

Identifying Resistance Mechanisms of *Nocardia* Strains to Trimethoprim-Sulfamethoxazole

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Antibiotic resistance has become a pressing international health issue. *Nocardia*, an emerging pathogen, are aerobic bacteria which can cause opportunistic infections and are often treated with the combination drug Trimethoprim-Sulfamethoxazole (TMP-SMX). TMP-SMX resistant *Nocardia* have been observed in clinical isolates. However, not much is known about how it becomes resistant to TMP-SMX. Our aim is to use experimental evolution to adapt nine strains of *N. nova* and *N. cyriacigeorgica* to TMP-SMX and use whole genome sequencing to identify mutations causing resistance. Following adaptation, we observed morphology and growth rates differences among strains which may be related to the mutations that confer resistance. Whole genomic sequencing data revealed mutation patterns and how they contributed to TMP-SMX resistance. We hope to uncover insight into how *Nocardia* evolve resistance to TMP-SMX which will help in the design of new treatment strategies for *Nocardia* that have developed resistance to this drug combination.