GR ENGR 1

Network resource management for cloud based networked control systems via adaptive sampling

A recent advancement in computing technology, referred to as cloud computing, enables control systems to access computational and storage resources over communication networks. Motivated by the benefits of using the cloud, several research efforts are going on to incorporate cloud into the traditional control system. However, signals, including control actions, are transmitted over a communication link which is associated with bandwidth limitation that could cause delay, packet drops which ultimately affects the performance and stability of the underlying control system. In this paper, we propose a real-time network resource management strategy to manage network resources to overcome such drawbacks. The proposed fuzzy based algorithms are implemented in an experimental platform to demonstrate the effectiveness of maintaining the successful operation of the plant under limited network resources.

GR ENGR 2

Agent-based Framework for Real-Time Detection of False Data Injection Attacks in Software Defined Networking Enabled Power Grid SCADA Systems

We study false data injection (FDI) attacks on measurement data and false data injection attacks on command data against a Supervisory Control and Data Acquisition (SCADA) system of the power grid. An attacker who knows the syntax and payload of SCADA control commands can craft a false data injection attack against commands causing them to appear legitimate which upon execution may put the energy delivery system in a critical state. On the other hand, an attacker who knows the topology of the power network can also craft a false data injection attack against measurement data such that conventional bad data detection schemes employed in state estimators fail to detect such attacks. We develop a distributed agent-based framework for detecting attacks that modify control signals such as control commands issued by the SCADA to remote substations and measurement data transmitted from substations to the SCADA. The distributed agent-based FDI detection framework proposed is composed of agents deployed at substations equipped with local substation data and the capability to exchange this data with agents at neighboring substations to detect malicious control commands and maliciously corrupted measurement data. In addition to detecting FDI attacks against legacy SCADA systems we extend our results to software defined networking (SDN) enabled SCADA systems to achieve some level resilience in the presence of false data. We develop an SDN framework which defines cyber threats and assigns a level of criticality on threats based on their location and impacted SCADA components for efficient and timebound detection and resolution of faults.

GR ENGR 3

The Synthesis and Mechanical and Structural Properties of Piezoelectric Polyvinylidene Fluoride Doped with Barium Titanate Nanoparticles

Authors: A. Joaquim, O. Paul, R. Turner, R. Parthasarathy, L. Ouyang, Yu. A. Barnakov and F. R. Williams

Project Funding: National Science Foundation HRD #1649934

Strain engineering is an innovative and prominent concept in the field of materials science. The coupling of materialsâ€™ strain/stress with their functional properties leads to a number of unprecedented phenomena ranging from surface enhanced Raman spectroscopy (SERS) enhancement in corrugated plasmonic structures to modification of the energy landscape in catalytic systems, from improving of nanoscale ferroelectricity in coherent epitaxial films to an increase of energy harvesting efficiency in photovoltaic devices. Herein, preliminary results of research work related to modification and improvement of piezoelectric properties of polyvinylidene fluoride (PVDF) nanocomposites by employing strain technology is presented. Two experimental approaches are utilized to produce polymer nanocomposites: (i) mechanical stretching of PVDF matrix doped with ferroelectric barium titanate nanoparticles and (ii) doping of PVDF with mechanochemically synthesized BaTiO3 nanoparticles. The overall goal is to improve elasticity of polymer composites in order to enhance their piezoelectric functionalities. The mechanical and structural properties of the synthesized materials will also be discussed.

GR ENGR 4

The Light Intensity Induced Phase Transitions in Graphene Oxide Doped Polyvinylidene Fluoride

Authors: O. Paul, A. Joaquim, M. Eguakun, V. P. Petranovskii, Yu. A. Barnakov, F. Williams

Project Funding: Office of Naval Research Grant #N00014-17-1-3060

The coupling of light (high frequency phenomena) with low frequency functionalities in materials is a long-standing problem. Often low frequency functionality can be manipulated in a material using mechanisms such as heat, mechanical strain, or electric stimulation. This research work presents data that indicates a fourth degree of freedom to stimulate our material through light.

In this work, an interesting finding of the light intensity induced phase transitions observed in 0.05 % weight graphene oxide (GO) doped piezoelectric polyvinylidene fluoride (PVDF) films with 100 Âµm thicknesses. Two effects were discovered in the Raman studies with wavelength of incident beam 532 nm: (i) an alternated modulation of integrated intensities of 797 and 840 cm-1 as a function of time, where wavenumbers stand for vibration modes of CH2 rocking of Î± non-piezoelectric and Î² piezoelectric phases, respectively and (ii) reversible switching between Î± and Î² phases depending on the light intensity (power within the range of 10 â€“ 40mW). A hypothesis on the mechanism and origin of observed effects within the framework of pyro-electricity of GO doped PVDF is also provided.

GR ENGR 5

Evaluation of Impact of Trucks on Intersection delay and Emission

Trucks have complex dynamics compared to passenger vehicles, they require a longer distance to stop, have lower acceleration/deceleration rates and takes longer time to maneuver when crossing the intersection, which causes disturbance to other vehicles. Such dynamics may impact overall intersection operation by increasing delays, which give rise to emission and total fuel loss. This study, therefore have two objectives, first to evaluates the impact of trucks volume on overall intersection operation, air pollution, and fuel loss. The Secondary objective is to suggest suitable mitigation strategies, to minimize delays, reduce emission and fuel loss. To achieve the objectives of this study nine-intersections in Shelby County were considered, twelve (12) hours traffic count survey (Turning Movement Count) was conducted at the selected intersections to observe traffic volume and vehicles composition. Also, existing traffic signal data were obtained from local traffic engineering office. Microsimulation software (VISSIM & SIMTRAFFIC) was adopted to simulate the traffic movement on the studied intersections and to estimates the total delay, emission, and fuel loss. The study found that intersection with higher trucks volume, associated with higher delays, emissions and fuels loss compared to those with lower trucks volume. The study explores various mitigation strategies, among others, optimizing signal time for trucks found to be effective. This attained by extending the green time in order to allow trucks to cross the intersection without stopping, this will not only benefit trucks but also reduce the travel time of all vehicles.

GR ENGR 6

Impact of Transit Signal Priority and Queue Jump lanes on Bus Travel Times in a Mixed Traffic Environment: A Microsimulation Approach

Transit Signal Priority (TSP); an effective means of improving bus regularity and punctuality has gained its popularity in the field of public transportation over the years. As a process of giving preferential treatment to transit vehicles in a mixed traffic environment, it gives a competitive edge to transit vehicles in comparison to the general traffic. TSP has the potential to greatly improve the attractiveness of transit vehicles to the general traffic even to automobile owners by reducing passenger waiting times at bus stops especially in areas where the demand for transit vehicle is low. This research therefore aims to evaluate through microsimulation the impact of transit preferential treatments such as Bus Signal Priority (BSP) and Queue Jump Lane (QJLs) on bus travel times, using a 0.8 mile section of Gallatin Pike corridor as a case study. This paper also aims to compare bus travel times with and without TSP. To achieve the research objectives this paper answers the following research questions: What is the expected bus travel time without TSP? What is expected bus travel time with TSP alone and with TSP and QJLs. Transit signal operations and phasing conditions were coded in Vehicle Actuated Programing (VAP) language with red truncation and green extension strategies which is provided as an add-on in VISSIM microsimulation software. Field data were also coded and calibrated in VISSIM to ensure that the simulated condition is close to the real situation. The findings indicates that priority treatments such as BSP and QJLs are effective to improving transit reliability, mobility and efficiency as it reduces bus travel times.

GR ENGR 7

Traffic Calming Measures: Simulating the Effects on Driving Speeds and Level of Pollution to the Environment

Traffic calming is the combination of mainly physical measures including speed hump and speed table and their role is to reduce the negative effects of motor vehicles use, change driver behavior and improve conditions for both motorized and non-motorized street users. However, traffic calming devices have impact on emergency vehicle response time. In this paper, VISSIM microsimulation software was used to study the influence of traffic calming measures on speeds of vehicles and on the level of noise and air pollution to the environment based on the type and location of traffic calming device. The influence of traffic calming measures on driverâ€™s behavior is characterized by speed, acceleration and deceleration parameters. In order to study their influence, several roadway segments on Nashvilleâ€™s residential and local streets were selected for traffic data collection focusing on traffic calming measures such as speed humps and speed tables. A high accuracy GPS device connected to a laptop and paired with Geographic Information System (GIS) was used on a probe vehicle to record a vehicleâ€™s accurate position (latitudinal and longitudinal coordinates) and speeds at specified 1 second interval

GR ENGR 8

Hoeffding Tree Algorithms for Anomaly Detection in Streaming Datasets: A Survey

This research aims to deliver an extensive and well-constructed overview of using machine learning for the problem of detecting anomalies in streaming datasets. The objective is to provide the effectiveness of using Hoeffding Trees as a machine learning algorithm solution for the problem of detecting anomalies in streaming cyber datasets. In this survey, we categorize the existing research works of Hoeffding Trees which can be feasible for this type of study into the following: distributed Hoeffding Trees, ensembles of Hoeffding Trees, and existing techniques using Hoeffding Trees for anomaly detection. These categories are referred to as compositions within this research and were selected based on their relation to streaming data and the flexibility of the techniques for use within different domains of streaming data. We discuss the relevance of how combining the techniques of the proposed research works within these compositions can be used to address the anomaly detection problem in streaming cyber datasets. The goal is to show how a combination of techniques from different compositions can solve a prominent problem, anomaly detection. The information surveyed in this research has helped bring forth an understanding of the state-of-the-art classification algorithms or compositions which can be combined to effectively address the anomaly detection problem in streaming cyber datasets. An ensemble approach using diversified proposed research is introduced and a further understanding determining if this type of proposed research is feasible and effective is reviewed through a discussion of the construction of our proposed combination of compositions along with the use of a diverse set of cyber datasets which allows for the flexibility to include public datasets, artificially generated attack datasets, and/or both.

GR ENGR 9

Detection of Distributed Denial of Service (DDoS) Attacks Using Artificial Neural Networks on Cloud Computing Platform

This research proposes a technique for detecting a significant threat to the availability of cloud services. By definition, a Distributed Denial of Service Attack (DDoS) refers to an attack in which multiple systems compromised by Trojan are maliciously used to target a single system. The attack leads to the denial of a particular service on the target system. In a DDoS attack, both the target system and the systems used to perform the attack are all victims of the action. This research first presents a survey of the various mechanisms, both traditional and modern, that are applied in detecting cloud-based DDoS attacks. We then proposed a DDoS detection system using artificial neural networks that will detect known and unknown DDoS attack. The proposed method has two major subsystems; (i) Data collection: a traffic generator has been developed to collect data corresponding to different DDoS types; and (ii) distributed DDoS detection: two different neural network algorithms, anomaly and signature-based approaches, are used for detection. The Amazon public cloud was used for running the fast cluster engine with varying cores of the machine. Finally, we have compared and evaluated our proposed system to other existing DDOS detection systems. The findings in this research can be extended to allow the application of the proposed technology for more complicated problems with considerable bigger network traffic.

GR ENGR 10

Evaluate Security of Multiple SDN Controllers Using Stochastic Petri Net

Software-defined networking (SDN) is a networking paradigm that provides automated network management at run time through network orchestration and virtualization. SDN control plane manages the network by applying rules using SDN protocols (e.g., OpenFlow) to switch that work as simple forwarding devices. SDN has received considerable attention in industrial and academia fields by its capability of network management centralization and programmability. However, there is increasing security concern that centralized controller in SDN introduces new network attacks. Compromising the network controller allows the attackers to have control of the entire network. Previous researches suggested to replicate controllers and distributed controllers, but there is still lack of research that studied the risk of using multiple of controllers. In this research, we present a model to analyze attacks on multiple SDN controllers and generate risk assessment scores that can aid mitigation. We build and analyze a Generalized Stochastic Petri Net (GSPN) model using PIPE tool. We explore the security impact of using multiple controllers vulnerabilities.

GR ENGR 11

Multi-Modality Sensor Modeling and Imagery Data Generation in the Virtual Environment Based on Robust Ray-Tracing Technique

Creating simulated Synthetic Aperture Radar (SAR) images as range maps thru virtual environments is helpful for the training and testing of proposed algorithms and techniques used for the analysis of SAR imagery and extraction of field information. The SAR imagery is achieved by modeling electromagnetic (EM) backscattering reflections patterns of objects in the environment. The SAR system, which operates based on radio wave transmission and receiving principles, projects narrow beams of EM radio waves in the azimuth-elevation planes and record time of flight of its transmitted and received signals to determine the environment objectsâ€™ ranges along its sight of view. This technique has various applications in the area of synthetic radar imagery generation, remote sensing, objects detection, localization, and tracking, as well as many aerial geographical surveying. In this paper, we propose an effective ray-tracking technique for SAR response modeling in a virtual environment simulation model (IRIS-VESM) developed at TSU. The approach is vigorously used to generate SAR imagery responses under different operating conditions. The environment objects, for this purpose, are generated using SolidWorks CAD software and imported into IRIS-VESM. Each SAR image represents a reflectivity map (i.e., 2D image) with pixel intensities scaled proportional to range of the nearest object corresponding to direction of projection of SAR in that particular direction in the environment. Using the proposed ray-tracing technique, we demonstrate two other applications of this technique including: (1) Light Detection and Ranging (Lidar), and (2) Infrared Thermal imaging. In the former technique, we take into consideration the optical characteristics of light illuminator and ranging. In the latter technique, we measure the thermal radiation reflectivity of heated objects in the virtual environment. Several examples of these techniques will be presented with appropriate technical details.

GR ENGR 12

Facial Expression Recognition and Learning

Face detection plays an important role in todayâ€™s world. It has many real-world applications like human/computer interface, surveillance, authentication and video indexing. However, research in this field is still young. Face recognition depends heavily on the particular choice of features used by the classifier. The recognition of facial expressions in image sequences is a difficult problem with many applications in human machine interaction. The State of the Facial expression analyzers achieve good recognition rates, but virtually all of them deal only with prototypic facial expressions of emotions and cannot handle temporal dynamics of facial displays. Human emotions are deeply intertwined with cognition learning. They tend to direct cognitive processes and mental cognitive processing of humans implicitly. The goal of this work is to design a model with the capability of classifying the uncertainty, contradiction, and the cognitive nature of the emotions â€“ particularly, for states of mental overload situations. Our approach constructs a multi-level framework utilizing multiple appearance-based learning methods to build corresponding face detectors and poses of human faces in the complex background situations. The completed system consists of an efficient computing technique with close to real-time response for dynamic facial expression recognition, tracking, and characterization. The proposed system offers appreciative improvements over existing technology and significantly enhances human-computer interfacing experience. Particularly, in terms of its capability to handle poorly illuminated facial expressions from within complex background situations. Other application of this technology is related to civilian, military, and homeland security surveillance.

GR ENGR 13

Visual Classification of Small Propeller Unmanned Aerial Vehicles Using Morphology Based Features

Small rotary blade UAVs (sUAVs) is an technology sector of extremely rapid growth. These devices change and evolve rapidly as the availability of small, efficient, and light components and materials become better and customersâ€™ needs change and evolve. These device are extremely maneuverable, capable of carrying a significant payload relative to their mass and size, and extremely easy to deploy anywhere anytime. These devices have been shown to be used to deliver various package types, to do monitoring, and to do search and rescue. Thus the need for remote recognition and tracking of these devices is becoming greater and greater for safety and security. Given that the majority of popular civilian sUAVs are physically similar with small or inferred features differentiating them. Due to the rapid pace of change and need to catch up to deployment speeds, some of the more sophisticated techniques trade too much speed and computational power for accuracy and robustness. In this paper, we present a more specialized classification approach using morphology based features such as propeller count, wingspan, and aspect ratio. Our dataset is generated by imaging CAD models of popular civilian sUAVS set in a 3D virtual environment at various distances from various angles. Using this dataset, we compare the descriptive accuracy of our descriptor, memory usage, and speed using a Support Vector Machine (SVM) against two generalized methods, Speed-up Robust Features (SURF) with a SVM and a neural network based on Hamming distance.

GR ENGR 14

Multi-Camera Target Tracking Via Imagery Data Fusion Techniques

Human activity detection and recognition capabilities have broad applications for civilian, military, and homeland security. However, monitoring of human activities are very complicated and tedious tasks especially when multiple persons involved perform activities in confined spaces that impose significant obstruction, occultation, and observability uncertainty. In advanced surveillance systems utilization of multi-cameras monitoring system is highly imperative for tracking, inference, and recognition of variety of group activities. Although single-camera tracking may be sufficient for small civilian surveillance spaces, however, many military and homeland surveillance applications require full large area coverage, tentative focus of attention, robust tracking accuracy, and even curiosity-based exploration and exploitation. With a single camera, tracking of multiple targets are very challenging to achieve reliably, at large due to presence of inevitable occultation. With multi-cameras systems, complexity of occultation can be dealt with by finding and correlating the correspondences from within multiple cameras views. In this project, we demonstrate one such a multi-person tracking system developed in a virtual environment and demonstrate how a bus group activity where multiple passengers are involved can be dynamically monitored using four operating surveillance camera systems simultaneously. Here, we present how processing tasks of multiple cameras are shared, what objects features they detect, tracks, and identify jointly. Furthermore, we present the computational intelligence techniques for the processing of multi-camera images for the recognition of objects of interest as well as for the annotation of observed activities. The proposed multi-camera processing system is shown to have respectable efficiency and effectively to track multiple targets exhibiting dynamic behavior of objects involved with their activities.

GR ENGR 15

Incorporating Rainfall into Storm Surge Prediction for Hurricane Irma

As increasing sea surface temperatures pave the way for more powerful hurricanes, and population growth remains unwavered in low-elevation coastal zones, the time is certainly ripe for accurate hurricane storm surge prediction. Emergency management officials need a reliable model to properly minimize loss of life, which also benefits authorities in preventing and limiting risks when designing coastal structure protection. A reliable model accurately portrays each parameter associated with hurricane storm surge.

As witnessed with Hurricane Harvey, a hurricane extends far beyond the wind-based Saffir-Simpson scale. The most powerful havoc occurred at its weakest moment as a storm. Tropical Storm Harveyâ€™s rainfall wreaked widespread flooding in southeast Texas, with up to $180 billion in overall damages. Yet some hurricane storm surge modeling programs lack a rain source term. This study employs rain, wind speed, and pressure data from the numerical weather prediction system Weather Research and Forecasting (WRF) with the Computation and Modeling Engineering Laboratory (CaMEL) to model Hurricane Irmaâ€™s storm surge. First, the model simulates Hurricane Irma without a rainfall parameter, and an ADvanced CIRCulation (ADCIRC) simulation is reproduced for validation. Second, Hurricane Irma is simulated in CaMEL applying a rain input from WRF. All three cases are compared to observational data collected from various NOAA stations along the Puerto Rico and Florida coasts. Hurricane Harvey and Hurricane Maria will eventually be simulated as well. Since hurricanes cannot be tamed, a more accurate model that includes rain is the only path to avoiding their destruction.

GR ENGR 16

Analysis of Hurricane Harveyâ€™s Wind Field Using Weather Research and Forecasting (WRF)

The challenge posed by the 2017 hurricane Harvey has highlighted the urgent need for the development and adoption of advanced hurricane prediction models. Harvey made its first landfall on 25 August 2017 and caused devastating impact on the middle and upper Texas coast resulting in over $ 180 billion in damages, more than any other natural disaster in U.S history. Contrary to many hurricanes that quickly weaken after landfall, Harvey was unique as it did not move inland quickly but instead stalled over the South and South-East Texas coast for days, producing torrential rainfall, flash and river flooding which were the major cause of devastation. For most hurricanes, wind is the primary meteorological parameter driving the storm surge as it directly forces the wave and storm surge models, and hence the accuracy of their forecast. Different techniques are available for forecasting hurricane winds. Most applications are based on analytical parametric formulations such as the Holland model which represent radial profiles of hurricane winds. However, a typical hurricane is rarely circular making such models often to underpredict the storm surge. This research proposes Weather Research and Forecasting (WRF) model that uses full physics to forecast the hurricane wind. This capability gives WRF a special property to support very high resolution and produce far field winds. The results of this study are compared with published early advisories for hurricane Harvey provided by National Hurricane Center (NHC) to validate our results.

GR ENGR 17

Implementation of Implicit Solver In Adcirc Storm Surge Model

Hurricanes are among the worst natural disasters, and storm surges caused by these hurricanes are the deadliest and most exorbitant contributors in the resulting destruction. To address this global challenge, the need for precise, fast, and reliable models that are capable of predicating storm surges, floods, and levee overtopping is inevitable. Storm surge models are computational programs, where the hurricanes get formulated mathematically by solving the Shallow Water Equations (SWEs), and simulation of the phenomena is performed before it happens to predict the water surge elevation and velocity. The algorithms used to solve the SWEs equations depends on explicit [1], semi-implicit [1], or implicit [2] methods.

Currently, Advanced Circulation (ADCIRC) [3] framework is a well-known model used by U.S. government to predict storm surge at the east coast; however, due to its explicit or semi-implicit method of solving the Shallow-Water Equations (SWEs), the stability of this model may turn out to be a concern in shallow water regions which needs more investigation [4].

In this research, we are proposing the implementation of an implicit solver in ADCIRC framework. Implicit solvers are found to be more stable than typical explicit or semi-implicit solvers, and hence capable of entertaining large timesteps. The proposed solver was originally presented by Akbar and Aliabadi [2] and Aliabadi et al. [5], and it uses hybrid finite element and finite volume methods to solve the Shallow Water Equations to model storm surges.

After an extensive comparison between ADCIRC explicit and semi-implicit solvers and the proposed solver [4], the authors concluded that implementing the implicit solver in ADCIRC framework would have a significant influence on storm surge research.

The objective of implementing the implicit solver in ADCIRC is to enhance the numerical stability, provide an option of using large timesteps, take advantage of the parallel architecture in ADCIRC framework,

GR ENGR 18

Design and Analysis of Variable Camber Compliant Wing Wrapped by thin Layer of Skin for Adaptive Morphing Wings Smart Technology

This research work is focused on design and analysis of variable camber compliant wing (VCCW) wrapped by a thin layer of seamless skin to predict the behavior of compliant membrane wings subject to camber shape adaptation. VCCW method is found to have a useful advantage comparing with other traditional morphing techniques. Some of VCCW benefits are: simple design, light weight, reduces airframe noise, improving the maneuverability, low operation power, single actuation mechanism to control a leading and trailing edges at the same time, and has the potential of increasing the lift/drag ratio.

In addition, an evaluation of the wing morphing which employs a continuous inextensible surface, continuous boundary conditions are presented here. SolidWorks used in this study as a solid modeling computer-aided design to model a fixed wing structure, ANSYS-FLUENT to extract an aerodynamic pressure around the wing, and ANSYS-Static Structural used for the analyzation of the stresses and other physical properties resulted from camber deformation design. The study intended to focus on the two wing morphing profiles i.e. NACA 2410 and NACA 8410.

GR ENGR 19

Effect of Temperature Distribution on the Efficiency of a Photovoltaic Module

The sun is the ultimate source for all the energy sources that we use today. Over time, people have developed devices and emerging technologies to collect solar energy for heat and to convert it into electricity. An example of these devices are solar photovoltaic cells. Solar cells convert radiation from sunlight directly into electricity and the efficiency of a photovoltaic (PV) solar cells is inversely proportional to their operating temperature [4]. The temperature distribution in a PV module will also give rise to thermal stresses within the module [1]. Hence, it is important to determine the operating temperature of solar cells accurately. This paper presents the finite element steady state thermal analysis of a typical PV module whereby the temperature distribution in each of the layers of the module is determined. The layers consist of a top glass cover, solar cells, ethylvinylacetate (EVA), tedlar back sheet and aluminum fins. To simulate the actual situation, the frame of the PV module is also modelled. The results shows that the addition of finned plates at the bottom surface of the module leads to increased convective heat transfer in the module and as well an increase in overall electrical efficiency. This analysis provides an understanding of how the convection heat loss affect the temperature of the solar cells and their efficiency.

GR ENGR 20

Closed Loop Analysis of the Geothermal System Containing a Heat Exchanger and a Deep, Water Basin

Geothermal systems have become an area of intrigue due to the attributes that are a result of what they provide to a given entity. Analysis of these systems are primarily done using computational fluid design capable programs such as COSMOL and ANSYS. Given an increase in the usage and need for understanding of the system, this research uses ANSYS Fluent to capitalize on formulating a model for a deep, water basin used by Metropolitan Nashville Airport Authority (MNAA) for recycling tarmac heat energy to analyze and simulate practical use of the system while providing in depth analysis as a bi-product of the computing capabilities of the software for a better understanding of effects. The focal point for development is to research and understand applications, gather systematic information to formulate the approach for analysis, configuration of a system in ANSYS Fluent, simulate to characterize thermodynamic properties, and provide conclusive results using benchmarks and intuitive results.

GR ENGR 21

Thermodynamic Analysis of CFRP for Early Detection of Failure

Carbon Fiber Reinforced Polymer (CFRP) composites are trending lightweight materials used in aircrafts due to favorable characteristics. However, aeronautical structures are subjected to continuous cyclic loading and are highly susceptible to damage by impact. Impact damage is considered the relative cause of fatigue in the composite. Fatigue has been found to be the major mode of failure within aircraftâ€™s structures. Developing theoretical and experimental methods for characterizing early stage failure in CFRP composites subjected to cyclic loading was the primary focus.

Experimentation requires quasi-static testing using tensile testing paired with NDI techniques, acoustic emissions (AE) and infrared thermography (IT), to study structural behavior of the CFRP. Correlating detection of failure from quasi-static testing allows interpretation of parameters needed for fatigue testing. Analysis techniques involve evaluating the structure as it experiences cyclic loadings, using data obtained from thermography and acoustic emissions with tensile testing. AE and IT provide energy data relevant to balance of interactive energy in the system. Understanding energy balances through structural changes can be derived with analysis of dissipated energy proportional to the overall energy balance of the system. Interpretation provides a new scope for analyzing energy accumulated through AE detection and IT to understand onset of failure.

GR ENGR 22

The Analysis of Aerodynamics and Optimization Design of Wind Turbine Blade

Wind turbines have become an economically competitive form of clean and renewable power generation. In the United States and abroad, the wind turbine blades continuing to be the target of technological improvements by the use of highly effective and productive design, materials, analysis, manufacturing and testing. Wind energy is a low density source of power [1]. The objective of this research is to develop a computational fluid dynamics (CFD) analysis for SERI-8 composite blade as it is shown in Figure 1 in order to maximize the aerodynamic efficiency of the wind turbine blades. The variables considered related to the aerodynamic performance of the wind turbine blade were the twist distributions of each profile and the pitch angle of the blade. Wind turbine blades are designed with a twist angles so they can present at an angle that takes advantage of lift and drag forces ratio. Those parameters can cause significant change value of the power coefficient (wind turbine efficiency). The achievement of the aerodynamic efficiency will be determine by the power output generated from the wind turbine blades. Finally, the obtain results of the CFD analysis are compared with an experimental reference SERI-8 model results.

GR ENGR 23

A Comparative Study: Aerodynamics of Morphed Airfoils Using CFD Techniques and Analytical Tools

This paper presents an aerodynamics study of wing morphing by creating a Computational Fluid Dynamics (CFD) model using ANSYS FLUENT. First, known National Advisory Committee for Aeronautics (NACA) 2410 and 8410 profiles of airfoils are modeled. Models are run using prescribed initial and boundary conditions to simulate the morphed wing and flow around it. The Shear Stress Transport (SST) ð ‘˜âˆ’ð œ” turbulence model is used to obtain an accurate comparison with the analytical results. Once satisfied with validation, variable cambers between NACA 2410 and 8410 are used in two ends of a wing to mimic a morphed wing situation. Drag and lift coefficients are analyzed for this configuration to understand effects of the airfoil shape on aerodynamic performance. A refined mesh is created near the airfoil wall to capture the flow details. This study is a step forward towards understanding how to accurately model the dynamic morphing of an airplane wing.

GR ENGR 24

A Survey of Team Mission Planning of Autonomous Sensor-based UAVs

Meeting emerging mission challenges, increasing accuracy in execution of mission, and eliminating the risk of failure requires newly crafted methods and technologies to increase autonomy and intelligence of UAVs which are already being tested by a number of civilian universities and military research institutions. To become truly autonomous, UAVs will need to get far better at sensing obstacles and reacting in time to avoid a collision. Fusion of data acquired from various sensors available in todayâ€™s drones gives the possibility to plan missions of multiple UAVs for completion of tasks in a more autonomous, durable, secure, adaptable, and integrated manner. Implementation of image processing algorithms in navigation helps UAVs to efficiently tackle dynamic threats and unplanned events. This paper presents the recent technological advances enabling successful navigation of autonomous UAVs in complex environment. A particular focus is devoted to control schemes, sensing, and team mission planning of UAVs operating in complex environments. Particularly, this paper discusses challenges associated to imaging and remote sensing of UAVs with adaptive learning.

GR ENGR 25

Modelling and Analysis of Micro-grids with Energy Storage Systems, with emphasis on Lithium-ion batteries for Load Balancing Applications.

Title: Modelling and Analysis of Micro-grids with Energy Storage Systems, with emphasis on Lithium-ion batteries for Load Balancing Applications

By

Frank Ajieh

Graduate Student

Department of Mechanical and Manufacturing Engineering

The traditional source of power from fossil fuel generators comes at significant cost and risk from the required huge logistics tail for fuel, heavy maintenance requirements, noise and environmental impact. This generally has led to coupling both renewables and fossil fuel with long-duration energy storage, thereby reducing the dependence and environmental impact of fossil fuel generators. Storage devices can provide frequency regulation to maintain the balance between the network's load and power generated, and they can achieve a more reliable power supply for industrial facilities. Also, batteries are required in order to advance towards smart electric grids that integrate discontinuous energy flow from renewable sources, optimizing the performance of clean energy sources as they balance micro-grids to achieve a good match between generation and load. In this research, study and analysis is done using HOMER and COMSOL software. HOMER is used for the economic analysis of the micro-grid system, while COMSOL is used for the analytic synthesis of the physical components of the lithium-ion battery, which would involve analyzing the capacity fade of the battery in order to predict the life-cycle of the battery and investigation into the state of charge estimation of the battery system.

GR AGSCI 26

Assesment of Biodiversity and Seasonal Patterns of Leech (Hirudinea) Parasitism of Semi-Aquatic Turtles in an Urbanized Wetland System

Aquatic turtles inhabiting a palustrine emergent wetland adjacent to Tennessee State University in Nashville, Tennessee were examined for leeches as a component of a multi-year mark and recapture study. Leeches serve as bioindicators in aquatic environments, and are useful in determining the biological condition of aquatic ecosystems based upon various evaluations such as species richness indices between parasite and host. This study investigated seasonal fluctuations in leech species diversity, abundance, and severity of infestation on hosts over a four-month period. Aquatic funnel traps were baited and deployed weekly from June â€“ October 2016 to sample the turtles. Each captured turtle was weighed, measured, sexed, marked, and examined for external leeches. All located leeches were removed and preserved for later identification. Turtle species captured during this study, included the Common Snapping Turtle (Chelydra serpentina), Stinkpot (Sternotherus odoratus), Spiny Softshell Turtle (Apalone spinifera), and the Red-eared Slider (Trachemys scripta elegans). The leeches that were collected from the turtles represented 3 different genera under phylum Hirudinea, including Batracobdella, Placobdella, and Helobdella, and 7 total species. Collectively, the interpretation of these data can be used to understand parasite-host relationships and how patterns in leech parasitism vary throughout the active season in a wetland system.

GR AGSCI 27

Detection of Salmonella typhimurium in Leafy Vegetables using a Surface Plasmon Resonance Biosensor

Salmonella contaminated leafy vegetables are responsible for 17 outbreaks, 762 illnesses and 26 hospitalizations in United States. Although different methods are available to timely detect Salmonella in foods, Surface Plasmon Resonance (SPR) has benefit of real-time, label-free and rapid detection with higher sensitivity and specificity. The purpose of this study was to develop a SPR method in conjugation with the Immunomagnetic Separation (IMS) for detection of low levels of Salmonella in leafy vegetables. Samples of romaine lettuce were inoculated with Salmonella typhimurium ATCC-13311 at low levels (101 to 102 CFU/g) and incubated overnight in Buffered Peptone Water at 37 oC. The numbers of naturally occurred bacteria and the inoculated Salmonella in the samples before and after incubation were determined by aerobic plate count and XLT-4 agars. Flagellin antigen was captured by the antibody immobilized on magnetic beads and then eluted by Glycine-HCl, pH 3.0. Flagellin antigen was neutralized and injected onto the SPR sensor surface immobilized with a flagellin-specific monoclonal antibody. SPR signals resulting from the binding of flagellin on sensor surface were observed and quantified. The IMS isolated samples yielded an average detection signal of 22.9 Â± 5.5 uRIU, whereas the average detection signal for non-isolated samples was 4.1 Â± 0.4 uRIU. The biosensor detection sensitivity was 2.4Ã—105 CFU/mL after enrichment. The lowest detection limit in inoculated samples before enrichment was 80 CFU/g. Four other bacteria (Enterobacter, Pseudomonas, Serratia and Aeromonas) were isolated from the vegetable samples after enrichment, but none of them were detected by the SPR when analyzed individually. Our results suggest that SPR can be used for faster detection of Salmonella typhimurium in leafy vegetables with higher specificity and sensitivity. Further study will be conducted to improve this developed method for detection of other serotypes.

GR AGSCI 28

Analysis of Flagellin Protein of Campylobacter Species with Monoclonal Antibodies

Campylobacter species are important enteric pathogens causing disease in humans and animals. The flagellar filaments of Campylobacter are complex, composed of two flagellin subunits primarily Fla A and secondary Fla B. Both are known to be highly homologous to each other. The objective of this study was to identify common epitope binding sites and molecular variations of flagellin among Campylobacter species using two sets of monoclonal antibodies (MAbs). Ten strains of Campylobacter from three species namely Campylobacter jejuni, Campylobacter coli and Campylobacter fetus were cultured in Campylobacter blood-free agar (CCDA). Flagellin proteins were extracted from the cell surfaces and separated by SDS-Polyacrylamide Gel Electrophoresis. Two sets of MAbs (Groups I and V), composed of seven clones of MAbs, were used in Western blot to detect the binding patterns with respect to naturally expressed flagellin proteins. Both groups recognized flagellin proteins with molecular weights around 64 kDa and divers of flagellin fragments with molecular weights between 20 and 55 kDa. The results showed that two distinct binding patterns between Groups I and V MAbs with all tested strains. Within the same group of MAbs, the differences were also observed among the tested strains with respect to the molecular weights and relative binding intensities of flagellin fragments. The diverse patterns of Western blots from distinct strains of Campylobacter were compared using image tool analysis. The result showed that the binding patterns were unique for different strains and consistent in the subsequent cultures from the same stains. These monoclonal antibodies therefore may be valuable in strain identification and immunological tests.

GR AGSCI 29

Comparison of concentration methods to facilitate the successful recovery and early detection of Phytophthora species from Tennessee nursery irrigation water

Diseases caused by Phytophthora are one of the most important problems for ornamental nursery production in the United States and water serves as an important means of introduction and spread of Phytophthora. The objective of this study was to develop methodology for reliable and sensitive screening of irrigation water for the presence of Phytophthora spp. in the complex environment of commercial nursery operations. P. nicotianae and P. capsici were used to spike 1L creek and chlorinated tap water samples with 102 and 104/ml zoospores. Phytophthora was concentrated by: 1) filtration (0.22 Âµm, 0.45 Âµm, 3 Âµm and 5 Âµm membrane filter), 2) centrifugation, and 3) baiting (1, 3, 5, and 7 days) and then tested directly with serological and molecular detection assays and culturing on selective PARPH-V8 medium. Filtration was the most effective and sensitive method for detecting low level of zoospores followed by baiting and centrifugation. Water samples (from small (<10 acres), medium (>10, <100 acres) and large (>100 acres) nursery production operations- 33 total samples) were processed with current accepted baiting procedure (USDA APHIS protocol). Six out of thirty tree water samples were confirmed as Phytophthora positive (3- P. syringae, 2- P. cryptogea and 1- P. hydropathica) using immunostrip, culturing on PARPH-V8 medium, PCR and sequencing. Reliable and sensitive detection of Phytophthora spp. in source and production water will be critical for making timely production management decisions by nursery growers and will help researchers and regulatory agencies to determine the distribution of Phytophthora species. This project was funded by the State of Tennessee, Department of Agriculture Specialty Crop Block Grant Program Agreement No. 32506-01117.

GR AGSCI 30

Integration of high frequency soil data for improving a microbial-enzyme-mediated decomposition model performance

Abstract. Soil organic carbon (SOC) response to climate warming is largely uncertain. The uncertainty lies in very poor parameterization of key microbial processes that can invoke critical feedbacks to climate warming. To improve the parameterization and model performance will require high-frequency observation data for model calibration such as soil microbial biomass. By working with a microbial-enzyme-mediated decomposition model (MEND), we integrated soil heterotrophic respiration and MBC data to MEND model based on 10 independent soil collections in a 180-day long soil incubation experiment. Multiple scenarios were designed by integrating 2, 4, 6, 8 and 10 measurements in MBC with the model while the same respiration and soil organic C pool data were included in all scenarios. In each scenario, the model simulations and observations will be compared in order to evaluate the model performance from integrating low frequency to high frequency data. Preliminary results showed that simulation with high frequency scenario showed better fit with observed heterotrophic respiration than that with low frequency (R2, 83% vs. 42%). The model projections over 1-year and one decade showed large discrepancies between low and high frequency scenarios. The preliminary output supports that integrating higher frequency MBC data can substantially improve model performance as compared with the traditional model calibration with low frequency data. Future field and laboratory experiment design should accommodate high frequency measurements of key soil and microbial variables. The proposed work is a collaborative project between TSU and Oak Ridge National Laboratory with funding sources of USDA and Department of Energy (DOE).

GR AGSCI 31

Interactive Learning to Educate Youth About Safe Handling and Preparation of Poultry and Eggs

Youth are an important population to understand regarding knowledge and perceptions of food safety because they are more prone to mishandling foods. Educating youth about best food practices is a time-honored tool to reach parents and families of youth to catalyze adoption of technologies and information. Our purpose was to evaluate dissemination of Poultry and Egg Education Project (PEEP) food safety using interactive instructional modules. Our goals were to 1) evaluate learning modules, each focusing on different messages regarding poultry and egg food safety and to 2) document knowledge of key messages/content. Youth participants were also asked to self-report impacts of the PEEP modules. With assistance from TSU students, six activities were chosen and delivered: Bacteria on a Stick, Bean Bag Refrigerator Toss, Microscope and Toy Bacteria, Pick the Right Thermometer, Bag Demonstration, and our PEEP Videos. Using convenience sampling, students (N = 247) participating students were asked to complete an online survey following completion of learning modules that measured knowledge gained and impacts of the modules. They also rated each of the activities on a scale of 0 = Nothing new learned and not interesting to 100 = Learned something and found very interesting. The results showed that out of 247 participants 47% knew how long they should wash their hands, 95% state they had learned something new about poultry and egg safety, 93% percent state they are adopting the safety standards, and 91% state they will share the information. Lastly, students reported the highest enjoyment for hands on activities, and the lowest for the informative videos. The significance is that participants learned and intend to share proper poultry and egg safety standards.

GR AGSCI 32

Effects of Elevated Hydrostatic Pressure for Decontamination of Raw Milk from Listeria monocytogenes and Background Microflora

Recent CDC epidemiological studies indicate approximately 99% of illnesses caused by Listeria monocytogenes are foodborne in nature, leading to hospitalizations in 94% of cases, and are responsible for collective annual death of 266 American adults. Current study evaluates effects of hydrostatic pressure at controlled temperatures for decontamination of raw milk. Various time (0 to 12 minutes) of elevated hydrostatic pressure (310 and 380 MPa e.g. 45K and 55K PSI) were investigated for inactivation of 4-strain mixture of Listeria monocytogenes (ATCCÂ® numbers 13932, 51779, 51772, BAA-2658) inoculated at target level of 6.0 log CFU/ml of raw milk. Temperature was monitored and maintained at 4, 25, and 50 ÂºC by a circulating water bath and a stainless steel water jacket. The experiments were conducted in two biologically independent repetitions, as blocking factors of a randomized complete block design, containing three repetitions per time/treatment/pressure within each block. Study was statistically analyzed by ANOVA using OpenEpi software. Inactivation indices were calculated using GInaFiT Software. At 380 MPa, for treatments of 0 to 12 minutes, D-values of 3.47, 3.15, and 2.94 were observed for inactivation of Listeria monocytogenes at 4, 25, and 50 ÂºC. Up to 3.73 and >4.26 log CFU/mL reductions (P<0.05) of Listeria monocytogenes at planktonic stage were achieved using application of pressure at 380 MPa for 3 and 12 minutes, respectively. Similarly, background microflora counts were reduced (P<0.05) by 1.3 and >2.4 log CFU/mL after treatment at 380 MPa for 3 and 12 minutes, respectively. Treatments below three minutes were less efficacious (P â‰¥0.05) against the pathogen and background microflora, in vast majority of time and pressure combinations. Results of this study could be incorporated as part of a risk-based food safety management systems and risk assessment analyses for mitigation of public health burden of listeriosis.

GR AGSCI 33

Agricultural Education an Mathematics Performance Among Secondar Students

Mathematics and science achievement in the US students continue to lag behind other developed nations. Reasons for this lag include unimaginative instructional methods, inexperienced teachers and lack of connection between school mathematics and the day-to-day experiences. Most students learn mathematics best when they see the connection between the concepts learned in school and their real life applications. Contextual learning enables students to link mathematics concepts and knowledge learned to learning environments of school, home and community. Agricultural education has great potential to deliver relevant curriculum, which engages students with hands-on learning environments that are rich with real life applications of mathematics. The purpose of this study was to determine the effects of agricultural education, Future Farmers of America (FFA) involvement, and Supervised Agricultural Experience (SAE) participation on the mathematics performance of secondary students. Our study explored these factors using an ex post facto research design. The findings of this study revealed that agricultural education students performed better than non-agricultural students on various Common Core math standards using a researcher-developed mathematics test. In terms of specific Common Core standards of mathematics, students overall, scored lowest on statistics and probability as compared to algebra and number systems. There was a positive, low relationship between mathematics score and the number of agricultural courses, as well as participation in SAE. There was a moderate, positive relationship between mathematics test scores and FFA participation. Agricultural educators should look for ways of integrating statistics and probability examples in agricultural education to improve scores in those areas. Agricultural education teachers should encourage students to enroll in as many agriculture courses as possible and emphasize FFA and SAE participation of the students.

GR AGSCI 34

The PRMT1 gene expression pattern in Panicum hallii

Title: The PRMT1 gene expression pattern in Panicum hallii.

Transcription factors (TFs) control gene expression precisely by significant binding to cis-regulatory DNA sequences in the promoters of their target genes. Some developing work put forward that transcriptional regulation may play more imperative roles in plants than in animals because of the large number of TF-coding genes in plant genomes. For this study, we chose PRMT1. PRMT1 belongs to the family of methyltransferases (Arginine specific) which leads to the formation of an epigenetic transcriptional memory. ChIP-Seq was done using the Next-Gen sequencing platform. Both HiSeq and MiSeq yielded more than 44 million raw reads per samples. This represents about 93% of the mapping ratio for the genome of Hallâ€™s grass (Panicum hallii, panhal2). Roughly 1300 to 34746 peaks were observed in the annotated gene regions. Fourteen common and 91 upregulated broad and narrow peaks were identified from the ChIP which sequenced the control and drought treated samples. After epigenetic modifications in Panicum hallii, some locations of the genome were enriched with high protein fold enrichment values. Out of these enriched areas, 69 genomic regions with a differential enrichment level had been chosen for qPCR. This confirmed that the presense of DNA-protein binding site occurred through methylase enzymes. Based on the gene ontology terms that follow biological processes, a higher percentage of these 69 genes involve in developmental process, metabolic process, response to stresses, as well as cell organization and involve in transport activity (including energy pathway). Some of the genomic areas are highly repetitive and involved in signal transduction.

GR AGSCI 35

Control of Phytophthora cinnamomi on flood stressed woody ornamental plants using preventive and curative fungicides

Phytophthora cinnamomi is an oomycete pathogen that attacks woody ornamentals; especially plants exposed to elevated soil moisture levels. During flooding events, Phytophthora root rot often causes damage in nurseries throughout the Southern and Eastern United States, sometimes leading to complete nursery crop loss. In this study, we evaluated the efficacy of fungicides and biofungicides for preventive and curative control of Phytophthora root rot on flooded dogwood seedlings. Fungicides or biofungicides were applied as preventive or curative drench treatments 7 d pre-flooding or 1 d post-flooding, respectively, to artificially inoculated dogwood, Cornus florida, seedlings. The plants were flooded by maintaining standing water for 1, 3, or 7 d, with five replications per treatment. After the experiment, plant growth data (fresh weight, root weight, plant height, plant width) were recorded, and roots were assessed for disease severity using a scale of 0-100% roots affected. Preventive treatments that reduced disease severity compared to a non-treated control included Subdue MAXX at 1, 3 and 7 d flooding and Orkestra Intrinsic at 1 and 3 d. Compared to the non-treated control, curative applications of Empress Intrinsic and Orkestra Intrinsic reduced disease severity at 1 and 3 d flooding. Fungicides and biofungicides can be incorporated into an integrated strategy to manage Phytophthora root rot on flood stressed nursery trees.

GR AGSCI 36

Inflammation Links Genetic Endogenous Retroviral Elements to Antibiotic Resistance in Guinea Fowl (Numida meleagris)

Inflammation Links Genetic Endogenous Retroviral Elements to Antibiotic Resistance in Guinea Fowl (Numida meleagris)

Alexis Pigg, Yongming Sang

Department of Agricultural and Environmental Sciences, College of Agriculture, Tennessee State University, Nashville TN 37209, USA

Gut health is a major aspect that affects the overall performance of poultry. The interaction between diet components and gut immune system is key to regulate gut health. Probiotics and antibiotics are among major food supplements to promote gut health; however, our understanding about the underlying molecular mechanism is largely unknown. Endogenous retroviral elements (ERV) comprise nearly 4-10% of animal genomes. ERV expression has been highlighted for the association with cell inflammatory status in studies of mice and humans. In regards to poultry, ERV expression has been related with reduced body size, appetite, and decreased disease resistance in layers. There is a void of data about ERVs in Guinea Fowl (Numidia meleagris) genomes and if they modulate physiological or immune functions. Determination of ERV composition will help genetically explain how Guinea Fowl respond to the food supplements of antibiotics and probiotics. I hypothesize that antibiotics and probiotics used as growth promoters interact with genetic endogenous retroviral elements to affect cellular inflammatory status and animal growth in Guinea Fowls. With experiments in this project, I expect to: (1) classify ERV composition and phylogenic relation in the Guinea Fowl genome and (2) clarify the correlation between endogenous retroviruses and inflammatory regulation by antibiotics and probiotics used as growth promoters.

This work is/was supported by the USDA National Institute of Food and Agriculture Evans-Allen 1013186.

GR AGSCI 37

The Co-Factorial Induction of Obesity Using High Fat Diet and Had-36 Adenovirus: A Transcriptomic Study

The Co-Factorial Induction of Obesity Using High Fat Diet and Had-36 Adenovirus: A Transcriptomic Study

Caitlin Gilmore, Yongming Sang

Department of Agricultural and Environmental Sciences, College of Agriculture, Tennessee State University

Obesity is defined as a multi-systemic disorder where abnormal or excess fat accumulates in adipose tissue to the extent that health may be impaired. It is considered a chronic disease caused by multiple factors, and a public health problem that is a worldwide epidemic. The United Statesâ€™ obese population has increased by 50%, resulting in more than one-third (34.9%, 78.6 million) of its adult population labeled as obese. A possible cause factor and consequence of obesity is the infection of the human adenovirus 36 (Had-36). Due to the higher susceptibility of obese persons to viral infection, it is possible that the prevalence of Had-36 is not just a cause of obesity, but a consequence. The infection upregulates the chronic inflammation, adipogenic commitment and differentiation of pre-adipocytes, which leads to an increased number of fat cells in animal models. Had-36 is also prevalent in 11% of the non-obese United Statesâ€™ adult population, implicating that the obese population infected with Had-36 must be due to co-effects from other cause factors. Given these findings, we hypothesize that a co-factorial obesity animal model induced with a high fat diet (HF) and Had-36 infection will better replicate and represent the obese population. We will use a co-factorial animal model of mice intestinal cells to (1) establish an animal obesity model with HF + Had-36 infection, (2) use a genome-wide profile signature to locate specific gene-responsive pathways using transcriptomic RNA-Seq, and (3) manipulate signature genes in an adipocyte cell line to study their role in adipogenesis.

This work is/was supported by the USDA National Institute of Food and Agriculture Evans-Allen 1013186.

GR AGSCI 38

Molecular and functional novelty of porcine interferon-Ï‰ subtype revealed through cross-species computational analysis

Molecular and functional novelty of porcine interferon-Ï‰ subtype revealed through cross-species computational analysis

Lauren Shields*, Yongming Sang

Department of Agricultural and Environmental Sciences, Tennessee State University, Nashville, Tennessee

Type I interferons (IFNs) are innate cytokine mediators that regulate antiviral immunity and have significant functional and molecular diversity in order to combat rapidly evolving viral pressures.

IFN gene families in the genomes of 155 animal species have been annotated and analyzed to reveal that pigs have the largest type I IFN family which consists of nearly 60 genes that encode for 7 IFN subtypes including multigene subtype IFNâ€“Ï‰. Subtypes such as IFN-Î± and â€“Î² have been extensively studied, whereas the unconventional subtypes such as IFN-Ï‰ remain under investigated. This research has evolutionarily defined the porcine IFN family and demonstrated that porcine IFN-ï · subtype possesses novel features including: a multi-gene subtype displaying specific expansion in bats and ungulates, emerging isoforms with higher antiviral potency than conventional IFNs, cross-species high antiviral activity in mammalian cells, and potential actions through non-canonical signaling pathways. By focusing on understanding porcine IFN-Ï‰s evolution, functional diversity, signaling specificity, and optimization of novel antivirals against viral diseases, the research has expanded the limited knowledge of the functional divergence of unconventional IFN subtypes and species-specificity of IFNs in livestock animals, while simultaneously demonstrating that IFN-Ï‰s exert broad and high antiviral activity. Finally, this research has furthered IFN-based novel antiviral design by establishing state-of-the-art procedures for efficient characterization of the molecular and functional spectrums of unconventional IFNs.

Supported by grants from USDA (NIFA AFRI 2013-67015-21236 and NIFA AFRI 2015-67015-23216)

GR AGSCI 39

Analysis of plant growth promoting traits of selected biological control agents

Analysis of plant growth promoting traits of selected biological control agents.

Asha Maheshwari1* and Margaret Mmbaga1

Department of Agricultural and Environmental Sciences, Tennessee State University, Nashville TN 37209

Bacterial endophytes are ubiquitous microorganism colonizing internal tissues of plants without causing any visible symptoms. Some of these endophytes employ direct or indirect mechanism to enhance plant growth and protect plants against phytopathogens. Eight isolates of endophytic bacteria (B17A, B17B, IMC8, Y, PS, PSL, Prt and E) were previously reported to have potential in biological control of phytopthora blight of pepper and powdery mildew in Cornus florida. Some of these biological control agents (BCAs) have also displayed plant growth promoting abilities in previous studies, but the mechanism of action has not been studied. The objective of this study was to analyze the selected BCAs for plant growth promoting (PGP) traits including the production indole-3-acetic acid (IAA), phosphate solubilization ability, ammonia synthesis, nitrogen fixation, and siderophore production using in vitro studies. All the BCAs tested were able to produce variable amounts of growth hormone IAA ranging between 3-65 Âµg/ml and ammonia ranging between 2-10 Âµmol/ml. Also, all eight BCAs showed ability to differentially fix atmospheric nitrogen while five isolates exhibited inorganic phosphate solubilization. Six BCAs exhibited siderophore production that is normally associated with transport of iron across cell membranes by formation of soluble Fe3+ complexes. Isolates B17B, PS, PSL, Prt, and E were positive for all five PGP traits tested, thus suggesting that their growth promotion ability is associated with different mechanisms involving growth hormone production and nutrient availability and uptake.

GR AGSCI 40

Controlling Powdery Mildew on Cucurbit Crops through Biological Control Agents

Cucumber and squash are cucurbits that have nutritional and medicinal benefits. These two crops contain essential provitamin, vitamins, and minerals such as potassium, iron, calcium, magnesium, manganese, copper, phosphorous, and calcium. In Tennessee, these cucurbit crops are affected by several major infectious diseases including anthracnose, Cercospora leaf spot, cucumber mosaic, downy mildew, Phytophthora fruit and crown rot, Septoria leaf spot, squash mosaic, Verticillium wilt and powdery mildew which severely reduce their productivity. Powdery mildew is ranked as the most severe disease of these cucurbits. Symptoms of powdery mildew appear as a white powdery residue on the upper leaf surface with circular patches or spots. Infected leaves become brown and shriveled and defoliate prematurely and infected fruits remain small and do not develop fully. Thus, the yield is reduced due to a decrease in the size or number of fruits and/or a decrease in the length of the harvest period. The purpose of this study is to control/treat powdery mildew in cucumber and squash using Biological Control Agents (BCAs). BCAs are known to reduce disease incidence directly or indirectly by inhibiting the development and activities of pathogens and/or promoting plant growth. The BCA mechanisms of actions include direct antagonism of the pathogens by selectively attacking pathogens through hyper-parasitism, production of antibiotics and/or lytic enzymes, competition for space and food source and by inducing systemic resistance in the host plants. Our study focuses in evaluating the effect of five previously isolated BCAs in controlling powdery mildew using weekly foliar sprays on cucumber and squash plants. Our preliminary results show a decrease in powdery mildew disease severity after four BCA applications. Extensive analysis of plant growth response to BCA applications is in progress.

GR AGSCI 41

Effect of UV-C irradiation on the nutritional quality and safety of cranberry flavored water using a dean flow continuous UV system

Effect of UV-C irradiation on the nutritional quality and safety of cranberry flavored water using a dean flow continuous UV system

Vybhav Gopisettya, Ankit Patrasa, Agnes Kilonzo-Nthengea, Sudheer Yannama, Micheal Sasgesb, Mallory Burnsc, Matthew J. Vergnec

aFood Biosciences and Technology Program, Department of Agricultural and Environmental Sciences, Tennessee State University, Nashville, 37209, TN, USA

bAquafine Corporation, Valencia, 91355, CA, USA

cDepartment of Pharmaceutical Sciences and Department of Chemistry and Biochemistry, Lipscomb University, Nashville, 37204, TN, USA

Abstract

The influence of short wave-length UV-C irradiation at 254 nm on microbial inactivation, anthocyanins stability, analysis of ascorbic acid, and cytotoxicity of formulated cranberry flavored water (CFW) was investigated. Pathogenic microbes like Escherichia coli ATCC 25922 and Salmonella typhimurium ATCC 13311 in UV-C treated formulated CFW were inactivated more than 5 log10 at UV-C fluence of 24 mJâˆ™cm-2 (p<0.05). Higher UV fluence up to 240 mJâˆ™cm-2 were applied to investigate the influence of UV-C irradiation on anthocyanins and ascorbic acid stability in CFW. The concentrations of ascorbic acid and anthocyanins such as (Cy3Ar), (Cy3Ga), (Pe3Ar), (Pe3Ga) in irradiated CFW were determined. UV-C irradiation of formulated CFW decreased concentration of anthocyanins at higher fluence levels (>120 mJ.cm-2). The content of ascorbic acid was retained up to 82% in irradiated CFW at a UV-C fluence of 40 mJâˆ™cm-2 (FDA recommended fluence levels for acidic fluids). This research study suggested that UV-C treatment of formulated CFW can achieve high levels of microbial inactivation without significantly decreasing the concentration of anthocyanins and ascorbic acid content. These results suggest that this non-thermal technique can be an alternative to thermal pasteurization in producing high quality beverages.

Sources of funding: USDA award number 2015-69003-23117

GR AGSCI 42

Detection of Personal Care Products (PCPs) in Surface Water of Collins River in Warren County, Middle Tennessee

Personal care products have been detected nationwide in different environmental matrices including wastewater effluents and surface water. The potential for these chemicals to pollute our rivers even at trace levels abounds. We conducted a monitoring study to detect the presence of personal care products in Collins River, Warren County. Collins River is a six-order river that drains a large portion of Warren County including McMinnville, Tennessee. Grab water samples were collected from Collins River for three seasons: (summer and fall of 2014 and 2015 and winter of 2015 and 2016) each year. Water quality parameters were also determined in situ using EurekaTM multi-parameter sondes. Water samples were analyzed for the presence of personal care products using GC-MS. Chemical Abstract Service Registry Numbers (CASRN or CAS) and subsequent use or descriptions of the detected chemical compounds were identified. Personal care products detected included flavor and fragrance agents, skin conditioning agents, surfactants in cosmetics, shampoos, moisturizer, antiperspirant, and deodorants. While the actual concentrations of these compounds were not determined in this study, their presence in surface water is noteworthy.

GR AGSCI 43

Analyzing Proteome of Bacillus cereus tsu1 for PHB Production Study

Analyzing Proteome of Bacillus cereus tsu1 for PHB Production Study

Hui Li*a, Suping Zhoua, Yong Yangb, Tara Fishb, Theodore Thannhauserb

a. College of Agriculture, Human & Natural Sciences, Tennessee State University, Nashville, TN 37209

b. Plant Soil and Nutrition Research Unit, USDA-ARS. Ithaca, NY, 14853-2901.

Abstract

Bacterium Bacillus cereus tsu1 was cultured in Rapeseed cake substrate (RCS, 25g/L) for continuous 12, 24 and 48 hours. Microscopy method was used to inspect intracellular PHB accumulation status. PHB accumulation was observed starting at early exponential phase and PHB degradation started after 12 hours at stationary phase. Bacterial cell pellet was collected by centrifugation at 12, 24 and 48 hours. Intracellular protein was extracted following SDS_Phenol_Based protein extraction protocol. Protein samples were quantified, 100 Î¼g protein from each sample was subjected for downstream proteome change study using TMT labeling followed by nanoLC-MS/MS analysis. All MS/MS raw spectra were processed and searched against Bacillus cereus tsu1 protein database. Principle component analysis (PCA) were conducted first followed by quantification analysis, in which the intensities of the constituent peptides were log2-transformed and subjected for normal distribution t-test (General linear model). A total of 2789 proteins were identified, out of which 144 proteins expressed a significant difference (p < 0.05) between bacterial cultured for 12 and 48 hours. Proteins involved in PHB biosynthesis regulation (PhaR and PhaC) expressed variation over time. Protein involved in cell division, endospore formation, signaling transduction pathways were found significantly changed. Results from this study, in addition revealing mechanism of PHB intracellular accumulation, provide systematic bacterial proteogenome analysis.

GR AGSCI 44

Bio-Industrial Relevant Enzymes Identified From Metagenomic Analysis in Rumen Environment

Bio-Industrial Relevant Enzymes Identified From Metagenomic Analysis in Rumen Environment

Santosh Thapa*, Hui Li, Joshua OHair, Sarabjit Bhatti and Suping Zhou

Department of Agricultural and Environmental Sciences, College of Agriculture, Human and Natural Sciences, Tennessee State University, Nashville, TN, 37209.

Microbial genome mining is a potential alternative route to traditional laboratory methods for the discovery and development of novel bioactive compounds and numerous biotechnological applications. The goat rumen harbors an assembly of microbes hypothesized to comprehend a rich source of lignocellulose degrading enzymes that could be exploited to enhance the bio-conversion efficiency of cellulosic ethanol production. The predominant cellulolytic bacteria and the fibrolytic mechanism(s) in the rumen remain elusive. This study aimed to isolate, identify and characterize the genes encoding novel cellulases in the goat rumen metagenome. To accomplish this goal, we extracted metagenome DNA from the goat rumen and sequenced using next-generation sequencing. Following assembly and annotation, several gene clones encoding for cellulases, hemicellulases and xylanases have been cloned and further sub-cloned using TOPO cloning strategy. Gene sequences were confirmed using Sanger sequencing and submitted to NCBI database. The genes encoding endo 1, 6 beta D-glucanase was functionally expressed in Escherichia coli and tested for clear halo zone formation around the colonies on the Phytagel plate containing the medium amended with CMC (carboxymethyl cellulose) demonstrating cellulolytic activities. The bio-functional enzymes were purified using NI-NTA purification method and further characterized through DNS assay. This finding corroborates that these multi-functional enzymes could impart potential industrial applications.

GR AGSCI 45

Controlling Powdery Mildew on Cucurbit Crops through Biological Control Agents

Cucumber and squash are cucurbits that have nutritional and medicinal benefits. These two crops contain essential provitamin, vitamins, and minerals such as potassium, iron, calcium, magnesium, manganese, copper, phosphorous, and calcium. In Tennessee, these cucurbit crops are affected by several major infectious diseases including anthracnose, Cercospora leaf spot, cucumber mosaic, downy mildew, Phytophthora fruit and crown rot, Septoria leaf spot, squash mosaic, Verticillium wilt and powdery mildew which severely reduce their productivity. Powdery mildew is ranked as the most severe disease of these cucurbits. Symptoms of powdery mildew appear as a white powdery residue on the upper leaf surface with circular patches or spots. Infected leaves become brown and shriveled and defoliate prematurely and infected fruits remain small and do not develop fully. Thus, the yield is reduced due to a decrease in the size or number of fruits and/or a decrease in the length of the harvest period. The purpose of this study is to control/treat powdery mildew in cucumber and squash using Biological Control Agents (BCAs). BCAs are known to reduce disease incidence directly or indirectly by inhibiting the development and activities of pathogens and/or promoting plant growth. The BCA mechanisms of actions include direct antagonism of the pathogens by selectively attacking pathogens through hyper-parasitism, production of antibiotics and/or lytic enzymes, competition for space and food source and by inducing systemic resistance in the host plants. Our study focuses in evaluating the effect of five previously isolated BCAs in controlling powdery mildew using weekly foliar sprays on cucumber and squash plants. Our preliminary results show a decrease in powdery mildew disease severity after four BCA applications. Extensive analysis of plant growth response to BCA applications is in progress. Funding Evans Allen, USDA

GR AGSCI 46

Improving Bioenergy Lignocellulosic Feedstocks Traits and Properties through CRISPR-Cas9 Technology in Switchgrass (Panicum virgatum L.)

Increasing greenhouse gas emissions (GHG) due to the use of fossil fuels has a negative impact on the climate, with an estimated increase in global temperature. To combat this increasing GHG, particularly CO2, biofuels have been proposed as replacement for petroleum-based fuels in transportation. Biofuels, energy sources generated from biomass have emerged as a potential route to meet energy demand and avoid political instability and environmental issues that could result from fossil fuel-related conflicts worldwide. Switchgrass (Panicum virgatum L.), a native North America grassland species is considered as an excellent bioenergy feedstock due to its high biomass yield, wide climatic adaptation, as well as its low energy input for production. However, there are major limitations of using switchgrass for biofuels including (i) the difficulty in degrading the main constituents of cell wall biomass, which in some instances is due to its recalcitrance behavior, (ii) difficulty in convectional breeding due to self-incompatibility and varied ploidy levels of the grass. These obstacles limit exploitation of this crop as a lignocellulosic biofuel, thus necessitate the development of genetic manipulation strategies to produce improved cultivars with better biomass quality. To achieve this, high-throughput efficient in-vitro cell culture systems capable of genetic transformation and regeneration are necessary for studying gene functions and germplasm improvement. Thus, our study focuses in developing reliable transformation and regeneration methods for switchgrass to enable cloning of biosynthetic lignin cell wall genes with CRISPR-Cas9 technology. This will lead us to a better understanding of lignin role in the recalcitrance of switchgrass biomass and provide fast and reliable methods to alter cell wall biosynthesis and improve biomass digestibility/conversion of this crop. Currently, we have established cell lines that are being used for transformation and regeneration.

GR AGSCI 47

Identification of long non coding RNAs in chicken divergently selected for leanness

Long non-coding RNAs (lncRNAs) are non-protein coding transcripts that are more than 200 nucleotides long. They lack an open reading frame of more than 100 amino acids and usually have one or two exons. Of all the transcripts from humans, only ~2% code for proteins. Until recently, the non-coding transcripts were thought of as â€œjunk DNAâ€ . LncRNAs play crucial roles in transcriptional regulation of biological processes. The objective of this study was to identify and characterize lncRNAs from adipose tissue of chickens divergently selected for leanness. 59,884,218 and 26,240,352 paired end sequence reads generated using Illumina platform using total RNA from adipose tissue of fat line (FL) and lean line (LL) respectively were downloaded from National Centre for Biotechnology Informationâ€™s (NCBI) SRA website were used. FastQc was used to analyze the quality of the reads and the high quality reads were retained for further processing. Cufflinks software was used to assemble the transcripts which were then submitted to Flexible Extraction of long non-coding RNAs (Feelnc) software to distinguish non-coding from the coding transcripts using a user generated coding potential score of 0.523. We predicted a total of 8986 putative lncRNAs from adipose tissue of the HF chicken. Of these, 4436 were further classified as genic while 4540 were classified as intergenic. The project adds to the database of chicken lncRNAs. Comparison between the expression of lncRNAs in the FL and LL chickens will help in highlighting the specific lncRNAs that may have regulatory roles in adipogenesis. These will provide targets for further analysis into their mode of action.

GR AGSCI 48

Evaluation of Bacterial isolates for Powdery Mildew Control in Cucumbers (Cucumis sativus)

Powdery Mildew is one the worldâ€™s most frequently encountered plant disease, infecting leaves, stems, flowers and fruits of nearly 10,000 species of angiosperms. Powdery mildew is particularly important and very common in cucurbits grown under field and greenhouse conditions in most areas of the world. The cucurbitaceae family (cucurbits) comprised of 90 genera and 750 different species include important vegetable crops such as cucumber, squash, water melon, bitter melon and others and powdery mildew is one of the most important diseases in these crops. Management of powdery mildew is limited to mostly chemical fungicides, and this practice is causing great concern to growers and vegetable consumers alike due to toxicity hazards posed by chemical fungicides to growers who apply the chemicals, to consumers and also to non-target organisms and environment. Public awareness on the hazards posed by pesticides has resulted in great demand for organic produce; hence, organic production of vegetables is the fastest growing sector in agricultural production systems. However, disease control is one of the biggest challenges in organic production systems and there is a need to actively develop alternative products for controlling such diseases. The objective of this study was to evaluate microbial isolates for the control of powdery mildew disease in cucumbers. In this study, five bacterial isolates previously selected for biological control of powdery mildew on other crops were tested on powdery mildew disease control of cucumbers and compared with chemical fungicide and non-treated control. Out of the five bacterial isolates tested one treatment, Bacillus sp. (Psl) showed significant disease suppression of powdery mildew of cucurbits and require further evaluation.

The 40th Annual University-Wide Research Symposium

April 2-6th, 2018

GR AGSCI 49

Hairy Root Transgene Expression Analysis of a Secretory Peroxidase (PvPOX1) from Common Bean Infected by Fusarium Wilt

Plant peroxidases (POXs) are one of the most important redox enzymes in the defense responses. However, the large number of different plant POX genes makes it necessary to carefully confirm the function of each paralogous POX gene in specific tissues and disease interactions. Fusarium wilt is a devastating disease of common bean caused by Fusarium oxysporum f. sp. phaseoli. In this study, we evaluated a peroxidase gene, PvPOX1, from a resistant common bean genotype, CAAS260205 and provided direct evidence for PvPOX1â€™s role in resistance by transforming the resistant allele into a susceptible common bean genotype, BRB130, via hairy root transformation using Agrobacterium rhizogenes. Analysis of PvPOX1 gene over-expressing hairy roots showed it increased resistance to Fusarium wilt both in the roots and the rest of transgenic plants. Meanwhile, the PvPOX1 expressive level, the peroxidase activity and hydrogen peroxide (H2O2) accumulation were also enhanced in the interaction. The result showed that the PvPOX1 gene played an essential role in Fusarium wilt resistance through the occurrence of reactive oxygen species (ROS) induced hypersensitive response. Therefore, PvPOX1 expression was proven to be a valuable gene for further analysis which can strengthen host defense response against Fusarium wilt through a ROS activated resistance mechanism.

GR AGSCI 50

Studies of Photosynthetic Efficiency In Eastern Redbud Varieties Important to the Ornamental Nursery of Tennessee

The Eastern Redbud Cercis canadiensis L. is a medium sized leguminous tree native to the forests of Tennessee and found growing as an ornamental throughout the Eastern United States and Canada. The objective of this research has been to evaluate the adaptation and limitations to redbud growth in nursery and greenhouse settings. Apart from a few biotic constraints, redbud is a very vigouros tree species with a fast growth rate. Redbud species and genus are a basal clade in the phylogeny of Papillinoid legumes, meaning that they are among the evolionarilly most ancient legumes within this subgroup of the second largest plant family on earth (the legumes). As such, redbud is a model species of photosynthetic and nutrient use efficiency in legumes and in trees more generally. The objective of this research, therefore, is to evaluate the photosynthetic and leaf mineral concentration differences existing in different genotypes of the redbud tree. The materials used included four different clonally reproduced varieties of redbud used by commercial nursery owners/growers in southern Tennessee and a population of wild collected seed reproduced trees of native redbuds from Kentucky. The varieties varied in leaf colors and growth habit including purple leafed weeping type â€œRuby Fallsâ€ , the yellow leafed upright type â€œRising Sunâ€ , the dark green dwarf type â€œAce of Heartsâ€ and the light green upright type â€œDon Egoffâ€ . All varieties were purple flowered and pure bred C. canadiensis varieties except for Don Egoff which was produced by backcrossing white flower color from C. chinensis, the Chinese Redbud into C. canadiensis, the Eastern (American) Redbud. The first two genotypes were transplanted from root limiting cloth bags and placed with nursery-grade potting mix in 15 gallon plastic containers like the other varieties which were already growing in 7.5 gallon plastic pots. The varieties were arranged in a randomized block design with five (5) replicates, each replicat

GR AGSCI 51

Prevalance of Antimicrobial Resistant Enterobacteriaceae in Almond Milk and Skins

Introduction: Consumption of plant-based milk is increasing rapidly as a result of increased health consciousness as well as changes in peoplesâ€™ lifestyle. With the demand for plant-based milk on the rise, concern for its microbiological safety has also raised. Antimicrobial resistance has also become a health challenge to the public.

Purpose: The aim of this study was to evaluate the prevalence of antimicrobial resistant Enterobacteriaceae isolated from almond milk and skins.

Methods: Almond milk was processed form raw almonds purchased from local stores in Davidson County. Enterobacteriaceae was isolated from raw almond milk and almond skins and thereafter identified using API 20E method. The antimicrobial susceptibility of identified isolates was determined using the Bauer and Kirby disk diffusion technique. Enterobacteriaceae isolates were then subjected to a panel of eight antibiotics: vancomycin (30Âµg), novobiocin (30Âµg), erythromycin (15Âµg), tetracycline (5Âµg), cefpodoxime (10Âµg), kanamycin (10Âµg), nalidixic acid (30Âµg) and imipenem (10Âµg).

Results: The main Enterobacteriaceae species found in raw almond milk and skins were: Enterobacter cloacae (40.7% and 37%), Pantoea spp3 (29.6% and 25.9%), Klebsiella pneumoniae spp ozaenae (22.2% and 3.7%), respectively. Pantoea spp4 was isolated in 3.7% of almond skins and not in the milk. Enterobacteriaceae from milk and skin significantly (P<0.05) indicated higher resistance for vancomycin (100%), novobiocin (96.3% and 100%), erythromycin (100% and 96.3%), than tetracycline (70.4% and 74.1%), cefpodoxime (55.6% and 59.3%), and kanamycin (3.7% and 18.5%) respectively. All Enterobacteriaceae isolates were susceptible to nalidixic acid and imipenem.

Significance: Based on our findings, plant-based milk is a reservoir of antimicrobial resistant Enterobacteriaceae, hence a concern since many consumers consider it a healthier option. Good Agricultural and food safety practices are recommend for growers and consumers.

GR AGSCI 52

Physicochemical and functional properties of Pigeon Pea (Cajanus cajan) protein isolates and non-starch polysaccharides

Introduction:

Pigeon pea (Cajanus cajan (L.) Millsp.) is a nutritive pulse crop containing multi bioactive components and is an important ingredient in diet for disease prevention. The finctioanl properties of pigeon pea protein and non-starch polysaccharides could be very beneficial food ingredient with regards to their functional and biological properties due to the heath benefits of the components.

Method:

Protein isolates (PI) were obtained from locally grown GA-2 pigeon pea variety, employing alkaline extraction- isoelectric point (IEP) method. Non-starch polysaccharides were extracted sequentially followed by alcohol precipitation. HPLC and GPC were employed to analyze amino acid composition and molecular weight of the isolated protein and monosaccharide composition, molecular weight and conformation of the isolated non-starch polysaccharides. The physicochemical and rheological properties including surface tension, emulsification, viscosity, and gelation properties were evaluated. A tensiometer was used for measuring surface tension. Zeta-potential and droplet size distribution were determined using Zetasizer 90 (Malvern Instruments Ltd, USA). ARES-G2 Rheometer (TA Instruments, USA) was used to measure viscosity and gelation properties of the samples.

Significance:

Emerging consumer trends keep food industry in continuous search for inexpensive, healthier, and alternative protein and polysaccharides ingredients.

Results:

Pigeon pea protein accounts for about 20% and non-starch polysaccharides accounts for about 6% of total seeds. Protein isolates were soluble between pH values of 3 and 10. . Pigeon Pea protein isolates exhibited 14% least gelation concentration. Non-starch polysaccharides were classified as pectic polysaccharides with shear thinning properties. The results exhibited that both fractions could be potential ingredients as food emulsifiers and stabilizers in terms of emulsification properties and rheological properties.

GR ENVSCI 53

Microhabitat Use by the Hellbender Salamander (Cryptobranchus alleganiensis) in East Tennessee

The Hellbender salamander (Cryptobranchus alleganiensis) is a long-lived, fully-aquatic salamander that inhabits cool, well-oxygenated streams and rivers in the eastern United States. Although once abundant, C. alleganiensis populations have experienced major declines across the historical range. Habitat degradation, siltation, aquatic contaminants, and infectious diseases are commonly suggested contributors to these declines. Although Tennessee provides areas of high-quality habitat for C. alleganiensis, microhabitat differences among life stages have not been well documented. We evaluated microhabitat use of larval, juvenile, and adult C. alleganiensis at three streams in east Tennessee by comparing sites occupied by C. alleganiensis to random sites within each stream. We used a generalized linear mixed model to evaluate what stream covariates best explained presence of C. alleganiensis, along with discriminant function analysis to evaluate differences in microhabitat use between C. alleganiensis life stages (i.e., larval, subadult, and adult). We completed habitat assessments for a total of 60 individuals. Our results showed a trend indicating a strong association between the percent large rock, the percent of low embedded rocks, and the number of rocks above 50 cm with C. alleganiensis presence. In addition, our results showed a trend indicating a strong difference in microhabitat use among life stages, which indicates that each life stage may select different microhabitat covariate within suitable streams. Overall, our analysis identified microhabitat covariates that are potentially important for long-term C. alleganiensis conservation, and provides guidance for stream protection and restoration practices that may mitigate sedimentation and habitat degradation in impacted streams.

GR ENVSCI 54

Detection and Habitat Modelling for the State Threatened Western Pygmy Rattlesnake (Sistrurus miliarius streckeri) in Tennessee

Shawn Snyder, Dr. William Sutton

Funding: Tennessee Wildlife Resource Agency

Globally, reptile populations are declining at a rate quicker than most other vertebrates. The Western Pygmy Rattlesnake (S. miliarius streckeri) occurs in a narrow range in west-central Tennessee along the Tennessee River drainages and Western Highland Rim. Little is known about the spatial ecology or habitat requirements of this species in Tennessee where it is listed as State Threatened. Previous studies on this species have reinforced the rarity of this species in the state with as little as 30 confirmed occurrences coming in the last 30 years. Our primary research objectives are to evaluate the distribution of the Western Pygmy Rattlesnake in Tennessee by using a variety of field-based survey methods and species distribution modeling techniques. Our preliminary habitat suitability model suggests most of the suitable habitat for pygmy rattlesnakes in Tennessee occurs on the East side of the Tennessee River and is predominantly associated with riverine and stream systems.

GR ENVSCI 55

Detecting the Presence and Abundance of Streamside Salamanders (Ambystoma Barbouri) in Middle Tennessee Using Environmental DNA

Amphibians represent the vertebrate taxa that has experienced the greatest declines globally. Declines tend to occur in species with geographically-isolated and/or fragmented populations. This is specifically true for the Streamside Salamander (Ambystoma barbouri), an Ambystomatid salamander that occurs in Middle Tennessee. This salamander species emerges to breed in low-order, ephemeral streams during the winter and spring months. As these animals are cryptic and only surface-active for several months, they can be difficult to detect using traditional survey methods. Surveys that target environmental DNA (eDNA) in the form of DNA sloughed into their aquatic environment could provide an effective method for detecting the presence of this species. Water samples were collected at 50 meter stretches of 17 streams across the A. barbouri range four times over 6 months (December 2016 â€“ May 2017). Stream segments were searched for all life-stages of salamanders using rock-turning and visual surveys. We used real-time PCR to quantify DNA amounts using an A. barbouri species-specific primer. We used Generalized Linear Mixed Models to evaluate relationships between A. barbouri adult, larval, and egg counts and biomass at each site. In addition, we evaluated the change in eDNA amounts across the active season of A. barbouri. Primary outputs from this study include a replicable eDNA approach to identify A. barbouri populations in Tennessee and sampling guidelines for appropriate times to collect eDNA survey data for A. barbouri. This information will provide a method which can be used by wildlife agencies to further the knowledge and conservation of this species.

GR PHYSCI 56

High Pressure Pasteurization for Inactivation of Rifampicin-Resistant Cronobacter sakazakii in Reconstituted Infant Formula

Infections associated with Cronobacter sakazakii are often fatal in infants born premature and those younger than two months. Two historic outbreaks of Cronobacter sakazakii associated with infant formula in Tennessee in 1988 and 2001, and a 2016 infection episode of the bacterium associated with a premature infant in Pennsylvania had brought increasing attention to endeavors for decontamination of the bacterium from infant formula. Current study investigated effects of high pressure pasteurization at 4 and 50 ÂºC for inactivation of the bacterium inoculated in reconstituted infant formula. Various times (0, 1, 4, 7 and 10 minutes) and two intensity levels of 310 and 380 MPa (e.g. 45K and 55K PSI) of elevated hydrostatic pressure were investigated for inactivation of 4-strain mixture of rifampicin-resistant Cronobacter sakazakii, inoculated in reconstituted infant formula. Experiment was conducted at 4 and 50 ÂºC, in two biologically independent repetitions, as blocking factors of a randomized complete block design. Samples were enumerated on TSA supplemented with rifampicin and yeast extract. Analysis of variance was conducted followed by LSD-based mean separation using OpenEpi software. During treatments at 380 MPa at 4 ÂºC, 1.59 and >6.01 log CFU/mL of inoculated pathogen were reduced (P<0.05) after 1- and 10-minute treatments, respectively. At 50 ÂºC and 380 MPa, corresponding reductions (P<0.05) were >5.00, >5.90, >5.81, and >6.00 log CFU/mL after treatments for 1, 4, 7, and 10 minutes, respectively. At 310 MPa the reductions (P<0.05) were ranging from 1.35 to 3.67 and 3.10 to >5.72 log CFU/mL for samples treated at 4 and 50 ÂºC, respectively. Over 5-log reduction of Cronobacter sakazakii in reconstituted infant formula is achievable as result of optimized high pressure pasteurization that could be utilized to assure safety of infant formula particularly for premature newborns and those with elevated risk of Cronobacter infection.

GR PHYSCI 57

Synergistic combination of luteolin and indole-3-carbinol selectively restrains estrogen receptor-positive breast cancer development

Dietary phytochemicals have emerged as modulators of multiple molecular or cellular components in various types of cancer. The rational of combining dietary phytochemicals is that phytochemicals at low dosages efficiently exert anticancer without side effects. In the present study, we firstly combined luteolin with indole-3-carbinol (I3C) at various concentrations to inhibit breast cancer cell growth using a cell proliferation assay in MCF7 (estrogen receptor alpha-positive, ERÎ±+), MDA-MB-231(triple negative breast cancer, TNBC) and BT-549 (TNBC) cells. Our results show that the combinations of luteolin and I3C (luteolin < 30ÂµM and I3C < 120 ÂµM) selectively inhibited ER+ MCF7 breast cancer cell growth but have no inhibitory effects either in MDA-MB-231 or BT-549 cells. Moreover, the selected combination of luteolin and I3C did not exhibit cytotoxicity in human normal endothelial cells (EA.hy926) compared to a couple of commercial anti-breast cancer drugs. Furthermore, immunoblot assays demonstrated that combination of luteolin and I3C down-regulated SIRT1 and ERÎ± protein expression in MCF7 cells. Finally, we found that co-administration of luteolin (8mg/body weight/day) and I3C (20mg/body weight/day) by intraperitoneal injection for 28 days significantly suppressed tumor growth while the individual luteolin or I3C injection have no significant anti-cancer effect in MCF7 xenograft mice. These results suggest that combination of luteolin and I3C may be an efficient approach to treat/prevent ER+ breast cancer without side effects.

GR PHYSCI 58

Anti-inflammatory Effects and Molecular Mechanisms of the Combination of Curcumin and Resveratrol in Vascular Cells and Mouse Aorta

Monocyte recruitment and adhesion to the endothelium is a crucial step the development of endothelial dysfunction and therefore induces cardiovascular disease (CVD), the number one killer of Americans. Emerging evidence shows that polyphenols, the secondary plant metabolites present in a large variety of foods, have the potential ability in reducing risk of CVD. The aims of this study are to investigate the synergistic anti-inflammatory effects of combined polyphenols at physiological levels and define relevant molecular mechanisms. Our results indicate that resveratrol and curcumin dose-dependently inhibited tumor necrosis factor-alpha (TNF-Î±)-induced monocytes adhesion to human EA.hy 926 endothelial cells. The half maximal effective concentration values of curcumin and resveratrol are 15 Î¼M and 26 Î¼M respectively. Particularly, combined curcumin (8 Î¼M) and resveratrol (13 Î¼M) significantly inhibited TNF-Î±-induced monocytes adhesion to endothelial cells while the individual chemicals did not have such effect at these concentrations. The combination index value of curcumin plus resveratrol at the selected concentrations is 0.82, indicating combination of these two polyphenols has synergistic anti-inflammatory effect. This synergistic anti-inflammatory effect was confirmed in the ex vivo assays using aorta from C57BL/6 mice fed with diet containing curcumin 500 mg/kg and resveratrol 200mg/kg for one week. Combination of resveratrol and curcumin also synergistically ameliorated the TNF-Î±-enhanced protein expressions of vascular cell adhesion molecule and monocyte chemotactic protein-1, two major indicators of vascular inflammation, both in cultured endothelial cell

GR PHYSCI 59

Nigrospora sphaerica products from the flowering dogwood exhibit antitumorigenic effects via the translational regulator, pS6 ribosomal protein

Research reports have shown that endophytic fungi that colonize plant tissues without any external symptoms produce novel bioactive metabolites that exhibit wide array of applications in biomedical field. In this study, Nigrospora sphaerica isolated from the flowering dogwood (Cornus florida L.), was examined for secondary metabolites that have anticancer properties on cell lines A549 (lung) and U251 (glioblastoma). Crude extracts of N. sphaerica exhibited antiproliferative and antimigratory effects on these solid tumors. Lung and glioblastoma cancer cells showed 17% and 25% decrease in cell viability when treated with 2 Î¼g/ml of N. sphaerica crude extract as compared to control. These quantitative effects on both cell lines were further supported by ANOVA analysis which showed a statistically significant differences (p < 0.05) across all concentrations examined. Boyden chamber assays revealed that cells treated with N. sphaerica crude extracts decreased tumor cell migration as compared to vehicle treated control cells (p < 0.05). Results also suggested that the antitumorigenic effects of N. sphaerica were as a consequence of negatively regulating the PI3K/Akt/mTOR translational control signaling pathway, a canonical mechanistic axis that contributes to the maintenance and progression of several human cancers. Thus, the results of this study provide experimental evidence that the endophytic isolate of N. sphaerica from flowering dogwoods is a promising source of bioactive metabolites with potential antitumor and antimetastasis properties.

GR PHYSCI 60

Harfmful Algal Blooms (HABs) in the TSU Wetland

The main campus of Tennessee State University (TSU) houses agricultural research facilities as well as a 26-acre wetland. Since 1996, beavers have established this wetland area, doubling its size every five years. The wetland becomes eutrophic during the spring and summer. Due to research livestock and wildlife having access to the wetland, concerns about the eutrophication and harmful algal blooms (HABs) has increased. TSU, the Tennessee Department of Health, the Tennessee Department of Environment and Conservation, and the U.S. Geological Survey conducted a study in the summer and fall of 2017 to determine if cyanotoxins were present. Water samples were collected at different locations within the wetland to measure nutrients (nitrogen, phosphorous, iron, sulfur), Secchi disk depth, type of algae present, and various cyanotoxins. Continuous water-quality instruments were maintained at the upper end of the wetland, mid-wetland and below the wetland to document dissolved oxygen, pH, temperature, specific conductance and turbidity. Several bacteria genera capable of producing cyanotoxins were present in the wetland during the sampling period, including Dolichospermum, Chrysosporum, Aphanizomenon, Anabaena, Oscillatoria, Pseudoanabaena, and Lyngba. Microcystin and saxitoxin levels in the wetland were ranged from trace amounts to 0.26 Âµg/L. The highest toxins concentrations were found in the mid-wetland area, near the livestock access point at levels approaching the US EPAâ€™s health advisory. Additional work is being done to determine the correlation between water chemistry parameters and cyanotoxin concentrations, which may provide an early and inexpensive indicator for cyanotoxins.

GR PHYSCI 61

SKP2 Knockdown Regulates AR/FOXA1 Expression and Inhibits Cell Proliferation in PCa

Increased levels of SKP2 (S-phase kinase-associated protein 2), an E3 ubiquitin ligase, are associated with prostate cancer (PCa) progression. This correlation is due to the ubiquitin-mediated degradation of key cell cycle regulators including p27 as well as regulating androgen receptor (AR) activity. However, the mechanisms involved in SKP2â€™s proto-oncogenic effects remain elusive. The pioneer transcription factor, FOXA1 (Foxhead box protein A1) is known to interact with AR inducing its activity and modulating downstream target genes. Dysregulation of the AR/FOXA1 complex contributes to the progression of PCa and castration-resistant prostate cancer (CRPC). We hypothesized that SKP2 impacts the function of the AR/FOXA1 complex contributing to the growth of CRPC. With application of shRNA technology, we established stable SKP2 knockdown PCa cell lines to investigate the effects of SKP2 on CRPC growth. Our results demonstrated that SKP2 plays a critical role in the regulation of AR and FOXA1 expression in CRPC cell lines. SKP2 knockdown resulted in an increase in both AR and FOXA1 levels in C4-2B and 22RV1 cells, two CRPC cell lines. Importantly, SKP2 knockdown led to a significant reduction in cell proliferation of both C4-2B and 22RV1 cells. Our findings present a potential SKP2-AR/FOXA1 signaling pathway that may be targeted as a therapeutic approach in the control of CRPC malignancy.

GR PHYSCI 62

FOXO3 regulates genome methylation by functioning as a competing endogenous RNA of DNMTs in chicken LMH cells

FOXO3 is an important transcription factor that belongs to the O subclass of the forkhead family. It plays multiple roles in cellular progression, including cell proliferation and differentiation, cell-cycle control, energy metabolism, protein degradation, DNA damage repair, oxidative stress response, and apoptosis. Several reports suggest that circFOXO3 is involved in cell growth and progression. DNA methylation exerts a crucial role in many biological processes like gene expression regulation, disease development, cellular homeostasis, DNA damage repair, cell differentiation, proliferation, and apoptosis. Three DNA methyltransferases (DNMTs), DNMT3A, DNMT3B, and DNMT1, have been implicated in the establishment or maintenance of DNA methylation. Both FOXO3 and DNA methylation is strongly associated with human longevity as well. The objective of the current study was to elucidate the relationship between FOXO3 and DNA methylation since these two factors have so many function overlaps. First, we cloned the full-length mRNA of chicken FOXO3 (cFOXO3) by 5â€™ rapid amplification of cDNA ends (5â€™RACE), and validated the existing of circular FOXO3 RNA (circFOXO3). After aligning the sequence with other species, we found that cFOXO3 and circFOXO3 had the same cellular functions as it in human and mouse by using flow cytometry analysis. Second, by using dual luciferase assay, we found that gga-miR-29-3p family (miR-29a-3p, miR-29b-3p, miR-29c-3p) could binding cFOXO3, circFOXO3, DNMT3A, DNMT3B and DNMT1. Third, Biotin pull-down assays showed that cFOXO3 and circFOXO3 competed with DNMT3A, DNMT3B and DNMT1 when combined with miR-29-3p family. Lastly, we found that over-expression of cFOXO3 and circFOXO3 could increase the protein expression of DNMT3A, DNMT3B and DNMT1 by using western blot, and 5-mC level of the genome was changed after over-expressed or knocked-down cFOXO3 and circFOXO3. Our results demonstrated that cFOXO3 and circFOXO3 regulate genome methylation by functi

GR PHYSCI 63

Preparation and testing of hsCAS9 lentiviral vector for genetic modifications chicken cells and embryos

Although the CRISPR-Cas9 technology has been successfully applied to a variety of mammalian cells and organisms, modifications in vivo to the chicken genome using this technology have proven to be more challenging, due to the sensitive nature of the developing chicken embryo which is protected within an egg shell and surrounded by a thick membrane critical for development. The single cell stage of avian zygotes is also hardly accessible. Based on the CRISPR-Cas9 technology, we designed a lentiviral vector utilizing a humanized Cas9 enzyme from Staphylococcus aureus, which has a short peptide sequence and has been demonstrated to have less toxicity effects on sensitive cell and tissue types. When paired with a separate gRNA vector, the Cas9 enzyme will become active, allowing for precise and efficient genetic knockout activity. For genetic modifications to take place in live chickens, we have prepared bacterial Cas9 gene cloned in a lentiviral vector. To validate the vector for its ability to transfer genes to chicken cells, we are testing the effectiveness of the vector to infection chicken embryonic fibroblast cells and preadipocytes. We are also developing microinjection techniques to deliver the hSaCas9 vector to target chicken primordial germ cells. We are also modifying methods that can be conveniently used to bring the microinjected chicken embryos to hatch.

GR PHYSCI 64

Isolation of transposon GFP-tagged mutants of Pectobacterium carotovorum in host signal-regulated genes

Pectobacterium carotovorum, a widely distributed gram negative enterobacterium is responsible for soft rot diseases in over 80 plant species. The major virulence factors are plant cell wall degrading exoenzymes (PCWDE) including pectate lyases, polygalacturonases, cellulases and proteases resulting in tissue maceration. Pathogenicity factor production is induced in the presence of plant host extracts. However molecular mechanisms of disease development are not completely understood. The goal of this research was to construct transposon mutant library of P. carotovorum in host signal regulated genes that may contribute to pathogenesis. Using a promoter-less green fluorescence protein (GFP) transposon, pCKD100 we constructed a pool of Chloramphenicol resistant mutants of P. carotovorum strain KD100 and selected 5264 for screening. The mutants were initially screened qualitatively for differences in the levels of GFP fluorescence in minimal media supplemented with and without host extract from celery (CE). Of this, 266 mutants were selected and screened further in the following round for quantitative GFP expression in the presence or absence of CE. We obtained 48 mutants with high GFP activity on CE. Five mutants also had high activities of extracellular protease. These are being analyzed to determine the identify the mutant genes.

GR PHYSCI 65

Esters from carboxylic acid through RCOOPdH species and styryltrifluoroborates

Palladium inserted hydridopalladium species is simply represented as RCOOPdH. Our focus is to use this species with potassium styryltrifluoroborates and to synthesize new kind of styryl carboxylate type ester compound. This kind of compound is largely unknown. In general, esters are chemical compounds with many practical uses. These uses include but are not limited to major industrial petrochemicals, medical inhibitors, and cosmetic ingredients. Esters are also found in the basic building blocks of life, animal cells. These are most commonly known as cholesterol esters, or neutral fats. One of the pioneer esterification reactions is called Yamaguchi esterification where anhydride is the initial product followed by reaction with alcohol and thus forms an ester. In our study, we explore an unprecedented approach for the synthesis of styryl esters. This new results and mechanism will be discussed.

GR PHYSCI 66

Organotrifluoroborates and discovery chemistry

Most important branches of organic chemistry are total synthesis, semi synthesis and methodology. Recently, we have discovered outstanding number of new reaction methodologies such as aroylation, nitration, C-H activation, aminoether synthesis, and amide styrylation in our laboratory at TSU. These new reaction methodologies and their mechanism will be displayed.

UG ENGR 67

The Design of a GPS Spoofing System

As modern warfare becomes more technological, new methods of attack become available to the technologically savvy. Many military operations are intended to be covert but rely on vulnerable Global Positioning System (GPS) information. Tech savvy attackers can penetrate the GPS network and obtain secret information, such as the locations of sensitive operations. This investigation focuses on the design and implementation of a GPS spoofing system that misleads attackers regarding the true position information by broadcasting false GPS data. A system engineering approach is used to design this system. Relevant mathematical, scientific, and engineering theories, principles, and tools are administered accordingly. The GPS spoofing system is composed of a software capable of manipulating a genuine GPS signal. We show that the cloaking of true GPS information is advantageous as both an offensive and a defensive military strategy.

UG ENGR 68

Design of a Remote Presence Device For Law Enforcement Agency and Road Safety

Intercepting vehicles to control drivers is an important day-to-day task performed by law enforcement and security personnel. However, such a task of intercepting vehicles and controlling drivers can be difficult and dangerous for the law enforcement personnel, the drivers, as well as civilians that may be present in the surrounding area where the interception is taking place. To this end, conventional law enforcement equipment that protects law enforcement personnel from injuries, such as bulletproof vests or other kind of body armors, or that slows down the progression of vehicles to be intercepted, such as road barriers or speed bumps, are employed. Although such conventional law enforcement equipment is employed, they present important drawbacks. Notably, this conventional law enforcement equipment provides limited efficiency as they require the law enforcement personnel to be in contact or in close distance with the drivers and or the vehicles to be intercepted or can be impracticable in highly dense traffic conditions. Thus, design a remote presence device for law enforcement and road safety that solves the aforementioned limitations of safety and efficiency is desired. Such a remote presence device has been designed and built as part of this project.

UG ENGR 69

Design of Power Efficient Stirling Engine

Efficiency optimization of the Stirling Engine presents the opportunity for expanding the use of renewable energy resource. Improvements upon this technology are made through modern approaches to material selection and mechanical design. This study is to investigate analytically how this can be done inexpensively and effectively. The Stirling Engine is currently a small-scale solution to the global problem of disengaging our reliance on carbon-based fossil fuels. The engine cycle has been shown to reach upwards of forty percent of Carnot efficiency, if not greater in personal projects. There have been many improvements upon the original engine patent presented by Robert Stirling; including breakthroughs made by Ivo Kolin and Jame Senft, with designs of a hand-held version of the engine known as the â€œringbomâ€ configuration. The ringbom configuration offers up the opportunity to change design elements such that the operation nature of the engine (expansion of gas in a volume upon heat exertion) can be optimized in the smallest versions taking vantage of lower temperature differentials. The analytical method in this study utilizes programs/simulations compiled by renown Stirling enthusiasts whom based such programs off different mathematical models estimating power output and efficiency. Results are compared and collectively show that heat capacity of the working gas and regenerator mesh/material distinctively impact engine performance across models. The volume of the gas is a minimal factor in performance, if properly sealed along displacer with proper room to sweep between the two temperature reservoirs. Influence of conductive materials regarding this fact is being studied. Research is also being done to find out scaling factors and issues that may arise in increasing the surface area of the heat flux entering the system and potential losses.

UG ENGR 70

Survey of Skin Design for Morphing Wing Aircraft: Status and Challenges

The main objective of this paper is to lay out current passive skin design efforts for morphing applications, their status, challenges, and a proposed approach to design a skin for a morphing wing. Passive lattice, corrugated, and elastomeric structures are considered for potential use. An approach to bridging the gap between the skin structure properties and application to a morphing wing is proposed. As a case study, stress and strain generation in a morphed wing under structural and aerodynamic loadings is studied using ANSYS Static Structural and ANSYS FLUENT. Structural loading that causes the morphing of the wing and skin is found to produce large stresses and strains, which must be considered during the skin design. The highest Von-Mises stress of 147MPa occurred at the leading edge of the free end of the wing skin as it morphed from a NACA 2410 to NACA 8410 profile when simulating a 5-mm thick polyethylene skin. Aerodynamic loading, on the other hand, seems to have a limited effect within the scope of this study.

UG AGSCI 71

Synergism of Natural Antimicrobials and High Pressure Pasteurization for Inactivation of Listeria monocytogenes in a Processed Dairy Product

Listeria monocytogenes is one of the leading causes of foodborne diseases and unlike vast majority of foodborne pathogens is halophilic in nature and could tolerate cold temperatures. A recent multistate outbreak associated with contaminated ice-cream with Listeria monocytogenes had drawn the attention of researchers and the popular press to safety of ice-cream products. Various time (0 to 9 minutes) of elevated hydrostatic pressure (380 MPa e.g. 55K PSI) were investigated for inactivation of 4-strain mixture of Listeria monocytogenes (ATCCÂ® numbers 13932, 51779, 51772, BAA-2658) inoculated at target level of 7.5 log CFU/ml of ice-cream base. Temperature was monitored and maintained at 4 ÂºC by a circulating water bath and a stainless steel water jacket surrounding the chamber. Control samples, and those containing 1% lactic acid, caprylic acid, and citric acid were studied. In a companion experiment, survival of the 4-strain mixture Listeria monocytogenes and background microflora in ice-cream base was investigated during aerobic storage at -20 ÂºC for control samples and those with 1% added citric acid. The experiments were conducted in two biologically independent repetitions, as blocking factors of a randomized complete block design, containing three repetitions per time/treatment within each block. Study was statistically analyzed at type one error level of 5% by LSD-based ANOVA using OpenEpi software. During the survival experiment, background microflora were 6.77 Â± 0.4 and 7.66 Â± 0.3 log CFU/mL on days 0 and 14, respectively. Similarly, Listeria monocytogenes counts were 5.72 Â± 0.2 and 5.86 Â± 0.4 log CFU/mL on days 0 and 14, respectively, after aerobic storage at -20ÂºC. A treatment at 380 MPa (55K PSI) for 9 minutes reduced (P <0.05) the pathogen counts for 1.66, 3.24, 1.51, 5.05 log CFU/ml of control samples and those with 1% lactic acid, caprylic acid, and citric acid, respectively.

UG AGSCI 72

Sensitivity of Foodborne Isolates of Salmonella serovars, Cronobacter sakazakii, and Listeria monocytogenes to Mild Hydrostatic Pressure and Heat in Phosphate Buffered Saline Medium

Application of high pressure processing in food manufacturing had been gaining increasing momentum in recent years due to advances in engineering of commercially available units. In the United States the market size of pressure-treated products are estimated to surpass $9B annually. Hydrostatic pressure of 103 to 380 MPa (15k PSI to 55K PSI) were applied at various time intervals (0 to 10 minutes) for inactivation of five strains of Salmonella serovars (at 35 and 55ÂºC), four strains of Listeria monocytogenes (at 25ÂºC), and four strains of Cronobacter sakazakii (at 25 and 55ÂºC), inoculated at target population of 7.0 log CFU/mL in phosphate buffered saline medium. The pressure processing unit was equipped with water jacket and circulating water bath surrounding the reaction chamber for precise application of hydrostatic pressure at controlled temperature. Experiments were conducted in Barocycler Reaction PULSE Tubes, with internal pressure, temperature, and compression rate monitored every 3 seconds using Barocycler HUB PBI Software. Results were analyzed using LSD-based ANOVA by OpenEpi software. Salmonella serovars were reduced (P < 0.05) below detection limit after 3, 6, and 9 minutes of treatment at 35 ÂºC and after 1, 3, 6, and 9 minutes of treatment at 55 ÂºC. At ambient temperature, Listeria monocytogenes was not reduced (P â‰¥ 0.05) after a 1-minute treatment at 380 MPa, and were reduced (P < 0.05) by >4 log CFU/mL after a 10 minute treatment at 380 MPa. Cronobacter sakazakii was reduced (P < 0.05) by 3.1 and 5.6 log CFU/mL after a 9-minute treatment at 380 MPa, at 25 and 55 ÂºC, respectively. Application of hydrostatic pressure up to 380 MPa, reduced Salmonella serovars, Listeria monocytogenes, and Cronobacter sakazakii by more than 4 log CFU/mL in phosphate buffered saline medium when applied for more than 3 minutes.

UG AGSCI 73

Multiple Displacement Amplification of Individually Isolated Sweet Sorghum Microsporeâ€™s Genomes

Multiple displacement amplification (MDA) is more efficient whole genome amplification (WGA) technology than the polymerase chain reaction (PCR) method. PCR procedure is used in WGA through primer extension pre-amplification (PEP) through melting, primer annealing, and extension temperatures during each amplification cycle. MDA utilizes random hexamer primers (small length) which can anneal to the template at 30Â°C while same constant temperature is needed for DNA strand synthesis by Phi 29 polymerase. This enzyme does not disassociate from the template DNA during synthesis, thus eliminates the potential for sequence bias and circumvents the need to melt the template at the growing fork. It can thus be hypothesized that DNA from individually isolated microspores of Sorghum bicolor L. amplified using MDA would have greater WGA success than that from the PCR-based PEP method. Two varieties of Sorghum bicolor L. (â€˜Daleâ€™ and â€˜Topper 76-6â€™) were grown in a greenhouse and closely monitored for physical indications around developing panicle (booting stage) for capturing microspores immediately after tetrad stage when the free microspores are without any exine (cell wall) and can be lysed. To isolate microspores, the individual sessile spikelets measuring 3.3-3.7 mm in length were dissected from spikes under a microscope to retrieve anthers. The anthers were crushed in sorbitol solution to release free microspores and cell-wall absence was confirmed under a high-power microscope. The microspores were then individually isolated into PCR tubes using a CellTram (Eppendorf North America, Hauppauge, NY) micro-injector mounted on an ultrafine move Marzhauser (HS-6) micromanipulator (ALA Scientific Instrument, Westbury, NY). Whole genome DNA amplifications were carried out using REPLI-g Single Cell Kit (QIAGEN, Germantown, MD) and comparatively quantified by NanoDropâ„¢ One (Fisher Scientific, Hampton, NH) UV-Vis Spectrophotometer. Funded by National Academies Sci., facilities Col Ag

UG AGSCI 74

Synergism of Natural Antimicrobials and High Pressure Pasteurization for Inactivation of Listeria monocytogenes in a Processed Dairy Product

Listeria monocytogenes is one of the leading causes of foodborne diseases and unlike vast majority of foodborne pathogens is halophilic in nature and could tolerate cold temperatures. A recent multistate outbreak associated with contaminated ice-cream with Listeria monocytogenes had drawn the attention of researchers and the popular press to safety of ice-cream products. Various time (0 to 9 minutes) of elevated hydrostatic pressure (380 MPa e.g. 55K PSI) were investigated for inactivation of 4-strain mixture of Listeria monocytogenes (ATCCÂ® numbers 13932, 51779, 51772, BAA-2658) inoculated at target level of 7.5 log CFU/ml of ice-cream base. Temperature was monitored and maintained at 4 ÂºC by a circulating water bath and a stainless steel water jacket surrounding the chamber. Control samples, and those containing 1% lactic acid, caprylic acid, and citric acid were studied. In a companion experiment, survival of the 4-strain mixture Listeria monocytogenes and background microflora in ice-cream base was investigated during aerobic storage at -20 ÂºC for control samples and those with 1% added citric acid. The experiments were conducted in two biologically independent repetitions, as blocking factors of a randomized complete block design, containing three repetitions per time/treatment within each block. Study was statistically analyzed at type one error level of 5% by LSD-based ANOVA using OpenEpi software. During the survival experiment, background microflora were 6.77 Â± 0.4 and 7.66 Â± 0.3 log CFU/mL on days 0 and 14, respectively. Similarly, Listeria monocytogenes counts were 5.72 Â± 0.2 and 5.86 Â± 0.4 log CFU/mL on days 0 and 14, respectively, after aerobic storage at -20ÂºC. A treatment at 380 MPa (55K PSI) for 9 minutes reduced (P <0.05) the pathogen counts for 1.66, 3.24, 1.51, 5.05 log CFU/ml of control samples and those with 1% lactic acid, caprylic acid, and citric acid, respectively.

UG AGSCI 75

Leaf Spot disease of Redbud (Cercis Canadensis)

Redbud (Cercis canadensis) is an ornamental tree native to North Americas. Red bud is a staple small tree in urban environments, beautifying landscapes with its bright, magenta pink flowers produced in large quantities in spring to early summer before the leaves, sometimes on the bare stems. Redbud trees are resilient and fairly disease free in Tennessee area, consequently, it is widely grown and commonly seen in diverse landscapes and as forest undergrowth tree. In 2017, a leafspot disease was observed in field grown plants in some nurseries in Mid-Tennessee; this disease has caused a lot of grower concerns over the marketability of infected trees and the fate of the redbud tree as an easy-to-grow small tree.Disease symptoms consisted of circular reddish-brown necrotic lesions resulting in unsightly summer foliage and reduced aesthetic value of the affected trees. Identification of the pathogen is needed as a pre-requisite to making recommendations for appropriate disease management strategies. The objective of this study was to isolate and identify the pathogen that caused the leafspot disease in red bud trees. One fungus was isolated from infected leaves and pathogenicity tests reproduced the re-brown lesions and confirmed cause and effect of the disease. Pathogen was identified using morphological features and DNA sequence analysis. Although effective fungicides can be recommended to growers, for the control of this disease, fungicides are potentially harmful to environment and applicators and they kill non-target organisms indiscriminately thereby eroding beneficial microorganism that buffer plants against pathogens. Evaluation of previously selected biological agents will be used to identify biological control agents (BCAs) for a more sustainable solution to disease management. Bacteria previously selected as effective BCAs will be evaluated in-vitro using dual culture assay and results will be confirmed in-vivo using redbud seedlings in greenhouse conditions

UG AGSCI 76

Molecular Attenuation of the Porcine Reproductive Respiratory Syndrome Virus toward Vaccine Design

Molecular Attenuation of the Porcine Reproductive Respiratory Syndrome Virus toward Vaccine Design

Amaris Daniels, Lauren Shields, Yongming Sang

Department of Agricultural and Environmental Sciences, College of Agriculture, Tennessee State University, Nashville TN 37209, USA

Abstract

Porcine Reproductive Respiratory Syndrome (PRRS), which was recognized in North America and European almost simultaneously in early 1990s, is still a significant disease devastating the swine industry to cause dramatic economic loss globally. Nearly 40-50% swine farms in the United States are PRRS positive. There is lack of effective vaccine to provide broad protection across heterologous PRRS viral strains (PRRSV). This project is designed to optimize vaccine protection by molecular manipulation of the viral genome. We hypothesize that molecular manipulation through a reverse genetic approach will speed up our need to attenuate the viral pathogenicity for generation of ideal vaccine backbones. Using a PRRSV infectious cDNA clone, we have engineered a PRRSV strain to express exogenous genes including fluorescent proteins and some antiviral cytokines (interferons) to essentially debilitating the engineered virus. A current research is to attenuate the PRRSV strain using a molecular handling to enrich the CG (cytosine and guanine)-dinucleotide content in the viral genome, which will elicit a zinc-finger antiviral proteinâ€™s (ZAP) response to suppress the viral replication and pathogenicity in anima cells. We expect that some attenuated laboratory strains will be produced to fulfill the need for vaccine production.

Supported by grants from USDA (NIFA AFRI 2013-67015-21236 and NIFA AFRI 2015-67015-23216)

UG AGSCI 77

Evaluation of the characteristics of Vimentin in French Pearl Guinea Fowl and the Effects on Gene Expression

Evaluation of the characteristics of Vimentin in French Pearl Guinea Fowl and the Effects on Gene Expression Justin McKinnie, Samuel Nahashon, and Thyneice Taylor, Tennessee State University , College of Agriculture, Human and Natural Science , Animal Biotechnolgy Lab, 3500 John A. Merritt Blvd. Nashville, Tn 37209

Vimentin is a protein that is encoded by the VIM gene in humans. Vimentin is a type III intermediate filament (IF) protein that is expressed in non- epithelial cells and mesenchymal cells and is attached to the nucleus, endoplasmic reticulum, or mitochondria and the protein encoded by this gene is responsible for maintaining cell shape, integrity of the cytoplasm, and stabilizing cytoskeletal interactions. It is involved in the immune response, and controls the transport of low-density lipoprotein (LDL)-derived cholesterol from a lysosome to the site of esterification. The objective of this research is to characterize and sequence the vimentin gene in guinea fowl. In this study we used Blast to align and compare expressed vimentin sequences in various avian species to find similarities that influence the function of Vimentin. Recently the guinea fowl genome has been sequenced, making primer design to further specific for vimentin. In this study we will be designing vimentin primers using NCBI which are specific to align with French Pearl Guinea Fowl. Extracted muscle tissue from guinea fowl was used to perform DNA extraction. The purified DNA was as the template to carry out polymerase chain reaction (PCR) with the primers that were designed specifically for vimentin. PCR samples are run on a 1.2% agarose electrophoresis gel and the presence of bands represents that ability of the primers to amplify the vimentin gene in guinea fowl. Then the purified PCR product will be used to sequence the vimentin gene in guinea fowl. These finding may lead to understanding the role vimentin may play in adipogensis.

UG AGSCI 78

Molecular Attenuation of the Porcine Reproductive Respiratory Syndrome Virus toward Vaccine Design

Amaris Daniels, Lauren Shields, Yongming Sang

Department of Agricultural and Environmental Sciences, College of Agriculture, Tennessee State University, Nashville TN 37209, USA

Abstract

In the early 1900â€™s, Porcine Reproductive Respiratory Syndrome (PRRS) was simultaneously recognized in North America and Europe. PRRS is a significant disease devastating the swine industry worldwide and cause about $800 million loss in the USA only. Nearly 40-50% of swine farms in the United States test positive for this virus. There is a lack of effective vaccines able to provide broad protection across heterologous PRRS viral strains (PRRSV). This project is designed to optimize vaccine protection by molecular manipulation of the viral genome. We hypothesize that molecular manipulation, through a reverse genetic approach, will facilitate our ability to attenuate the viral pathogenicity for generation of ideal vaccine backbones. Using a PRRSV infectious cDNA clone, we have engineered a PRRSV strain to express exogenous genes, which include fluorescent proteins and some antiviral cytokines (interferons) to essentially debilitate the engineered virus. Our current research is to attenuate the PRRSV strain using molecular handling to enrich the CG (cytosine and guanine)-dinucleotide content in the viral genome. This will elicit the zinc-finger antiviral proteinâ€™s (ZAP) response to suppress the viral replication and pathogenicity in animal cells. We expect that laboratory generated attenuated strains will be produced to fulfill the need for vaccine production.

Supported by grants from USDA (NIFA AFRI 2013-67015-21236 and NIFA AFRI 2015-67015-23216)

UG AGSCI 79

Biological Controls Agents against Botryosphaeria dothidea

Biological Controls Agents against Botryosphaeria dothidea

Steve Osborne1*, Margaret Mmbaga1, Asha Maheshwari1

1 Department of Agricultural and Environmental Sciences, Tennessee State University, Nashville TN 37209.

* Presenter, Undergraduate student, College of Agriculture, Oral presentation

Botryosphaeria dothidea is an economically important pathogen known to cause the formation of cankers on a wide variety of tree and shrub including dogwood (Cornus florida L). It has broad geographical distribution as a pathogen, but it has also been identified as an endophyte, existing in association with plant tissues on which disease symptoms were not observed. Previous studies reported that B. dothidea causes canker in dogwood branches leading to its die-back. Currently chemical fungicides are used for management of this disease. Concerns over harmful effects of chemical fungicides have led to extensive search for environmentally friendly alternative products including the use of microorganisms as biological control agents (BCAs). Pathogenicity of B. dothidea using detached leaf assay confirmed its pathogenicity on dogwood. The objective of this study was to evaluate microbial agents for biocontrol of B. dothidea previously isolated as an endophyte from stems of C. florida. Eight bacterial isolates previously reported to have potential as biological control agents of plant diseases were used in this study: B17A, B17B, IMC8, A2B1, PS, PSL, Prt and E. These bacterial BCAs were evaluated for biocontrol activity against B. dothidea using in vitro dual culture technique. All eight BCAs had the ability to inhibit the mycelium growth of B. dothidea. Percentage of inhibition growth ranged from 38.18 to 59.88 percent with Bacillus spp. expressing maximum inhibition of B. dothidea mycelium growth. In-vivo studies using C. florida seedlings in growth chamber and greenhouse conditions will be used to confirm bioactivity of these biocontrol agents against B. dothidea.

UG AGSCI 80

Survival and Inactivation of Wild-Type and Rifampicin-Resistant Cronobacter sakazakii and Background Microflora of Infant Formula using Repeated Cycles of Hydrostatic Pressure

Previously known as Enterobacter sakazakii from 1980-2008, Cronobacter sakazakii could survive and proliferate in dry, low moisture environments such as infant formula. Infections caused by the bacterium are often fatal in infants born premature and those younger than two months. Sporadic cases have been investigated in Florida, Oklahoma, Missouri, Illinois, Tennessee, and more recently Pennsylvania in 2016. There have been occurrence of two outbreaks associated with Cronobacter sakazakii in infant formula in Memphis, TN (1988) and Knoxville, TN (2001). Up to 9 cycles of elevated hydrostatic pressure (350 MPa, 30 seconds) were investigated for inactivation of 4-strain mixture of wild-type and rifampicin-resistant Cronobacter sakazakii, at 4 and 55 ÂºC, respectively. In a companion experiment, survival of the 4-strain mixture Cronobacter sakazakii in infant formula was investigated during aerobic storage at 10 and 25 ÂºC. The experiments were conducted in two biologically independent repetitions, as blocking factors of a randomized complete block design, containing three repetitions per cycle/phenotype within each block. Study was analyzed by LSD-based ANOVA using OpenEpi software. Counts of Cronobacter sakazakii were reduced (P <0.05) from 5.50Â±0.5 to 4.74Â±0.2 log CFU/g (approximately <90% reduction) during a 14-day aerobic storage at 25ÂºC. Counts of background microflora were similarly reduced (P <0.05) from 7.19Â±0.4 to 5.03Â±0.2 log CFU/g (approximately >99% reduction), during a 14-day aerobic storage at 25ÂºC. At 55ÂºC, >2.04 and up to 6.56 log reductions (P<0.05) of wild-type Cronobacter sakazakii were observed as result of application of elevated hydrostatic pressure at 350 MPa (51K PSI). At 4ÂºC, >1.06 and >5.23 reductions (P <0.05) of wild-type Cronobacter sakazakii were observed as result of application of elevated hydrostatic pressure at 350 MPa (51K PSI).

UG PHYSCI 81

Synthesis of melanin-like pigments from phenols using peroxide

Melanin-like pigments are synthesized from phenolic or other compounds using a combination of Fe(II) and hydrogen peroxide. By varying the reaction conditions, pigments with different physical-chemical properties can be generated. Experiments are conducted to evaluate the reproducibility of the experimental results. In addition, experiments are conducted to scale up select reactions in order to be able to purify and characterize the materials generated.

UG PHYSCI 82

Synthesis of melanins from catecholamines under varying reaction conditions

Melanin-like pigments are synthesized from catehcolamines or other compounds using a combination of Fe(II) and hydrogen peroxide. By varying the reaction conditions, pigments with different physical-chemical properties can be generated. Experiments are conducted to evaluate the reproducibility of the experimental results. In addition, experiments are conducted to scale up select reactions in order to be able to purify and characterize the materials generated.

UG PHYSCI 83

Flame Retardant, Hexabromocyclododecane, Alters Secretion of Interleukin 6 from Human Immune Cells

Hexabromocyclododecane (HBCD) is a brominated flame retardant compound. It is used in polystyrene insulation, accumulates in living organisms and is highly toxic to aquatic organisms. Interleukin 6 (IL-6) is a pro-inflammatory protein that is produced by T lymphocytes and monocytes (as well as other cells). It regulates cell growth, tissue repair, and immune functions. Previous studies have shown that HBCD alters the secretion of cytokines IL-1Î², TNFÎ±, and INFÎ³ from human immune cells. Due to the important role IL-6 plays in immune responsiveness, it is important to understand whether exposures to HBCD are able to disrupt its secretion. HBCD is found in human blood and previous studies have shown that it inhibits the ability of human NK lymphocytes to destroy tumor cells. This study examines whether HBCD affects the secretion of IL-6 from monocyte-depleted (MD) human peripheral blood mononuclear cells (PBMCs). IL-6 secretion was measured by enzyme linked immunosorbent assay (ELISA). Results indicate that exposures of MD-PBMCs to different concentrations of HBCD (ranging from 5-0.05 ÂµM) for 24 increase secretion of IL-6 from these immune cells. Thus, exposure to HBCD may potentially disrupt the immune regulation mediated by IL-6. Supported by NIH grant 2 T34GM007663.

UG PHYSCI 84

The Combined Effect of Canagliflozin and Metformin in Human Prostate Cancer Cells

There is still a need to identify effective treatments for castration-resistant prostate cancers. Recent studies have shown that two drugs used to treat type 2 diabetes, metformin and canagliflozin, may be effective treatments for castration-resistant prostate cancer. Both drugs have individually been shown to inhibit proliferation of 22Rv1 and PC3 prostate cancer cell lines. However, it is not known if combined treatment with metformin and canagliflozin suppresses the growth of prostate cancer cells better than each drug alone. The goal of this study was to determine the effectiveness of the combination of canagliflozin and metformin as an alternative treatment for prostate cancer. Presto Blue Assays were used to assess the effect of metformin and canagliflozin on proliferation prostate cancer cell lines. Western blot analysis was performed to determine effects of metformin and canagliflozin on androgen receptor (AR) protein levels. Canagliflozin produced a significant decrease in the proliferation of PC3 and 22Rv1 cells. While metformin showed no significant decrease in proliferation of PC3 cells, metformin did significantly decrease 22Rv1 cell proliferation. The combination of canagliflozin and metformin showed a significant decrease in both PC3 and 22Rv1 cells. However, the effect of the combination was no greater than canagliflozin alone. AR protein levels were reduced by canagliflozin, metformin, and the combination of both drugs. The combination of metformin and canagliflozin was most effective in reducing AR protein levels. The combination of canagliflozin and metformin was equally effective as canagliflozin alone at reducing prostate cancer cell proliferation. However, this drug combination was more effective at suppressing AR protein levels within castration-resistant prostate cancer cells. These data suggest that combination treatments involving metformin and canagliflozin could be used to decrease tumor growth and AR expression in prostate cancer.

UG PHYSCI 85

A Comparison of Leaf Chlorophyll Content Measurements by Different Chlorophyll Meters on Switchgrass under Different Precipitation Treatments

A Comparison of Leaf Chlorophyll Content Measurements by Different Chlorophyll Meters on Switchgrass under Different Precipitation Treatments

Denton Musick, Sunil Gurung, Kripa Dhakal, Katherine Miller, and Dafeng Hui

Leaf chlorophyll content is an important indicator of leaf N status, plant stresses, and photosynthetic capacity. Fast and non-destructive measurements are needed for field experiments. In this study, we used three chlorophyll meters (SPAD-502, CCM 200 and At-Leaf) and measured switchgrass leaf chlorophyll contents under different precipitation treatments. Results showed that readings of SPAD-502 and At-Leaf were significantly correlated at both leaf and plot mean levels, but readings of CCM 200 were lower and had no correlations with SPAD-502 and At-Leaf. Precipitation treatment had no significant influences on leaf chlorophyll contents measured by all three meters. The SPAD-502 and At-Leaf appeared to produce better estimation of precipitation effects on leaf chlorophyll contents of switchgrass. Further studies will be conducted to investigate the measurements at different environmental conditions and plant growth stages.

UG PHYSCI 86

Responses of Switchgrass Ecosystem Productivity to Precipitation Changes

Responses of Switchgrass Ecosystem Productivity to Precipitation Changes

Katherine Miller, Qi Deng, Chih-Li Yu, Denton Musick, and Dafeng Hui

The quantification of ecosystem productivity response to climate change has been heavily investigate. However, it is still not clear how grassland ecosystem productivity respond to precipitation changes. A degree of controversy exists in the literature as to whether the relationship is linear or nonlinear and asymmetric or symmetric. We conducted two experiments to investigate ecosystem productivity and soil CO2 emission responses to precipitation changes in switchgrass, Panicum virgatum, over two growing reasons. One is a mescosom (big pot) study in a greenhouse and another one is field precipitation experiment. Both experiments used randomized complete block design with 5 precipitation treatment levels (-50%, -33%, ambient, +33%, and +50%). The results demonstrated consistent changes, though there was variation between the field and greenhouse experiments. Precipitation changes highly influenced the physiology, growth, and soil respiration of switchgrass. Responses of (ANPP) were indeed nonlinear and asymmetric. Yet, responses of soil respiration to precipitation were close to symmetric and linear. Future research should focus on further testing of the double asymmetry model with more precipitation levels and longer time frames.