Program Addendum, p 1

**Attendee Additions**
- Ed Cesa, U.S. Forest Service
- Min Chen, Penn State University
- Chase Crowell, Cornell University
- Jonathan Cumming, West Virginia University
- Mary Ann Fajvan, U.S. Forest Service
- Glenn Kenny, Ernst Conservation
- Lew McCreery, U.S. Forest Service
- Sandy Simon, West Virginia University

**Opening Session Thrust Short Reports**
Dan Ciolkosz, Penn State University, will present the Education Report

**NARA/ASCENT Survey**: All AFRI CAPs are participating in a NARA/Ascent survey run by Min Chen, PhD Candidate in Ag/Bioengineering at Penn State. Chen will provide a brief description of the survey just prior to the Panel Discussion at 10 a.m. The survey is paper-based, and is included in the [green] annual meeting folder. All attendees are asked to complete the survey and return it to a location that will be announced.

**Team Huddle Advisory Board Report Out**
Tom Foust, NREL and NEWBio Advisory Board Chair, will report on the board meeting scheduled for Tuesday evening.

**Poster Session Student Abstract Corrections/Additions**
- **Stephanie Aniyika, Delaware State University**
  Title Correction: Identification of Domains-Rearranged Methyltransferases (DRM1) in Switchgrass (*Panicum Virgatum* L.)
  Switchgrass (*Panicum virgatum*) is a native grass and under suitable soil conditions can be found throughout most of the United States except California and the Pacific Northwest. It is an excellent sustainable renewable energy crop that can be converted into cellulosic biofuels like ethanol for fuel needs. This work focuses on DNA methylation, which is an epigenetic modification that regulates key developmental and stress processes. We are analyzing DNA methyltransferases, which are a group of enzymes that catalyze the transfer of a methyl group to bind onto the 5' carbon of the cytosine residue. There are four types of DNA methyltransferases (Dnmt); DNA methyltransferase I (MET I), Chromo-methyltransferase (CMT), Domain-Rearranged Methyltransferase (DRM) and DNA methyltransferase2 (DNMT2). DRM1 is a Dnmt that is responsible for *de novo* methylation that is a process that adds new methylated patterns to a DNA sequence. This research will focus on the presence of DRM1 expression in switchgrass under salinity stress using qPCR analysis. Our goal is to understand the role these enzymes play in *de novo* methylation. To determine the presence of DRM1 in switchgrass, we identified it using a model species in order analyze gene expression under salt stress conditions.

- **Isaac Fisher, Delaware State University**
  Title Correction: Comparison of Stress Genes in Switchgrass (*Panicum Virgatum* L.) Genotypes under Drought Conditions
  Switchgrass (*Panicum virgatum* L.) is being examined as a potential biofuel feedstock because of its large biomass and minimal required input for growth. Drought is an abiotic stress that can affect all agricultural crops and can be combated by farmers via more drought-tolerant cultivars. Plants have adapted to overcome harsh environmental conditions by expressing stress-specific genes that allow them to withstand unfavorable conditions. We set out to measure the expression of such genes, (RAB18, RD22, and DREB2α), which are known to be active under drought and other stresses such as extreme temperatures and salinity. For this work we are comparing two ecotypes, a lowland Alamo and an upland Cave-In-Rock, which originate from different areas and environments. We grew the two ecotypes within the greenhouse to subject half of the samples to drought conditions while the other half received full watering. Samples were collected for RNA isolation, cDNA synthesis, and qPCR to compare expression levels of the genes. Currently, our results showed that the drought-treated plants expressed a higher level of RAB18 compared to that of the control plants, as well as the lowland Alamo expressing a higher expression level in comparison to the upland Cave-In-Rock. This information can be further used in attempting to understand the genes and their functions, or for future breeding programs geared toward a higher tolerance to drought conditions. Our future research will be to test different genotypes as well as different stress-related genes in the same manner.

- **Ryne Davis, Delaware State University**
  Title: Identifying Transcriptionally Active Regulatory DNase I Hypersensitive Sites in Switchgrass (*Panicum virgatum* L.) genotypes AP13 and VS16
  Switchgrass has potential to be used as a source for producing bioethanol, while reducing greenhouse gas emissions by up to 86% when com-
pared with gasoline. The objective of this research is to utilize DNase I digestion and high-throughput sequencing (DNase-seq) to identify active site locations, referred to as DNase I Hypersensitive Sites (DHSs). DHSs are areas in nucleosomes that are hypersensitive to DNase and are correlated with gene activation in eukaryotes. DNase-seq will be conducted using two switchgrass genotypes (AP13 and VS16). Nuclear isolation will be employed to extract chromatin from plant nuclei. Isolated nuclear DNA is then digested using DNase I enzyme resulting in smaller fragments sensitive to DNase digestion and are considered DHSs. DNase-seq data will provide information that will help identify differences between the active regulatory sites found in the two genotypes. Once regions responsible for specific gene regulation are identified and understood, selective breeding and/or genetic modification can be used to develop more efficient switchgrass clones capable of increased yield and tolerance to stress factors.

Preliminary results indicate successful nuclear DNA isolation and DNase treatment. PCR results have confirmed the presence of DNase-digested nuclear DNA, which will undergo size selection for library preparation and sequencing. Future work may involve analyzing the same genotypes after exposure to abiotic and biotic stressors. Results can then be compared to other epigenetic studies in order to gain a better understanding of the biological processes taking place at DHSs and determine how gene expression differs between the two genotypes.