

Implementing AMR reporting via WGS data to TESSy – current status

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Outline

- Currently available services at ECDC for FWD WGS analysis
- New features to be added in the near future
- Short demo
- Comparison of predicted resistance and phenotypic

WGS data upload options

- ECDC WGS upload app
- Submission of ENA/SRA accession numbers
- Submission of assemblies through Bionumerics

<https://tessy.ecdc.europa.eu/TessyHelp/index.aspx?navigation=TechnicalGuidelines>

ECDC upload app



- Configure once
- One-click submission of both epi data and WGS reads/assembly to TESSy
- Makes submissions easier and also eliminates manual work at ECDC
- Shows the most common variables by default, but more TESSy variables can easily be added
- For technical assistance, contact typing@ecdc.europa.eu

ECDC WGS upload app v1.0.9

Data Setup Submission View

Isolate table Total entries: 10 Selected: 0

ECOLIISO LISTISO MYCOISO SALMISO

RecordId	SampleId	DateOfSampling	DateOfReceiptS...	DateOfReceiptR...	Gender	Age	AgeMonth	SampleOrigin	Specimen	PlaceOfResidence	Imported	ProbableCountr...	WgsProtocol	WgsAssembler	Modified date	Ready for upload	ECDC event (UI)
															2021-11-19 09:1...		
															2021-11-19 09:1...		
															2021-11-19 09:1...		
															2021-11-19 09:1...		
															2021-11-19 09:1...		
															2021-11-19 09:1...		
															2021-11-19 09:1...		
															2021-11-19 09:1...		
															2021-11-19 09:1...		
															2021-11-19 09:1...		

Epidemiological typing

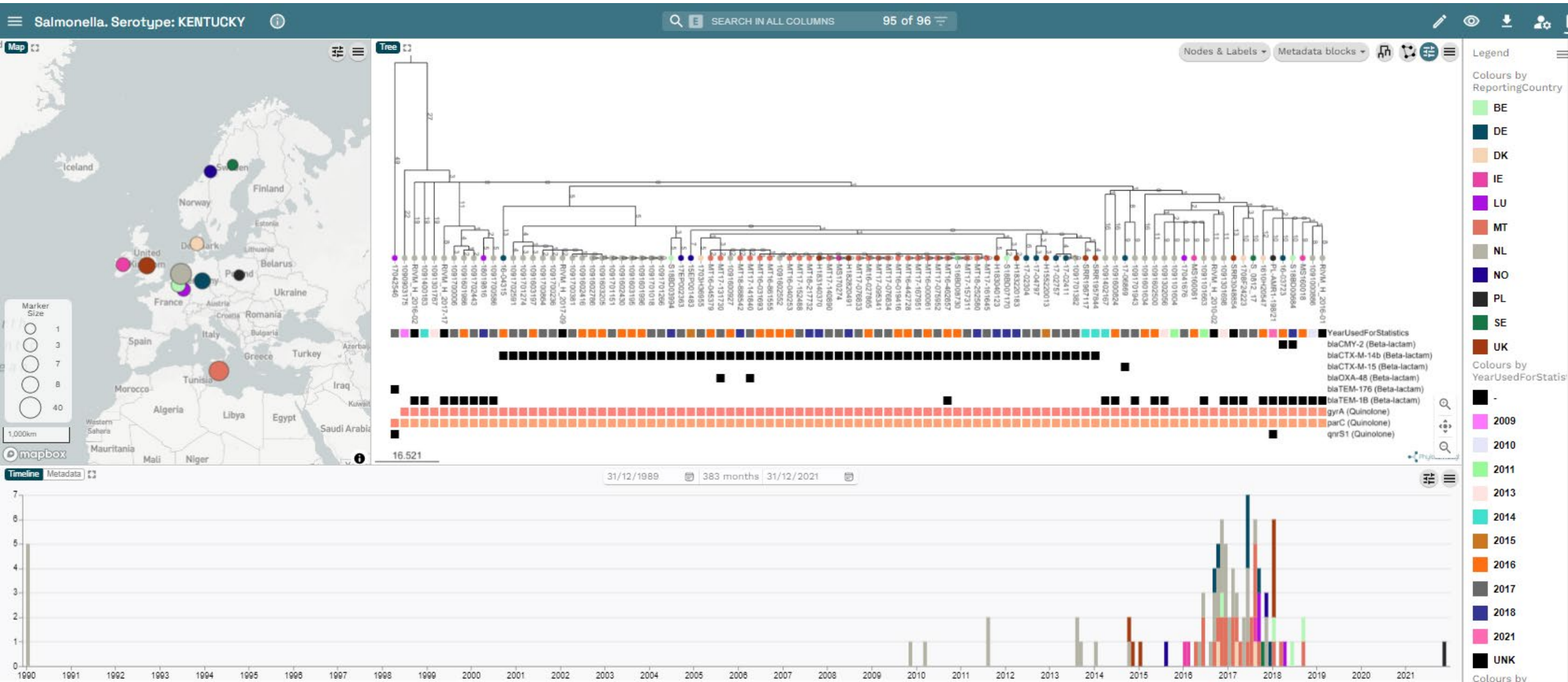
- The submitted WGS data are analysed using the Bionumerics cgMLST schema (Pasteur for *Listeria*, Enterobase for *Salmonella* and *E. coli*)
- Currently weekly cluster analysis is performed for *Listeria*, this will be expanded to include further pathogens soon

AMR analysis for FWD pathogens at ECDC



- ResFinder+PointFinder have been chosen as the initial tools for AMR analysis
 - Managed within the EU
 - Well-curated and supported
 - Technically compatible with the ECDC platform
- ResFinder+PointFinder are run on all submitted WGS data for relevant organisms
- The results are available through EpiPulse, the ECDC Surveillance Atlas and the annual report on antimicrobial resistance in zoonotic and indicator bacteria

Data visualisation in EpiPulse using MicroReact



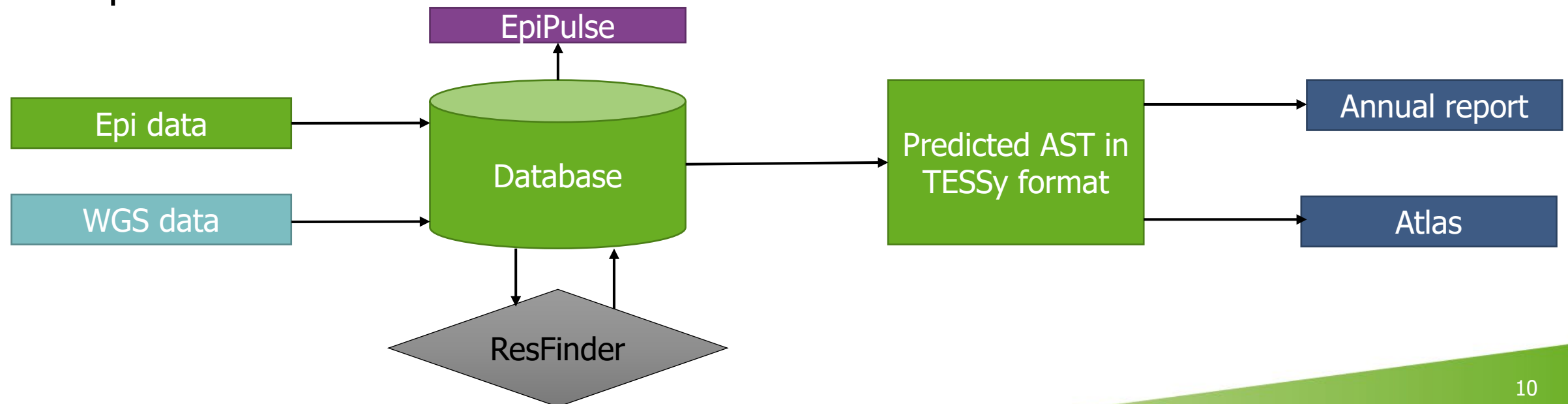
Available and planned visual elements for AMR in EpiPulse



- Available now:
 - Tabulated ResFinder/PointFinder results for all visualisations, can be downloaded
 - Integration of results with MicroReact
 - Visualisations can be created for e.g. country, time period, serotype, cluster, event
- Planned:
 - Tabulated predicted resistance per antibiotic (WT/non-WT)
 - Integration of predicted resistance with MicroReact
 - Download link for each TESSy batch

Predicted AMR phenotypes for annual AMR data collection for *Salmonella* and *Campylobacter*

- Member States can now upload WGS data instead of phenotypic AST data
- If WGS data are uploaded, phenotypes will be predicted using ResFinder
- The phenotypes will be transformed into an identical format to the phenotypic AST data in TESSy (predicted wild type/non-wild type, no MIC predictions)
- The predicted data will be included in the annual epidemiological report, AMR report and in the Surveillance Atlas



Summary and timelines

- Available WGS services for FWD right now:
 - WGS data upload for Listeria, Salmonella, STEC, Campylobacter
 - Cluster analysis for Listeria
 - ResFinder/PointFinder
 - Visualisation of WGS data through EpiPulse
- FWD AMR-related activities with estimated delivery dates:
 - Regular cluster analysis for Salmonella (2023)
 - Individual isolate reports with detailed ResFinder/PointFinder results in EpiPulse (2023)
 - Predicted resistance in EpiPulse, AER, Atlas, and AMR report (2023)
 - Improved download options for ResFinder/PointFinder results (2023-2024)

Contacts

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Discussion/Q&A and Demo

Comparison between predicted resistance vs phenotypic – *Salmonella* TESSy data

Possible reasons for discrepancies

- problems with phenotypic testing, e.g. too old discs, incubation, reading etc.
- mistakes in reporting the phenotypic quantitative results to TESSy
- other mechanisms resulting in higher MIC/smaller zones or resistance genes or mutations not yet identified or added to database
- Most discrepancies in CIP/NAL
 - will look into further, all related to mutation in parC (T57S), mix of countries

Antibiotic	PWT/ WT	PNWT/ NWT	PWT/ NWT	PNWT/ WT	Total
AMP	764	137	16	9	926
AMX	172	35	0	0	207
AZM	747	3	7	2	759
CAZ	882	24	1	3	910
CHL	847	16	3	3	869
CIP	508	314	17	87	926
COL	5	0	0	0	5
CTX	896	24	2	3	925
ETP	20	0	0	0	20
FOX	89	1	0	0	90
GEN	884	25	0	2	911
MEM	915	0	5	0	920
NAL	384	262	21	66	733
SMX	5	0	0	0	5
TCY	732	106	13	6	857
TGC	700	0	28	0	728
TMP	799	12	8	2	821
Total	9,349	959	121	183	10,612

Comparison between predicted resistance vs phenotypic – *Campylobacter* TESSy data

Antibiotic	PWT/WT	PNWT/NWT	PWT/NWT	Total
CIP	3	28	2	33
ERY	33	0	0	33
GEN	33	0	0	33
TCY	7	26	0	33
Total	76	54	2	132

Only 2 discrepancies for *Campylobacter* so far but few isolates that have both phenotypic data and sequences in TESSy

Comparison between predicted WT/NWT vs phenotypic interpreted with clinical breakpoints - *Salmonella*



WGS predicted	Interpretation with clinical breakpoints			
	S	I	R	Total
PWT	7,565	11	252	7,828
PNWT	115	21	648	784
Total	32	900	7,680	8,612

Expected to find isolates that are PNWT but not considered clinically resistant – matter of dose, MICs for clinical resistance often higher than the ECOFF

Not expected to find isolates PWT but with MIC or zone mm indicating I or R

- majority of these due to colistin – many *Salmonella* (particularly *S. Enteritidis* and *S. Dublin*) have MIC above the clinical breakpoint without carrying any (known) resistance determinants

Antibiotic	PWT/I or R
AMP	15
CAZ	3
CHL	20
CIP	17
COL	170
CRO	1
CTX	2
MEM	5
SMX	25
TMP	5
Total	263

How do we separate between sequences submitted as part of an outbreak investigation and official annual data



- Routine continuous submission of sequences to TESSy
 - Would that be representative subset for all *Salmonella*/*Campylobacter* infections or mainly outbreak isolates?
- If not representative, how to separate from annual AMR sequence submission?
 - Use other data source?
 - Add a variable to discriminate?

Thank you for you interest!

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