness the explosion of work on soil-rhizosphere-root interactions
- Non-disruptive technologies to monitor root growth and plasticity.
- Genetic diversity within elite breeding genepools and genetic resources.
- Improve understanding of root interaction with source:sink and their role in hormone signaling to above ground organs.

Threats:

- Disentangling biotic from abiotic threats underground.
- Reductionist approaches; e.g. studies at single root positions
- Influence of soil characteristics largely ignored in root research.
- Research in sophisticated growth facilities prioritized over field studies, while the former ignore the real conditions (temperature gradients, oxygen levels, plough layers, increasing pressures with depth and the living fauna) of roots at different soil layers in cropping systems.

Opportunities for investment and translational research on root traits to improve crop productivity, climate resilience and input use efficiency:

1. **Improving Root Depth:** Root depth is a primary determinant of water and nitrogen capture, as well as biosequestration of carbon dioxide. Substantial genotypic variation for root depth is present within crops, which can be selected for using high throughput remote sensing tools.
2. **Leveraging high throughput phenotyping (HTP) platforms and deep-sequencing** to identify genes and haplotypes associated with favorable root-traits for deployment in breeding; capitalizing on research that has identified root phenotypes that substantially improve crop yield under stress.
3. **Translating promising strategic research outputs** to a breeding context using multidisciplinary/multiscale approaches, including a comprehensive root-trait and marker database, also leading to development of deep learning models to facilitate deployment of root traits in mainstream breeding.

Role of Efficiency of Maintenance Respiration in Crop Productivity

Focus Group Summary

Strengths:

- Foundational knowledge exists on respiratory cost of growing crop biomass
- There is genetic variation in respiration in the field, potentially translating into yield differentials
- Rapid measurement of respiration rates – Q2 fluorophore robotic system; hyperspectral reflectance; machine learning for prediction to aid in screening

Weaknesses:

- Field-based methodologies for quantifying whole-crop respiration must be developed
- Variation in respiration among tissues complicates generalizations and scaling to whole-plant performance
- Distinguishing genetic and environmental effects on respiration requires extensive data, well-designed experiments, and genetically diverse panels

Opportunities:

- Evolving technologies for genetic engineering are opening doors to improving respiration biochemistry, e.g., genetic engineering of enzymes
- Improving the efficiency of respiratory ATP synthesis and efficiency of energy use (via reducing cellular maintenance energy costs)
- Tiller dynamics & in-/determinate flowering as proxies for measuring maintenance respiration

Threats:

- Warming climate negatively affects photosynthesis–respiration balance and crop productivity
- Focus on spot (time/developmental phase) measurements on tiny portions of crops – without ability to scale spatially, temporally, and/or developmentally – will delay understanding of crop respiration
- The complex, multi-pathway nature of respiratory metabolism and its interactions with other processes may limit the ability to alter overall respiration via single-gene/trait changes

Opportunities for investment and translational research on “efficiency of maintenance respiration” to improve crop productivity:

1. **Phenotyping:** Validate and modify/develop high throughput and proxy methods to quantify respiration and translate/use them in research and breeding.
Impact: Ability to prioritize targets and effectively select to increase efficiency of respiration, differentiating genetic and environmental effects.
2. **Genetic Resources:** Establish genetic diversity for maintenance respiration among elite breeding gene pools and diverse/exotic genetic resources.
Impact: Ability to prioritize and use/mine genetic resources to improve respiration efficiency at crop or plant levels and phenological or diurnal stages.
3. **Apply evolving technologies for discovery, validation and translational research:** Gene editing or bioengineering to modify or replace key enzymes; apply artificial intelligence to model and predict targets.
Impact: Validate hypotheses for step-changes in respiration efficiency for later translation into breeding programs.

Role of Integrated Biology and Modeling in Crop Productivity

Focus Group Summary

Strengths:

- Simulation modeling is a potentially effective technology
- New modelling tools that combine statistical, mathematical and AI principles becoming available
- Good empirical foundational knowledge in many areas
- Industry becoming skillful in the practical use of models
- Computing capabilities-practical application of crop growth models within agronomic and breeding programs

Weaknesses:

- Funding opportunities overly focused on model applications making model development difficult to support
- Lack of researchers that combine modeling expertise (systems thinking, engineering), robust understanding of crop performance at the field scale, and basic plant biology
- Gaps in knowledge is where tremendous research potential exists including key feedbacks for the whole plant system

Opportunities:

- Unprecedented ability to perturb crop systems at the gene level (gene editing, nanotechnology) to understand, model and predict gene effects
- Better linkages between IB&M and remote sensing might enable better understanding of crops and in-season management where that is a realistic option.
- IB&M might be more deeply imbedded in basic plant biology and crop production
- Smart & sparse designs enables physiology and breeding experimentation for applications in breeding programs
- Mature phenotyping technologies to understand systems and train models for prediction within breeding programs

Threats:

- Lack of compelling case studies
- Unwillingness to share data, knowledge, resources that connect various streams of research
- Siloed thinking, lack of a common language, and training in system thinking by various practitioners
- Reward systems focus on individuals and not teams

Opportunities for investment and translational research on integrated biology and modeling of research bottlenecks topics:

1. **Harness AI for gene function prediction.** Generate a large language model with genetic sequence information to understand relationships (source-sink, hormones, etc.) and drive modeling of specific traits. Involves collaboration with GEMS modeling, a broad transdisciplinary consortium open to sharing knowledge, expertise and resources on genomics, phenomics and enviromics for designing targeted experiments, collecting quality data and integrated genomic specific modelling of crop growth by genotype-specific dynamic control systems for bottleneck traits. Set the global standard for collaboration, from ontologies to IT.
2. **BottleNext modeling:** Define and explore quantitative “what-if” modeling questions to formulate hypotheses in biology, crop improvement and adaptation to climate change.
3. **Validation of research and modelling outputs:** Strategic crossing and progeny selection suggested by outputs of ‘bottleneck’ research and simulation, and multilocation testing of selected progeny for proof of concept.