TITLE: COMMERCIALIZATION OF AN INEXPENSIVE, MODULAR, ROBOTIC PLANT PHENOTYPING PLATFORM

Team Members (alphabetical order)

Max Feldman Ph.D (Entrepreneurial Lead)
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Dr. Feldman, a postdoc in Dr. Ivan Baxter's lab at Donald Danforth Plant Science Center, has successfully designed and prototyped a scalable robotic phenotyping module by leveraging funds from the Donald Danforth Plant Science Center's "Maker - Internal Equipment Funds" competitive grant program and establishing a collaboration with the Washington University in St. Louis Mechanical Engineering Department through supervision of a Capstone Design Project. He possesses appreciable experience constructing parallelizable computational pipelines to automate extraction of plant traits from multiple sensor types using computer vision[1] and mapping of quantitative trait loci (QTL) in high-throughput phenomics studies[2]. Additionally, he completed an eight-week Entrepreneurial Training Workshop offered by the University of Missouri – St. Louis in 2015.

Christopher Topp Ph.D (Principal Investigator)
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Dr. Topp is a Principal Investigator/Assistant Member at the Donald Danforth Plant Science Center who has been previously awarded an USDA-NIFA Postdoctoral Fellowship to develop multidimensional imaging platform to analyze root system dynamics in response to changing environments (Grant No. 2011-67012-30773). His experience collaborating with mechanical engineers, computer scientists and other plant biologists to develop this platform have led to important biological discoveries[3] and development of novel methods to extract biological meaning from complex multidimensional phenotypic datasets[4]. He currently supervises/mentors a research group composed of graduate students, scientific technicians and postdocs focused on understanding the functional basis and identifying genetic components associated with root system architecture in crop plants.

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Dr. Wang possesses extensive experience performing plant genetics research in both an academic setting as a postdoc in Detlef Weigel's group[5–8] and transitioning technologies developed in Dr. Weigel's lab into the commercial sector. Most recently, Dr. Wang served in the role of President of Computomics USA where he commercialized both a stationary phenomics platform and consultant based services assisting customers with interpretation of genomic sequencing data to answer biological questions. His experience in handling the business aspects of running a private company and handling the backend data storage/management required for our innovation will be extremely valuable for this project. Discussions between him and Feldman (Entrepreneurial Lead) initiated earlier in 2017 have been paramount for identifying significant challenges on the path towards commercialization of this invention.

Relevant current/previous NIFA awards
Award number (Grant No.): 2011-67012-30773

Title of the Project: A Multidimensional Imaging Platform to Analyze Crop Root System Dynamics in Response to Changing Environments

NIFA program name: Post Doctoral Fellowships

NIFA program area name: Agriculture and Food Research Initiative

Brief description of the potential commercial impact

Feldman (Entrepreneurial Lead) has invented a plant phenotyping instrument (optimal hardware configuration) that provides scientists and educators with the ability to simulate natural or artificial environments while simultaneously collecting data on plant performance in large genetically structured populations. This utility is important for many parties engaged in plant science research and education. As a research tool, this innovation enables scientists to maintain consistent soil moisture levels across experimental treatment blocks and quantify plant (plant size, transpiration) and environmental variables (temperature, humidity, irradiance and CO_2 concentrations) at hourly intervals. Such measurements are critical for investigating the genetic basis of ecophysiological plant traits and predicting plant performance across multiple environments.

The modular nature and simplicity of our design ensures that hardware costs will be dramatically lower than other commercial solutions currently available in the marketplace (also potentially more mechanically robust) and is designed to be compatible with greenhouse and growth chamber infrastructure currently in place at most academic institutions and private companies. From a research perspective, our design greatly enhances the temporal resolution of data collection and allows scientists to easily exchange hardware components enabling use of different plant imaging sensors and providing the flexibility to conduct experiments on species that require different pot sizes. By selling our instrument in modular units, customers can scale their research programs to experimentally study dozens-to-thousands of plants easily without having to invest in expensive customized solutions. This flexibility has the added benefit of enabling Principal Investigators to initiate multiple exploratory, confirmatory or genetic fine-mapping without the set up and take down of new experiments interfering with experiments already underway.

Utilization of this tool in combination with the computational resources developed by Feldman and Topp have the potential to add tremendous value to the undergraduate educational curriculum. By automating many of the laborious tasks that prevent such studies from being performed in undergraduate lab courses students can assist in setting up, conducting and analyzing data from publication quality plant phenomics experiments. This has the benefit of introducing students to simple programming tasks, data visualization, and statistics, in addition to more advanced topics in plant physiology and quantitative genetics.

Brief description of the current commercialization plans for the innovation

Funds awarded through the I-FAST Prize Competition will be used to contract a mechanical engineering firm to finalize a production quality prototype and perform market research to estimate consumer demand and market price point. The production quality prototype will undergo tests to examine the robustness of the mechanical and software design with the goal of obtaining >95% uptime in a typical application environment. Once these objectives have been achieved we will file a utility patent to protect this intellectual property.

After a provisional patent has been issued we will assess options for licensing our design to an established hardware manufacturer or form a new company to manufacture, deliver and setup this instrument for customers. Customers will be identified through our existing network of scientific collaborators in addition to the identification of new customers through interactions at major scientific conferences and industry tradeshows.

References

1. Fahlgren, N. *et al.* A Versatile Phenotyping System and Analytics Platform Reveals Diverse Temporal Responses to Water Availability in Setaria. *Mol. Plant* **8,** 1520–1535 (2015).
2. Feldman, M. J. *et al.* Time dependent genetic analysis links field and controlled environment phenotypes in the model C4 grass Setaria. *PLOS Genet.* **13,** e1006841 (2017).
3. Topp, C. N. *et al.* 3D phenotyping and quantitative trait locus mapping identify core regions of the rice genome controlling root architecture. *Proc. Natl. Acad. Sci.* **110,** E1695–E1704 (2013).
4. Li, M. *et al.* Persistent homology: a tool to universally measure plant morphologies across organs and scales. (2017). doi:10.1101/104141
5. Wang, G. & Dillon, M. E. Recent geographic convergence in diurnal and annual temperature cycling flattens global thermal profiles. *Nat. Clim. Change* **4,** 988–992 (2014).
6. Hagmann, J. *et al.* Century-scale Methylome Stability in a Recently Diverged Arabidopsis thaliana Lineage. *PLoS Genet.* **11,** e1004920 (2015).
7. Smith, L. M. *et al.* Rapid divergence and high diversity of miRNAs and miRNA targets in the Camelineae. *Plant J.* **81,** 597–610 (2015).
8. Liu, C. *et al.* Genome-wide analysis of chromatin packing in *Arabidopsis thaliana* at single-gene resolution. *Genome Res.* **26,** 1057–1068 (2016).