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This work was published as: Wuyts *et al.* Whole genome sequence analysis of *Salmonella* Enteritidis PT4 outbreaks from a National Reference Laboratory's viewpoint. PLOS Currents Outbreaks, 11 September 2015

## AIM OF THE STUDY

Added value of whole genome sequencing (WGS) for outbreak investigation?  
WGS data analysis feasible for average NRL or NRC?

### OUTBREAK FLANDERS

Social event: food supplied by catering service → ± 220 guests  
Disease onset: April 23<sup>rd</sup> 2014  
Outbreak: 45 cases with 5 hospitalised persons

### OUTBREAK WALLONIA

Social event: bbq meal prepared by volunteers → ± 300 guests  
Disease onset: May 1<sup>st</sup> 2014  
Outbreak: ± 40 cases with some people hospitalised

Standard questionnaire for epidemiological information + food samples → NRL-FBO  
Isolates of human cases → NRCSS

## MICROBIOLOGICAL INVESTIGATION

All outbreak isolates: serotyped as *Salmonella enterica* subsp. *enterica* serovar Enteritidis

Outbreak	Isolate	Origin	Phage type	MLVA	Antimicrobial resistance
Flanders	S14FP01640	Chocolate mousse <sup>a</sup>	PT4	3-10-5-4-1	Colistin
Flanders	S14FP01642	Chocolate mousse <sup>a</sup>	PT4	3-10-5-4-1	Colistin
Flanders	S14BD01605	Human	PT4	3-10-5-4-1	Colistin
Flanders	S14BD01672	Human	PT4a	3-10-5-4-1	Colistin - ampicillin
Wallonia	S14FP01877	Raw egg <sup>b</sup>	PT4	3-10-5-4-1	Colistin
Wallonia	S14BD01753	Human	PT4	3-10-5-4-1	Colistin

Same source  
or different sources  
for the 2 outbreaks?

<sup>a</sup> Prepared with non-commercial eggs from privately kept laying hens

<sup>b</sup> Non-commercial egg from privately kept laying hens, which were used to prepare tiramisu

## WHOLE GENOME SEQUENCING DATA ANALYSIS

WGS:  
Illumina HiSeq 2000  
100 bp paired-end reads

Raw  
FASTQ reads

CLC Genomics Workbench:  
1) quality trim  
2) *de novo* assembly  
3) read mapping on *S. Enteritidis*  
P125109 chromosome + *de novo*  
assembly of unmapped reads

Center for Genomic Epidemiology:  
CSI Phylogeny<sup>5</sup>

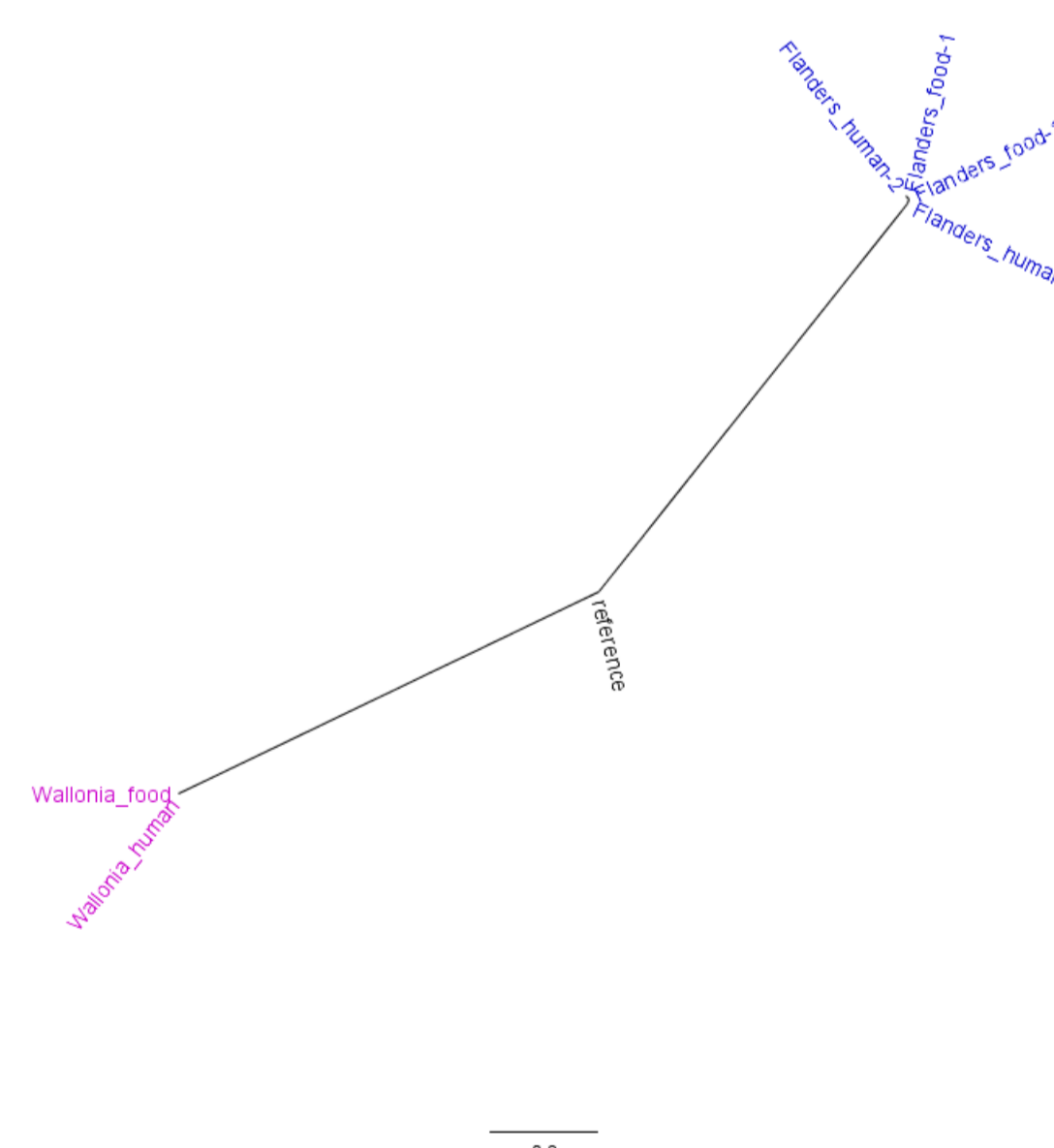
Contigs:  
chromosome  
+ plasmids

Contigs:  
plasmids

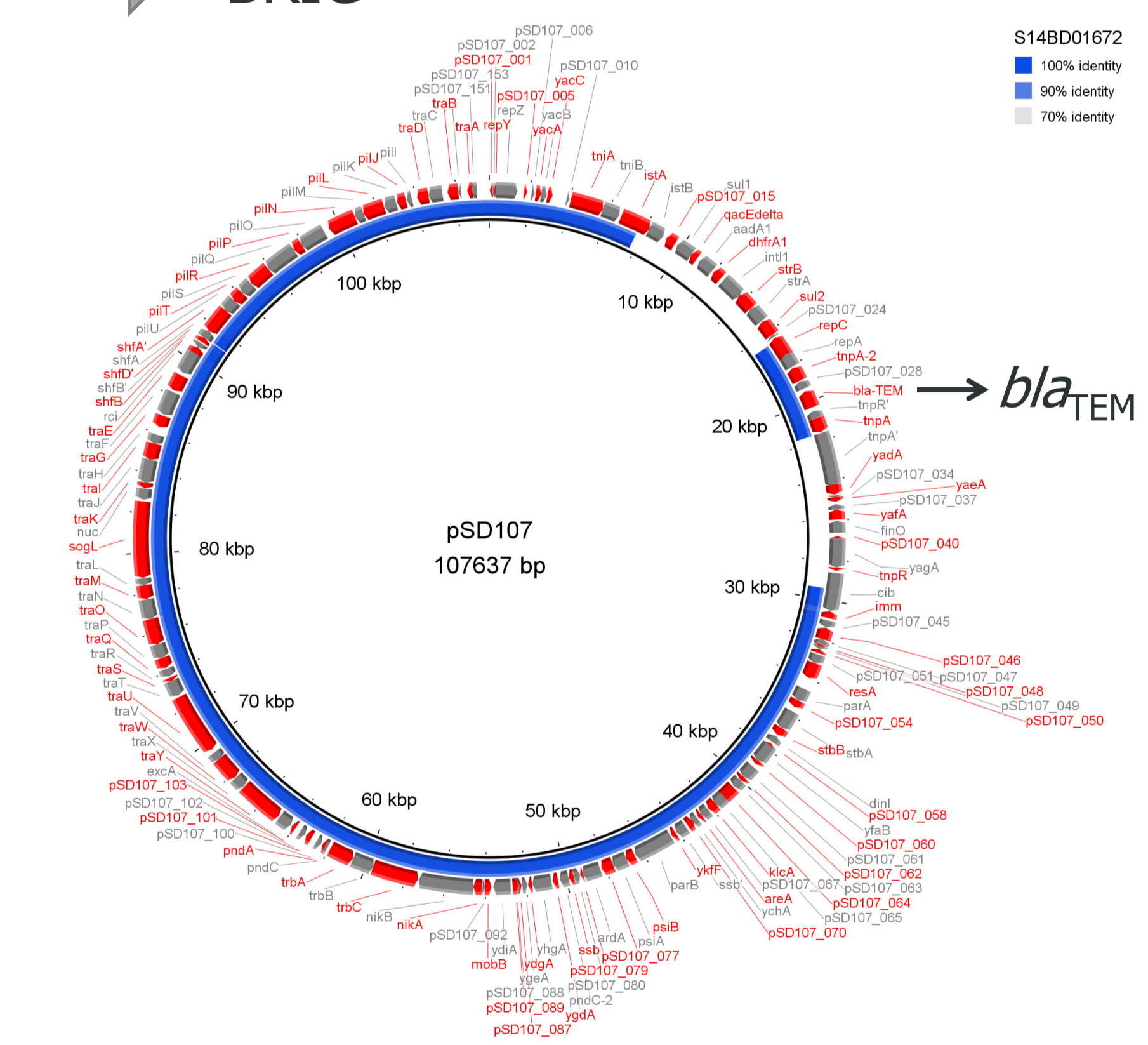
Center for Genomic Epidemiology:  
MLST<sup>1</sup> + ResFinder<sup>2</sup> +  
PlasmidFinder<sup>3</sup>

BRIG<sup>4</sup>

Outbreak	Isolate	MLST	ResFinder	PlasmidFinder
Flanders	S14FP01640	ST-11	-	pSLA5
Flanders	S14FP01642	ST-11	-	pSLA5
Flanders	S14BD01605	ST-11	-	pSLA5
Flanders	S14BD01672	ST-11	<i>bla</i> <sub>TEM-1B</sub>	pSLA5 – pSD107
Wallonia	S14FP01877	ST-11	-	pSLA5
Wallonia	S14BD01753	ST-11	-	pSLA5



CSI Phylogeny



BRIG: pSD107 – S14BD01672

## CONCLUSIONS

WGS: confirmation of link between food and human isolates  
= initial epidemiological and microbiological investigation

SNP analysis: discrimination between both outbreaks  
> initial epidemiological and microbiological investigation

Exploration of plasmids: fine-tuning of SNP analysis results

Added value of WGS for outbreak investigation  
WGS is feasible for an average NRL or NRC

if user-friendly tools are available

Need for database on circulating strains  
to estimate background variability

## REFERENCES

<sup>1</sup>Larsen MV *et al.* (2012) J Clin Microbiol 50(4):1355-1361; <sup>2</sup>Zankari E *et al.* (2012) J Antimicrob Chemother 67(11):2640-2644; <sup>3</sup>Carattoli A *et al.* (2014) Antimicrob Agents Chemother 58(7):3895-3903; <sup>4</sup>Alikhan N-F *et al.* (2011) BMC Genomics 12:402; <sup>5</sup>Kaas RS *et al.* (2014) PLoS ONE 9(8):e104984.