A comparative genomics analysis of the T3SS2α pathogenicity island of *Vibrio parahaemolyticus*

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Vibrio parahaemolyticus

- **Vibrio parahaemolyticus (Vp)** is ubiquitous in the environment
- May acquire **virulence factors** that make them pathogenic
- Virulence factors have been found in **pathogenicity islands**
- Pathogenicity islands can be acquired or transferred in a process called **horizontal gene transfer**
Virulence factors of *Vibrio parahaemolyticus*

- **Virulence factors** are molecules expressed by an organism that enables them to propagate to the detriment of a host organism.
- In *Vibrio parahaemolyticus*, these can be:
  - capsules (physical protection)
  - flagella (movement)
  - iron uptake (competition for scarce nutrient)
  - quorum sensing (communication)
  - secretion systems (transfer of genetic material/toxins)
- **tdh** (thermostable direct hemolysin) is a toxin that destroys host cells.
- **Type 3 secretion system** (T3SS) is a secretion system that can transfer this toxin to the target cell.
- Some virulence factors (T3SS, tdh toxin) are found in pathogenicity islands.
**Pathogenicity Islands and Horizontal Gene Transfer**

- **Pathogenicity islands (PAI)** are discrete genetic units.
- Flanked by direct repeats, insertion sequences, or tRNA.
- Pathogenicity islands are unstable.
- Pathogenicity islands can be acquired or transferred in a process called horizontal gene transfer.

- **Horizontal gene transfer (HGT)** is the direct transfer of genes between organisms through processes such as injection of the relevant genes.
- Continuous HGT introduces variations in the PAI.
- One facilitator of horizontal gene transfer is the type 3 secretion system.
Type 3 secretion system

- **Type 3 secretion system (T3SS)** is a needle-like structure commonly found in pathogenic bacteria.
- Some bacteria that contains has T3SS mediated virulence are *Yersinia* (plague), *Salmonella* (typhoid fever), *E. coli* (food poisoning), *Chlamydia* (STD), and *Vibrio*.

- *Vibrio parahaemolyticus* has 3 known T3SS systems.
  - T3SS1
  - T3SS2α – encodes for tdh (*tdhA* & *tdhS*)
  - T3SS2β – encodes for trh
  T3SS2α and T3SS2β are variants of each other.
T3SS2α pathogenicity island (VpPAI) of *Vibrio parahaemolyticus* RIMD 2210633

From the outside:
1\textsuperscript{st} 2\textsuperscript{nd} = CDS on the plus and minus strands
3\textsuperscript{rd} = pathogenesis-related genes (red)
4\textsuperscript{th} = GC skew
5\textsuperscript{th} = percentage G+C/mean G+C

- from http://genome.bio.titech.ac.jp/
Methodology

A. BLAST

B. ALIGN

C. MAUVE
tdh+/T3SS2α+/trh-
tdh+/T3SS2α+/trh-
Vibrio parahaemolyticus RIMD 2210653 (unknown)
Vibrio parahaemolyticus VP2007-007 (unknown)
Vibrio parahaemolyticus NW605 (unknown)
Vibrio parahaemolyticus AQ4037 (unknown)
Vibrio parahaemolyticus VIP4-0447 (unknown)
tdh+/ T3SS2β +/trh+
T3SS2α

PERU-466
RIMD 2210633
VIP4-0439

EKP-021
EKP-026
605

VP2007-07
M0605
V-223/04
949
VP-NY4
V14/01

Northeastern Vibrio parahaemolyticus?

T3SS2β

0.250
• The approach is a viable method to understand incompletely assembled sequences
• Several lineages of the VpPAI can be discerned
• Several lineages may be available in a single locale
• The USA *Vibrio parahaemolyticus* are mostly a tdh+ T3SS2β