Insights into the evolution of *Yersinia pestis* through whole-genome comparison with *Yersinia pseudotuberculosis*


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History of *Y. pestis* and *Y. pseudotuberculosis*

- *Y. pestis* diverged from *Y. pseudotuberculosis*
  - possibly 1500 to 20,00 years ago
  - comparatively very little new genetic material
    - 32 chromosomal genes and 2 plasmids in *Y. pestis*

- Massive gene loss
  - about 13% of *Y. pseudotuberculosis* are pseudogenes in *Y. pestis*
  - caused by insertions and rearrangements
Yersinia pestis vs Yersinia pseudotuberculosis

- **Y. pestis**
  - responsible for bubonic and pneumonic plagues
  - 3 biovars (Antiqua, Medievalis, and Orientalis)
    - 3 different strains correspond to 3 pandemics

- **Y. pseudotuberculosis**
  - causes yersiniosis (Far East scarlet fever), enteric
  - soil and water borne, most commonly acquired through food
Infectious Process

- Virulence plasmid pCD1
  - “responsible for injecting into host cells a number of cytotoxins and effects that inhibit phagocytosis and processes of innate immunity”
- Besides plasmids, other causes are mostly unknown

Goal: Comparing whole genome to understand possible areas that could have coded for the emergence of *Y. pestis*
Methods

- PHRAP - used to assemble *Y. pseudotuberculosis* IP32953
- ARTEMIS Comparison tool (ACT): [http://www.webact.org/WebACT/prebuilt](http://www.webact.org/WebACT/prebuilt)  
  - used to view comparisons between the sequences

![ARTEMIS Comparison tool screenshot](image)
Results

IP32953 has 3 parts, a circular chromosome, the pYV virulence plasmid, and an atypical cryptic plasmid

KIM10+ and CO92 are two different biovars of *Y. pestis*
Fig. 2. Functional classification of genes missing or inactivated in *Y. pestis*. Distribution of *Y. pestis*-specific lost functions by gene region deletion (light blue) or by gene inactivation (i.e., pseudogene, dark purple) in COG functional groups: C, energy production; D, cell division and/or chromosome partitioning; E, amino acid metabolism; F, nucleotide metabolism; G, carbohydrate metabolism; H, coenzyme metabolism; I, lipid metabolism; J, translation; K, transcription; L, DNA replication and/or repair; M, cell envelope biogenesis; N, cell motility, secretion; O, posttranslational modification; P, inorganic ion metabolism; R, general function prediction only; S, function unknown; T, signal transduction; conserved, conserved hypothetical genes with no significant COG hits; and unique, hypothetical genes with no significant COG hit.
Future Work

Continued analysis of the genome to understand the virulence

Using this study as a basis for other diseases (i.e. spread of TB strains in Los Angeles)
Credits

Insights into the evolution of *Yersinia pestis* through whole-genome comparison with *Yersinia pseudotuberculosis* - Various Authors: [http://www.pnas.org/content/101/38/13826.full](http://www.pnas.org/content/101/38/13826.full)

WebACT - Imperial College London: [http://www.webact.org/WebACT/prebuilt](http://www.webact.org/WebACT/prebuilt)