

# Genome Characterization and Antimicrobial Resistance Gene Profile of Non-Typeable *Streptococcus pneumoniae* Isolates in Indonesia

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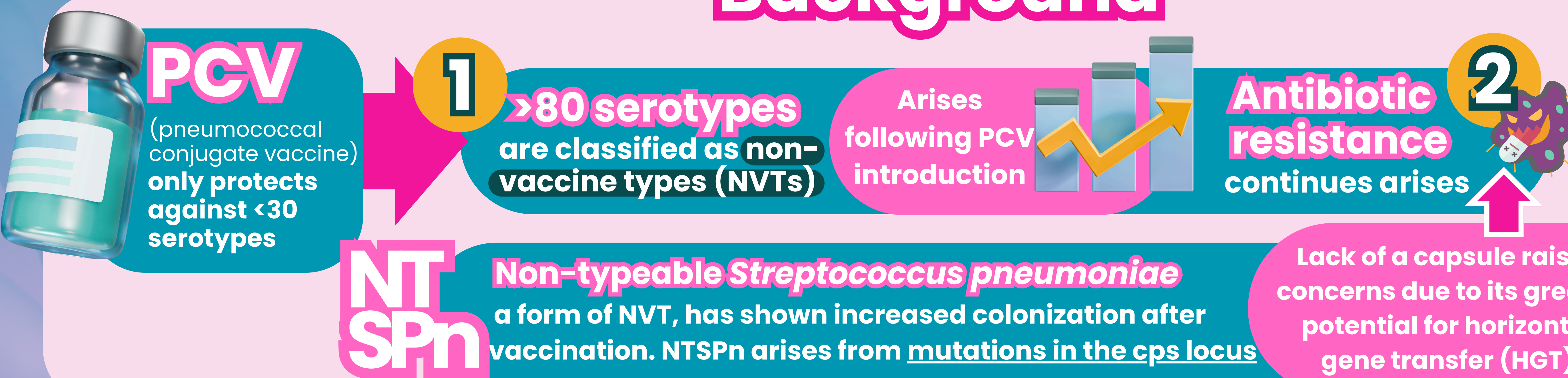
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## Background

## Aim

This study aims to identify the antimicrobial resistance (AMR) gene profile in NTSPn isolates.



## Methods

### Sample Collection



### Bacterial Isolation & Identification



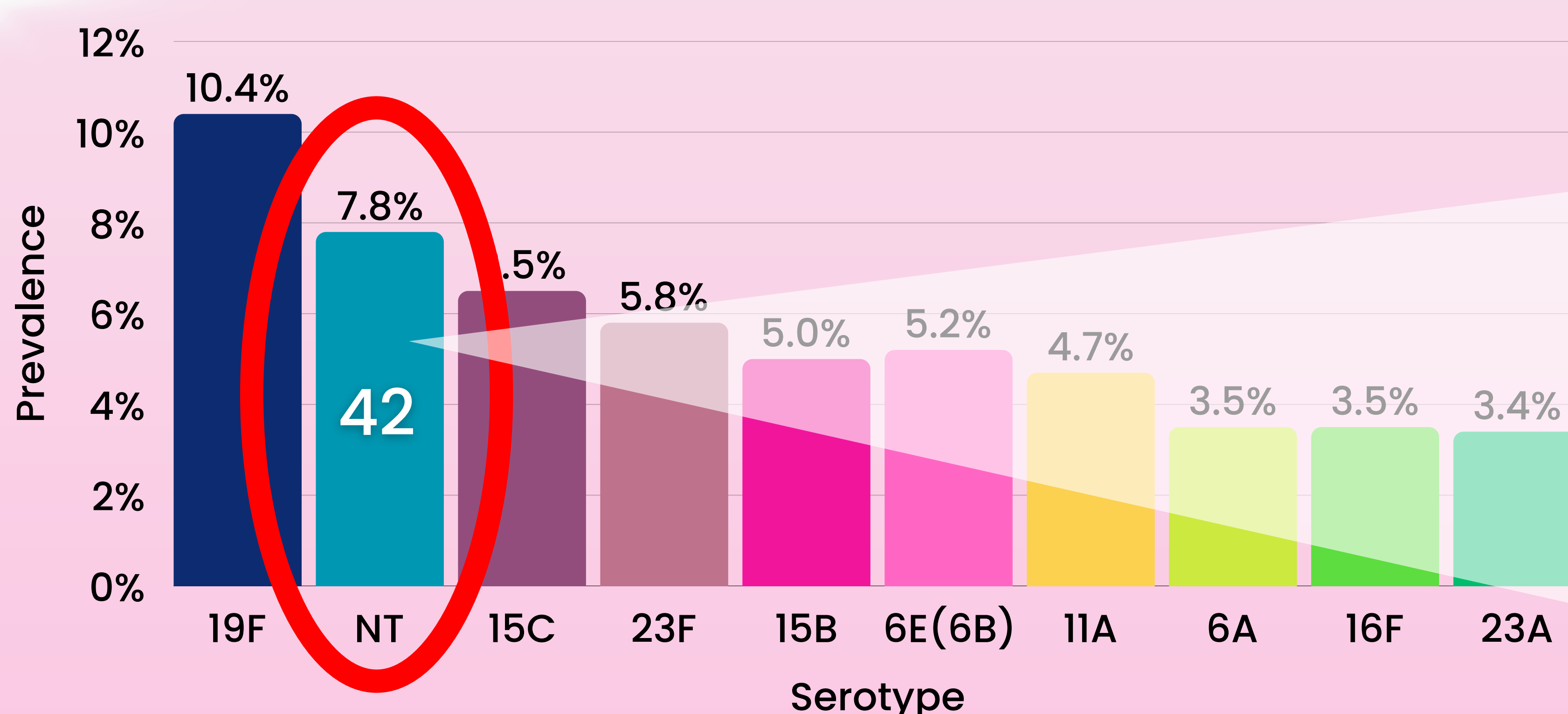
### DNA Extraction



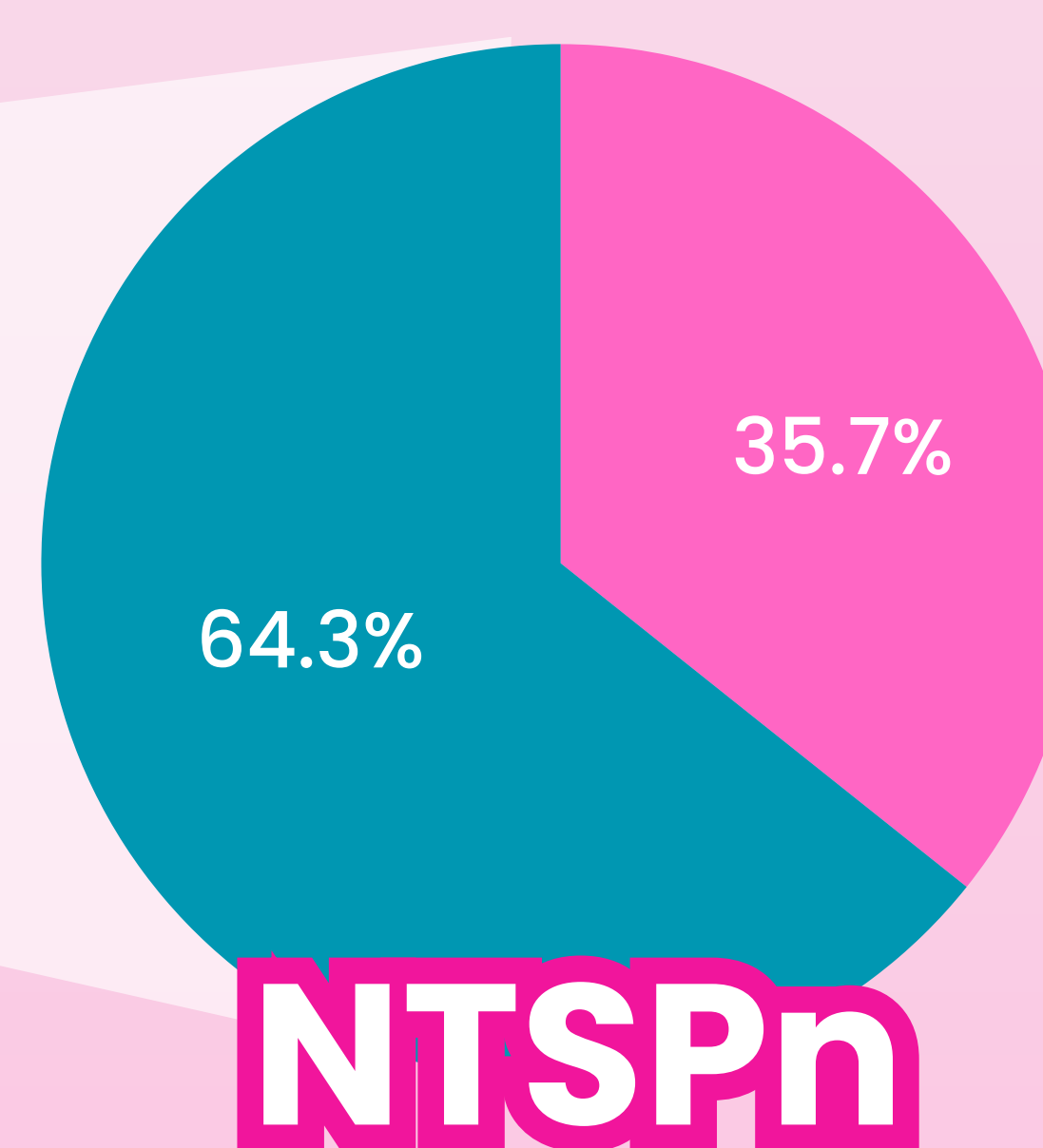
### Whole Genome Sequencing (WGS)



### Bioinformatic Analysis



Carried *pspK* gene  
Did not carry the *pspK* gene



## Results

Among 536 *Streptococcus pneumoniae* isolates, 42 isolates (7.8%) were identified as NTSPn, with 15 isolates carried the *pspK* gene, thus classified non-encapsulated clade NCC1.

	Spn_003	Spn_019	Spn_027_a	Spn_028	Spn_072	Spn_074	Spn_076	Spn_079	Spn_083	Spn_085	Spn_111	Spn_252	Spn_279	Spn_288	Spn_315	Spn_325	Spn_327	Spn_334	Spn_350	Spn_372	Spn_410	Spn_420	Spn_439	Spn_454	Spn_80	Spn_1051	Spn_1293	Spn_1308	Spn_1321	Spn_1385	Spn_1404	Spn_1528	Spn_011	Spn_028	Spn_053	Spn_079	Spn_086	Spn_142	Spn_188	Spn_151	Spn_027_b	Spn_322	
<i>folP</i>																																											
<i>folA</i>																																											
<i>tetM_12</i>																																											
<i>tetM_2</i>																																											
<i>tetM_1</i>																																											
<i>mefA_10</i>																																											
<i>ermB</i>																																											

Co-trimoxazol

Tetracycline

Macrolides

AMR determinant gene were detected in 35 NTSPn isolates (83.3%), with in silico predictions. Notably, 33 isolates (78.6%) exhibited resistance or intermediate susceptibility to co-trimoxazole, associated with point mutations of *folA* and *folP* genes, tetracycline resistance was observed in 28 isolates (66.7%) carrying the *tetM* gene, while macrolide resistance (7.1%) was associated the presence of *ermB* and *mefA* genes.

## Conclusion

This study highlights significant AMR profile in NTSPn isolates, with co-trimoxazole showing the highest resistance rate associated with mutations in *folA* and *folP* genes