The idea: Integrated, Accessible Knowledge Platform for Accelerating Plant Breeding in Africa

There is an urgent need for rapid increase in the robustness and productivity of crops. The need is especially urgent in developing regions that are facing the greatest needs, yet seriously lack access to the infrastructure needed to achieve rapid improvements. As a result, current crops are often not optimized for local needs. **Our aim is to develop and deploy an accessible, cutting-edge plant measurement and big data analytics platform to accelerate plant breeding for the specific conditions found in developing countries. The platform will guide users to design optimized field trials and automatically gather and analyze the results to rapidly identify quantitative trait loci (genetic components) that can guide plant breeders to make improved varieties.** The project will take advantage of our PhotosynQ platform (www.photosynq.org), and the MultispeQ plant instrument, breakthrough technologies that are already providing access to sophisticated plant phenotyping and analytical tools to hundreds of users around the world. We will integrate into this platform new analytical and experimental tools to optimize field trials, rapidly collect integrated data sets, and use this large database to rapidly map quantitative trait loci (QTL), i.e. genetic components that control plant performance. Successful identification of these QTLs is a critical towards step in modern plant breeding approaches. The platform will be demonstrated in a collaborative pilot project that will immediately benefit ongoing research on cowpea in Nigeria, and test the hypothesis that the new tools can significantly accelerate the discovery of genes, and ultimately lead to accelerated improvement of cowpea varieties. To our knowledge, this will be the first platform to have these integrated capabilities, and if successful, will effectively allow its users to leapfrog bottlenecks in the current technology.

Proposed Project: Our pilot project focused on using the platform to identify critical genetic traits that could improve the drought resistance of cowpea, an important crop in Nigeria, constituting both critical sources of protein and income. Currently, cowpea production is constrained by its low inherent photosynthetic efficiency which is highly sensitive to abiotic and biotic stresses, including diseases, pests, low soil fertility, heat and drought. However, cowpea also has great genetic potential, and with the appropriate tools, it should be possible to generate improved cowpea varieties. The proposed project will combine the strengths in cowpea breeding and genetics by the groups of Dr. Ousmane Boukar at International Institute of Tropical Agriculture (IITA), which is located in Nigeria, the largest producer of cowpea, and Drs. Philip Roberts and Bao Lam Huynh at UC Riverside, and plant phenotyping and analytical platforms developed in the lab of Drs. David Kramer and Dan TerAvest at Michigan State University. Our collective preliminary work has shown that 1) identified mapping populations of cowpea with large diversity responses to drought and other stresses; 2) the PhotosynQ platform and MultispeQ instrument can sensitively detect these differences; 3) the resulting data can, when appropriately analyzed, generate high resolution QTL maps. We have also developed a series of PhotosynQ-linked analytics programs and thus we have confidence in the feasibility of the project.

Implementation: The project can move very rapidly because it will take advantage of the existing PhotosynQ and MultispeQ platforms, which already provide openly-accessible, inexpensive yet sophisticated plant phenotyping instruments and informatics pipelines. In addition, we will integrate our efforts into ongoing field experiments at IITA sites, allowing work to begin immediately and keeping the costs low.

The platform development at MSU will focus on integrating and refining existing open source QTL mapping applications with PhotosynQ to work seamlessly and automatically, allowing even beginners to map loci, while allowing more experienced users to rapidly test and assess different analytical procedures to determine the most sensitive indicators of plant status and crop yield. It will also optimize analyses to obtain the highest resolution QTL mapping and provide rapid feedback to users so they can optimize their trials on the fly. The MSU group will deploy PhotosynQ instruments to IITA partner groups and provide user training, both over the internet and in person.

The field trials in Nigeria will focus on identifying QTLs related to efficient and robust cowpea productivity. Cowpea is grown in several distinct agroecological zones in Nigeria, and deploying the new platform to these regions offers the opportunity to determine if a single elite variety of cowpea can be developed for all regions or if it is more effective to develop separate varieties for each region. For instance, we may find common QTLs from experiments from all field locations, indicating strong genetic targets for genetic improvement. Alternatively, it may be that distinct genetic loci are important under different environments, indicating that site-optimized varieties are needed.

The UC Riverside group will supply seed stocks for the IITA experiments and help analyze and interpret the results. Preliminary work has determined conditions and mapping populations, including a multi-parent advanced generation intercross (MAGIC) and three biparental recombinant inbred line (RIL) populations, are best suited for QTL mapping of photosynthetic responses to drought and heat. These panels will be grown in 3-5 research or farm locations, under drought and watered field conditions at IITA. Plants will be assayed at multiple growth stages using the MultispeQ device and for key phenotypes (photosynthesis, water use efficiency, growth, pigmentation canopy architecture). The final biomass and grain yields will be measured and uploaded to PhotosynQ. These results will be analyzed using both the existing QTL mapping software and the new integrated platform. From our experience in dealing with complex field data from PhotosynQ projects, we expect to find that combining information from multiple parameters will greatly enhance the power of the approach, and one important outcome will be the identification of sets of parameters and conditions that provide the most powerful discrimination of plant performance.

Based on our past experience, we expect the development aims to take 3-4 months of time from our programmer, and cost approximately $30,000. The field pilot projects will require funds to support salaries two technicians at IITA, cover travel costs to field sites and provide MultispeQ instruments, computers and internet access at a cost of approximat0ly $40,000. The production of pure seed stocks and genetic analyses at UC Riverside will require approximately $20,000. The remaining $10,000 will cover the travel costs for in-person training and coordination meetings between U.S. and IITA participants in Nigeria.

The major outcomes will include the integrated PhotosynQ-QTL-breeding-platform, together with assessments of the platform and methodologies for identifying QTLs, as well as the identification of cowpea QTLs that can be used to guide subsequent plant breeding efforts. If successful, subsequent phases will focus on developing the tools to use these data to optimize the breeding of new varieties. We will make the platform, tools and methods accessible and easy to use through the PhotosynQ platform, so that they can be deployed and operated to a broader community around the world.