

Recap Exercise 2

ResFinder

Known Mutations

parE

No mutations found in parE

parC

No known mutations found in parC

folP

No mutations found in folP

gyrA

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
gyrA p.S83A	TCG → GCG	S → A	Quinolones,Fluoroquinolones	15848289

pmrB

No known mutations found in pmrB

pmrA

No mutations found in pmrA

16S_rrsB

No known mutations found in 16S_rrsB

16S_rrsH

No known mutations found in 16S_rrsH

gyrB

No mutations found in gyrB

ampC

No known mutations found in ampC

16S_rrsC

No known mutations found in 16S_rrsC

23S

No known mutations found in 23S

GyrA and *GyrB* in *E. coli* are difficult cases as it is often a **combination** of mutations that leads to resistance

- According to ResFinder-3.0, the *E. coli* strain that caused the German outbreak has **one** point mutation in *gyrA* (S83A)
- Mutations at this position are usually related to resistance to quinolones/ flouroquinolones (ciprofloxacin, nalidixic acid)
- According to Grad et al, 2012, the *E. coli* strains are resistant to nalidixic acid, while susceptible to ciprofloxacin
- For ciprofloxacin, studies have shown that single mutations in *gyrA* only lead to modest increment in resistance - isolates would still be considered clinically susceptible. Only a second mutation in *gyrA* or a mutation in *parC* leads to a clinical level of resistance (PMID: 15942878)
- ResFinder-3.0 currently outputs resistance according to the environmental break point, not the clinical breakpoint

ResFinder

Unknown Mutations

parC		
Mutation	Nucleotide change	Amino acid change
parC p.E62K	GAA → AAA	E → K

gyrA		
No unknown mutations found in gyrA		

pmrB		
Mutation	Nucleotide change	Amino acid change
pmrB p.D283G	GAC → GGC	D → G
pmrB p.Y358N	TAC → AAC	Y → N

16S_rrsB	
Mutation	Nucleotide change
16S_rrsB r.80A>C	A → C
16S_rrsB r.89T>G	T → G
16S_rrsB r.93T>C	T → C
16S_rrsB r.250A>T	A → T
16S_rrsB r.253A>T	A → T
16S_rrsB r.273T>A	T → A
16S_rrsB r.474G>A	G → A

16S_rrsH	
Mutation	Nucleotide change
16S_rrsH r.80A>C	A → C
16S_rrsH r.89T>G	T → G
16S_rrsH r.90C>T	C → T
16S_rrsH r.93T>C	T → C
16S_rrsH r.250A>T	A → T
16S_rrsH r.253A>T	A → T
16S_rrsH r.273T>A	T → A
16S_rrsH r.1036A>G	A → G
16S_rrsH r.1120T>C	T → C

ampC		
Mutation	Nucleotide change	Amino acid change

SerotypeFinder-1.1 Server - Results

H type						
Serotype gene	%Identity	Query/HSP length	Contig	Position in contig	Predicted serotype	Accession number
<i>fliC</i>	100.00	1050 / 1050	Supercontig_1.4	70365..71414	H4	AJ605764

O type						
Serotype gene	%Identity	Query/HSP length	Contig	Position in contig	Predicted serotype	Accession number
<i>wzx</i>	100.00	1278 / 1278	Supercontig_1.4	215774..217051	O104	KB021482
<i>wzy</i>	99.64	1113 / 1113	Supercontig_1.4	218280..219392	O104	AF361371

Predicted Serotype: O104:H4

[extended output](#)

[Results as text](#)

[Results tab separated](#)

[Hit in genome sequences](#)

[Serotype gene sequences](#)

Selected %ID threshold: 85.00 %

Selected minimum length: 60 %

Input Files: *escherichia_coli_c227-11.fsa*

CITATIONS

For publication of results, please cite:

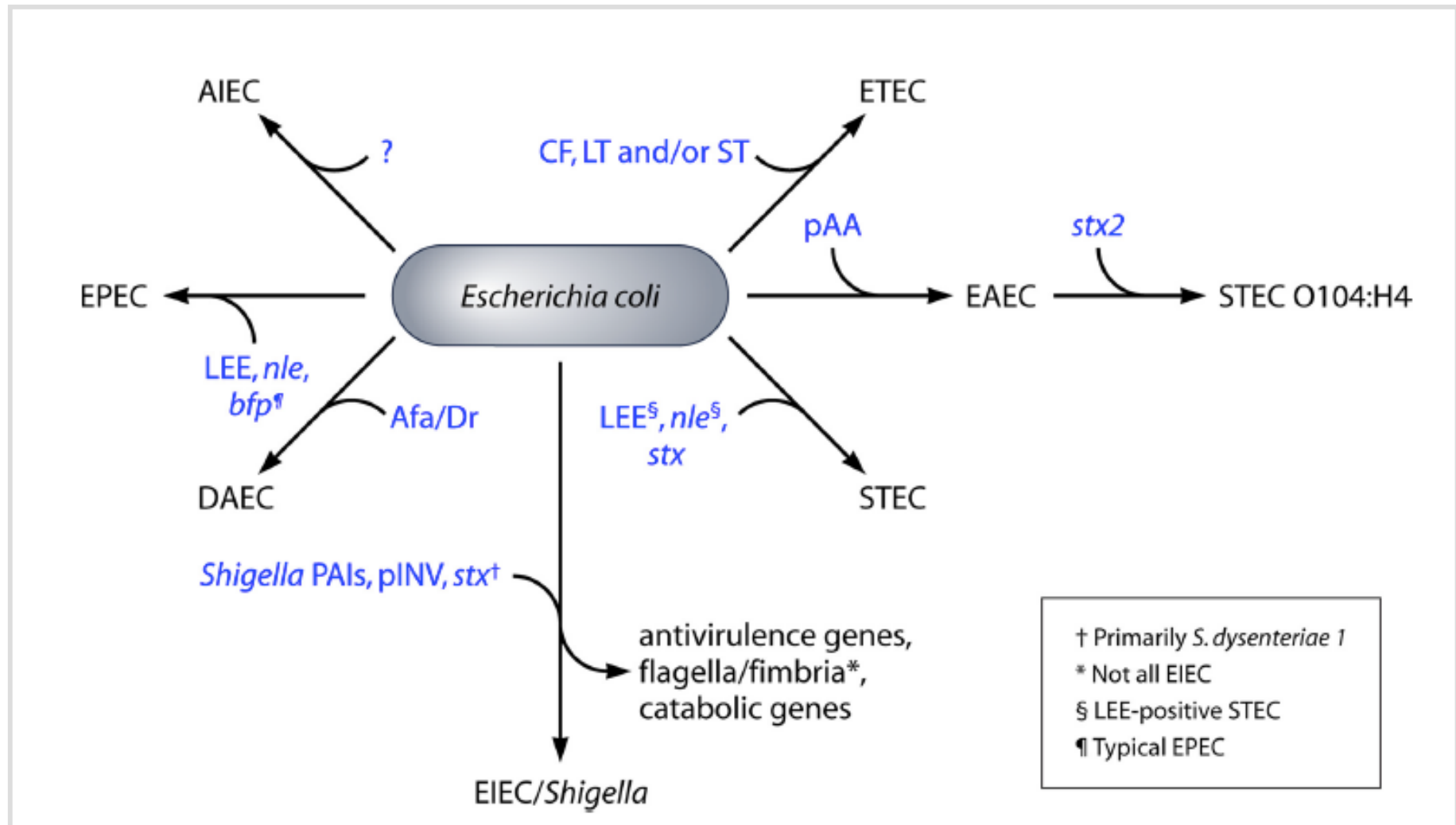
- Joensen, K. G., A. M. Tetzschner, A. Iguchi, F. M. Aarestrup, and F. Scheutz. 2015. Rapid and easy in silico serotyping of *Escherichia coli* using whole genome sequencing (WGS) data. *J.Clin.Microbiol.* 53(8):2410-2426. doi:JCM.00008-15 [pii];10.1128/JCM.00008-15 [doi]

Link to the [article](#)

VirulenceFinder results

Gene	Associated pathotype	Present in isolate
<i>iroN</i>	UPEC	-
<i>papG</i>	UPEC	-
<i>Stx1a</i>	EHEC	-
<i>Stx1b</i>	EHEC	-
<i>Stx2a</i>	EHEC	+
<i>Stx2b</i>	EHEC	+
<i>pic</i>	EAEC	+
<i>pet</i>	EAEC	-
<i>astA</i>	EAEC	-
<i>aggR</i>	EAEC	+
<i>sta1</i>	ETEC	-
<i>stb</i>	ETEC	-
<i>ltaA</i>	ETEC	-

Pathogenic gene acquisition and loss for different pathotypes



The positive control

Center for Genomic Epidemiology

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MyDbFinder-1.1 Server - Results

User database				
Fasta header	%Identity	Query/HSP length	Contig	Position in contig
<i>PapG</i>	98.32	1011 / 1011	CFT073_NC_004431	3429593..3430603
<i>PapG</i>	98.52	1011 / 1011	CFT073_NC_004431	4940831..4941841
<i>dsbD</i>	98.17	1698 / 1698	CFT073_NC_004431	4972379..4974076

[extended output](#)[Results as text](#)[Results tab separated](#)[Hit in genome sequences](#)[Database gene sequences](#)

Selected %ID threshold: 98.00 %

Selected minimum length: 60 %

Input Files: EC4.fsa

escherichia_coli_c227-11.fsa

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MyDbFinder-1.1 Server - Results

User database				
Fasta header	%Identity	Query/HSP length	Contig	Position in contig
<i>dsbD</i>	99.06	1698 / 1698	Supercontig_1.6	34344..36041

Selected %ID threshold: 98.00 %

Selected minimum length: 60 %

Input Files: *escherichia_coli_c227-11.fsa*