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Characterisation of a Type Six Secretion System in *Neisseria cinerea*

Author(s)

Rachel M. Exley, n/a

Departmental Lecturer

Sir William Dunn School of Pathology, University of Oxford

Rafael Custodio, n/a

Post Doctoral Researcher

University of Exeter

Veronika Bakulova, n/a

PhD student

University of Oxford

Rene Baerentsen, n/a

Post Doctoral Researcher

University of Oxford

Cara Ellison, n/a

Post Doctoral Researcher

University of Oxford

Gerda Mickute, n/a

PhD student

University of Oxford

Rhian Ford, n/a

PhD student

University of Nottingham

Christoph M. Tang, PhD

Professor

Sir William Dunn School of Pathology, University of Oxford

Background

Colonising bacteria generally exist in complex microbiomes, and interactions within and between species can shape community composition and host interactions. Type six secretion systems (T6SS) are dynamic injection

systems that deliver effectors with degradative, lytic and other activities directly into neighbouring cells, resulting in their elimination. T6SS-mediated interactions can lead to genotypic and phenotypic changes in either the secreting or target populations. Thus, understanding the impact of T6SS in interactions among bacteria could provide insights into their biology and behaviour in communities.

Aim/Methods

We have shown that *Neisseria cinerea* expresses a T6SS. To better understand the impact of the T6SS in interactions between *Neisseria* species we are characterising the activity of effectors and identifying elements contributing to survival following T6SS-mediated attack. We have used sequence and structural homology analysis to predict effector structure/function. Inducible expression in *E. coli*, and in vitro analysis has been used to define the activities of *N. cinerea* T6SS effectors. *N. cinerea* mutants and a combination of agar plate based competition assays and microscopy have been used to dissect the contributions of effectors and other factors to survival of interacting bacteria.

Results

We previously identified six putative T6SS effector-immunity pairs (Nte/Nti1-6) in *N. cinerea* strain CCUG346T. Based on homology searches, conserved domain analysis and structure prediction, Nte1 is a putative phospholipase, Nte2 is a putative ribonuclease, and Nte3, 4, 5 and 6 are putative nucleases. Expression of effectors in *E. coli* results in significantly impaired growth and leads to changes in cell morphology and membrane and/or nucleoid integrity. We have identified key residues required for toxicity, consistent with predicted catalytic activities. In parallel we have shown a T6SS-dependent reduction of meningococci and gonococci grown in co-culture with *N. cinerea* and provide evidence that this is affected by expression of virulence factors such as capsule and pili.

Conclusions

We have demonstrated that T6SS can confer competitive fitness advantage in *Neisseria* co-culture. Understanding the activity and targets of effectors could reveal how interactions between close relatives shape *Neisseria* biology.