Growth of Community-Acquired MRSA strain USA300 Multi-drug Transporter Mutants is inhibited by Extracts of Tyrol Knapweed, *Centaurea nigrescens*. Kyra P. Lasko, Kathryn D. Robinson, and Dr. Luke G. Huggins. Department of Biology and Environmental Science, West Virginia Wesleyan College, Buckhannon, WV.

The rates of infection by community-acquired multi-drug resistant *Staphylococcus aureus* (CA-MRSA) have risen dramatically over fifteen years in the United States. CA-MRSA is responsible for rapidly progressive diseases, including necrotizing pneumonia, severe sepsis, and necrotizing fasciitis. Consequently, novel antibacterial strategies are needed to combat the rising antibiotic resistance seen in CA-MRSA strains. The USA300 CA-MRSA strain has been mutagenized using the *Bursa aurealis* transposon to create the Nebraska Transposon Mutant Library (NTML). We have screened the 1920 non-essential, defined transposon insertions in the NTML for strains that are either susceptible or resistant to methanol extracts of *Centaurea nigrescens* (CnME) leaves and flowers. 30 strains containing mutations affecting transporter proteins were identified as having either significant resistance or susceptibility to *Centaurea* extract. Insertions in two different drug efflux transporter families have been identified. The EmrB/QacA drug resistance transporter subfamily is a multi-drug efflux pump responsible for the export of toxic molecules from bacteria and yeast. The ABC transporters are involved in drug import and export. These results confirm the effectiveness of the screen as a means for identifying drug-resistance genes affected by the *C. nigrescens* methanolic extract and suggest a role for drug efflux proteins in the resistance of *S. aureus* CA-MRSA to antibacterial plant metabolites. Current work is focused on determining the effect of CnME on the expression of selected drug-resistance transporters via qRT-PCR.