

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

P. S. G. Chain - E. Carniel - F. W. Larimer - J. Lamerdin - P. O. Stoutland - W. M. Regala - A. M. Georgescu - L. M. Vergez - M. L. Land - V. L. Motin R. R. Brubaker - J. Fowler - J. Hinnebusch - M. Marceau - C. Medigue - M. Simonet - V. Chenal-Francisque - B. Souza - D. Dacheux - J. M. Elliott
A. Derbise - L. J. Hauser - E. Garcia

Mara Keledei

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>
 - used to view comparisons between the sequences

WebACT | [Select Sequences](#) | [Select Region](#) | [Select Locus](#) | Results

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Results

Overview of Selection (Mouse over for sequence details)

BX936398

AL590842

Yersinia pseudotuberculosis (serovar I, strain IP32953)
chromosome

View Comparison -

Selection contains full sequence of BX936398, from base 1
to 4744671

Open overview in separate window. 

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*

Table 1. General features of *Y. pseudotuberculosis* IP32953 and chromosomal comparison with *Y. pestis* KIM10+ and CO92

Property	<i>Y. pseudotuberculosis</i> IP32953			<i>Y. pestis</i> KIM10+	<i>Y. pestis</i> CO92
	pYV32953	pYptb32953	Chromosome	Chromosome	Chromosome
Size, bp	68,526	27,702	4,744,671	4,600,755	4,653,728
G+C, %	44.60	44.59	47.61	47.64	47.64
CDS, total*	99	43	3,974	4,090	4,016
CDS, %	80.7	86.5	83.6	83.4	83.9
RNA operons	0	0	7	7	6
tRNAs	0	0	85	73	70
Total IS	0	0	20	117	138
IS100			5	35	44
IS1541			5	55	65
IS1661			3	8	8
IS285			7	19	21
Pseudogenes†					
Total	4	1	62	54 (+202)	149 (+149)
Role unknown	0	0	10	8 (+60)	34 (+58)
Unique regions‡					
Total	0	0	35	21	21 (+1)
Phage regions	0	0	5	3	3 (+1)
Unique CDS‡					
Total	0	0	304	112	112 (+12)
Phage-related			183	59	59 (+12)
Assigned role			56	11	11
Role unknown			65	42	42
Pseudogenes			6	5	5

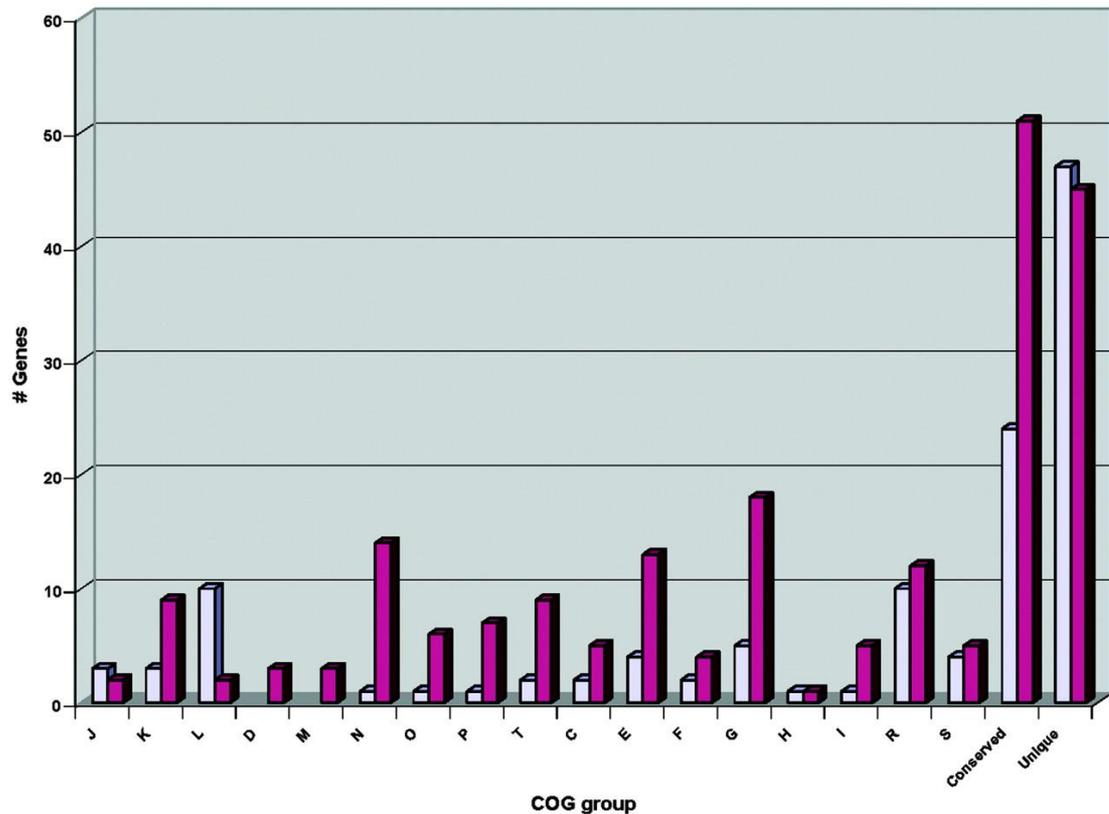


Fig. 2.

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>

WebACT - Imperial College London: <http://www.webact.org/WebACT/prebuilt>