



Microbiology of the Nasopharynx in Children Hospitalized with Suspected Pulmonary Tuberculosis

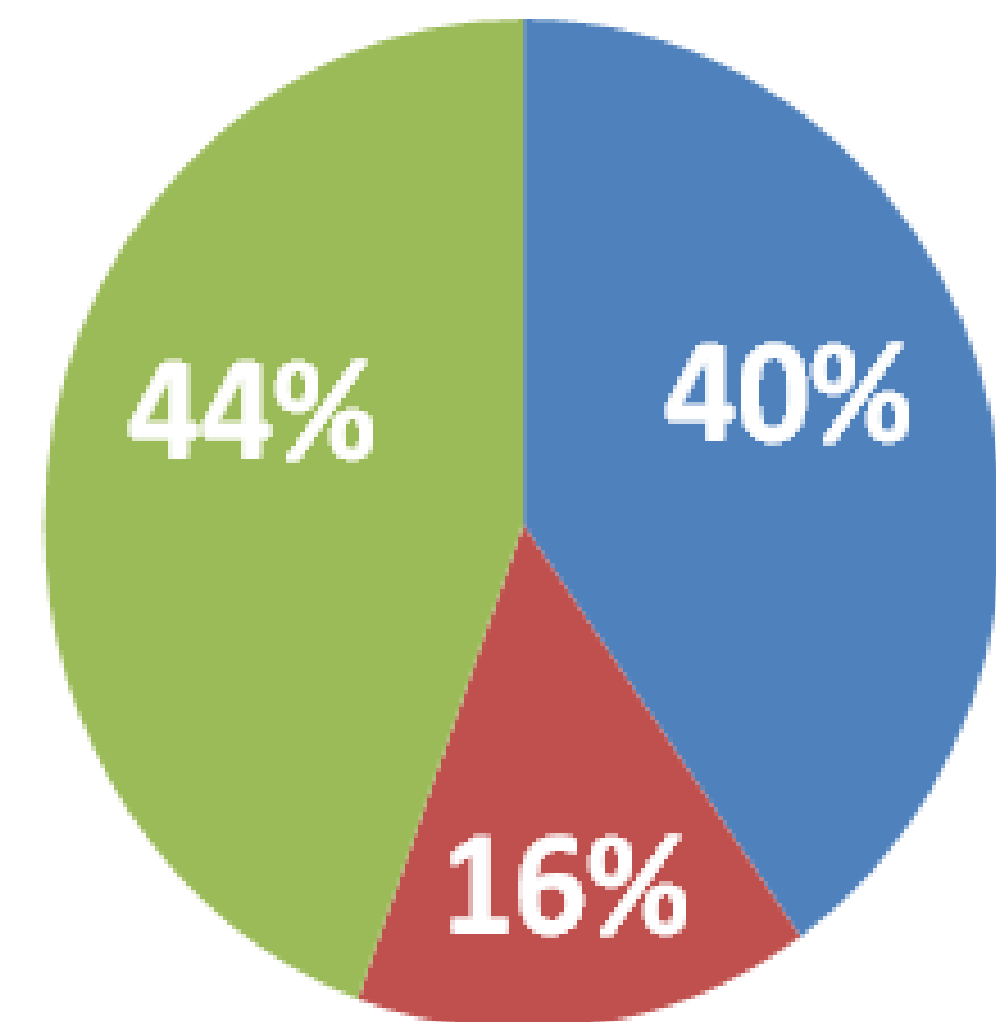


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Background and rationale:

- Lower respiratory tract infections : - leading causes of mortality and morbidity in children under the age of 5 years.
 - **nearly 1.4 million deaths** every year globally [1].
- The burden of childhood tuberculosis and its impact on child health has been under-recognized, partly due to difficulties in confirming diagnosis [2]. This is further confounded by other concurrent respiratory tract infections [3].
- In our setting: - **only 16%** of children with pulmonary tuberculosis (TB) are treated based on culture confirmed TB;
 - **40% of patients** are treated based on clinical and radiological features, whereas **TB is clinically excluded in 44%** of patients.

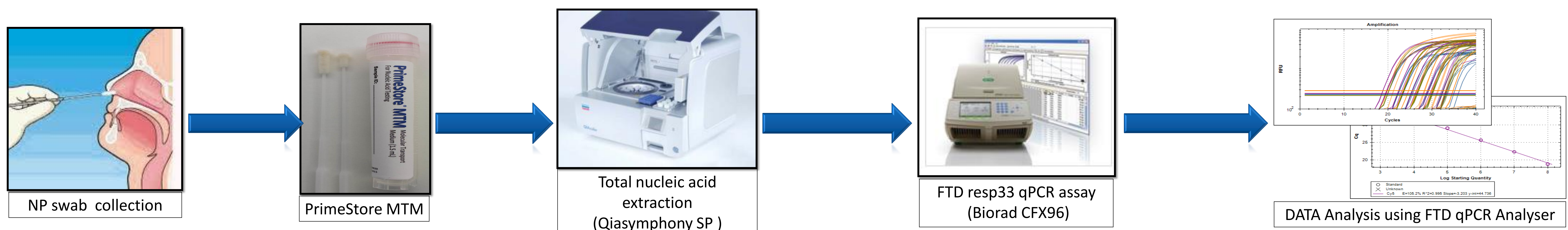


Aim:

- To identify other potential respiratory pathogens in children hospitalised with suspected pulmonary TB

Materials and methods:

- Children with signs or symptoms suggestive of TB were investigated for TB and were categorized as definite TB (culture confirmed), NOT TB (not clinically diagnosed and improved on follow-up without TB treatment) and others (Possible TB). A nasopharyngeal (NP) swab was taken from all children, placed in PrimeStore and processed as below.



Results:

- 214 children** enrolled: median age, 36 months (interquartile range, [IQR] 5 – 17 months).
- Most common bacteria detected (Figure 1):** *Moraxella catarrhalis* (64%), *Streptococcus pneumoniae* (42%), *Haemophilus influenzae* (29%) and *Staphylococcus aureus* (22%).
- Other bacteria: *Mycoplasma pneumoniae* (9%), *Bordetella pertussis* (7%) and *Chlamydomphila pneumoniae* (4%).
- M. catarrhalis* and *S. pneumoniae* appeared concurrently in 49% of cases where at least one was detected.**
- Most common viruses (Figure 2):** metapneumovirus (19%), rhinovirus (15%), influenza C (9%), adenovirus (7%), cytomegalovirus (7%) and coronavirus OC43 (5.6%).
- Coronavirus OC43** was associated with definite TB ($p = 0.024$).
- Linear discriminant analysis (Figure 3):**
 - could not discriminate distribution of respiratory pathogens detected in the **three** TB categories.
 - no clear difference in the distribution of respiratory pathogens between children with and without TB.

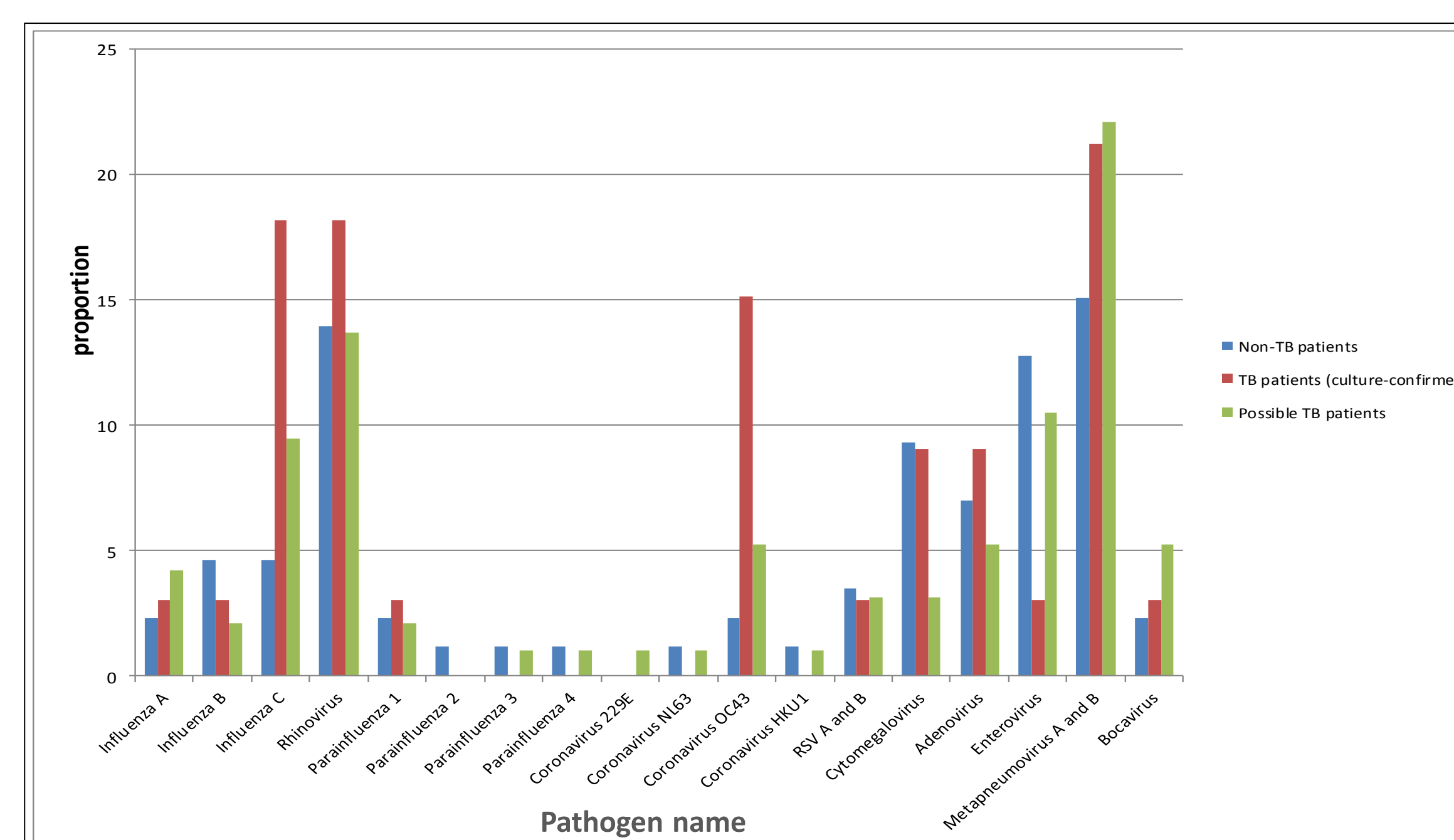


Figure 1. Diversity of bacterial and fungal pathogens detected

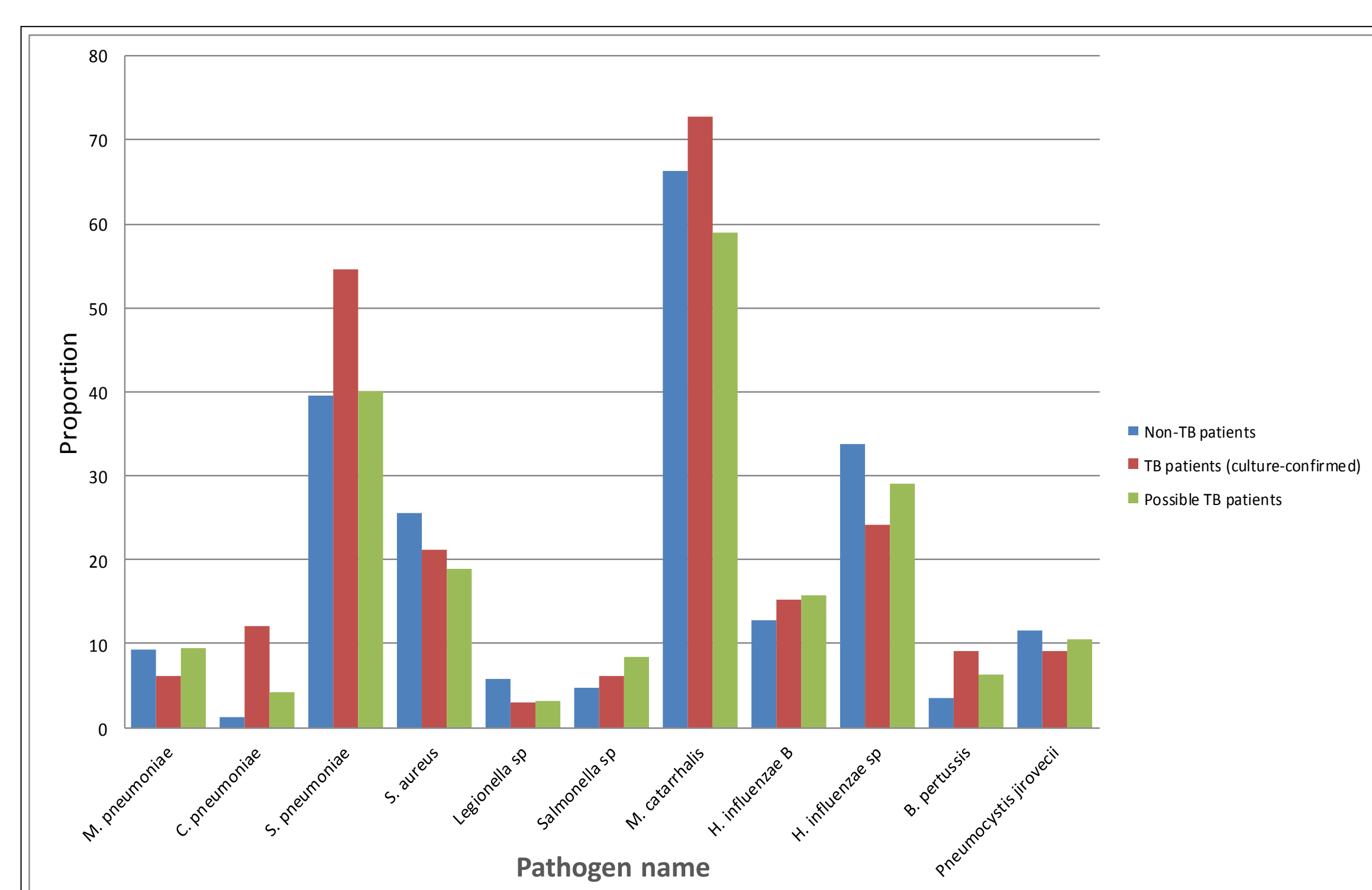


Figure 2. Diversity of respiratory viruses detected

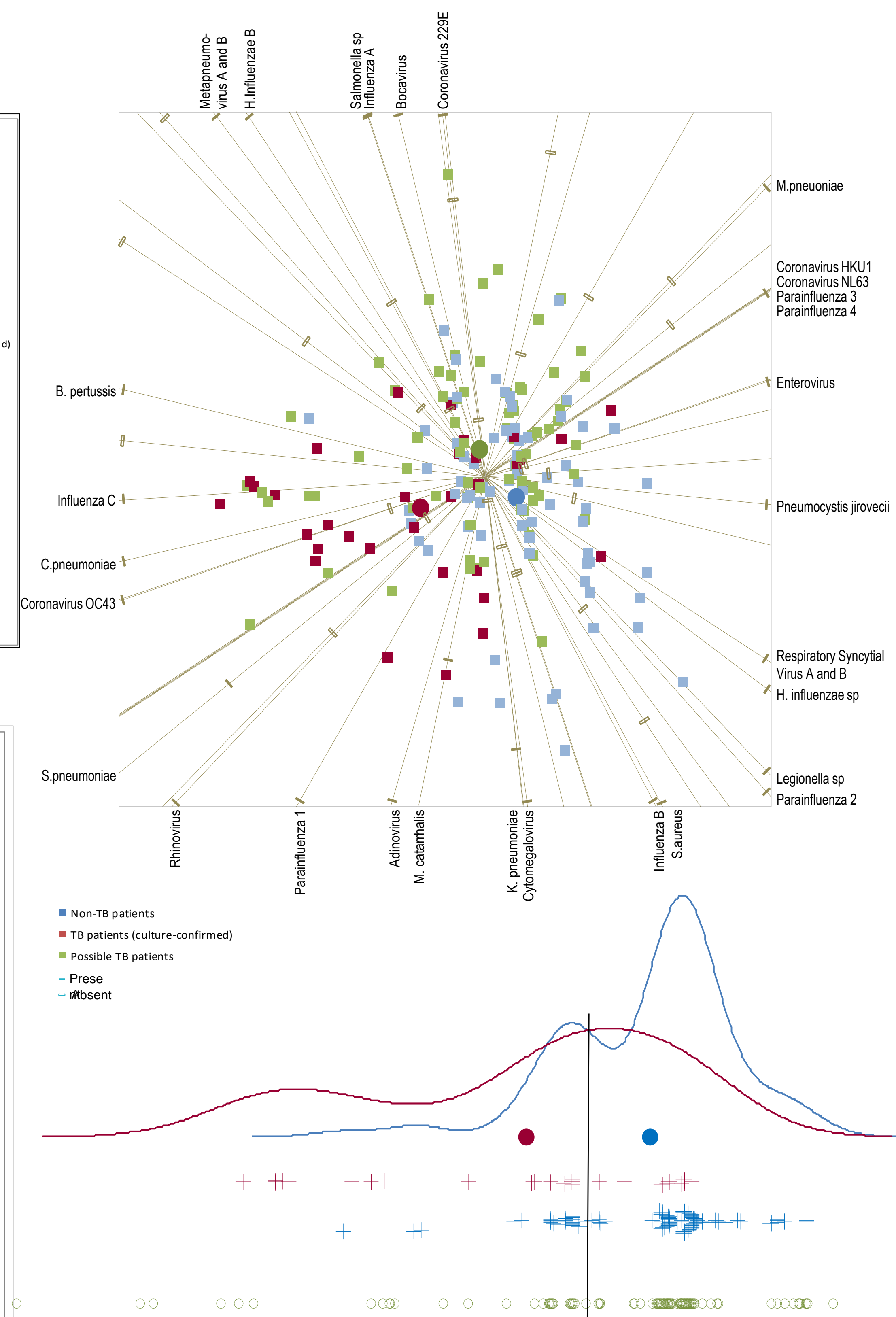


Figure 3. Cononical variate analysis (CVA) plot

Discussion and Conclusion:

- There was no relationship between TB categorization and co-infection/colonisation with other pathogens detected; either when comparing all 3 categories (TB, Non-TB and Possible TB) or when restricting the comparison to TB and Non-TB patients
- Further work is needed to explore possible pathogen interactions and determine prevalence, in a control group of children, of nasopharyngeal colonisation with the pathogens identified.

References:

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- Zar HJ, Workman L, Isaacs W, Munro J, et al. Rapid molecular diagnosis of pulmonary tuberculosis in children using nasopharyngeal specimens Clin Infect Dis 2012, 55(8):1088-1095
- Moore DP, et al Role of Streptococcus pneumoniae in hospitalization for acute community-acquired pneumonia associated with culture-confirmed M. tuberculosis in children: a pneumococcal conjugate vaccine probe study. Pediatr Infect Dis J. 2010 Dec;29(12):1099-04.

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