

IMPROVING PLANT BREEDING EFFICIENCY WITH QUANTITATIVE
METHODOLOGIES

By

LIN XING

A DISSERTATION PRESENTED TO THE GRADUATE SCHOOL
OF THE UNIVERSITY OF FLORIDA IN PARTIAL FULFILLMENT
OF THE REQUIREMENTS FOR THE DEGREE OF
DOCTOR OF PHILOSOPHY

UNIVERSITY OF FLORIDA

2017

© 2017 Lin Xing

To my parents for their support and love

ACKNOWLEDGMENTS

When writing this note of thanks and wrap up on my dissertation, it is excited to know that I am very close to the finish of my Ph.D. study. It has been a period of intense learning for me, not only in the scientific arena, but also on a personal understanding on life. I would like to reflect on the people who have supported and helped me so much throughout this period.

I would first like to thank my advisors, Dr. Patricio Munoz and Dr. Kevin Kenworthy for their strong guidance on the research directions and creation of excellent opportunities for me to conduct a very interesting dissertation. I also would like to express the deepest appreciation to my committee member Dr. Salvador Gezan, who always is helpful and set aside time for prompt communications. Without his guidance and persistent help this dissertation would not have been possible. Special thanks to Dr. Schwartz for helping me improve considerably my understanding on the biology and statistics related to turfgrass studies. In addition, a very important thank you to Dr. Md Ali Babar, who has provided excellent insight regarding the applications of sensor technology on crop biology.

Nobody has been more important to me in the pursuit of this degree than the members of my family. I would like to thank my parents, whose love is always with me in whatever I pursue. Most importantly, I wish to thank my loving girlfriend, Yu, who spend countless late night staying up with me to provide unending inspirations.

I am very grateful to all of those with who I have had the pleasure to work during this and other related projects. Thanks to my friends and colleagues, especially Yolanda Lopez, Luis Inostroza for their support and friendship.

TABLE OF CONTENTS

	<u>page</u>
ACKNOWLEDGMENTS	4
LIST OF TABLES	7
LIST OF FIGURES	8
LIST OF ABBREVIATIONS.....	9
ABSTRACT.....	10
CHAPTER	
1 INTRODUCTION	12
2 IMPROVED GENETIC PARAMETER ESTIMATIONS IN ZOYSIAGRASS BY IMPLEMENTING POST HOC BLOCKING	23
Background.....	23
Materials and Methods	23
Experiment	23
Statistical Analysis	24
Results.....	27
Discussion.....	29
3 STATISTICAL ANALYSES OF MULTIPLE RESPONSE MEASUREMENTS TO UNDERSTAND IMPACT OF DROUGHT AND GROWTH IN ZOYSIAGRASS	37
Background.....	37
Materials and Methods	37
Experimental Data	37
Statistical Analysis	39
Results.....	41
Discussion.....	45
4 IMPROVING PREDICTABILITY OF MULTI-SENSOR DATA WITH NONLINEAR STATISTICAL METHODOLOGIES.....	56
Background.....	56
Materials and Methods	56
Experiment Description.....	56
Measurements.....	57
Feature Engineering.....	58
Criteria of Model Performance.....	58
Evaluation of the Prediction Methodologies	59

Evaluation of Predictor Variables	61
Results.....	62
Discussion.....	64
5 CONCLUSIONS	73
APPENDIX	
A VARIANCE-COVARIANCE MATRIX OF GXE AND THE TEMPERATURE INFORMATION AT VARIOUS LOCATIONS OF CHAPTER 3	76
B SUMMARY OF GXE INTERACTION AND BROAD-SENSE HERITABILITY CONSIDERING ALL LOCATIONS WITHIN SERIES	78
C PREDICTABILITY AND STANDARD ERROR FOR CHAPTER 4 MODELS	82
LIST OF REFERENCES	85
BIOGRAPHICAL SKETCH	95

LIST OF TABLES

<u>Table</u>	<u>page</u>
2-1	Experimental site information for the five zoysiagrass trials, average turf quality scores (TQ, scale 1 to 9), and number of measurements33
2-2	Post-hoc blocking designs IB and R-C, at the site level, including all repeated measurements.....34
2-3	Calculated genetic gains (%) from selecting overall top 10, 15, and 20% of parental genotypes.34
3-1	Summary of five response variables in each of the seven trails including all series..49
3-2	Summary of broad-sense heritability estimates for different calculated response variables in different trials for each series.50
A-1	The variance-covariance matrix reflects the covariance (lower diagonal), variance (diagonal), and correlation (upper diagonal) of seven sites.76
A-2	The average precipitation and temperature of selected sites within given months.....77
B-1	Site-to-site Type-B genetic correlations for different response variables in various series. Values in parenthesis correspond to the standard error of the estimates.78
B-2	Summary of broad-sense heritability of calculated response variables considering all trials within series.79
B-3	Bivariate analysis of TQD against TQND and TQG against TQNG traits with all the data from sites within years.80
B-4	The correlation matrix obtained by modeling data from seven trails in series 2011 with CORGH variance-covariance structure.81
C-1	Prediction performance of target harvest date in dry matter yield trait with sensor data measurements using statistical models built with all previous harvest data82
C-2	Use of dataset from one harvest to predict another in dry matter yield trait82
C-3	Predictability of agronomical important traits with applications of statistical methodologies, PLS regression, ridge regression, SVM, and RF.....83

LIST OF FIGURES

<u>Figure</u>	<u>page</u>
2-1	Geographical location of the five experimental sites within Florida.....35
2-2	Likelihood ratio test (LRT) comparison..35
2-3	Estimation of narrow-sense heritability h^2 for the analysis of each of the five sites.36
2-4	Changes of rankings of top 10 genotypes at different sites based on all available measurements per site.....36
3-1	Distribution of measurements at different trails. The x-axis marks the measurement month and the y-axis shows the corresponding trails..52
3-2	Site-to-site Type-B genetic correlations, r_B , for different calculated response variables by series. The whisker bars represent the standard errors of the mean.53
3-3	Summary of broad-sense heritability estimates, H^2 , of calculated response variables considering data from all trails within a series..53
3-4	Trait-to-trait Type-A genetic correlations, r_A , for each trail based on the bivariate analysis of TQD against TQND with data from all trails within series.....54
3-5	Percentage of top genotype matching from series 2011 to 2014 with the selection intensities of 10%, 20% and 30%.55
4-1	An example of nested cross-validation with outer and inner loops both set as 5-fold.68
4-2	Predictability, correlation between predicted and test dataset values, of agronomically important traits.69
4-3	Predicted vs. observed values of dry matter yield and total digestible nutrient traits..70
4-4	The agriculturally important traits and their corresponding normalized root-mean-square error (NRMSE) with applications of statistical methodologies71
4-5	The model performance in dry matter yield after removing each of the variables in sequence from the dataset..72

LIST OF ABBREVIATIONS

AIC	Akaike information criteria
BIC	Bayesian information criteria
IB	Incomplete block
PLS	Partial least square
RC	Row-column
RCB	Randomize complete block
RF	Random forest
TQ	The score rating of turf quality trait
TQD	The turf quality rated under drought conditions
TQG	The turf quality rated under growth period
TQND	The turf quality rated under non-drought conditions
TQNG	The turf quality rated under non-growth period

Abstract of Dissertation Presented to the Graduate School
of the University of Florida in Partial Fulfillment of the
Requirements for the Degree of Doctor of Philosophy

IMPROVING PLANT BREEDING EFFICIENCY WITH QUANTITATIVE
METHODOLOGIES

By

Lin Xing

December 2017

Chair: Kevin Kenworthy
Cochair: Patricio Munoz
Major: Agronomy

By 2050, the food demand is expected to increase at least 59% worldwide, which has imposed a tremendous challenge to current agricultural infrastructures and practices. Besides utilization of improved pesticides and better understanding of field management, breeding crop cultivars efficiently becomes a key point of achieving the goal, feeding the world.

Plant breeding has been described from its origin as the art and science of the selection process. Today the statement still hold true, however, with the evolution of the complex data, the improvement of analytical methodologies becomes an important component of plant breeding which can make the decision-making process more efficient. The goal of this dissertation is to test different statistical methodologies to improve analytical challenges related to plant breeding.

Due to various field conditions, the environmental variation undoubtedly affects the performance of experimental units, which makes unbiasedly evaluating genotype performance very challenging. To alleviate the environmental impact, post hoc blocking was tested, which improved genetic parameter estimations by considering the heterogeneous environmental variation, and showed to help with decision making in plant breeding. This study also used zoysiagrass data as model crop to evaluate the impact of drought conditions, being more

prevalent in the past years, on the estimations of broad-sense heritability and genotype by environment interaction. In addition to the improved estimation and understanding about the drought, being able to collect phenotypic data in a fast manner will boost the breeding efficiency. Hence, this study focused on evaluation of statistical methodologies to improve the prediction performance of multi-sensor system. With competitive prediction accuracy, the current implemented sensor system could be a more lucrative alternative to traditional data harvest.

In summary, this study indicates that appropriate statistical methodologies could be very helpful to enhance plant breeding efficiency and has showed potential solutions to existing issues known to breeding programs.

CHAPTER 1 INTRODUCTION

Plant breeding has been described from its origin as the art and science of the selection process. However, with the evolution of complex data collection and improved analytical methodologies, the process of decision-making relies more on scientific information. The goal of this dissertation is to test different statistical methodologies to improve analytical challenges related to plant breeding.

Randomized complete block (RCB) designs are widely used in plant science because of their simplicity to design, analyze (Clewer and Scarisbrick, 2013) and compare treatments, including different genotypes (Anderson and McLean 1974, Montgomery et al. 1984). For the RCB design to be effective, the environmental variation within a given block should be relatively small. However, this is usually not the case when numerous (hundreds or thousands) genotypes are tested in a single breeding experiment (Montgomery et al. 1984). The block size increases as the number of genotypes tested increases, causing a loss in the design's capacity to appropriately control for environmental variation. Several alternatives exist for this challenge at both the design and analysis stages. At the design stage, more efficient experimental designs that consider some control of spatial variation, can be implemented, such as incomplete block (IB) designs and row-column (R-C) designs (Welham et al., 2014), which use smaller and incomplete strata to group genotypes. At the analysis stage, there are statistical alternatives such as spatial analysis (Gilmour et al., 1997) and post-hoc blocking that can provide relevant improvements in the estimation and prediction of parameters (Gezan et al., 2006).

Post-hoc blocking is a tool that superimposes a new experimental layout onto the original design and then the data are analyzed assuming this new design (Patterson and Hunter 1983).

This method was initially proposed as a low cost alternative to evaluate new potential

experimental designs without the necessity of establish the experiments in the field (Patterson and Hunter 1983, Gezan et al. 2006). For example, implementation of resolvable IB on top of an RCB design increases the homogeneity within the smaller incomplete blocking structure. In other cases, if a two-trend gradient environmental variation exist, then a R-C design can be superimposed to increase uniformity of the experiment by considering two-way spatial blocking (John and Eccleston 1986). The increase in efficiency at controlling experimental errors for both the IB and R-C designs over the original RCB designs has been previously presented using experimental field data in wheat, *Triticum spp.* (Qiao et al., 2000), and with simulated data (Fu et al. 1998, Fu et al. 1999, Qiao et al. 2000, Gezan et al. 2006, Kravchenko et al. 2006).

In breeding programs, often many genotypes are screened using RCB designs. By evaluation of the application of post hoc blocking methods on already established experiments, we expect to improve the estimation accuracy of genetic effects; and therefore, increase the reliability of information when making selections, that, in turn, will result in greater genetic gains. Moreover, the evaluation of post hoc blocking may provide evidence of more efficient experimental designs, which can be implemented in future.

Zoysiagrass (*Zoysia spp.*) is an important warm-season turfgrass species adapted for states in humid, warm, transitional zones and into the Midwest and Northeastern United States. Two species are important to the turfgrass industry, *Z. japonica* Steud. and *Z. matrella* (L.) Merr. (Brede and Sun, 1995). Both species are tetraploids, $2n = 4x = 40$. Phenotypically they can be differentiated by leaf texture, where *Z. japonica* typically has leaves that range from medium to coarse leaf texture, and leaves of *Z. matrella* are fine textured (Forbes, 1952). Because zoysiagrass is a tetraploid and the species can hybridize, breeding programs typically observe significant phenotypic variation. Variation in zoysiagrass has been reported to occur for turf

quality, seed head density (Schwartz et al., 2009), DNA content (Schwartz et al., 2010a), shade (Morton et al., 1991), salinity (Marcum et al., 1998; Qian et al., 2000), drought (Marcum et al., 1995; White et al., 2001), temperature adaptations (Patton and Reicher, 2007), diseases (Green et al., 1994), nematodes (Busey et al., 1982; Schwartz et al., 2010b), insects (Braman et al., 2000; Reinert and Engelke, 1992) and fusillade herbicide resistance (Leon et al., 2014). With the extensive presence of genetic variation within this genus and the development of several breeding programs across the US, it is important to determine the most efficient analytical tools that provide best accuracy of estimation of genetic parameters. Therefore, in the second chapter of this study, the post hoc blocking will be tested to check if it could improve the accuracy of genetic parameter estimations.

To further improve the selection efficiency in cultivar development and provide critical information regarding its performance in various locations, establishment of experiments at multiple sites to learn about the heritability, breeding values of genotypes and related genotype by environment (GxE) interaction become more and more important. The concept of interaction between genotype and environment was first raised (Haldane, 1946) in an article, 'The interaction of Nature and Nurture', stating in a broad sense that the combination of species and environment would have an impact on the phenotypic features of creatures. Later, in Allard and Bradshaw (1964), the genotype-by-environment (GxE) interaction concept was revisited again and emphasized in context of plant breeding. Moreover, this concept has been reviewed many times in various disciplines, such as plant science (Eberhart and Russell, 1966; Hoeck et al., 2000), animal behavior (Bergeman and Plomin, 1989; Plomin and Hershberger, 1991; Plomin et al., 1977), and plant breeding (Allard and Bradshaw, 1964; Annicchiarico, 2002; Becker and Leon, 1988).

The concept of GxE interaction has a critical role in cultivar development, specifically in evaluating the phenotypic stability in crop breeding (Kang, 1997). In the scenario of plant breeding, the genotype usually refers to a cultivar or tested genotypes (i.e. with genetically homogeneous materials or heterogeneous) and the term environments relate to the climate, soil, pest pressure at a given location of the year. The GxE interaction is reflected in the performance of genotypes at various locations and impact differing traits such as extreme temperatures and water shortage (Billings, 1987; Hoekstra et al., 2001). Specifically, some genotypes may thrive in particular regions, whereas, in other regions they may perform poorly (Finlay and Wilkinson, 1963; Lin and Binns, 1988; Otoo and Asiedu, 2006). In plant breeding, multiple locations with the same genotypes are typically set up of cultivar development, especially, the selection of genotypes targets macro-regions (Finlay and Wilkinson, 1963).

The establishment of multiple-location trials to estimate the GxE interaction has been found quite often in various crop species. Johnson et al. (1955) estimated genetic and environmental variability in soybeans and found significant environmental variability occurred in one of the test populations. Al-Jibouri et al. (1958) conducted experiments with eight yield and fiber traits in upland cotton and reported that the interaction between progeny and environment is small. Similarly, there was one study showing small GxE interaction for all traits except yield and bolls per plant in upland cotton (Miller et al., 1958). Not only is GxE interaction reflected in traditional phenotypic data analysis, but there are studies exploring the GxE interaction for genetic mapping. Jansen et al. (1995) illustrated the MQM mapping that considers the GxE interaction to provide a better mapping method with *Arabidopsis thaliana* data. In plant breeding, best linear unbiased prediction (BLUP) can provide a good estimation of variance-covariance structure for the GxE interaction (Piepho et al., 2008). Moreover, to have a more reliable and

accurate understanding on genotype, environment, and their interaction, Chapman (2008) used crop models to simulate plant breeding traits and reported the analysis.

In addition to the impact of the GxE interaction on cultivar development, the global climate also plays an important role in the genotype selection process. Many studies are pointing out the occurrence of global drought and probability of extreme heat events (Allen et al., 2010; Hayhoe et al., 2010; Luber and McGeehin, 2008), hence breeding for drought resistant cultivars seem to be a reasonable consideration. Moreover, since the water availability in the United States may be limited during certain months of the year, especially in July and August, there are turfgrass breeding programs actively breeding cultivars in response to the climate change.

The drought condition usually occurs when the precipitation drops below the long-term average of several years, leading to soil moisture decreases to the point that negatively impact plant development. Drought resistance-or drought tolerance indicates how well the turf holds quality and color during the dry period when there is no irrigation or rainfall. Favorable drought responses could also include holding of turf color during the drought conditions, recovery of color after the irrigation, or even the reduced usage of water to maintain healthy conditions. Huang et al. (1997a) showed that shoot dry matter production partially recovered for zoysiagrass after re-watering. Similar drought effect studies were carried out for the root response and found that root dry weight recovered partially for zoysiagrass after re-watering as well and the drought resistance may be associated with enhanced root growth, rapid water uptake at deeper soil layers, and rapid root regeneration after re-watering (Huang et al. 1997b). Additional studies indicate that the rooting depth, weight and branching at lower depth are responsible for drought resistance mechanism in zoysiagrass (Marcum et al., 1995). Hays et al. (1991) showed that the root mass significantly correlated with turf quality at multiple levels during drought conditions but there

was no direct impact on root carbohydrate distribution. More research related to zoysiagrass also showed that the turfgrass rooting and drought resistance level could be markedly affected by the genetic tolerance, providing support of turf breeding effort on the drought resistance cultivars. Even though there are plenty of physiological evidences to prove that breeding for drought resistance cultivars are necessary and approachable, not much direct breeding data is available in the literature. Hence, in the third chapter, the broad-sense heritability (H^2) and GxE interactions will be estimated and, subsequently, the impact on estimation of drought will be explored.

The traditional rating system in turfgrass breeding is very common and well recognized as it is straightforward and intuitive. However, when it comes to the phenotyping data, especially dry matter yield and other quality traits, in forage crops, the process becomes very time consuming, labor intensive and expensive. Bermudagrass is an excellent warm-season forage species native to southeast Africa, and has been adapted and extensively used in southeastern United States (Sleper et al., 1989). Due to its excellent active production during the months of May through October, in which most other forage species decreasing the production activities (Bouraoui et al., 2002), it fits into a unique niche among forages. Extensive efforts have been spent on testing its nutritional responses and management (Franzluebbers et al., 2001; Overman et al., 1990).

The evaluation of the biomass of bermudagrass usually takes multiple harvests that are traditionally considered time-consuming and labor intensive, requiring additional drying facilities as an additional expense. To assess the nutritional values of bermudagrass, the forage nutritive value analysis has been the traditional choice, which involves evaluations performed through wet and ignition laboratory (Kellems and Church, 2009) and NIRS laboratory analysis (Norris et al., 1976). Even though the test results were considered accurate and reliable, the

analysis process could take weeks to complete, leading to high turnaround time (Pittman et al., 2016).

To solve the drawbacks of traditional labor- and time-consuming bermudagrass harvests and nutritive value evaluation, mainly two kinds of approaches, advanced machinery and sensor technology, have been proposed (Srivastava et al., 2006; Stoll and Kutzbach, 2001). Since sensor technology has significant advantages over machinery in terms of expenses and flexibility, there have been many studies examining the application of sensors on bermudagrass. Utilization of remote sensing strategies for prediction of the forage nutritive values and biomass could potentially allow efficient adjustment of grazing management and rapid decision making on the inclusion of feed supplements (Pittman et al., 2016). The sensor combinations (ultrasonic, laser, and spectral sensors) were expected to outperform the traditional remote sensing approach as various sources of data could provide more relevant information and complement each other. Ultrasonic proximity sensors reflect the approximate distance to target by calculate the time interval between the signal sending and receiving. In agricultural practice, they have been extensively used to characterize the canopy coverage in orchards and corn (*Zea mays* L.) (Aziz et al., 2004; Escolà et al., 2011), growth in wheat (*Triticum aestivum* L.) (Scotford and Miller, 2004), and to measure height in cotton (*Gossypium hirsutum* L.) (Sui and Thomasson, 2006). Laser proximity sensors work either through the phase-shift method that compares the reflection of beams with the time-of-flight method that is based on calculation of the time taken to capture the reflected optical pulse. Due to its measurement mechanism, laser sensors have been successfully employed in multiple scenarios to characterize the height of targets. Laser sensors have been used to predict the leaf area index (LAI) that is related to grapevine foliage and indirectly determining grape (*Vitis* L. spp) yield and quality (Arnó et al., 2013).

Laser sensors have also been successfully utilized to quantify and characterize forest structure, ecozones, and stem measurements of standing trees (Henning et al., 2006; Hopkinson and Chasmer, 2009; van Leeuwen and Nieuwenhuis, 2010). Genc et al. (2017) utilized light detection and ranging (LIDAR) to determine the vegetation height on wetlands. Laser sensors have also been employed to measure biomass density in oilseed rape (*Brassica napus* L.), rye (*Secale cereale* L.), and wheat (Ehlert et al., 2008); to approximate winter wheat height (Ehlert et al., 2010; Hosoi and Omasa, 2009); and to characterize properties of corn stands (Selbeck et al., 2010). An application to provide measurement comparison in apple (*Malus pumila* Mill.) orchards for various spray volume deposition models also illustrated the wide adaptation properties of laser sensors (Walklate et al., 2002). The spectral strategies rely on the responses to plants and their ambient environments with respect to reflectance and absorption of various wavelengths. Successful applications of spectral strategies have been documented in various literatures. At the leaf level, the spectral values depend on the content of chlorophyll, and the reflectance measurements partially illustrated the relationship (Cartelat et al., 2005). The diurnal changes of photosynthesis efficiency of sunflower (*Helianthus annuus* L.) canopies could also be captured with a spectral index (Gamon et al., 1992). Additionally, Vogelmann et al. (1993) reported the spectral properties from measurements on sugar maple (*Acer saccharum* Marshall) leaves. At the canopy level, spectral strategies are responsive to variation in moisture content (Bowyer and Danson, 2004), vegetation water content (Ceccato et al., 2002), and tropical pasture quality (Mutanga et al., 2005).

In addition, spectral strategies could provide information regarding the photosynthetic light-use efficiency of Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco) forests (Middleton et al., 2009) and indirectly reflect the lignin and nitrogen concentrations (Martin and Aber, 1997).

At the landscape level, the spectral strategies could capture the structural measurements of forest vegetation (Roberts et al., 2004) and reflect the effects of prescribed burning on pine forests (Finney et al., 2005). These studies indicate that the spectral strategies are very useful in different applications and could be used to derive various indexes such as normalized difference vegetation index (NDVI) and reflected photosynthetically active radiation (RPAR) among others. However, the spectral strategies could be less reliable when the saturation of reflectance occurs (Gnyp et al., 2014; Hong et al., 2007).

In term of sensor usage in bermudagrass, the spectral reflectance type of sensor was initially focused on by researchers. Various ranges of wavebands were explored to find good estimations of different traits; for example, multiple wavebands in the 368 to 1100 nm and 350 to 1125 nm ranges to estimate N concentration (Starks et al., 2008; Starks and Brown, 2010). Since some spectral devices may depend on consistent lighting and limited sampling conditions, researchers actively sought alternative approaches. Pittman et al. (2015) examined the usage of combined sensors to estimate biomass and later reported crude protein estimation with active-spectral and canopy-height data (Pittman et al., 2016). Most of these studies use traditional analytical methodologies (Partial Least Square, PLS) to study the capacity of different sensor(s) as a proxy to predict economically important trait. However, they ignore the contribution that different analytical methods could have in this process. Thus, this study will focus on testing different statistical methodologies to improve the estimation of economically important bermudagrass traits.

Partial least square regression is a widely-used methodology to regress predictor data against target prediction traits based on the assumption that the response variables are from a process generated by unobserved latent variables (Rosipal and Krämer, 2006). It is a competitive

prediction model both due to its light computational requirements and superior performance when collinearity exists in the data set (Wold et al., 1984). Even though PLS regression initially gained popularity in chemometric studies for its superior prediction performance (Sjöström et al., 1983; Geladi and Kowalski, 1986; Frank, 1987; Tobias, 1995), its application has been expanded to various research fields, such as genetics and ecological studies (Nguyen and Rocke, 2002; Carrascal et al., 2009). In spectral sensor data analysis, PLS regression was initially used as the default statistical methodology to predict variables of interest [e.g., estimation of grass biomass and measurement of nitrogen status (Hansen and Schjoerring, 2003; Cho et al., 2007)]. However, there are other prediction methodologies, such as ridge regression and random forest, which have been used in other applications and shown competitive performance, which could potentially outperform PLS regression. Ridge regression is a methodology initially proposed by Hoerl and Kennard (1970) to address the potential instability in the least square estimations by adding a small constant value to the diagonal entries of the matrix $X^T X$ before taking its inverse. Even though the ridge regression estimators are biased, the prediction performance of this methodology is quite competitive. Because of the small noise added to the diagonal entries of the matrix $X^T X$, the ridge regression can handle multicollinearity very neatly, which is especially helpful in the sensor data as the collinearity is not uncommon (Mahajan et al., 1977; Rook et al., 1990). Support vector machine regression was based on the classification algorithm that projected the data into hyperplanes for differentiation and has been adapted to regression problems through a fixed feature-space transformation (Bishop, 2007). Considering the flexibility of kernel functions to capture the nonlinearity relationships, it has been widely adapted for various usage such as prediction of corporate financial distress, exchange rate prediction, wind speed prediction, and remote sensing (Mohandes et al., 2004; Pai et al., 2006; Hua et al.,

2007; Mountrakis et al., 2011). Random forest is an ensemble learning method based on constructing multiple decision trees and obtaining the regression prediction by the mean of each tree's prediction (Liaw and Wiener, 2002). The combination of random selection of variables at each tree node split, full tree length growth, and multiple tree copies gives RF superior performance in multiple problems and effectively avoids overfitting issues.

In the fourth chapter of this study, the performance of prediction methodologies regarding the agronomic important traits will be evaluated and, based on the dry matter yield trait, the impact of sensor variables on predictive model performance will be studied.

CHAPTER 2
IMPROVED GENETIC PARAMETER ESTIMATIONS IN ZOYSIAGRASS BY
IMPLEMENTING POST HOC BLOCKING¹

Background

Randomized complete block (RCB) designs are widely used in plant science because of their simplicity to design, analyze and compare treatments, including different genotypes. However, since plant breeding programs usually set up hundreds or thousands of genotypes in a single experiment, the assumptions of RCB designs usually cannot be fulfilled. To alleviate the issues to accommodate the already set up experiments in the analyzing phase, the post-hoc blocking was introduced. In this chapter, the post hoc blocking will be tested to check if it could improve the accuracy of genetic parameter estimations and subsequently illustrate its impact on the ranking of top genotypes.

Materials and Methods

Experiment

The data used in this study was from five zoysiagrass trials established across Florida, USA (Figure 2-1) between 2011 and 2012, representing different soil types and weather conditions (Table 2-1). All five experiments were established as RCB designs with three replicates and 80 genotypes per replicate. These genotypes consisted of F1 hybrids, parental breeding lines, and two commercial cultivars used as checks. Experimental units corresponded to plots of 1.52×1.52 m². Plots were established by planting 10, 5 × 5 cm clonal plugs. Standard turfgrass maintenance practices were utilized to maintain all experiments (Brede, 2000). Mowing frequency varied by location, with Citra, Duda Sod (Duda), Bethel Farms (Bethel), Jay, and RB Farms mowed weekly, biweekly, biweekly, biweekly, and monthly, respectively.

This Chapter published in *Euphytica*, 213(8), 195

Statistical Analysis

The performance of the post hoc blocking was compared with the original experimental design at the single measurement level across sites, and later using all measurements within a site. The software ASREML v. 3 (Gilmour et al., 2009) was used to fit linear mixed models that provided variance component estimates, best linear unbiased prediction (BLUP) for each genotype, and REML log-likelihood values. After analyses, the best post hoc blocking experimental design was selected, and its impact on genetic parameter estimation and predictability was assessed.

At a first stage, comparisons of post hoc blocking with the original experimental design were implemented with the data from all 100 measurements belonging to the five sites. Only two measurements with extremely low genetic signal obtained from single measurement analysis were removed. Here, for each measurement-site dataset, the linear mixed model for the original RCB experimental design was fitted (2-1). Then, a model was fitted by superimposing an IB design (2-2) with a total of eight genotypes per incomplete block, and a superimposed R-C design that considered the specified rows and columns within a block of each experimental unit (2-3). These fitted models were

$$\text{RCB: } \mathbf{y} = \mu \mathbf{1} + \mathbf{Xb} + \mathbf{Z}_1 \mathbf{g} + \mathbf{e} \quad (2-1)$$

$$\text{IB: } \mathbf{y} = \mu \mathbf{1} + \mathbf{Xb} + \mathbf{Wi} + \mathbf{Z}_1 \mathbf{g} + \mathbf{e} \quad (2-2)$$

$$\text{R-C: } \mathbf{y} = \mu \mathbf{1} + \mathbf{Xb} + \mathbf{W}_1 \mathbf{r} + \mathbf{W}_2 \mathbf{c} + \mathbf{Z}_1 \mathbf{g} + \mathbf{e} \quad (2-3)$$

where \mathbf{y} is the vector of phenotypic value (i.e. turf quality rating score); μ is the overall mean effect; \mathbf{b} is the fixed vector of replicate (or block) effects; \mathbf{i} is the random vector of incomplete block effect nested in the original replicate, with $i \sim N(0, \sigma_i^2 \mathbf{I})$; \mathbf{r} is the random vector of row effect nested in the original replicate, with $r \sim \text{MVN}(0, \sigma_r^2 \mathbf{I})$; \mathbf{c} is the random vector of column

effected nested in the original replicate, with $c \sim N(0, \sigma_c^2 \mathbf{I})$; g is the random vector of parental effects with $g \sim MVN(0, \sigma_g^2 \mathbf{A})$; and e is the random vector of error, with $e \sim MVN(0, \sigma_e^2 \mathbf{I})$. The letters X , Z_1 , W , W_1 , W_2 represent the incidence matrices for their respective effects. The matrix A is the additive relationship matrix obtained from pedigree information, and I is an identity matrix of its proper size.

After fitting the above models, log-likelihood values were recorded and likelihood ratio tests (LRT, Gilmour 2009) were performed for IB design vs. RCB design and R–C design vs. RCB design with $\alpha = 0.05$ (Eq. 4), as: $d = 2[\text{LogL2} - \text{LogL1}] \sim \chi^2_{df2-df1}$, where LogL2 is the log-likelihood values for R-C or IB designs and LogL1 is the log-likelihood values for original RCB design, and similarly for $df2$ and $df1$.

In a second stage, data from each location were pooled and three different linear mixed models were fitted (2-4, 2-5 and 2-6) to evaluate the effect of post hoc blocking when repeated measurements were considered. This was done for each site individually and later the results were used to compare the post hoc blocking performance. The fitted models were

$$\text{RCB: } y = \mu \mathbf{1} + X_1 u + X_2 b(u) + Zg(u) + e \quad (2-4)$$

$$\text{IB: } y = \mu \mathbf{1} + X_1 u + X_2 b(u) + Wi(u) + Zg(u) + e \quad (2-5)$$

$$\text{R-C: } y = \mu \mathbf{1} + X_1 u + X_2 b(u) + Wr(u) + Wc(u) + Zg(u) + e \quad (2-6)$$

where y is the vector of phenotypic values; μ is the overall mean effect; u is the fixed vector of measurement; $b(u)$ is the fixed vector of block effect within measurement; $i(u)$ is the random effects vector of incomplete block effect nested within block within measurement, with $i(u) \sim MVN(0, D_{iu})$; $r(u)$ is the random effect vector of row effect nested within block within measurement, with $r(u) \sim MVN(0, D_{ru})$; $c(u)$ is the random effect vector of column effect nested within block within measurement, with $c(u) \sim MVN(0, D_{cu})$; $g(u)$ is the random vector of parent

effect within each measurement, with $g(u) \sim \text{MVN}(0, A \otimes G)$; and e is the random vector of errors, with $e \sim \text{MVN}(0, R \otimes I)$. The matrices D_{iu} , D_{ru} , D_{cu} are diagonal matrices where each of the j th measurement has a different and independent incomplete, row and column variance component, σ_{iuj}^2 , σ_{ruj}^2 , σ_{cuj}^2 , respectively. The matrix A is the numerator relationship matrix for parents, G is a matrix of variance-covariance (dimension determined by the number of measurements within site) between genotypes across measurements, modeled by considering a single genetic correlation term, r_B , and a unique j^{th} variance term, σ_{gui}^2 for each measurement (i.e., CORUH), R is a matrix of variance-covariance components (dimension determined by the number of measurements within site) between residuals of measurements defined as an autoregressive heterogeneous order 1 error structure with a correlation between residuals of p_e and a different residual variance for each j^{th} measurement, σ_{ej}^2 . All the other matrices were previously defined.

Based on the estimated variance components for each of the analyses, a narrow-sense heritability was calculated based on the expression:

$$h^2 = \frac{\sigma_a^2}{\sigma_T^2} = (\bar{\sigma}_{gu}^2 \times r_B) / (\bar{\sigma}_{gu}^2 + \bar{\sigma}_{biu}^2 + \bar{\sigma}_{bru}^2 + \bar{\sigma}_{bcu}^2 + \bar{\sigma}_e^2) \quad (2-7)$$

where the components correspond to averages of estimates across all measurements.

Later, the log-likelihood values of different models were recorded, based on which the Bayesian Information Criterion (BIC) (Liddle, 2007) and Akaike information criterion (AIC) were calculated and used to assess the goodness-of-fit of the evaluated models. Moreover, the reliability was calculated serving as additional model selection criterion, which reflected the correlation between true and predicted breeding values. The reliability was calculated based on the expression:

$$r^2(\hat{g}_i) = 1 - c^{ii} \times \frac{\bar{\sigma}_e^2}{\sigma_{gu}^2 \times rB} \quad (2-8)$$

Finally, to assess the impact of post hoc blocking on the selection process, the response of parental selection, i.e. genetic gain, for different selection intensities was evaluated. For a given site, the predicted mean values for each genotype tested in the experiment across all measurements were used to calculate the genetic gains in relative terms by fitting a randomized complete block (RCB, 2-5) and a row–column (R–C, 2-7) design. Genetic gains were obtained by averaging the prediction values of the top 10, 15, and 20% of the genotypes and dividing them by the average phenotypic response. Additionally, as during the turfgrass genotype selection, the ranking of the genotypes will affect which genotypes selection for the next breeding cycle. Understanding the impact of post hoc blocking on this process can be critical. Hence, the genotype rankings based on breeding values within sites were plotted for each site to illustrate the effect of post hoc blocking.

Results

First, we determined whether data fitting, at the single measurement level, with post hoc blocking was significantly better than the original RCB design (Figure 2-2). When comparing the post hoc IB design against the RCB design, in 44% of the comparisons, post hoc IB designs performed significantly better than the original RCB designs ($\alpha < 0.05$) (Figure 2-2). Additionally, we found that for 77% of comparisons, the post hoc R–C designs were significantly better than the original RCB designs, with no statistical significant differences in the remaining comparisons (Figure 2-2).

For the fitted model, considering all repeated measurements within a site, in the case of the LRT, the post hoc blocking designs performed overall better than the original RCB designs (Table 2-2). At the Jay site, the model fitting of the IB design was significantly better than RCB

($p < 0.001$), while there was no significant difference between R–C and RCB designs ($p = 0.999$). In contrast, for Duda, the data fitting of the post hoc R–C design was better than the original design ($p < 0.001$), but there was no significant difference between IB design and RCB ($p = 0.199$). At RB Farms and Bethel Farms, both post hoc IB and R–C designs were significantly better than the original RCB designs ($\alpha < 0.05$). However, due to the smaller p -values with the R–C designs for the hypothesis testing and their respective AIC values, the R–C designs were found to have a better fit than the RCB designs. At PSREU, AIC and reliability all indicated that the IB design was better than the R–C design (Table 2-2). Overall, for the combined information from measurements across a site, the R–C design performed marginally better.

From the analyses at the site-level, the narrow-sense heritability (h^2) varied between 0.239 and 0.399 for the R–C design while it ranged from 0.248 to 0.398 for the RCB design (Figure 2-3). The h^2 from Jay and RB Farms were the highest and lowest among all the locations, respectively (Figure 2-3). The $G \times M$ interaction, presented as a genetic correlation across measurements varied from 0.558 at RB Farms to 0.996 at Jay for the R–C design, whereas it ranged from 0.566 at RB Farms to 0.991 at Jay for the RCB design (Figure 2-3).

The genetic gains, calculated based on selection of the top 10, 15, and 20% parental genotypes, resulted, with some minor exceptions, in marginally higher values for the original RCB designs in relation to the R–C designs at all three selection intensities for PSREU, RB Farms and Bethel Farms (Table 2-3). For Jay, at 10% selection intensity, the genetic gain of R–C design was slightly higher, whereas, at 15 and 20%, the opposite was true. Interestingly, at Duda, the application of the post hoc R–C design yielded higher genetic gains in all selection intensities.

Comparisons between the original RCB and R–C designs based on the top 10 genotype performers (~12% of total genotypes) at each of five sites were presented in Figure 2-4. The site with the highest h^2 and GxM, Jay, had no genotype ranking change. At the other sites, there were changes in genotype ranking and the degree of change varied from site to site. For example, at Bethel Farms, the genotype UFZ11 ranked fifth in the original design, but with post hoc R–C design it ranked second. Even more relevant for breeding, is that some of the genotypes originally ranked in the top 10 performers dropped out of selection after the implementation of post hoc blocking with an R–C design (Figure 2-4). This last phenomenon would have a considerable impact on selections.

Discussion

Post-hoc blocking by superimposing incomplete block (IB) and row–column (R–C) designs were compared to the original randomized complete block (RCB) design. At the single measurement level, for the datasets analyzed, the post hoc R–C design was found to perform better than the original RCB and IB designs (Figure 2-2). These comparisons were also performed at the site level with multiple measurements using a likelihood ratio test, Akaike Information Criterion (AIC), and Bayesian Information Criterion (BIC). Again, the post hoc R–C design resulted in the best performance at Duda, RB Farms, and Bethel Farms; whereas, the post hoc IB design was better at Jay and PSREU. However, when the R–C designs were compared to the original RCB designs, they almost always had a better fitting model than the RCB design except at Jay. In addition, the residual variance was reduced an average of 18.7% by implementing the post hoc R–C design over the original RCB design. The residual variance decreased by 2, 13, 24, 27 and 27% at Jay, PSREU, Duda, Bethel and RB Farm, respectively. This indicates a very strong local environmental heterogeneity in this experimental site that is successfully controlled for by the added row and column effects. Because the residual variance

decreased significantly at most sites, even with different criteria, such as relative efficiency (Simon and Maitournam, 2004), the R–C design would be considered to have better performance than other designs tested. The superior performance of the post hoc R–C over the IB designs may be due to the existence of dominant global gradients (that are better controlled for by row and columns) instead of small patches (controlled by incomplete blocks) (Gezan et al., 2006). The different decrease in residual variance among locations could also be influenced by the layout conditions at each location. However, we could not find a trend associated with the planting layout (square versus rectangular blocks) of the location in this specific study.

The size of the incomplete block, another factor to consider, determines the effectiveness of the IB design. In this case, the number of genotypes within each post hoc IB design was based on the criteria proposed by Williams 2002 to use a value marginally smaller than the square root of the number of treatments (here, $8 < 8.9 = \sqrt{80}$). Other incomplete block sizes were not investigated, but larger blocks are expected to be less efficient, and smaller blocks might capture a portion of the genetic signal reducing heritability (Gezan et al., 2006).

The post hoc R–C design did not seem to have a big effect in terms of the estimated h^2 values when compared to the RCB design estimates. As expected, there was some positive association between heritability and measurement-by-measurement genetic correlation estimates, indicating that sites with better genetic signals tend to have lower levels of $G \times M$ interaction.

The magnitude of $G \times M$ reported here provides useful information for turfgrass breeders who might want to optimize the frequency of data collection in the selection process. For example, in Jay, r_B between measurements is 0.996, indicating a very high agreement between consecutive measurements (Figure 2-3). Therefore, in this and other experimental sites, the frequency of data collection could be reduced without affecting genetic gains and the accuracy of

the final selections. However, at Duda and RB Farms, the correlations were around 0.6, indicating that some loss of information might occur if fewer measurements are considered. The consistency of measurements at various sites may be impacted by many factors such as weather conditions, disease prevalence, and management practices.

The change of genotype ranking (Figure 2-4) illustrates the direct impact from implementation of the post hoc designs. For example, UFZ126 and UFZ154 were the genotypes at Duda, which were estimated to be in the top 10 with the RCB design. However, with the implementation of post hoc R–C design, they dropped out of this potential selection list. This could be critical information for plant breeders, particularly when the selection intensity is high and limited resources are available. Bethel was one of the most affected locations, in terms of ranking change, with the implementation of post hoc blocking. The significant slope, compared to other locations, could have contributed to this change and this reinforced the idea of implementation of post hoc blocking to control these potential intra-blocks environmental variation.

Besides post hoc blocking, others have tried to address this challenge in different ways. (Cullis et al., 1989) showed that some spatial model could be incorporated to enhance the estimation of BLUP of genotypic values in early generation variety trials. Stroup and Muiltze (1991) developed nearest neighbor adjusted BLUP and found it to have considerable estimation efficiency improvement. Moreover, some geostatistical methods such as Kriging, provide local predictions utilizing the observation information at neighbors based on spatial correlation (Schabenberger and Gotway, 2017).

Even though the selection criteria and cultivar development procedures of multiple testing sites for selections in turfgrass breeding are very well developed (Ebdon and Gauch,

2002; Raymer and Braman, 2006; Watkins et al., 2011), for this species, there is not information available on how different experimental designs may impact genotype testing and selection. Results from this study indicate that genetic parameters, ranking of genotypes and genetic gain could be impacted when the environmental variation is better controlled. Implementation of post hoc blocking analysis will allow turfgrass, and other plant breeders, to utilize their data more efficiently. In addition, implementation of R–C designs, followed by its analysis, is recommended for future testing efforts in turfgrass for Florida. The utilization of multiple testing sites is common, which add valuable information regarding genotype stability (Fan et al., 2007) and provide an indication of genotype-by-environment interaction ($G \times E$). In future studies, it would be worthy to determine the post hoc blocking on the estimation improvement of $G \times E$ by combining analyses of multiple data resources.

In conclusion, in this study, the contrasting of different post hoc experimental designs indicated that R–C designs clearly outperformed RCB and are marginally better than IB designs. It was shown here, that post hoc blocking analysis could provide important spatial control of the local environmental variation.

Table 2-1. Experimental site information for the five zoysiagrass trials, average turf quality scores (TQ, scale 1 to 9), and number of measurements. Standard deviations in parentheses.

Sites	Jay	PSREU*	Duda	RB farm	Bethel
Planting Date	June 2011	July 2011	July 2012	May 2012	Aug. 2011
Soil Type	Sandy loam	Deep sand	Flat wood soil	Muck soil	Flat wood soil
County	Santa Rosa	Alachua	Seminole	Highlands	DeSoto
Location	Jay	Citra	Cocoa Beach	Lake Placid	Arcadia
TQ average	5.93 (1.12)	3.45 (1.54)	4.85 (1.55)	5.03 (1.42)	4.78 (1.63)
Measurement #	13	27	18	18	24

*Plant Science Research and Education Unit

Table 2-2. Post-hoc blocking designs IB and R-C, at the site level, including all repeated measurements. incomplete block (IB) and row-column (R-C) designs were compared with original randomized complete block (RCB) design with data from five different locations analyzed by all measurements available by site (Eq. 2-5, 2-6 and 2-7). For the Akaike information criteria (AIC) and the Bayesian information criteria (BIC) the smaller value the better goodness-of-fit, whereas, for the log-likelihood value (LogL), the larger value, the better the fit. Reliability is the correlation between true and predicted breeding values. df is the degree of freedom for the likelihood ratio test. The models with best fitting within a site are highlighted with bold.

Site	Design	LogL	BIC	AIC	Reliability	df	<i>p-value</i>
Jay	RCB	-8200.23	16625.27	16456.46	0.792		
	IB	-8175.79	16680.76	16433.58	0.792	13	< 0.001
	R-C	-8195.6	16824.75	16499.2	0.796	26	0.999
PSREU	RCB	-8029.23	16526.53	16170.46	0.729		
	IB	-7947.42	16588.59	16060.84	0.731	27	< 0.001
	R-C	-7949.53	16818.49	16119.06	0.725	54	< 0.001
Duda	RCB	-2749.66	5816.94	5575.32	0.698		
	IB	-2738.27	5944.61	5588.54	0.699	18	0.199
	R-C	-2576.35	5771.22	5300.7	0.708	36	< 0.001
RB Farms	RCB	-2732.13	5781.88	5540.26	0.666		-
	IB	-2712.68	5893.43	5537.36	0.668	18	0.003
	R-C	-2609.44	5837.40	5366.88	0.668	36	< 0.001
Bethel	RCB	-7382.38	15196.72	14864.76	0.786		
	IB	-7361.17	15361.64	14870.34	0.790	24	0.012
	R-C	-7117.69	15082.02	14431.38	0.763	48	< 0.001

Table 2-3. Calculated genetic gains (%) from selecting overall top 10, 15, and 20% of parental genotypes based on the all available measurements per site by fitting a randomized complete block (RCB, Eq. 2-5) and a row-column (R-C, Eq. 2-7) design. Number in parenthesis correspond to the number of genotypes selected. Note that the total number of parental genotypes considered here are only those tested in the experiment.

Design	Selection	Jay	PSREU	Duda	RB farms	Bethel
RCB design	10% (8)	12.69	37.21	21.63	18.54	28.78
	15% (12)	11.46	33.87	20.48	17.14	25.90
	20% (16)	10.60	31.89	19.55	15.62	23.54
R-C design	10% (8)	12.70	36.53	22.93	17.54	26.48
	15% (12)	11.45	33.32	21.15	16.27	24.25
	20% (16)	10.57	31.38	19.81	14.74	22.52

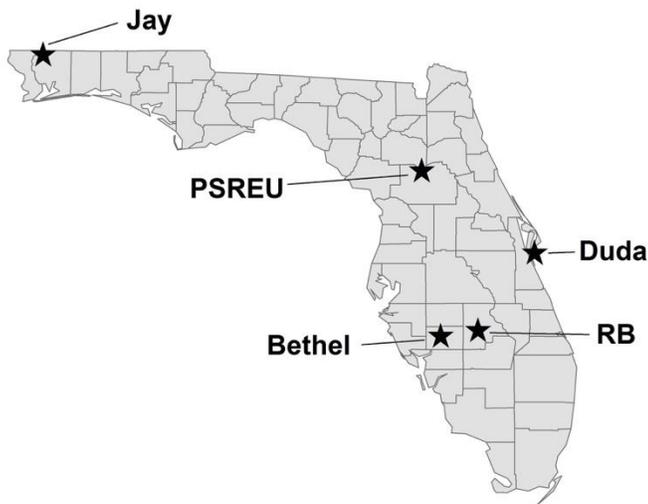


Figure 2-1. Geographical location of the five experimental sites within Florida

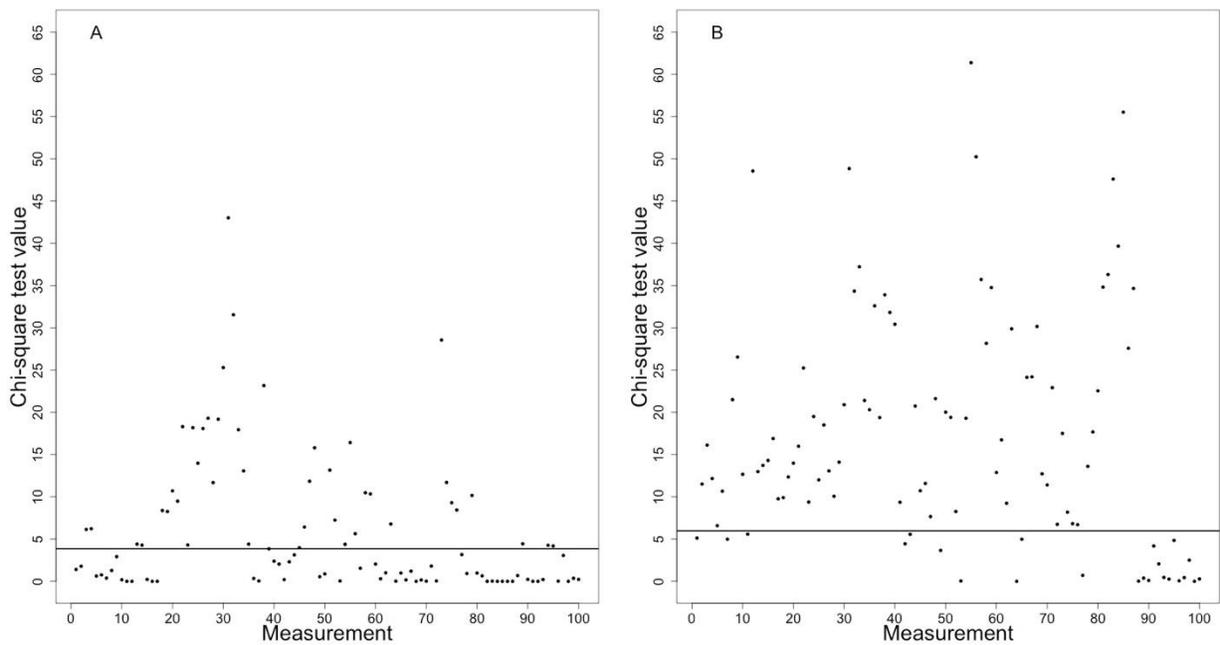


Figure 2-2. Likelihood ratio test (LRT) comparison between post-hoc IB design and RCB design (A), and between post-hoc R-C design and RCB design (B). The lines indicate the critical value of two-sided chi-square test with 1 degree of freedom (3.84, in A) and with 2 degrees of freedom (5.99, in B).

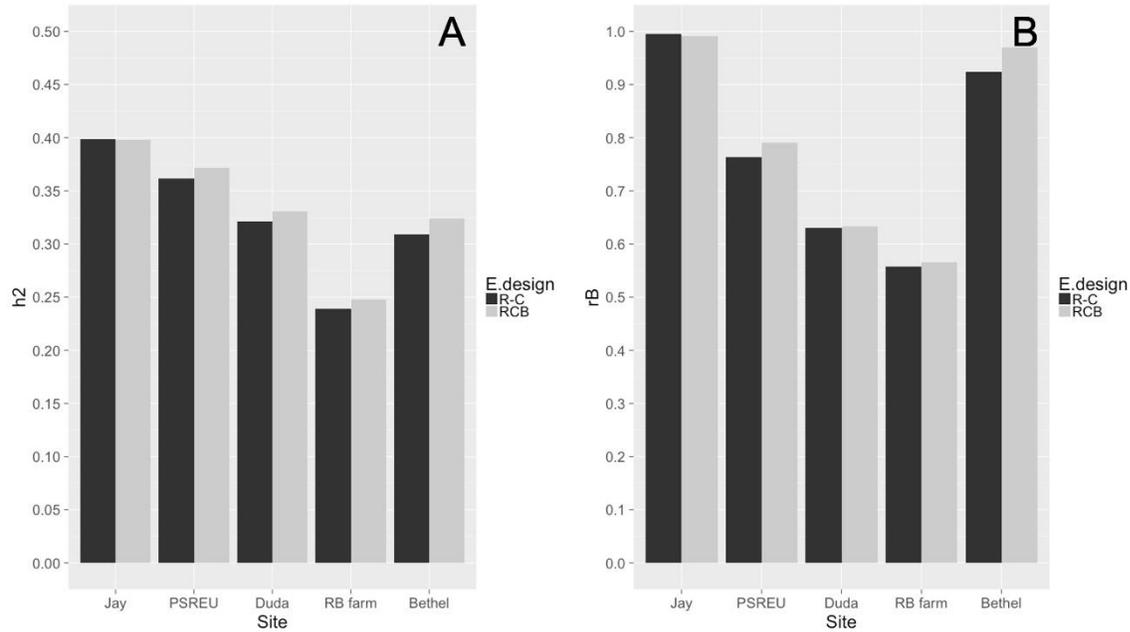


Figure 2-3. Estimation of narrow-sense heritability h^2 (2-8) (A) and genotype-by-measurement interaction r_B (B) for the analysis of each of the five sites with all their available measurements by fitting a randomized complete block (RCB, 2-5) and a row-column (R-C, 2-7) design.

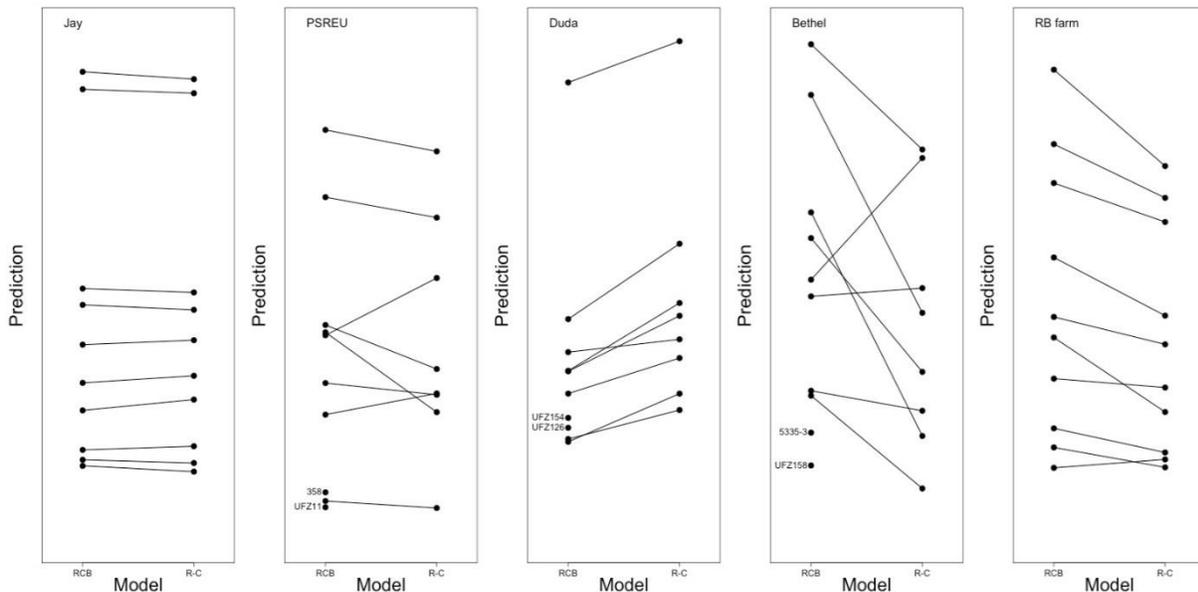


Figure 2-4. Changes of rankings of top 10 genotypes at different sites based on all available measurements per site by fitting a randomized complete block (RCB, 2-5) and a row-column (R-C, 2-7) design. Points with line connected are the same genotypes and the cross of lines indicate the ranking changes. Points with the names are genotypes that move out of the top 10 after implementation of post-hoc blocking with an R-C design.

CHAPTER 3
STATISTICAL ANALYSES OF MULTIPLE RESPONSE MEASUREMENTS TO
UNDERSTAND IMPACT OF DROUGHT AND GROWTH IN ZOYSIAGRASS

Background

The concept of GxE interaction has a critical role in cultivar development, specifically in evaluating the phenotypic stability in crop breeding. The GxE interaction is reflected in the performance of genotypes at various locations and impact differing traits such as extreme temperatures and water shortage. In plant breeding, multiple locations with the same genotypes are typically set up of cultivar development, especially, the selection of genotypes targets macro-regions. To improve cultivar development efficiency, understanding GxE of target species is an important step.

The drought condition usually occurs when the precipitation drops below the long-term average of several years, leading to soil moisture decreases to the point that negatively impact plant development. As the probability of extreme heat events in global scale increases, the breeding for drought resistant cultivar seem to be a reasonable consideration. Even though there were research related to zoysiagrass showed that the turfgrass rooting and drought resistance level could be markedly affected by the genetic tolerance, providing support of turf breeding effort on the drought resistance cultivars, there is still limited literature describing the impact of drought conditions on the genetic parameter estimations. Therefore, in this chapter, the broad-sense heritability (H^2) and GxE interactions will be estimated and, subsequently, the impact on estimations under drought conditions will be explored.

Materials and Methods

Experimental Data

The data used in this study originates from zoysiagrass trails that were established between 2011 and 2014 in five states (seven locations) in the United States, including Florida

(1), Texas (2), Georgia (2), North Carolina (1), and Oklahoma (1), representing different soil types and climate zones. A total of four series of seven trials each (identified as series 2011, 2012, 2013 and 2014) were established as randomized complete block (RCB) designs with two replicates and they include repeated measurements taken on an approximate monthly basis. Standard turfgrass maintenance practices were utilized to manage all experiments (Brede, 2000) and mowing frequency varied by location and was determined by local turfgrass breeding programs. There were 164, 164, 164, and 84 experimental genotypes tested in series 2011, 2012, 2013, and 2014, respectively, half of which originated from the Texas A&M University and half from the University of Florida breeding programs. Four common cultivars ('El Toro', 'Empire', 'Palisades', and 'Zeon') were also planted in all four series and served as checks. Genotypes were different across the series but identical within a series; hence, series were explored independently.

The response variable evaluated was turf quality (RTQ) rated with a 1-9 scale as described by the National Turfgrass Evaluation Program (NTEP) (Morris and Shearman, 1998), which was recorded in every evaluation. Here, a rating of 9 indicates outstanding or ideal turf, and 1 reflects very poor or dead turf. In general, a rating of 5 is considered the minimum acceptable turf quality. Due to different planting dates, the number of rating measurements differs by series, trials, and years.

To simplify further analyses, a new variable, TQ, was obtained by averaging the repeated measurements over time and replication within a given experimental unit. In addition, to facilitate the exploration of turf quality ratings at various conditions, other response variables were defined corresponding to averages of repeated measurements under: drought conditions (TQD); normal non-drought conditions (TQND); actively growing months, April/May to

October/November (TQG); and non-growing months, November/December to March April (TQNG). Drought conditions and active growing months were defined based on field observations of conditions and active growth period of plants during the year for each trial. Further details of phenotypic data are presented in Figure 3-1 and Table 3-1.

Statistical Analysis

The statistical analyses were carried out at different levels following some data cleaning procedures. First, to better understand the genetic signals, the individual RTQ measurements were fitted separately using the following linear mixed model

$$y = I\mu + X\beta + Zg + e \quad (3-1)$$

where y is the vector of phenotypic value (i.e. turf quality rating score); μ is the overall mean effect; β is the fixed vector of replicate (or block) effects; g is the random vector of genetic effect with $g \sim \text{MVN}(\mathbf{0}, \sigma_g^2 \mathbf{I})$; and e is the random vector of error, with $e \sim \text{MVN}(\mathbf{0}, \sigma_e^2 \mathbf{I})$. The letters X , Z represent the incidence matrices for their respective effects, I is a vector of ones, and \mathbf{I} is an identity matrix of its proper size.

Based on the estimated variance components for each of the analyses, a broad-sense heritability (H_y^2) was calculated as

$$H_y^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2} \quad (3-2)$$

First, Measurements with very low genetic signals ($H_y^2 < 0.05$) were removed.

Second, TQ, TQD, TQND, TQG, and TQNG were calculated with the remaining measurements to be used for further analysis. Since the majority of genotypes tested in the four series were different, the analyses were performed separately by series considering all their corresponding seven trails. Within series, the levels of genetic control and genotype by environment (GxE) interactions were assessed by fitting the model

$$\mathbf{y} = \mathbf{I}\mu + \mathbf{X}_1\mathbf{u} + \mathbf{X}_2\mathbf{b}(\mathbf{u}) + \mathbf{Z}\mathbf{g}(\mathbf{u}) + \mathbf{e} \quad (3-3)$$

where \mathbf{y} is the vector of phenotypic values (TQ, TQD, TQND, TQG and TQNG); μ is the overall mean effect; \mathbf{u} is the fixed vector of trial; $\mathbf{b}(\mathbf{u})$ is the fixed vector of block effect within trial; $\mathbf{g}(\mathbf{u})$ is the random vector of genetic effect within each trial, with $\mathbf{g}(\mathbf{u}) \sim \text{MVN}(\mathbf{0}, \mathbf{I} \otimes \mathbf{G})$; and \mathbf{e} is the random vector of errors, with $\mathbf{e} \sim \text{MVN}(\mathbf{0}, \mathbf{R})$. \mathbf{G} is a matrix of variance-covariance (dimension determined by the number of trials within a series) between genotypes across trials, modeled by considering a single Type-B genetic correlation term, r_B , and a unique i^{th} variance term, σ_{gui}^2 , for each trial (i.e., CORUH). \mathbf{R} is a block diagonal matrix of variance-covariance components (dimension determined by the number of trials within a series) with a different residual variance for i^{th} trial, σ_{ei}^2 . The letters \mathbf{X}_1 , \mathbf{X}_2 and \mathbf{Z} represent the incidence matrices for their respective effects, \otimes is the Kronecker or direct product, and all other matrices were as previously defined.

Based on the estimated variance components for each of the analyses, the broad-sense heritability at each site ($H_{(i)}^2$) and overall broad-sense heritability (H^2) of a series were calculated for each of the responses with the following expressions

$$H_{(i)}^2 = \frac{\sigma_{gui}^2}{\sigma_{gui}^2 + \sigma_{ei}^2} \quad (3-4)$$

$$H^2 = (\overline{\sigma_{gu}^2} \times r_B) / (\overline{\sigma_e^2} + \overline{\sigma_{gu}^2}) \quad (3-5)$$

where the bars over the variance components identify averages of variance components over the trial estimates.

Third, to understand the level of pleiotropy of genotype performance at various environmental conditions, bivariate analyses were performed for TQD against TQND, and TQG against TQNG. As before, these bivariate analyses were done to each series separately, as different genotypes were tested in each series. The model fitted corresponded to

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = X_1 t + X_2 \beta(t) + Z g(t) + e$$

where y_1 and y_2 are the data vectors for the two traits of interest; t is the fixed vector of group effects, where each was defined as the combination of trait and trial; $\beta(t)$ is the fixed vector of block effects within group; $g(t)$ is the random vector of genetic effect within group, with $g(t) \sim \text{MVN}(0, I \otimes G)$; and e is the random vector of errors, with $e \sim \text{MVN}(0, I \otimes R)$. The matrix G is a 2 x 2 variance-covariance matrix between traits defined by a single trait-to-trait Type-A genetic correlation term (r_A), and a unique j^{th} variance term, σ_{gtj}^2 for each trait (i.e., CORUH). The matrix R is a uniform heterogeneous 2 x 2 matrix of variance-covariance components between residuals of the same group. All the other matrices were previously defined.

Finally, even though the relationship between genotype performances under different conditions were explored with the above models, specific performance of genotypes needs to be further explored. In order to provide further insights, the top 10%, 20% and 30% genotypes under TQD and TQND were compared.

All linear mixed models were fitted with the software ASreml v. 3 (Gilmour et al., 2009) that estimates variance component under REML and provides BLUP values for each genotype.

Results

The analyses that were carried out on the single-measurement level of RTQ provide insight on the level of genetic signal of the collected data. The total number of measurements available for RTQ over all series corresponded to 206 with the highest broad-sense heritability, H_y^2 , of 0.839 and the lowest of 0.001. Six measurements with $H_y^2 < 0.05$ were removed from dataset before calculating the other aggregated response variables.

The variables TQ, TQD, TQND, TQG, and TQNG help to summarize the data from different trails that have been collected over multiple measurements. The response variable TQ

had an average value by trial that ranged from 4.13 (Dallas) to 6.65 (Griffin), and there were different number of measurements at locations (Table 3-1). In total, there were 200 measurements across all combinations of trial-series with the lowest number of measurements collected at Tifton (10) and highest number of measurements at Citra (37) (Table 3-1). The number of measurements for response variable TQD and TQND was similar (92 and 102, respectively). As expected, the average value of TQ under non-drought (TQND) was consistently higher than that under drought (TQD) at multiple trials except for Dallas. On the other hand, TQ under growth measurements (TQG) had higher number of measurements (187) than that under non-growth measurements (TQNG), which indicated that the focus of data collection of turfgrass by the breeders was concentrated on the growing seasons. The average values of the TQG were higher than those of TQNG at Citra and Dallas and lower at College Station and Stillwater. Overall, there was no clear pattern identified between TQG and TQNG, and there were no measurements for some of the trails (Griffin, Sandhills, and Tifton) for the non-growth period.

The site-to-site Type-B genetic correlations (r_B), used indirectly to evaluate the GxE interaction, varied for TQ from its lowest value of 0.350 in series 2011 to its highest value of 0.727 in series 2012, with an average of 0.519 (Figure 3-2 and Table B-1). In series 2011, the performances of genotypes at various locations were quite different; whereas, in series 2012, genotype performances were more alike. Moreover, when comparing the responses TQND and TQD, the yearly Type-B genetic correlations of TQND were 0.296, 0.724, 0.598, 0.689; consistently higher than those of TQD, 0.277, 0.608, 0.308, 0.425. Similar results were found for TQG and TQNG, which showed that the Type-B genetic correlations of TQNG were consistently higher than those of TQG (Figure 3-2 and Table B-1). By comparing the average of the correlations across the five response variables (TQ, TQD, TQND, TQG and TQNG), series 2011

had the lowest values (0.378), and series 2012 had the highest value (0.734), which holds across all the traits except for TQNG (Figure 3-2 and Table B-1).

The broad-sense heritability, $H_{(i)}^2$, of the calculated average response variables were analyzed by sites and year to reflect the site-specific and year-specific genetic information. In series 2011, TQND had the highest heritability (0.485), and TQNG had the lowest (0.236), which can be explained by the active expression of genetic signals during normal non-drought conditions and the difficulty of differentiating phenotypic performance across genotypes during the non-growing season (Table 3-2). In series 2012, TQG had the highest $H_{(i)}^2$ (0.558), which was very close to that of TQ (0.557). On the other hand, TQNG still had the lowest $H_{(i)}^2$ (0.337) across all the response variables. Interestingly, in series 2013, TQD had the highest $H_{(i)}^2$ (0.509), followed by TQ (0.500) and TQG (0.500), indicating that drought conditions in this series did not have an important impact on the phenotypic signal of the genotypes evaluated. In series 2014, TQND had the highest $H_{(i)}^2$ (0.561) and TQNG had the lowest value (0.239) (Table 3-2).

Given that the previously reported heritability values were calculated on a by-site and by-series basis, these estimates may be inflated by other sources of variance such as GxE interaction. To eliminate this bias, an analysis was carried out considering all the sites within a series. For TQ, the H^2 ranged from 0.165 to 0.397 with an average of 0.290 (Figure 3-3 and Table B-2). The H^2 of TQD were consistently higher than that of TQND. Similar trends were found for TQG with higher heritability values than TQNG with an exception of series 2014, in which the two estimates were very close (Figure 3-3 and Table B-2). When averaged across series, the H^2 values of the five calculated responses ranged from 0.181 (TQD) to 0.296 (TQND).

The bivariate analysis by series on TQD and TQND, TQG and TQNG were carried out to compare the performance of genotypes under different environmental conditions (in this case drought and non-drought, and growth and non-growth), providing useful information to assist in effects of indirect selection. Since for each series, the genotypes were different, the analyses were carried out separately by series. Series 2011 presented a trait-to-trait Type-A genetic correlation (r_A) between TQD and TQND, at various trials, with values ranging from -0.032 to 0.820 with most of the values between 0.703 to 0.878 (Figure 3-4 and Table B-3). Moreover, the Type-A correlation between TQG and TQNG varied from 0.070 to 0.959, which indicated, within some of the trials, that TQG and TQNG were almost independent traits, while in other trials, TQG and TQNG were almost identical traits (Figure 3-4 and Table B-3). In series 2012, the Type-A correlation between TQD and TQND within all the sites varied from 0.708 to 0.999. Similar trends were observed in series 2013 for TQD and TQND as well, when Type-A correlation values ranged from 0.622 to 0.976 with most values above 0.873 (Figure 3-4 and Table B-3). Interestingly, the correlation between TQG and TQNG in 2012-2013, at College Station, Dallas and Stillwater were 0.948, 0.851, 0.999, respectively; indicating that selections under growth and non-growth periods in this season were very similar (Figure 3-4 and Table B-3). Similar trends were observed in series 2014 with Type-A correlations ranged from 0.852 to 0.929. In contrast, for series 2014, Type-A correlations between TQD and TQND differed for different locations considerably (ranging from 0.079 to 0.999), which indicates that the impact of drought conditions on genotype performance varied considerably at different sites (Figure 3-4 and Table B-3).

Top genotypes BLUP values were compared for the analyses on the calculated response variables TQD and TQND, in which the percentage of genotypes (10, 20 and 30%) on both top

performers lists, was obtained (Figure 3-5). The identified top genotypes that agreed for TQD and TQND in series 2011 and 2014 were lower than those from series 2012 and 2013 (Figure 3-5). As the selection pressure decreased, the percentage of top genotype matching increased. Overall, the percentage of top genotypes matching under drought and non-drought conditions peaked at 30% selection intensity and the mean across multiple series was 57.75%, leading to poor agreement of top identified genotypes in TQD and TQND (Figure 3-5); thus, reflecting the difference nature of these traits.

Discussion

The level of GxE interaction between sites was explored by calculating a single correlation value (i.e. Type-B genetic correlation) within series estimated by fitting a complex linear mixed model (using the CORUH structure), giving an overall indication of the genotype performance across trials. For example, in series 2011, the r_B of sites was 0.350 (0.048), indicating a relatively high level of GxE across trials. However, by modeling the data in less parsimonious way with a different correlation parameter between pairs of trials (i.e. CORGH), it is not hard to note that the genetic correlation between Tifton and Citra, Tifton and Griffin were 0.728, 0.624, respectively, which indicates lower GxE interaction levels for those sites than previously estimated (Table B-4). By comparing the overall H^2 (Figure 3-3 and Table B-2) with the GxE effect (Figure 3-2 and Table B-1), a trend was identified, where lower GxE interaction levels usually are accompanied by higher H^2 values, and vice versa, which can be found across the five calculated response variables (TQ, TQD, TQND, TQG, and TQNG). However, the direct comparisons of response variables between series in terms of H^2 and GxE are not very reasonable as the genotypes differ from series to series.

The available literature on zoysiagrass breeding is limited. Some studies reported heritability values for relative leaf firing, shoot, and root growth (Qian et al., 2000), but there is

not much information available regarding the estimation of the heritability in turf quality traits. Schwartz et al. (2009) reported heritability estimates of turf quality based on three leaf textures: very fine, fine, coarse. These values ranged from 0.70 to 0.76 for different textured zoysiagrass species based on one location data. These values are considerable high when compared to the estimated heritability presented in our study of TQ trait, that ranged from 0.165 to 0.397 (Figure 3-3 and Table B-2); which were estimated by considering multiple sites, and the estimate from Schwartz et al. (2009) may be inflated by GxE effects.

The measurements in this study were mainly collected during the growth period, which is reasonable considering the biological conditions of turfgrass. However, the number of measurements between trials and series vary considerably. For example, for TQ measurements in Citra, there were 37 across multiple series, but there were only 10 in Tifton, which created unbalanced datasets for evaluation and estimation of genetic effects. In addition, by observing the frequency of measurements taken, some trials had consistently one or two measurements per month, a fact that might favor estimation of effects on some trials over others. According to Xing et al. (2017) that evaluated the estimations of genotype-by-measurement interaction in zoysiagrass, the authors suggested that monthly rating could be potentially reduced without significant impacting on reducing the quality of the information.

The drought effects on zoysiagrass have been well studied on the root and shoot, and after drought recovery responses (Huang, et al., 1997; Marcum et al., 1995), but most of the studies were focused on the physiological aspects without covering their impact on breeding selections. By comparing the TQD against TQND in terms of GxE interaction and H^2 , it was shown in this study that drought effects induce differential genetic expressions of turf quality. In detail, the estimation of Type-B correlation and heritability of the response variable TQD were

consistently lower than these of TQND, a phenomenon that could be caused by many factors. One possibility is that the drought conditions may have some masking effect by limiting the genetic expressions, reflected as more similar phenotypic responses.

To better understand the drought effect to breeding selections, bivariate analyses between TQD and TQND were performed. Most of the genetic correlations (i.e. 11 out of 12), in series 2011 and 2012, were higher than 0.7. Thus, it appears that both responses provide with similar genetic information. However, because breeding selection is based on the top performance genotypes, the bivariate analyses regarding the overall correlation between two responses may not completely reflect the relationship between top performers. From observing the matching percentage of top genotypes for TQD and TQND, it is reasonable to assume that the drought conditions create very different breeding selection sets of genotypes (Figure 3-5). On the other hand, the correlations from bivariate analyses between TQG and TQNG were fluctuated in a wide range, from being almost independent to highly correlated, which make the two response measurements unreliable to represent each other. Therefore, plant breeders need to be aware of the difference in data information collected at different growth conditions and, based on breeding goals, carry out the data collection accordingly.

In summary, this study reported the levels of GxE interaction and heritability of zoysiagrass with data from seven locations measured over time over a range of environmental conditions, which add reliable genetic information to the understanding of this species for breeding purposes. It was noted that drought conditions affect the estimated genetic parameters and the rank of top genotypes. To have more reliable plant breeding selections, it is recommended to use the data from the non-drought conditions to perform rankings. Finally, the analytical approach used in this study can be potentially used as a template to answer similar

questions in other commercially relevant crops, particularly those that deal with several observations over one or multiple sessions, such as phenotypic scores or harvests.

Table 3-1. Summary of five response variables in each of the seven trails including all series.
 The first and second values represent the mean and its standard error, respectively.
 Number of measurements is shown in parenthesis.

Response	College						
	Citra	Station	Dallas	Griffin	Sandhills	Stillwater	Tifton
TQ	4.15±0.02 (37)	4.83±0.02 (36)	4.13±0.02 (35)	6.65±0.02 (15)	4.83±0.02 (31)	4.42±0.02 (36)	5.03±0.03 (10)
TQD	3.80±0.02 (21)	4.30±0.02 (23)	4.56±0.03 (13)	5.68±0.04 (3)	4.12±0.02 (11)	3.60±0.02 (18)	3.86±0.04 (3)
TQND	4.59±0.02 (16)	5.68±0.02 (13)	3.90±0.02 (22)	6.91±0.02 (12)	5.22±0.02 (20)	5.41±0.02 (18)	5.53±0.03 (7)
TQG	4.18±0.02 (35)	4.77±0.02 (34)	4.31±0.02 (29)	6.65±0.02 (15)	4.83±0.02 (31)	4.35±0.02 (33)	5.03±0.03 (10)
TQNG	3.67±0.07 (2)	5.64±0.06 (2)	3.36±0.03 (6)	- (0)	- (0)	5.35±0.05 (3)	- (0)

Table 3-2. Summary of broad-sense heritability estimates for different calculated response variables in different trials for each series. Values in parenthesis correspond to standard error of the estimates. TQ, averages of repeated measurements of turf quality; TQD, averages of repeated measurements of turf quality under drought conditions; TQND, averages of repeated measurements of turf quality under non-drought conditions; TQG, averages of repeated measurements of turf quality in growing months (April/May to October/November); TQNG, averages of repeated measurements of turf quality in non-growing months (November/December to March April); College Stn, abbreviation of location, College Station.

Series	Trial	TQ	TQD	TQND	TQG	TQNG
2011	Citra	0.404 (0.064)	0.385 (0.067)	0.347 (0.067)	0.405 (0.065)	0.086 (0.052)
	College Stn	0.346 (0.069)	0.363 (0.068)	0.523 (0.059)	0.323 (0.070)	0.319 (0.071)
	Dallas	0.552 (0.054)	0.557 (0.054)	0.536 (0.055)	0.538 (0.055)	0.540 (0.055)
	Griffin	0.344 (0.068)	.	0.359 (0.068)	0.347 (0.068)	.
	Sandhills	0.382 (0.066)	0.000 (0.000)	0.462 (0.062)	0.384 (0.066)	.
	Stillwater	0.411 (0.067)	0.299 (0.072)	0.485 (0.061)	0.438 (0.066)	0.000 (0.000)
	Tifton	0.687 (0.041)	.	0.685 (0.041)	0.686 (0.041)	.
	Average	0.447	0.321	0.485	0.446	0.236
2012	Citra	0.264 (0.057)	0.347 (0.065)	0.234 (0.065)	0.278 (0.058)	.
	College Stn	0.571 (0.051)	0.398 (0.062)	0.473 (0.062)	0.507 (0.055)	0.325 (0.070)
	Dallas	0.872 (0.019)	0.828 (0.024)	0.831 (0.024)	0.873 (0.019)	0.676 (0.043)
	Griffin	0.412 (0.058)	0.414 (0.062)	0.141 (0.062)	0.419 (0.059)	.
	Sandhills	0.502 (0.055)	0.386 (0.063)	0.580 (0.063)	0.510 (0.055)	.
	Stillwater	0.487 (0.055)	0.249 (0.061)	0.601 (0.061)	0.529 (0.055)	0.010 (0.014)
	Tifton	0.794 (0.056)	0.571 (0.053)	0.803 (0.053)	0.794 (0.029)	.
	Average	0.557	0.456	0.523	0.558	0.337

Table 3-2. Continued.

Series	Trail	TQ	TQD	TQND	TQG	TQNG
2013	Citra	0.357 (0.067)	0.324 (0.069)	0.274 (0.065)	0.357 (0.067)	.
	College Stn	0.246 (0.072)	0.116 (0.066)	0.384 (0.067)	0.246 (0.072)	.
	Dallas	0.592 (0.050)	0.698 (0.040)	0.533 (0.055)	0.592 (0.050)	.
	Griffin	0.297 (0.069)	.	0.253 (0.064)	0.297 (0.069)	.
	Sandhills	0.509 (0.057)	0.406 (0.064)	0.503 (0.057)	0.509 (0.057)	.
	Stillwater	0.824 (0.026)	0.837 (0.024)	0.588 (0.051)	0.824 (0.026)	.
	Tifton	0.674 (0.044)	0.676 (0.044)	.	0.674 (0.044)	.
	Average	0.500	0.509	0.423	0.500	.
2014	Citra	0.636 (0.069)	0.566 (0.079)	0.533 (0.080)	0.604 (0.074)	0.477 (0.088)
	College Stn	0.000 (0.000)	0.000 (0.000)	0.359 (0.087)	0.000 (0.000)	.
	Dallas	0.634 (0.068)	0.638 (0.066)	0.618 (0.068)	0.633 (0.069)	.
	Griffin	0.457 (0.082)	0.135 (0.087)	0.539 (0.074)	0.457 (0.082)	.
	Sandhills	0.720 (0.052)	0.443 (0.087)	0.700 (0.056)	0.720 (0.052)	.
	Stillwater	0.689 (0.057)	0.550 (0.075)	0.614 (0.068)	0.685 (0.058)	0.000 (0.000)
	Tifton
	Average	0.523	0.388	0.561	0.516	0.239

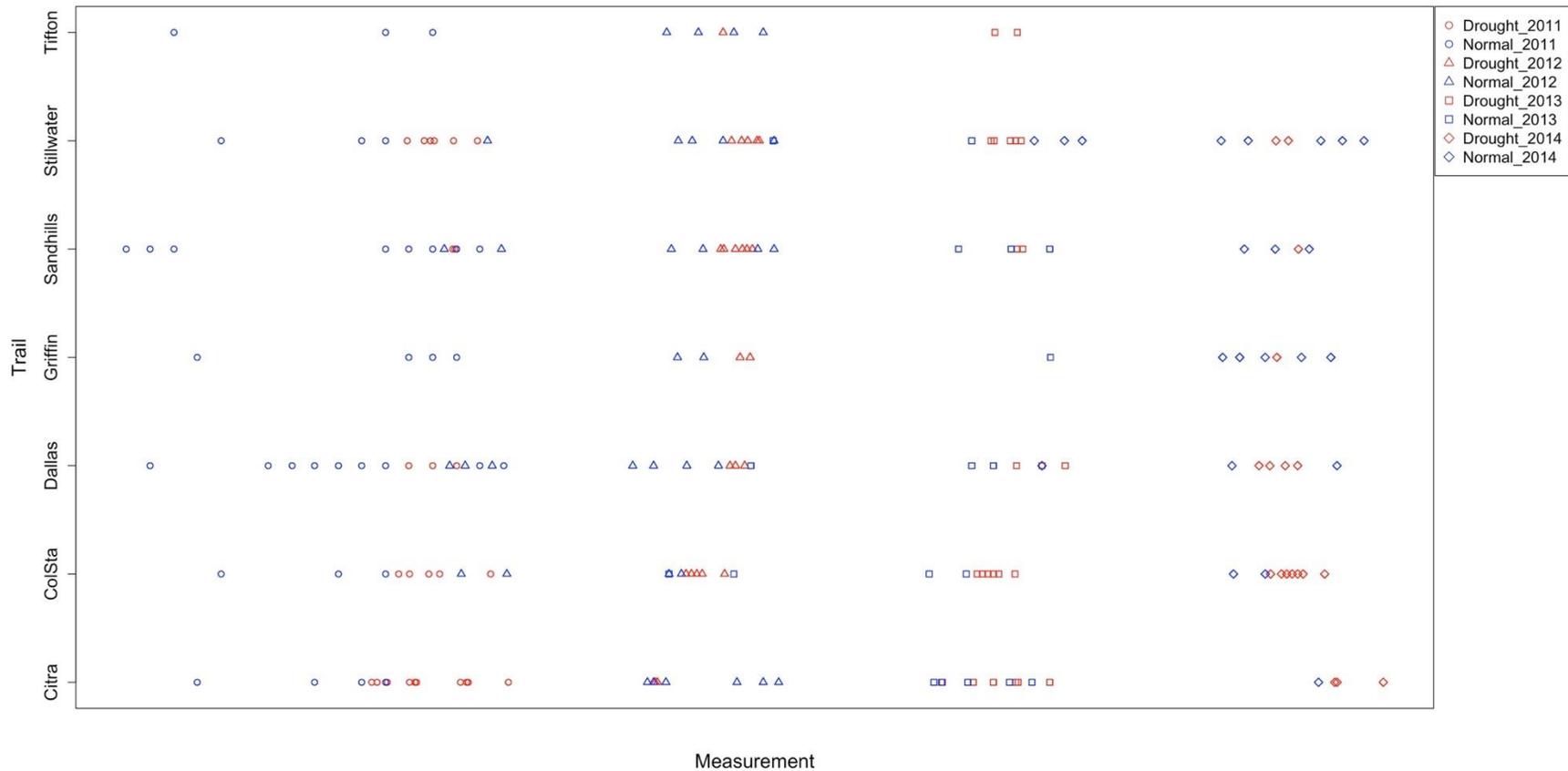


Figure 3-1. Distribution of measurements at different trails. The x-axis marks the measurement month and the y-axis shows the corresponding trails. Different shapes indicate which series the measurements belong to. The red and green color identifies those measurements were taken under drought or normal conditions, respectively.

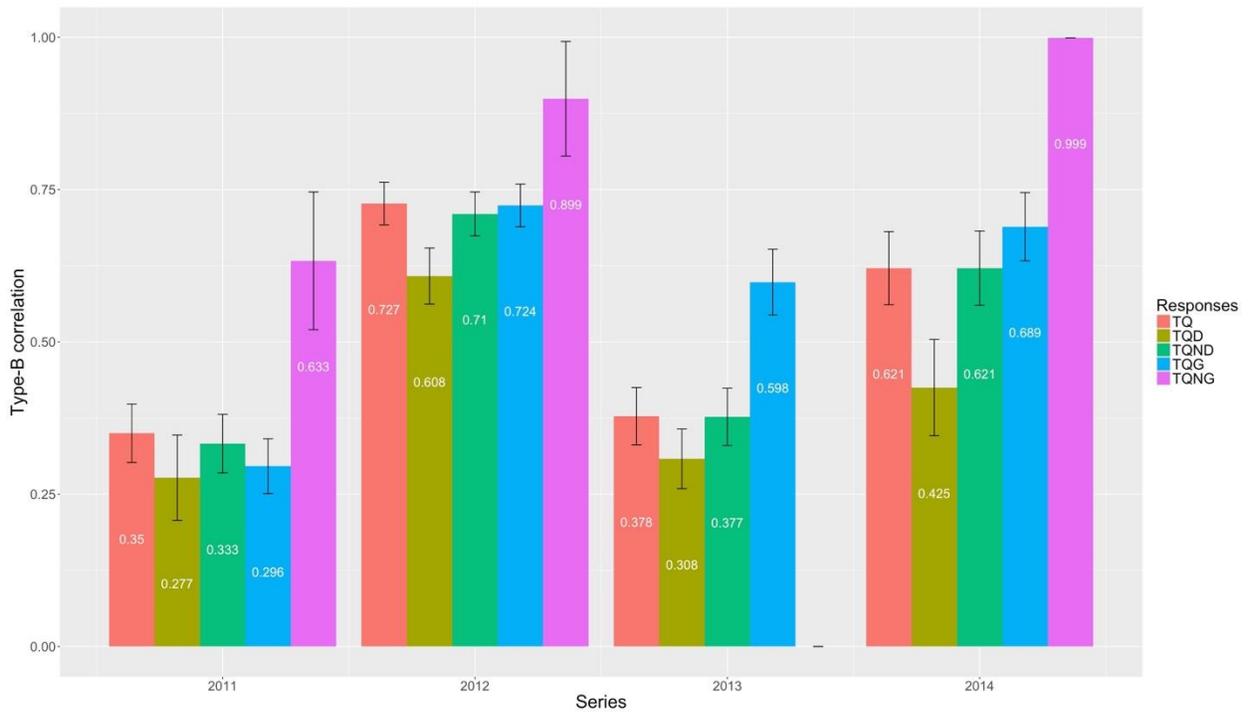


Figure 3-2. Site-to-site Type-B genetic correlations, r_B , for different calculated response variables by series. The whisker bars represent the standard errors of the mean.

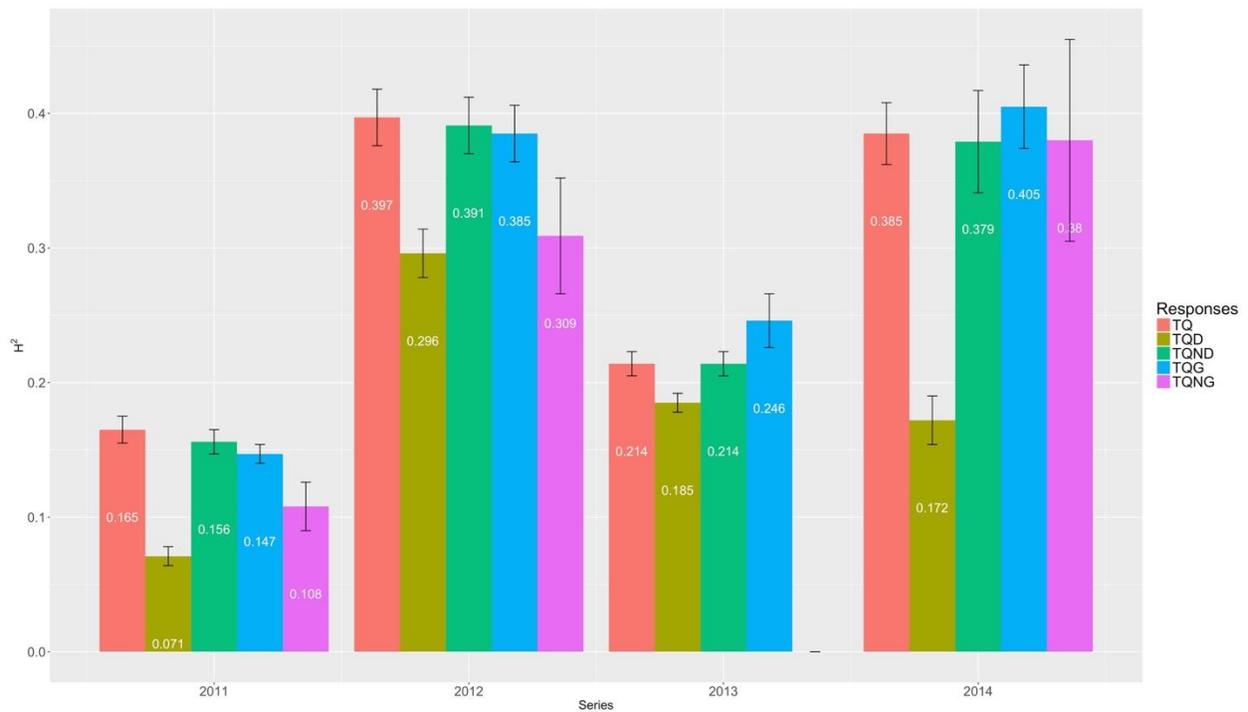


Figure 3-3. Summary of broad-sense heritability estimates, H^2 , of calculated response variables considering data from all trails within a series. The whisker bars represent the standard errors of the mean.

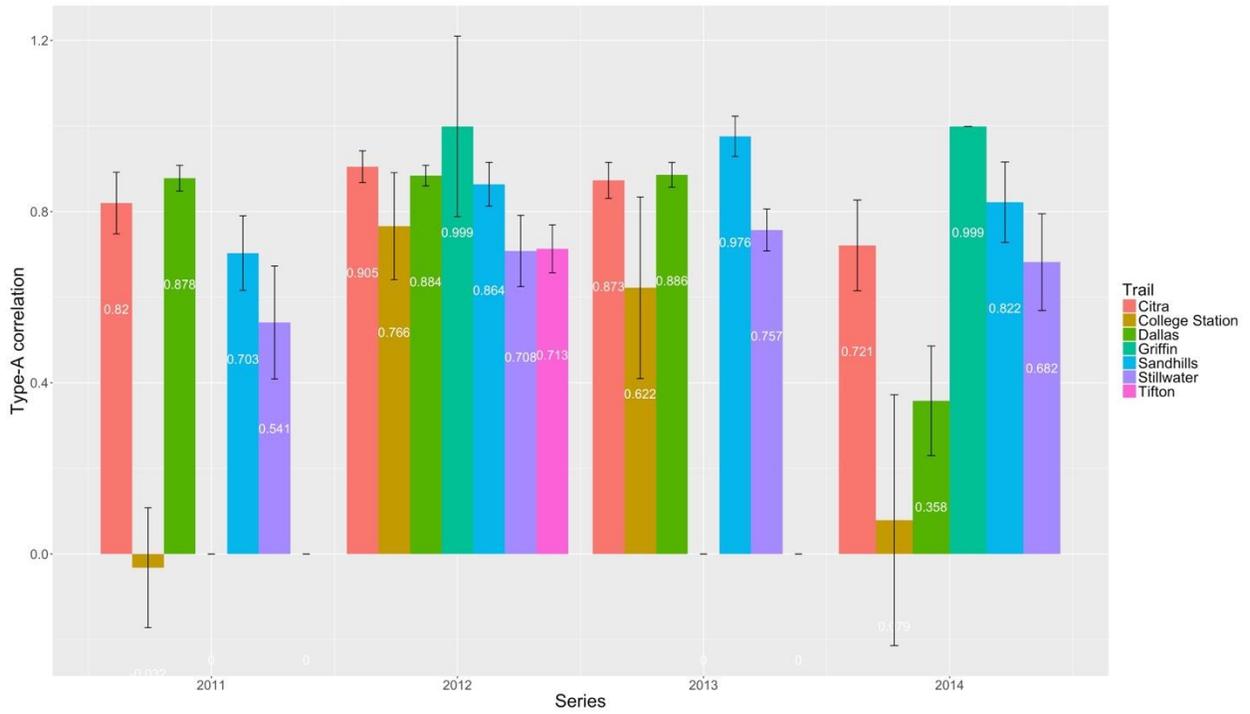


Figure 3-4. Trait-to-trait Type-A genetic correlations, r_A , for each trail based on the bivariate analysis of TQD against TQND with data from all trails within series. The whisker bars represent the standard errors of the mean.

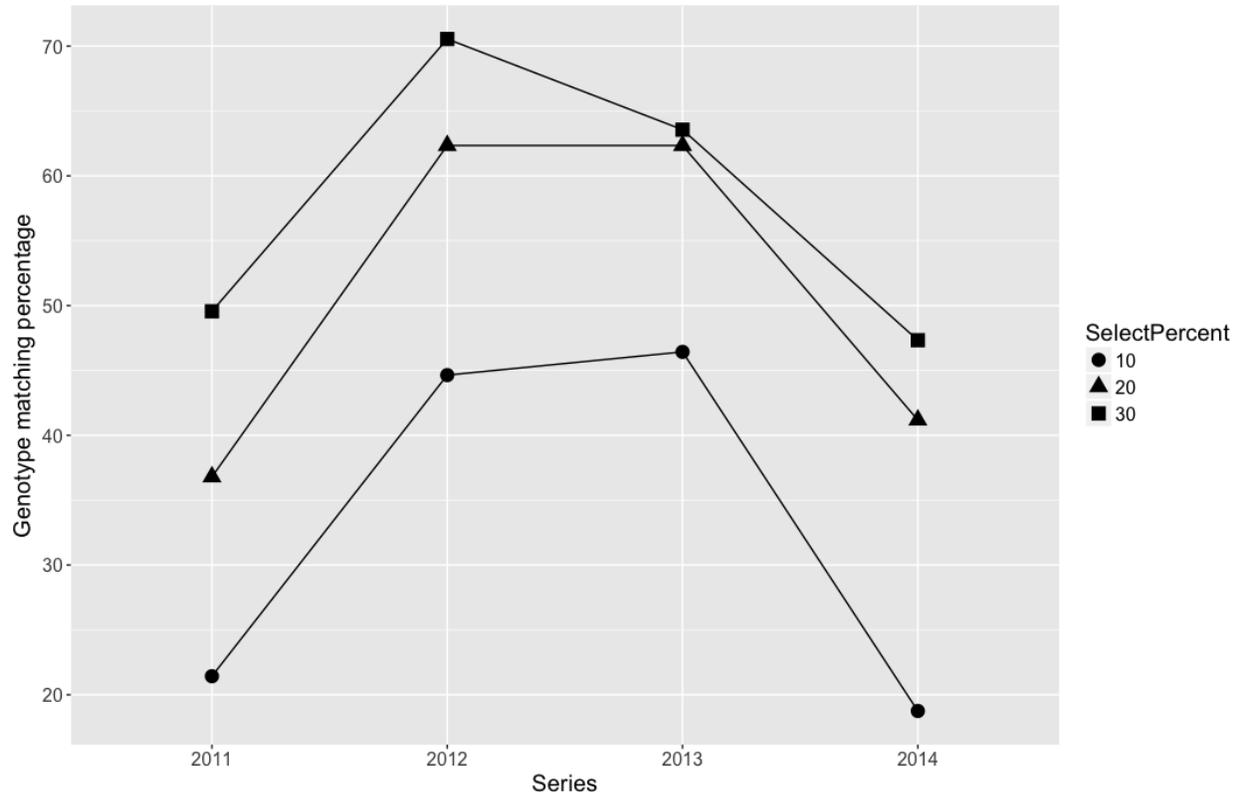


Figure 3-5. Percentage of top genotype matching from series 2011 to 2014 with the selection intensities of 10%, 20% and 30%.

CHAPTER 4 IMPROVING PREDICTABILITY OF MULTI-SENSOR DATA WITH NONLINEAR STATISTICAL METHODOLOGIES¹

Background

The evaluation of the forage quality nutritive value and biomass usually takes multiple harvests, and is considered time-consuming, labor intensive, and expensive. The use of sensors to evaluate different forage traits has been proposed as a method to alleviate this problem. However, most analytical techniques involve the use of traditional linear methods to predict and the prediction models can still be improved with the use of non-linear methods. In this study, nonlinear methodologies were evaluated for their prediction accuracy in 16 agronomic important traits compare to traditional approaches and the importance of prediction variables were explored.

Materials and Methods

Experiment Description

The experiment was carried out on a >15-year old well established 'Midland 99' bermudagrass field at the Noble Research Institute, LLC Red River Research and Demonstration Farm near Burneyville, OK (33.88° N, 97.28° W; elevation 234 meters). The soil was characterized as Slaughterville fine sandy loam (coarse-loamy, mixed, superactive, thermic Udic Haplustolls) with N-nitrate, P and K soil test values of <5, and 64017 g kg⁻¹, respectively, and pH of 6.3. Soil was amended with 178 kg K ha⁻¹ (0-0-60, muriate of potash) (Pittman et al., 2015).

The trial was setup as a RCBD with seven levels of N treatments (0, 28, 56, 84, 112, 168, and 224 kg N ha⁻¹), and four blocks (3.0 m x 6.0 m plot size). The treatment design was

Chapter submitted to Crop Science Journal in August 2017

structured to ensure maximum variability in responses (DMY and nutritive value), which is needed for model construction. The N treatments were initially applied on 1 May 2015 and reapplied on 15 June 2015 (Pittman et al., 2015).

Measurements

Data were collected in 2015 using both standard physical methods and sensor measurements with a multi-sensor array including ultrasonic, laser, and spectral sensors described by Pittman et al. (2015). Seven harvests occurred across the summer, with first harvest on May 18th and the last harvest on August 18th with an average of 14-days harvest interval. The total number of measurements was 532 with 17 predictors and 16 response variables. The measurement variables include lasers (Pittman et al., 2015), ultrasonic, NDVI from GreenSeeker® (Trimble Inc., Sunnyvale, CA), infrared reflectance vegetative index (IRVI), normalized difference red edge index (NDRE), NDVI from Crop Circle ACS-430 active canopy sensor (HSNDVI) (Holland Scientific, Lincoln, NE), leaf area index proxy index (LAIVI), chlorophyll content index (CCCVI), red-edge reflectance (RE), near-infrared reflectance (NIR), red reflectance (RED), vegetation temperature (VegTemp), intercepted photosynthetically active radiation (IPAR), RPAR, reflectance at 532 nm (nm532), reflectance at 550 nm (nm550), and reflectance at 700nm (nm700).

The agronomically important traits were DMY and concentrations of crude protein (CP), Ca, P, K, Mg, acid detergent fiber (ADF), neutral detergent fiber (NDF), total digestible nutrients (TDN), lignin, in vitro true dry matter digestibility (IVTDMD), ash, 48 hr digestible NDF (dNDF48), fructana, sugars, and water-soluble carbohydrates (WSC). The DMY and forage nutritive value analyses were estimated by hand clipping two 0.11 m² quadrats per plot to a 2.5-cm stubble height. Samples were dried in a forced draft oven at 50 °C for five days, weighed, ground in a Wiley mill (Thomas Scientific, Swedesboro, NJ) to pass a 1-mm screen, and

submitted for nutritive value analysis. All nutritive value analyses were conducted using the Foss 6500 NIRS instrument. The samples were scanned using Foss ISIScan software (Infrasoft, 2003) and nutritive values were estimated using 2013 prediction equations for grass hay developed by the NIRS Forage and Feed Testing Consortium (Hillsboro, WI).

Missing values of sensor measurements were handled in two ways. If the missing values for a single observation were found in more than three sensor variables, the observation was removed. If the missing values were in less than three sensor variable measurements, then they were filled with imputation from a linear model. To impute the missing values, all the sensor variables without missing values on the target imputation rows were fitted on a linear model, then a stepwise AIC was utilized to reach the final model. Thereafter, the prediction values from the final models were used to fill in the missing values in the target rows. In this study, five sonar data points were imputed.

Feature Engineering

Based on the variables in dataset, the canopy temperature depression (CTD) index and fraction intercepted photosynthetically active radiation (FIPAR) were calculated with

$$\text{CTD} = \text{airTemp} - \text{VegTemp} \quad (4-1)$$

$$\text{FIPAR} = \frac{\text{IPAR} - \text{RPAR}}{\text{IPAR}} \quad (4-2)$$

where airTemp is the air temperature; VegTemp is the vegetation temperature; IPAR is the incident photosynthetically active radiation; RPAR is the reflected photosynthetically active radiation.

Criteria of Model Performance

To evaluate the performance of models to predict a target trait, the root-mean-square error (RMSE) was proposed. However, because there are multiple traits with different

measurement units in the dataset and comparison among the performance of different traits were also of interest, the normalized root-mean-square error (NRMSE) was utilized. The RMSE and NRMSE were calculated as

$$\text{RMSE} = \sqrt{\sum_{i=1}^n (\hat{Y}_i - Y_i)^2 / n} \quad (4-3)$$

$$\text{NRMSE} = \frac{\text{RMSE}}{\bar{y}} \quad (4-4)$$

where Y_i denoted the observed value and \hat{Y}_i denoted the predicted value of corresponding observation; \bar{y} is the mean of the observations in the test dataset.

Even though the usage of NRMSE makes the model performance across all the traits comparable, the accuracy of the prediction was not very well characterized. Therefore, the predictability (the correlation between predicted and observed values) was also calculated.

Evaluation of the Prediction Methodologies

Partial least square regression is a widely-used methodology to regress predictor data against target prediction traits based on the assumption that the response variables are from a process generated by unobserved latent variables (Rosipal and Krämer, 2006). It is a competitive prediction model both due to its light computational requirements and superior performance when collinearity exists in the dataset (Wold et al., 1984). Even though PLS regression initially gained popularity in chemometric studies for its superior prediction performance (Sjöström et al., 1983; Geladi and Kowalski, 1986; Frank, 1987; Tobias, 1995), its application has been expanded to various research fields, such as genetics and ecological studies (Nguyen and Rocke, 2002; Carrascal et al., 2009). In spectral sensor data analysis, PLS regression was initially used as the default statistical methodology to predict variables of interest [e.g., estimation of grass biomass and measurement of nitrogen status (Hansen and Schjoerring, 2003; Cho et al., 2007)]. However, there are other prediction methodologies, such as ridge regression and random forest, that have

been used in other applications and shown high performance, which could potentially outperform PLS regression. Ridge regression is a methodology initially proposed by Hoerl and Kennard (1970) to address the potential instability in the least square estimations by adding a small constant value to the diagonal entries of the matrix $X^T X$ before taking its inverse. Even though the ridge regression estimators are biased, the prediction performance of this methodology is quite competitive. Because of the small noise added to the diagonal entries of the matrix $X^T X$, the ridge regression can handle multicollinearity very neatly, which is especially helpful in the sensor data as the collinearity is not uncommon (Mahajan et al., 1977; Rook et al., 1990). Support vector machine regression was based on the classification algorithm that projected the data into hyperplanes for differentiation and has been adapted to regression problems through a fixed feature-space transformation (Bishop, 2007). Considering the flexibility of kernel functions to capture the nonlinearity relationships, it has been widely adapted for various usage such as prediction of corporate financial distress, exchange rate prediction, wind speed prediction, and remote sensing (Mohandes et al., 2004; Pai et al., 2006; Hua et al., 2007; Mountrakis et al., 2011). Random forest is an ensemble learning method based on constructing multiple decision trees and obtaining the regression prediction by the mean of each tree's prediction (Liaw and Wiener, 2002). The combination of random selection of variables at each tree node split, full tree length growth, and multiple tree copies gives RF superior performance in multiple problems and effectively avoids overfitting issues.

In this study, PLS regression was used as the benchmark, and other statistical methodologies need to surpass its performance to be considered as alternatives. The methodologies tested included ridge regression, SVM and RF. The tuning of the model parameters was determined with the inner loop of the nested cross-validation and their

performance was evaluated with the hold out dataset in outer loop (Figure 4-1). For the PLS regression and random forest, the tuning parameters tested were 'ncomp' (1-15) and 'mtry' (1-10), respectively. Additional tuning parameters, such as number of trees, were determined by internal algorithms used by 'caret' package (in R (version 3.3.2)) and were combined with pre-defined testing parameters to form the tuning grids. For ridge regression and SVM, the number of parameters tested and selected by 'caret' package was set to 20, which is a compromise between the computing time and reliability of parameter selections. The tuning parameter of ridge regression was weight decay, lambda, whereas, SVM had two parameters, sigma and cost, to tune. After the determination of model parameters, the models could be potentially used to predict future harvests with upcoming sensor data measurements.

The estimation of model performance with cross-validation could be biased (Varma and Simon, 2006), therefore to have a solid evaluation on the performance of predictive models in this study, the nest cross-validation was used (Krstajic et al., 2014). In the nest cross-validation setup, the data were split into k-fold and each time one-fold was retained for testing and the remaining k-1 folds were used for training and validation (Figure 4-1). Different from k-fold cross-validation, the hold out sets do not have impacts on the parameter tuning and selections, only providing performance measurements of models.

Evaluation of Predictor Variables

Since biomass is the most important agronomical trait in this study, it was utilized as prediction target to illustrate the model performance after the removal of variables. The deterioration of performance after removal of a variable was used to measure the importance of the removed variable. The importance of variables was determined with a step by step elimination. The NRMSE was recorded for each removed variable, and after each variable had been eliminated, the one with the lowest NRMSE was removed. In each round, only one variable

was removed and the rest were used for model training and prediction testing. The assumption of removing the variable with the lowest NRMSE is that if the variable is important, by removing it, the performance of model should deteriorate quickly, resulting in high NRMSE. By repeating the process until only two variables remained, the importance of each sensor variable was determined. Statistical analysis was done using R (version 3.3.2), packages ‘caret’, ‘e1071’, ‘ggplot2’, and ‘MASS’ (Team, 2014).

Results

Predictability, which is the correlation between predicted and test dataset values, of the four methodologies was compared (Figure 4-2 and Table C-3). The RF and SVM with radial kernel were consistently better in prediction accuracy than PLS regression and ridge regression. In all the traits except DMY, SVM predicted better than the RF with higher predictability values. Both PLS regression and ridge regression had similar performance and were not statistically different in all traits. By the criteria of the predictability of traits greater than 0.85 for the best performance model, CP, DMY, dNDF48, IVTDMD, TDN, K, Mg, P, ADF, fructan, and NDF could be reliably predicted by sensor data (Figure 4-2 and Table C-3).

The DMY and TDN traits were selected based on largest and smallest NRMSE and to represent biomass and forage quality for further detailed investigation on the prediction performance (Figure 4-3). For DMY, most of the values clustered between 0 and 2500 kg ha⁻¹, in which the prediction values in PLS regression and ridge regression had greater variance than SVM and RF. At observations of high DMY, the prediction of all the methodologies tended to underestimate the observed value (Figure 4-3). The prediction patterns between SVM and RF were very similar and the predictability of RF (0.887) and SVM (0.883) was almost the same (Figure 4-3). Conversely, the overall value distribution of TDN was relatively uniform across the value range. The SVM and RF had more accurate predictions on TDN compared to PLS

regression and ridge regression, which reflected as data points were closer to the 1:1 perfect prediction line (Figure 4-3). There was no obvious bias found in the SVM model and its correlation is 0.934, indicating it could be reliably used for future predictions (Figure 4-3).

Even though the predictability reflects the overall trends of relative model performance, it does not provide a good measurement of total missing prediction loss and the bias, which are the magnitude of prediction deviations from the real measured values. Therefore, the NRMSE of the models were also reported to reflect the absolute missed prediction. It was apparent that model prediction performance of RF and SVM with radial kernel were more accurate better than PLS regression and ridge regression (Figure 4-4). Between RF and SVM, the performance greatly depends on the traits in the study. For ash and TDN, RF and SVM have quite similar performance. The RF had a more accurate prediction performance in DMY trait, whereas the SVM was slightly better in CP, sugars, WSC, dNDF48, IVTDMD, Ca, K, Mg, P, ADF, fructans, lignin, and NDF (Figure 4-4). Comparisons among the traits indicate that CP, DMY, sugars, and WSC are more difficult to predict than the other traits in terms of the total prediction loss. Out of all the traits, DMY is the most difficult trait to predict, whereas TDN, dNDF48, ADF, and NDF do not have much bias in predictions and are the traits most easily predicted. The results from NRMSE and predictability were not perfectly matched as some of the traits, such as DMY and CP, had decent predictability but its NRMSE had quite high values.

After the performance of the models was compared in different traits, the importance of sensor variables was studied as well. As DMY is the most important trait, it was used to represent the impact of removing of variables on the model prediction performance. In this study, the interval between harvests was approximate 14-day. The average DMY of seven harvests across the summer from the first to last were 1757, 2408, 2857, 2062, 2621, 1893, 1746 kg ha⁻¹,

respectively. The greatest yield occurred at the 3rd harvest (June 22nd) and lesser yields measured in early and late summer. Since NRMSE could reflect the performance of models on both the prediction and bias aspects, it was used in the study of impact of removed variables on the model performance. The removal of the first eight variables, NDRE, RE, LaiVI, FIPAR, HSNDVI, CCCVI, CTD, and IRVI, did not have much impact on the prediction of DMY trait and the performance of all predictive methods was stable (Figure 4-5). For PLS regression and ridge regression, after removal of the 9th variable, IRVI, the prediction performance exhibited a steep drop, and similar situation occurred when the 14th variable, RED, was removed, at which NRMSE increased at least 40% compared to the starting point. On the other hand, following the removal of the variable NDVI and the remaining variables, RF prediction performance gradually decreased while NRMSE increased around 21% compare to the original. Moreover, the NRMSE of SVM started at a greater value than RF, but was stable in the variable reduction process, resulting in a 9% increase of NRMSE. Overall, RF and SVM were more stable than PLS regression and ridge regression when there is variable information missing in the dataset.

Discussion

To describe model performance, two criteria, predictability and NRMSE, were used. Some traits (e.g. CP) were very high in terms of predictability, but not as good as expected measured in NRMSE, which could result from the bias of the prediction. Some of the predictions at high values may be under-predicted by the models (e.g. DMY) however, they are still higher in values compared to the predictions with lower observation values, which would be reflected in NRMSE but would not be covered by the correlations (Barnston, 1992). Regardless of criteria used to represent model performance, SVM always performed better than PLS regression and ridge regression with higher predictability and lower NRMSE values. In other words, the

prediction accuracy of nonlinear models is better than the linear models, which could be caused by some nonlinear trend in the mixed sensor dataset (Fan et al., 2009).

In forage crop experiments, multiple harvests within one year is not uncommon (Woodard and Prine, 1991; Robins et al., 2007; Tahir et al., 2011; Inostroza et al. 2015; Inostroza et al. 2016). When multiple harvests are involved in the experiment, determination of harvests that should be included in the future harvest prediction become very important. In this study, the results of utilizing all the previous harvests to predict future harvest indicate that usage of all the harvests to predict future harvest may not be the ideal condition (Table C-1). Harvests 4 and 5 have the best prediction performance compared to the predictions on the remaining harvests. At the same time, by increasing the number of harvests used for the model building, harvest 6 and 7 did not have a superior prediction performance (Table C-1). When a single harvest was used in model building and prediction for future harvest, some of the future harvests could be well predicted by the previous harvests. For example, harvest 4 was predicted with harvest 3 data (NRMSE = 0.14), while others were not (Table C-2). Hence, the prediction performance heavily depends on whether previous harvest could provide useful information to predict the future harvest. In future studies, if the research interest is to predict future harvest, it may be worth determining how many harvests should be included for model building to have the optimal prediction performance even though the harvest frequency may greatly depend on the physiological nature of the forage crops (Woodard and Prine, 1991; Sanderson et al., 1999).

Compared to other applications of sensor technology in forage crops, our analysis showed high prediction performance. Zhao et al. (2007) studied the prediction of forage biomass and quality parameters of bermudagrass with canopy reflectance measurements in which NDF, ADF, CP, and biomass had predictability around 0.72, 0.45, 0.85, and 0.74, respectively. In

comparison, by analyzing the combined sensor data with the SVM model, NDF, ADF, CP, and DMY in our study had predictability around 0.94, 0.93, 0.94, and 0.88, respectively. Knox et al. (2011) reported the total variance explained by regression for fiber and P traits were 65 and 57%, respectively, when hyperspectral Carnegie airborne observatory sensor was used to predict African savanna forage quality. In our study, the predictability of fiber and P were 90 and 87%, respectively, which could be considered an improvement compared to previous studies. Additionally, Zhao et al. (2007) reported bermudagrass r^2 values of NDF, ADF, and CP of 0.23, 0.21, 0.51, respectively, with two-band reflectance ratios ($R_{\text{NIR}}/R_{\text{red}}$). However, in our study, the same three traits had r^2 values > 0.87 (Figure 4-2). Similarly, Lee et al. (2005) reported $r^2 = 0.85$ when predicting P concentration with multispectral image analysis on bahiagrass (*Paspalum notatum* Flugge), which was lower than our measurement of $r^2 = 0.90$. Additionally, in their evaluation of prediction performance, neither any form of cross-validation nor hold out dataset was utilized, which may lead to the overoptimistic results and model prone to overfitting issue. Moreover, compared to the cross-validation used by Pittman et al. (2016) to evaluate the model prediction, nested cross-validation in this study provided more reliable estimation as the testing set is not encountered by the model construction even by indirect manners (Cawley and Talbot, 2010).

In summary, by observing 11 out of 16 of traits in this study that could be reliably predicted by the sensor data (with the correlation between observation and prediction greater than 0.85), the application of combined sensor systems in this type of research seems very promising. Additionally, this study provided some evidence that some nonlinear models had superior performance and they were more robust when there was limited information available. Even though the removal of variables may have had some impact on the prediction performance, the

degree of prediction accuracy change was quite different. It is interesting to observe that the removal of the first eight variables, NDRE, RE, LaiVI, FIPAR, HSNDVI, CCCVI, CTD, and IRVI, had little impact on prediction performance, which may be interesting information to be considered by engineers in future product development. Moreover, SVM and RF have a more robust prediction performance compared to the PLS regression and ridge regression, showing superior prediction accuracy even with reduced information.

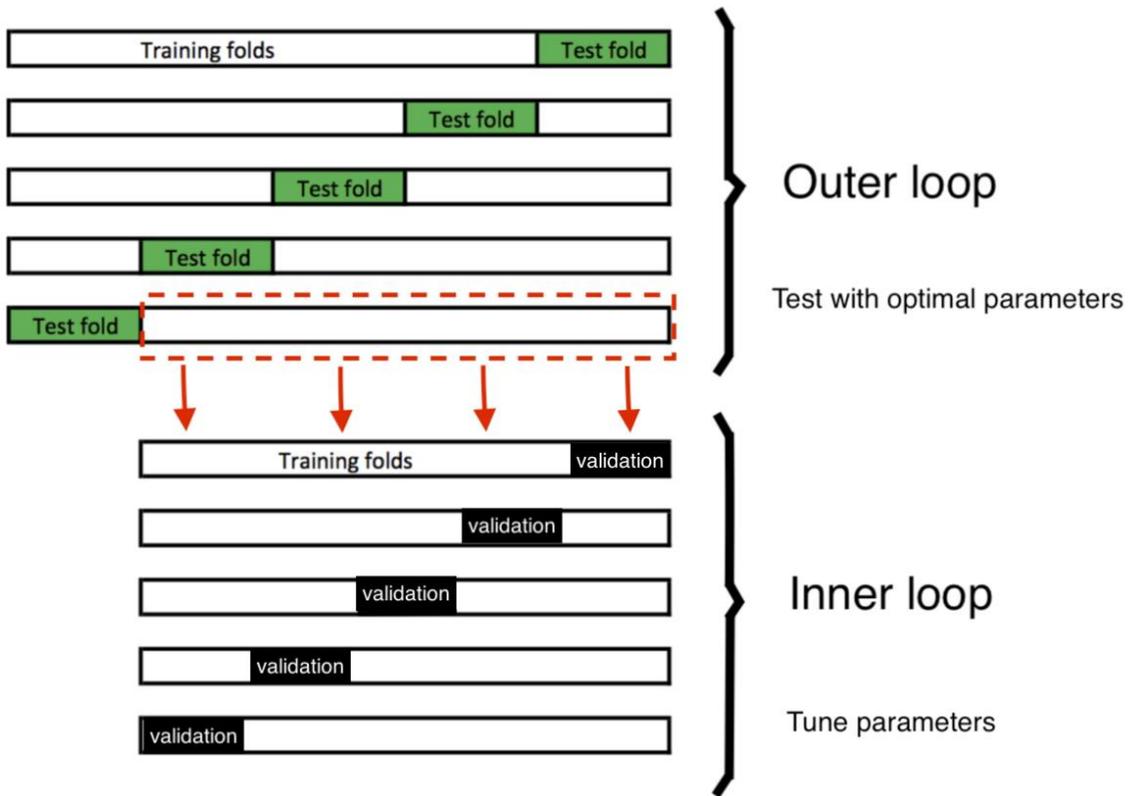


Figure 4-1. An example of nested cross-validation with outer and inner loops both set as 5-fold.

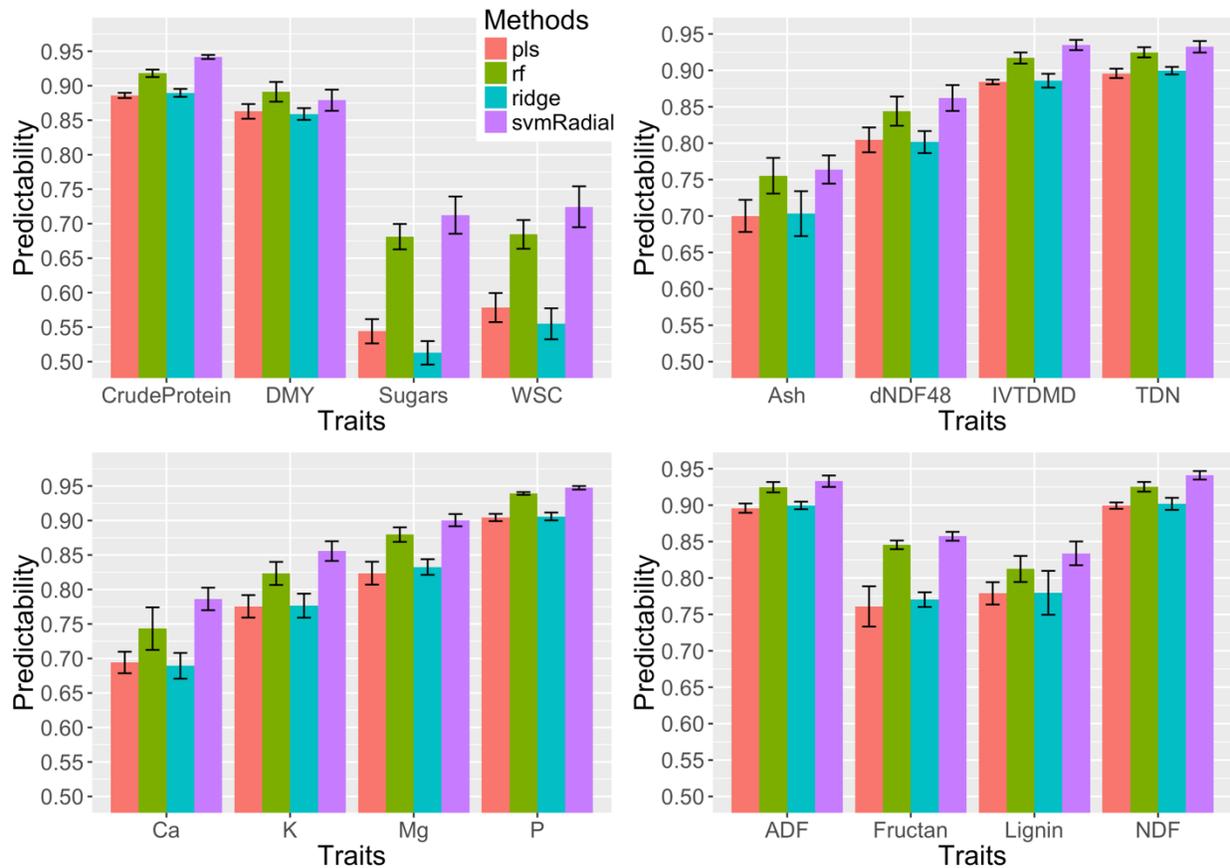


Figure 4-2. Predictability, correlation between predicted and test dataset values, of agronomically important traits with applications of statistical methodologies, partial least square regression, ridge regression, support vector machine (with radial kernel), and random forest. The whisker bar represents the standard error of the mean.

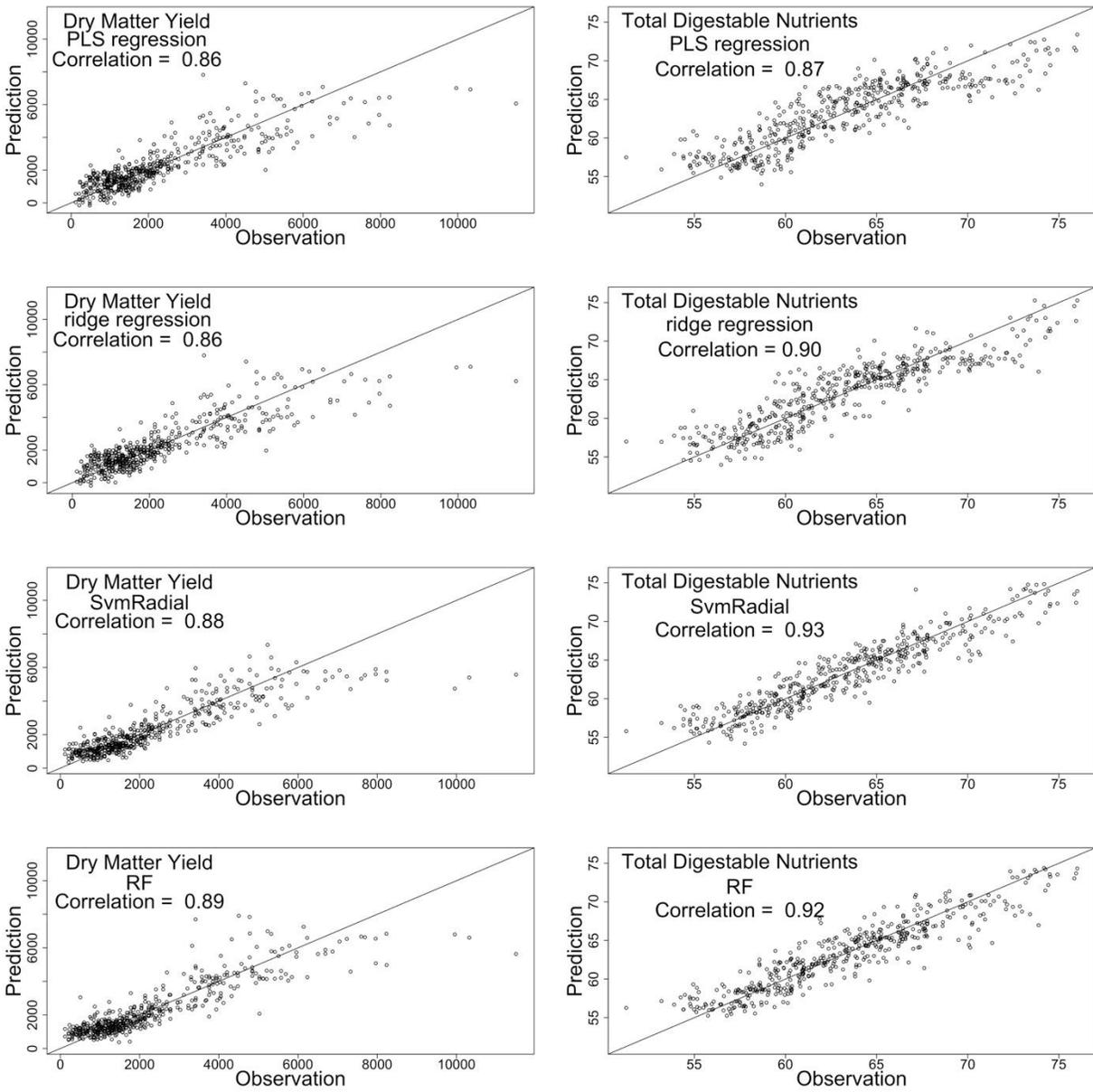


Figure 4-3. Predicted vs. observed values of dry matter yield and total digestible nutrient traits. The 1:1 line was used to illustrate a perfect matching for the predictions and observations. PLS regression, partial least square regression; SvmRadial, support vector machine with radial kernel; RF, random forest.

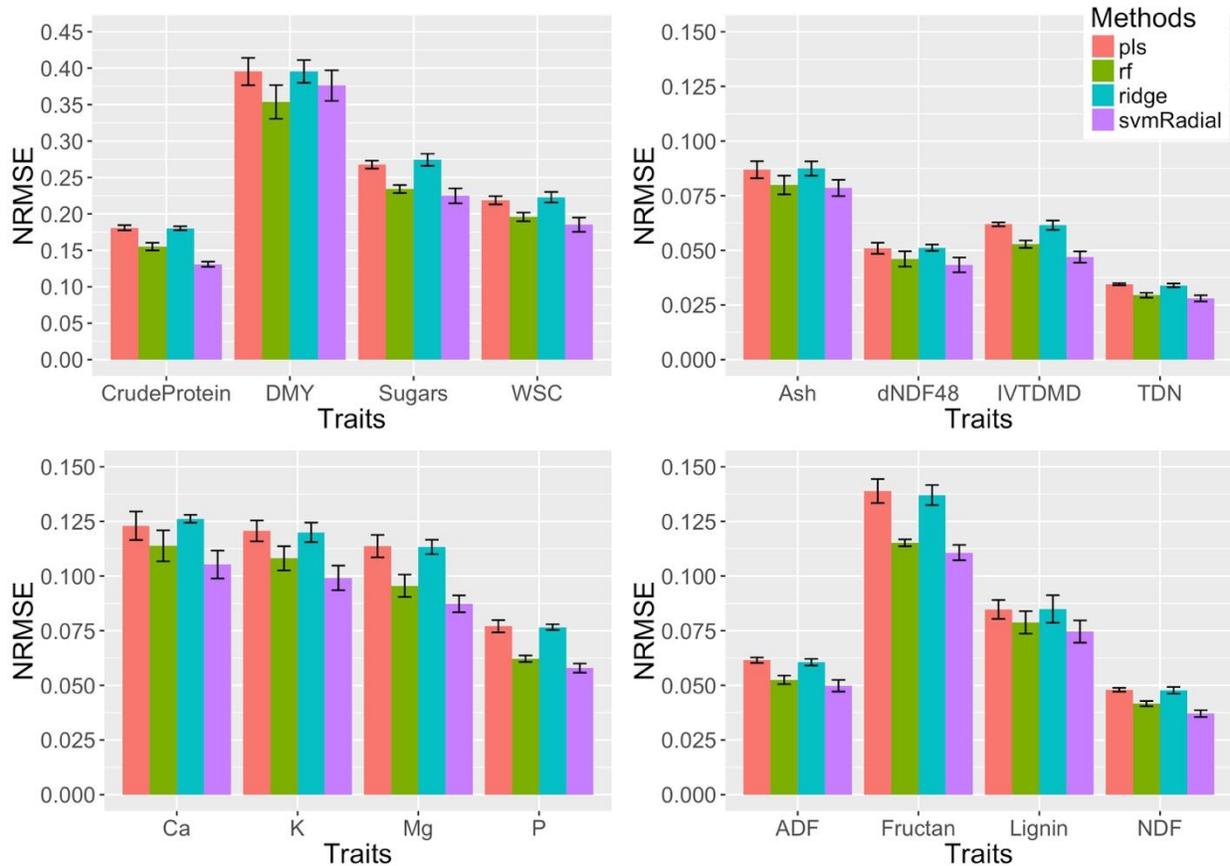


Figure 4-4. The agriculturally important traits and their corresponding normalized root-mean-square error (NRMSE) with applications of statistical methodologies. Lower value of NRMSE reflects better model prediction performance. The whisker bar represents the standard error of the mean

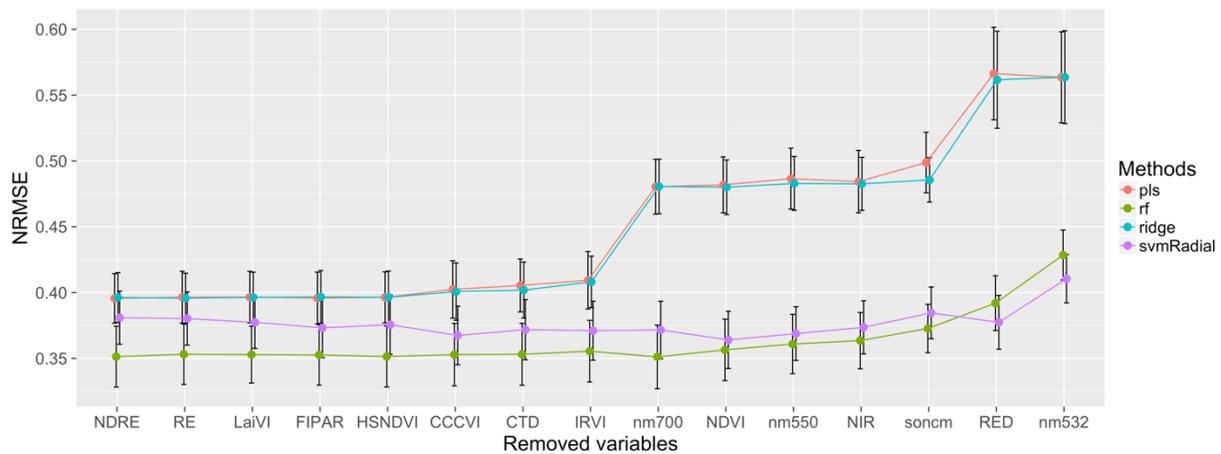


Figure 4-5. The model performance in dry matter yield after removing each of the variables in sequence from the dataset. Each of variable names denotes the normalized root-mean-square error (NRMSE) after removal of that variable and lower value of NRMSE indicates better prediction performance. The whisker bar represents the standard error of the mean. Pls, partial least square regression; rf, random forest; ridge, ridge regression; svmRadial, support vector machine with radial kernel; NDRE, normalized difference red edge index; RE, red-edge reflectance; LAIVI, leaf area index proxy index; FIPAR, fraction intercepted photosynthetically active radiation; HSNDVI, NDVI from Crop Circle ACS-430 active canopy sensor (Holland Scientific, Lincoln, NE); CCCVI, chlorophyll content index; CTD, canopy temperature depression index; IRVI, infrared reflectance vegetative index; nm700, reflectance at 700nm; NDVI, NDVI from GreenSeeker® (Trimble Inc., Sunnyvale, CA); nm550, reflectance at 550 nm; NIR, near-infrared reflectance; soncm, ultrasonic measured in cm; RED, red reflectance; nm532, reflectance at 532 nm.

CHAPTER 5 CONCLUSIONS

To embrace the fast generation of data information and improve the cultivar development efficiency, the utilization of powerful statistical methodologies become more and more important when facing with the present challenges in plant breeding. The adoption of improved statistical methodologies should include both the advanced experimental design, reliable analysis tools, and accurate prediction machines.

To solve the problem associated with testing large number of genotypes, causing the blocks of randomized complete block (RCB) design losing its environmental control capability, the post-hoc blocking designs were tested. In our study, the post-hoc R-C design are superior compared to the post-hoc IB designs and the original RCB designs both at the single measurement level and at site level. The narrow-sense heritability estimate, h^2 , after post-hoc blocking did not change considerably, but the ranking of the top performance genotypes varied and this can have a significant impact on the breeding selection process. The h^2 estimated with post-hoc R-C design were 0.399, 0.362, 0.321, 0.239, 0.309 for Jay, PSREU, Duda, RB farm and Bethel trials, respectively. The type B correlation followed a similar trend as the h^2 except for Bethel with a lower h^2 value than expected. Since the post-hoc blocking providing superior estimation accuracy of genetic parameters, when analyzing experimental trails with large number of genotypes, we recommend using the post-hoc blocking, sometimes, even better, at the experimental setup stage, planning a more efficient experimental design that provide better control of the smaller size environmental variation of genotypes should be implemented.

The issues that the post-hoc blocking employed to tackle are mostly related to local heterogeneous environmental variation; however, there are also other challenges existed at a larger scale to the plant breeding. As the unpredictability of temperature change happening in the

past few years, drought effects have become more frequent and stronger in many plant science field, especially in turfgrass breeding. To facilitate the selection of genotypes under the occurrence of drought conditions, the multiple-site trails were analyzed to report the genotype by environment (GxE) interaction and broad-sense heritability (H^2) in zoysiagrass. The GxE interaction estimated from all the data were ranging from 0.350 to 0.727 at different years, indicating a wide variation of GxE interaction exists. When the GxE interaction and H^2 were estimated with only drought and non-drought data, the genetic parameters from non-drought data showed stronger signals. Hence, we recommend utilizing the data without drought condition to calculate the breeding values for genotypes in selection of general turf quality traits. From bivariate analysis, the agreement of genotype performance under drought and non-drought conditions varied significantly based on year and sites. Similar trends were found in the bivariate analysis of turf quality under growth and non-growth conditions, however, most of the time, the performance of genotypes was highly correlated. To alleviate the impact of drought on the cultivar development, turfgrass breeders could potentially consider focusing on non-drought and the growth season data to aid with breeding selections.

Besides the implementation of statistical approaches to handle the environmental variations and the impact of drought on phenotypical evaluations of genotypes, this study also provided an alternative to fast accessing the forage quality and biomass, which are usually time-consuming, labor intensive, and expensive. By improvement of prediction performance through nonlinear statistical methodologies, the utilization of sensor technologies becomes more appealing for the applications in agricultural related research fields. The non-destructive multi-sensor system that accommodate spectral, ultrasonic, and laser data were tested on a bermudagrass experiment, from which the random forest (RF) and support vector machine with

radial kernel (SVM) were found to be most competitive. The RF had the best performance with correlation being 0.89 in dry matter yield (DMY) trait prediction, whereas SVM performed best in the rest 15 traits with correlation ranging from 0.72 to 0.95. Besides the prediction performance of statistical models, this study also provided some insight about the importance of variables by removing variables and re-evaluates the model performance in DMY trait. As most of the traits in this study could be reliably predicted by the SVM and RF, we are expecting to see more of sensor technology applications in the agronomic field in future.

Overall, the results of this study support the plant breeding from the statistical methodology aspect, which can be extended beyond the turfgrass or forage breeding. While the species zoysiagrass and bermudagrass were used as models here, the recommendations from this study can extend to different plant breeding programs.

APPENDIX A
 VARIANCE-COVARIANCE MATRIX OF GXE AND THE TEMPERATURE
 INFORMATION AT VARIOUS LOCATIONS OF CHAPTER 3

Table A-1. The variance-covariance matrix reflects the covariance (lower diagonal), variance (diagonal), and correlation (upper diagonal) of seven sites.

	Citra	ColSta	Dallas	Griffin	Sandhills	Stillwater	Tifton
Citra	0.415	0.340	0.511	0.406	0.380	0.019	0.728
ColSta	0.101	0.212	0.578	0.066	0.017	0.046	0.300
Dallas	0.223	0.180	0.458	0.286	0.291	0.057	0.592
Griffin	0.075	0.009	0.056	0.083	0.145	-0.114	0.624
Sandhills	0.192	0.006	0.154	0.033	0.611	0.618	0.397
Stillwater	0.006	0.011	0.020	-0.017	0.249	0.265	0.148
Tifton	0.448	0.132	0.383	0.172	0.297	0.073	0.914

Table A-2. The average precipitation and temperature of selected sites within given months. The calculation of average following three steps: 1). manually confirm the data collection months within a File (includes two years), 2). search the precipitation information related to confirmed months, 3). get an average of precipitation of the months.

File	Site	Average precipitation (inch)	Average temperature(F)
2011-2012	Citra	5.48	73.64
	College Station	2.26	76.98
	Dallas	2.52	72.83
	Stillwater	1.31	.
	Tifton	8.41	75.85
	Average	4.00	74.83
2012-2013	Citra	2.48	75.58
	College Station	1.44	80.06
	Dallas	2.16	77.61
	Stillwater	2.86	.
	Tifton	5.19	.
	Average	2.83	77.75
2013-2014	Citra	4.7	77.32
	College Station	3.3	82.12
	Dallas	2.11	81.97
	Stillwater	4.05	.
	Tifton	2.61	80.83
	Average	3.35	80.56
2014-2015	Citra	3.02	72.77
	College Station	2.16	83.55
	Dallas	3.04	81.6
	Stillwater	4.09	.
	Tifton	.	.
	Average	3.08	79.31

APPENDIX B
SUMMARY OF GXE INTERACTION AND BROAD-SENSE HERITABILITY
CONSIDERING ALL LOCATIONS WITHIN SERIES

Table B-1. Site-to-site Type-B genetic correlations for different response variables in various series. Values in parenthesis correspond to the standard error of the estimates.

Series	TQ	TQD	TQND	TQG	TQNG
2011	0.350 (0.048)	0.277 (0.070)	0.296 (0.045)	0.333 (0.048)	0.633 (0.113)
2012	0.727 (0.035)	0.608 (0.046)	0.724 (0.035)	0.710 (0.036)	0.899 (0.094)
2013	0.378 (0.047)	0.308 (0.049)	0.598 (0.054)	0.377 (0.047)	-
2014	0.621 (0.060)	0.425 (0.079)	0.689 (0.056)	0.621 (0.061)	0.999 (-)
Average	0.519	0.405	0.577	0.510	0.844

Table B-2. Summary of broad-sense heritability of calculated response variables considering all trials within series. The calculation of heritability was based on Eq. 5 and their respective variance components were estimated with Eq. 3. Values in parenthesis correspond to the standard error of the estimates. TQ, averages of repeated measurements of turf quality; TQD, averages of repeated measurements of turf quality under drought conditions; TQND, averages of repeated measurements of turf quality under non-drought conditions; TQG, averages of repeated measurements of turf quality in growing months (April/May to October/November); TQNG, averages of repeated measurements of turf quality in non-growing months (November/December to March April).

Series	TQ	TQD	TQND	TQG	TQNG
2011	0.165 (0.010)	0.071 (0.007)	0.147 (0.007)	0.156 (0.009)	0.108 (0.018)
2012	0.397 (0.021)	0.296 (0.018)	0.385 (0.021)	0.391 (0.021)	0.309 (0.043)
2013	0.214 (0.009)	0.185 (0.007)	0.246 (0.020)	0.214 (0.009)	-
2014	0.385 (0.023)	0.172 (0.018)	0.405 (0.031)	0.379 (0.038)	0.380 (0.075)
Average	0.290	0.181	0.296	0.285	0.266

Table B-3. Bivariate analysis of TQD against TQND and TQG against TQNG traits with all the data from sites within years. College Stn, abbreviation of location, College Station.

Series	Trail	TQD vs. TQND	TQG vs. TQNG
2011-2012	Citra	0.820 (0.072)	0.959 (0.276)
	College Stn	-0.032 (0.140)	0.224 (0.170)
	Dallas	0.878 (0.030)	0.956 (0.016)
	Griffin	-	-
	Sandhills	0.703 (0.087)	-
	Stillwater	0.541 (0.132)	0.070 (0.202)
	Tifton	-	-
2012-2013	Citra	0.905 (0.037)	-
	College Stn	0.766 (0.125)	0.948 (0.128)
	Dallas	0.884 (0.024)	0.851 (0.032)
	Griffin	0.999 (0.000)	-
	Sandhills	0.864 (0.051)	-
	Stillwater	0.708 (0.083)	0.999 (0.427)
	Tifton	0.713 (0.056)	-
2013-2014	Citra	0.873 (0.042)	-
	College Stn	0.622 (0.212)	-
	Dallas	0.886 (0.029)	-
	Griffin	-	-
	Sandhills	0.976 (0.047)	-
	Stillwater	0.757 (0.049)	-
	Tifton	-	-
2014-2015	Citra	0.721 (0.106)	0.852 (0.072)
	College Stn	0.079 (0.293)	-
	Dallas	0.358 (0.128)	-
	Griffin	0.999 (0.000)	-
	Sandhills	0.822 (0.094)	-
	Stillwater	0.682 (0.113)	0.929 (0.036)
	Tifton	-	-

Table B-4. The correlation matrix obtained by modeling data from seven trails in series 2011 with CORGH variance-covariance structure. College Stn, abbreviation of location, College Station.

	Citra	College Stn	Dallas	Griffin	Sandhills	Stillwater	Tifton
Citra	1	0.334	0.511	0.406	0.380	0.019	0.728
College Stn		1	0.578	0.066	0.017	0.046	0.300
Dallas			1	0.286	0.291	0.057	0.592
Griffin				1	0.145	-0.114	0.624
Sandhills					1	0.618	0.397
Stillwater						1	0.148
Tifton							1

APPENDIX C
PREDICTABILITY AND STANDARD ERROR FOR CHAPTER 4 MODELS

Table C-1. Prediction performance of target harvest date in dry matter yield trait with sensor data measurements using statistical models built with all previous harvest data. The calculated values are the normalized root-mean-square error (NRMSE).

Harvest Date	NRMSE
June 2 nd	0.77
June 22 nd	0.57
July 9 th	0.23
July 21 st	0.29
August 6 th	0.77
August 18 th	0.70

Table C-2. Use of dataset from one harvest to predict another in dry matter yield trait. Column names are the harvests to be predicted and the row names are the harvests used to build the models for prediction. All the predictions are based on one harvest and the calculated values are the normalized root-mean-square error (NRMSE).

	Harvest2	Harvest3	Harvest4	Harvest5	Harvest6	Harvest7
Harvest1	0.77	0.74	0.29	0.52	0.99	0.84
Harvest2	.	0.62	0.34	0.27	0.73	0.87
Harvest3	.	.	0.14	0.40	0.72	0.80
Harvest4	.	.	.	0.47	0.80	0.86
Harvest5	0.65	0.59
Harvest6	0.76

Table C-3. Predictability of agronomical important traits with applications of statistical methodologies, PLS regression, ridge regression, SVM, and RF. The predictability corresponds to prediction vs. observation values and SE is the standard error of respective means.

Trait	Methods	Predictability	SE
CrudeProtein	pls	0.886	0.004
CrudeProtein	rf	0.918	0.005
CrudeProtein	ridge	0.890	0.006
CrudeProtein	svmRadial	0.942	0.003
DMY	pls	0.863	0.011
DMY	rf	0.891	0.014
DMY	ridge	0.859	0.008
DMY	svmRadial	0.879	0.015
Sugars	pls	0.544	0.018
Sugars	rf	0.681	0.018
Sugars	ridge	0.513	0.017
Sugars	svmRadial	0.712	0.027
WSC	pls	0.578	0.021
WSC	rf	0.684	0.021
WSC	ridge	0.555	0.022
WSC	svmRadial	0.725	0.030
Ca	pls	0.694	0.016
Ca	rf	0.743	0.031
Ca	ridge	0.689	0.019
Ca	svmRadial	0.786	0.016
K	pls	0.776	0.016
K	rf	0.823	0.017
K	ridge	0.777	0.017
K	svmRadial	0.856	0.014
Mg	pls	0.824	0.017
Mg	rf	0.880	0.011
Mg	ridge	0.833	0.011
Mg	svmRadial	0.900	0.009
P	pls	0.904	0.005
P	rf	0.939	0.002
P	ridge	0.906	0.006
P	svmRadial	0.947	0.003
Ash	pls	0.700	0.022
Ash	rf	0.755	0.025
Ash	ridge	0.703	0.031

Ash	svmRadial	0.764	0.019
dNDF48	pls	0.805	0.017
dNDF48	rf	0.844	0.020
dNDF48	ridge	0.802	0.015
dNDF48	svmRadial	0.862	0.018
IVTDMD	pls	0.884	0.003
IVTDMD	rf	0.917	0.008
IVTDMD	ridge	0.886	0.009
IVTDMD	svmRadial	0.935	0.007
TDN	pls	0.896	0.006
TDN	rf	0.925	0.007
TDN	ridge	0.900	0.005
TDN	svmRadial	0.932	0.008
ADF	pls	0.896	0.006
ADF	rf	0.925	0.007
ADF	ridge	0.900	0.005
ADF	svmRadial	0.933	0.008
Fructan	pls	0.761	0.028
Fructan	rf	0.846	0.006
Fructan	ridge	0.770	0.010
Fructan	svmRadial	0.857	0.006
Lignin	pls	0.779	0.015
Lignin	rf	0.812	0.018
Lignin	ridge	0.780	0.030
Lignin	svmRadial	0.834	0.016
NDF	pls	0.899	0.004
NDF	rf	0.925	0.007
NDF	ridge	0.902	0.008
NDF	svmRadial	0.941	0.006

LIST OF REFERENCES

- Al-Jibouri, H., Miller, P. A., & Robinson, H. F. (1958). Genotypic and environmental variances and covariances in an upland cotton cross of interspecific origin. *Agronomy Journal*, 50(10), 633–636.
- Allard, R. W., & Bradshaw, A. D. (1964). Implications of Genotype-Environmental interactions in applied plant breeding. *Crop Science*, 4(5), 503.
- Allen, C. D., Macalady, A. K., Chenchouni, H., Bachelet, D., McDowell, N., Vennetier, M., ... Cobb, N. (2010). A global overview of drought and heat-induced tree mortality reveals emerging climate change risks for forests. *Forest Ecology and Management*, 259(4), 660–684.
- Annicchiarico, P. (2002). Genotype x environment interactions: challenges and opportunities for plant breeding and cultivar recommendations. *Food & Agriculture Org.*, 174
- Arnó, J., Escolà, A., Vallès, J. M., Llorens, J., Sanz, R., Masip, J., Palacin, J., & Rosell-Polo, J. R. (2013). Leaf area index estimation in vineyards using a ground-based LiDAR scanner. *Precision Agriculture*, 14(3), 290–306.
- Aziz, S. A., Steward, B. L., Birrell, S. J., Kaspar, T. C., & Shrestha, D. S. (2004). Ultrasonic Sensing for Corn Plant Canopy Characterization. *Paper Number 041120, 2004 ASAE Annual Meeting, August 1 - 4, 2004*, 1–11.
- Barnston, A. G. (1992). Correspondence among the correlation, RMSE, and Heidke Forecast Verification Measures; Refinement of the Heidke Score. *Weather and Forecasting*, 7(4), 699–709.
- Becker, H. C., & Leon, J. (1988). Stability analysis in plant breeding. *Plant Breeding*, 101(1), 1–23.
- Bergeman, C. S., & Plomin, R. (1989). Genotype-environment interaction. In M. H. Bornstein & J. S. Bruner (Eds.), *Interaction in human development*, 157-171. Hillsdale, NJ: Erlbaum.
- Billings, W. D. (1987). Constraints to plant growth, reproduction, and establishment in arctic environments. *Arctic and Alpine Research*, 19(4), 357.
- Bishop, C. (2007). *Pattern Recognition and Machine Learning (Information Science and Statistics)*, 1st edn. 2006. corr. 2nd printing edn. *Springer, New York*.
- Bouraoui, R., Lahmar, M., Majdoub, A., Djemali, M., & Belyea, R. (2002). The relationship of temperature-humidity index with milk production of dairy cows in a Mediterranean climate. *Animal Research*, 51(6), 479–491.
- Bowyer, P., & Danson, F. M. (2004). Sensitivity of spectral reflectance to variation in live fuel moisture content at leaf and canopy level. *Remote Sensing of Environment*, 92(3), 297–308.

- Braman, S. K., Duncan, R. R., & Engelke, M. C. (2000). Evaluation of turfgrass selections for resistance to fall armyworms (Lepidoptera: Noctuidae). *HortScience*, *35*(7), 1268–1270.
- Brede, D. (2000). *Turfgrass maintenance reduction handbook : sports, lawns, and golf*. Ann Arbor Press.
- Busey, P., Reinert, J. A., & Atilano, R. A. (1982). Genetic and environmental determinants of zoysiagrass adaptation in a subtropical region. *Journal of American Society for Horticultural Science*, *107*(1), 79–82.
- Carrascal, L. M., Galván, I., & Gordo, O. (2009). Partial least squares regression as an alternative to current regression methods used in ecology. *Oikos*, *118*(5), 681–690.
- Cartelat, A., Cerovic, Z. G., Goulas, Y., Meyer, S., Lelarge, C., Prioul, J.-L., ... & Moya, I. (2005). Optically assessed contents of leaf polyphenolics and chlorophyll as indicators of nitrogen deficiency in wheat (*Triticum aestivum* L.). *Field Crops Research*, *91*(1), 35–49.
- Cawley, G. C., & Talbot, N. L. C. (2010). On Over-fitting in Model Selection and Subsequent Selection Bias in Performance Evaluation. *Journal of Machine Learning Research*, *11*(Jul), 2079–2107.
- Ceccato, P., Gobron, N., Flasse, S., Pinty, B., & Tarantola, S. (2002). Designing a spectral index to estimate vegetation water content from remote sensing data: Part 1: Theoretical approach. *Remote Sensing of Environment*, *82*(2), 188–197.
- Chapman, S. C. (2008). Use of crop models to understand genotype by environment interactions for drought in real-world and simulated plant breeding trials. *Euphytica*, *161*(1–2), 195–208.
- Cho, M. A., Skidmore, A., Corsi, F., van Wieren, S. E., & Sobhan, I. (2007). Estimation of green grass/herb biomass from airborne hyperspectral imagery using spectral indices and partial least squares regression. *International Journal of Applied Earth Observation and Geoinformation*, *9*(4), 414–424.
- Clewer, A. G., & Scarisbrick, D. H. (2013). *Practical Statistics and Experimental Design for Plant and Crop Science*. John Wiley & Sons.
- Cullis, B. R., Lill, W. J., Fisher, J. A., Read, B. J., & Gleeson, A. C. (1989). A New Procedure for the Analysis of Early Generation Variety Trials. *Applied Statistics*, *38*(2), 361.
- Ebdon, J. S., & Gauch, H. G. (2002). Additive Main Effect and Multiplicative Interaction Analysis of National Turfgrass Performance Trials. *Crop Science*, *42*(2), 497–506.
- Eberhart, S. A., & Russell, W. A. (1966). Stability parameters for comparing varieties. *Crop Science*, *6*(1), 36.
- Ehlert, D., Heisig, M., & Adamek, R. (2010). Suitability of a laser rangefinder to characterize winter wheat. *Precision Agriculture*, *11*(6), 650–663.

- Ehlert, D., Horn, H. J., & Adamek, R. (2008). Measuring crop biomass density by laser triangulation. *Computers and Electronics in Agriculture*, *61*(2), 117–125.
- Escolà, A., Planas, S., Rosell, J. R., Pomar, J., Camp, F., Solanelles, F., ... & Gil, E. (2011). Performance of an ultrasonic ranging sensor in apple tree canopies. *Sensors*, *11*(3), 2459–2477.
- Fan, W., Hu, B., Miller, J., & Li, M. (2009). Comparative study between a new nonlinear model and common linear model for analysing laboratory simulated-forest hyperspectral data. *International Journal of Remote Sensing*, *30*(11), 2951–2962.
- Fan, X.-M., Kang, M. S., Chen, H., Zhang, Y., Tan, J., & Xu, C. (2007). Yield Stability of Maize Hybrids Evaluated in Multi-Environment Trials in Yunnan, China. *Agronomy Journal*, *99*(1), 220.
- Finlay, K., & Wilkinson, G. (1963). The analysis of adaptation in a plant-breeding programme. *Australian Journal of Agricultural Research*, *14*(6), 742.
- Finney, M. A., McHugh, C. W., & Grenfell, I. C. (2005). Stand- and landscape-level effects of prescribed burning on two Arizona wildfires. *Canadian Journal of Forest Research*, *35*(7), 1714–1722.
- Forbes, I. (1952). Chromosome Numbers and Hybrids in *Zoysia*1. *Agronomy Journal*, *44*(4), 194.
- Frank, I. E. (1987). Intermediate least squares regression method. *Chemometrics and Intelligent Laboratory Systems*, *1*(3), 233–242.
- Franzluebbers, A. J., Stuedemann, J. A., & Wilkinson, S. R. (2001). Bermudagrass Management in the Southern Piedmont USA. *Soil Science Society of America Journal*, *65*(3), 834.
- Gamon, J. A., Peñuelas, J., & Field, C. B. (1992). A narrow-waveband spectral index that tracks diurnal changes in photosynthetic efficiency. *Remote Sensing of Environment*, *41*(1), 35–44.
- Geladi, P., & Kowalski, B. R. (1986). Partial least-squares regression: a tutorial. *Analytica Chimica Acta*, *185*, 1–17.
- Genc, L., Dewitt, B., & Smith, S. (2004). Determination of wetland vegetation height with LIDAR. *Turkish Journal of Agriculture and forestry*, *28*(1), 63–71.
- Gezan, S. A., Huber, D. A., & White, T. L. (2006). Post hoc blocking to improve heritability and precision of best linear unbiased genetic predictions. *Canadian Journal of Forest Research*, *36*(9), 2141–2147.
- Gilmour, A., Cullis, B., & Verbyla, A. (1997). Accounting for Natural and Extraneous Variation in the Analysis of Field Experiments. *Journal of Agricultural, Biological, and Environmental Statistics*, *2*(3), 269–293.

- Gilmour, A., Gogel, B., Cullis, B. & Thompson R. (2009). ASReml user guide release 3.0. VSN International Ltd, Hemel Hempstead.
- Gnyp, M. L., Miao, Y., Yuan, F., Ustin, S. L., Yu, K., Yao, Y., ... & Bareth, G. (2014). Hyperspectral canopy sensing of paddy rice aboveground biomass at different growth stages. *Field Crops Research*, 155, 42–55.
- Green, D., Fry, J., Pair, J., & Tisserat, N. A. (1994). Influence of management practices on Rhizoctonia large patch disease in zoysiagrass. *HortScience*, 29, 186–188.
- Haldane, J. B. S. (1946). The interaction of nature and nurture. *The Annals of Human Genetics*, 13(1), 197–205.
- Hansen, P. M., & Schjoerring, J. K. (2003). Reflectance measurement of canopy biomass and nitrogen status in wheat crops using normalized difference vegetation indices and partial least squares regression. *Remote Sensing of Environment*, 86(4), 542–553.
- Hayhoe, K., Sheridan, S., Kalkstein, L., & Greene, S. (2010). Climate change, heat waves, and mortality projections for Chicago. *Journal of Great Lakes Research*, 36(SUPPL. 2), 65–73.
- Hays, K. L., Barber, J. F., Kenna, M. P., & McCollum, T. G. (1991). Drought avoidance mechanisms of selected bermudagrass genotypes. *HortScience*, 26(2), 180–182.
- Henning, Jason G.; Radtke, P. J. (2006). Detailed Stem Measurements of Standing Trees from Ground-Based Scanning Lidar. *Forest Science*, 52(14), 67–80.
- Hoek, J. A., Fehr, W. R., Murphy, P. A., & Welke, G. A. (2000). Influence of genotype and environment on isoflavone contents of soybean. *Crop Science*, 40(1), 48.
- Hoekstra, F. A., Golovina, E. A., & Buitink, J. (2001). Mechanisms of plant desiccation tolerance. *Trends in Plant Science*, 6(9), 431–438
- Hoerl, A. E., & Kennard, R. W. (1970). Ridge Regression: Biased Estimation for Nonorthogonal Problems. *Technometrics*, 12(1), 55–67.
- Hong, S., Schepers, J. S., Francis, D. D., & Schlemmer, M. R. (2007). Comparison of Ground-Based Remote Sensors for Evaluation of Corn Biomass Affected by Nitrogen Stress. *Communications in Soil Science and Plant Analysis*, 38(15–16), 2209–2226.
- Hopkinson, C., & Chasmer, L. (2009). Testing LiDAR models of fractional cover across multiple forest ecozones. *Remote Sensing of Environment*, 113(1), 275–288.
- Hosoi, F., & Omasa, K. (2009). Estimating vertical plant area density profile and growth parameters of a wheat canopy at different growth stages using three-dimensional portable lidar imaging. *ISPRS Journal of Photogrammetry and Remote Sensing*, 64(2), 151–158.

- Hua, Z., Wang, Y., Xu, X., Zhang, B., & Liang, L. (2007). Predicting corporate financial distress based on integration of support vector machine and logistic regression. *Expert Systems with Applications*, 33(2), 434–440.
- Huang, B., Duncan, R. R., & Carrow, R. N. (1997a). Drought-resistance mechanisms of seven warm-season turfgrasses under surface soil drying: i. shoot response. *Crop Science*, 37(6), 1858.
- Huang, B., Duncan, R. R., & Carrow, R. N. (1997b). Drought-resistance mechanisms of seven warm-season turfgrasses under surface soil drying: II. Root aspects. *Crop Science*, 37(6), 1863–1869.
- Inostroza, L., Acuña, H., Muñoz, P., Vásquez, C., Ibáñez, J., Tapia, G., ... & Aguilera, H. (2016). Using aerial images and canopy spectral reflectance for high-throughput phenotyping of white clover. *Crop Science*, 56(5), 2629–2637.
- Inostroza, L., Acuña, H., & Méndez, J. (2015). Multi-physiological-trait selection indices to identify *Lotus tenuis* genotypes with high dry matter production under drought conditions. *Crop and Pasture Science*, 66(1), 90–99.
- Jansen, R. C., Van Ooijen, J. W., Stam, P., Lister, C., & Dean, C. (1995). Genotype-by-environment interaction in genetic mapping of multiple quantitative trait loci. *Theoretical and Applied Genetics*, 91(1), 33–37.
- Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, 270(7), 314–318.
- Kang, M. S. (1997). Using genotype-by-environment interaction for crop cultivar development. *Advances in Agronomy*, 62(C), 199–252
- Kellems, R. O., & Church, D. C. (2009). *Livestock Feeds and Feeding*. Livestock Feeds and Feeding. Prentice Hall.
- Knox, N. M., Skidmore, A. K., Prins, H. H. T., Asner, G. P., van der Werff, H. M. A., de Boer, W. F., ... & Grant, R. C. (2011). Dry season mapping of savanna forage quality, using the hyperspectral Carnegie Airborne Observatory sensor. *Remote Sensing of Environment*, 115(6), 1478–1488.
- Krstajic, D., Buturovic, L. J., Leahy, D. E., & Thomas, S. (2014). Cross-validation pitfalls when selecting and assessing regression and classification models. *Journal of Cheminformatics*, 6(1).
- Lee, W. S., Jordan, J. D., In, A., Craig, J. C., & Manager, R. S. (2005). Multispectral Image Analysis for Phosphorus Measurement in Bahia Grass. *Plant Science*, 300(5), 1–7.
- Leon, R. G., Unruh, J. B., Brecke, B. J., & Kenworthy, K. E. (2014). Characterization of Fluazifop-P-butyl Tolerance in Zoysiagrass Cultivars. *Weed Technology*, 28(2), 385–394.

- Liaw, A., & Wiener, M. (2002). Classification and Regression by randomForest. *R News*, 2(December), 18–22.
- Liddle, A. R. (2007). Information criteria for astrophysical model selection. *Mon. Not. R. Astron. Soc.*, 377, 74–78.
- Lin, C. S., & Binns, M. R. (1988). A superiority measure of cultivar performance for cultivar \times location data. *Canadian Journal of Plant Science*, 68(1), 193–198.
- Luber, G., & McGeehin, M. (2008). Climate Change and Extreme Heat Events. *American Journal of Preventive Medicine*, 35(5), 429–435.
- Mahajan, V., Jain, A. K., & Bergier, M. (1977). Parameter Estimation in Marketing Models in the Presence of Multicollinearity: An Application of Ridge Regression. *Journal of Marketing Research*, 14(4), 586.
- Marcum, K. B., Anderson, S. J., & Engelke, M. C. (1998). Salt Gland Ion Secretion: A Salinity Tolerance Mechanism among Five Zoysiagrass Species. *Crop Science*, 38(3), 806.
- Marcum, K. B., Engelke, M. C., Morton, S. J., & White, R. H. (1995). Rooting characteristics and associated drought resistance of zoysiagrass. *Agronomy Journal*, 87(3), 534–538.
- Martin, M. E., & Aber, J. D. (1997). High spectral resolution remote sensing of forest canopy lignin, nitrogen, and ecosystem processes. *Ecological Applications*, 7(2), 431–443.
- Middleton, E. M., Cheng, Y.-B., Hilker, T., Black, T. A., Krishnan, P., Coops, N. C., & Huemmrich, K. F. (2009). Linking foliage spectral responses to canopy-level ecosystem photosynthetic light-use efficiency at a Douglas-fir forest in Canada. *Canadian Journal of Remote Sensing*, 35(2), 166–188.
- Miller, P., Williams, J., Robinson, H., & Comstock, R. (1958). Estimates of genotypic and environmental variances and covariances in upland cotton and their implications in selection. *Agronomy Journal*, 50(3), 126–131.
- Mohandes, M. A., Halawani, T. O., Rehman, S., & Hussain, A. A. (2004). Support vector machines for wind speed prediction. *Renewable Energy*, 29(6), 939–947.
- Morris, K., & Shearman, R. (1998). NTEP turfgrass evaluation guidelines. *Turfgrass Evaluation Workshop, Beltsville, MD*, 17, 1–5.
- Morton, S. J., Engelke, M. C., & White, R. H. (1991). Performance of four warm-season turfgrass genera cultured in dense shade. II. *Stenotaphrum secundatum*. *PR-Texas Agricultural Experiment Station (USA)*.
- Mountrakis, G., Im, J., & Ogole, C. (2011). Support vector machines in remote sensing: A review. *ISPRS Journal of Photogrammetry and Remote Sensing*, 66(3), 247–259.

- Mutanga, O., Skidmore, A. K., Kumar, L., & Ferwerda, J. (2005). Estimating tropical pasture quality at canopy level using band depth analysis with continuum removal in the visible domain. *International Journal of Remote Sensing*, 26(6), 1093–1108.
- Nguyen, D. V., & Rocke, D. M. (2002). Tumor classification by partial least squares using microarray gene expression data. *Bioinformatics*, 18(1), 39–50.
- Norris, K. H., Barnes, R. F., Moore, J. E., & Shenk, J. S. (1976). Predicting forage quality by infrared reflectance spectroscopy. *Journal of animal science*, 43(4), 889–897.
- Otoo, E., & Asiedu, R. (2006). Cultivar evaluation and mega-environment investigation of *Dioscorea cayenensis* cultivars in Ghana based on the GGE biplot analysis. *Journal of Food, Agriculture and Environment*, 4(3–4), 162–166.
- Overman, A. R., Neff, C. R., Wilkinson, S. R., & Martin, F. G. (1990). Water, harvest interval, and applied nitrogen effects on forage yield of bermudagrass and bahiagrass. *Agronomy journal*, 82(5), 1011–1016.
- Pai, P.-F., Hong, W.-C., Lin, C.-S., & Chen, C.-T. (2006). A hybrid support vector machine regression for exchange rate prediction. *International Journal of Information and Management Sciences*, 17(2).
- Patton, A. J., & Reicher, Z. J. (2007). Zoysiagrass Species and Genotypes Differ in Their Winter Injury and Freeze Tolerance. *Crop Science*, 47(4), 1619.
- Piepho, H. P., Möhring, J., Melchinger, A. E., & Büchse, A. (2008). BLUP for phenotypic selection in plant breeding and variety testing. *Euphytica*, 161(1–2), 209–228.
- Pittman, J. J., Arnall, D. B., Interrante, S. M., Wang, N., Raun, W. R., & Butler, T. J. (2016). Bermudagrass, wheat, and tall fescue crude protein forage estimation using mobile-platform, active-spectral and canopy-height data. *Crop Science*, 56(2), 870–881.
- Pittman, J. J., Arnall, D. B., Interrante, S. M., Moffet, C. A., & Butler, T. J. (2015). Estimation of biomass and canopy height in bermudagrass, alfalfa, and wheat using ultrasonic, laser, and spectral sensors. *Sensors (Basel, Switzerland)*, 15(2), 2920–2943.
- Plomin, R., DeFries, J. C., & Loehlin, J. C. (1977). Genotype-environment interaction and correlation in the analysis of human behavior. *Psychological Bulletin*, 84(2), 309–322.
- Qian, Y. L., Engelke, M. C., & Foster, M. J. V. (2000). Salinity effects on zoysiagrass cultivars and experimental lines. *Crop Science*, 40(2), 488.
- Qiao, C. G., Basford, K. E., DeLacy, I. H., & Cooper, M. (2000). Evaluation of experimental designs and spatial analyses in wheat breeding trials. *TAG Theoretical and Applied Genetics*, 100(1), 9–16.
- Raymer, P., & Braman, K. (2006). Breeding seashore paspalum for recreational turf use. *JL Nus (Ed.)*, 36.

- Reinert, J. A., & Engelke, M. C. (1992). Resistance in zoysiagrass (*Zoysia spp.*) to the tropical sod webworm (*Herpetogramma phaeopteralis*). *PR-Texas Agricultural Experiment Station (USA)*.
- Roberts, D. A., Ustin, S. L., Ogunjemiyo, S., Greenberg, J., Dobrowski, S. Z., Chen, J., & Hinckley, T. M. (2004). Spectral and Structural Measures of Northwest Forest Vegetation at Leaf to Landscape Scales. *Ecosystems*, 7(5), 545–562.
- Robins, J. G., Bauchan, G. R., & Brummer, E. C. (2007). Genetic mapping forage yield, plant height, and regrowth at multiple harvests in tetraploid Alfalfa (*Medicago sativa* L.). *Crop Science*, 47(1), 11–18.
- Rook, A. J., Dhanoa, M. S., & Gill, M. (1990). Prediction of the voluntary intake of grass silages by beef cattle. 2. Principal component and ridge regression analyses. *Animal Production*, 50(3), 439–454.
- Rosipal, R., & Krämer, N. (2006). Overview and Recent Advances in Partial Least Squares (pp. 34–51). Springer, Berlin, Heidelberg.
- Sanderson, M. A., Read, J. C., & Reed, R. L. (1999). Harvest management of switchgrass for biomass feedstock and forage production. *Agronomy Journal*, 91(1), 5–10.
- Schabenberger, O., & Gotway, C. (2017). Statistical methods for spatial data analysis. *CRC Press*.
- Schwartz, B. M., Kenworthy, K. E., Crow, W. T., Ferrell, J. A., Miller, G. L., & Quesenberry, K. H. (2010). Variable Responses of Zoysiagrass Genotypes to the Sting Nematode. *Crop Science*, 50(2), 723.
- Schwartz, B. M., Kenworthy, K. E., Engelke, M. C., Dennis Genovesi, A., & Quesenberry, K. H. (2009). Heritability estimates for Turfgrass performance and stress response in *Zoysia spp.* *Crop Science*, 49(6), 2113–2118.
- Schwartz, B. M., Kenworthy, K. E., Engelke, M. C., Genovesi, A. D., Odom, R. M., & Quesenberry, K. H. (2010). Variation in 2C Nuclear DNA Content of spp. as Determined by Flow Cytometry. *Crop Science*, 50(4), 1519.
- Scotford, I. M., & Miller, P. C. H. (2004). Combination of Spectral Reflectance and Ultrasonic Sensing to monitor the Growth of Winter Wheat. *Biosystems Engineering*, 87(1), 27–38.
- Selbeck, J., Dworak, V., & Ehlert, D. (2010). Testing a vehicle-based scanning lidar sensor for crop detection. *Canadian Journal of Remote Sensing*, 36(1), 24–35.
- Simon, R., & Maitournam, A. (2004). Evaluating the Efficiency of Targeted Designs for Randomized Clinical Trials. *Clinical Cancer Research*, 10(20).

- Sjöström, M., Wold, S., Lindberg, W., Persson, J.-Å., & Martens, H. (1983). A multivariate calibration problem in analytical chemistry solved by partial least-squares models in latent variables. *Analytica Chimica Acta*, 150, 61–70.
- Sleper, D. A., Asay, K. H., Pedersen, J. F., & Burton, G. W. (1989). Progress and Benefits to Humanity from Breeding Warm-Season Forage Grasses. In *Contributions from Breeding Forage and Turf Grasses* (pp. 21–29). Crop Science Society of America.
- Srivastava, A. K., Goering, C. E., Rohrbach, R. P., & Buckmaster, D. R. (2006). *Engineering principles of agricultural machines* (NO. 631.3/S774). St. Joseph, Mich.: American society of agricultural engineers.
- Starks, P. J., & Brown, M. A. (2010). Prediction of forage quality from remotely sensed data: Comparison of cultivar-specific and cultivar-independent equations using three methods of calibration. *Crop Science*, 50(5), 2159–2170.
- Starks, P. J., Zhao, D., & Brown, M. A. (2008). Estimation of nitrogen concentration and in vitro dry matter digestibility of herbage of warm-season grass pastures from canopy hyperspectral reflectance measurements. *Grass and Forage Science*, 63(2), 168–178.
- Stoll, A., & Kutzbach, H. D. (2001). Guidance of a forage harvester with GPS. *Precision Agriculture* (Vol. 2, pp. 281–291). Kluwer Academic Publishers.
- Stroup, W. W., & Muhlitz, D. K. (1991). Nearest Neighbor Adjusted Best Linear Unbiased Prediction. *The American Statistician*, 45(3), 194–200.
- Sui, R., & Thomasson, J. (2006). Ground-based sensing system for cotton nitrogen status determination. *Transactions of the ASABE*, 49(6), 1983-1991.
- Tahir, M. H. N., Casler, M. D., Moore, K. J., & Brummer, E. C. (2011). Biomass Yield and Quality of Reed Canarygrass under Five Harvest Management Systems for Bioenergy Production. *Bioenergy Research*, 4(2), 111–119.
- Team, R. (2014). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. 2013.
- Tobias, R. D. (1995). An Introduction to Partial Least Squares Regression. In *Proceedings of the twentieth annual SAS users group international conference* (pp. 1250-1257). SAS Institute Cary, NC
- van Leeuwen, M., & Nieuwenhuis, M. (2010). Retrieval of forest structural parameters using LiDAR remote sensing. *European Journal of Forest Research*. Springer-Verlag.
- Varma, S., & Simon, R. (2006). Bias in error estimation when using cross-validation for model selection. *BMC Bioinformatics*, 7(1), 91.
- Vogelmann, J. E., Rock, B. N., & Moss, D. M. (1993). Red edge spectral measurements from sugar maple leaves. *International Journal of Remote Sensing*, 14(8), 1563–1575.

- Walklate, P. J., Cross, J. V., Richardson, G. M., Murray, R. A., & Baker, D. E. (2002). IT—Information Technology and the Human Interface: Comparison of Different Spray Volume Deposition Models Using LIDAR Measurements of Apple Orchards. *Biosystems Engineering*, 82(3), 253–267.
- Watkins, E., Fei, S., Gardner, D., Stier, J., Bughrara, S., Li, D., ... Diesburg, K. (2011). Low-Input Turfgrass Species for the North Central United States. *Ats*, 8(1), 0.
- Welham, S. J., Gezan, S. A., Clark, S. J., & Mead, A. (2014). *Statistical methods in biology: Design and analysis of experiments and regression*. CRC Press.
- White, R. H., Engelke, M. C., Anderson, S. J., Ruemmele, B. A., Marcum, K. B., & Taylor, G. R. (2001). Zoysiagrass Water Relations. *Crop Science*, 41(1), 133.
- Wold, S., Ruhe, A., Wold, H., & Dunn, III, W. J. (1984). The Collinearity Problem in Linear Regression. The Partial Least Squares (PLS) Approach to Generalized Inverses. *SIAM Journal on Scientific and Statistical Computing*, 5(3), 735–743.
- Woodard, K. R., & Prine, G. M. (1991). Silage characteristics of Elephantgrass as affected by harvest frequency and genotype. *Agronomy Journal*, 83(3), 541–546.
- Xing, L., Gezan, S., Kenworthy, K., Unruh, J. B., & Munoz, P. (2017). Improved genetic parameter estimations in zoysiagrass by implementing post hoc blocking. *Euphytica*, 213(8), 195.
- Zhao, D., Starks, P. J., Brown, M. A., Phillips, W. A., & Coleman, S. W. (2007). Assessment of forage biomass and quality parameters of bermudagrass using proximal sensing of pasture canopy reflectance. *Grassland Science*, 53(1), 39–49.

BIOGRAPHICAL SKETCH

Lin Xing was born in a military family in Beijing, China and he is the only child in his family. Later his family moved to Weihai, a beautiful coastal city, where he lived during his childhood. Inspired by the urgent of agricultural development in China, he would like to be an agronomist when he was at young age. In late 2006, he started his journey in China Agricultural University to study plant protection and began to explore his interest in research. In 2010, he went to University of Florida to study entomology and received a Master of Science degree in entomology and nematology, during which he mainly focused on the research of termite molting and the mechanism of chitin synthesis inhibitor on termite control. In early 2014, he started to study plant breeding and work with forage crops at the University of Florida. In late 2014, coincidentally asked by his lab mate to take one statistics course together, from which he developed his interest in statistics. Followed his passion, he began to study statistics as a dual degree with Doctor of Philosophy and also received a master's degree in statistics in 2016. To be more efficient in conducting data exploration and analysis, he began to develop programming skills as well. In the short term, he looks forward to working to help other people making sense of their data and providing insight to their questions.