

Project #: 126593

Progress Report Year: 3 of 3 years (maximum of 3 year funding cycle)

Title: Intelligent Prediction and Association Tool to Facilitate Wheat Breeding

PI: Dr. Zhiwu Zhang

Cooperators: Dr. Michael Pumphrey, Dr. Arron H. Carter, and Dr. Kimberly Campbell

Executive summary: *We released one software package and published two articles in this fiscal year. The software package is named as the name of our project: iPat (integrated Prediction and Association Tool). This is a user friendly software for breeders and genetic researchers to map genes and conduct molecular breeding. Its manuscript has been published recently by bioinformatics leading journal, Bioinformatics. iPat has two major features. One is graphic user interface. Breeders can simplify use any computer pointing device to drag their datasets into the interface and then click on the graphical icons for analyses. With data analyzed by this software, we published a article on Plant Genome. The other feature is it is upgraded easily for internal engines. Currently, iPat's internal engines include GAPIT, FarmCPU and BLINK. FarmCPU is ten time faster than GAPIT and BLINK is ten time faster than FarmCPU. We applied a data size restriction to the public version of BLINK, but gave WSU/USDA-ARS breeders the advantage of assembling any size dataset from all available genotypic and phenotypic data. Our manuscript describing BLINK is currently under review for publication. We also publish an article on Wheat Life entitled "Genomics tools turncharge classical breeding".*

Impact: *Our collabrative research positions WSU/USDA-ARS research team as one of the the world's leading institutions to conduct fundamental and applied research, publish academic articles, and update and release software packages. Our project's success not only benefit Washington, but will also benefit the entire world through the dissemination of knowledge. In short term, breeders can conduct most of data analyses without frustration on data formating and selecting different analytical functions. They have more oppertunities to find the casative genes controlling traits of interest. They have more confidence to eliminate lines with low genetic potentials to reduce the cost of field trials. In long term, breeders have more chances to retain the genetic lines with desirable genes, and recombine them to create superior varieties.*

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Project PI(s): *Zhiwu Zhang, Michael Pumphrey, Arron H. Carter, and Kimberly Campbell*

Project initiation date: 1-Jul-15

Project year: 3 of 3

Objective	Deliverable	Progress	Timeline	Communication
3) Integrate IPAT with Agrobase	iPat was released and the paper was published on Bioinformatics leading journal: Bioinformatics	Advanced data management system has been identified, HDF5 to manage big data collected from fields across multiple years and location, as well sequencing data from molecular labs. HDF5 was used by NASA for data management.	December 31, 2017: Develop source code on elementary functions; June 30, 2018: Complete system testing on real data from all the Co-Pis	1) One article was published on Wheat Life; 2) One presentation was given at WGC annual meeting; 3) Two presentations were given at national/international conference; and 4) Two papers were published on academic journal