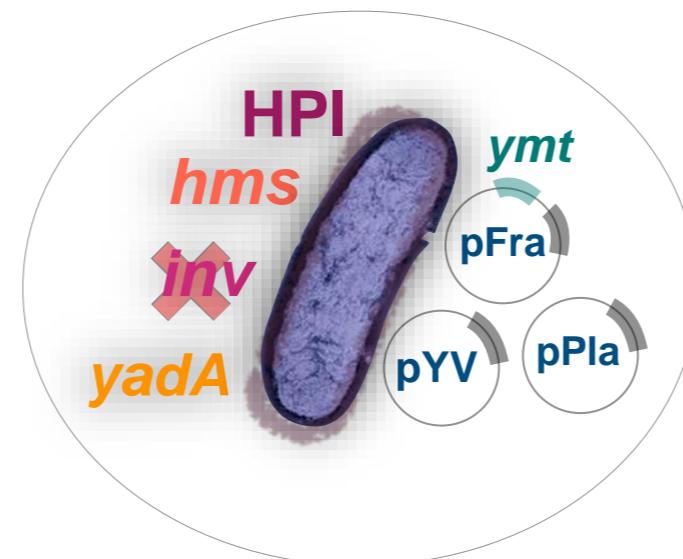




Pathogen X

August 29th-30th, 2022

Bacterial evolution & Plague



javier.pizarro-cerda@pasteur.fr



World Health Organization

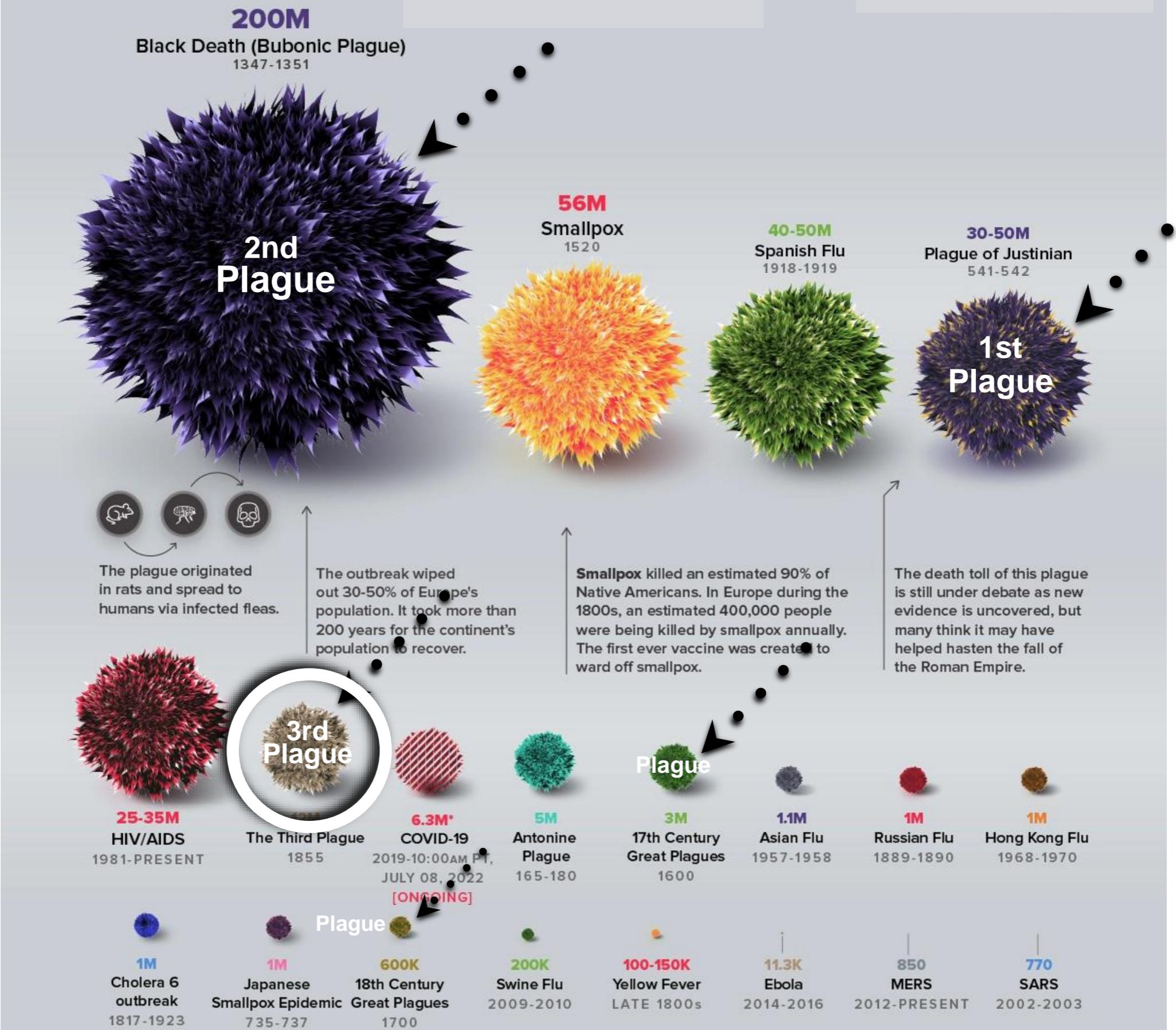
Collaborating Centre for Plague (FRA-140)



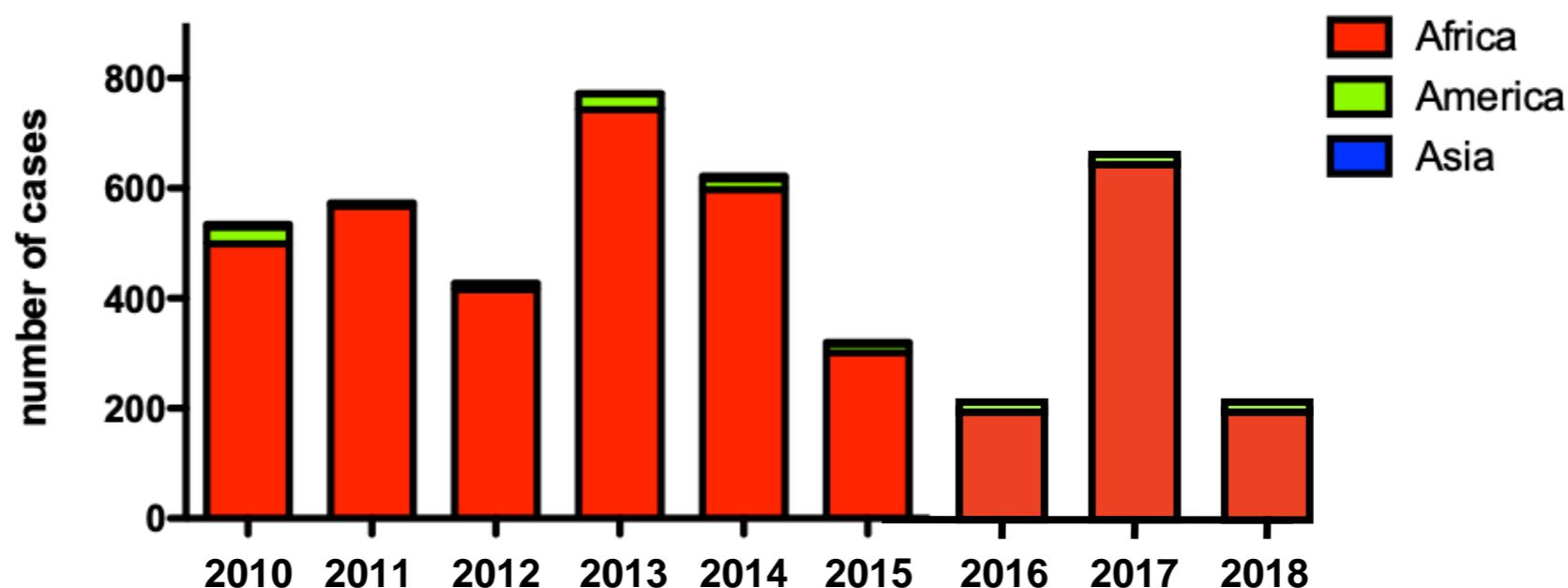
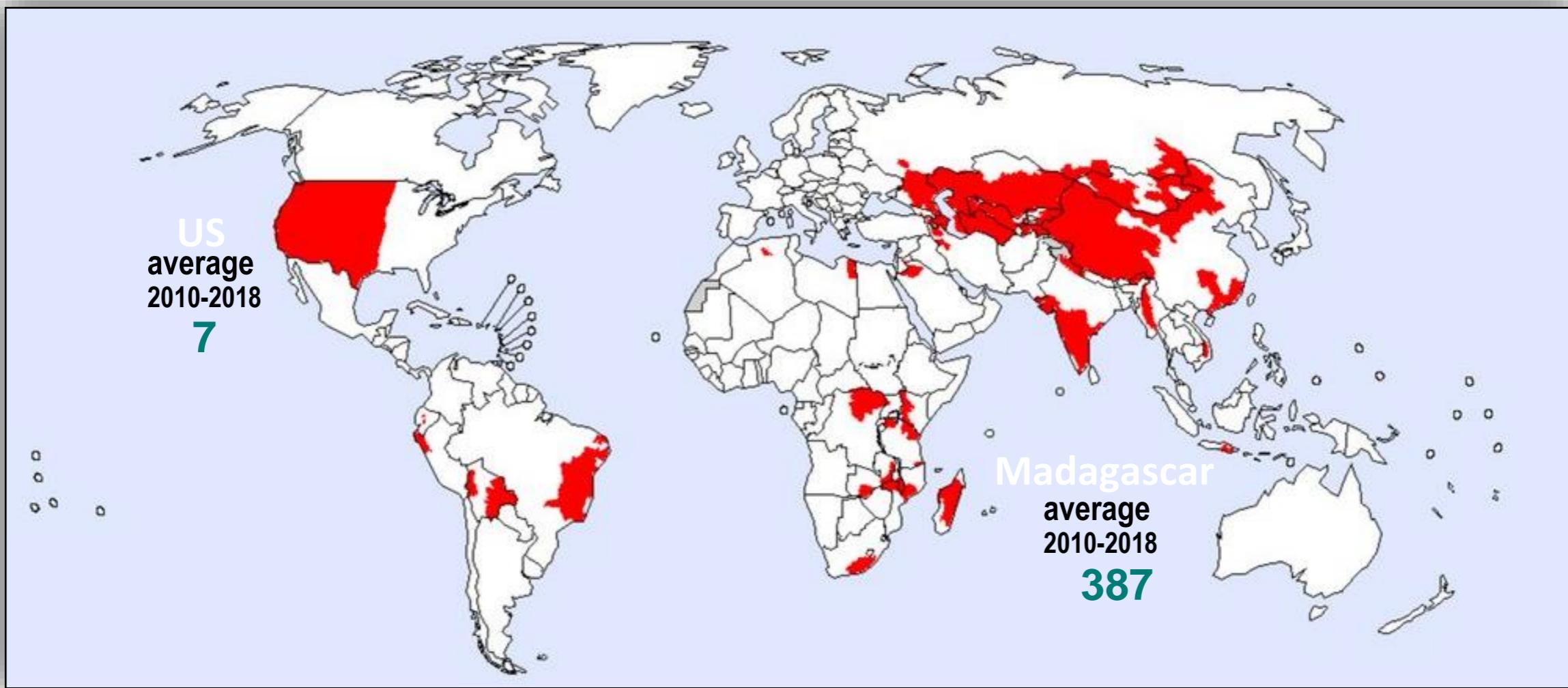
NATIONAL REFERENCE LABORATORY
Plague & Other Yersinioses

INSTITUT
PASTEUR
Yersinia Research Unit

Death toll of historical pandemics

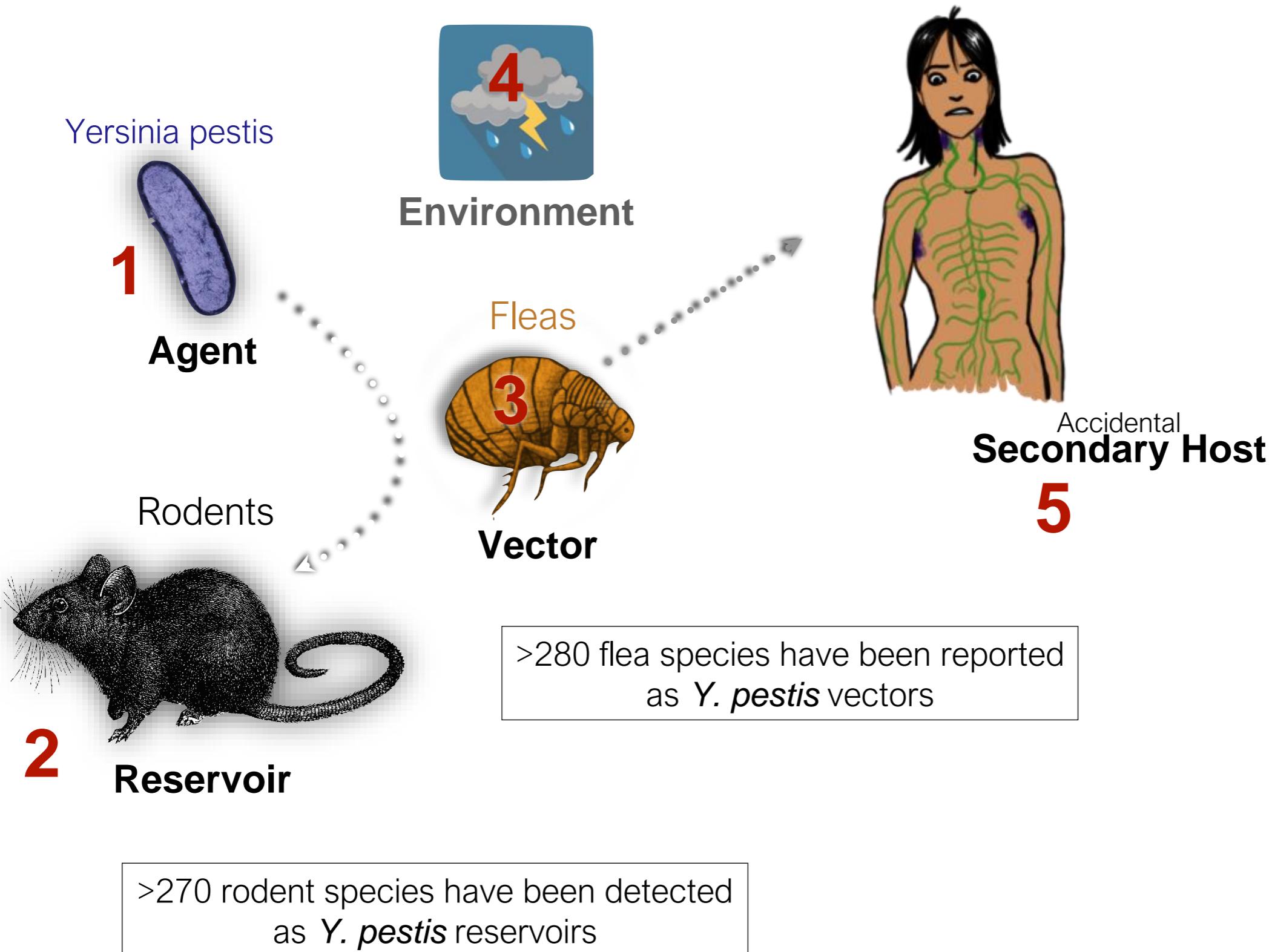


World Plague Distribution (2016)



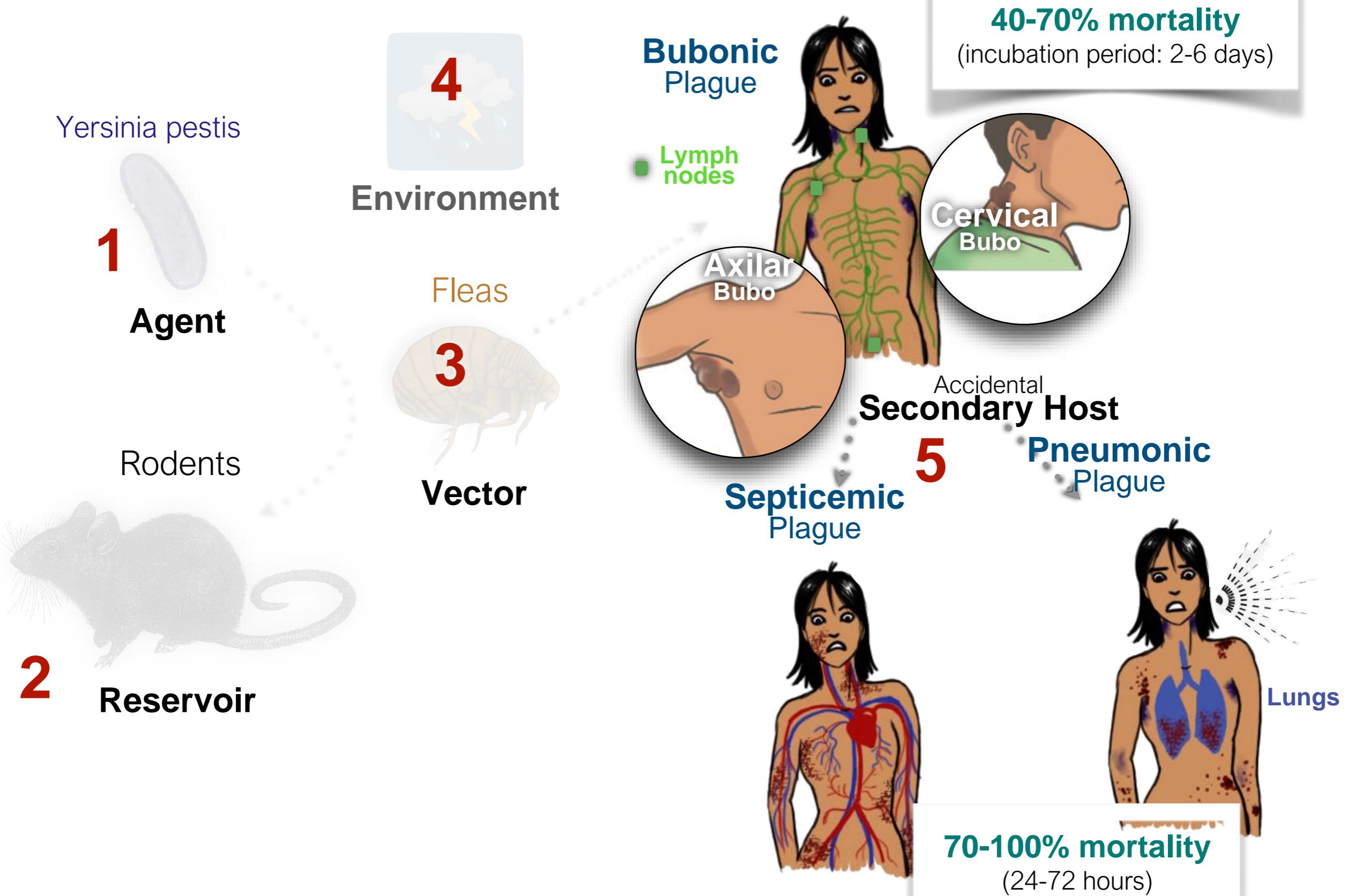
Plague:

5 players in a complex ecosystem



Human plague:

Three major forms: bubonic, pulmonary & septicemic



The recent ancestor of *Yersinia pestis*

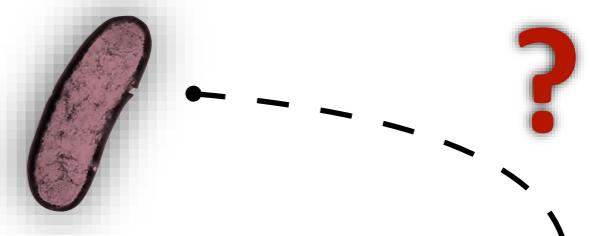
is the enteropathogen *Y. pseudotuberculosis*



Lethal Dose 50 (I.V.)



100 000 bacteria



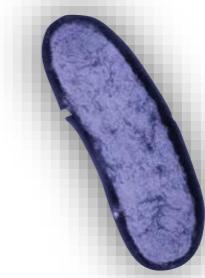
Flea



Lethal Dose 50 (I.V.)



<10 bacteria



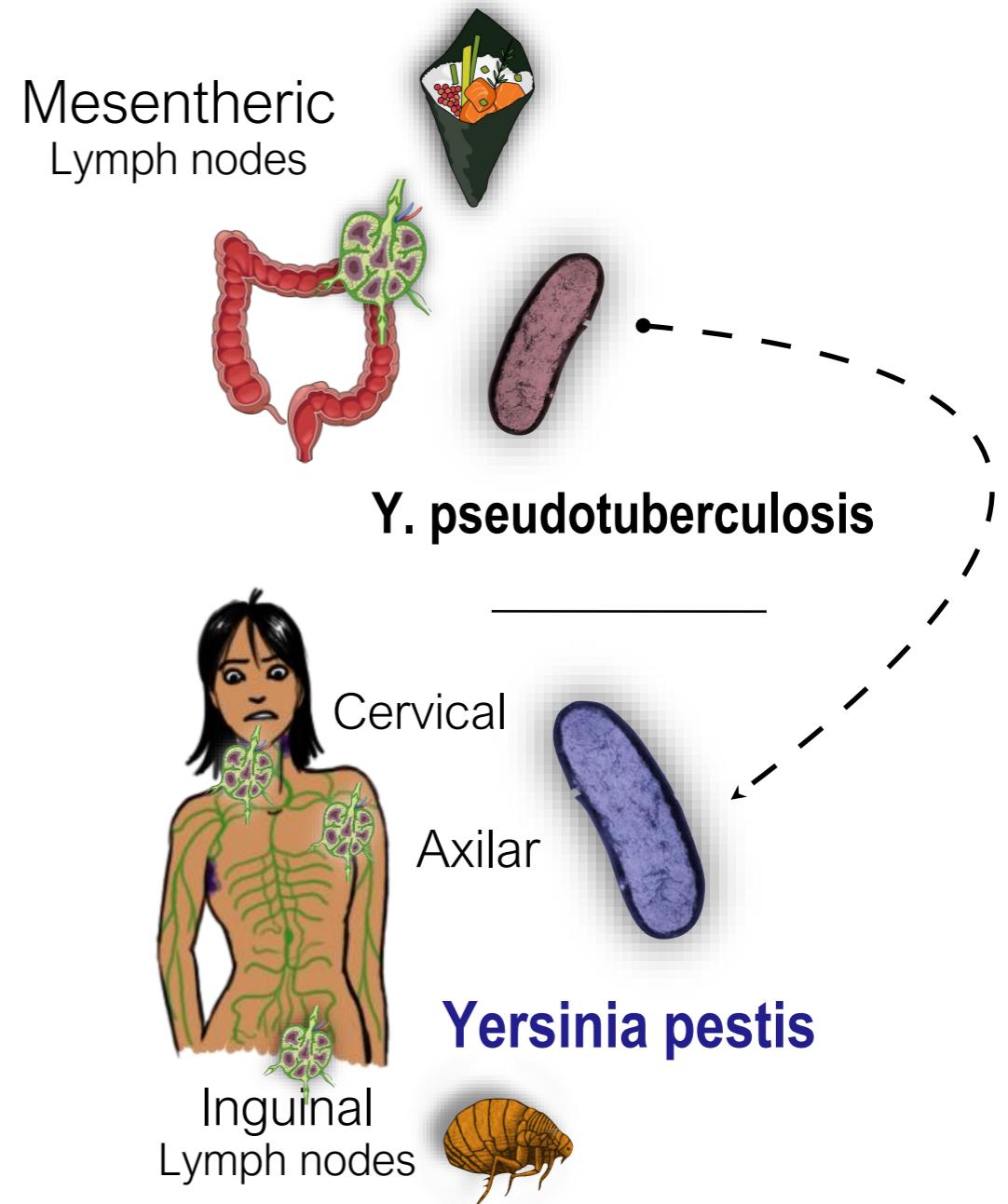
Transmission

Disease

Pathogenicity

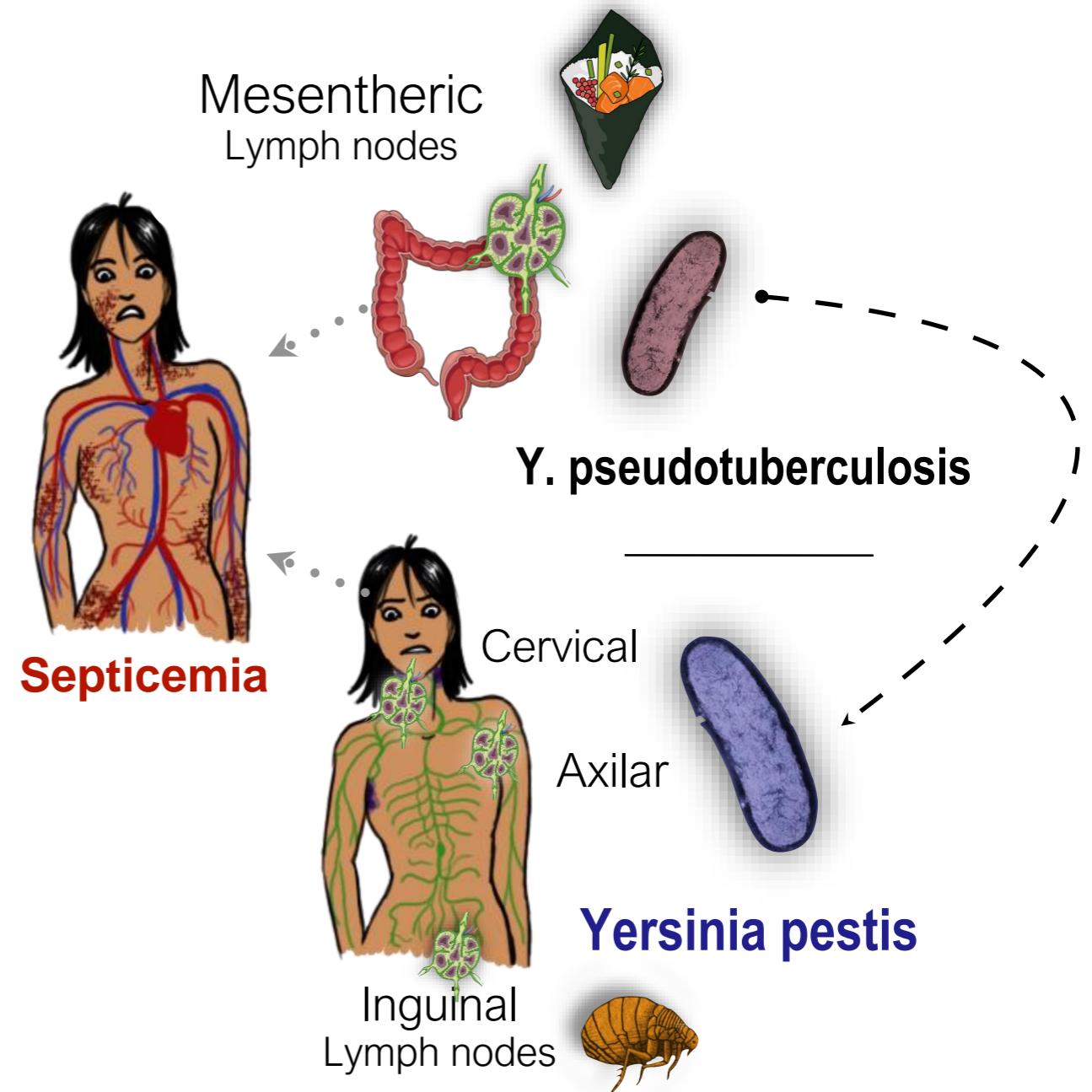
***Y. pestis* shares virulence mechanisms**

with the enteropathogen *Y. pseudotuberculosis*



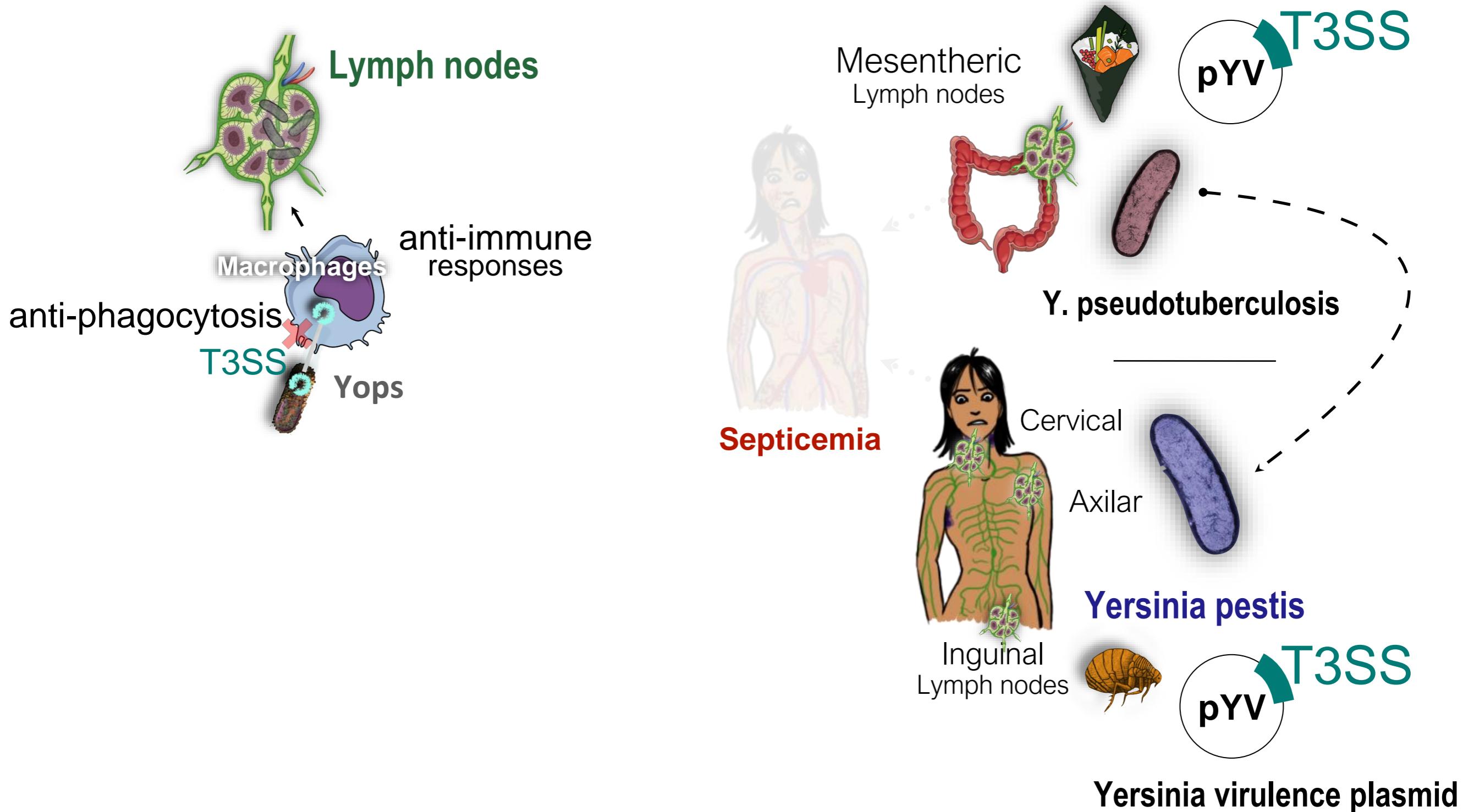
***Y. pestis* shares virulence mechanisms**

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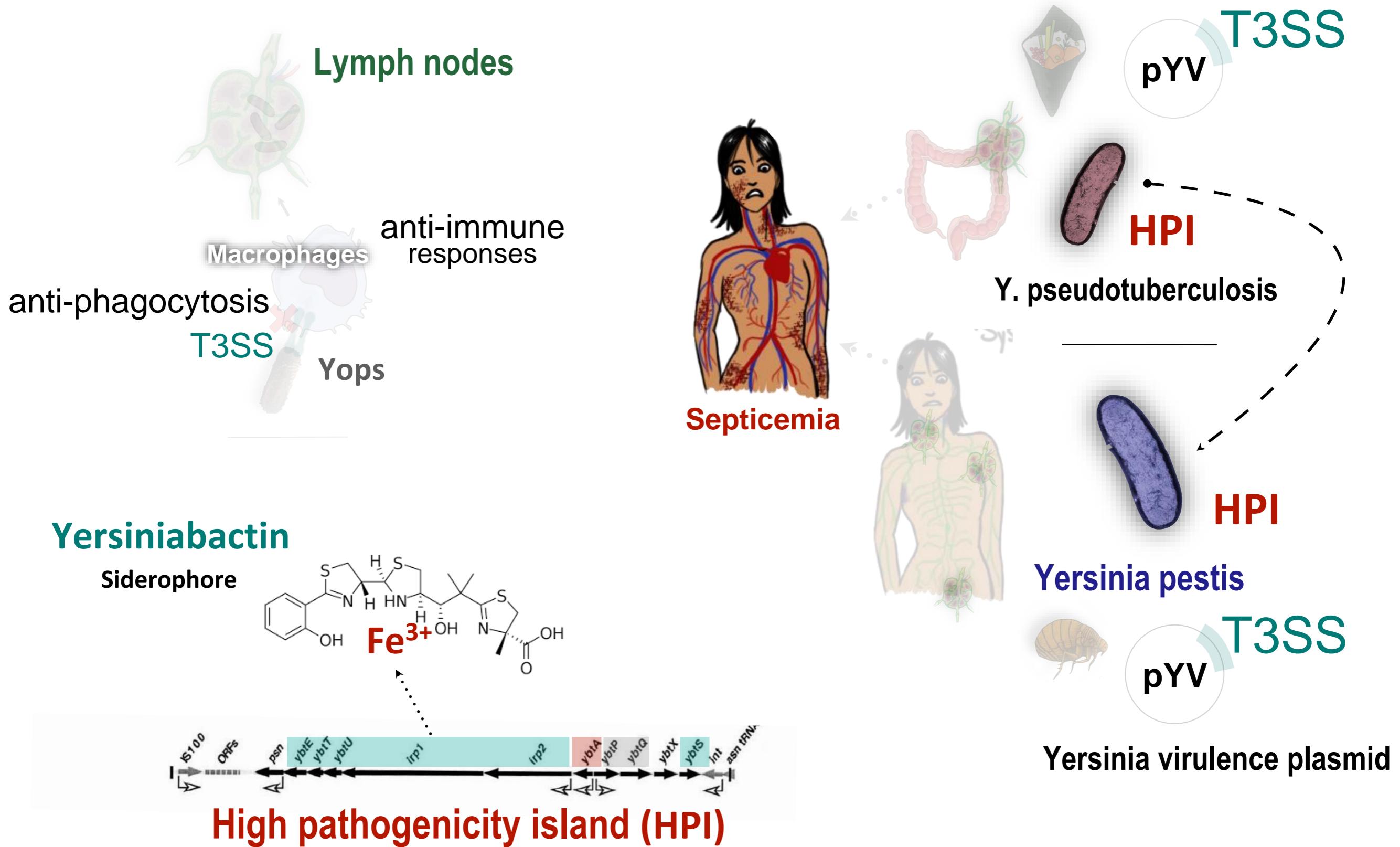
Yp & Ypstb share a Type 3 Secretion System

- a molecular syringe to inject bacterial proteins into host cells



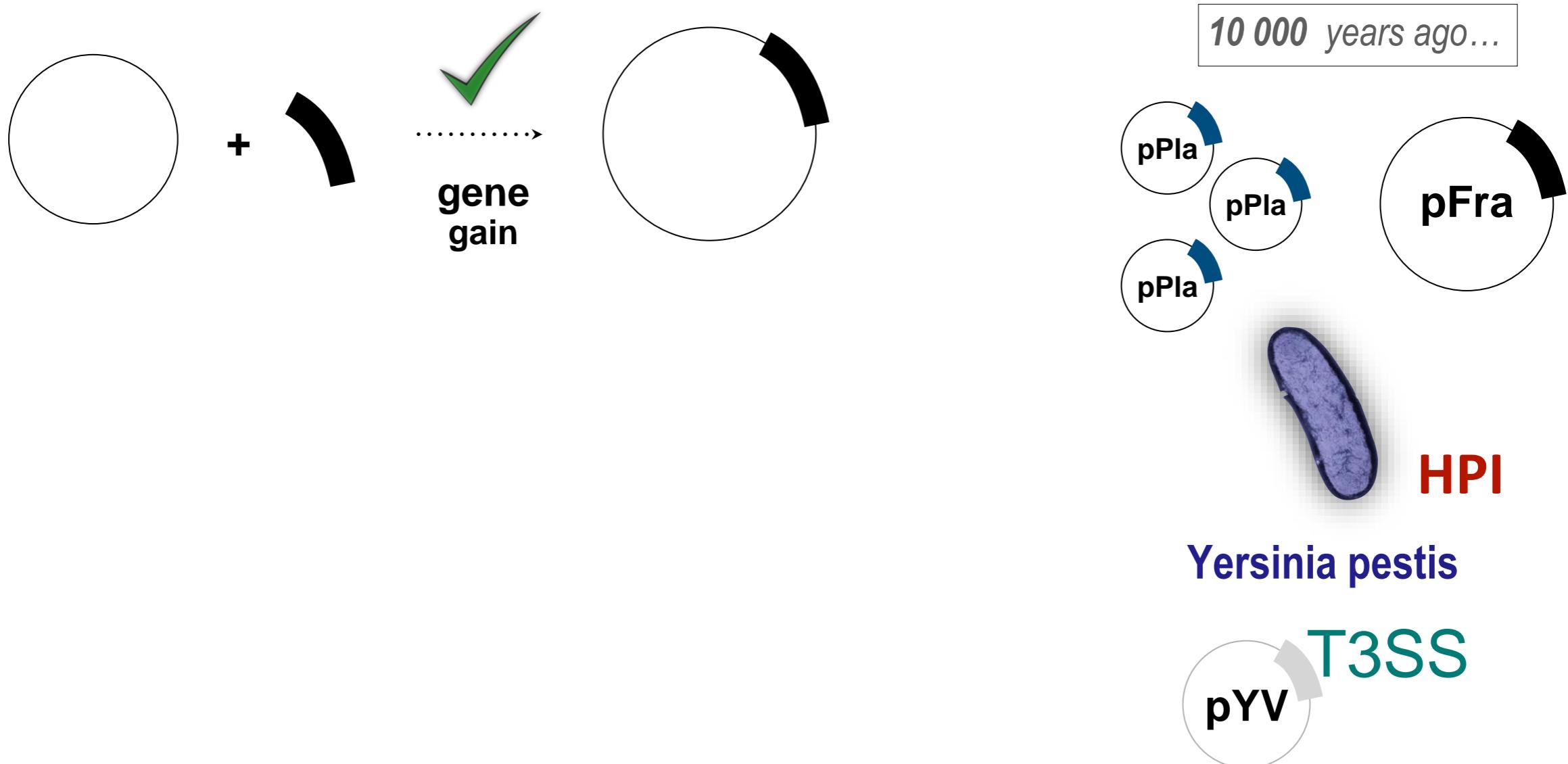
Yp & Ypstb share an iron acquisition system

- the High Pathogenicity Island



***Yersinia pestis* acquired two plasmids**

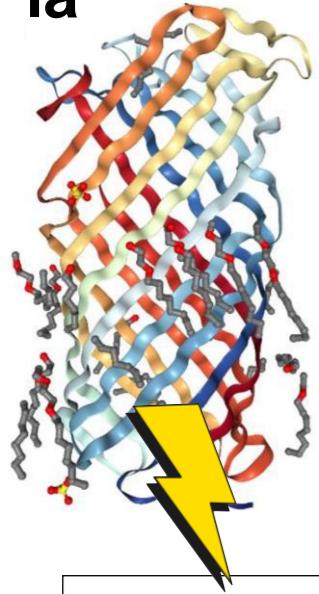
critical for pathogenicity and vectoriality



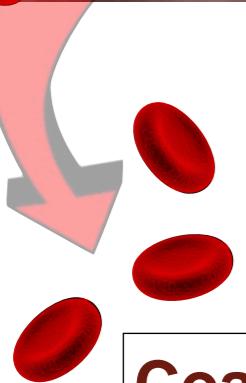
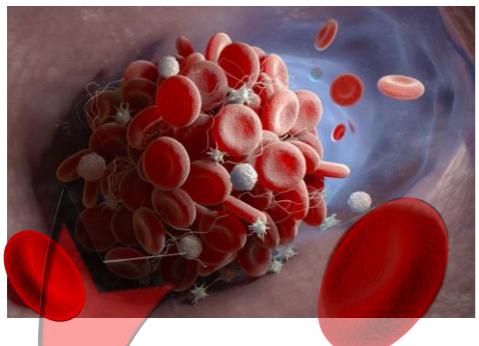
Pla is a broad-range protease

that favors **Yp** dispersion from lymph nodes & lungs

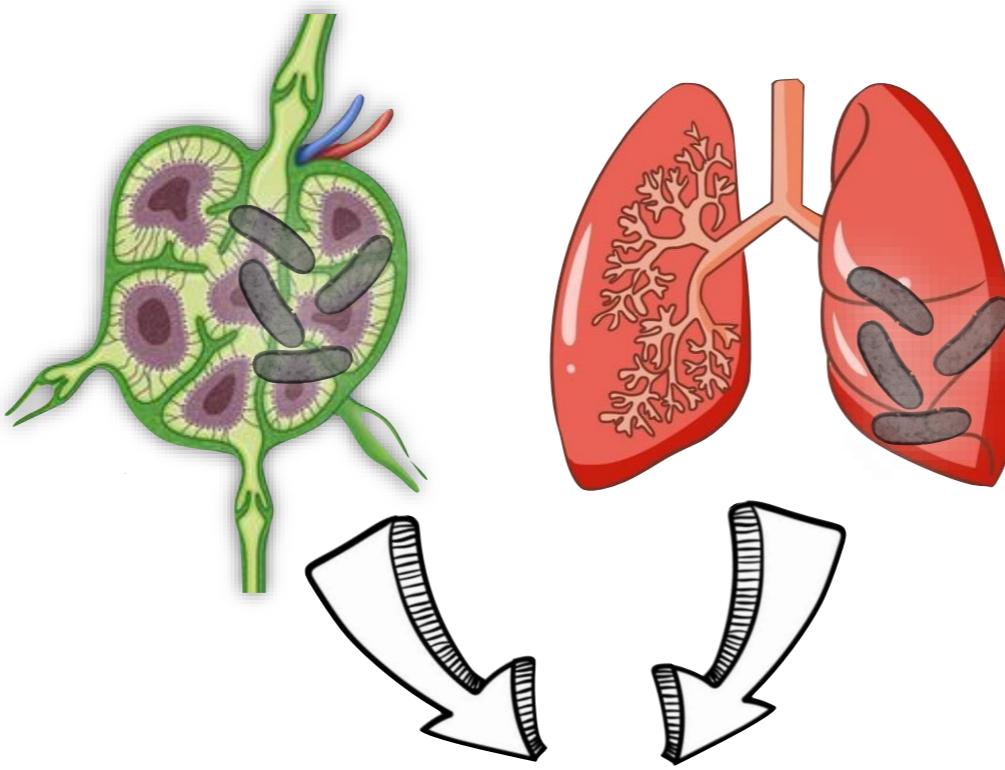
Pla



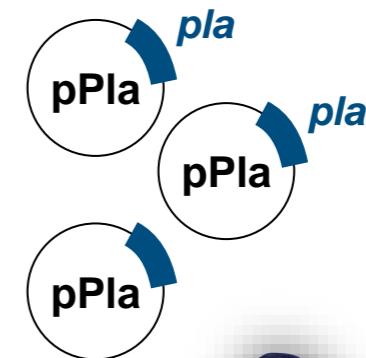
Plasminogen



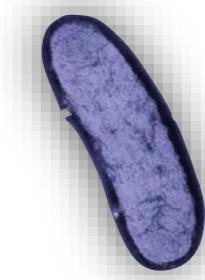
Coagulation disruption



Dispersion to other organs

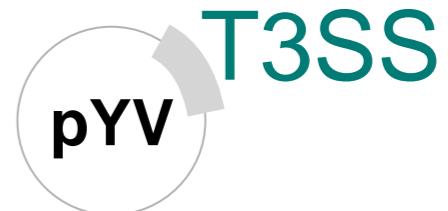


pFra



HPI

Yersinia pestis

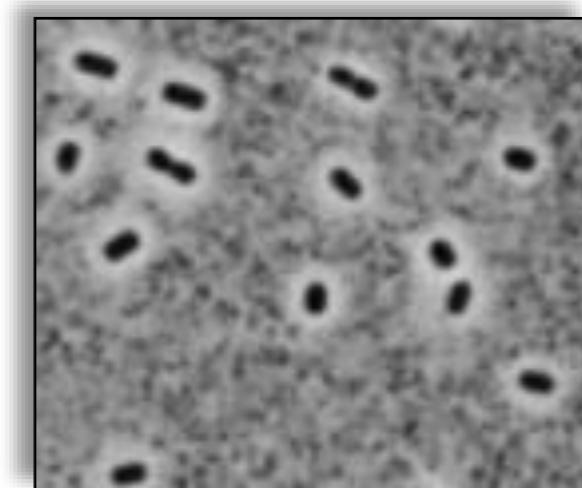
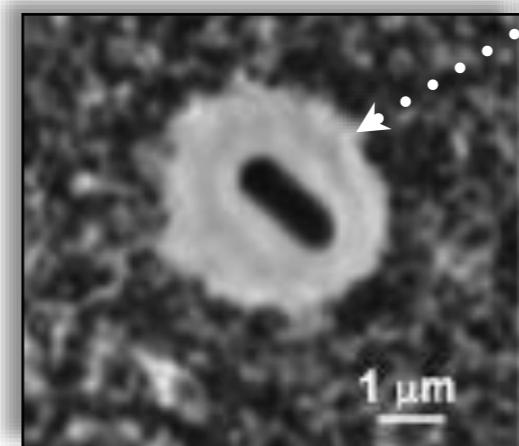
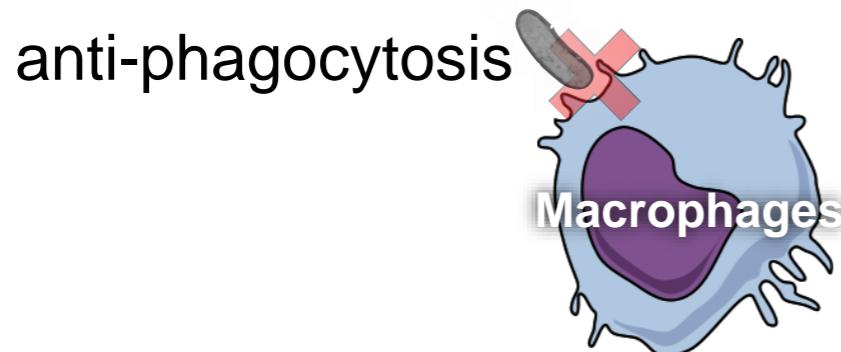


T3SS

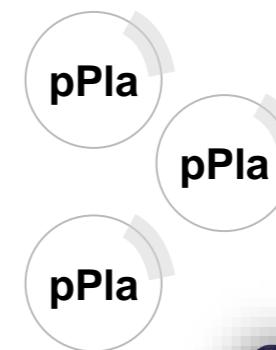
pYV

F1 forms a pseudocapsule

that hampers **Yp** phagocytosis

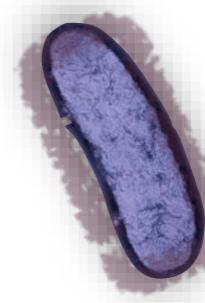


Pseudocapsule



F1
↑
caf1

pFra



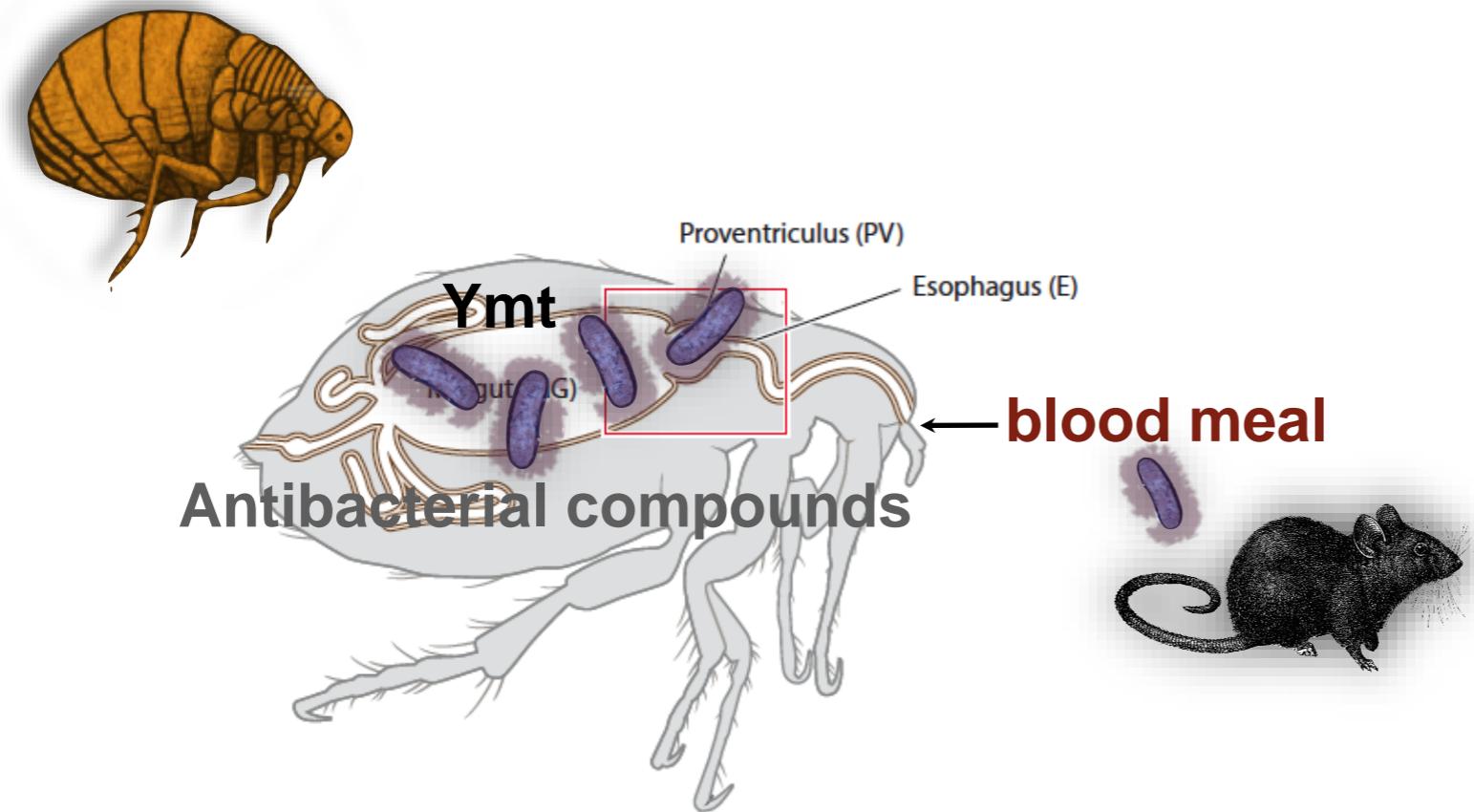
HPI

Yersinia pestis

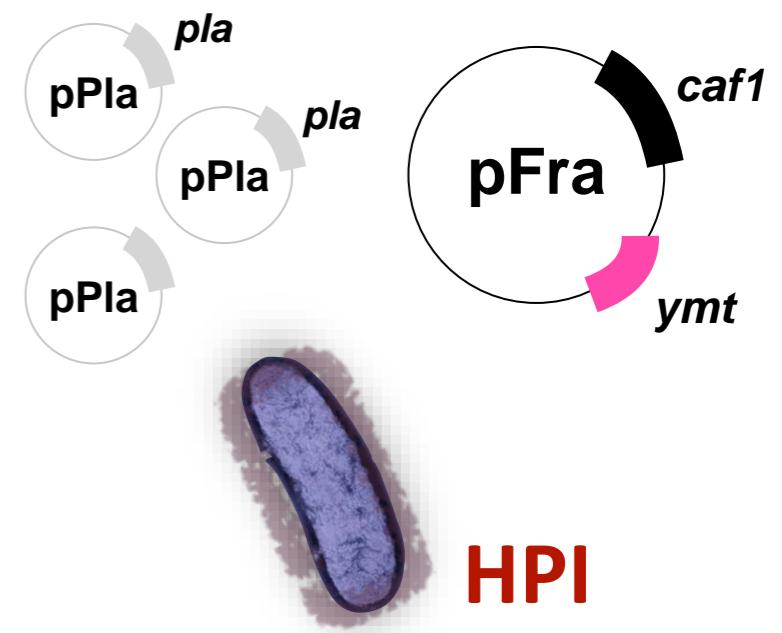


Ymt encodes a phospholipase

critical for *Y. pestis* survival in the flea intestine



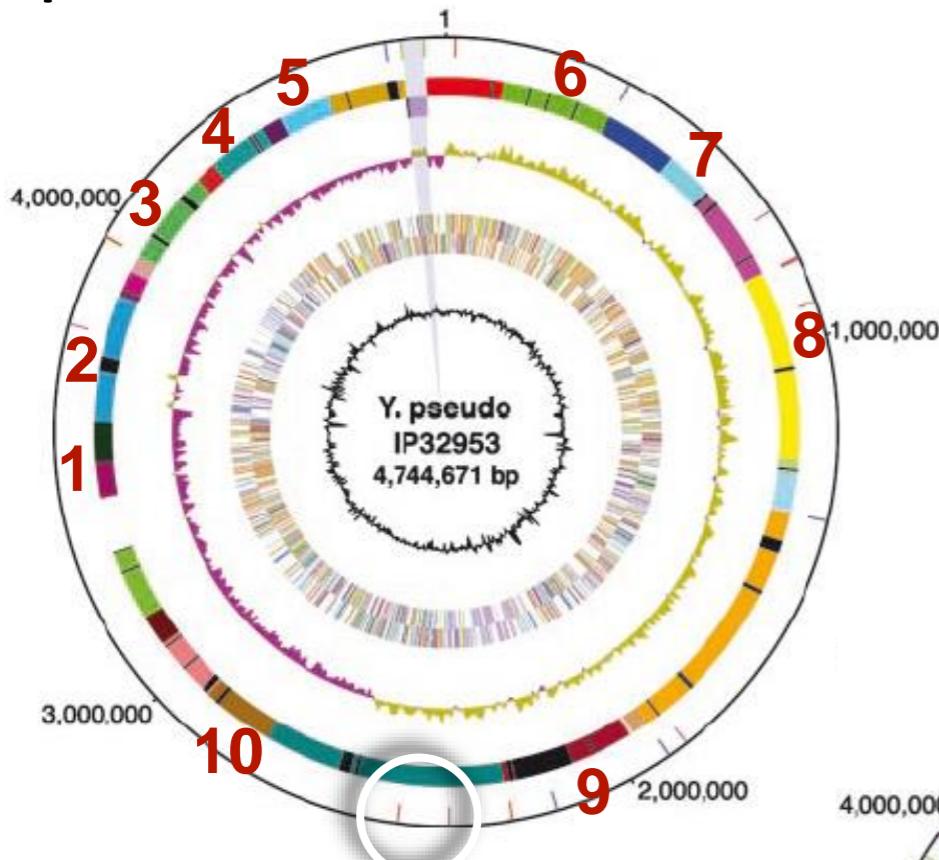
5 000 years ago...



Gene inactivation

has been a major driver of *Y. pestis* evolution

***Y. pseudotuberculosis* chromosome: 20 IS**



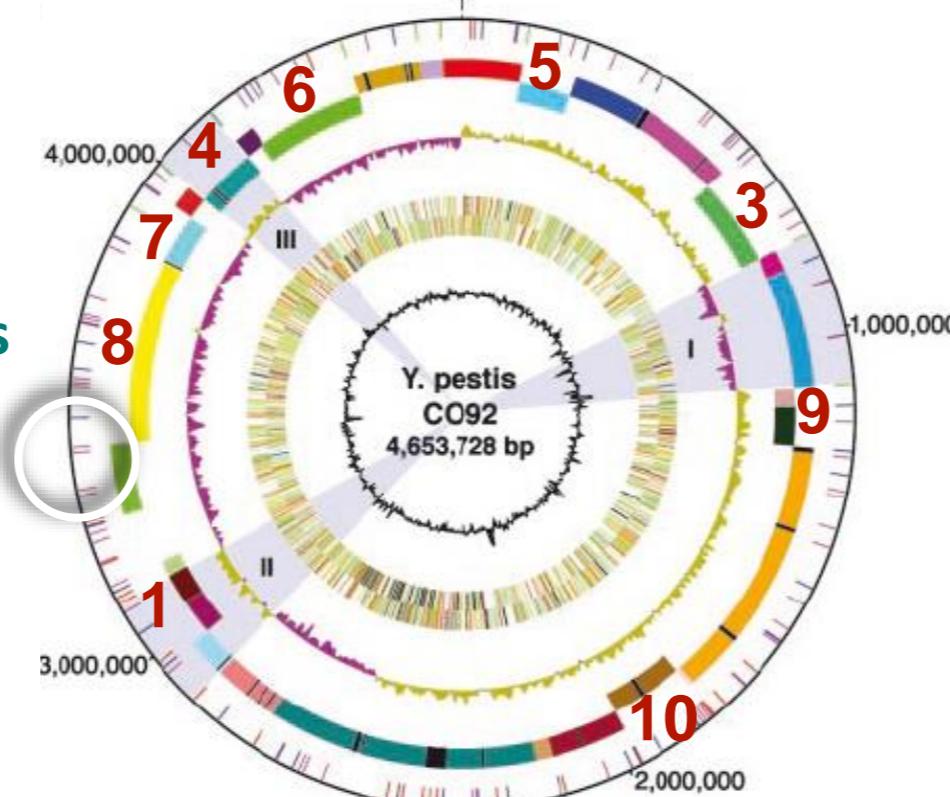
insertion sequences

13% of the genome

is inactivated in *Y. pestis*

1. genome rearrangements
2. insertion sequences
3. non-sense point mutations

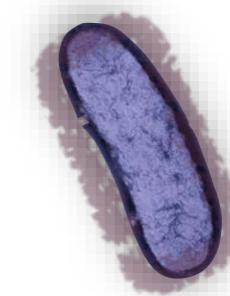
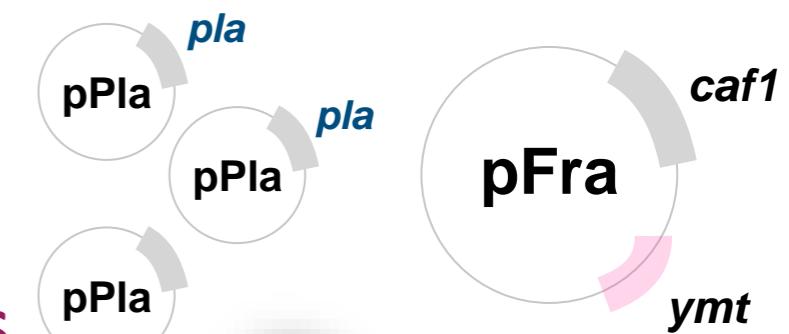
***Y. pestis* chromosome: 138 IS**



Yersinia pestis

T3SS

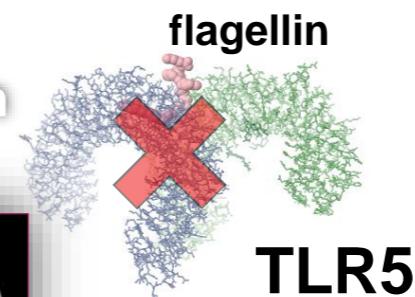
pYV



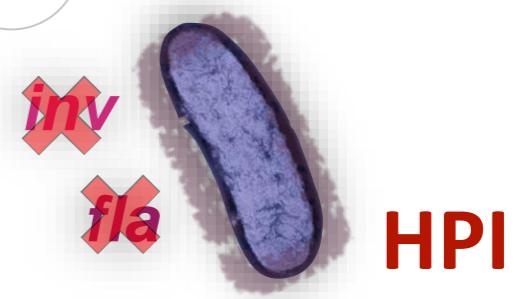
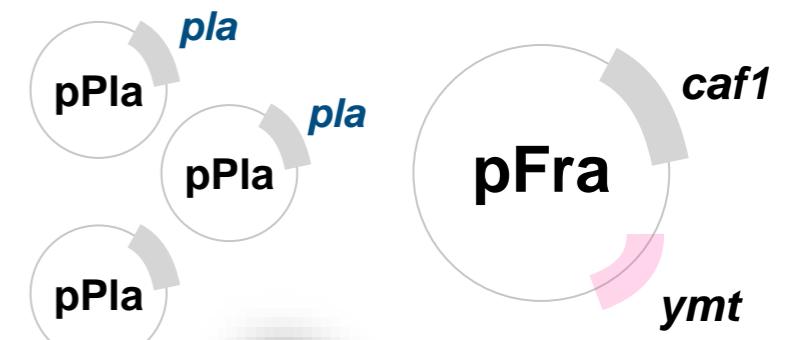
HPI

Gene inactivation impacted host tropism

& escape from immune responses



TLR5



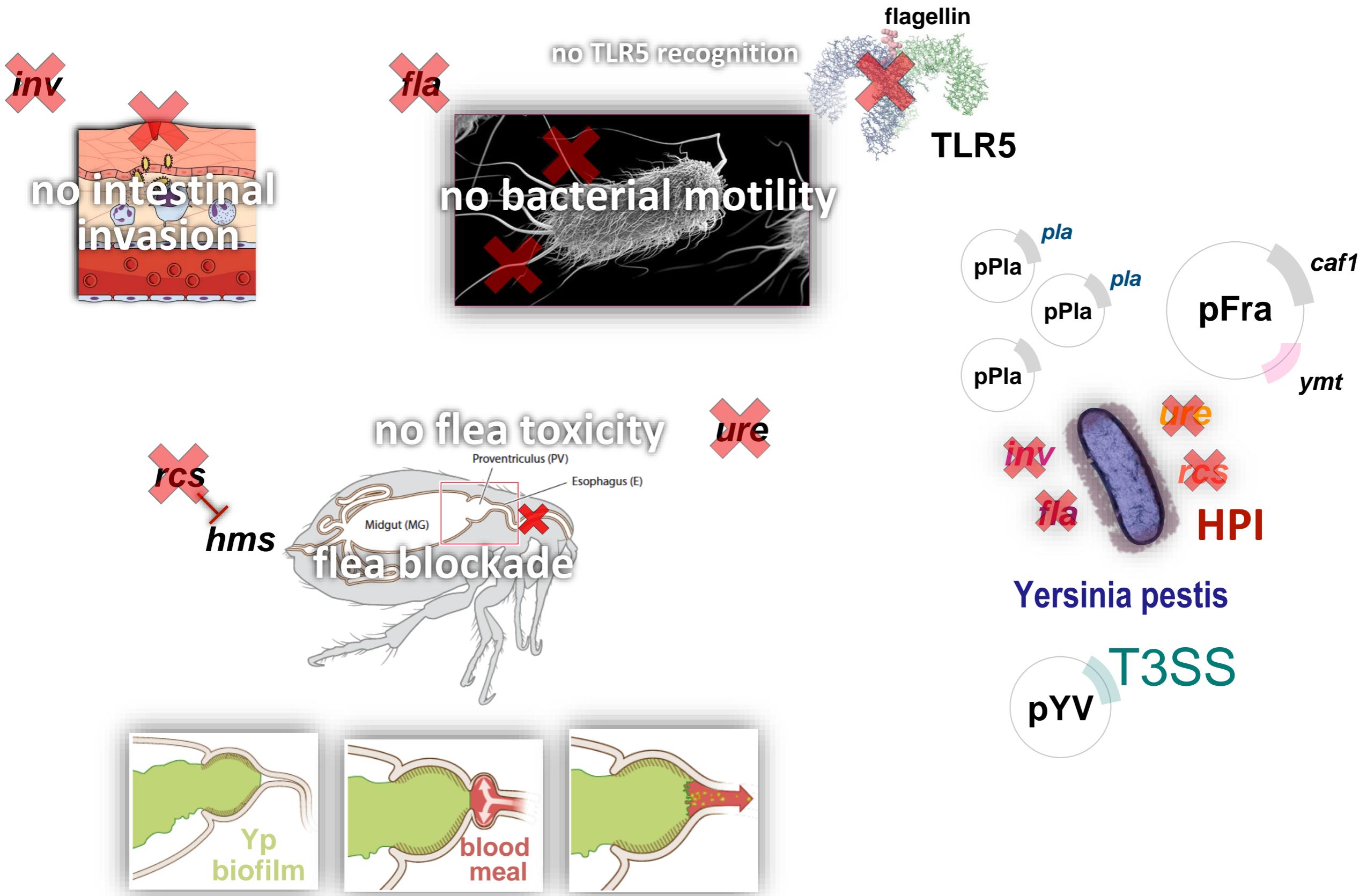
Yersinia pestis



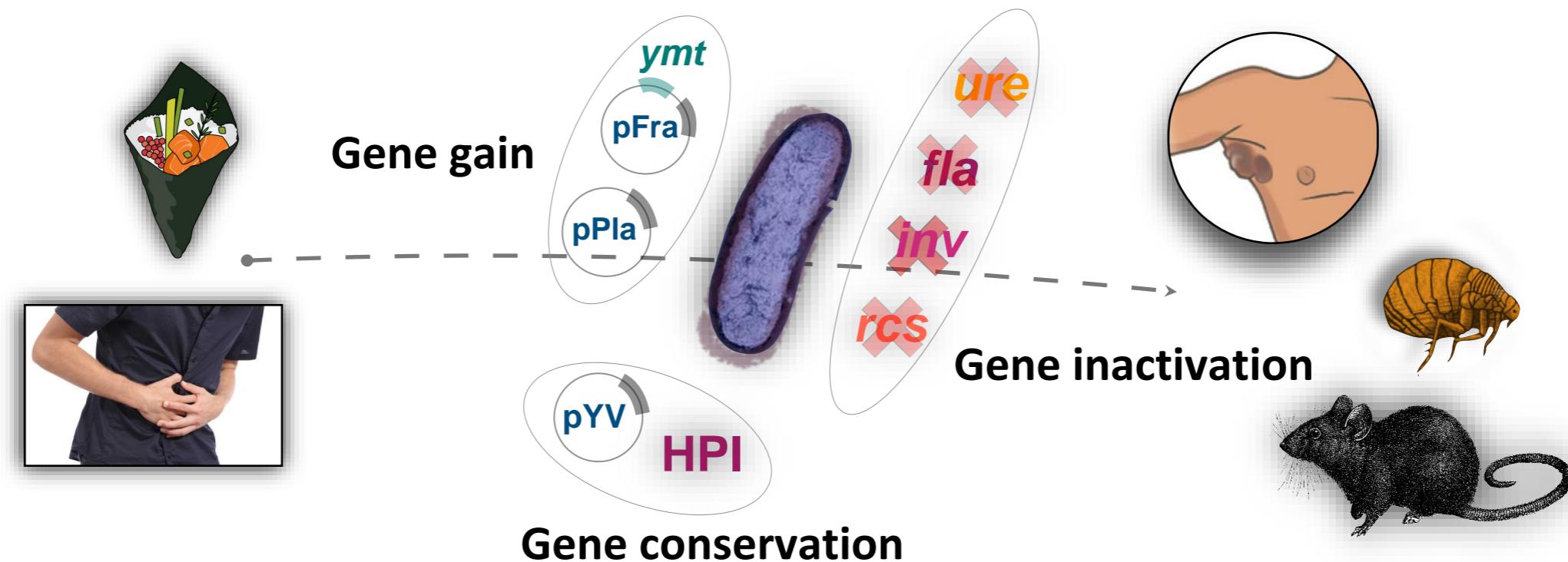
T3SS

Gene inactivation impacted host tropism

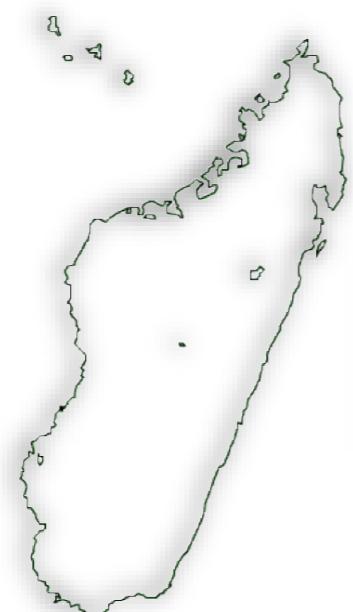
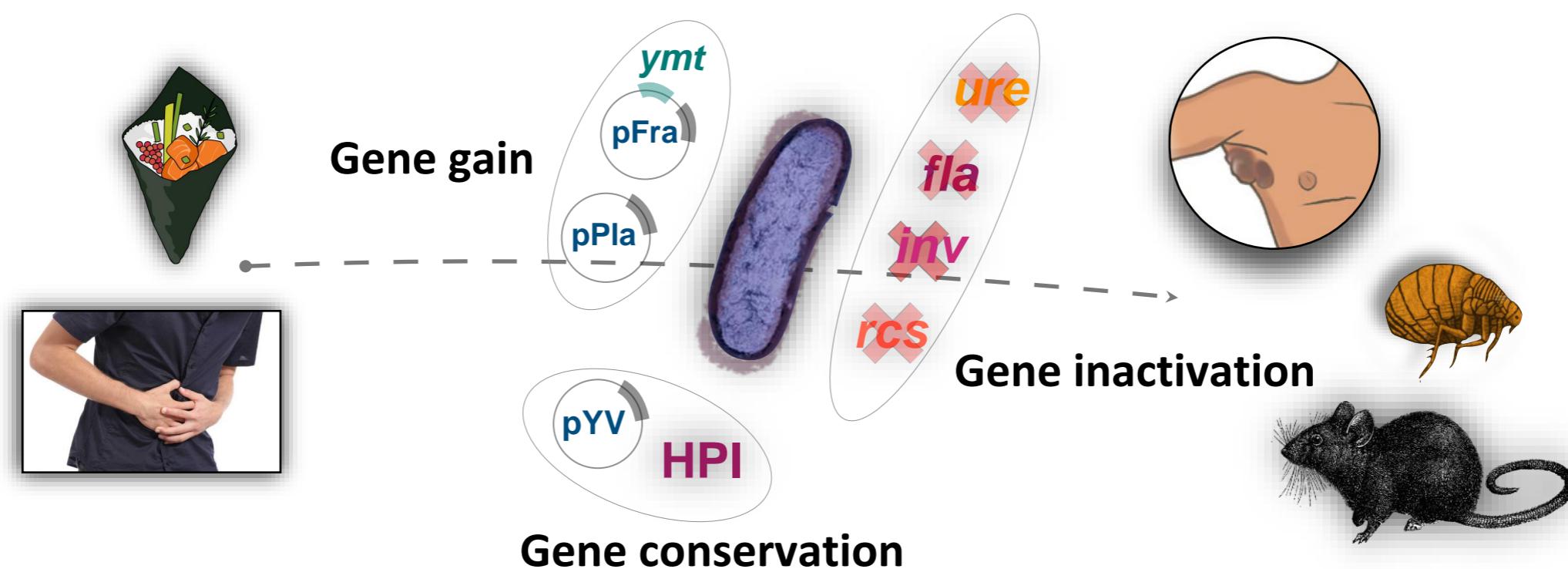
& escape from immune responses



Take Home Messages



Take Home Messages



Madagascar
1997

8

MULTIDRUG RESISTANCE IN
YERSINIA PESTIS MEDIATED BY
A TRANSFERABLE PLASMID

N Engl J Med 337: 667



Pathogen X

August 29th-30th, 2022

Bacterial evolution & Plague

Thank you!

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World Health Organization

Collaborating Centre for Plague (FRA-140)



NATIONAL REFERENCE LABORATORY
Plague & Other Yersinioses

**INSTITUT
PASTEUR** 
Yersinia Research Unit