

## 2018 BIOAg Final Report

**Title:** Rapid Evaluation of Winter Wheat Residue Decomposition Potential

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**Key words:** wheat straw, fiber analysis, near infrared spectroscopy, residue decomposition

**Abstract:** Managing crop residue is essential to conservation farming systems that enhance soil quality and reduce soil erosion. Growers, and the seed dealers they work with, regularly request information on residue decomposition of winter wheat cultivars, but none is currently available. Previous analysis of winter wheat residue has shown that hard and soft cultivars differ significantly in their neutral detergent fiber, acid detergent fiber, acid detergent lignin, carbon (C), nitrogen (N), C/N ratio, and near infrared spectroscopy (NIR) readings, and that many can be categorized as having characteristics for either “rapid” or “slow” residue decomposition. A recombinant inbred line (RIL) population between Finch (slow breakdown) and Eltan (fast breakdown) and a diversity panel of 480 lines was grown under field conditions at Spillman Farm, Pullman, WA and Mansfield, WA, in 2015, 2016, and 2017. Residue was collected at harvest, scanned using NIR, and validated using traditional forage fiber, carbon and nitrogen analyses. Populations were genotyped using the 9K and 90K Infinium wheat SNP chip. Significant QTL were found on chromosomes 1A, 1D, 3B, 4A, 5A, 6B, and 7D and are associated with the different traits tested. None of the QTL were consistent across locations or traits, and most only accounted for 2-6% of the phenotypic variation. NIR prediction models were only moderately correlated to trait values, attributed to the narrow genetic divergence between the two parents used. The diversity panel should have enough genetic diversity present to develop better NIR prediction models, although these analyses are still under development and not proven yet. A genetic analysis of the 2016 data from the diversity panel shows a similar genetic story as the RIL population showed. Significant marker-trait associations were identified, yet again most were minor QTL which did not span traits or environments. The genetic composition of straw breakdown traits is complex, and highly influenced by the environment. It is unlikely that a marker-assisted selection program could be used to select new cultivars based on breakdown potential. NIR prediction appears to have promise as a high-throughput method of estimating straw breakdown potential in wheat.

**Project Description:** This project is focused on developing a NIR prediction model to evaluate and predict the ability of wheat straw residue to decompose under field conditions. Many areas of Washington State practice conservation farming systems in order to enhance soil quality and reduce soil erosion. In many counties with less than 12 inches of annual precipitation, a wheat-summer fallow rotation is used to conserve moisture. This farming practice leads to high amounts of soil erosion due mainly to wind events. Having a cultivar which has a slow straw breakdown would be beneficial to these growers. Not only would it

help reduce soil erosion by wind, but would also help trap more moisture in the soil. In locations where annual rainfall exceeds 18 inches, many growers are altering their production systems to prevent soil erosion from rainfall. Furthermore, these conservation systems are also leading to improved soil health, mainly through the reduction of tillage practices. The reduction of tillage has slowed the decomposition of wheat straw residue from the previous winter wheat crop. As a result, when growers try to direct seed into the winter wheat stubble in the spring, it can oftentimes be difficult due to the high amount of residual residue. Growers are searching for cultivars with residue which has a rapid decomposition. With the need for cultivars which have both rapid and slow decomposing residue, many growers are eager to use residue decomposition as a criterion for cultivar selection. Unfortunately, there is very little information available for this trait. The objective of this research was to develop a predictive NIR calibration to screen breeding material in order to select cultivars with rapid and slow residue decomposition. A large panel of 480 lines was grown in two locations. Data will be collected on fiber characteristics using wet chemistry methods as well as NIR. NIR calibration models will be developed to allow rapid evaluation of this trait, as the wet chemistry method is laborious and time-consuming. Once completed, the NIR prediction method will become routine in the WSU winter wheat breeding program to evaluate germplasm for this trait. The ultimate goal is to release cultivars which can be adopted into different conservation farming systems in order to meet production goals, ensure sustainability, and increase economic return to the growers.

## **Outputs**

**Work Completed and in Progress; Methods and Results:** We have two different populations that are being used for this research. The first population is a bi-parental recombinant inbred line (RIL) population with Finch and Eltan as the parents. Previous work identified Finch as a slow residue breakdown line whereas Eltan has fast residue breakdown. The RIL population consists of 151 lines and previous work genotyped this population and developed a genetic linkage map of these lines to map stripe rust resistance, cold tolerance, and snow mold tolerance. We have completed processing of samples from Pullman in 2011, and Pullman, Mansfield, and Central Ferry in 2015, and Pullman and Mansfield in 2017. All samples and locations have been analyzed for C and N content and NIR, and the wet chemistry looking at ADF, NDF, and ADL. BLUPs were calculated on all data from all locations to help correct for variations in environments across years. Initial QTL analysis from the data indicate genetic regions on chromosome 1A, 1D, 3B, 4A, 5A, 6B, and 7D to be associated with the different traits tested. None of these genetic regions appears to be a major QTL. Most are minor QTL which contribute between 2-6% of the phenotypic variation. Heritability estimates are low to moderate for the traits analyzed, indicating environmental conditions influence the trait values more than genetics does. Furthermore, we have identified lines within the population with fast and slow residue decomposition from this population. Some of these lines have already been used in the breeding program as parents, allowing us to go into these breeding populations and begin making selections out of them. NIR predictions models showed good distribution of phenotypes, but was inconclusive during validation, we think because of the limited variation in

the population using only two parents. This prompted us to continue this testing in a more diverse genetic population.

The QAM population consists of 480 Soft white winter wheat lines from the Pacific Northwest and represents maximized allelic and phenotypic diversity. This population has already been genotyped using 90K SNP markers and genotyping-by-sequencing. Genome-wide associations studies have been performed on this panel for *Cephalosporium* stripe resistance, stripe rust, drought stress, agronomic characteristics, end-use quality, and pre-harvest sprouting. We have completed all phenotyping of this populations for fiber analysis and C&N from Pullman and Central Ferry, 2016, locations. We harvested straw in 2017 from Pullman, Central Ferry, and Mansfield. These locations have had the straw prepared for analysis, and we are currently on track to have the phenotyping completed by August 2018. Because of the large nature of this population, we were not able to complete testing of this population before the end of the granting period; we were only able to complete the RIL population as originally proposed. Regardless, we have found additional funding leveraged from our grant funding to continue the work. For the QAM panel, we will have the same data generated on it as we did for the RIL population. We will perform GWAS on the trait data to further explore the genetics underlying decomposition rates. Furthermore, we can use these two populations to validate the results found to improve use in breeding programs. We also believe the NIR data from the QAM will provide better predictive model development for future NIR use in breeding programs. NIR models will be further developed in the Fall of 2018 and then validated using the two populations in order to develop a high-throughput method for testing straw decomposition.

**Discussion:** This research is one of the first we can find which looks to identify the genetic control of straw decomposition in winter wheat. The QTL identified will help assist selection of lines which have either fast or slow straw decomposition. Unfortunately, the QTL identified were only minor and contributed to less than 10% of the phenotypic variation, although we did find that some QTL were additive in nature, indicating that pyramiding these QTL within the same cultivar would prove useful. The other limiting factor is that few of the QTL were significantly associated across environments. This supports our findings of low to moderate heritability estimates. Basically, the environmental conditions at each location controls more of the variation for straw breakdown than does genetics. We hypothesize this has to do with many factors such as rainfall, temperature, and other disease pressures that the plant might be faced with. Further analysis is being done to see if we can identify which environmental factor might be contributing the most to this variation.

The limited number of QTL identified may also point to a trait which is very complex in nature. For example, a recent study we did involving *Cephalosporium* stripe resistance (which has been very difficult for us to breed resistance for), identified more than 70 minor QTL associated with resistance (now we know why it was so hard to breed for!). Straw breakdown may have a similar level of complexity. With the knowledge of strong environmental interactions, the genetic control of straw breakdown may involve several biochemical pathways which are difficult to account for using only two parents in a RIL population. Basically, you can only find the QTL which are segregating between these two parents even though there may be several more to identify. Again, using the power of the 480 lines in the QAM panel and a GWAS, we may be able to further unravel the complexity of this trait.

Since the environment may have a strong impact on the development of straw constituents which then subsequently have an impact on straw decomposition in the field, only general recommendations about cultivars may be given to growers. This will still allow growers to select cultivars based on categorical placings even though we could not give them quantitative rankings. To this end, we are also very eager to complete the NIR prediction equations to see if these can do a better job at predicting straw breakdown over the limited genetic information we have.

#### **Publications, Handouts, Other Text & Web Products:**

Roa, A., Kruse, E., Stubbs, T., and Carter, A.H. 2018. QTL analysis of straw residue components as it relates to the rate of straw decomposition. To be submitted to the Journal of Agriculture and Food Chemistry.

**Outreach & Education Activities:** Discussion of the project, current progress, and anticipated outputs were presented at 18 farmer field days, six county wheat grower meetings, and at two Washington Grain Commission meeting. Individual grower discussions have been held at events such as the WSU wheat academy, the Tri-State grain growers meeting, Wilke and Lind Field days, and the WSCIA annual meeting. We have also used remnant straw residue from this project to assist with two other lignin research project within the department, further leveraging the support given to further research at WSU. One supports the research into another high-throughput method of determining lignin and cellulose composition, and the other looks at cellulose composition as it related to biofuels. We have also supported a USDA group to do similar research in a second population for research into nematode resistance. All output and outreach has recognized the BIOAg program as the funding source.

#### **Impacts**

**Short-Term:** The short-term knowledge gained upon completion of the project will be information on the residue decomposition potential of two diverse collections of winter wheat germplasm (containing almost all currently grown cultivars), and the ability of NIR to predict residue quality traits. Information gathered using traditional wet chemistry fiber characterization methods, and combustion methods for nutrient analysis will be compared to the ability of NIR to predict those same traits and relate to residue decomposition. QTL identified begin to give plant breeders an understanding of the genetic control of straw decomposition.

**Intermediate-Term:** We will gain the ability to quickly process and scan small quantities of winter wheat residue from large numbers of samples, such as breeding populations, using NIR analysis to screen for residue decomposition potential. This information will be useful in determining suitability of potential new varieties for conservation farming systems in both high rainfall, annual cropped regions and low rainfall, winter wheat-fallow regions. Use of this tool for residue screening would occur in the year following completion of the research.

**Long-Term:** The ability to process and test a small quantity of winter wheat residue for the characteristics that determine decomposability using NIR predictions will become a standard test toward deciding which potential cultivars move forward in developing new varieties at

Washington State University. Use of NIR to screen winter wheat residue for decomposition characteristics would be used in subsequent years following completion of the research. Cultivars that decompose slowly will help to protect soils in low rainfall regions where conventional tillage with fallow is practiced. Cultivars that decompose rapidly and allow for ease of direct seeding will hasten adoption of conservation farming practices; minimize the need for conventional tillage, burning and winter wheat residue removal; and lead to practices that build soil quality. There may also be impact with regards to decisions about baling straw residue and removing it from the farm, as well as impact of new wheat pulping facilities.

**Additional funding applied for/secured:** Funds have been obtained from a USDA-NIFA grant and from the Washington Wheat Commission to make NIR testing a standard process within the WSU winter wheat breeding program. We secured funding from private endowment funds to hire Nathan Nielsen to continue the work on the QAM population in the 17/18 crop year (OA Vogel and Willard Hennings Endowment). Nathan submitted a research grant to the Western SARE program, and was awarded funds for his research stipend to continue the work on the QAM population and the NIR prediction models into the next academic year. Upon completion of the project, breeding lines will be tested annually for this trait and used in the selection process.

**Graduate students funded:** Alex Callaway was a MS student funded on this project starting July 5<sup>th</sup>, 2016. Unfortunately, Alex passed away on October 11<sup>th</sup>, 2016 due to complications from an undiagnosed medical condition. Alejandra Roa started as a graduate student in January 2017 and has continued work on this project, focusing on the RIL population and the 2016 QAM panel. Nathan Nielsen was hired as a MS graduate student in August 2017 to complete the QAM project, partial funded on BIOAg money and partially on endowment money. He will be funded this upcoming year on a Western SARE proposal to complete additional work on this subject. Both students attended a FOSS training in September 2017 on NIR prediction model development.

**Recommendations for future research:** The Finch by Eltan RIL population will be submitted for genotyping-by-sequencing to further enhance the genetic map. One reason we may have found few QTL is because the D genome of this population is sparsely covered by genetic markers. The additional genotyping should help improve this coverage. Once this work is completed, testing new cultivars released in the Pacific Northwest would be beneficial to growers so that every variety has a rating, similar to how they currently rate disease resistance or end-use quality in buyer's guides. Additionally, testing the hard red cultivars to see if the NIR prediction works across market classes would be beneficial.