



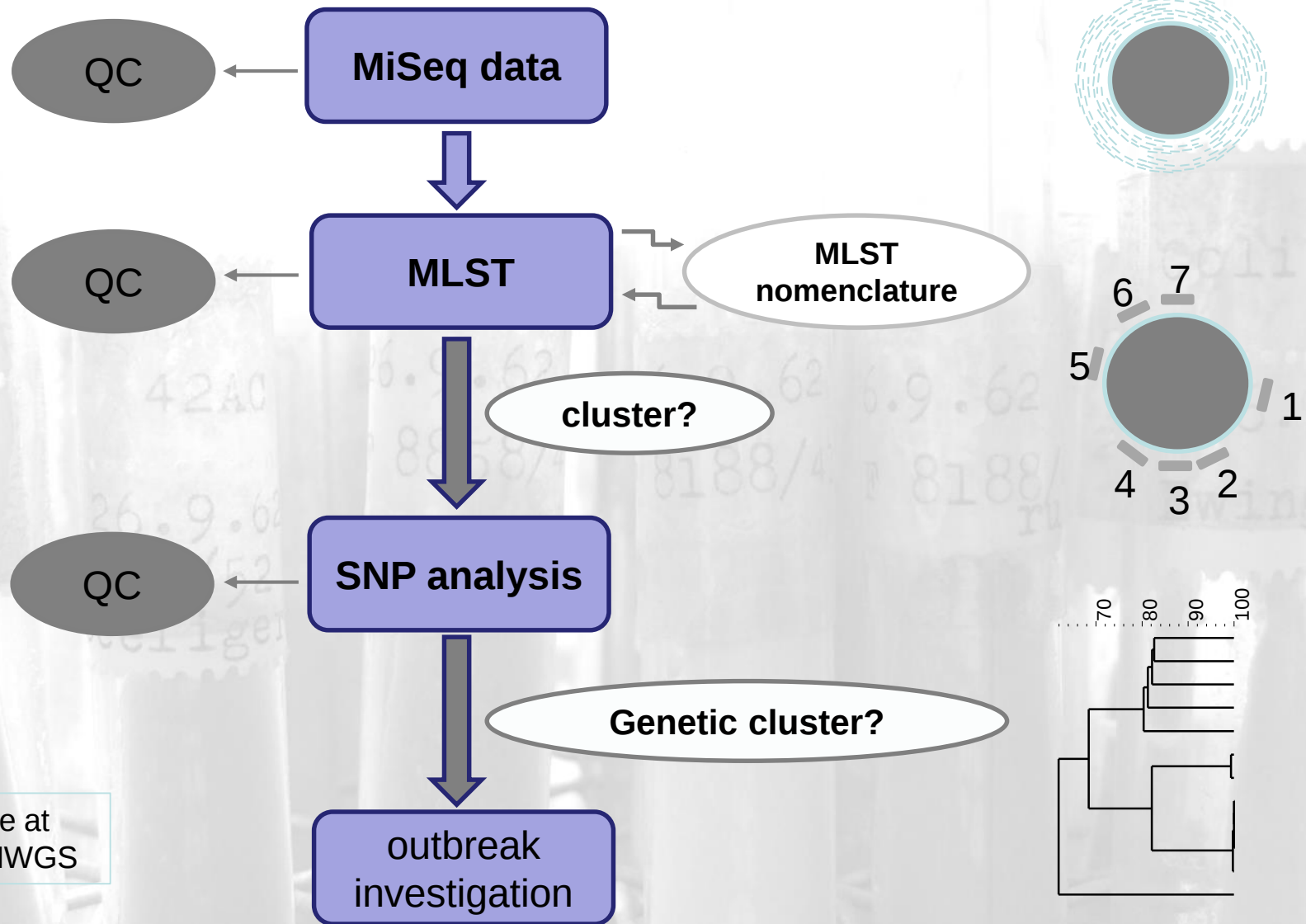
Whole genome sequencing (WGS) surveillance of VTEC and Shigella

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Workflow – outbreak detection

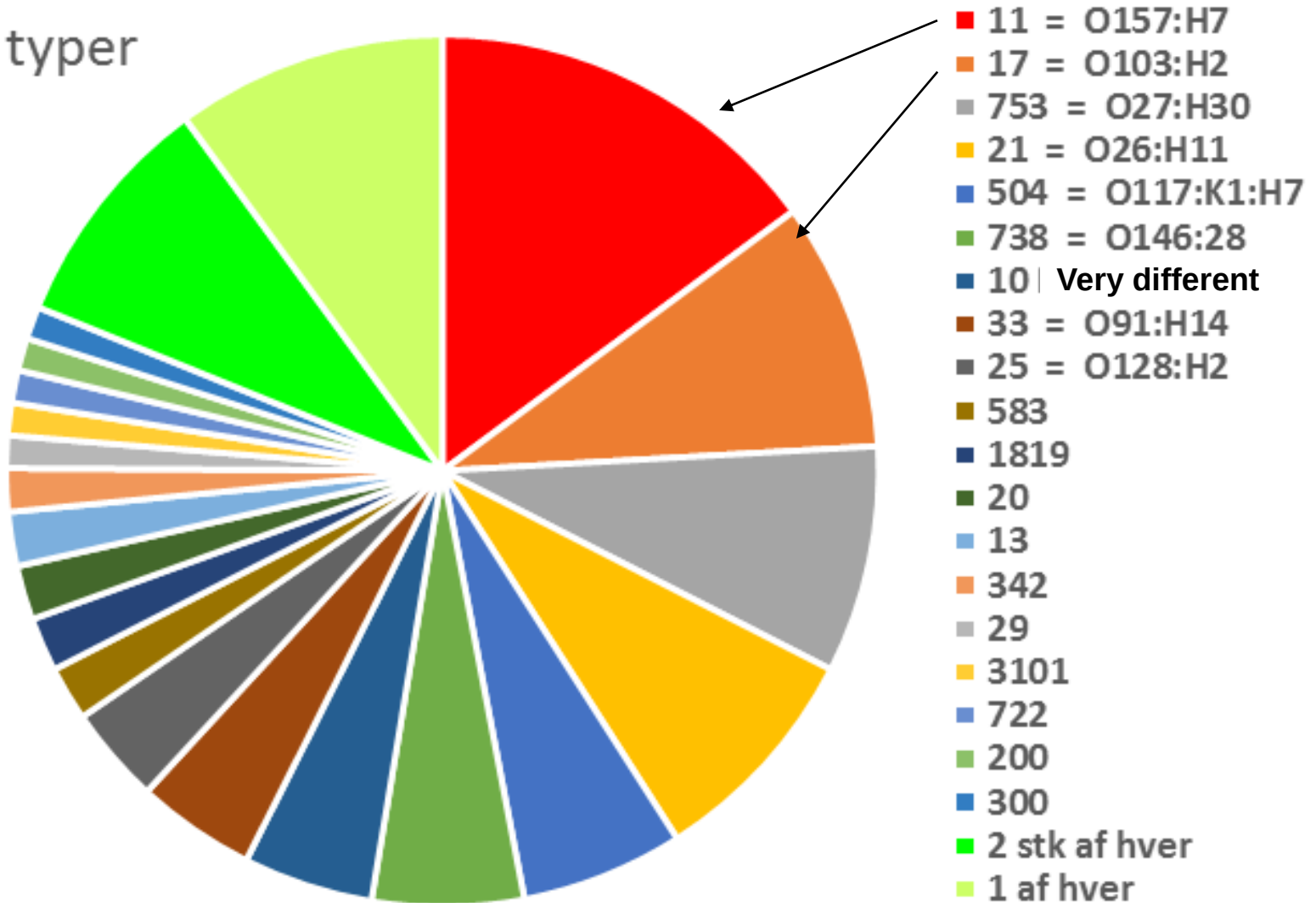


ssi-snp-pipeline at
github.com/PHWGS

Multi Locus Sequence Typing = MLST types (>10 with serotype)



MLST typer





VTEC outbreaks by SNP in 2015

10 Genomic clusters

- 2-3 persons in each cluster
- 4 institutional clusters
- 2 family clusters
- 4 spread over time & place

All interviewed

No sources identified (1 case related to kebab outbreak)

Serotypes:

- O157:H7 (5)
- O103:H2 (2)
- O26:H11 (2)
- O128:H2 (1)



VTEC real-time O:H serotype during 2015

116 isolates typed:

- **33 no phenotype; only WGS**
- **8 only phenotype**
- **~85 phenotype & WGS**

Discrepancies:

- **1 H**
- **2 O**
- **29 non-motile were H typed**

New insights:

- **O91:H14 (ST 33)**
- **New variants of O40**



WGS *E. coli* & VTEC typing 2015-2016

	Total	O group	Htype
n	510	455	443
Percent	100	89	87

	VTEC		
n	283	266	250
Percent	100	94	85

***vtx* subtypes
279 (98.6%)**



WGS *vtx* subtyping 2015-2016

<i>vtx1a</i>	89	<i>vtx2e</i>	4
<i>vtx2b</i>	45	<i>vtx1d</i>	3
<i>vtx1a; vtx2c</i>	24	<i>vtx2a + vtx2c</i>	3
<i>vtx1a; vtx2a</i>	21	<i>vtx1a; vtx2d</i>	2
<i>vtx2f</i>	20	<i>vtx2d</i>	2
<i>vtx1c; vtx2b</i>	17	<i>vtx1a; vtx2a + vtx2c</i>	1
<i>vtx2a</i>	14	<i>vtx1a; vtx2b + vtx2d</i>	1
<i>vtx1c</i>	13		
<i>vtx2c</i>	8		
<i>vtx1a; vtx2b</i>	7		
<i>vtx2g</i>	5		



WGS vtx subtyping 2015-2016

<i>vtx1a</i>	89	<i>vtx2e</i>	4
<i>vtx2b</i>	45	<i>vtx1d</i>	3
<i>vtx1a; vtx2c</i>	24	<i>vtx2a</i> + <i>vtx2c</i>	3
<i>vtx1a; vtx2a</i>	21	<i>vtx1a; vtx2d</i>	2
<i>vtx2f</i>	20	<i>vtx2d</i>	2
<i>vtx1c; vtx2b</i>	17	<i>vtx1a; vtx2a</i> + <i>vtx2c</i>	1
<i>vtx2a</i>	14	<i>vtx1a; vtx2b</i> + <i>vtx2d</i>	1
<i>vtx1c</i>	13		
<i>vtx2c</i>	8		
<i>vtx1a; vtx2b</i>	7	HUSEC: <i>vtx2a</i> & <i>vtx2d</i>	
<i>vtx2g</i>	5		

44 = 15.8%

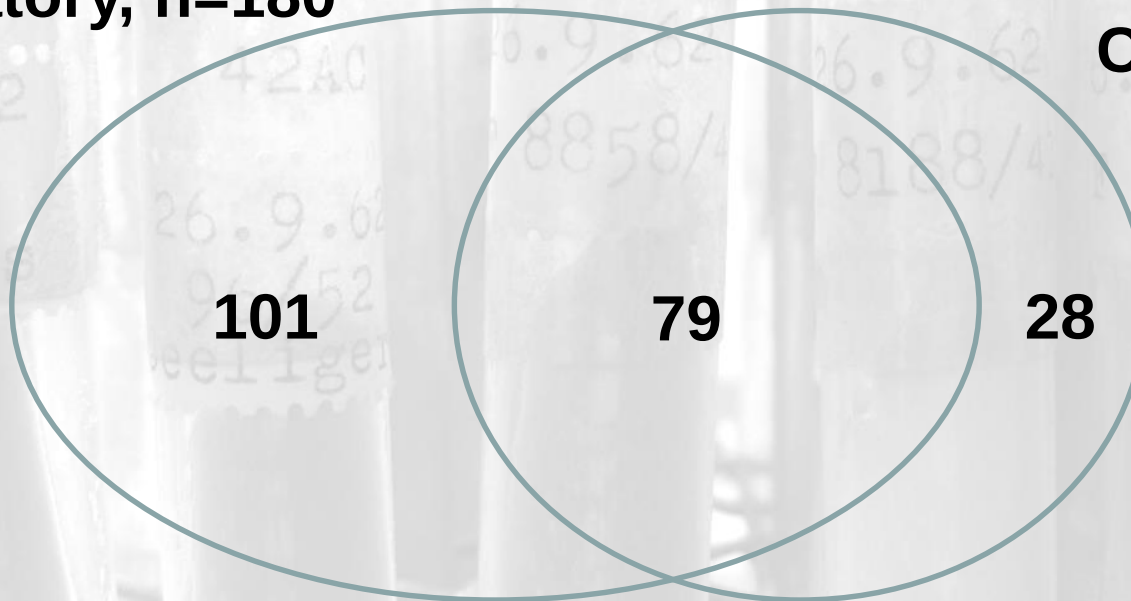


Shigella notification clinical & lab 2015

Shigella notifications 2015 total = 208

Laboratory, n=180

Clinical, n=107





Shigella Laboratory 2010-15

Type	2010	2011	2012	2013	2014	2015	Total
EIEC	36	14	17	14	28	20	129
<i>ipaH</i>	14	11	7	1	2		35
<i>S. boydii</i>	6	4	2	4	3	6	25
<i>S. dysenteriae</i>	2	2	5	1	1	3	14
<i>S. flexneri</i>	45	39	18	20	24	21	167
<i>S. sonnei</i>	77	66	38	57	70	68	376
<i>S. spp.</i>	6	2	4	18	12	70	112
Total	186	138	91	115	140	188	858



Clinical Shigella notifications 2010-15

Type	2010	2011	2012	2013	2014	2015	Total
Not specified	2	1	3	2		5	13
S.boydii	6	4	2	3	2	3	20
S.dysenteriae	2	4	5	1	3	13	28
S.flexneri	21	26	10	18	15	11	101
S.sonnei	57	53	36	57	35	25	263
Unknown	3	1	1	7	18	39	69
NA		2	2	6	3	21	34
Total	91	91	59	94	76	117	528



Shigella/EIEC in MiBa 2015

Laboratory results	n
<i>ipaH</i> Invasion associated gene	5
Shigella species DNA	9
Shigella species/Enteroinvasive <i>E. coli</i> DNA	175
Total	189

Country of infection Shigella 2015

Country	Clinical notification		Laboratory	
	n	Percent	n	Percent
Denmark	23	20	11	6
Egypt	13	11	10	6
India	10	9	12	7
Pakistan	10	9	1	1
Other	59	50	50	28
NA	2	2	96	53
Total	117	100	180	100

WGS Shigella serotyping; n = 76

ST type	Serotype	Species	n	Shigella
1273	O32:H45	<i>Shigella boydii</i>	1	B14
145	O147:H45	<i>Shigella boydii</i>	2	F6 (1-5)
152	:H16	<i>Shigella sonnei</i>	32	SS
5517	:H16	<i>Shigella sonnei</i>	3	SS
245	O13:H14	<i>Shigella flexneri</i>	8	F2a
630	O13:H14	<i>Shigella flexneri</i>	1	F2a
270	O136:H7	<i>Escherichia coli</i>	1	EIEC
270	O28ac:H7	<i>Escherichia coli</i>	3	B13
311	O28ac:H7	<i>Escherichia coli</i>	2	B13
4627	O28ac:H7	<i>Escherichia coli</i>	1	B13
281	O144:H25	<i>Escherichia coli</i>	4	D10
4267	O8/O40:H19	<i>Escherichia coli</i>	3	D9
4627	O173:H7	<i>Escherichia coli</i>	1	
59	O1:H7	<i>Escherichia coli</i>	1	
6	O121:H30	<i>Escherichia coli</i>	2	D10
99	O96:H19	<i>Escherichia coli</i>	10	EIEC
Unknown	O38:H26	<i>Escherichia coli</i>	1	D8

Classical & **New** EIEC O:H serotypes



O group

H antigen

O28ac	H-	= <i>S. boydii</i> 13
O29	H-	= <i>S. dysenteriae</i> 11
O112ac	H-	= <i>S. dysenteriae</i> 2
O112ab		= <i>S. boydii</i> 15
O115	H-	
O121	H-	= <i>S. dysenteriae</i> 7
O124	H-; H7; H30; H32	= <i>S. dysenteriae</i> 3
O135	H-	
O136	H-	= <i>S. dysenteriae</i> 3/SB1?
O143	H-	= <i>S. boydii</i> 8
O144	H-; H25	= <i>S. dysenteriae</i> 10
O152	H-	= <i>S. dysenteriae</i> 12
O159	H2	
O164	H-	= <i>S. dysenteriae</i> 3 ?
O167	H-; H4; H5	= <i>S. boydii</i> 3
O173	H-	

Shigella IDs & **New** EIEC O groups



O40

~ *S. dysenteriae* 9/sonnei S?

O58

S. dysenteriae 5

O130

H-

~ *S. dysenteriae* 6 (SR form)

O147

S. flexneri 6 & 1-5)

O148

~ *S. dysenteriae* 1

O149

S. boydii 1

O150

S. dysenteriae 13

O168

S. dysenteriae 4

Shigella IDs & **New** EIEC O groups



O9	H-	
O13	H-	<i>S. flexneri</i> (F2a)
O15	H-	
O32		<i>S. boydii</i> 14
O36	H14	
O38		<i>S. dysenteriae</i> 8
O53		<i>S. boydii</i> 4
O44	H-	
O79		<i>S. boydii</i> 5
O82, O87?		<i>S. flexneri</i> 6?
O87		<i>S. boydii</i> 2
O89	H19	
O96	H19	Italian and English outbreak strain
O105		<i>S. boydii</i> 11
O106		<i>S. boydii</i> 1a, 4a
O129		<i>S. flexneri</i> 5b and Y
O131		<i>S. flexneri</i> X
O130	H-	~ <i>S. dysenteriae</i> 6 (SR form)
O132	H21	
O135		<i>S. flexneri</i> 1b, 3a and 5b
O151		<i>S. dysenteriae</i> 9
OX183		<i>S. boydii</i> 10
OX188		<i>S. boydii</i> 16



SHIGELLA INTERNATIONAL MEETING

May, 28-29, 2012 – Buenos Aires – Argentina

Funding for this meeting was made possible by the Bill & Melinda Gates Foundation, PATH and PAHO/WHO

“as a long term goal, it was proposed to revise the classification of *Shigella* spp. including it in the same scheme as *Escherichia coli*, given the evidence of close genetic relation between these organisms...”

2nd version: . . . “As a long term goal, **some participants** proposed that the classification of *Shigella* spp. should be revised and **perhaps** to fold it into the same scheme as *Escherichia coli* . . . “!!