

**Project #: 126593**

**Progress Report Year:** *1 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 update two software package and published two articles partially under support of this project in this fiscal year. The two software package are GAPIT (Genome Association and Prediction Integrated Tool) and iPat (integrated Prediction and Association Tool). Both of the packages can be used to conduct GWAS (Genome Wide Association Study) and GS (Genomic Selection). GAPIT is R Package for users with programming skills in R language. Analyses can be programmed to process large amount of analyses with same settings. iPat has 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. Bot of these packages implemented the two new methods we published in 2018 by Wang and et al. (Heredity, 121, 648–662). We also publish an article on Wheat Life in November of 2018 entitled “Empowering breeders for success”.*

**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-18

Project year: 1 of 3

<b>Objective</b>	<b>Deliverable</b>	<b>Progress</b>	<b>Timeline</b>	<b>Communication</b>
1) Develop a sophisticated, single-step method that combines MAS and GS to boost prediction accuracy	Two peer reviewed paper was published (Wang and Et. Al., <i>Heredity</i> , 121, 648–662, 2018; and Chen and Zhang, <i>Bioinformatics</i> , Volume 34, Issue 11, 1 June 2018, Pages 1925–1927). The paper describes two newly developed methods which have been implemented in GAPIT and iPat.	The manuscript is in progress for implementation of the methods to combine GWAS (genome wide association study) and GS (genomic selection).	December 31, 2018: investigate multiple variable linear regression methods. Published one peer reviewed paper; June 30, 2019: published one peer reviewed paper to describe methods to combine GWAS (genome wide association study) and GS (genomic selection).	1) One article published bt <i>Wheat Life</i> (November 2018); 2) One presentation to WGC meeting; 3) One presentation at international conference of plant and animal genome; and 4) two papers on academic journal (Wang and et. Al., <i>Heredity</i> , 121, 648–662, 2018; and Chen and Zhang, <i>Bioinformatics</i> , Volume 34, Issue 11, 1 June 2018, Pages 1925–1927).