



# ***The role of phages in the evolution of VTEC and their presence in food and the environment***

Maite Muniesa

Department of Microbiology, University of Barcelona

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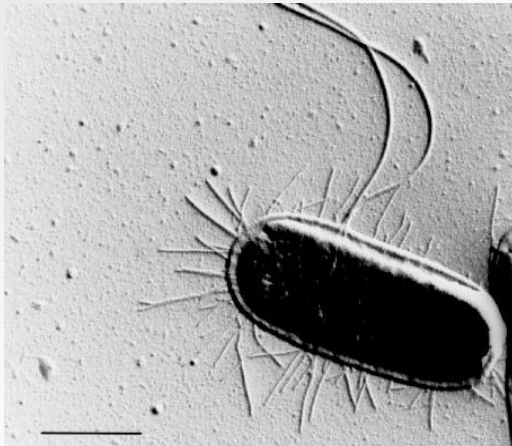


# Phages encoding virulent genes in *E. coli*

## ➤ Shiga Toxin

Smith *et al.*, J. Gen Microbiol. 1983.

O'Brien *et al.*, Science 1984



## ➤ Genes encoding effector proteins

- nleA bacteriophages

- Cif bacteriophages

Marchés *et al.*, Molec. Microbiol. 2003

Loukiadis *et al.*, J. Bacteriol. 2008

Creuzburg *et al.*, 2005

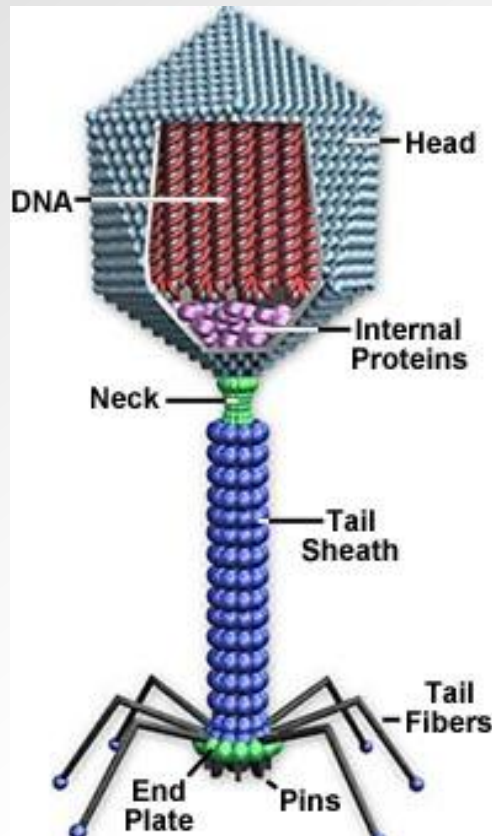
## ➤ CDT (cytolethal distending toxin)

Janka *et al.*, Inf. Immun. 2003

Asakura *et al.*, PNAS. 2007

Allué-Guardia *et al.* Inf. Immun. 2011. J. Virol 2013

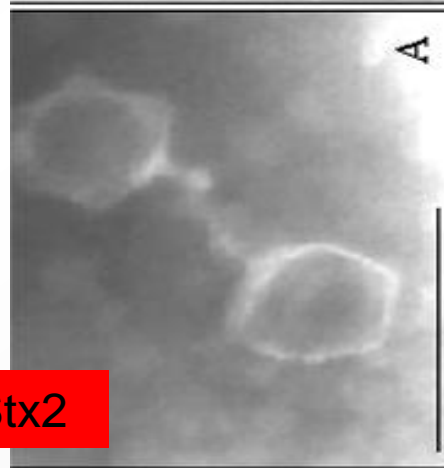
# Stx1 and Stx2 phages



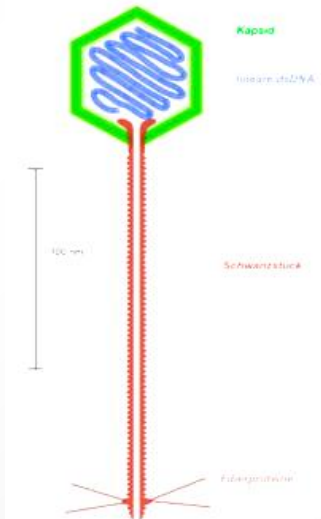
Stx1



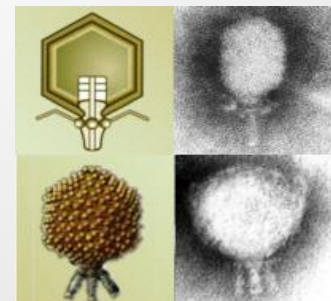
Stx2



Schematisches Gezeichnet des Lambda Phagen



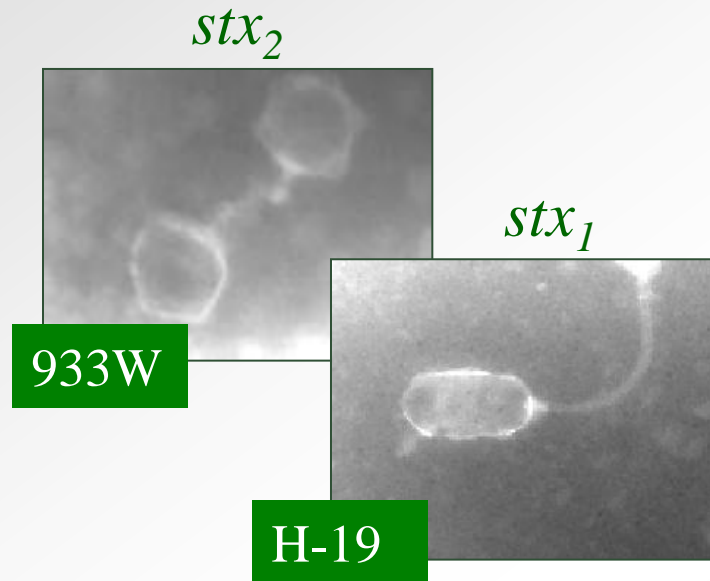
Siphoviridae



Podoviridae

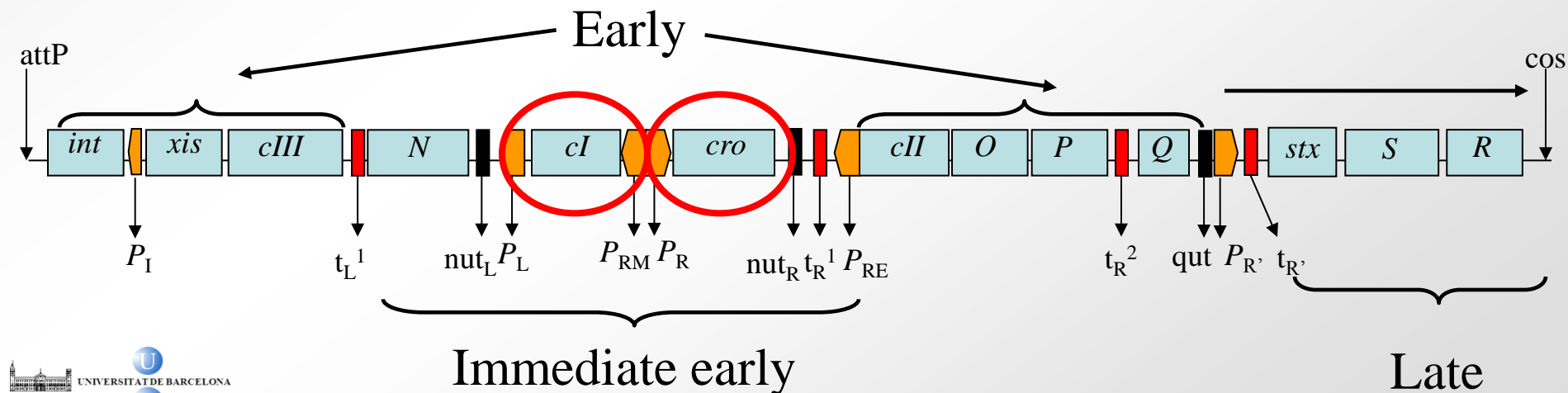
But in general Stx phages are quite diverse (morphology, host range, genetics...)

# Shiga-like toxins: Stx<sub>1</sub>, Stx<sub>2</sub>, variants of Stx<sub>2</sub>

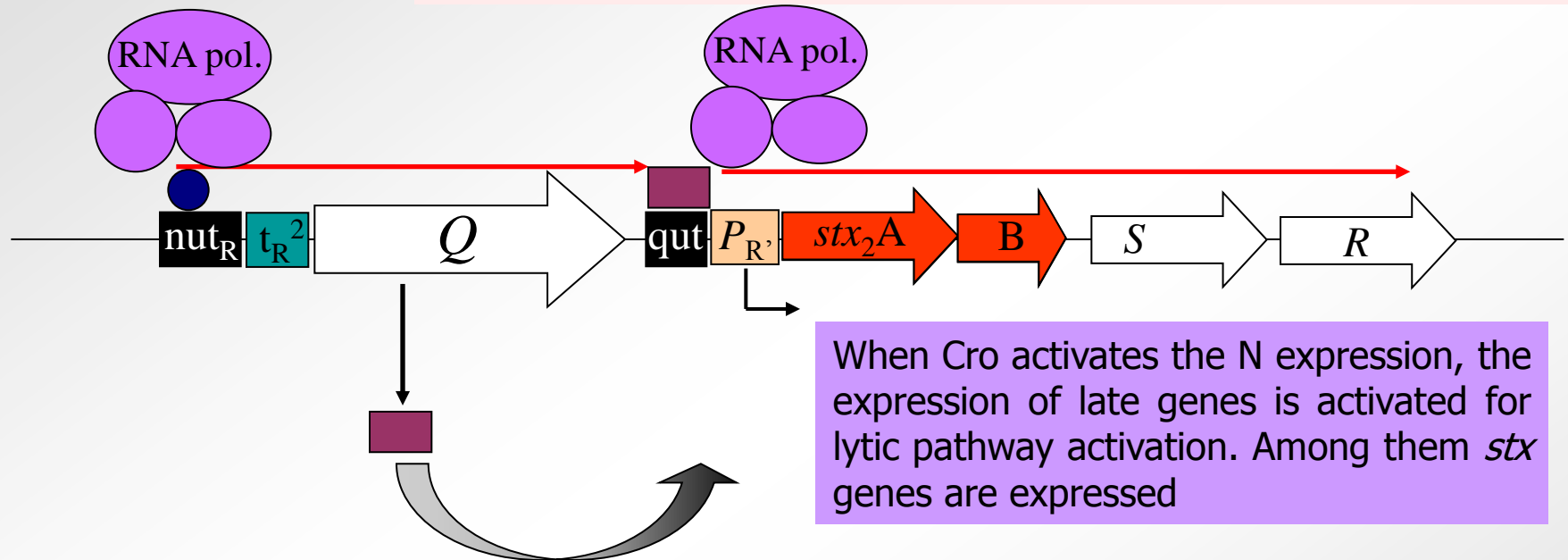


*stx* genes are encoded in the genome of temperate bacteriophages

*stx2e, stx2d, stx2c, stx2g*



# Induction of Stx phages



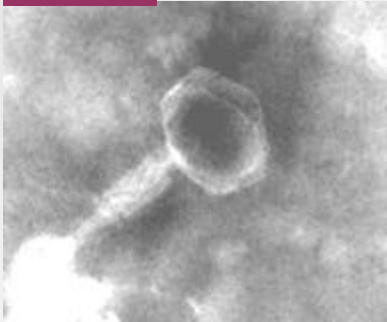
♣ Phage lytic cycle induction by activation of bacterial **SOS response** (recA dependent or not) can be activated by:

- U.V. radiation.
- Certain antibiotics (Mitomycin C, fluoroquinolones, beta-lactamics...)
- EDTA and other chelating agents
- Hydrogen peroxide
- Iron depletion: only for Stx1 without phage lysis
- Food treatments !!! (heat, radiation in low doses, antibiotics as prophylactics, HHP...)



# Diversity: Morphology

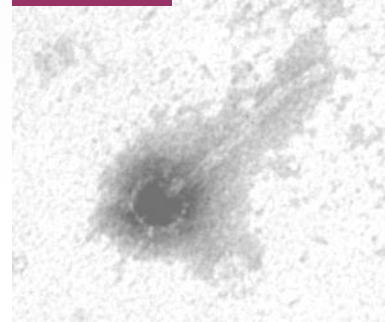
$\phi 1a$



$\phi 4$



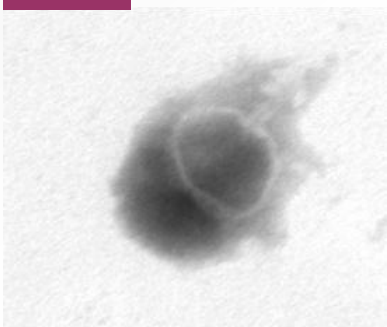
$\phi 13a$



$\phi 16a$



$\phi 1b$



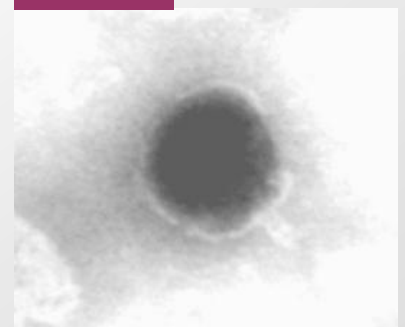
$\phi 12$



$\phi 13b$



$\phi 16b$



# Diversity: Host range

Host bacteria	Strain	Phages									
		φ1a	φ1b	φ3	φ4	φ5	φ6	φ12	φ13a	φ13b	φ16b
<i>Shigella dysenteriae</i>	500	+	+	+	+	+	+	-	+	+	+
<i>Shigella boydii</i>	316	-	+	-	+	-	-	-	-	-	-
<i>Shigella boydii</i>	351	-	+	+	+	-	-	-	-	-	-
<i>Shigella sonnei</i>	866	+	+	+	+	+	+	-	+	+	+
<i>Shigella sonnei</i>	635	+	+	+	+	+	+	-	+	+	-
<i>Shigella flexnery</i>	805	-	+	-	+	-	-	-	-	-	-
<i>Shigella flexnery</i>	668	+	+	+	+	+	+	+	+	+	+
<i>E. coli</i> O111	209	-	-	-	+	-	-	-	-	-	-
<i>E. coli</i> O26	216	-	-	-	+	-	-	-	-	-	-
<i>E. coli</i> O26	224	-	-	+	+	+	+	-	-	+	+
<i>E. coli</i> O157:H7 ATCC43888		-	-	-	+	-	-	+	-	-	-
<i>E. coli</i> C600	-	+	+	+	+	+	+	+	+	+	+
<i>E. coli</i> DH5 α	-	+	+	+	+	+	+	+	+	+	+
<i>E. coli</i> WG5	-	+	+	+	+	+	+	+	+	+	+

*Shigella dysenteriae* 90 %

*Shigella sonnei* 25 %

*E. coli* O111 10 %

*E. coli* O157:H7 20 %

*Shigella boydii* 85 %

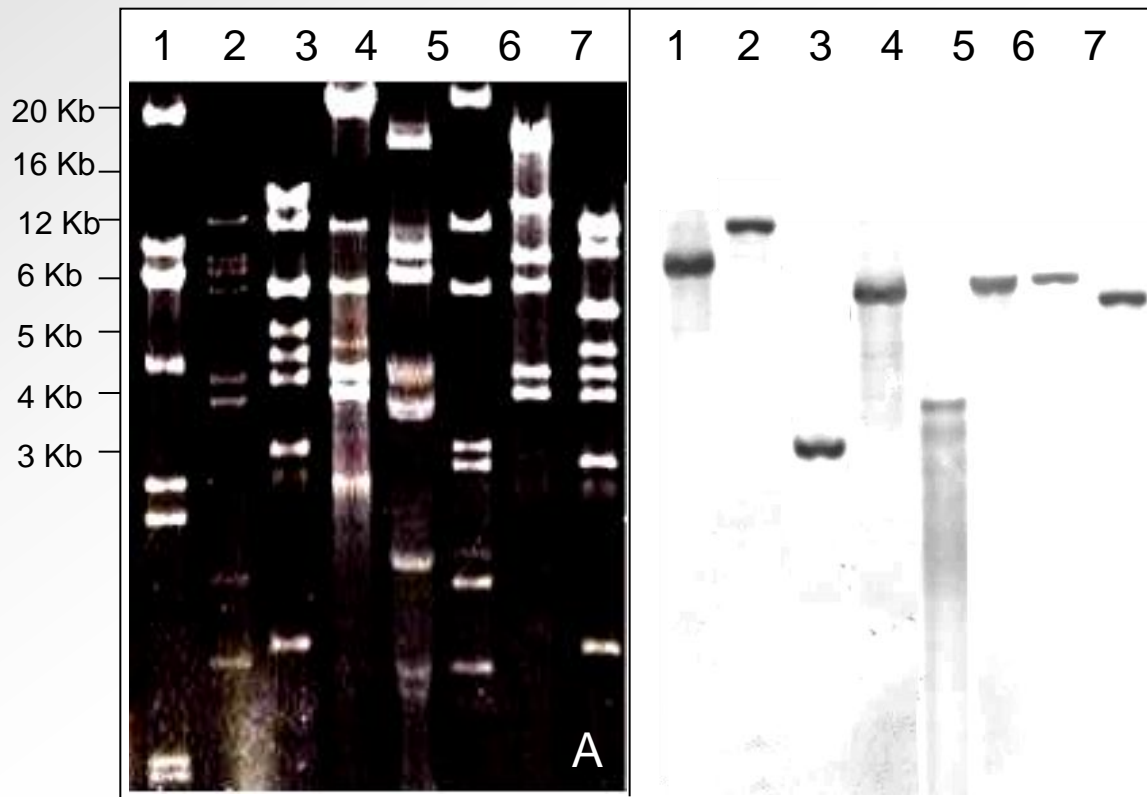
*Shigella flexnery* 60 %

*E. coli* O26 35 %

*E. coli* C 100 %



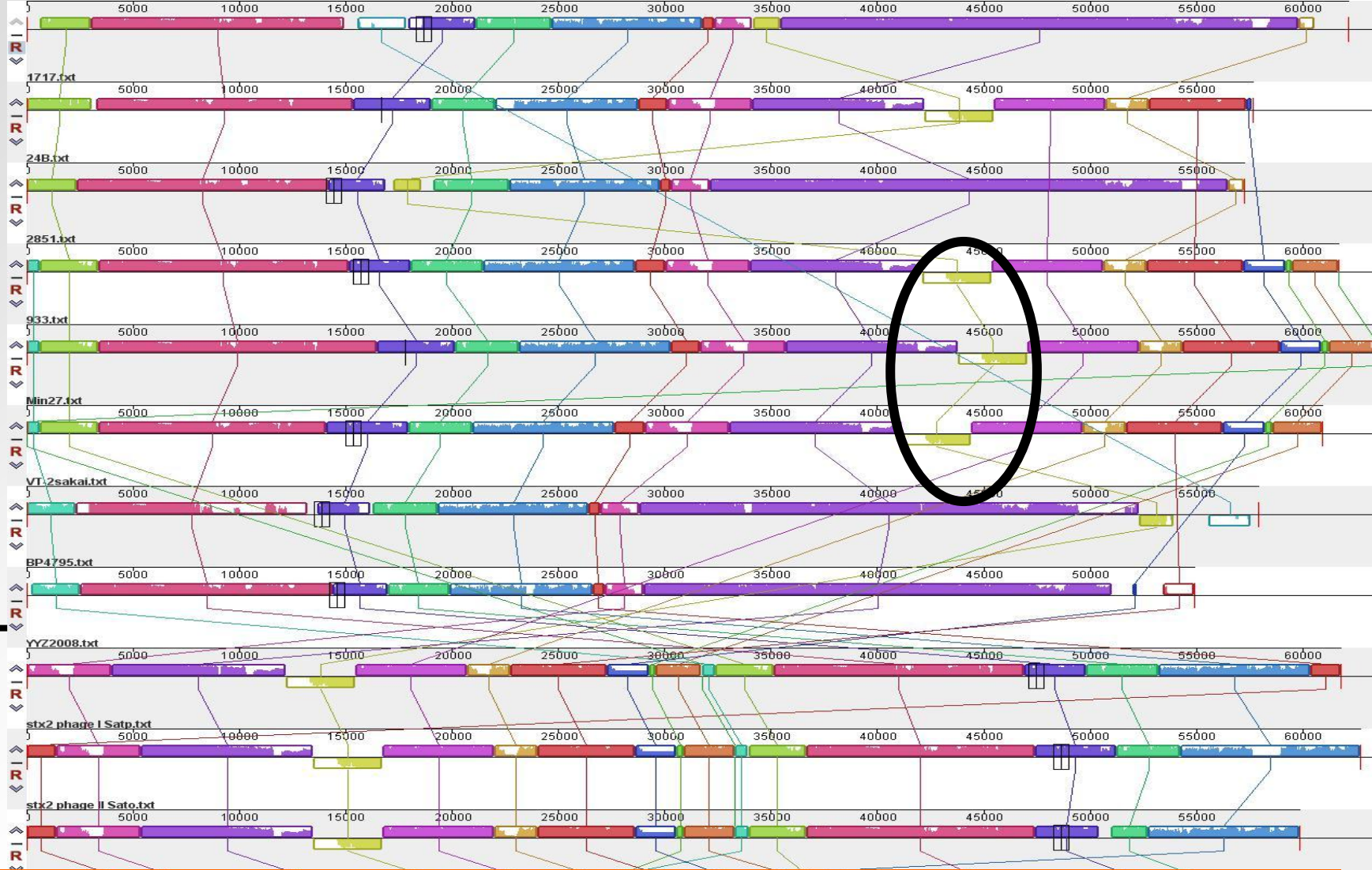
# Variability among phages



phage DNA of 7  
different Stx phages  
isolated from the  
environment

Southern blot stx2A-DIG  
probe

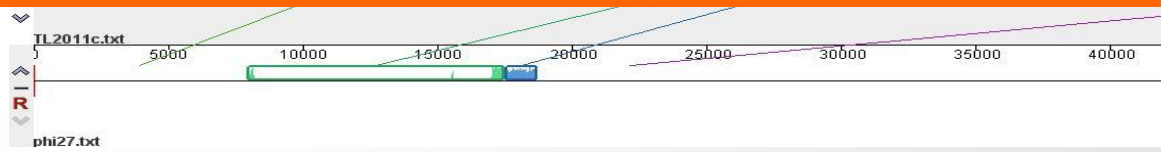
Stx2 phages



Stx1 phages

**Genetic exchange between phages in the same STEC genome**

**There are not two phages identical after passing through a new host**

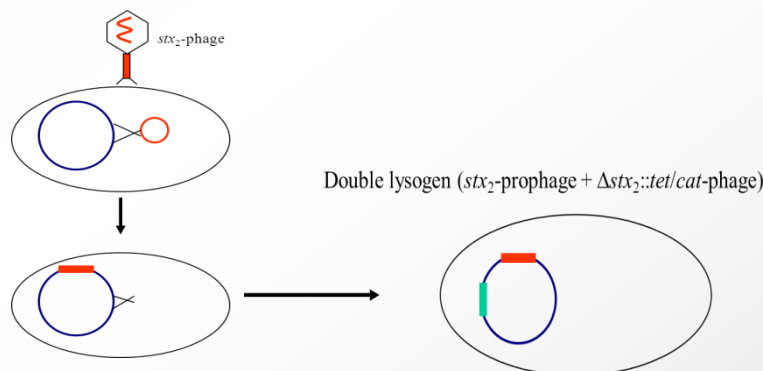


- Stx phages are involved in the **horizontal transmission** of the gene: TRANSDUCTION
  - ❖ in the lab (Schmidt *et al.*, 1999)
  - ❖ in the intestinal tract (Toth *et al.*, 2003; Cornick *et al.*, 2006)
  - ❖ in biofilm (Solheim *et al.*, AEM 2013)
  - ❖ In food and water

Emergence of new virulent strains

## Double lysogens

- Some STEC strains isolated from food, environment and clinic carry more than one inducible Stx phage in their genome (65 %)
- In the double lysogeny of Stx phages does not apply the phage immunity described for phage lambda

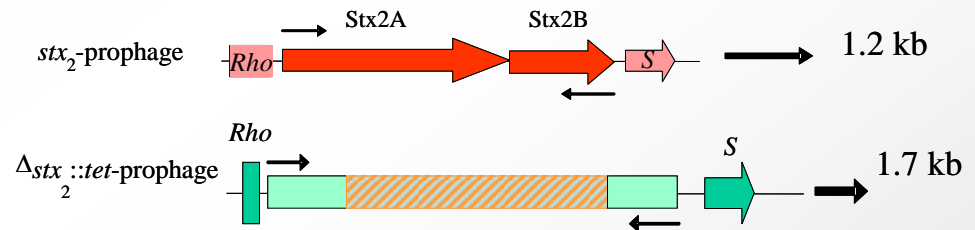
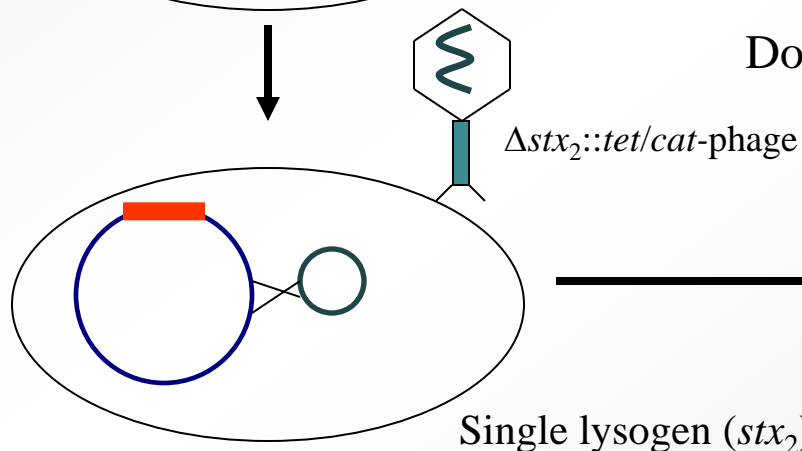
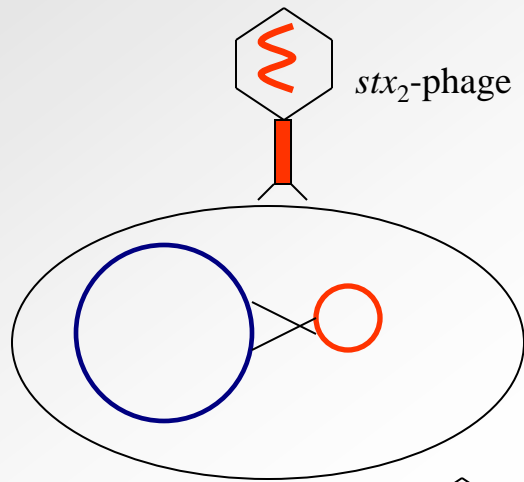


- Have a direct implication in Stx production
- Increase **genome** variability by allowing recombination between both phages.

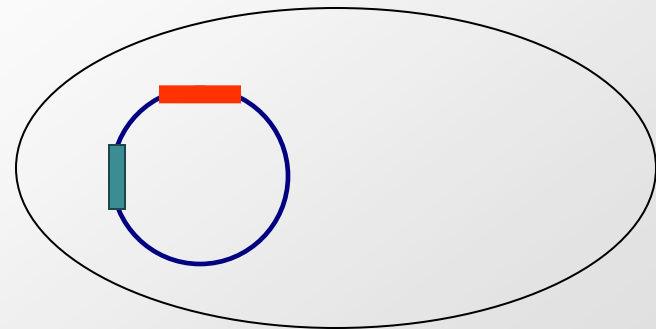
## *Stx* phages search for insertion in *E. coli* chromosome

Double and even triple lysogens of the Same *Stx* phage could be generated

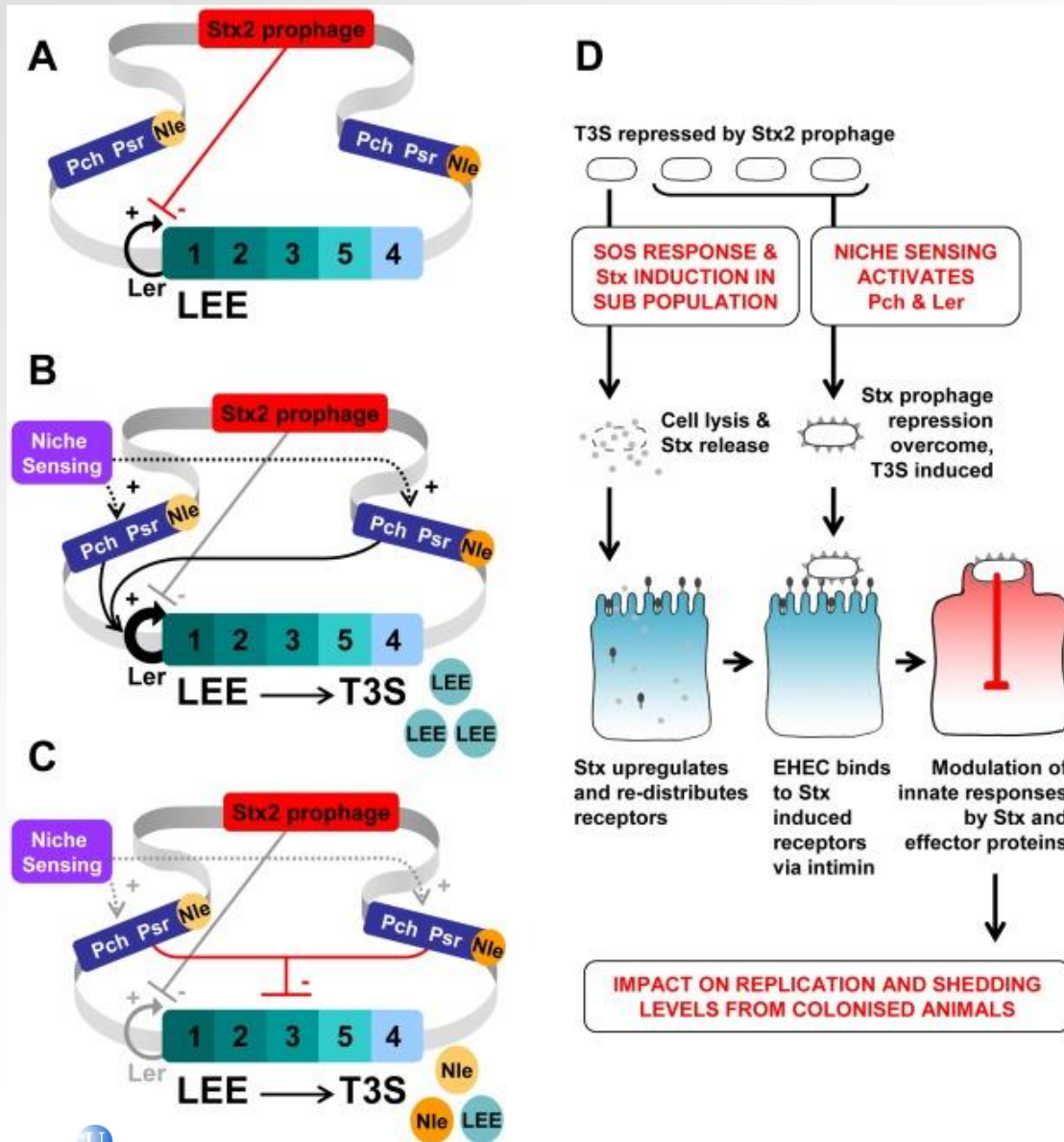
They have a preferred insertion site. If it is not available they search for a secondary site for insertion.



Double lysogen (*stx*<sub>2</sub>-phage +  $\Delta stx_2::tet/cat$ -phage)



# Stx2 phages down regulate LEE expression



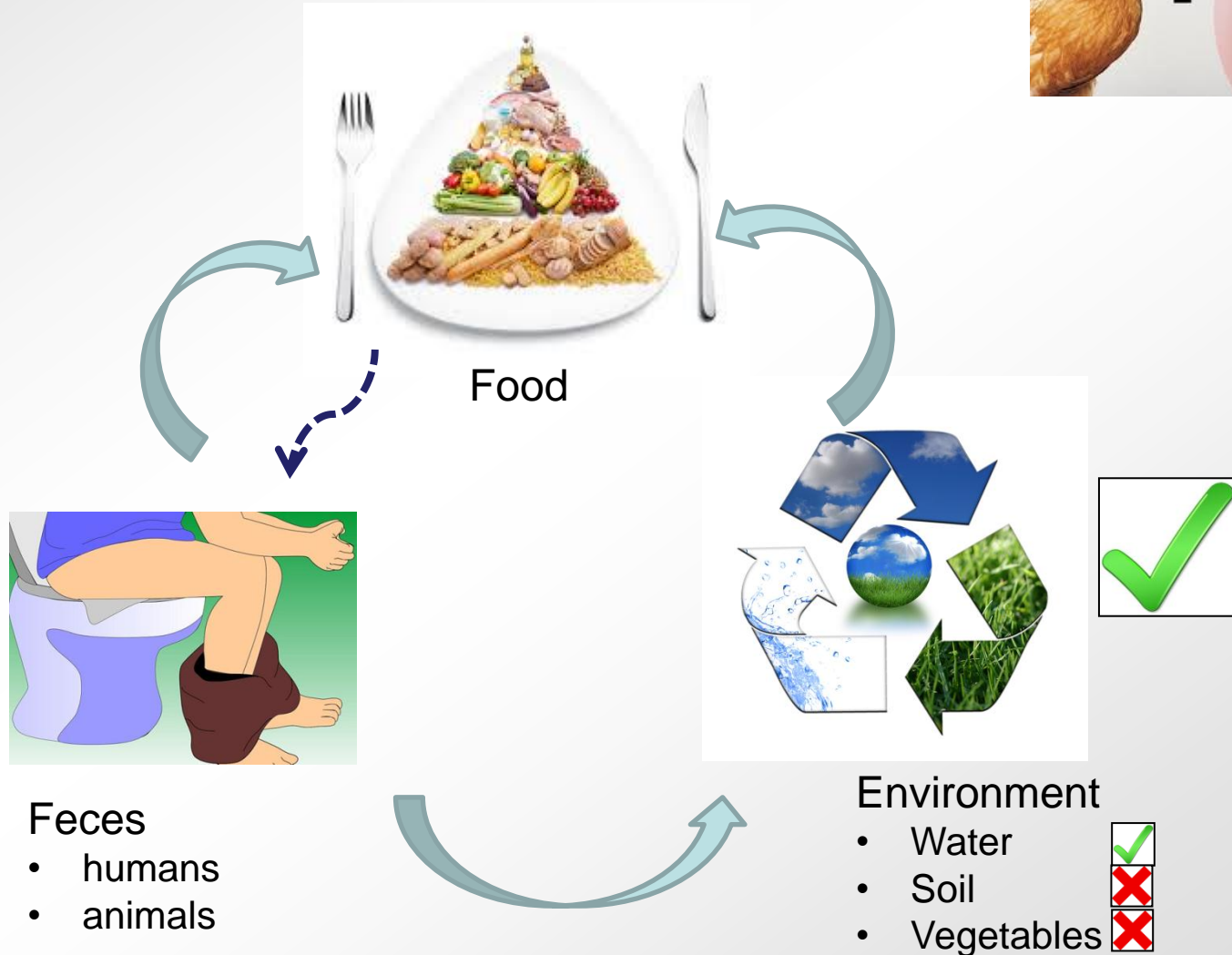
Deletion of Stx2 phages from EHEC strains increased the level of T3SS in LEE whereas lysogeny by Stx2 phages decreased T3SS.



# What is the origin of Stx phages?

Are they induced from VTEC?

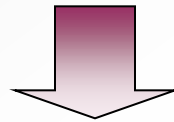
Are free-Stx phages moving around and generate new VTEC?





# Stx phages in the environment

Stx2 phages occurring in sewage were detected by qPCR.



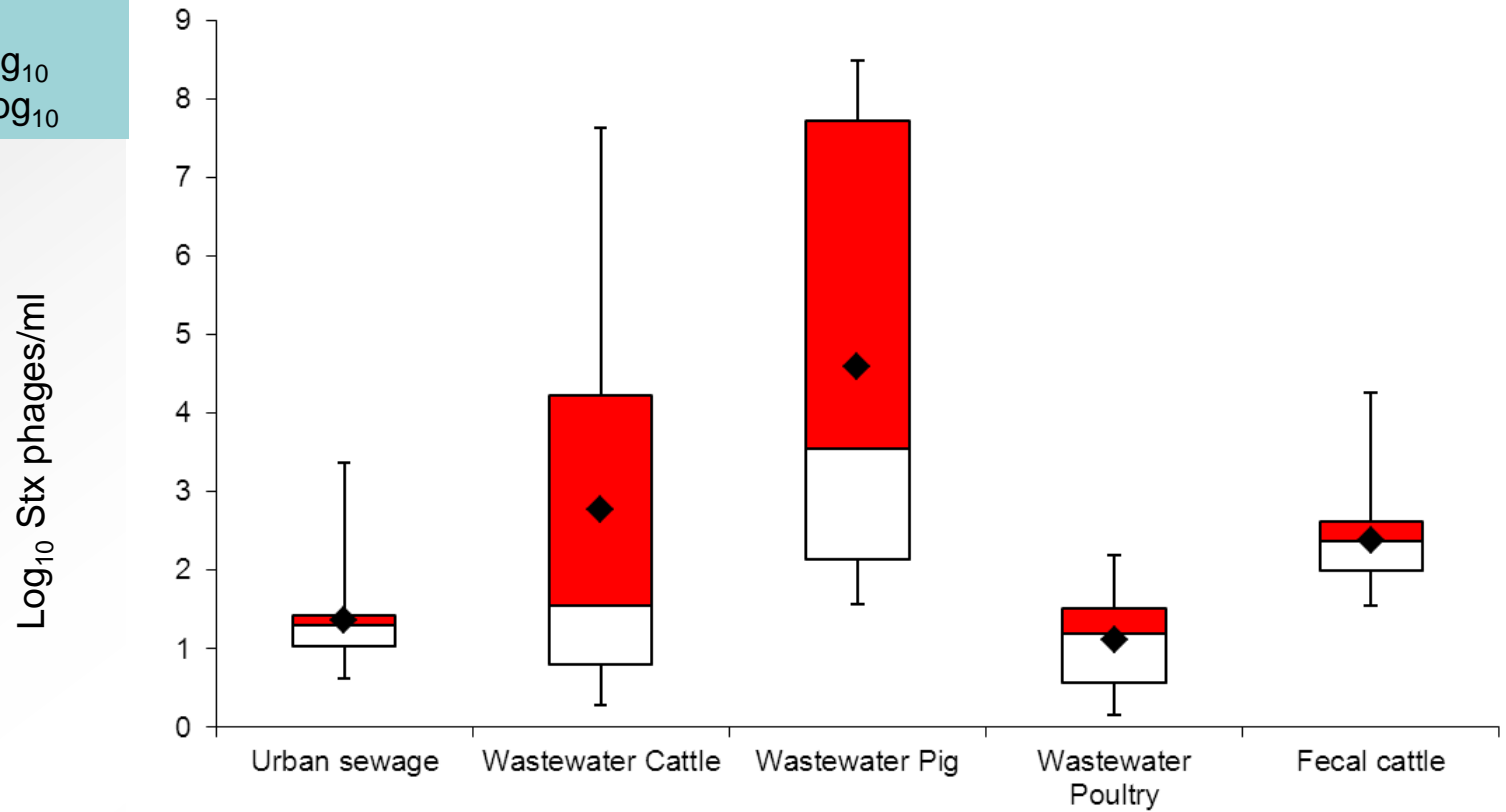
- Abundant in fecal polluted water (human and animal) in Barcelona
  - More than 1000 per ml of sewage
- Present in different geographical areas
  - Austria, France, **Germany**, Ireland, UK, New Zealand, Spain, Sweden or South Africa
- Persistent
  - Chlorination, natural inactivation, thermal treatment, UV light

Stx phages from these samples can propagate in *E. coli*, showing that some of the phages detected are infectious.

**Infectivity means they are potentially able to transduce *stx*.**

# Faecally polluted environments

Human: 1.4 log<sub>10</sub>  
Cattle: 2,8 log<sub>10</sub>  
Pig: 4,6 log<sub>10</sub>  
Poultry: 1.1 log<sub>10</sub>  
Slurries: 2,3 log<sub>10</sub>

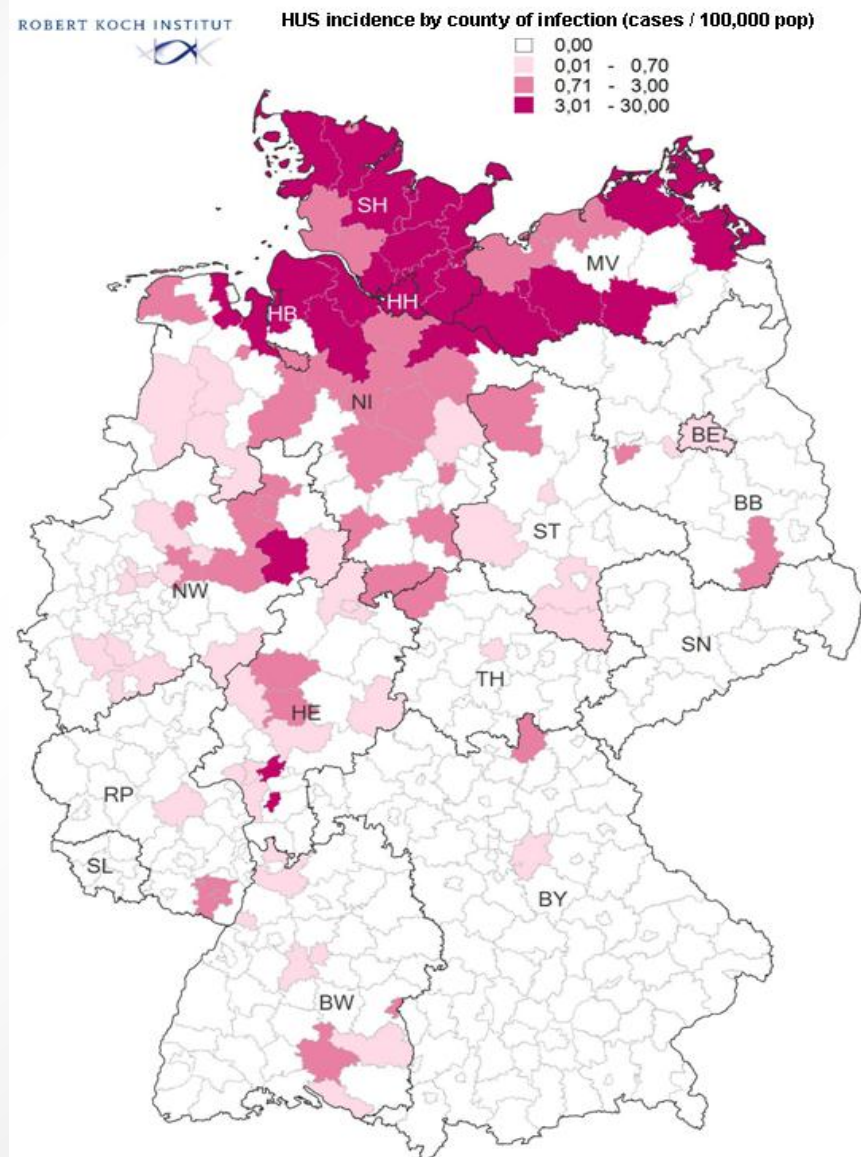


# ***0104:H4 outbreak in Germany***

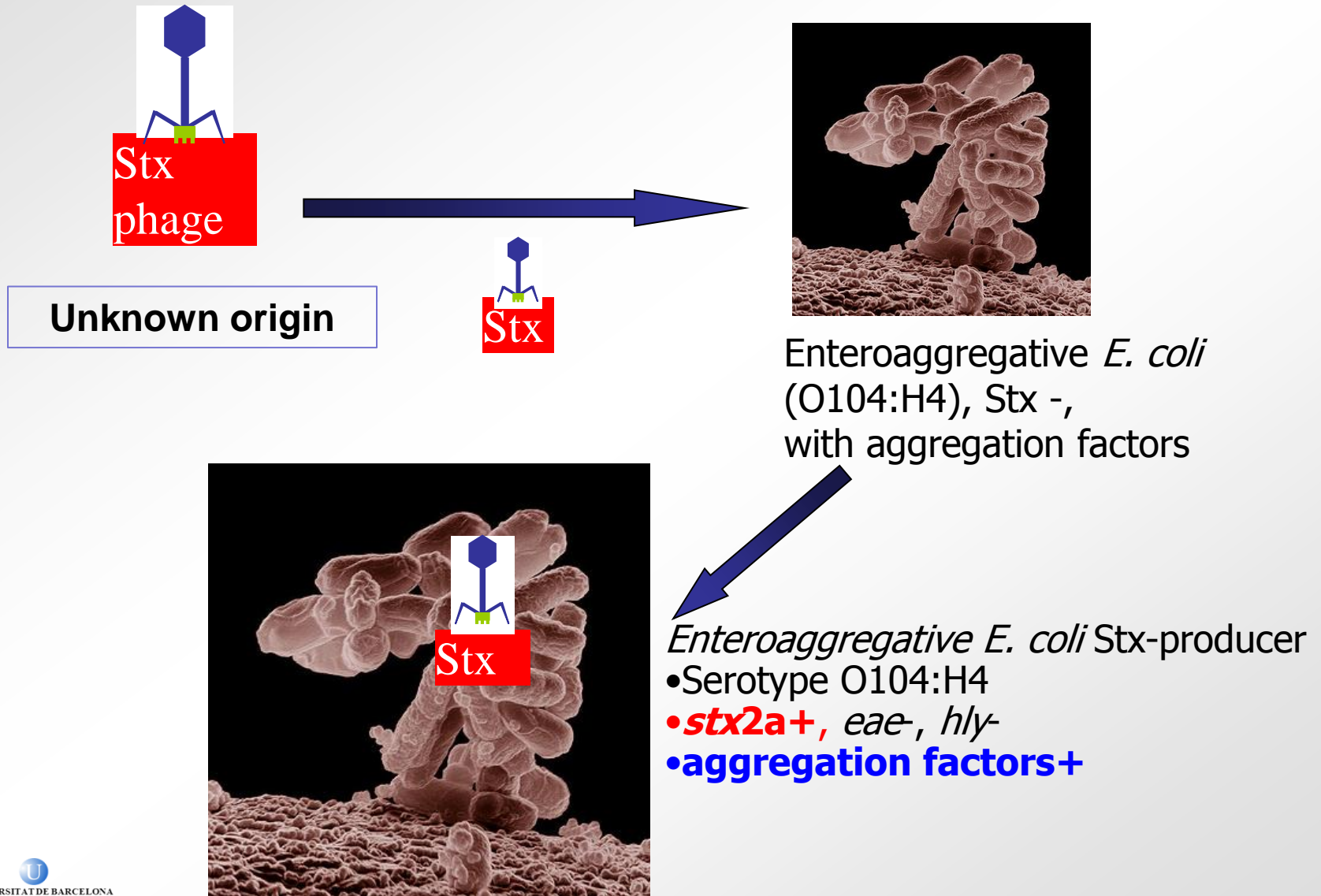
Shiga toxin-producing *E. coli* in Germany. May 2011

2nd June 2011 more than 3255 confirmed cases, 800 with HUS high number of deceased (33).

The 3<sup>rd</sup> most relevant outbreak of *E. coli* in recent history and the greatest in Germany



# Emergence of a new strain



# *What is the origin of O104:H4 ?*

Epidemiological data showed vegetables as the source of the strain.

However, O104:H4 was **NOT** isolated from more than 800 samples of sprouts analyzed.

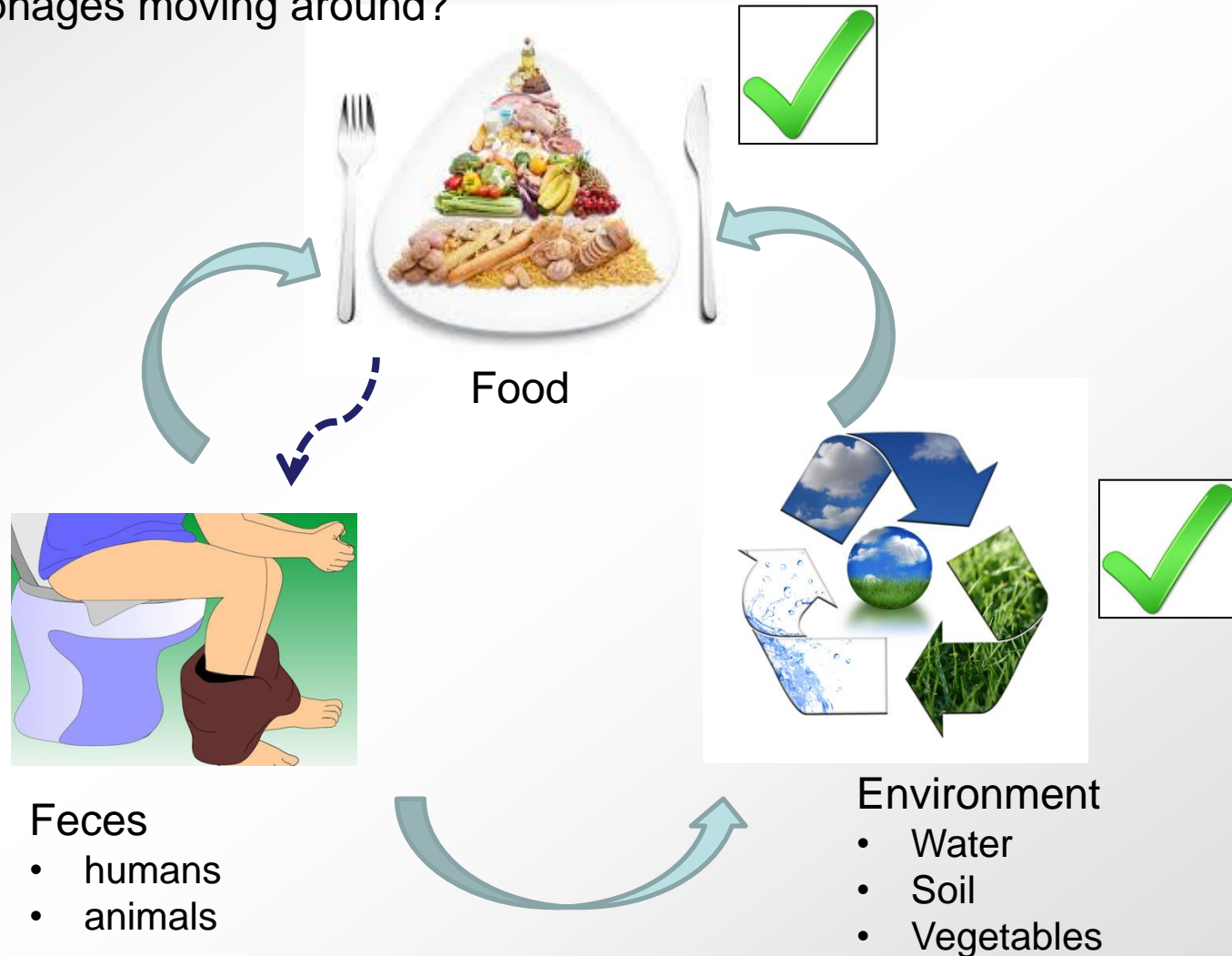
All indicated that **Fenugreek sprouts** from **Egypt**, with a clear coincidence in France and Germany, could be the origin of the causative agent of the German outbreak.





# *What is the origin of Stx phages?*

Are they induced from VTEC?  
Are free-Stx phages moving around?





# Stx phages in food

## Food

Microbiological criteria EU regulation



$10^2$ - $10^5$  Stx phages / 25 g minced beef. 100% of the samples  
 $10^2$ - $10^3$  Stx phages / 25 g fresh salad. 69 % of the samples

Bar: qPCR

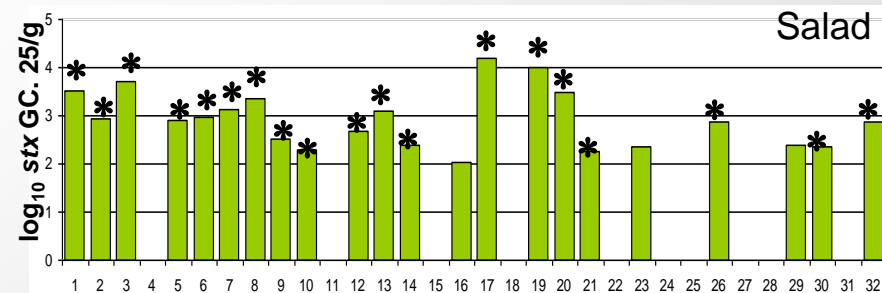
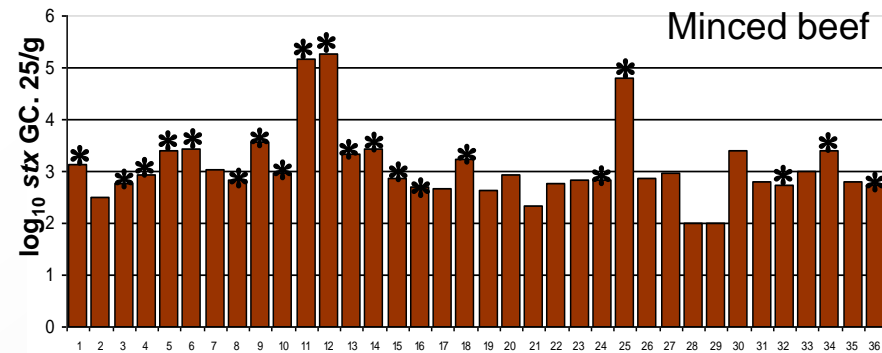
\*: + end point PCR



**At least 50 % of the Stx phages in these samples were infectious**

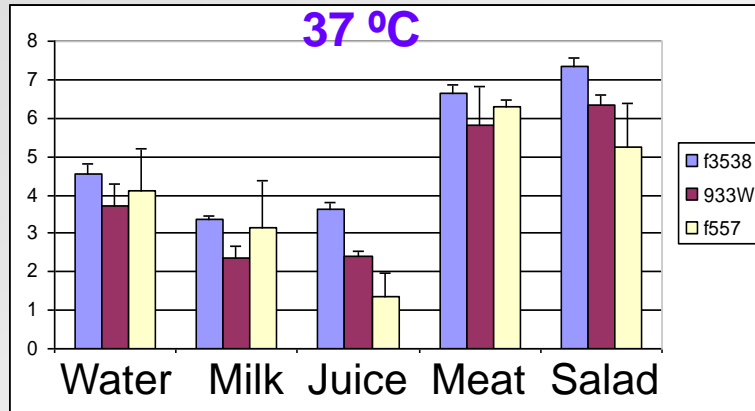
Able to propagate in host strains

Barcelona area has a low incidence of VTEC infections

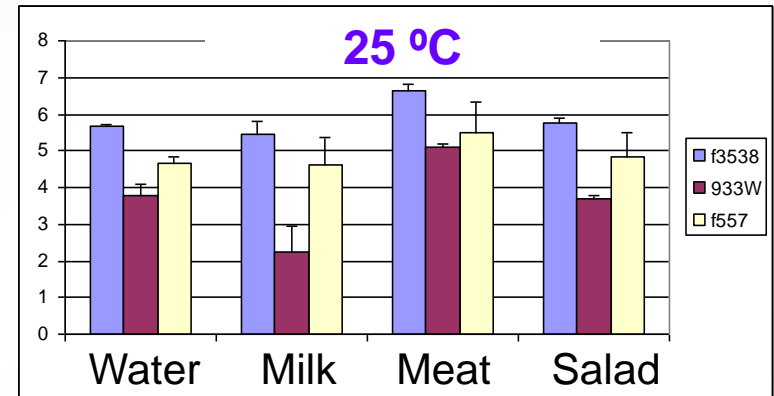
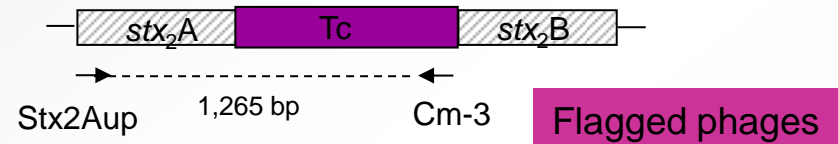


Sample n°

# Stx phage transduction to *E. coli* can take place in food



- To various *E. coli* strains (including O157:H7)
- In liquid or solid matrices
- A minimal number of host and phages are required
- Without inducing agent



Imamovic et al., AEM. 2009

- Not at 4°C!
- Not at low pH (below 4)

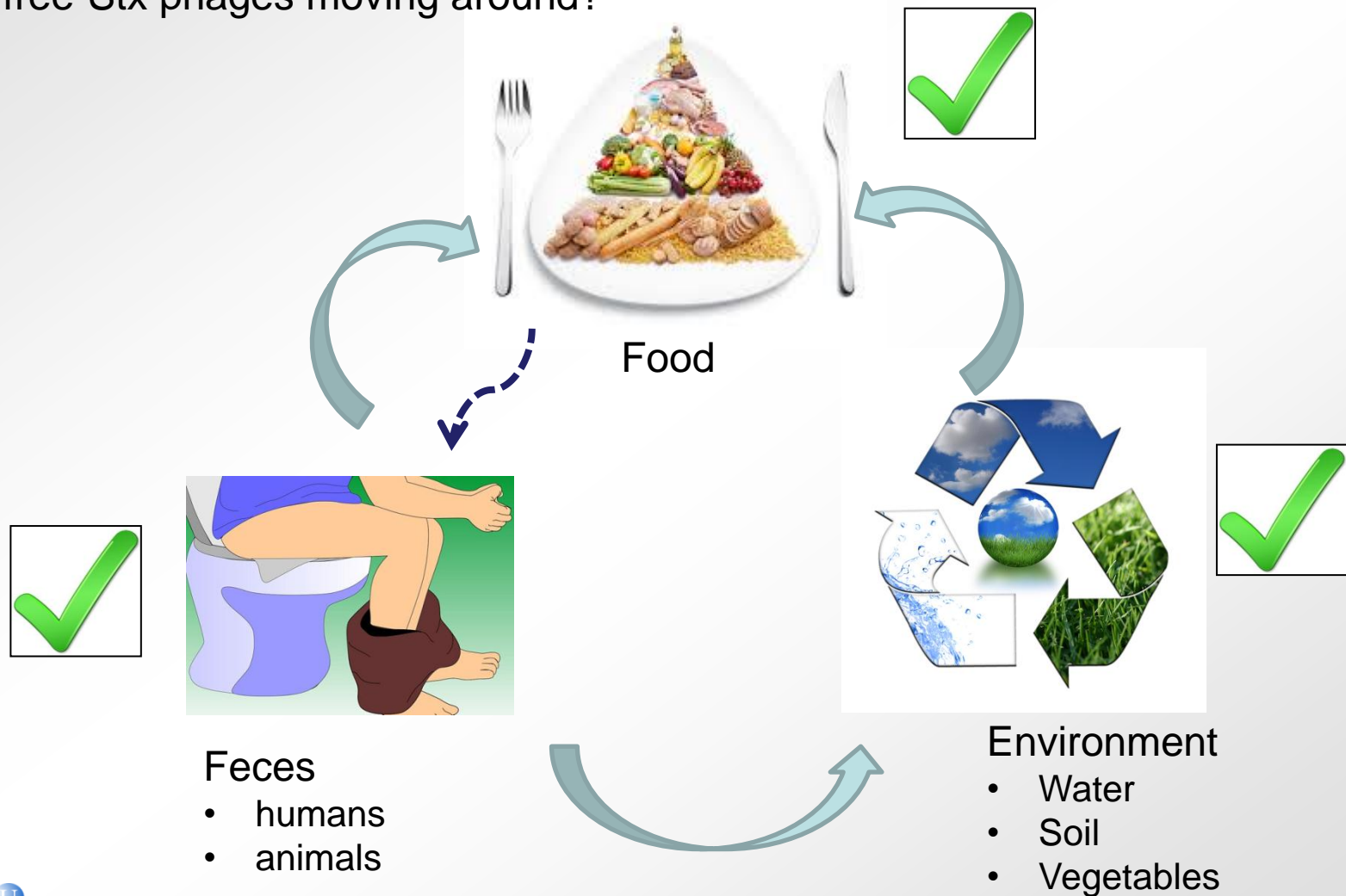
## Transduction in milk at different temperature profiles and cell concentrations

- Transduction was not affected by initial or final concentration of donor or recipient strains.
- occurs when the cells are metabolically active
- it does not take place at low temperatures.

# *What is the origin of Stx phages?*

Are they induced from VTEC?

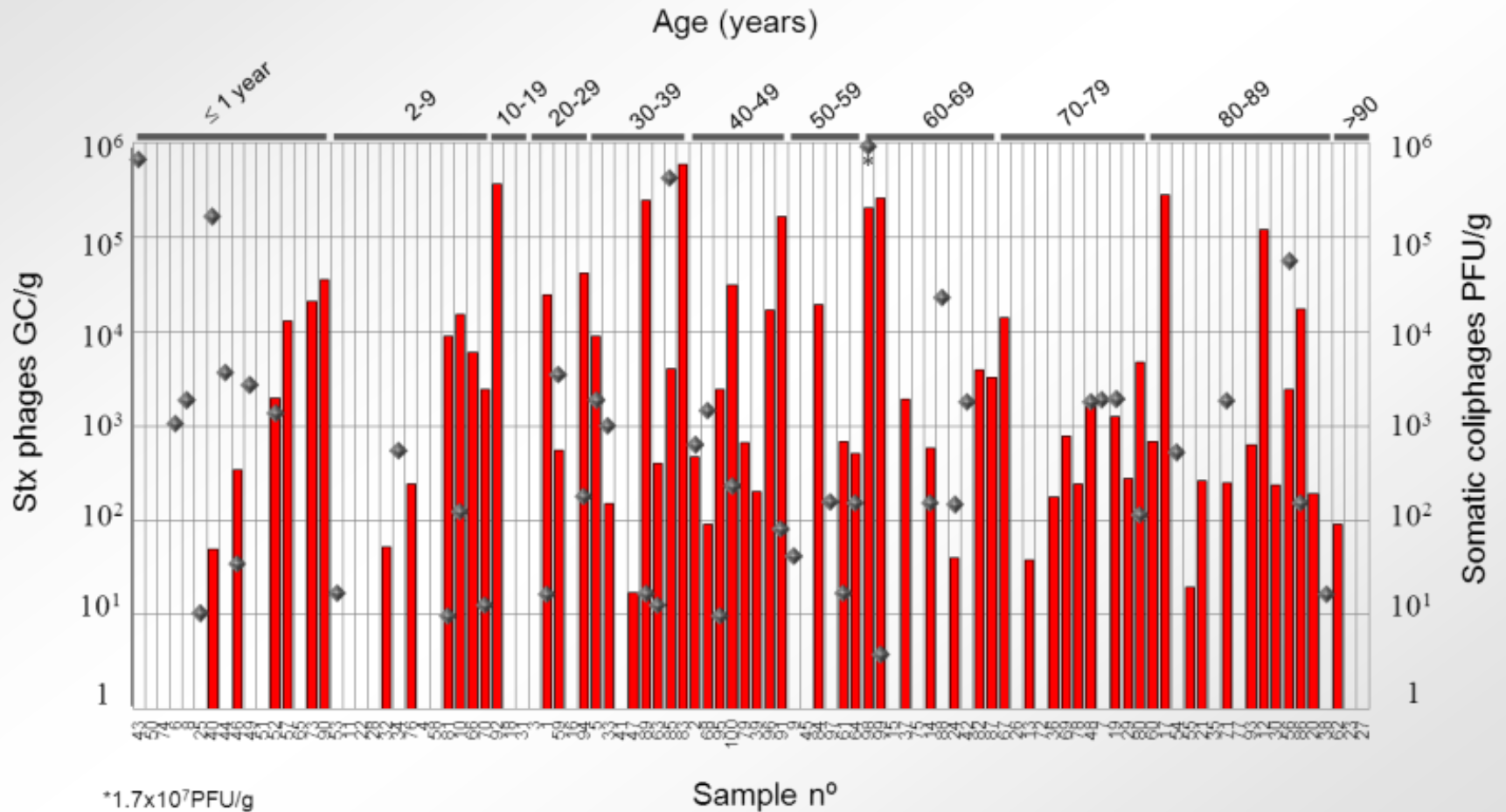
Are free-Stx phages moving around?

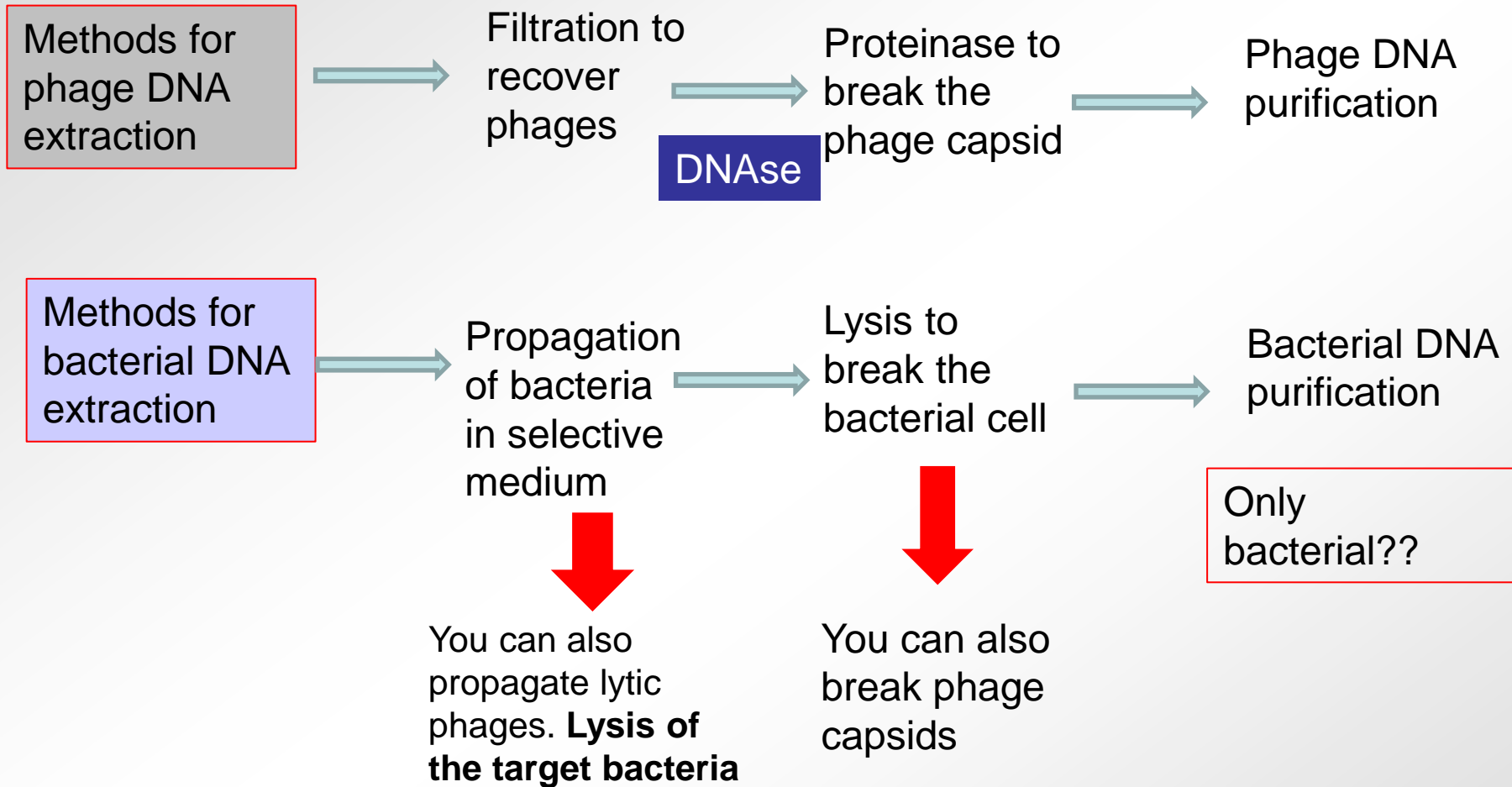


# Stx phages in human feces (healthy individuals)

$2.6 \times 10^4$  Stx phages/g  
62 % positive samples

Infectious Stx phages in 95% of positive samples

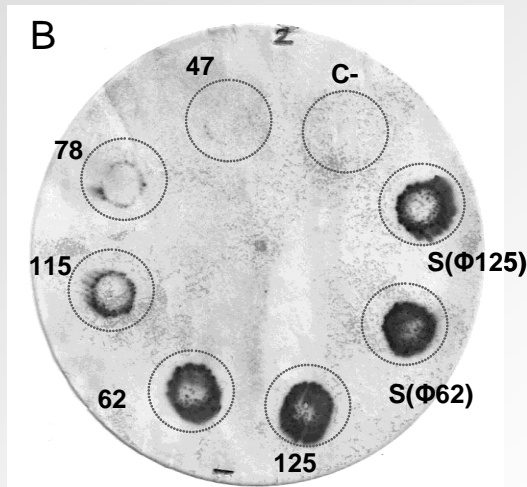




When looking at *stx* genes in stools (or in other samples) by PCR are we always detecting STEC or could be detecting Stx phages?

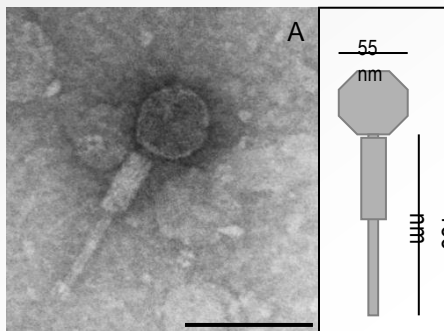
DNA extraction methods can include both!!!

# Other phages in STEC. Cdt phages

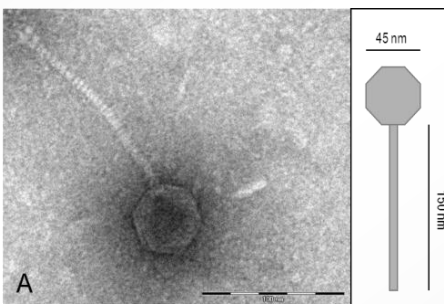


Phages carrying diverse *cdt* variants

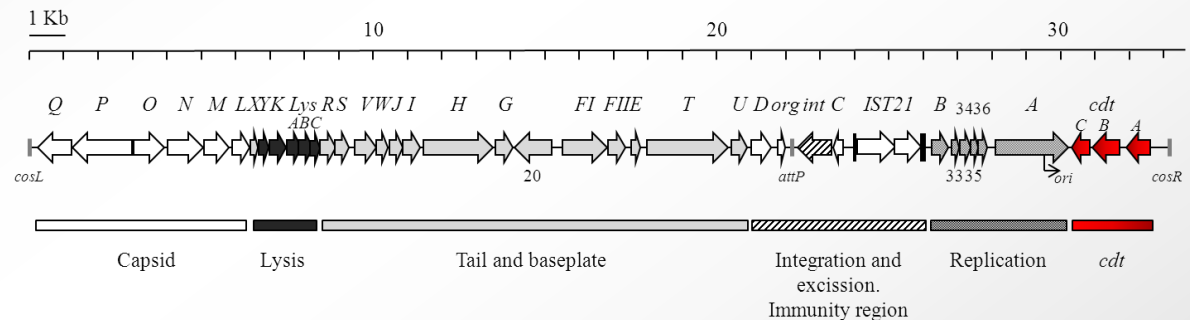
**Cytolethal distending toxin**, causes distension in the cells and blocks mitosis



P2-like phage



Lambda phage



- Variability among phages described
- Transduce *cdt* to *E. coli* and to *Shigella*
- Present in wastewater ( $10^3$  GC/ml)
- High persistence to disinfection



# Phages encoding genes of effector proteins

## Cif bacteriophages



Cif: T3SS mediated effector protein that cause cytostatic effect

Is encoded in a lambdoid prophage present in EPEC and EHEC

Other genes encoding effector proteins (nle) are found in the genome of these phages

Hot spot for insertion of bacterial genes

Loukadis et al.  
J. Bacteriol.  
2008

## nleA bacteriophages

nleA gene and also linked to other effector genes

Apparently these phages were not inducible

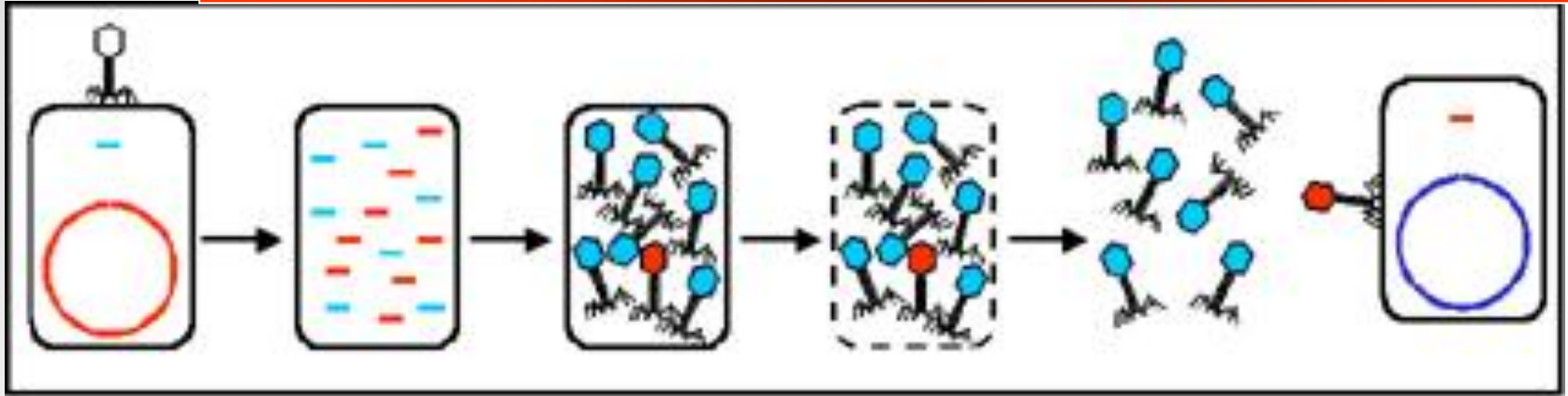
Prophages may have integrated type III effector genes during recombination events in the lytic life cycle

Creuzburg et al. AEM 2011

The majority of functional effector genes are encoded by 9 exchangeable effector loci that lie within lambdoid prophages. Thus, T3S in *E. coli* is linked to a vast phage "metagenome". **The major function of lambdoid prophages in EHEC is to carry T3S effectors.**

Tobe et al., PNAS. 2006

Phages can mobilize **ALL GENES** through **generalized transduction!**



- Phage-derived generalized transducing particles are a phage capsid with bacterial DNA inside.

- 1.-Equal high persistence in the environment
- 2.-They can infect new hosts and transduce these genes
- 3.-They will not release as new phages again

- Some processes increase the amount of transducing particles and hence the frequency of transduction and emergence of new strains.



Anna Allué-Guardia  
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Department of Microbiology  
University of Barcelona

Thanks!

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*mmuniesa @ub.edu*

