

Title: Prevalence of zinc resistance encoded by the *czrC* gene in US swine-associated MRSA ST5 strains - **NPB 15-145**

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Scientific Abstract: Zinc resistance in livestock-associated methicillin resistant *Staphylococcus aureus* (LA-MRSA) sequence type (ST) 398 is primarily mediated by the *czrC* gene co-located with the *mecA* gene, encoding methicillin resistance, within the type V SCC*mec* element. Because *czrC* and *mecA* are located within the same mobile genetic element, it has been suggested that the use of in feed zinc as an antidiarrheal agent has the potential to contribute to the emergence and spread of MRSA in swine through increased selection pressure to maintain the SCC*mec* element in isolates obtained from pigs. In this study we report the prevalence of the *czrC* gene and phenotypic zinc resistance in US swine associated LA-MRSA ST5 isolates, MRSA ST5 isolates from humans with no swine contact, and US swine associated LA-MRSA ST398 isolates. We demonstrate that the prevalence of zinc resistance in US swine associated LA-MRSA ST5 isolates was significantly lower than the prevalence of zinc resistance in MRSA ST5 isolates from humans with no swine contact, swine associated LA-MRSA ST398 isolates, and previous reports describing zinc resistance in other LA-MRSA ST398 isolates. Collectively our data suggests selection pressure thought to be associated with application of zinc in feed is not playing a role in the prevalence and persistence of LA-MRSA ST5 in the US swine population. Additionally, our data indicate that zinc resistance is more associated with MLST lineage suggesting a potential link between genetic lineage and carriage of resistance markers.

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