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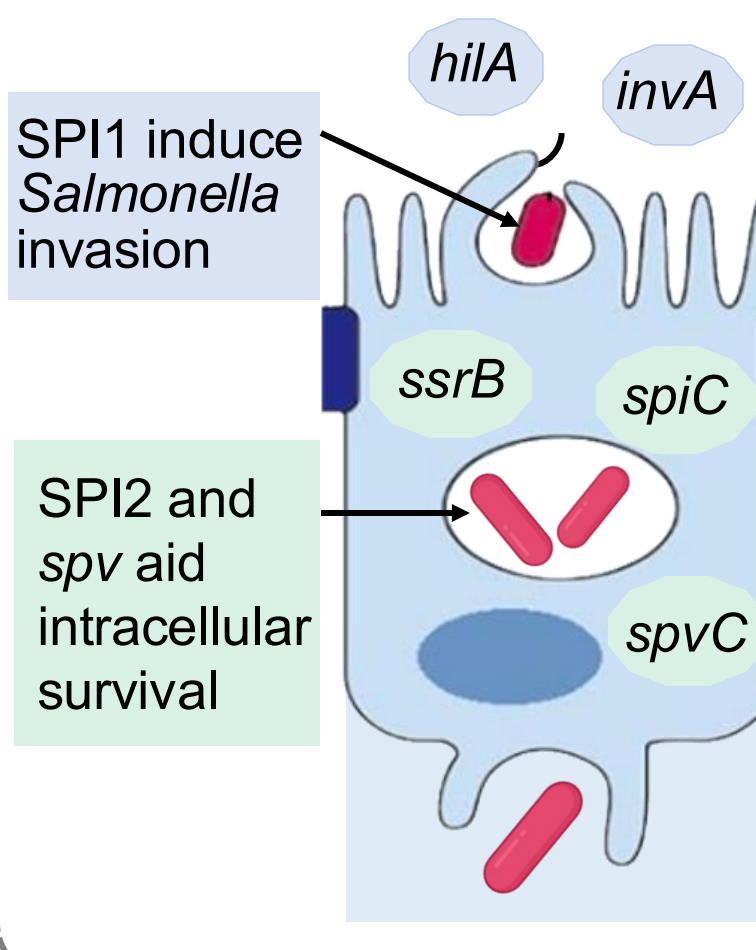
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Introduction

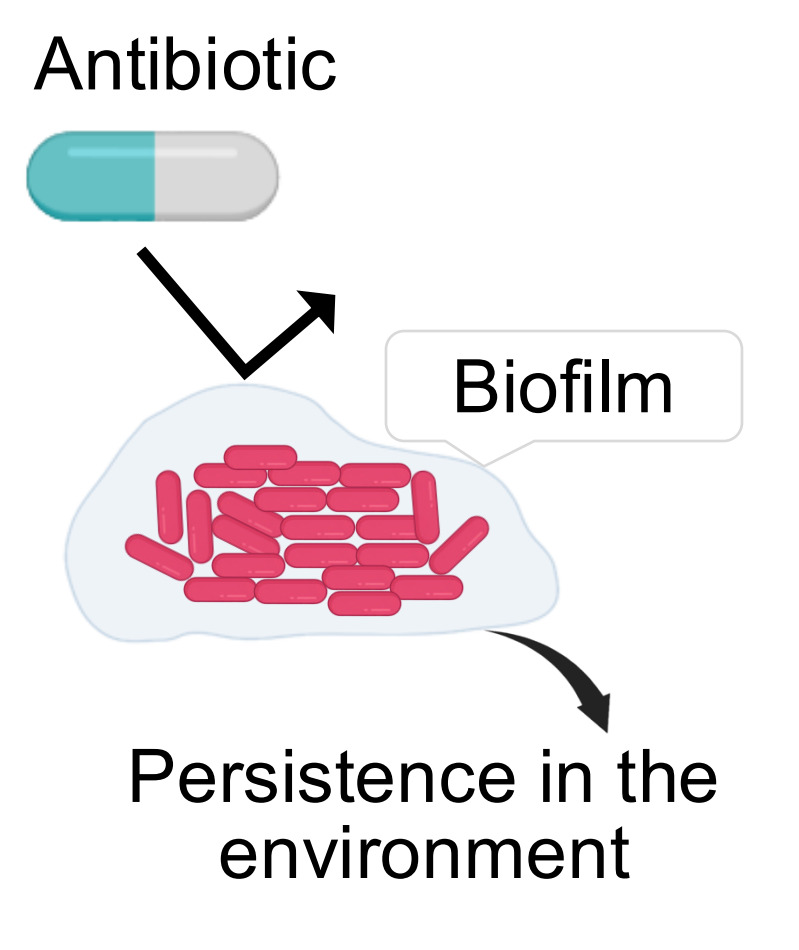
Non-typhoidal *Salmonella* (NTS)

- Gram-negative, rod-shaped bacilli, facultative anaerobe
- Over 2500 serotypes reported
- Causes food poisoning in humans

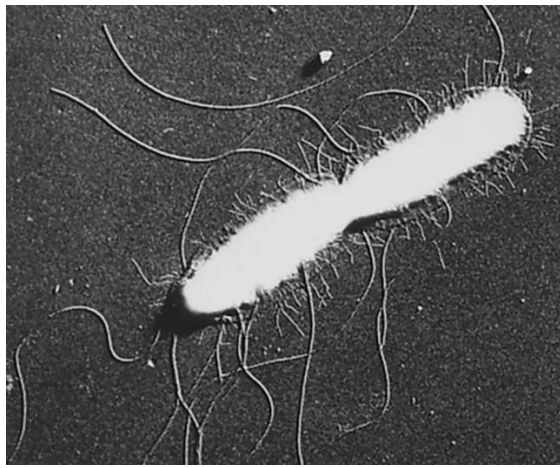
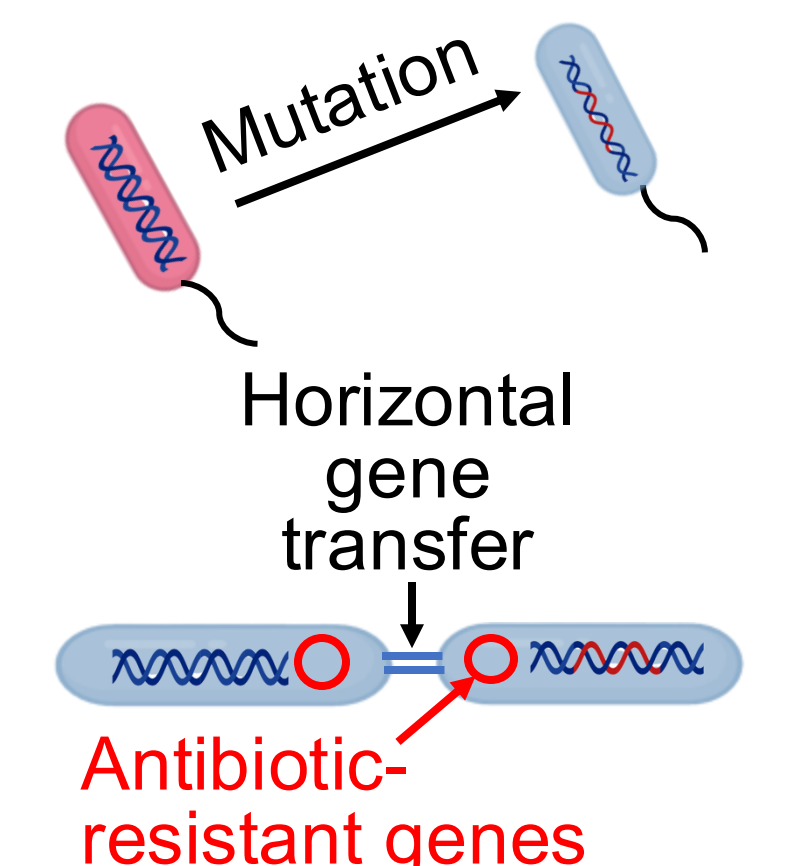
Virulence genes



Biofilm formation



Antimicrobial resistance (AMR)



Enhanced bacterial survival and spread

Serious risks to human

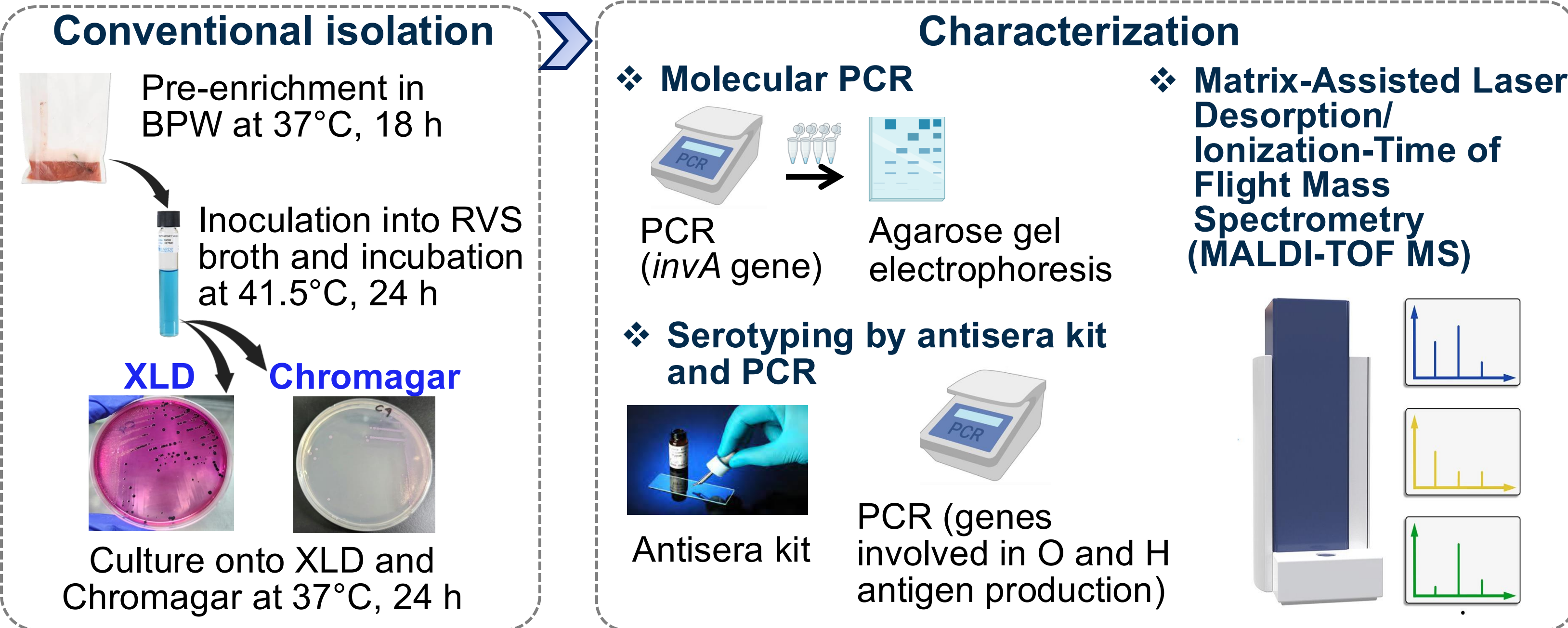
Objectives

- To determine the prevalence and serotype of NTS from chicken meat
- To characterize the virulence genes and biofilm formation ability of NTS isolates
- To investigate the antimicrobial resistance of NTS isolates
- To estimate the genetic diversity of NTS isolates

Materials and Methods

1. Detection of NTS in chicken meat

- A total of 50 chicken samples were collected from retail shops in Fukuoka, Japan.

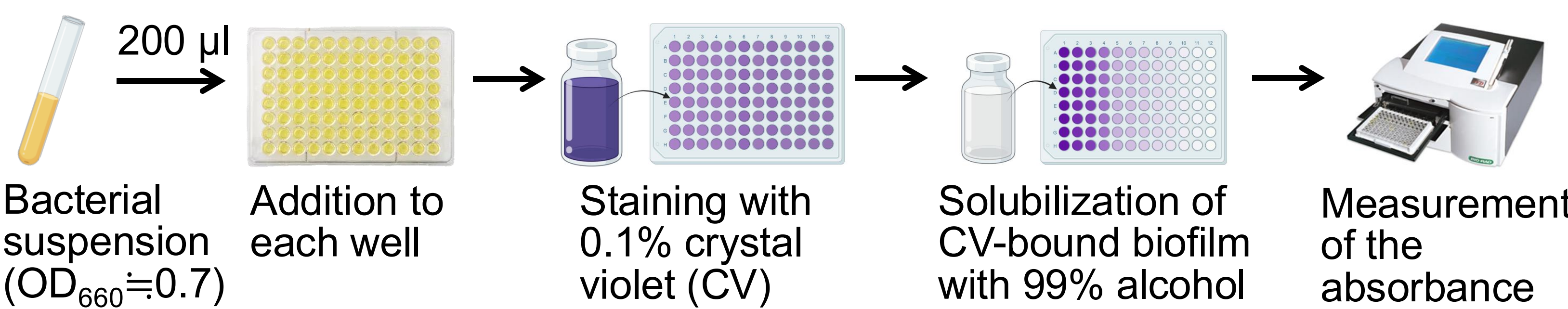


2. Virulence genes detection

- *hilA*, *ssrB*, *spiC*, and *spvC* genes were detected by PCR.

3. Biofilm formation

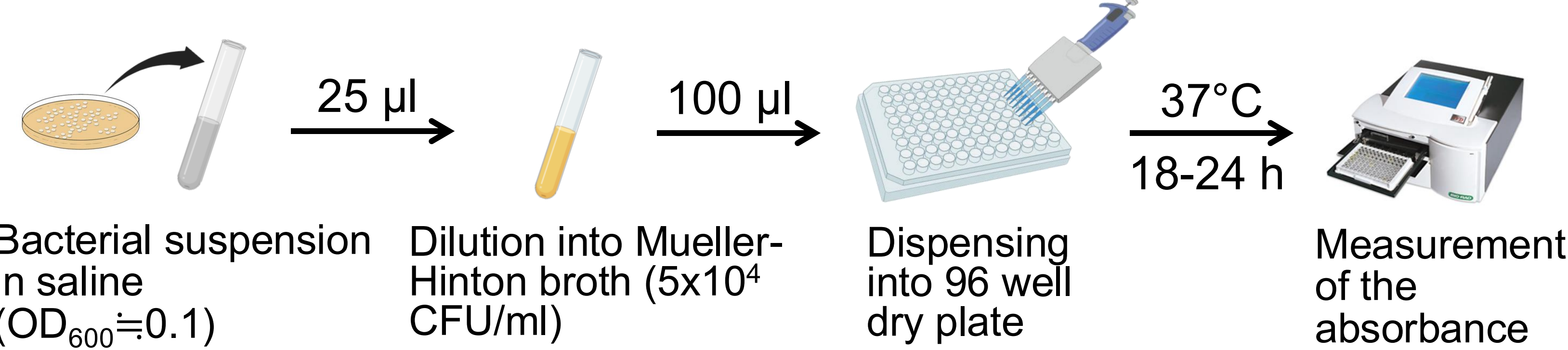
- All the *Salmonella* strains were evaluated by microtiter plate assay.



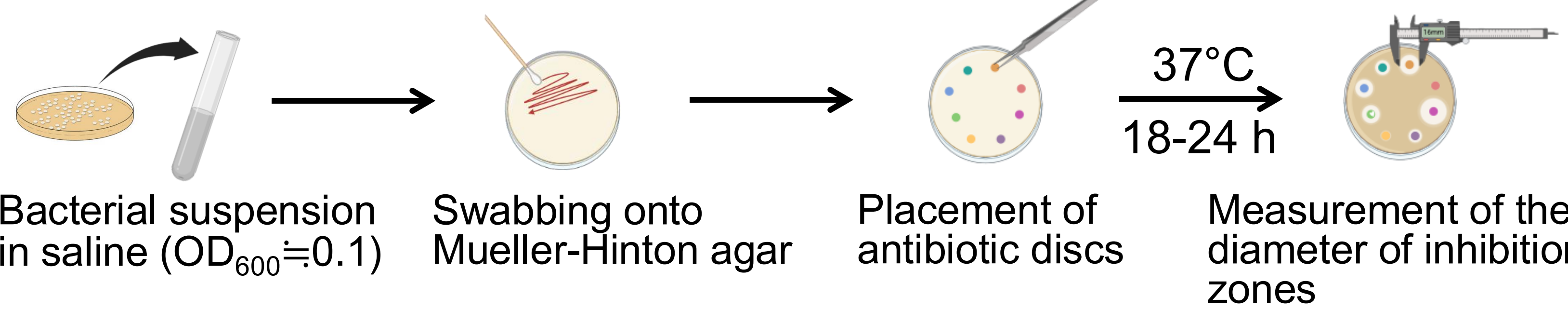
4. Antimicrobial susceptibility test

- Susceptibility against 25 antimicrobials was tested by two methods.

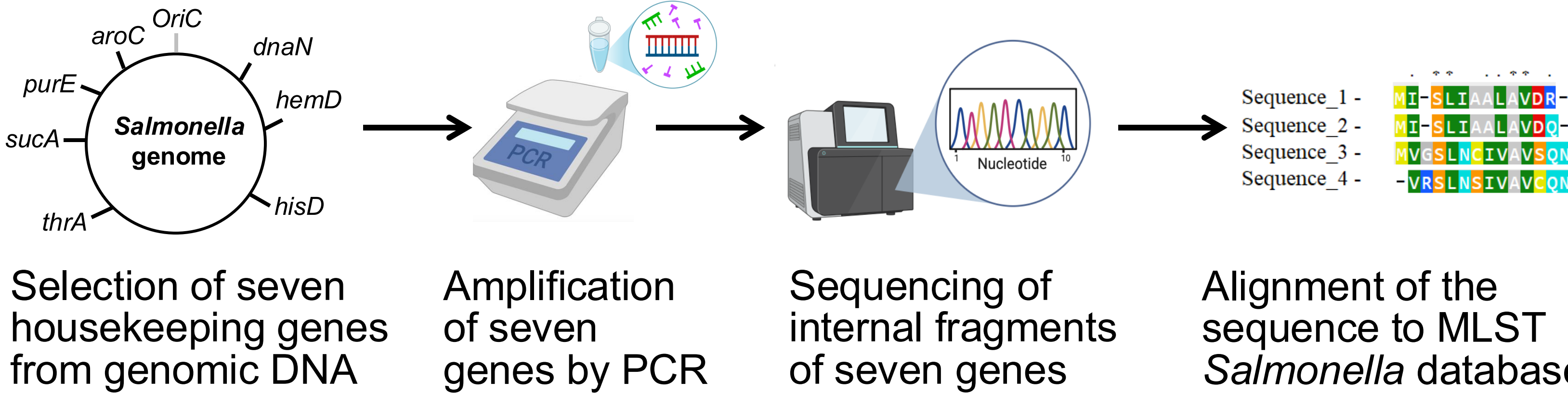
- ❖ Microbroth dilution method using DP-31 96-well dry plate



- ❖ Disc diffusion method using antibiotic discs



5. Multi-locus sequence typing



Conclusion

	<i>S. Schwarzengrund</i>	<i>S. Thompson</i>	<i>S. Oranienburg</i>
Prevalence	78.1%	15.6%	6.3%
Virulence genes			
<i>hilA</i>	100%	100%	100%
<i>ssrB</i>	100%	100%	100%
<i>spiC</i>	96%	100%	100%
Biofilm strength	Strong (84%) Moderate (16%)	Moderate (20%) Weak (80%)	Weak (100%)
AMR profile	MDR	No resistance	No resistance
Sequence type	241	26	23

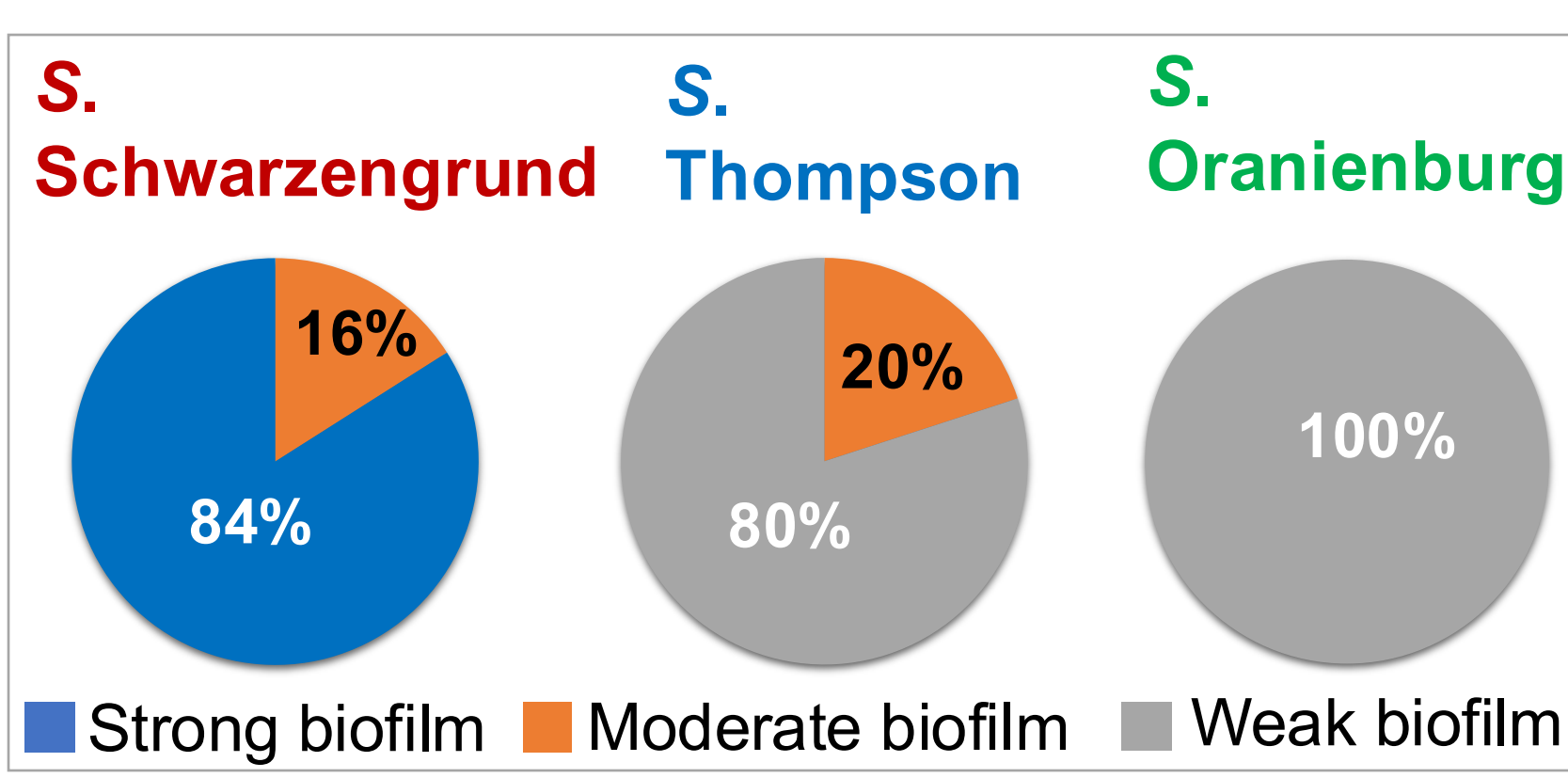
The findings in this study highlight the need for ongoing surveillance and control efforts on broiler farms.

Results

1. Prevalence of NTS in chicken meat

No. Serotype	No. of isolate (%)
1 <i>S. Schwarzengrund</i>	25 (78.1)
2 <i>S. Thompson</i>	5 (15.6)
3 <i>S. Oranienburg</i>	2 (6.3)

3. Biofilm formation



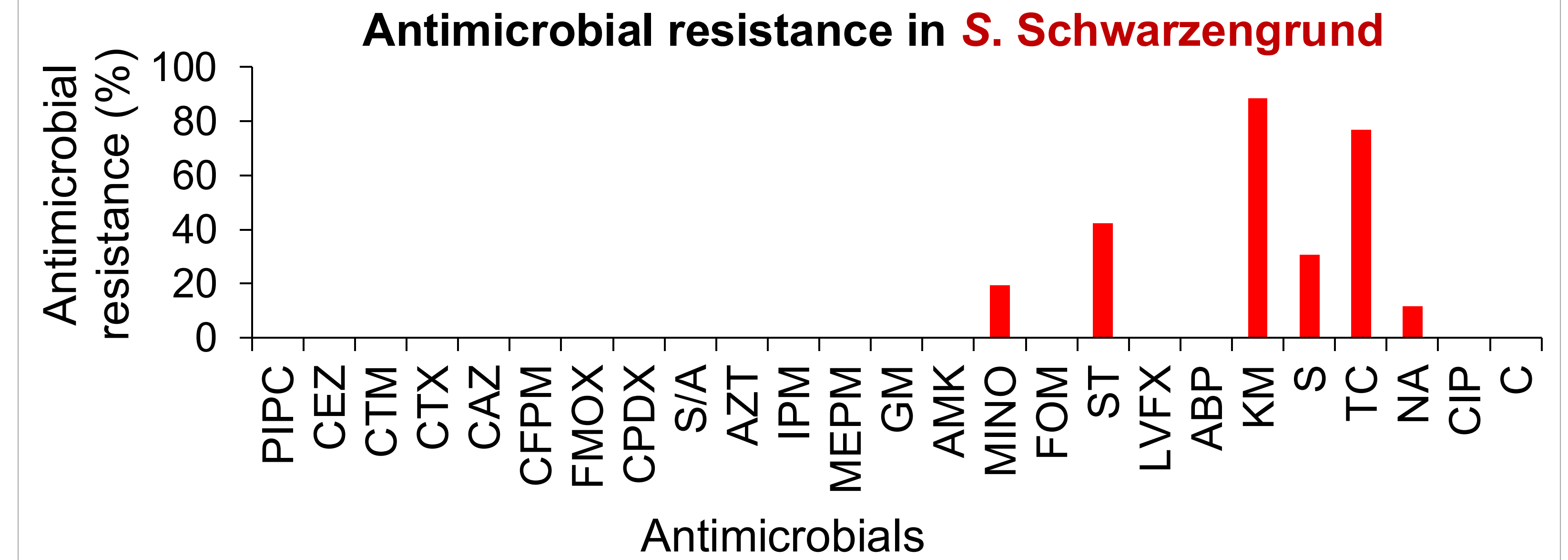
2. Virulence genes

Genes	No. of positive strains (%)		
	S. Schwarzengrund	S. Thompson	S. Oranienburg
hilA	25 (100)	5 (100)	2 (100)
ssrB	25 (100)	5 (100)	2 (100)
spiC	24 (96)	5 (100)	2 (100)
spvC	ND (0)	ND (0)	ND (0)

ND: Not detected

4. Antimicrobial resistance

- All the *S. Thompson* and *S. Oranienburg* isolates were susceptible to all the antimicrobials tested.
- *S. Schwarzengrund* isolates were resistant to multiple antimicrobials.



5. Sequence types

ST	No. of isolate	Clonal complex	Serotype
241	25	33	<i>S. Schwarzengrund</i>
26	5	28	<i>S. Thompson</i>
23	2	41	<i>S. Oranienburg</i>

Methods

6. Principal component analysis (PCA) dendrogram

- A PCA dendrogram was generated from MALDI-TOF MS spectral data.

Results

6. PCA dendrogram

- ❖ It showed six clusters (I-VI), indicating considerable protein diversity among the isolates.
- ❖ Some isolates with the same serotypes, STs, AMR profiles, virulence genes, and biofilm formation patterns were clustered together.

