Development of New Measurements and Tools to Mitigate Fescue Toxicosis in Beef Cattle

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Summary and Implications

The objective of this study was to identify new ways to determine the severity of fescue toxicosis and identify genetic differences in fescue impacted traits as a basis in understanding how cattle could be selected for tolerance to fescue toxicosis. We identified across breed and within breed differences in heat stress related traits and growth rate in pregnant cows exposed to toxic fescue. In addition, new biomarkers were identified to differentiate susceptible and tolerant cattle in the form of specific fecal and vaginal microbes. Finally, we identified differentially expressed (DE) genes in high versus low tolerant cattle on toxic fescue. These findings may allow more accurate diagnosis of fescue toxicosis and provide a glimpse into the genes and microorganisms that may impact tolerance or susceptibility to toxic fescue.

Introduction

Fescue toxicosis (FT) is estimated to cost the beef industry between $600 million to $1 billion dollars, annually. Tall fescue is a common forage source because it has exceptional nutrient content and is heat and drought tolerant.

Its hardy growth also makes it the grass of choice for erosion control on hilly terrain. Tall fescue contains a fungus that confers heat and drought tolerance to the grass, but also produces toxic mycotoxins (e.g. ergot valine). Cattle grazing tall fescue often experience increased heat stress in warm weather, and have poor health, reproductive success and growth rate. With so many different impacts on cattle health, it is often difficult to determine the extent of fescue toxicosis in an animal because symptoms are not easily defined. Hair shedding has been used as an indicator of fescue toxicosis since animals grazing toxic fescue do not shed their winter coat. However, this method is subjective and only captures one of a variety of different traits impacted by toxic fescue.

A host of management strategies are needed to reduce the losses caused by toxic fescue. Despite the development of low toxin, novel fescue and other agronomic mitigation strategies, no one solution mitigates all incidences of fescue toxicosis. A relatively simple to implement solution would be to breed cattle that are tolerant to fescue toxins. This solution is attractive because it is inexpressive and would require little change on farms. Evidence of across and within breed variation for performance of cattle pastured on toxic fescue has been documented; however, these differences have not been utilized for selection.

Materials and Methods

Data and analyses are presented from two studies of fescue toxicosis at The University of Arkansas and North Carolina State University. Arkansas: A total of 100 fall-calving cows were selected for allocation to pasture treatments (N=50 toxic; N=50 non-toxic) in 2016, with ergot valine levels monitored monthly. Within pasture, two different sire breeds (Hereford and Charolais) were phenotyped during cold (March) and hot (August) ambient temperatures. Phenotypes collected included: hair shedding, body weight, body condition score (BCS), respiration rate, caudal vein blood pressure, and rectal temperature. Samples were also collected to assess fecal and vaginal bacterial content (microbiomes). DNA were isolated and 16S rRNA were amplified for microbiome profiling using Illumina chemistry. North Carolina: Forty pregnant purebred Angus cows were selected from a larger group based on their growth at two locations (high (H-ToxF) and moderate levels (L-ToxF) of toxic fescue), and classified as either high tolerant (HT) or low tolerant (LT) to FT with 20 cows in each group balanced by location. Fecal samples were collected on the last week (13) of the trial for microbiome analysis as described above. Blood samples were collected on weeks 1, 5, 9, and 13 for RNA sequencing to identify differentially expressed genes when comparing high vs. low tolerant cattle. Normalized gene counts were analyzed with a negative binomial statistical model.

Results and Discussion

Arkansas: We observed breed differences in rectal temperature, with Charolais being cooler than Hereford when fed toxic-fescue without pond access ($P<0.001$). Significant differences due to pasture treatment were observed for a variety of phenotypes, including: body weight ($p<0.02$), BCS ($p<0.05$), respiration rate ($p<0.002$) and blood pressure ($p<0.02$), independent of breed effects. Significant pasture–by-ambient temperature interactions were identified for rectal temperature and respiration rate

(p<0.0001) as well as BCS (p<0.007). Analysis of vaginal microbiota indicates that animals fed toxic-fescue have greater microbial diversity (P<0.001) than animals fed non-toxic-fescue. Fecal microbial analysis did not identify a difference in the diversity, but did identify more total number of microbes present with some predictive of exposure to toxic fescue.

North Carolina: Angus cows with contrasting growth performance (20 high- and 20 low-growers) exposed to toxic fescue during the summer were considered more or less tolerant, respectively. Animals with greater growth rates (HT) harbored significantly different microbial communities (P<0.001) than LT animals, suggesting that the gastrointestinal microbial communities may have an impact on susceptibility of cattle to FT. Animals fed fescue with higher toxin levels (high toxic-fescue group; H-ToxF) compared to those fed less toxic-fescue (high toxic-fescue group; L-ToxF) also had greater fecal microbial diversity (P<0.001). There were more DE genes ($P < 0.01$) between HT and LT animals at one location (high toxic levels; 550) than the other (moderate; 83). At greater toxic level, DE genes were enriched for relevant functions such as cardiac,

protein metabolism, stress response, and other metabolic-related functions, supporting the idea that FT impacts vasoconstriction, immune response, and digestive capacity in cattle. These genes may be used to identify candidate genes to improve response to FT.

These results support the previous evidence that genetics impact fescue tolerance. In addition, microbial and gene expression biomarkers may provide new ways to quantify the severity of fescue toxicosis, which is needed to help select cattle for improved tolerance to fescue toxicosis. Research is ongoing to identify how selection could be used in concert with these findings to select cattle that are tolerant to the negative effects of toxic fescue.