



EFSA WGS SYSTEM

Mirko Rossi, Scientific Officer BIOHAW

OUTLINE

- **System Overview**
Brief refresher on the system's key components and current functionality.
- **Expected Changes in 2026**
Detailed look at upcoming updates, anticipated impacts, and implementation plans.
- **Conclusion**
Summary of key points and next steps.

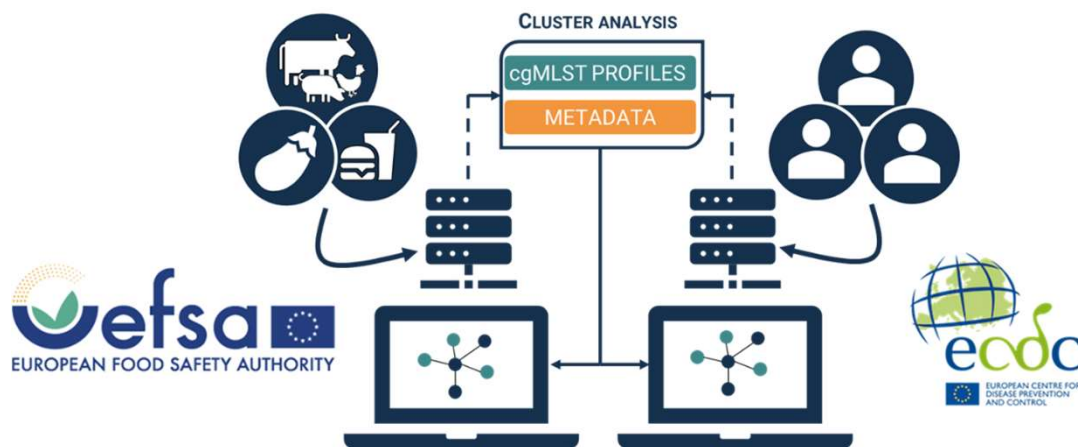


EFSA WGS SYSTEM



EFSA AND ECDC JOINT ONE HEALTH WGS SYSTEM

- Mandate from EC received in 2019
- The Joint One Health WGS system is **operative since July 2022**



Secure Collaboration



Responsible Data Use



EU Complexity



Operational Efficiency



Constantly evolving



WHO CAN ACCESS THE SYSTEM AND SHARE DATA?

USERS AT COUNTRY LEVEL



COUNTRY OFFICER

Coordinate data provider organisations
Contact point for EFSA



- Can submit on behalf of their country (any organisation)
- Can see all data from their country
- Can explore all the queries from ECDC



DATA PROVIDER

Share typing data to EFSA Database
Manage shared information



- Can submit on behalf of their organisation
- Can see all data from their organisation
- Can explore all the queries from ECDC

NOMINATION PROCEDURE



Controlled Access: Only appointed users from food authorities can access the data, ensuring the maintenance of the chain of custody.



WHAT ARE THE DATA STORED IN THE EFSA WGS SYSTEM PLATFORM?



EXPERIMENTAL DATA

Information related to the experiment



TYPING DATA

Genomic profile and other typing data

Different Data/Different Owners: Asynchronous submission of WGS data and epidemiological data.



EPIDEMIOLOGICAL DATA

Information related to food/ feed/ animal samples from which the pathogen has been detected

WGS DATA

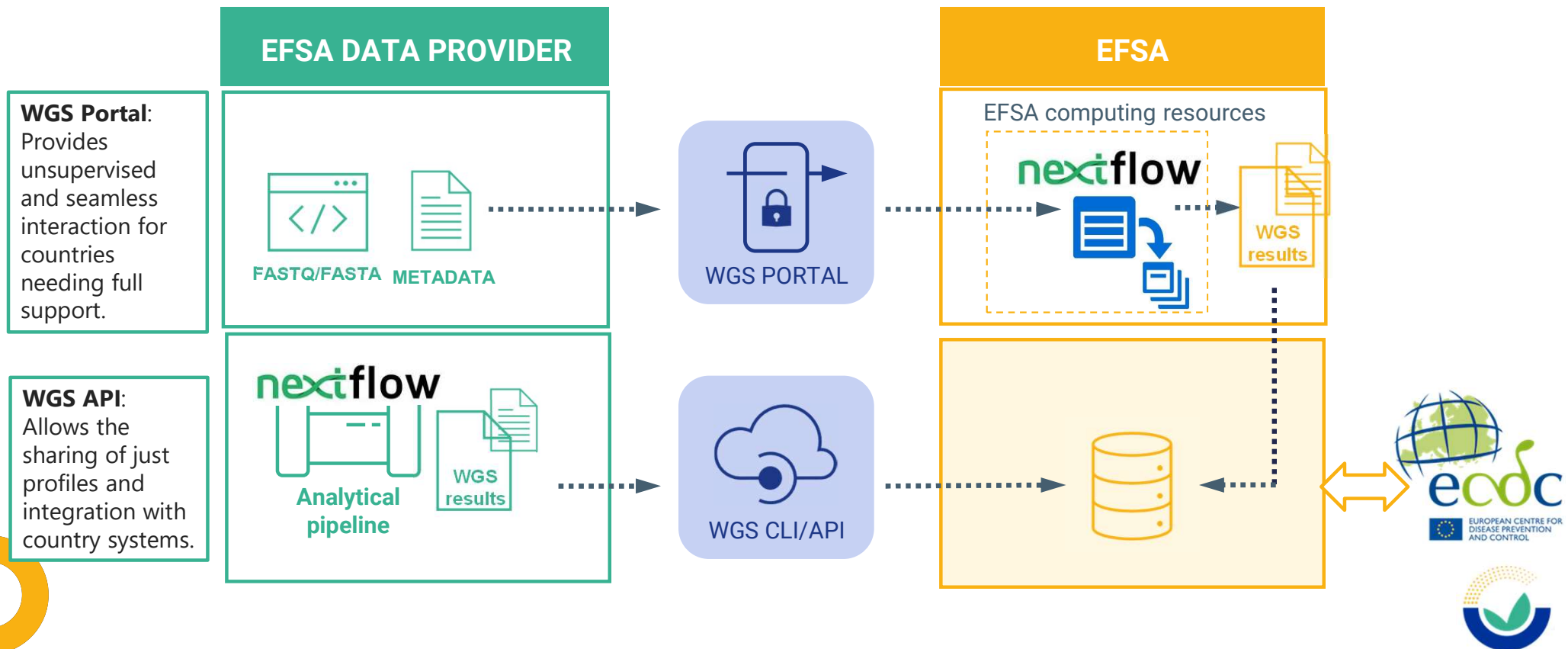
Controlled Data Sharing:

Countries have the authority to decide at any time whether to share, edit, or withhold the data (release/unrelease).



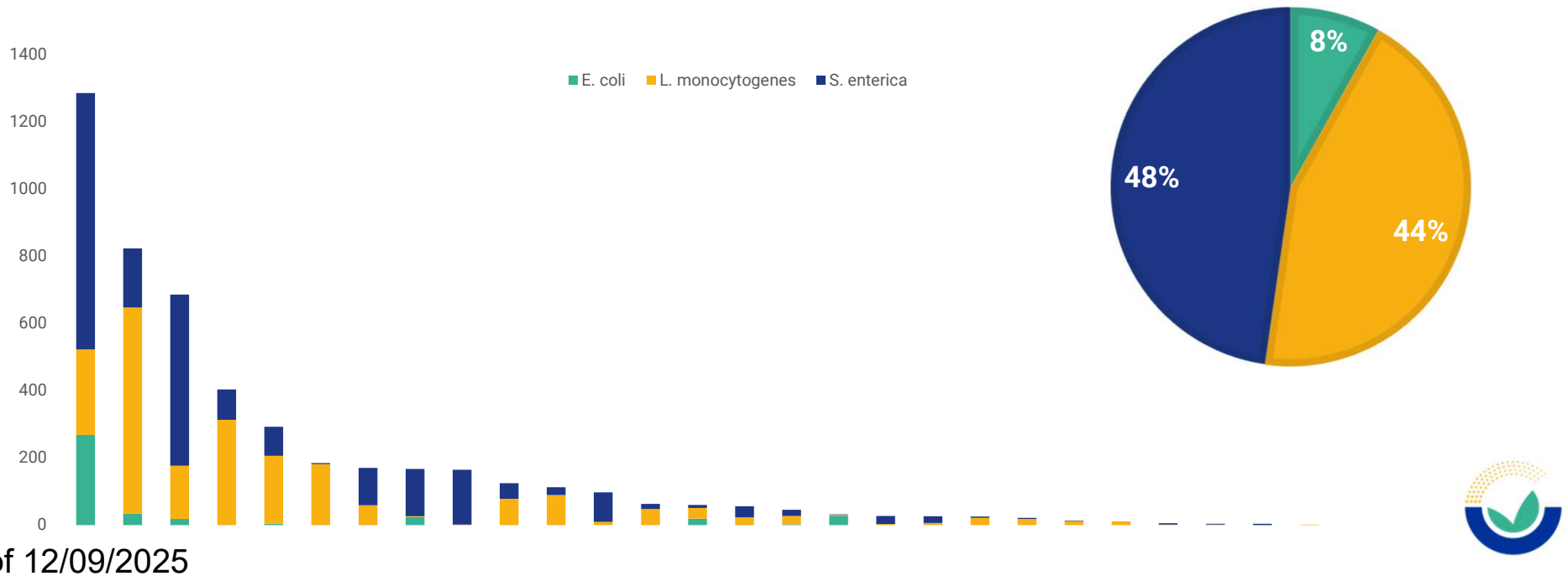
HOW ARE DATA SUBMITTED?

TAILORED SOLUTIONS FOR VARIOUS SETTINGS



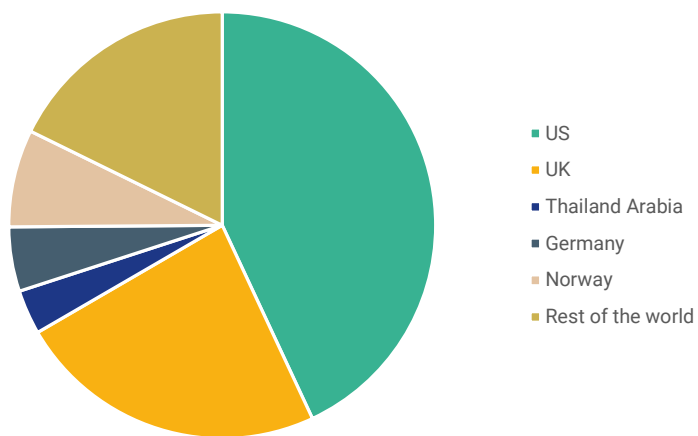
CONTRIBUTION MEMBER STATES (PROFILE RELEASED) SINCE 2022

- Frequency >100 uploads/month
- Total uploads **5,033**
- 97.3% successful release for comparison with ECDC profiles
- Total profile released **4,897** (**2684 – 55% - found matching ECDC clusters**)



ENRICHMENT WITH PUBLIC DATA

- Since March 2025 EFSA automatically import food/animal/environmental data from NCBI for a total of **12,108 (32% found matching ECDC clusters)**



TOTAL NCBI/ENA	12,108
<i>Escherichia coli</i> (STEC)	103
<i>Listeria monocytogenes</i>	5,182
<i>Salmonella enterica</i>	6,823

As of 12/09/2025



USE OF THE DATA

- EFSA and ECDC use the data from the users to identify clusters across-sectors (joint clusters) to support **ECDC-EFSA Joint Rapid Outbreak Assessments**
- **EFSA – ECDC interaction**
 - **Weekly Queries:** ECDC sends queries to EFSA recurrently using a fixed-threshold
 - **Ad Hoc Queries:** ECDC can send queries to EFSA using variable-threshold as needed
 - **Automatic Data Exchange:** data exchange only occurs between ECDC and EFSA when a match across-sector is found
 - **Cross-sectoral Analyses:** Data are included only in ECDC-EFSA food-borne outbreak assessments



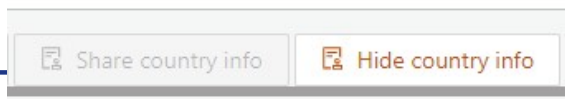
WHAT DO EFSA AND ECDC SHARE?

Always shared

- **cgMLST profile**
- Other typing data (MLST ST, AMR profile, Serotype, Virulence genes)
- Sampling year
- Food category (e.g. fish and fishery products thereof)

Shared only if agreed by Data Provider

- Country of owner organisation
- Country of submitting organisation
- Country of sampling
- Country of origin



EFSA Data Providers have the freedom to decide if **any country information** is sharable with ECDC system or not by selecting “hide/share country info”



SERVERLESS CG-MLST ALLELE DESIGNATION

WITH NOMENCLATURE SERVER

Locus A > allele sequences

```
1 ATGATAGAAATGAATACACGTAATTTATCTACGAGCTTCAACTA
AAGATCAAGATGCAAAAAGGGCTTTGCAGATTTCTTCAGGATCT
AAACCAAACTTGAATTTGGGCGAAACCATTTGTGTACGTGGAA
AACTATAGTGGTACGAAGTTAGACCGACCTGAATTGAATAAGC
TACTGTGAGAAGCAATCAGGGTGACACCTTGTAGTTGAAAG
TATTGACCGCTTATCAGCCTTAACCCAACGAGATTTTCAAGAG
CTGAAGCGCAGGATCCAGGAAAAGGGACTTCGTTTAGTCGTAG
CAGATCTTCCTACTACTACCAATGATTCAAGCCAGTGACAG
CAATTAATCAATCTGGAATCATCAATAATATGTTGATT
GATCTCCTGGCAACAATGGCTCGCCTGGCAATGAGAAACGTA
TAGAACGTATTAAGCAGGGCCTAGCGCTTCAGGTTACAAGCC
AACAGGTAAGAAGGCTAATGAGGCTAAACATAAAGCAATAAAA
GAAGCTGCTGGTGGCTGCAATATGACTAAGGAAGAAATTGCAA
AAGCAGTGAATTGTGGAGTTGCAACTGTCTATCGAGTTGCTAA
GGTTATCTA
```

=

Locus A > allele sequences

```
1 ATGATAGAAATGAATACACGTAATTTATCTACGAGCTTCAACTA
AAGATCAAGATGCAAAAAGGGCTTTGCAGATTTCTTCAGGATCT
AAACCAAACTTGAATTTGGGCGAAACCATTTGTGTACGTGGAA
AACTATAGTGGTACGAAGTTAGACCGACCTGAATTGAATAAGC
TACTGTGAGAAGCAATCAGGGTGACACCTTGTAGTTGAAAG
TATTGACCGCTTATCAGCCTTAACCCAACGAGATTTTCAAGAG
CTGAAGCGCAGGATCCAGGAAAAGGGACTTCGTTTAGTCGTAG
CAGATCTTCCTACTACTACCAATGATTCAAGCCAGTGACAG
CAATTAATCAATCTGGAATCATCAATAATATGTTGATT
GATCTCCTGGCAACAATGGCTCGCCTGGCAATGAGAAACGTA
TAGAACGTATTAAGCAGGGCCTAGCGCTTCAGGTTACAAGCC
AACAGGTAAGAAGGCTAATGAGGCTAAACATAAAGCAATAAAA
GAAGCTGCTGGTGGCTGCAATATGACTAAGGAAGAAATTGCAA
AAGCAGTGAATTGTGGAGTTGCAACTGTCTATCGAGTTGCTAA
GGTTATCTA
```

Server 1



Collection of allele designations
Local premises

Locus A > allele "1"

Sample	Locus A	Locus B
A	1	3
B	1	4
C	4	3

≠



Server 2

Locus A > allele "23"

Sample	Locus A	Locus B
A	23	13
B	23	8
C	8	13

WITHOUT NOMENCLATURE SERVER

Locus A > allele sequences

```
1 ATGATAGAAATGAATACACGTAATTTATCTACGAGCTTCAACTA
AAGATCAAGATGCAAAAAGGGCTTTGCAGATTTCTTCAGGATCT
AAACCAAACTTGAATTTGGGCGAAACCATTTGTGTACGTGGAA
AACTATAGTGGTACGAAGTTAGACCGACCTGAATTGAATAAGC
TACTGTGAGAAGCAATCAGGGTGACACCTTGTAGTTGAAAG
TATTGACCGCTTATCAGCCTTAACCCAACGAGATTTTCAAGAG
CTGAAGCGCAGGATCCAGGAAAAGGGACTTCGTTTAGTCGTAG
CAGATCTTCCTACTACTACCAATGATTCAAGCCAGTGACAG
CAATTAATCAATCTGGAATCATCAATAATATGTTGATT
GATCTCCTGGCAACAATGGCTCGCCTGGCAATGAGAAACGTA
TAGAACGTATTAAGCAGGGCCTAGCGCTTCAGGTTACAAGCC
AACAGGTAAGAAGGCTAATGAGGCTAAACATAAAGCAATAAAA
GAAGCTGCTGGTGGCTGCAATATGACTAAGGAAGAAATTGCAA
AAGCAGTGAATTGTGGAGTTGCAACTGTCTATCGAGTTGCTAA
GGTTATCTA
```

CRC-32

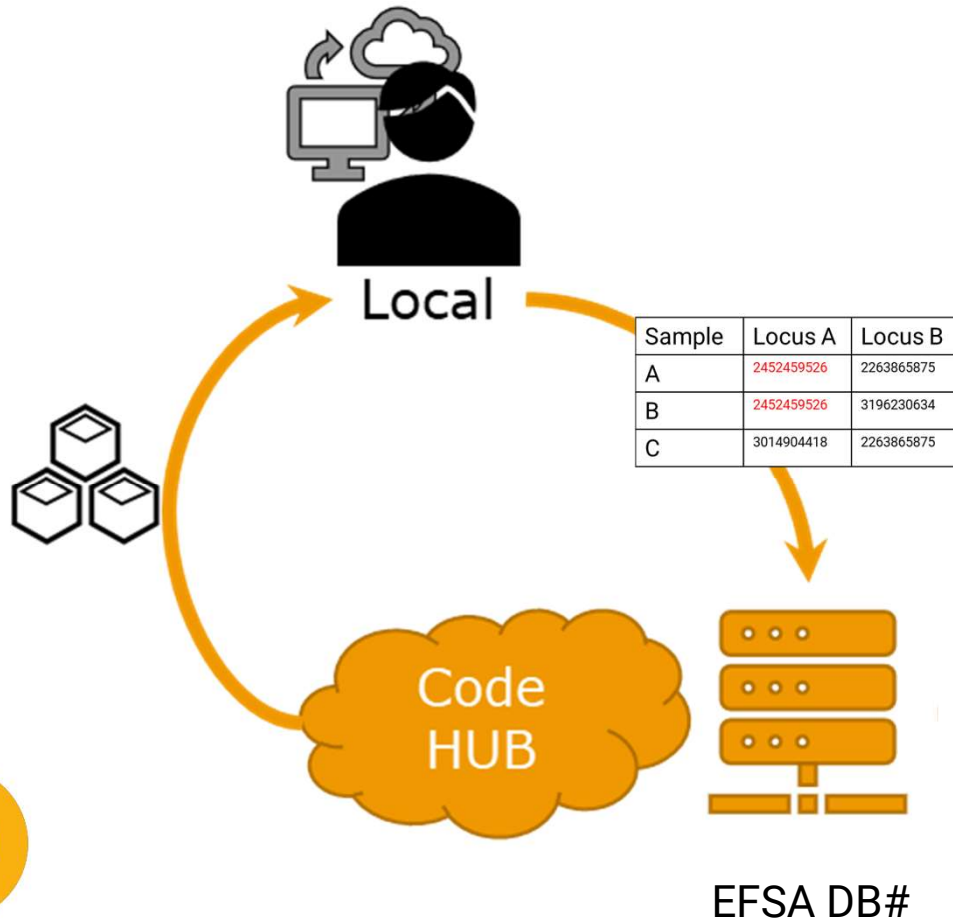


Locus A > allele "2452459526"

Sample	Locus A	Locus B
A	2452459526	2263865875
B	2452459526	3196230634
C	3014904418	2263865875

Unique profile

DECENTRALIZATION OF DATA GENERATION



Cons

Possible collisions ($\neq$ sequences same allele)

No curation of alleles (spurious alleles)

Pro

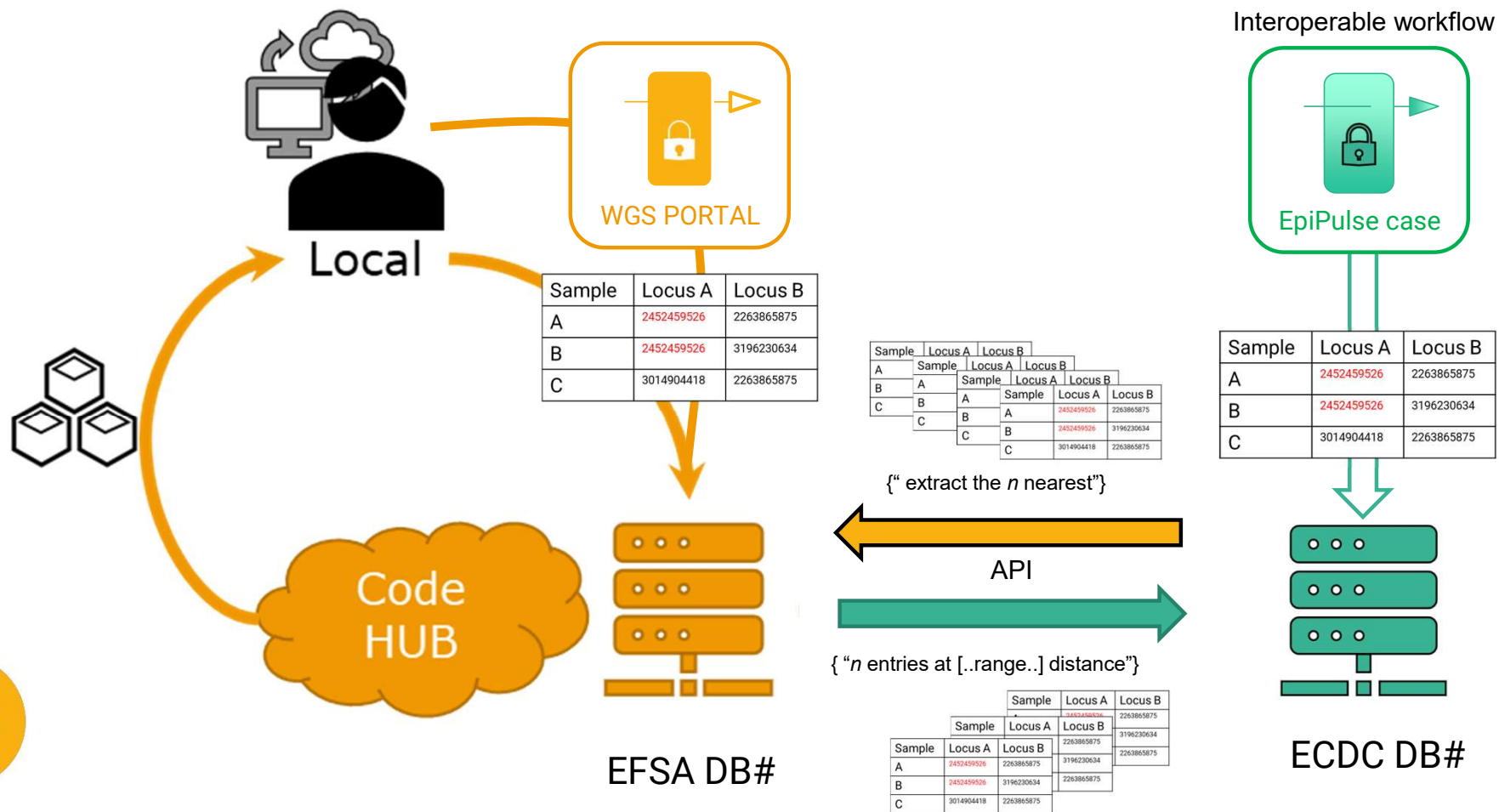
Seamless integration cross-sectors

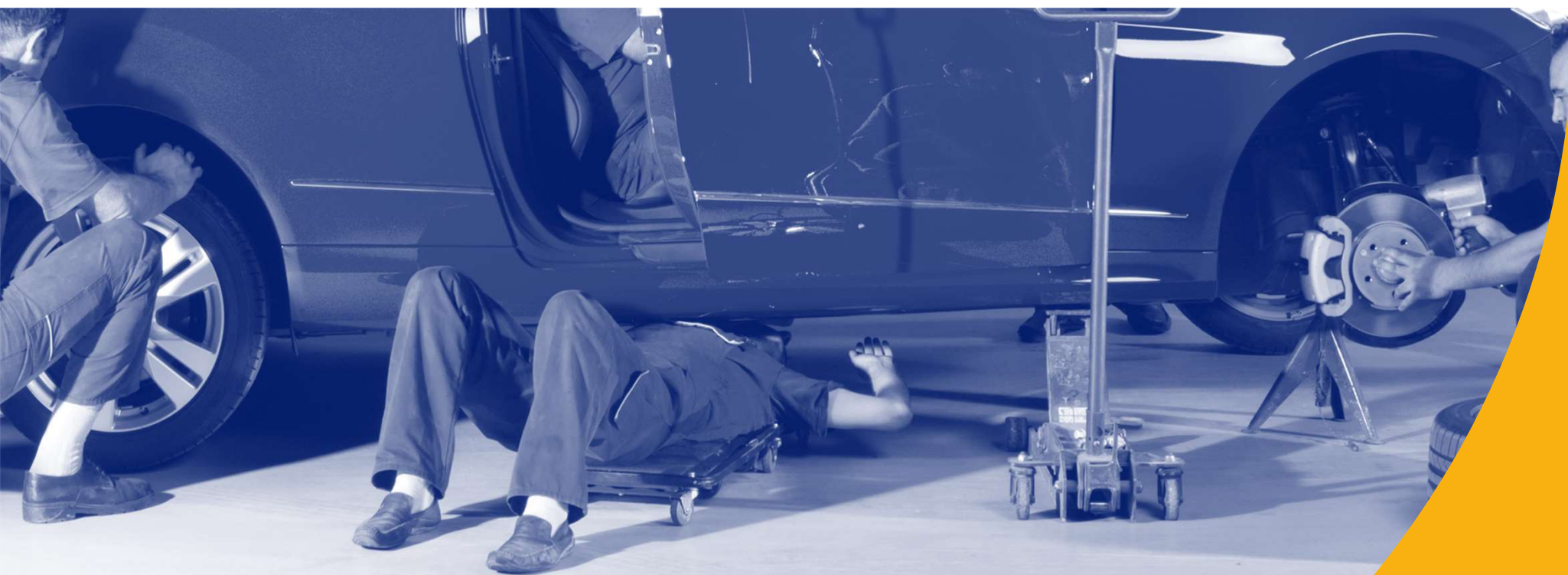
No possible to generate the sequence from the hash

No need to maintain the nomenclature server

No need to access same nomenclature server

SEAMLESS INTEGRATION WITH ECDC





EXPECTED CHANGES IN 2026



COMMISSION IMPLEMENTING REGULATION (EU) 2025/179 –

- **Purpose:** Improve outbreak investigations by mandating WGS of foodborne pathogens, enabling swift identification of contaminated consignments and outbreak sources.
- **Scope:** Applies to isolates from food, feed, animals, and related environment associated or suspected to be associated to foodborne outbreak.
- **Pathogens Covered:** *Salmonella enterica*, *Listeria monocytogenes*, *Escherichia coli*, *Campylobacter jejuni*, *Campylobacter coli*.
- **Requirements:**
 - WGS must be performed in **ISO 17025-accredited labs**.
 - Data must be transmitted **without undue delay** to EFSA.
 - Metadata must include **sampling date, origin, outbreak identification**, and more.
- **Food Business Operators:** Must cooperate with national food authorities.

F.A.Q from EC

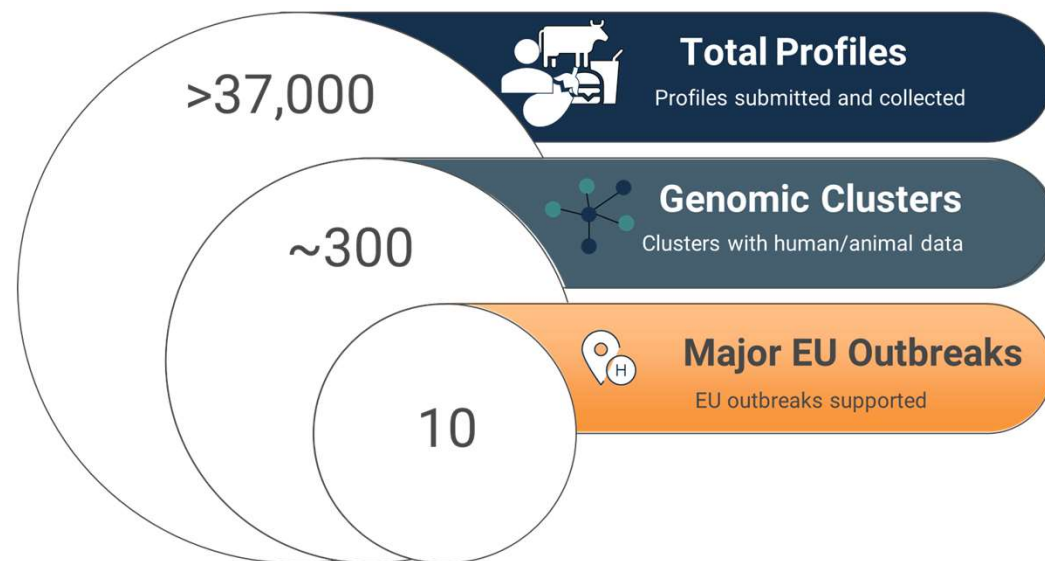


EFSA WGS SYSTEM PLANNED CHANGES

- Major system update planned for **Summer 2026**.
 - Expanded data scope: FASTQ, assembly FASTA, cgMLST profiles.
 - Clear separation of voluntary vs mandatory submission workflows.
 - Enhanced metadata to meet new regulatory requirements.
 - Inclusion of *Campylobacter* species.
 - Robust data transmission with full workflow redundancy via both the UI and API.
 - Enhanced batch upload and batch edit
 - New user roles for specific cases (e.g., submissions on behalf user, Northern Ireland user).
 - Testing mode
- Change management plan with webinars and training in early 2026.



IN SUMMARY



- **EFSA:** Over 17,000 profiles submitted by 29 countries or imported from public domains
- **ECDC:** Over 20,000 profiles

This has led to:

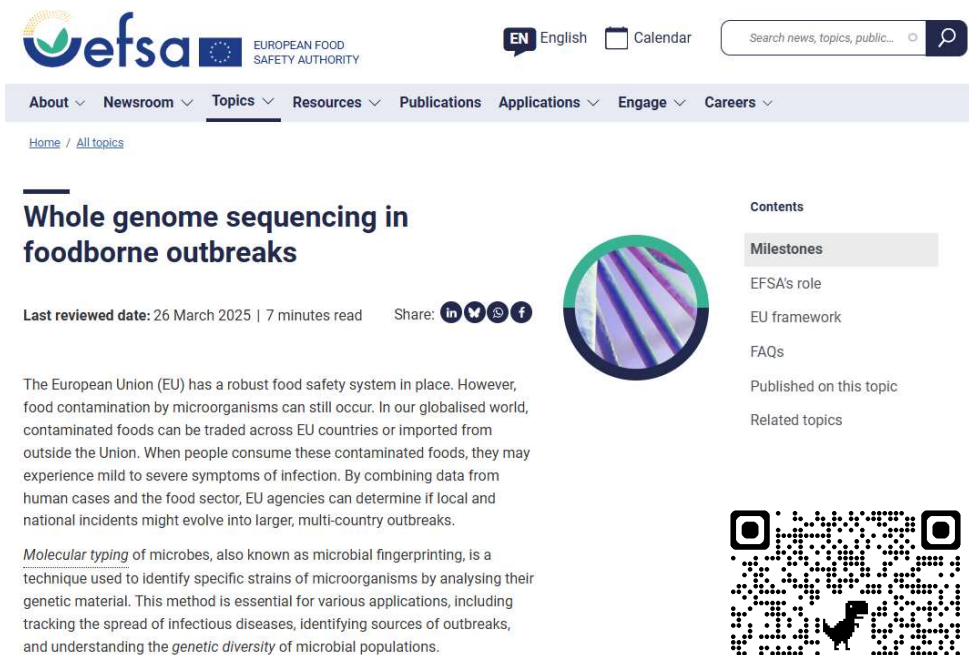
- **Hundreds of thousands of interactions** between the platforms
- **Approximately 300 genomic clusters identified** containing both food/animal and human data
- Support for assessment of **10 EU major multi-country foodborne outbreaks**, involving hundreds of human cases

The system has proven effective in linking human cases to foodborne sources, enhancing outbreak response and surveillance



MORE INFORMATION

Topic page in the EFSA website

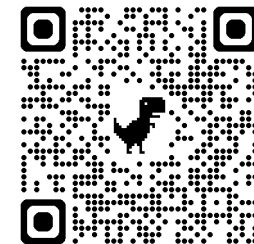
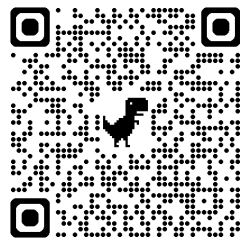


The screenshot shows the EFSA website interface. At the top, the EFSA logo and name are displayed alongside a language selector (EN English) and a calendar icon. A search bar is also present. Below the header, a navigation menu includes links for About, Newsroom, Topics, Resources, Publications, Applications, Engage, and Careers. The main content area features the title 'Whole genome sequencing in foodborne outbreaks' with a sub-header 'Last reviewed date: 26 March 2025 | 7 minutes read'. A circular image of a DNA helix is shown. To the right, a 'Contents' sidebar lists: Milestones, EFSA's role, EU framework, FAQs, Published on this topic, and Related topics. The main text begins with 'The European Union (EU) has a robust food safety system in place. However, food contamination by microorganisms can still occur. In our globalised world, contaminated foods can be traded across EU countries or imported from outside the Union. When people consume these contaminated foods, they may experience mild to severe symptoms of infection. By combining data from human cases and the food sector, EU agencies can determine if local and national incidents might evolve into larger, multi-country outbreaks.' A paragraph follows, starting with 'Molecular typing of microbes, also known as microbial fingerprinting, is a technique used to identify specific strains of microorganisms by analysing their genetic material. This method is essential for various applications, including tracking the spread of infectious diseases, identifying sources of outbreaks, and understanding the genetic diversity of microbial populations.'

Promotional video



The screenshot shows a YouTube video thumbnail. It features the YouTube logo in the top left corner. The EFSA logo and name are centered. Below the logo, the text reads 'HOW THE EU USES WHOLE-GENOME SEQUENCING TO COMBAT FOODBORNE OUTBREAKS'. At the bottom, a black bar contains the text 'to combat foodborne outbreaks.'



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