RORI SCHREIBER, EMILY YOUNG, JORDAN GIBSON, SIENA MCGOVERN, EMMA BEATTY, CLAIRE KELLY, KENDALL SOUDER, JUSTIN RICE, Department of Biomedical Sciences, West Liberty University, West Liberty, WV, RYAN J. PERCIFIELD, Department of Biology, West Virginia University, Morgantown, WV, DONALD A. PRIMERANO, Department of Biomedical Sciences, Joan C. Edwards School of Medicine, Marshall University, Huntington, WV, NICOLE GARRISON and DEANNA M. SCHMITT. Department of Biomedical Sciences, West Liberty University, West Liberty, WV. Role of KatG in *Francisella tularensis* Susceptibility to Resazurin.

The CDC classifies Francisella tularensis as a Category A bioterrorism agent. Due to the risk of potential release of antibiotic-resistant F. tularensis strains, new therapeutics against F. tularensis must be developed. Resazomycins are resazurin (Rz)-based compounds that exhibit antimicrobial activity against F. tularensis and other gram-negative bacteria. The mode of action of resazomycins is not understood, but potential targets of the antibiotic were identified in a high throughput screen for Rz-resistant isolates. The FTL 1504 gene was identified as being mutated in all of the Rz-resistant (Rzr) strains sequenced. FTL 1504 encodes for the catalase KatG which catalyzes the decomposition of hydrogen peroxide to water and oxygen. Moreover, KatG has also been shown to play an essential role in the activity of a different antibiotic, isonazid. Four different coding mutations were characterized in katG that included single base pair substitutions and a deletion with all resulting in the introduction of a premature stop codon. All Rzr mutants tested had reduced catalase activity compared to wild-type F. tularensis LVS with three of the four mutations resulting in loss of KatG expression. Based on this data, we hypothesize KatG plays a role in the susceptibility of *F. tularensis* to resazurin. To address this, we are generating a katG deletion mutant in F. tularensis LVS and measuring its Rz susceptibility via agar dilution assays. Investigation of the contribution of KatG may unveil a unique role for the oxidative stress response in the mode of action of this family of antibiotics.