

Data for one component of an RND efflux system does not reflect the function of the tri-partite complex

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AcrAB-TolC is a well studied tri-partite RND efflux system of *Escherichia coli* and *Salmonella enterica* serovar Typhimurium which has an established role in antibiotic resistance and virulence. The literature describing this efflux system contains multiple examples of data concerning one of the components being extrapolated to make assumptions about the role or behaviour of all three components or the system as a whole. We present data from this, and other laboratories, showing that *acrA* and *acrB* can be expressed independently of each other and discuss the potential consequences of this for published research and for future investigations.

Furthermore, we propose that phenotypic data for mutants lacking single components of this efflux system should not be assumed to inform about function of the entire tri-partite system because it is clear from numerous studies that *AcrA*, *AcrB* and *TolC* have different contributions and roles in the complex as mutants lacking individual components have distinct phenotypic profiles. We present the case, using *AcrAB-TolC* of *S. Typhimurium* as a paradigm system, that future studies should consider the value of studying all three of the components of *AcrAB-TolC*, and other homologous systems, separately and as a complete complex. This will allow more information to be gathered about these systems as a whole, clinical relevance in antibiotic resistant isolates and about the contributions of the individual components. We advocate that study of one component as indicator of expression or an effect on the whole tripartite system should be discouraged.