An update of the Invasive Bacteria *E. coli-Shigella* Study (IBESS) after an inclusion period of one year

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Introduction

Shigella spp. and entero-invasive *Escherichia coli* (EIEC) are difficult to distinguish and cause a similar disease. Shigellosis is a notifiable disease, while infections with EIEC are not notifiable. To gain insight in diagnostics, incidence, disease outcome, transmission and socio-economic consequences of infections with EIEC and *Shigella* spp., a cross-sectional Invasive Bacteria *E. coli-Shigella* Study (IBESS) has started in January 2016. The outcomes of this study will also provide tools for evidence-based optimalization of national guidelines regarding infectious diseases caused by *Shigella* spp. and EIEC. Fourteen medical microbiological laboratories (MMLs) and their adjacent public health services (PHS) are participating in IBESS. This is a dissemination of preliminary results after one-year inclusion.

Methods

Inclusion criteria: 1) the patient suffers from gastro-enteric complaints, 2) positive diagnostics for *Shigella* or EIEC from a fecal sample is performed by a participating MML as part of regular clinical diagnostics.

The fecal sample, a DNA eluate and, if applicable, an isolated strain or the original selective agar plates were sent to the IBESS research group. All DNA-eluates were screened with a molecular serotyping PCR, an extended culture procedure was applied if original agar plates were provided, and all isolated strains were identified and serotyped with classical methods. Simultaneously, a public health nurse collected clinical and epidemiological data from the patients, from which consent was received. The sample size of IBESS was estimated to be 560 inclusions per year, of which in 225 (40%) cases a strain is isolated and in 335 (60%) cases patient data is available.

Conclusions

-The response percentage of 64.9% was higher than estimated (60.0%), while the percentage of feces with cultured isolates (36.5%) was lower than expected (40%).
- The *wzx*-genes of most isolated *Shigella* spp. were detected in the feces with molecular serotyping.
- For identification, MALDI-TOF analysis was not in concordance with classical methods.
- A reasonable geographic distribution of patients was accomplished. In the north of Noord-Holland and Gelderland inclusion was not optimal.
- The age peaks around 30 and 55 years are in concordance with Dutch demographics, in contrast with the peak around 5 years of age.
- To analyze laboratory data in correlation with patient data, more inclusions are necessary.
- The inclusion period of IBESS will last until January 2018.

Results

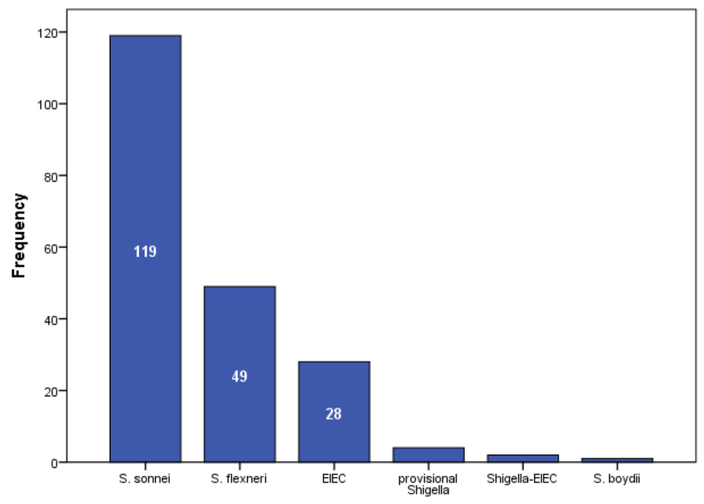
Inclusions and response data collection

Inclusions: 554 patients. Exclusions: 5 patients, of which 2 samples were offered for clinical diagnostics during the same disease episode.

Description	n	%
Inclusions	**554**	
Data collection finalized	**515**	**100**
Physician disagree	-56	-10,9
Patient disagree	-64	-12,4
Total approached patients	**395**	**76,7**
Patients reached by phone	310	60,2
Questionnaires returned by mail	+24	+4,7
Total response for data collection	**334**	**64,9**

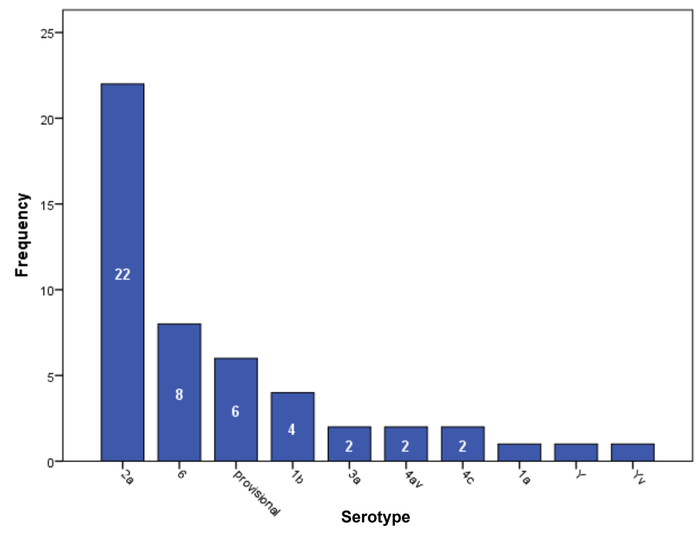
Cultured strains and identifications (n=203)

From the fecal samples of 202 patients, a total of 203 *Shigella* and EIEC strains were isolated.



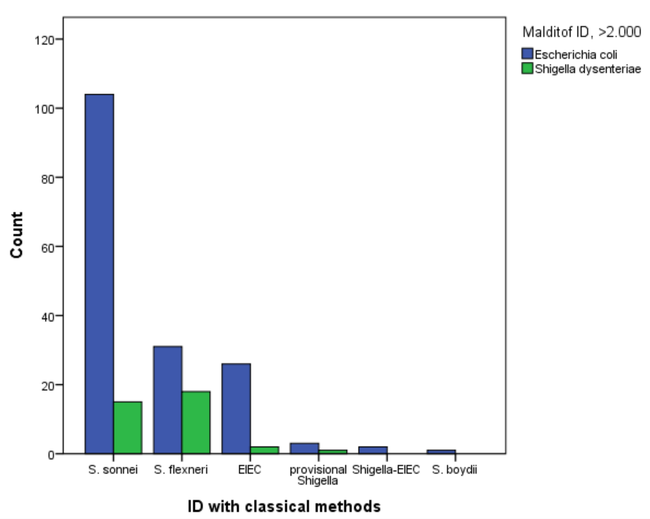
Serotypes *S. flexneri* (n=49)

From the cultured isolates; 49 were *S. flexneri,* displaying10 different serotypes.



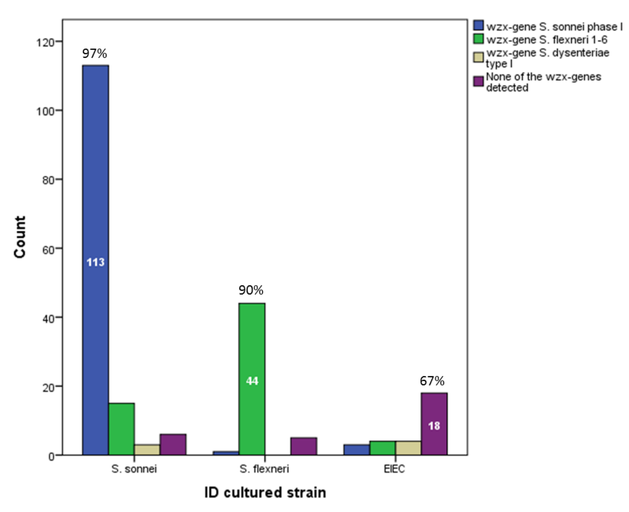
MALDI-TOF vs classical identification (n=203)

MALDI-TOF analysis with Bruker Maldi Biotyper classification software, including Bruker's Security Relevant Library.



Molecular serotyping PCR (n=203)

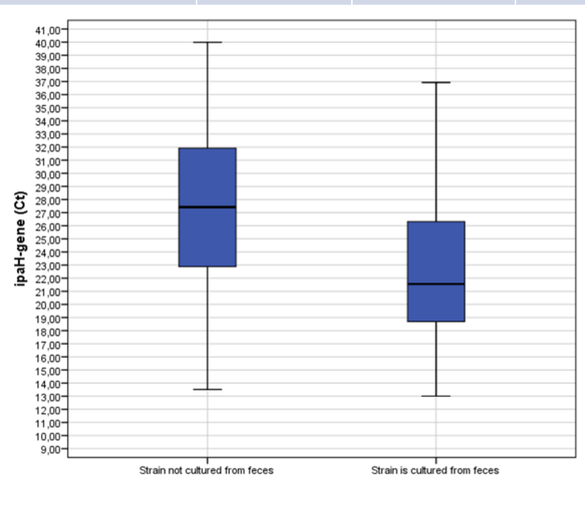
Detection of the *wzx*-genes of *S. sonnei*, *S. flexneri* and *S. dysenteriae* serotype 1 in the feces of which a strain was cultured and identified with classical methods.



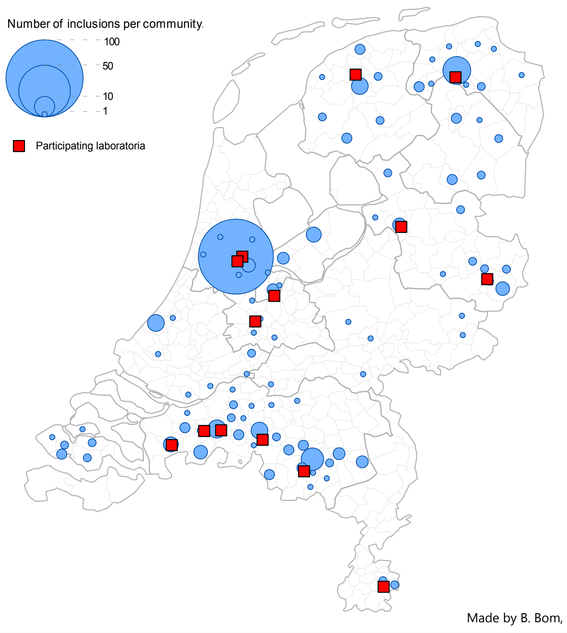
Ct-values of *ipaH*-gene in feces (n=553)

Detected in the molecular serotyping PCR at Certe.

	Cultured	Not cultured	p (T-test)
Ct-value (mean ± SD)	22.60 ± 5.39	27.47 ± 5.41	<0.001



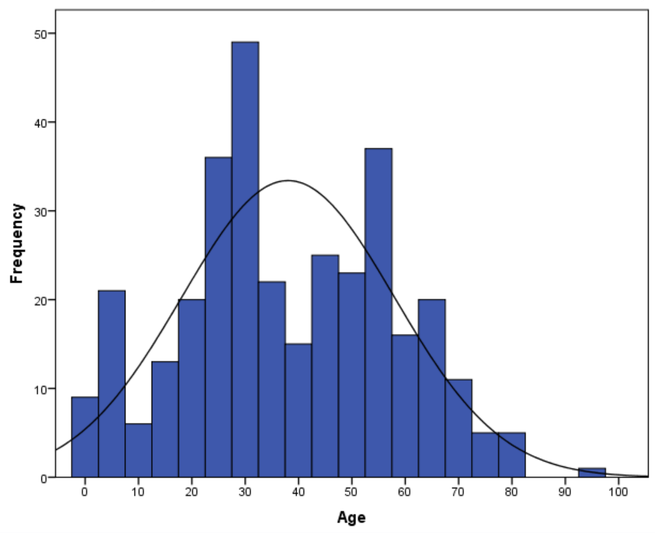
Residence of patients (n=334)



Age and sex of patients (n=334)

Sex: 164 (49.1%) male and 170 (50.9%) female

Age: not normally distributed, median (IQR) = 35.50 (24.00-54.25) year, minimum=0 and maximum 96 year



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