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Establishment and public release of a whole-genome database of multi-sectoral antimicrobial resistant bacteria

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Background

Methods

- ❖ The World Health Organization (WHO) recognizes antimicrobial resistance (AMR) as a major global health concern and emphasizes the role of whole-genome sequencing (WGS) in high-resolution pathogen characterization.
- ❖ WGS-based approaches are essential for tracing resistant pathogens, identifying resistance mechanisms, and supporting diagnostic and therapeutic strategies.
- ❖ A publicly accessible multi-sectoral WGS database strengthens AMR surveillance across human, animal, food, and environmental sectors, enabling harmonized monitoring and timely responses. It also provides standardized genomic data to support cross-sector comparison and early detection of resistance threats.

Results

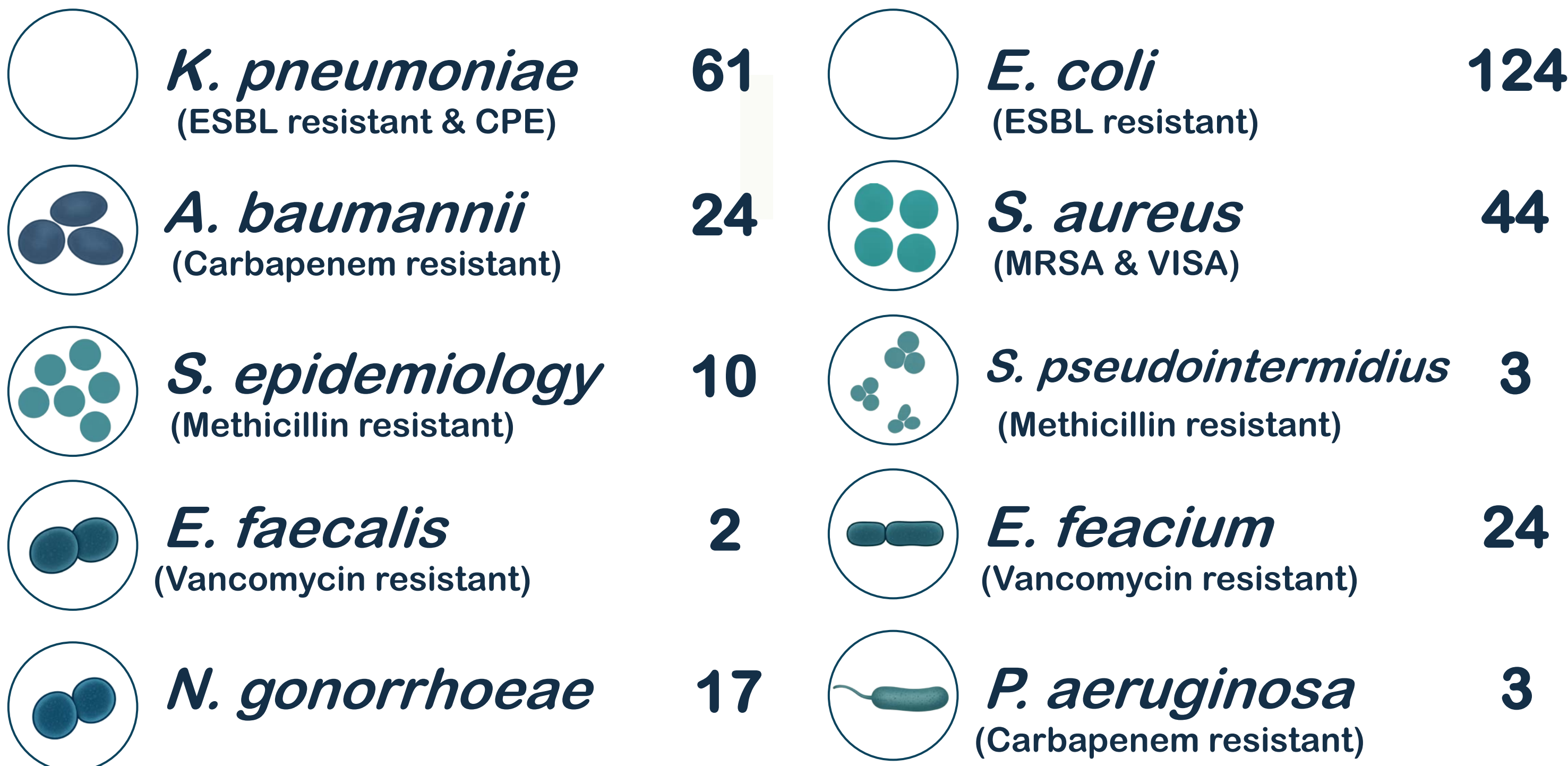


Figure 1. Current Status of Publicly Available Whole-Genome Data of Antimicrobial-Resistant Bacteria

- ❖ A comprehensive collection of 312 isolates representing 10 clinically and epidemiologically important AMR species.
- ❖ Includes key clinical pathogens such as *K. pneumoniae*, *E. coli*, and *A. baumannii*, as well as *E. coli*, *K. pneumoniae* and *Staphylococcus* spp. from One Health sectors.
- ❖ Each isolate is linked to resistance phenotype and WGS data, providing an integrated view of genotypic and phenotypic characteristics.

Table 1. Summary of AMR Isolates by Human, Animal, Environmental, and Food Sources with Resource Links

Species	No. of isolates					Phenotype		Resource		
	Total	Human				AMR	NCCP	NCBI		
		Patient	Community	Industrial	Companion					
<i>K. pneumoniae</i>	61	57	20	-	-	2	-	ESBLs CPE	61	58
<i>E. coli</i>	124	30	20	27	16	23	8	ESBLs	124	124
<i>A. baumannii</i>	24	24	-	-	-	-	-	CRAB	24	24
<i>S. aureus</i>	44	29	1	10	-	3	1	MRSA VISA	44	25
<i>S. epidermidis</i>	10	-	6	-	3	1	-	MRS	10	13
<i>S. pseudointermedius</i>	3	-	-	-	2	1	-	MRS	3	3
<i>N. gonorrhoeae</i>	17	17	-	-	-	-	-	-	17	17
<i>E. faecium</i>	24	24	-	-	-	-	-	VRE	24	20
<i>E. faecalis</i>	2	2	-	-	-	-	-	VRE	2	-
<i>P. aeruginosa</i>	3	3	-	-	-	-	-	CRPA	3	-
Total	312	186	47	37	21	30	9	-	312	284

- ❖ The collection encompasses antimicrobial-resistant bacteria from diverse sources, including clinical patients, healthy individuals, animals, environmental samples, and food.
- ❖ Among the 312 isolates, 186 originated from human patients and 126 from non-clinical sources such as livestock, companion animals, and the environment.
- ❖ All isolates were characterized by both antimicrobial susceptibility profiles and genomic sequencing, with viable strains distributed through the National Culture Collection for Pathogens (NCCP) and corresponding genome assemblies deposited in the NCBI database.
- ❖ This cross-sectoral dataset provides a foundational resource for comparative analysis and supports integrated AMR surveillance across human, animal, and environmental domains.

Conclusions

- ❖ This integrated WGS-based AMR resource represents a unique national platform that combines genomic, phenotypic, and strain-level information. Future expansions incorporating isolates from national surveillance programs such as Kor-GLASS will strengthen multidisciplinary AMR research and enhance Korea's capacity for AMR monitoring, prevention, and control.

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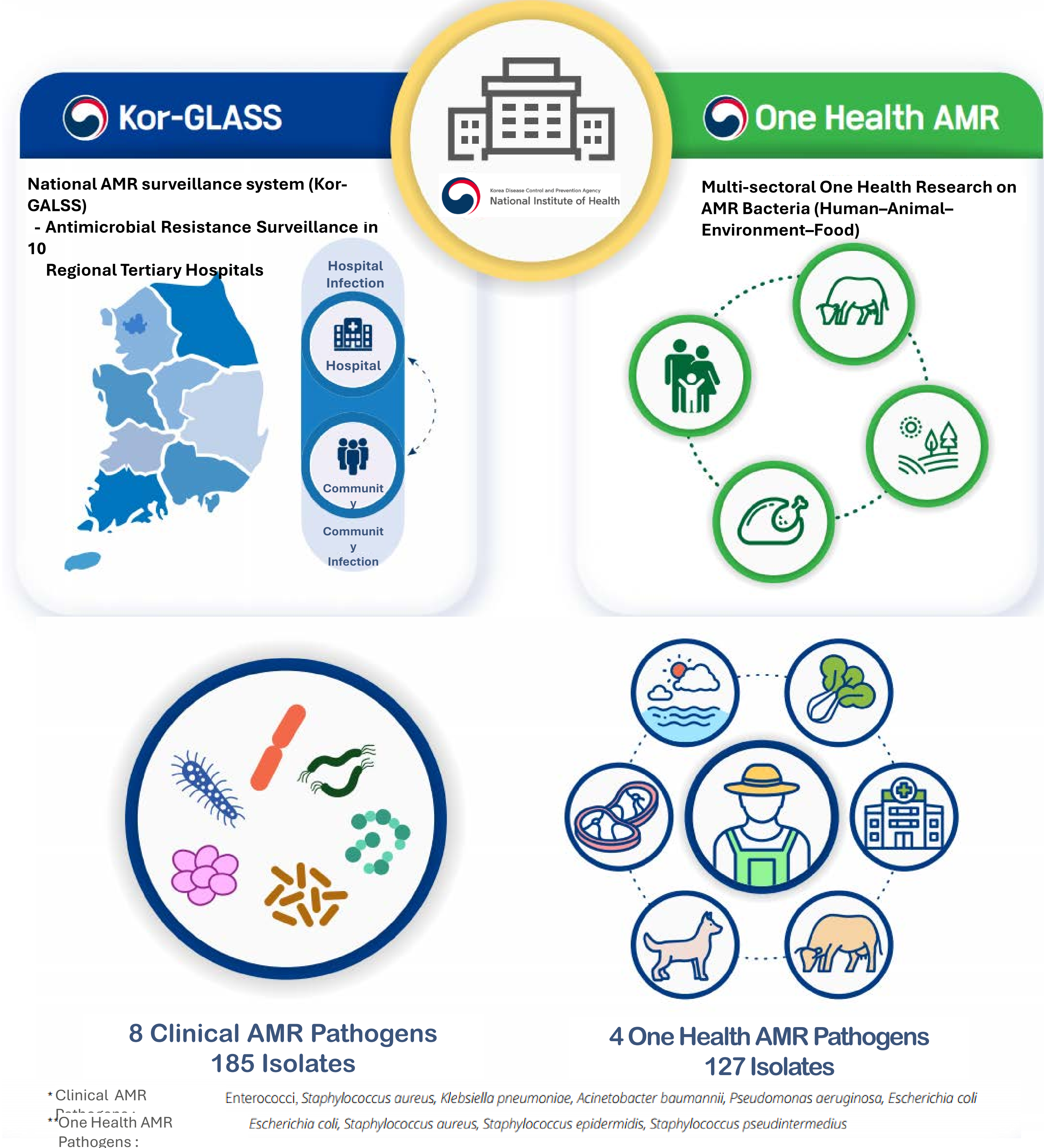


Figure 2. Clinical and One Health Surveillance Data Released as Public AMR Genomes

- ❖ In 2019, the Antimicrobial Resistance Research Division of the Korea National Institute of Health (KNIH) established the One Health AMR portal to connect antimicrobial resistance data from human, animal, environmental, and food sectors.
- ❖ This platform complements the national Kor-GLASS surveillance system, which monitors clinical AMR trends in tertiary hospitals, by expanding the scope to community and environmental reservoirs of resistance.
- ❖ Through this integrated framework, isolates and genomic data collected from both clinical and One Health surveillance programs are harmonized and shared, enabling cross-sectoral comparison and national-level resource management for AMR monitoring.

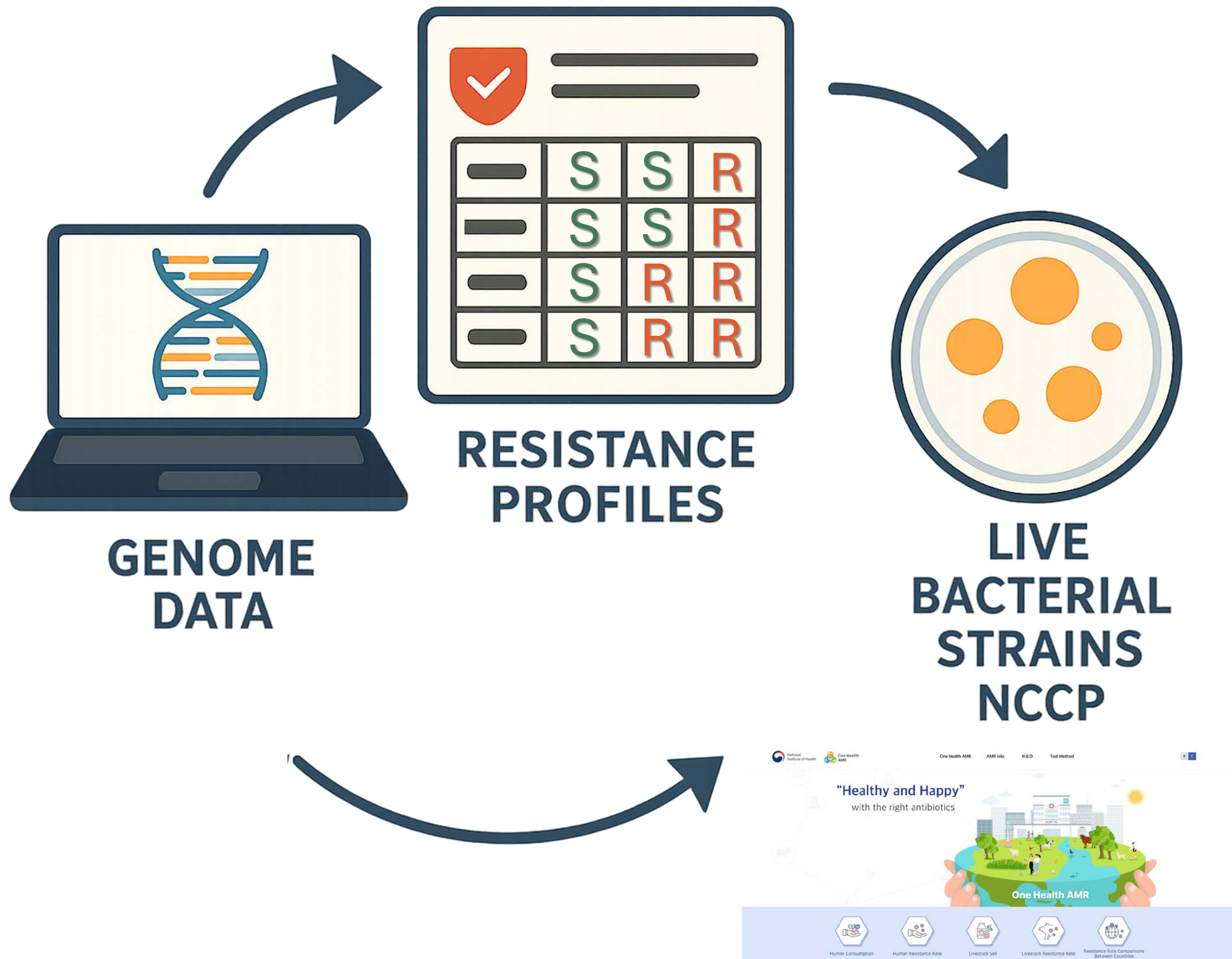


Figure 3. AMR Genomes with Resistance Profiles and Live Isolates

- ❖ In 2025, the portal was expanded through a national research program to include a new resource of multidrug-resistant (MDR) bacterial genomes. The platform integrates three components—genome data, resistance profiles, and live bacterial strains—providing matched datasets for advanced investigations.
- ❖ Live strains are supplied in collaboration with the National Culture Collection for Pathogens (NCCP), enabling access to both genomic data and corresponding isolates.

Reference

- ❖ Korea Disease Control and Prevention Agency. (2025). Open release of multidrug-resistant bacterial genome resources (다제내성균 유전체자원 공개) [Card news]. Cheongju: KDCA.
- ❖ Korea Disease Control and Prevention Agency, National Institute of Health. (2025). National AMR Genome Resource Portal. Retrieved from <https://www.nih.go.kr/nohas/>

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