SURVEY RESULTS ON WGS CAPACITY AND METHODS

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REFERENCE DIAGNOSTICS AND CHARACTERISATION

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Salmonella

Requirements	Serotyping	Antimicrobial resistance	Cluster detection
Minimum	Phenotypic or genotypic: common serovars	Phenotypic AST or genotypic AMR prediction	High resolution molecular typing (e.g. MLVA)
Optimal	Phenotypic or genotypic: all serovars	Phenotypic AST and WGS-based AMR prediction*	WGS-based (e.g. cgMLST, wgMLST, SNP)

Campylobacter

Requirements	Species	Antimicrobial resistance	Cluster detection
Minimum	Phenotypic or genotypic: *C. jejuni, C. coli*	Phenotypic AST or genotypic AMR prediction	Not applicable**
Optimal	Phenotypic or genotypic: all species	Phenotypic AST and WGS-based AMR prediction*	WGS-based (e.g., cgMLST, wgMLST, SNP)

* a defined proportion of isolates or selected isolates are periodically tested phenotypically to ensure detection of novel resistance mechanisms

** Some laboratories may use Pulsed-field gel electrophoresis (PFGE) for cluster detection but this is not considered as a minimum requirement

WGS - BASED PREDICTION OF AMR

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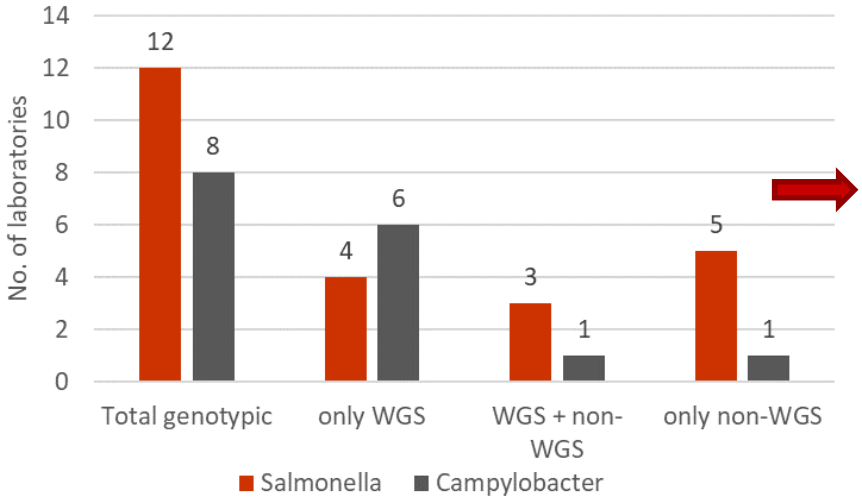
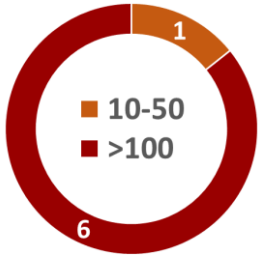
Molecular methods in use for testing of AMR



Salmonella

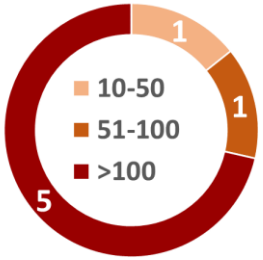
- <u>7 WGS-based</u>
- 8 non - WGS

No. of isolates tested using WGS



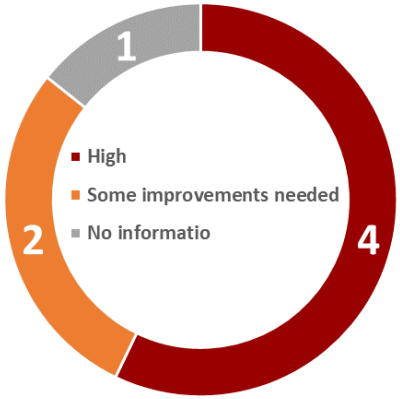
Campylobacter

- <u>7 WGS – based</u>
- 2 non - WGS



Perceived performance of AMR prediction using WGS

Salmonella



Campylobacter

GENETIC MARKERS TESTED AND DATABASES IN USE

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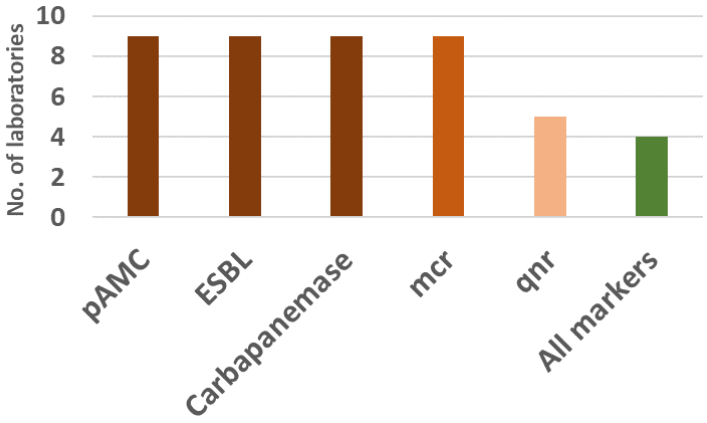
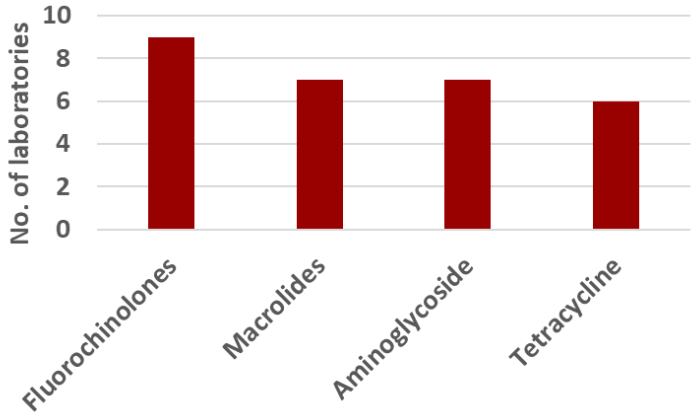
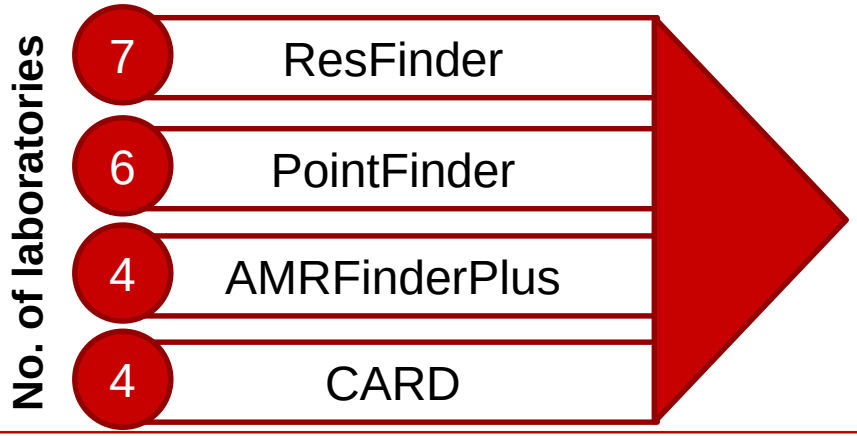
Genetic markers tested routinely in *Salmonella* and *Campylobacter**





*at least one genetic marker from each class is tested

Databases in use for prediction of AMR in *Salmonella* and *Campylobacter*



All laboratories use a combination of databases, and often they are incorporated into certain tools or in-house build pipelines

WGS - BASED STRAIN SUBTYPING

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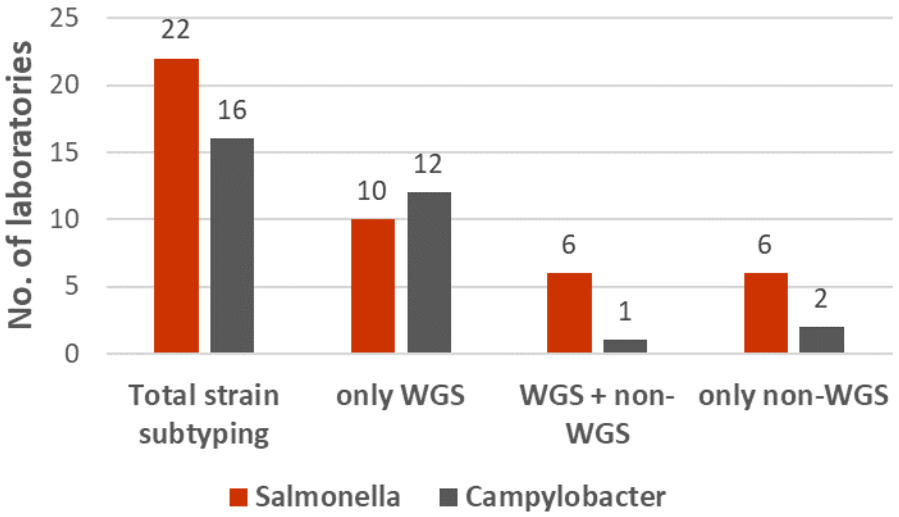
Molecular methods in use for strain subtyping



Salmonella
- 16 WGS-based
- 12 non – WGS

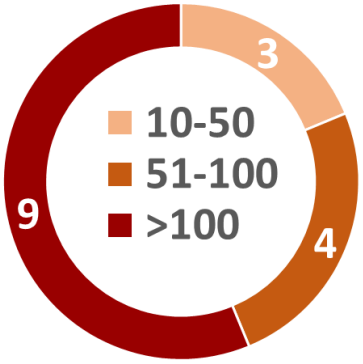
(PFGE, MLVA)

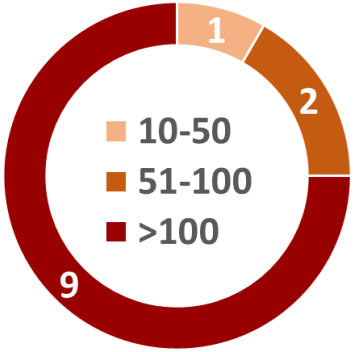
Campylobacter
- 12 WGS – based
- 3 non – WGS

(PFGE, *flaA*)

No. of isolates tested using WGS anually

Salmonella





Campylobacter

WGS – BASED STRAIN SUBTYPING

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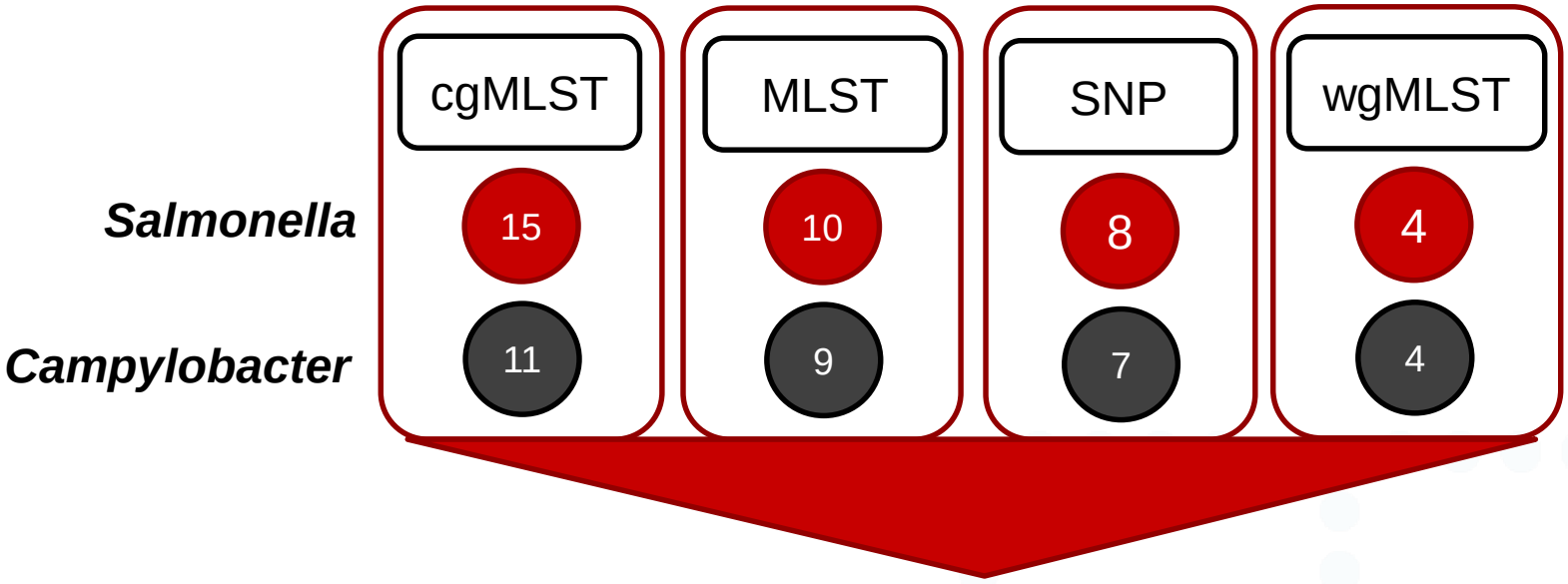
WGS- based methods in use for strain subtyping



Often a combination of methods are used

WGS CAPACITY AND UTILISATION

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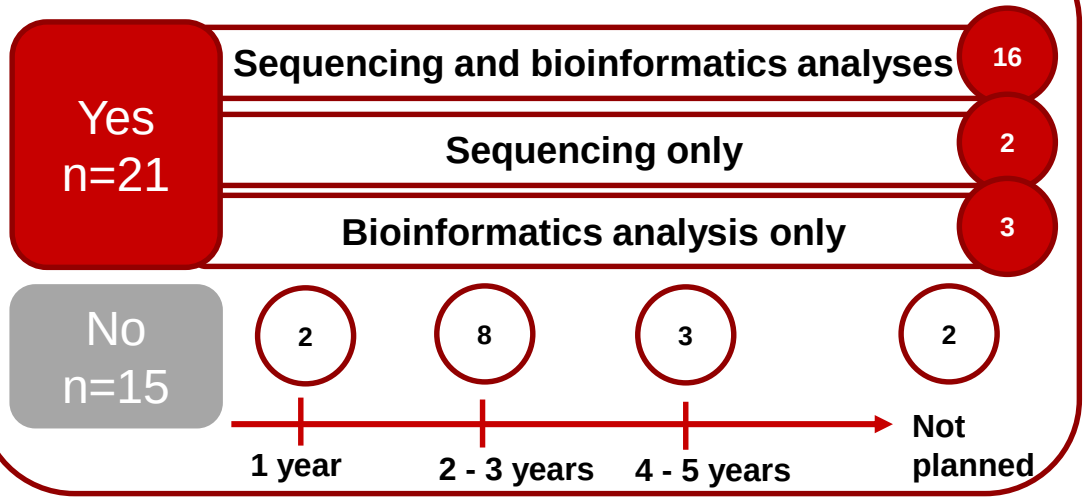
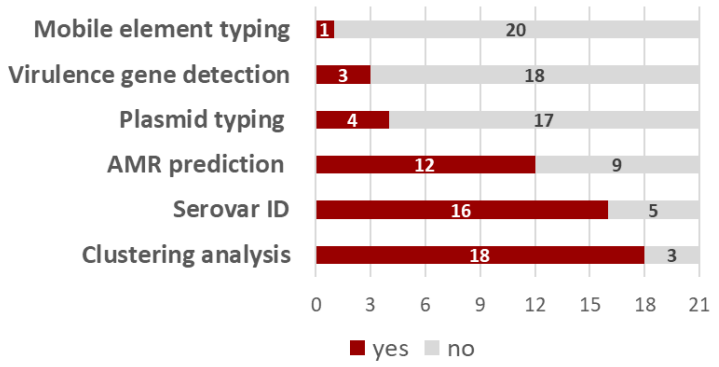
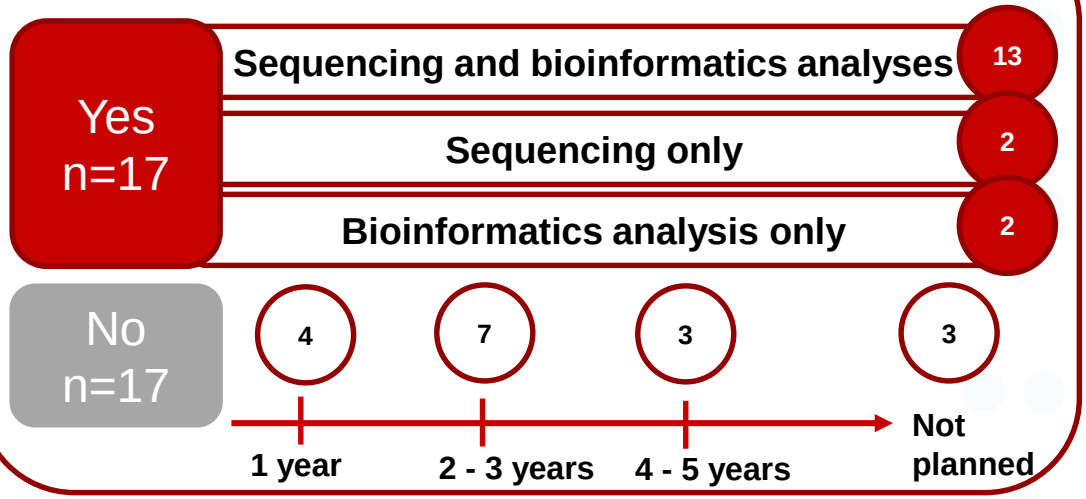
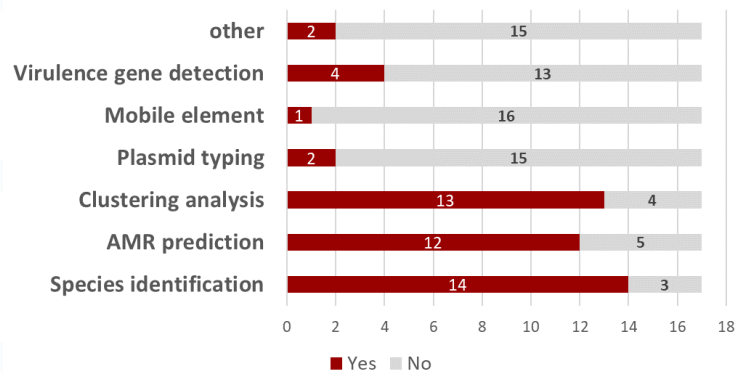
Current WGS status in 36 countries for *Salmonella*





Current WGS status in 34 countries for *Campylobacter*





BIOINFORMATICS TOOLS IN USE

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Commercial softwares in use

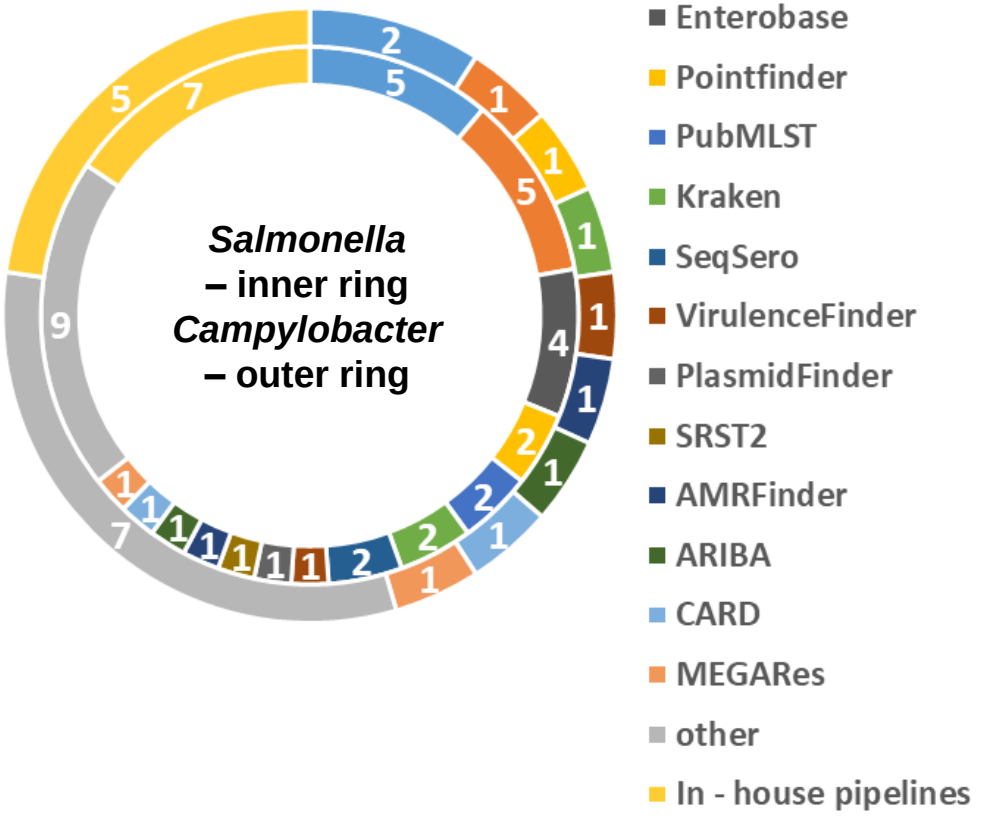
Salmonella

- SeqSphere 10
- Bionumerics 4
- CLC Genomic Workbench 4

Campylobacter

- SeqSphere 6
- Bionumerics 2
- CLC Genomic Workbench 3
- Genious 1

Open source tools in use



SUMMARY

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- Up to 61% of countries have WGS capacity, however:
  - Up to 52% use WGS for strain subtyping routinely
  - 23% use WGS for prediction of AMR routinely
- High variation of bioinformatics methods, tools and softwares are used in different countries performing WGS – based prediction of AMR and strain subtyping of *Salmonella* and *Campylobacter*