PI: Jean-Luc Jannink	**PI's E-mail:** jeanluc.jannink@usda.gov
Project ID: FY20-DI-003	**ARS Agreement #:** *N/A*
Research Category: EC-HQ	**Duration of Award:** 1 Year
Project Title: US Wheat & Barley Scab Initiative's Networking & Facilitation Office and Website	

PROJECT 1 ABSTRACT
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This project is in support of the USWBSI's Networking & Facilitation Office (NFO). The NFO has been working on the development of a web-based database containing public sector breeding data, facilitating collaboration and data-sharing across programs since FY10. This database is called The Triticeae Toolbox (T3). The development is now largely complete and we are at the stage where historical data from the various breeding programs and scab nurseries needs to be uploaded to the database. To assist with this process, the NFO will utilize 10% of a curator's time. A Research Support Specialist I (RSS) will do this work under the direction of Dr. Jean-Luc Jannink. Funding for this project will pay 10% of the RSS annual salary for one year as curator/gatekeeper to facilitate uploading and troubleshooting of wheat and barley data from USWBSI public breeding programs to T3.

PI: Jean-Luc Jannink	**PI's E-mail:** jeanluc.jannink@usda.gov
Project ID: FY20-BA-012	**ARS Agreement #:** *N/A*
Research Category: BAR-CP	**Duration of Award:** 1 Year
Project Title: Optimizing Parent Combinations to Improve FHB/DON Resistance in Barley	

PROJECT 2 ABSTRACT
(1 Page Limit)

We will use funding to expand an analysis tool on T3 to suggest crosses to breeders. The current genomic selection tool in T3 allow a user to select the trials that will form the training population, and the genotypes to be predicted. The tool proceeds to make the desired predictions. To this tool, we will add the possibility of specifying a set of individuals to be used as parents. The tool output will then be a list of possible crosses among the parents, ranked according to their superior progeny mean. To maximize gain despite negative correlations between desirable traits, the user will be able to input selection index weights for multiple traits, and the tool will output crosses ranked by superior progeny mean for the index. The analyses will be accomplished by using deterministic estimates of progeny variance