RCN: Broadening and Energizing the Maize Genetic Research Community

White Paper Year 1 – Defining research opportunities, infrastructure and technology needs, and approaches to build and empower the maize community

This white paper is a summary of discussions at the mid-year conference held September 19 to 21, 2018 in Madison, WI

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Mid-Year Conference Participants

Teams were identified in advance of the conference to coordinate and address the following areas: Functional Genomics Tools and Resources; Informatics Tools, Resources, and Services; Community Breadth and Developing Country Interface; Industry Interface; Training and Student Recruitment.

In addition, a portion of the conference was devoted to defining functional genomic resource opportunities and needs, and some conference participants led discussions of that topic area. The following list describes those participating and the primary area that they represented.

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Executive Summary

The Maize Genetics Community is a vibrant global assembly of more than 4,500 researchers and related people with yearly conference attendance of around 600 scientists. The overall goals of the community are to 1) facilitate coordination and prioritization of funding for research, 2) support exchange of genetic stocks and germplasm, 3) advocate for funding for centralized databases and tools, and 4) provide forums to exchange scientific information – primarily via the annual Maize Genetics Conference and the Maize Genetics Cooperation Newsletter.

Maize is a premiere species for basic and translational research. It is one of the major crops that sustains humanity worldwide, and has had a coordinated research community for more than a century. Maize is a research substrate specifically well-suited to address grand challenges addressed at understanding basic biological mechanisms and meeting global food, feed, fiber and sustainability needs.

Maize was identified as being specifically well-positioned to meet the following grand challenges:

1. Understanding Genome Structure, Evolution, and Transposon Biology
2. Predictive Phenomics: Genes and phenes controlling plant adaptation in diverse and variable environments
3. Heterosis: The basis of hybrid yield
4. Agroecosystem Sustainability: Meeting crop system productivity needs while reducing environmental impacts and maintaining ecological, economic, and social stability

A number of technological needs were identified that will support the research enterprise in this community in the next 10 years:

1. Systematic gene modification in one or more relevant genetic backgrounds
   a. Achieving this goal requires improved cost and system efficiency in transformation and gene-editing
   b. Creation of collections of mutant or modified alleles will enable scientists to take full advantage of maize genetics tools and resources

2. Development of advanced phenotyping approaches (Transparent Plant concept)
   a. Cellular imaging and -omics, including omics of single cells, will support characterization of temporal responses and identify regulatory networks
   b. Chromatin structure and function characterization in time and with cell to organ specificity will elucidate regulatory control mechanisms
   c. Organ and whole-plant imaging and sensors will detect developmental and biochemical responses of plants interacting with their environment

    d. Field and landscape scale imaging, sensing, and monitoring to evaluate agroecosystem (biological and socio-economic) impacts of genetically variable cultivars will support optimization of cropping systems

    e. Integration of phenome data into modelling and prediction will support discovery and intervention

3. Databases and computation

    a. Databases to coordinate and support data collection are needed to provide access to large, well-curated datasets

    b. Computational approaches will provide mechanisms to turn data into useful information

    c. Training and collaboration will empower biologists to develop and evaluate hypotheses using "big data"

The Maize Genetics Community must evolve to remain effective and relevant. Important discussion points related to the community are:

1. Broadening diversity of underrepresented groups and international researchers
2. Identifying a path to disciplinary diversity – likely enabled through strategic linkages
3. Exploring structures to formalize the community to maximize effectiveness

Evolution of the Maize Genetics Community

The maize community was initially formalized in 1918 through a "Cornfest" at the AAAS meeting organized by R.A. Emerson to discuss maize gene symbols and mapping (Kass et al. 2005 – Genetics 169:1787-1797). Cornfests evolved into "Cornfab" in 1928, with the goal of determining a convention to order linkage groups and to parcel them out for oversight by researchers. Enabling research founded in the accumulating genetic mapping projects required a mechanism to share and distribute genetic stocks. In 1934, the Rockefeller Foundation provided $5,000 to support a Maize Genetics Stock Center. The initial stock center was at Cornell University until 1953, when it moved to the University of Illinois where it currently resides. A Maize Genetics Cooperation Newsletter was initiated in 1931 to facilitate rapid sharing of information. This newsletter complemented the standard process of publishing in refereed journals, allowing genetic mapping data and other technical details to be made rapidly available and synergizing research in the community. A Maize Genetics Database was initiated in 1991, soon after the broad availability of the World Wide Web, to facilitate rapid sharing and storage of genetic information. The initial database was housed at the University of Missouri, and transitioned to Iowa State University in 2003 as growing amounts of sequence information required redesign of the original architecture.

Annual maize genetics-oriented conferences were initiated in 1959. The first conferences were held at the Allerton House Conference Center associated with the University of Illinois. A Maize Genetics Conference Steering Committee was formalized by charter in 2006, with the primary goal of organizing the yearly conferences. The meetings have grown in attendance to around 600 participants annually, and now rotate to locations throughout the world.

A Maize Genetics Executive Committee (MGEC) was formally initiated through an election by the maize community in 2000. The executive committee was formed following a visioning process in 1998, with a goal of positioning the maize community within the context of the then newly formed National Plant Genome Initiative. The primary role of the MGEC has been to serve as a unified voice of the community, and to advocate for funding to support key research activities. One example of these activities was to advocate for support to sequence the genome of the maize inbred line B73. In 2007, the MGEC organized a second retreat at the Allerton Conference Center to discuss positioning the community in the post-genome era. Our current Research Coordination Network (RCN) project is an extension of these visioning activities, coordinated by the MGEC, to articulate needs of the research community and support its expansion and promote broader impacts.

This brief overview of the evolution of the community describes that the purpose of organizing the Maize Genetics Community was 1) to provide a forum to discuss coordination of research activities and rapidly disseminate results, synergizing research in the community, 2) to provide a mechanism to share valuable genetic stocks and germplasm, and 3) to provide central repositories to gather and share information. These principles remain keystones of the purpose of the community as we look to the future.

Overview of current maize community and composition

The current vibrancy and breadth of this maize group are highlighted by data from Carson Andorf at Maize Genetics and Genomics Database (MaizeGDB). Among our total 4,544 Maize Genetics Cooperators, substantially more than three quarters have attended annual meetings during the past 10 years (Figure 1A). Especially important is the notable involvement of early-career scientists in our annual meetings (Figure 1B). Data from 2018 indicates that two-thirds of our attendees are either graduate students (41%) or postdoctoral associates (22%). This diversity of career levels means we have an outstanding opportunity to connect and integrate new, young people into the professional scientific network at this meeting. Also, all attendees are able to integrate on-site with the international scientific community. This meeting has increasingly become the global forum for maize research. We currently draw approximately a quarter of our attendees from around the world, and our RCN is implementing strategies to increase underrepresented and disciplinary diversity, as well as global participation. Maize researchers travel from almost every continent to attend the annual meetings and arrange collaborative studies. These interactions are also invaluable to our students and postdoctoral associates.

The geographic distribution of Maize Genetics Cooperators spans essentially the entire U.S. Although membership is prominent in the corn states of Iowa, Illinois, Indiana, Missouri, Minnesota, and Wisconsin, the same is also true for California, New York, North Carolina, and Florida. In addition, scientists and students from almost all other states in the US are included in our current community. Finally, an even broader community is evident among those who access maize genetics resources via online portals. Statistics from MaizeGDB.org, a core resource for maize researchers, show its widespread use by many in addition to the Maize Genetics Cooperators. For example, in 2016 there were over 60,475 users in the U.S., distributed across every state. The broad reach and active use of MaizeGDB make it invaluable to our RCN effort.
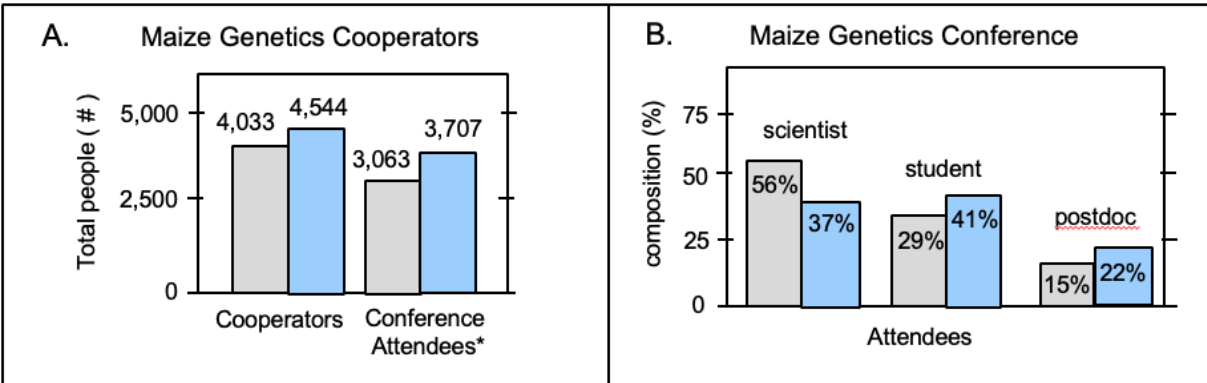
Figure 1. The Maize Genetics Community: A. Maize Genetics Cooperators. Total numbers are based on the e-mail database from MaizeGDB.org (2018 and 2019). The conference attendees* include meetings held in the US from 2008 to 2017 compared to data from 2018.   Each attendee is counted only once during this time. **B**. Maize Genetics Conference attendee composition. Data from 2012 and 2015 are compared to 2018. (Courtesy of MaizeGDB)

Maize as a Substrate for Basic and Translational Research

Maize is a crop grown in vast areas across the world, having impact on socio-economic, ecological, production, and industrial systems. World-wide production is currently more than 40 billion bushels (1 billion metric tons), and more than 89 million acres planted with corn in the U.S. in 2018. Driven by dramatic genome and sequence variation, maize hybrids and populations that are adapted to climates ranging from lowland equatorial regions to northern short-day latitudes have been developed. The resulting grain and plant material are used for a vast array of food, feed, fuel, and raw materials uses.

Maize has many strengths as a research subject. Over a century of innovative science has established a strong research community centered around this species. Seminal discoveries in maize, including discoveries of imprinting, paramutation, and transposons, have had dramatic impacts across biology. The unique structure of the female inflorescence (ear) has made maize a valuable organism to dissect developmental and biochemical processes during ear and kernel development (Figure 2). Maize is an annual species with an average life-cycle of ~100 days, although some varieties can go from seed-to-seed in less than 60 days, and others need more than 200 days. The large size of the plant facilitates gathering tissue for biochemical and 'omics analyses. Adaptation of maize to field environments has facilitated large-scale, inexpensive plant growth, and is fundamentally important in the emerging "Genome to Phenome" era with a goal of understanding plant responses to environment. The striking visible nature of maize

mutations makes this species an engaging educational tool to attract students to basic and applied plant biology careers.
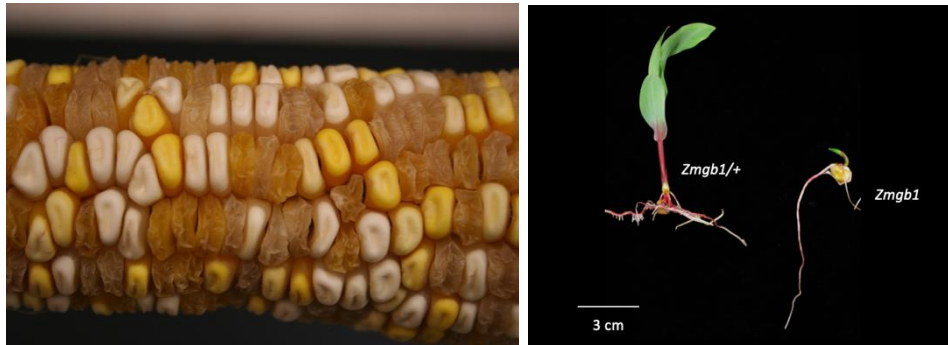
Figure 2: Maize Phenotypes. (<u>Left</u>) Kernels segregating for carotenoid content and carbohydrate composition on a maize ear. The organized arrangement of hundreds of kernels on each ear has supported genetic studies and training for decades. (<u>Right</u>) A CRISPR derived knockout of the maize G beta gene leads to a seedling lethal autoimmune phenotype (Dave Jackson and Bing Yang, unpublished).

Due to the role of maize as both a long-standing basic research platform, as well as a crop that supports modern societies, the maize community is ideally positioned to both make basic scientific discoveries and translate them to products that will benefit growers and consumers. Coordinated efforts between the public sector and industry to support utilization of relevant research substrates, and identify paths to collaborative translational research and development, will maximize the probability that federal research funding can provide societal benefit.

<u>Grand Challenges Addressable Using Maize as a Research Substrate.</u>

The RCN group meeting discussed the following key focus areas that should be promoted in maize research:

1. <u>Genome Structure, Evolution, and Transposon Biology</u>. Maize is an outcrossing diploid of ancient tetraploid origin. Segregating populations (landraces) have been grown for centuries by farmers and indigenous peoples. This process of domestication and selection resulted in accumulation of a rich collection of alleles, many of which were identified and selected for their impact on adaptation and morphological phenotypes. The maize genome, as with many crop genomes, is populated with a large proportion of transposable elements resulting in substantial intergenic space. Important regulatory regions that are critical for development of cultivars responsive to environmental conditions can be located far from genes and within transposable elements. Studies of chromatin, coupled with the rapidly growing arsenal of genomic tools, will help to document functional elements in the maize genome and provide insights into genome evolution and transposon biology of crop plants.

2. <u>Predictive Phenomics:</u> Predictive phenomics involves the characterization of genes and phenes controlling plant adaptation to diverse and variable environments. The growing Genome to Phenome initiative promises to support research discovery, improve plant breeding, and provide options for enhancing intervention during the growing season to protect yield potential and maximize product output. Temporal and spatial measurements of plant growth and development with high precision and frequency will provide insights into plant processes at a level of detail that was not previously possible. We discussed how research in this area can be grouped into two levels of detail and complexity: cell to plant, and plant to system.

    a. The Transparent Plant - Cell to Plant Level: At this level of detail, a goal is to understand the molecular and cellular processes that control meristem formation and development from meristems into adult plant structures. Single-cell -omics across time points, reporters and sensors to monitor plant processes, and imaging across scales from microscopic to whole organ or plant level will provide high-resolution information on the mechanisms by which gene expression orchestrates progression from germinating seed through the whole plant life cycle, including fertilization, embryogenesis and to mature seed.

    b. Predictive Phenomics in the Field: Maize plants are grown in very diverse field environments which precludes extension of the Transparent Plant concept to large-scale field studies. However, field-level experiments have the advantage that hundreds of thousands of plants can be grown and studied at many

locations, combining synergistic genetic and phenomic tools to develop predictive models of performance, and to inform plant growth models. New low-cost sensors and high-throughput imaging will facilitate measurement of plant growth and physiology throughout the season, dissecting end-of-season measurements, which result from a complex interaction of processes, into basic phenomic response with simpler genetic control. Coupled with detailed genomic information across thousands of lines, a new level of understanding of genotype by environment interactions will be achieved, predicting gene and pathway effects, and supporting improved modeling of plant adaptation to environments.

3. <u>Heterosis:</u> Heterosis underlies the amazing hybrid yields achieved by growers. Since the development of hybrid maize cultivars, the phenomenon of heterosis has captivated growers, breeders, and researchers. Heterosis was discovered in maize, and it exhibits the highest level of heterotic vigor for yield among all crops. Record yields exceeding 540 bu/ac have been reported in recent years, and inbred parents rarely yield 1/3 of this value. Yield is a highly complex trait, involving an accumulation of molecular actions directing development in the context of environmental queues and challenges. A holistic grand challenge, such as heterosis for yield (a measure of fitness and fecundity) is the sort of problem that engages and integrates disciplines from biology to engineering to mathematics. Maize remains the exemplary case study of heterosis.

4. <u>Agroecosystem Sustainability</u>. Maize is a dominant organism across the agricultural landscape. In this role, it impacts multiple processes, including soil health and water quality, ecosystem services, rural community vitality, and global industry and policy. While sometimes viewed as an ecologically challenging species, maize is among a small number of major crops that sustain humanity, and will not be easily replaced. Within the scope of the Maize Genetics Community, there are numerous aspects of biology that potentially impact the overall system. Nutrient and water acquisition and resource efficiency impact the energy balance of production and nutrient cycling. Research toward perennial maize, or production of maize in perennialized systems, can support the sustainability of maize production. Identification of new characteristics of maize can support expanded markets and profitability. Blockchain technology holds the potential to grow and market a more diverse group of products, avoiding complexities of edited or transgenic varieties unintentionally reaching the global market, and providing premiums for high-quality products. Maize basic research has substantial potential to provide the foundation to capture these new opportunities.

Technological Needs to Support Next-Generation Discovery and Translation

1. Genetic Tools. The RCN team strongly supported the need for improved genetic tools. Stocks with altered alleles form the basis of genetic research. The ideal research substrate will 1) vary only at the target locus without linkage drag or a background mutation load, 2) be altered in a genetic background(s) of interest, and 3) be immediately available to answer a research question. Populations generated by chemical or radiation-based mutagenesis, in addition to naturally occurring mutations, were the initial tools of maize geneticists. These highly efficient and cost-effective procedures produced many useful mutations. Transposon mutagenesis was the next resource that was harnessed. Transposon-tagged mutations led to cloning of the first maize genes connected to a biological function. Screenable or sequence-tagged transposon resources, such as the Pioneer Hi-Bred TUSC resource and the Uniform-Mu resource (McCarty and Meeley, 2009) or Ac-Ds populations (Vollbrecht al, 2010) have been major drivers in the maize community over the last 20 years. While chemical or transposon resources are efficient to produce, they generate random events, carry a substantial genetic load, and their use incurs a knowledge and expertise barrier for researchers from other species' communities. In addition, less than half of gene models have one effective allele among current resources, and two alleles are available for only a small proportion of all genes.

Gene editing coupled with new approaches to transformation, or using free ribonuclear protein particles (RNPs), has the potential to efficiently produce specific targeted alleles, including loss-of-function, allele replacement, and altered regulation. However, loss-of-function alleles are much easier to produce than allele replacement or mis-expression. Methods for direct CRISPR reagent delivery are being developed in animal systems, and should be tested in maize. It is possible to use genome editing to produce alleles in multiple inbred backgrounds, with minimal or no off-target changes. The cost to produce validated gene edited stocks is currently high, mainly due to high transformation costs. Improved efficiencies to the process, coupled with targeted pooling approaches is likely the most promising path to success in the short-term. "Traditional" transgenics should also not be discounted as, coupled with seed markers, it is easy to follow transgene events without molecular assays that would be required for segregating edits. One point that requires additional thought is whether editing can become efficient enough to be considered "on-demand", or if collections containing stocks edited in "all" genes should be produced. The benefit of collections of mutant lines – however they are produced – is that seed is available immediately to conduct an experiment. However, there is a large up-front investment to produce collections, *e.g.*, seed storage and renewal can be costly, and some lines may never be used. Genome-

wide CRISPR knockout collections have been produced in rice, and feasibility studies to perform similar screens in maize must be considered. However, appropriate optimization, including multiplexing of constructs and transformations, and knocking out paralogous gene pairs to optimize the chance to find phenotypes, will reduce cost while increasing utility of such collections.

There are unique stewardship concerns with edited and transgenic seed with special training and handling requirements, although some CRISPR edits may be considered non-transgenic if produced by non-integrating reagents or if the editing transgene has segregated away. Clearly, additional discussion of trade-offs and benefits, coupled with the strong need to increase the efficiency (cost and time) of transgenics and editing is needed in the very near term. Incredible advances in transformation efficiency and range of lines that can be transformed have come from advances such as the BBM-WUS systems developed by Pioneer/Corteva (Lowe et al, 2016, Mookkan et al. 2017). Use of transformation and editing systems developed by industry may be accompanied by stewardship agreements and/or licensing terms that can be difficult for individual researchers to complete. Novel systems of access, coupled with continued development of publicly accessible technologies will be needed for the research community to make a step-change in research.

In addition to the process of producing genetic tools, the genetic background in which those tools are developed is highly impactful for translation. Modern breeding has produced high-performing inbreds and hybrids that overcome the deficiencies of older and less-selected materials. A genetic alteration that will have a strong positive effect in one genetic context will not necessarily have the same effect in modern hybrids. On the other hand, a good allele is defined, in a relative context, to a bad allele. Germplasm containing undesirable alleles may allow us to define gene function and biological pathways and networks, even if that function does not immediately result in a new product. Insights into the genetic and epigenetic chromatin level variation that can explain the differences between different inbreds and hybrids can arise from genomic and epigenomic profiling techniques that are becoming cheaper with the reduction in Next Gen sequencing costs. Cooperation of industry and the public sector should also be promoted, in order to make advanced inbreds available to support translational research. This will be important in maintaining the relevance of the research community, and maximizing the proportion of federally supported discoveries that are translated into products. Increasing the diversity of fully sequenced maize inbreds, particularly targeting tropical inbreds, will create germplasm and genomic resources that will enable and connect global research. At the same time, discovery from random, blue sky research can be quite impactful, and a balance

should be struck between coordinating and synergizing research while still supporting *ad hoc* discovery projects.

2. <u>Phenotyping</u>. It is widely recognized that the benefits of the genome revolution can be more fully realized by improving our ability to measure, record, and interpret attributes of organisms. Wearable devices to monitor biological attributes in humans are revolutionizing human health, and coupled with genome information, are supporting development of personalized medicine. Increasing information about crops has a similar potential to not only gain an in-depth biological understanding in maize but also match cultivars with micro-environments, enabling timely interventions to maximize and protect productivity and quality, and will alter yield prediction and marketing of crops.

The Iowa Corn Growers Association together with the National Corn Growers Association and a team of public researchers have spearheaded a campaign to fund an agricultural Genome to Phenome initiative (genomes2fields.org). This is the same seminal group that advanced the National Plant Genome Initiative, which ultimately funded the NSF Plant Genome Research Program and spurred funding across agencies. The goal of the current Genome to Phenome project is to have the same transformational effect on research funding, with an additional goal of promoting translational research, providing benefit to growers and consumers.

Development of new phenotyping tools is paramount to achieving this new vision. Large-scale expensive infrastructure will play a role in providing ground-truth information and setting research standards. But low-cost flexible solutions that can be broadly deployed, will enable the broader community to access and benefit from high-throughput phenotyping and will allow sampling broadly across individual plants and environments.

The scale of phenotyping advances can be from sub-cellular to field, and even region level. Ultra-high throughput single cell assays, coupled with novel molecular probes, can revolutionize research in multiple biochemical processes, including signaling and metabolism. Such assays have revolutionized research in mammalian systems, and their development should be encouraged in maize, where efficient protoplast transformation systems already exist. Single cell mRNA sequencing and other 'omics approaches are now commonplace in other systems, and should be promoted in maize research, as they can help in understanding the fundamental developmental and physiological pathways that drive maize growth and productivity, as well as their regulation at multiple levels including transcriptional and chromatin based. Communication among cells, regulatory cascades, and gradients of proteins, RNAs and metabolites are also critical in

organizing cellular processes in complex organisms. Measuring and monitoring gene expression proteins and chromatin states at the multi-cell scale is critical to understand these dynamic processes. At the whole plant level, response to environmental cues and developmental programs can be monitored by imaging devices and sensors on an organ to plant to field scale. Imaging devices and sensors deployed on rovers, drones, planes, and satellites, coupled with detailed measurements of environments and microenvironments, will provide plant information on an unprecedented depth and scale. The Maize Genetics Community must play a central role in this rapidly developing research area.

Databases and Computation

The genomics, phenomics, and technologies highlighted above are all highly data intensive, and terms like networks and interactions highlight the need for advanced computational approaches to support these projects.

1. Databases.
    a. Capturing Data. The first critical step in utilizing big data sets is that the data are systematically captured using consistent controlled ontologies, safely stored and readily accessible, and accompanied by sufficient metadata to ensure usability. The ability to produce high-quality, integrated large datasets is facilitated by large multi-investigator projects with dedicated database support personnel and centralized goals. This funding mechanism is not necessarily optimal for all aspects of the scientific enterprise, but it provides the clearest path to useful, integrated big datasets. Given the breadth of funding sources and project sizes, coordination of data collection across researchers within a country, and ideally globally, would synergize the research enterprise. In addition to availability of data, access to germplasm connected to the datasets would also be enabling, and is expected when publishing in most scientific journals.

    b. Data Analysis and Visualization. Gathering data is the first step in enabling research. Turning data into useful information and research outcomes requires expertise, including computer programming and harnessing available analysis tools. Training current and next generation scientists is critical in the near-term, and should be prioritized in graduate curricula and supported by connections among diverse researchers. There is value in generating tools and visualizations, but caution must be exercised, as the details that underlie simplified and consolidated data summaries are important in correctly interpreting outcomes.

c. Immediate Priority: Pan-genome integration and annotation. An immediate high priority data integration activity is annotation of the maize pan-genome. Multiple genomes representing substantial diversity in maize have been sequenced and assembled, and others are in process. For basic reasons, including coordinating and communicating results, it is critical that genes be systematically named and connected between genomes. High quality genome annotation is also of utmost priority. Annotation includes both identifying correct transcription initiation, termination, and splice sites, in addition to providing current experimentally validated and/or predicted information on function. Updating functional annotations, using computational methods to incorporate ongoing research across biology, is a daunting but critical task. Researchers must also better understand the limitations of computationally-based functional annotation. Experimentally-based evidence of function will be supported by Technological Priority Areas 1 and 2 above – systematically generating altered plants and phenotyping them in high detail.

Community Building and Training

Substantial discussion at the mid-year conference related to expanding and diversifying the community. The scope of our current community is Maize Genetics. This has evolved over time to include – with peaks and valleys – transmission genetics, developmental genetics, cytogenetics, molecular genetics, genomics, quantitative genetics/breeding, evolutionary genetics, and other areas. There was strong support for broadening the community related to gender balance, underrepresented minorities, industry and academia, small college (Primarily Undergraduate Institutions, PUI) participants, and international scientists and strategies for increasing recruitment in these areas were discussed and several ideas will be piloted at the Maize Genetics Conference this year. There was less consensus in terms of desirable disciplinary broadening of the community. A central focus of the Maize Genetics Community has always been on maize, with some connections to "allied species" such as sorghum and oats. Genome sequencing and resurgence of some crops raises the question of whether communities working on other species, with sorghum being the next closely related, should be considered as partners. It was also clearly recognized that a variety of disciplines, including plant physiology, crop modelling, engineering, mathematics, and others are highly valuable in advancing genetic research objectives, and these connections are also valued by funding agencies. While the value of these connections was recognized, concern was raised that substantial diversification would diminish the current community focus of maize genetics, and could result in undesirable changes to the format and size of our annual meeting. Additional discussion is needed to determine how to maintain the

positive "family" aspect of the current community, while supporting disciplinary inclusion and stimulating synergies.

There has also been discussion within the Maize Genetics Executive Committee (MGEC) and at the mid-year conference regarding organization of the Maize Genetics Community. Currently, the MGEC is elected by a community defined by whoever is on an email listserv. The listserv is populated by attendance, or by request of a person or on behalf of a person to be added to the list. There is no formal membership and no process of screening "applicants" for relevance to the community. The primary charge of MGEC is to organize and communicate needs to funding agencies, and this activity is largely aimed at U.S. funding agencies. The MGEC does not have a budget or any monetary authority. The MGEC has recently taken on a role of organizing and choosing winners of maize community awards. A separate group, the Maize Genetics Conference Steering Committee (MGCSC), is a self-perpetuating volunteer committee with the primary charge of organizing the yearly Maize Genetics Conference. There is a representative of the MGEC to MGCSC, but formal connections and hierarchy of the two groups should be established and documented by MGEC. The community is not otherwise formalized or incorporated, but it may be necessary to take this step to address liability and fiduciary issues. In terms of monetary issues, the conferences have been recently organized by the University of Missouri Conference Center, and carry-over funds from conferences are maintained in an account at the University of Missouri.

The possibility of adding virtual and online participation to the Maize Genetics Conference was discussed as a way to increase international attendance. Many maize community members do not have the possibility of traveling internationally to attend the Conference due to financial or visa constraints. Live streaming presentations, uploading posters to the conference website, and web-based conferencing, from individual participant's computers or a regional hub, would maximize information exchange and collaborative opportunities. Mechanisms to prevent the Maize Genetics Conference from losing in-person participants can be put in place. A registration fee for virtual attendance could offset costs of the hardware and software needs of such an interactive, online system. Further development of databases of Maize Genetics Community members, including research interests, needs, and capabilities, may facilitate future collaborations between researchers from different countries. Discussion was also raised about international funding, for example at MaizeGDB, where close to half of all current users are from China.

Given the current growing concerns related to professional ethics and professional behavior, in addition to concerns about properly assigning fiduciary responsibility of the community, there was initial discussion about whether the community would benefit from either formally incorporating, or conducting some components of activities under the

umbrella of an organized society. Examples include ACSESS, the Alliance of Crop, Soil, and Environmental Science Societies, which is the oversight organization of the American Society of Agronomy, Crop Science Society of America, Soil Science Society of America that also supports some activities for partner societies; or ASPB, the American Society of Plant Biologists. There are some immediate reasons that this formality should be at least partially addressed in the near future. First, if a complaint is filed, or an incident occurs at the yearly conference or during an activity within the context of the Maize Genetics Community, issues of liability and path to resolution are currently unclear. Second, there has been a desire to codify ethical and professional expectations for the community and its leadership. In the absence of a formalized membership, it is unclear if MGEC or MGCSC is empowered to make such a proclamation and what the implications would be for community members if it were in place. As societies and communities evolve in the context of global research trends in publication, communicating science via conferences and other methods, and diversification of research enterprises, it should be a high priority for the maize community to address organizational structures that will enable its effectiveness moving forward.

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Appendix A: Meeting Agenda

Maize 2018 mid-Year Conference Agenda
The Edgewater Hotel
Madison, WI

Begin: September 19, 2018: 5:00 p.m.
Adjourn: September 21, 2018: Noon

Outcomes:
1. Initiate RCN Priority Theme Activities
    a. Draft plan of activities to strengthen annual meeting including topical focus by year, and to deliberately broaden the community
    b. development of subcommittees and networks to address community needs in five priority areas.

2. Topical Focus: Functional Genomics Tools and Resources
    a. Produce white paper on functional genomic tools and resource needs to enable maize research in the next 20 years.

Day 1: Wednesday September 19, 2018

Optional:	Tour of WCIC, presentations, maize transformation discussion
1:00 – 3:00	Depart The Edgewater (time will be determined by # of participants)
4:00	Return to The Edgewater
5:00 to 6:00	Dinner (hot/cold hors d'oeuvres, coffee, tea, water)
6:00 to 6:30	US/World Maize Production and Needs/Challenges: <u>Presenter – David Ertl</u>
6:30 to 7:00	Future Role of Scientific Societies and Collaboratives: <u>Presenter – Shawn Kaeppler</u>
7:00 to 7:30	Paths to Impact – Technology Transfer and Discovery to Product: <u>Presenter – Pat Schnable</u>
7:30 to 8:30	Group Visioning Session I – Defining our Context
8:30 to 9:30	Subgroup breakout meetings
9:30	Social (local pub in hotel)

Day 2: Thursday September 20, 2018

7:00 to 8:00   Breakfast (pastries, muffin, bagel, fruit, coffee, water, tea, soda)

Functional Genomics Tools Theme area

8:00 to 8:30   Introduction and Goals <u>Presenter – David Jackson</u>

8:30 to 9:00   Overview of Maize Functional Genomics Research including EMS and Transposon Resources: <u>Presenter – Nathan Springer</u>

9:00 to 10:00   Maize Transformation: <u>Presenters – Kan Wang, Heidi Kaeppler, Bill Gordon-Kamm</u>

10:00 to 10:15   Break

10:15 to 10:55   Gene Editing: <u>Presenters – Bing Yang, Feng Zhang</u>

10:55 to 11:35   Free DNA transformation and RNP/Nanoparticles: <u>Presenters – Mark Cigan, Krishanu Saha</u>

11:35 to 12:00   Uses of transgenes in maize research: <u>Presenter – David Jackson</u>

12:00 to 1:00   Lunch (buffet outside meeting room)

1:00 to 1:40   Epigenome: <u>Presenters – Bob Schmitz/Nathan Springer</u>

1:40 to 3:00   Functional Genomics Visioning Session I – Defining Opportunities and Needs

RCN Team Updates

3:00 to 3:30   Training and Student Recruitment Team: <u>Presenter – Mark Lubkowitz</u>

3:30 to 4:00   Informatics Tools, Resources, and Services Team: <u>Presenter – Ed Buckle</u>r

4:00 to 4:30   Industry Interface Team: <u>Presenter – Paul Chomet</u>

4:30 to 5:00   Envisioning a Broader Community: <u>Presenter – Marilyn Warburton</u>

6:00 to 7:00   Dinner (Wine Room---same room as Wednesday evening meeting)

7:00   Group Visioning Session II – Prioritizing Community Issues and Opportunities and Defining Desired Outcomes

8:30   Social and Discussion

Day 3: Friday September 21, 2018

7:00 to 8:00   Breakfast (pastries, muffin, bagel, fruit, coffee, water, tea, soda)

8:00 to 8:30   Utilizing Natural Variation: Presenter – Ed Buckler

8:30 to 9:00   Maize Breeding and Quantitative Genetics: Presenter – Natalia de Leon

Supporting Functional Genomics Research
9:00 to 9:20   Databases and Data Management: Presenter – Carson Andorf

9:20 to 9:40   Infrastructure: Germplasm Centers: Presenter – Marty Sachs

9:40 to 10:00   Centralized and Distributed Components of Research Pipeline:
                     Presenter – Shawn Kaeppler

10:00 to 10:15   Refreshment Break

10:15 to 10:45   Single Cell Methods: Presenter – Mike Scanlon

10:45 to 11:15   Omics and Networks: Presenter – Andrea Eveland

11:15 – 12:00   Functional Genomics Visioning Session II – Imagining Tools and Resources
                     to Support Scientific Discovery

12:00   Meeting adjourns