

Human & Bordetella Pertussis Co-expression Networks

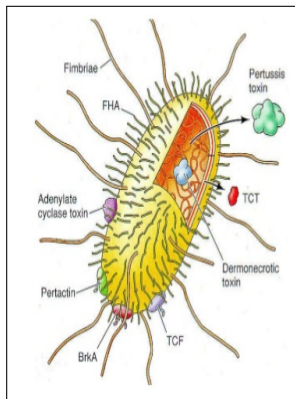
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TBI Winterseminar

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Bordetella Pertussis



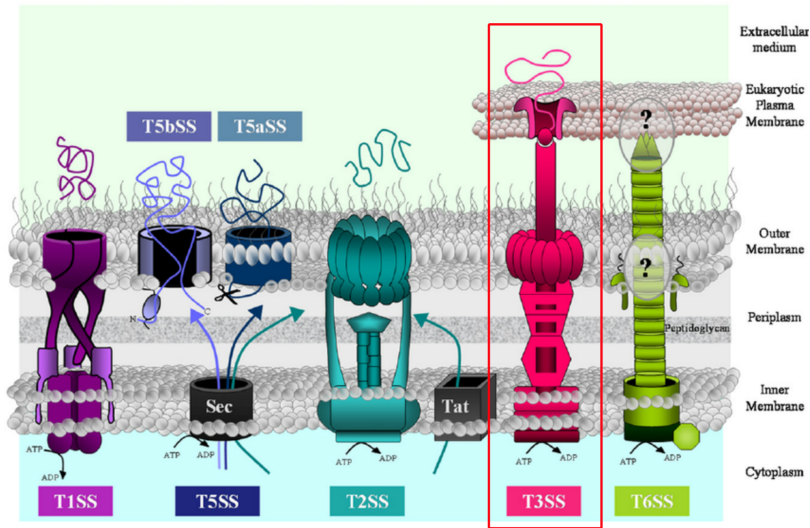
Source: Wikipedia

- Gram negative bacteria
- Highly contagious respiratory disease
- One of the ten most common causes of death from infectious diseases
- Least controlled vaccine preventable respiratory disease

Problem

Little is known about its pathogenesis

Pertussis Invasion into Host



Source: S Badr et al, 2016

Human Pertussis Interplay

Pertussis

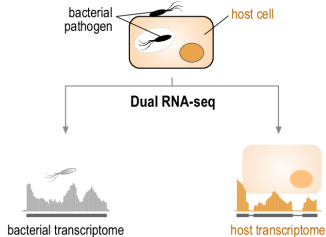
- Invasion
- Escapes killing
- Survival
- Hideout to spread infection
- Uses host machinery for infection

Human

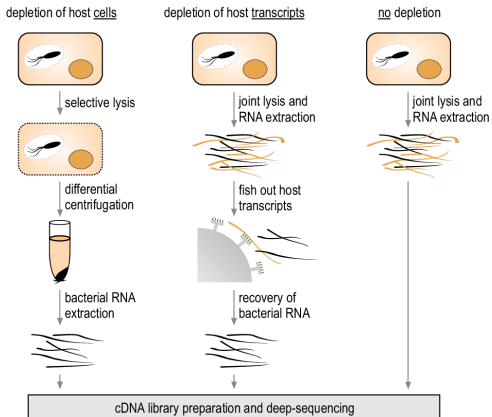
- Immune response
- Killing of bacteria
- Apoptosis

Dual RNAseq

a



b



Source: A Westermann et al, 2017

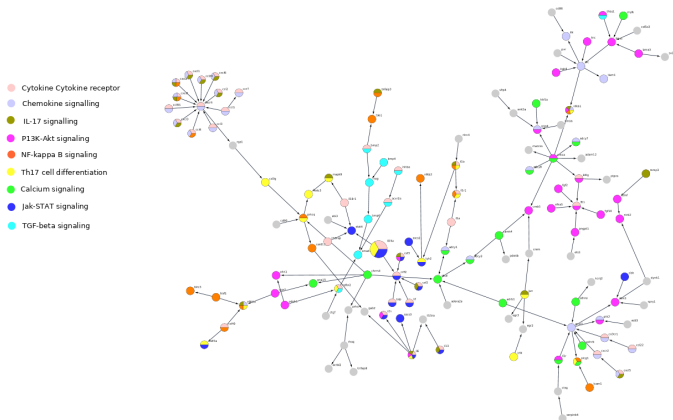
- Heuristic approach in Java
- Identifies concerted modulated directed sub-graphs in the global cell signaling network
- Identifies perturbation points of the modulated sub-graphs as sources
- Allows to read the flow of information from the perturbation source to the effectors.
- Provides impact score for sources

How does MSF work

- Input files
 - ① Good quality directed network
 - ② Differential gene expression analysis (DGEA) results
- Combines individual gene p -value (from DGEA) to generate sub-graph p -value
- Considers complete DEG list
- Most upstream genes are the sources (perturbation points)

Pertussis Infection Data

| | Control-6H | 2h-6H | 6H-24H |
|-----------------------|------------|-------|--------|
| IL23A | Yes | Yes | Yes |
| IL23A <i>p</i> -value | 4.55E-28 | 0.14 | 0.21 |
| IL23A impact Score | 2.2% | 1.4% | 28% |



Whats Next?

- Investigate other sources with high impact score
- Correlate the sources identified by **MSF** with Pertussis secretory proteins

- MSF paper (under review)

<https://f1000research.com/articles/7-1346/v1>

- MSF tool on github

<https://github.com/MariamFarman/Modulated-SubPath-Finder>

Try it !

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