

## FOLLOWING A DECADE OF PCV IN THE GAMBIA SHOULD A DECLINE IN RESISTANCE BE ANTICIPATED? (ID 1205)

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### Abstract

#### Background

*Streptococcus pneumoniae* is one of the priority pathogens in need of new antibiotics. Vaccines have the potential to curb anti-microbial resistance. Here we employ genomics to examine the distribution of AMR genes within vaccine and non vaccine serotypes in rural areas of The Gambia prior to the nationwide introduction of PCV7.

#### Methods

We studied a genomic dataset of 150 [85 (56.7%) VT and 65 (43.3%) NVT] *S. pneumoniae* isolated through a carriage surveillance conducted in 2009, before the introduction of PCV7. We compared the profiles of anti-microbial resistant genes in vaccine and non-vaccine serotypes.

#### Results

Three resistant genes were found in the dataset *tet*, *cat*, and *ermC*, which conferred resistance to tetracycline, chloramphenicol, and erythromycin, respectively. The *tet*, *cat* and *ermC* genes were present in 66(46%), 12(8%) and 1(0.7%), genomes respectively. The rates of *tet* gene presence in vaccine serotypes was higher although this difference was not significant (OR 2.34, p-value 0.997, CI 0-4.38), *cat* and *ermC* genes had low prevalence, which resulted to no significant differences.

#### Conclusions

We have observed that AMR genes prevailed more in VT than NVT. It will be interesting to measure the distribution of *tet*, *cat* and *ermC* resistant genes post vaccine era.