

## Identification of bacteria by amplification gene encoding 16s rRNA and antibiotics resistance test from pneumonia outpatients

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### Abstract

The bacteria that cause upper respiratory tract infections (URTI) pneumonia have become resistant due to the use of various antibiotics. The aims of this study were to identify the bacteria in URTI pneumonia outpatient samples and test resistance to some antibiotics. The bacteria were isolated from sputum sample of outpatients in a hospital in Garut West Java Indonesia and tested for gram staining. Then, isolation of bacterial chromosome and amplification of gene encoding 16s rRNA was performed using polymerase chain reaction method. The isolated bacteria were analyzed for antibiotic resistance to amoxicillin 30 µg/10 µg, cefadroxil 30 µg/10 µg, trimethoprim 5 µg/10 µg, sulfamethoxazole 300 µg/10 µg, ceftriaxone 30 µg/10 µg and cefotaxime 30 µg/10 µg. The PCR primers for the gene encoding 16s rRNA of *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Klebsiella variicola*, *Pseudomonas geniculata*, and *Serratia marcescens* were designed based on gene database; <http://blast.ncbi.nlm.nih.gov>. The result of resistance test showed that ceftriaxone and cefotaxime inhibited those bacteria while there were no inhibition zones of amoxicillin and cefadroxil except against to *K. variicola*. In addition, trimethoprim had no activity on *P. aeruginosa* and *P. geniculata*. Likewise, sulfamethoxazole had no activity against *E. cloacae* and *P. geniculata*. The isolated bacteria from URTI pneumonia outpatients are believed to cause hospital acquired pneumonia which had become resistant to amoxicillin, cefadroxil, trimethoprim and sulfamethoxazole.

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**Keywords:** URTI pneumonia bacteria; 16s rRNA; PCR; sequencing; resistance test

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