Salmonella Pathogenicity Island SPI is an Integrative and Conjugative Element with a Close Relative in Salmonella bongori

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1. SPI-7 background

- SPI-7 is a large pathogenicity island encoding virulence functions:
  - Vi antigen
  - SopE effector
  - Type IVB pilus
- SPI-7 is found in most strains of Salmonella Typhi and Salmonella Paratyphi C, as well as some strains of Salmonella Dublin, ranging in size from 82kb to 129kb

2. SPI-7 shares features with ICEs

- SPI-7 shares features with characterised integrative and conjugative elements (ICEs):
  - Genes are not essential for conjugation.
  - Many genes are conserved between SPI-7, ICESt1 and ICEHin1056.
  - This phenotypic analysis indicates which genes are involved in excision, circularisation and conjugation.

3. A related ICE in Salmonella bongori

- A relative of SPI-7 has been identified within a strain of Salmonella bongori, isolated from a dog with diarrhoea.
  - This element, ICESb1, shares 98% nucleotide identity with SPI-7 along the ICE backbone.
  - ICESb1 carries an alternative cargo, which includes:
    - putative autotransporter
    - putative antibiotic resistance determinants and drug efflux
    - putative immunoglobulin binding regulators lbrAB
    - Von Willebrand A homologue

4. Mobility of SPI-7 and ICEs

- SPI-7 from Salmonella Typhi is not able to transfer itself into new hosts, although it can promote the conjugation of other resident plasmids [Baker, 2008].
- Nested PCR shows that SPI-7 from S. Typhi strains is not able to excise from the chromosome and circularise, whereas SPI-7 from strains of S. Dublin and S. Paratyphi C is able to do this (data not shown).

5. ICE comparisons identify homologues and candidate knockouts

- Many genes are conserved between SPI-7, ICESt1 and ICEHin1056.
- Some genes have putative assigned functions:
  - The "left" region is involved in the integration/excision of the ICE
  - The "replication region" is involved in replicating the circular intermediate
  - The "transfer" region is involved in the formation of the novel "GI" (Genomic Island) Type 4 Secretion System (T4SS) [Juhás, 2007].

6. Knockouts imply function

- Excision is the first step in the process: if this is abolished, no further steps occur (as seen in Δ57, Δ76, (to a large degree), Δ117 (preliminary data) and Δ118).
- Circularisation is the next step and is non-functional in mutants Δ3, Δ4, Δ5 and Δ11.
- Conjugation requires many gene products, forming the GI T4SS and controlling DNA transfer. This is abolished in Δ9, Δ12, Δ40-42, Δ44-54, Δ58 and Δ61-69.
- Genes not involved in the process include Sb1_34, Sb1_35 and Sb1_43.
- Mutants Δ56 and Δ59 demonstrate a reduction in conjugation efficiency, but these genes are not essential for conjugation.

7. Why is SPI-7 immobile?

- SPI-7 from S. Typhi has been shown to promote conjugation, thus must contain all the genes essential for conjugation.
- This phenotypic analysis indicates which genes are involved in excision, circularisation and conjugation.

8. References

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