

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 updated one software package, released a new software package, and published one article partially under support of this project in this fiscal year. The GAPIT software package updated for new functions for both GWAS (Genome Wide Association Study) and GS (Genomic Selection) (<http://zzlab.net/GAPIT>). 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. The new software package is MMAP (<http://zzlab.net/MMAP>). The manuscript of update GAPIT (version 3) is under review by Genomics, Proteomics and Bioinformatics. The manuscript is released to public b [preprint](#). The MMAP was published by [Bioinformatics](#).*

Impact: *Our collaborative 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 formatting and selecting different analytical functions. They have more oppertunities to find the causative 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: 3 of 3

Objective	Deliverable	Progress	Timeline	Communication
3) Develop a web-driven molecular breeding pipeline to enable breeders to conduct analyses and make decisions anywhere with internet access.	New tools named MMAP with integration of web based data and calculation through internet access.	We have developed iPat under previous WGC support. The software has graphic user interface and ability to use third-party packages as internal engines for data analyses. The functions of iPat will be transformed into web based software.	December 31, 2020: Functions have been developed ; June 30, 2021: Complete system testing on real data from all the Co-PIs.	1) One presentation at WGC annual meeting; 2) One presentation at International Conference of Plant and Animal Genome; and 3) one paper was published by Bioinformatics for MMAP.