



WAGENINGEN
UNIVERSITY & RESEARCH



Nederlandse Voedsel- en
Warenautoriteit
Ministerie van Economische Zaken

Wageningen Food Safety Research (WFSR)

Rapid detection and differentiation of *Salmonella* species, *S. Typhimurium* and *S. Enteritidis* by multiplex Real-time PCR

Bart Wullings

Team bacteriology K&E



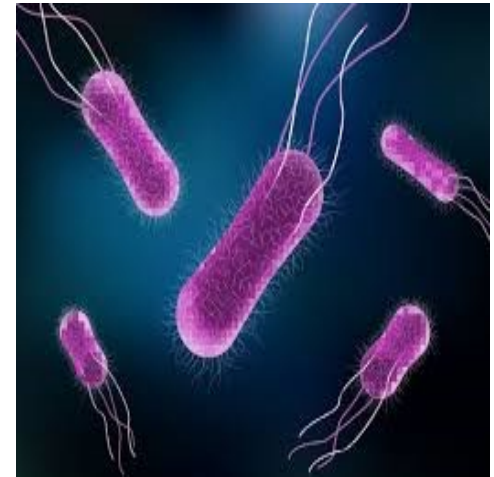
Salmonella

Different strategies:

- *Salmonella* spp.
 - › processed poultry meat and other food samples
- *Salmonella* top 2 serotypes
 - › Enteritidis and Typhimurium
 - › unprocessed poultry meat

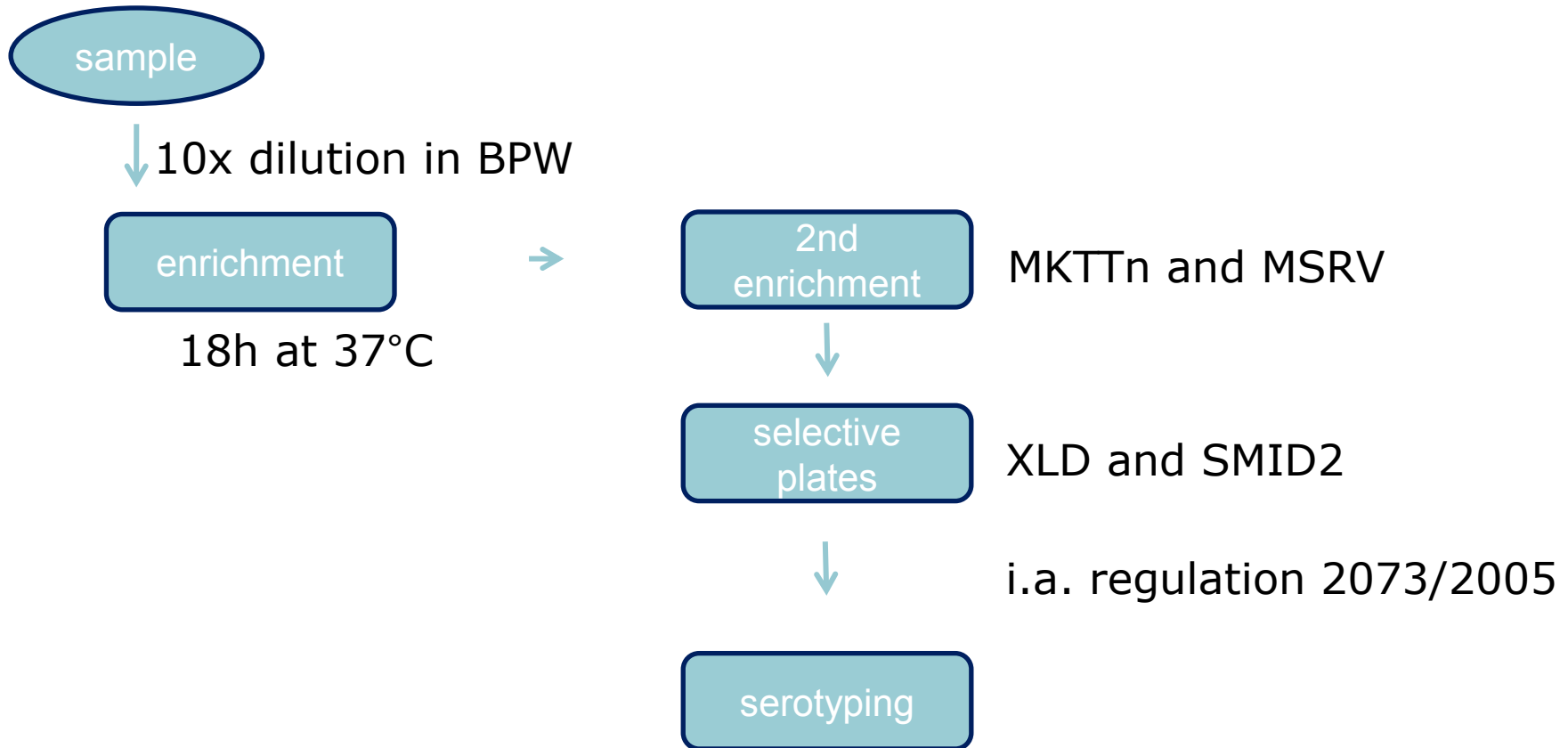
Farm monitoring:

- 6 serotypes of importance
 - › Enteritidis, Typhimurium (incl. monop.), Hadar, Infantis, Virchow and Java





Salmonella ISO protocol ISO 6579-1





Salmonella serotyping (WFSR approach)

- serotyping by Check&Trace (over 300 serotypes)
 - › Includes all main serotypes
 - › microarray based detection

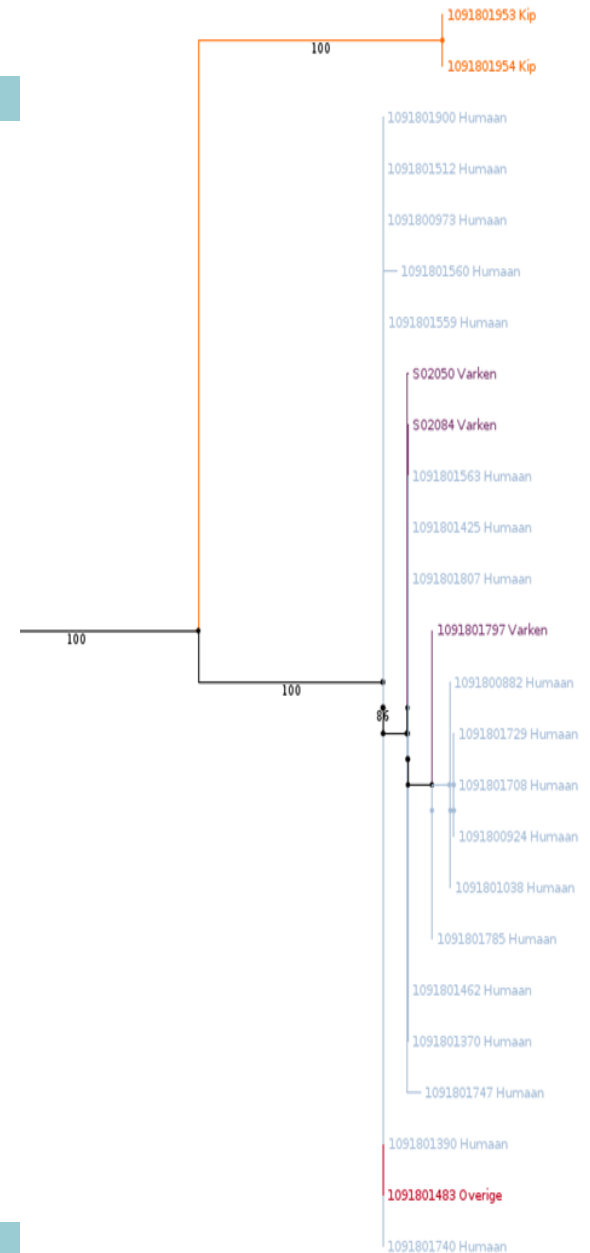


- Additional serotype isolates are send to Public health institute (RIVM)
 - SE and ST are additionally typed by MLVA



Salmonella WGS

- Use of Whole-genome Sequencing analysis
- Quick identification of source
- Collaboration with RIVM (human – food)



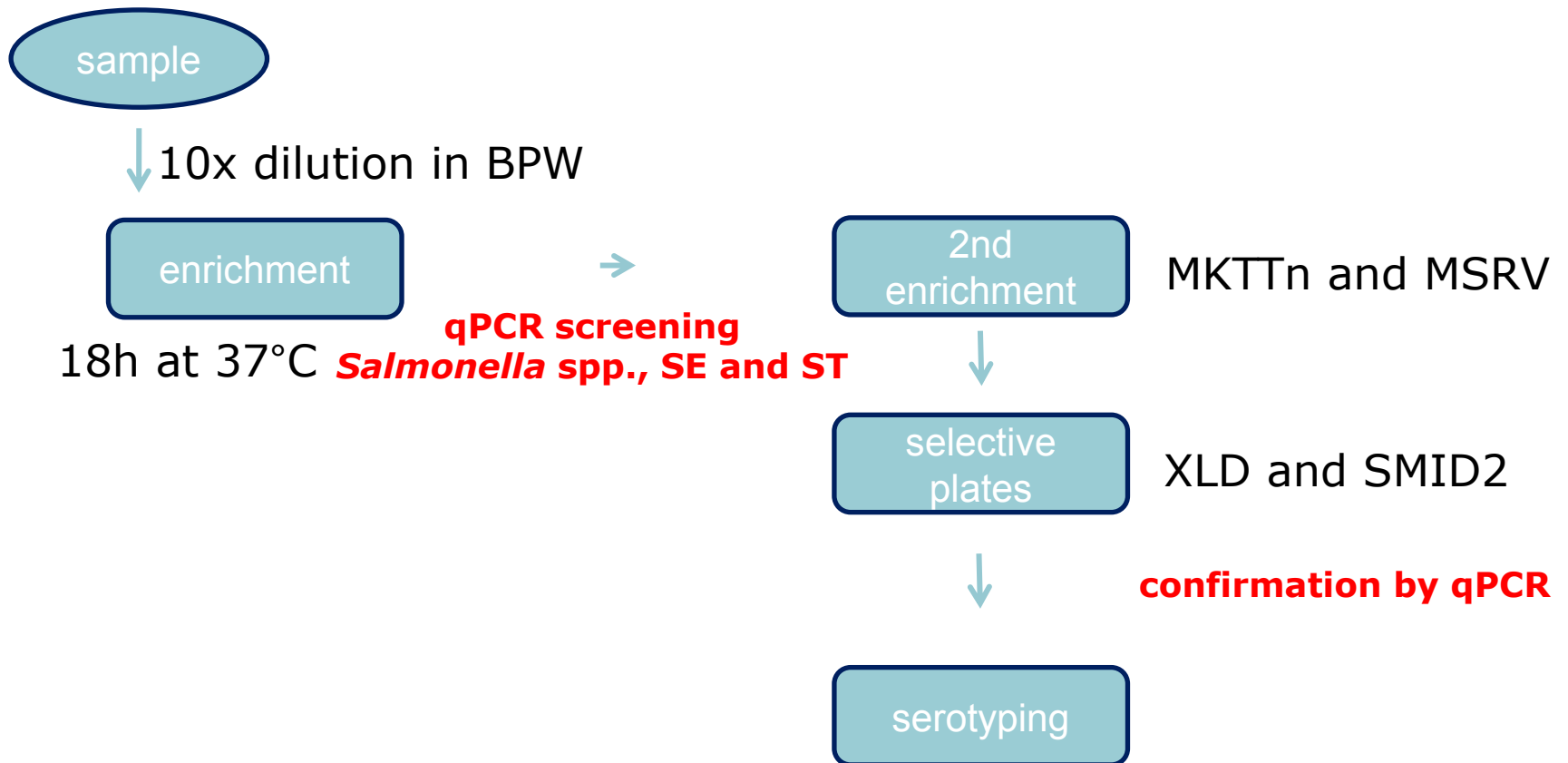


Salmonella monitoring 2018

- Almost 12000 samples tested – 370 positive (3%)
- Meat
 - porcine, bovine, poultry, small ruminants, exotic meat
- Vegetables, herbs and spices
- Fish and sea products
- National and import
 - retail, warehouse, slaughterhouse
 - conventional, organic



Salmonella ISO protocol ISO 6579-1





Publication of PCR



PUBLISH

ABOUT

BROWSE

SEARCH



advanced search

OPEN ACCESS PEER-REVIEWED

RESEARCH ARTICLE

Rapid detection and differentiation of *Salmonella* species, *Salmonella* Typhimurium and *Salmonella* Enteritidis by multiplex quantitative PCR

Raymond Heymans, Amir Vila, Caroliene A. M. van Heerwaarden, Claudia C. C. Jansen, Greetje A. A. Castelijin, Menno van der Voort , Elisabeth G. Biesta-Peters

Published: October 25, 2018 • <https://doi.org/10.1371/journal.pone.0206316>

0 Save	1 Citation
1,599 View	0 Share



Primer & probe design

Target	Gene	Function	PCR product size(bp)
<i>Salmonella</i> spp.	<i>invA</i>	Invasion protein	95
<i>S. Typhimurium</i> (ST)	STM4200	Putative phage tail fiber protein	101
<i>S. Enteritidis</i> (SE)	SEN1392	Predicted phage protein	77



PCR primer/probe specificity

- *InvA* gene for *Salmonella* spp.
 - Target analysed in 30 scientific paper
 - Total 4023 isolates of *Salmonella* spp. and 758 non *Salmonella* spp. isolates screened
 - **Inclusivity: >99,7%**, 11 isolates with different serovars negative
 - **Exclusivity: 100%**

- SEN1392 for SE
 - Analysed in one additional paper
 - Total 156 isolates of SE, 72 ST and 35 non *Salmonella* spp. isolates screened
 - **Inclusivity: 100%**
 - **Exclusivity: ~100%** (one isolates SEN1392 and STM4200 positive)



PCR primer/probe specificity

- STM4200 for ST
 - Total 72 St isolates, 49 isolates of SE and 35 non *Salmonella* spp. isolates screened
 - **Inclusivity:** 100%
 - **Exclusivity:** 94,6%: cross reaction with Derby, Rissen en Goldcoast and one isolate SEN1392 and STM4200 positive

Target	Cross reaction isolates (from 2013)	Poultry	Most
STM4200	5,2% (95/1833)	6% (9/95)	Derby (77/95)



Multiplex qPCR assay and relative accuracy

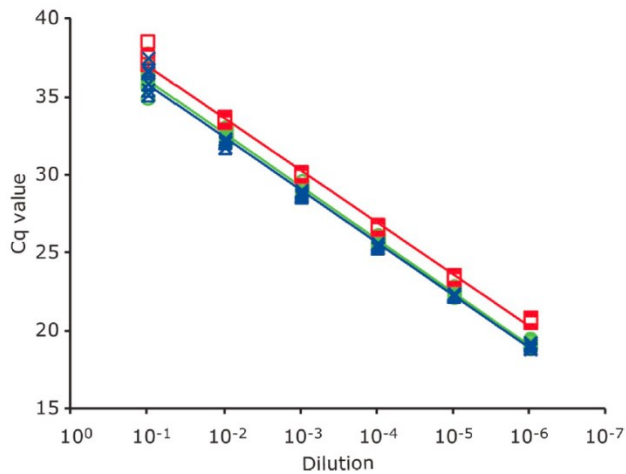


Fig 1. Standard curves for targets *invA*, SEN1392, and STM4200. *invA*: green line and symbols; SEN1392: red line and symbols; STM4200: blue line and symbols.

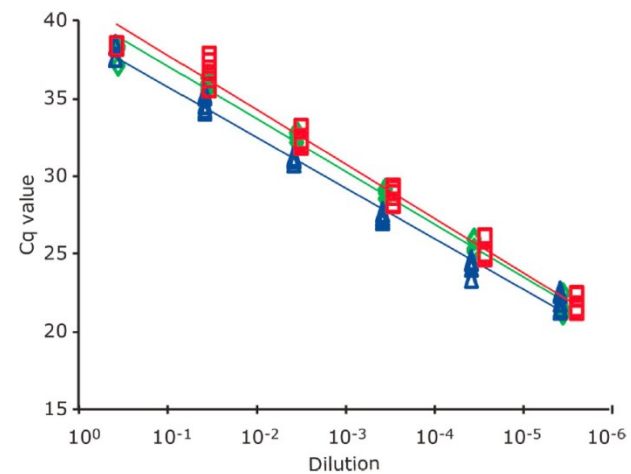


Fig 2. Cell standard curves for target *invA* from *S. Typhimurium* STM4200 for the matrices BPW, Chicken, and curcuma spice. BPW: Blue line and symbols; Chicken: red line and symbols; curcuma spice: green line and symbols.



Level of detection of multiplex qPCR assay

Matrix	Contamination level (CFU/25g)	Screening using Real-time qPCR method	ISO method
Chicken	4	+ (6/6)	+ (6/6)
Fish (Shrimps)	4	+ (5/6)	+ (6/6)
Powdered milk	11	+ (6/6)	+ (6/6)
Herbs/spices	11	+ (6/6)	+ (6/6)
Egg	11	+ (6/6)	+ (6/6)
Feed	11	+ (6/6)	+ (6/6)
<i>Down</i>	8,5	0 (0/6)	+ (3/6)
Swabs	3	+ (6/6)	+ (6/6)
Minced meat	4	+ (6/6)	+ (6/6)
Boot-socks with chicken feces	43/4	+ (3/6)	+ (5/6)



Conclusions (1)

- qPCR methods specific for *Salmonella* spp., Se and ST were design and validated
 - S spp.: inclusivity: >99,7% and exclusivity: 100%
 - SE: inclusivity: 100%, exclusivity: ≈100%
 - ST: inclusivity: 100%, exclusivity: 94,6% (cross reaction with Derby, Rissen en Goldcoast)
- Three qPCR method can be combined in one multiplex assay with high efficiency, linear relationship with and without matrix
- The multiplex qPCR method is validated for screening of enrichments broths and isolates
- Results are comparable to the ISO method, and allows for detect of low levels (around or below 10 CFU/25g) of *Salmonella* in various (food) matrices.



Conclusions (2)

- By using the multiplex qPCR method, instead of conventional culture methods, for screening of enrichments broths, the analysis time of samples is reduced from 48h to 24h.
 - In 2018 \approx 11,000 samples were negative after qPCR screening
- The ability to differentiate between SE and ST makes it a robust tool to easily detect both serotypes as requested by regulation no 2073/2005. However, ST positives must be further confirmed
- This method therefore facilitates effective and faster intervention when contaminated food products are on the market.



Thank you!



Bart Wullings
bart.wullings@wur.nl