

## EXPANSION OF MULTIPLE VIRULENCE DETERMINANTS HARBOURING *Escherichia coli* WITHIN A CLINICAL SETTING OF NORTH-EAST INDIA

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### INTRODUCTION

An evolutionary route to pathogenicity is considered to be provided by the acquisition of virulence genes. Presence of specific virulence gene combinations in *Escherichia coli* is linked to various infections. One major public health concern is the presence of pathogenic *Escherichia coli* in the clinical settings as they are the most common organism causing nosocomial infections. Therefore, this study aimed at investigating the occurrence of different virulence determinants harbouring *Escherichia coli* isolates in a tertiary referral hospital in the North-Eastern part of India.

### OBJECTIVES

- Identification and characterization of virulence genes in clinical *Escherichia coli* isolates
- Antibioqram profiling of the virulent isolates

### METHODOLOGY

Consecutive non-duplicate, clinical isolates of *Escherichia coli* were obtained from the patients admitted to different wards of Silchar Medical College and Hospital

Genotypic characterization of different types of virulence genes of *Escherichia coli* was performed by Multiplex PCR and further confirmed by Simplex PCR

Antibioqram profiling of the virulent *Escherichia coli* isolates against various antibiotics was determined by using Kirby-Bauer Disc Diffusion Method

Clonal analysis of the virulence determinants harbouring *Escherichia coli* isolates was performed by ERIC PCR and a supporting dendrogram was plotted by using NTSYS software

### RESULTS

Out of the tested 61 *Escherichia coli* isolates, 25 isolates were harboring different virulence genes. Seven different types of virulence genes namely *chuA*, *arpA*, *yjaA*, *iutA*, *fyuA*, *fimH* and *papC* were detected within the tested clinical *Escherichia coli*. Highest resistance pattern against Ampicillin followed by Imipenem and Ceftriaxone were observed. ERIC PCR revealed twenty-three different haplotypes of *Escherichia coli*.

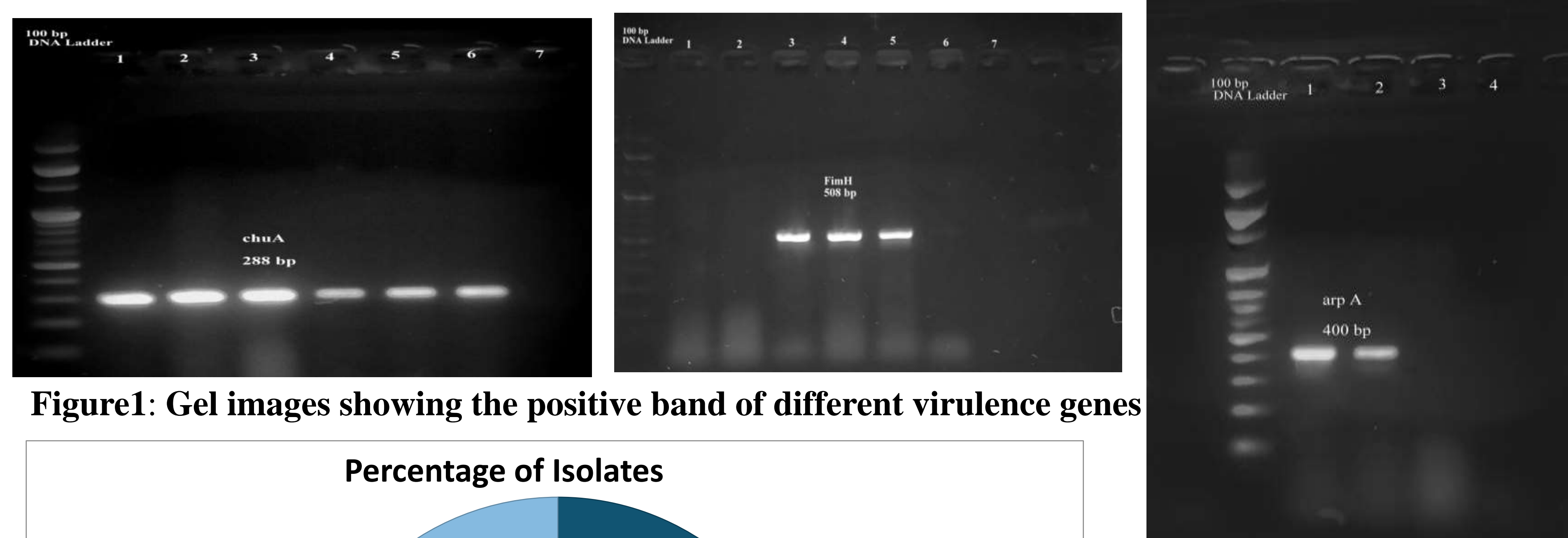


Figure1: Gel images showing the positive band of different virulence genes

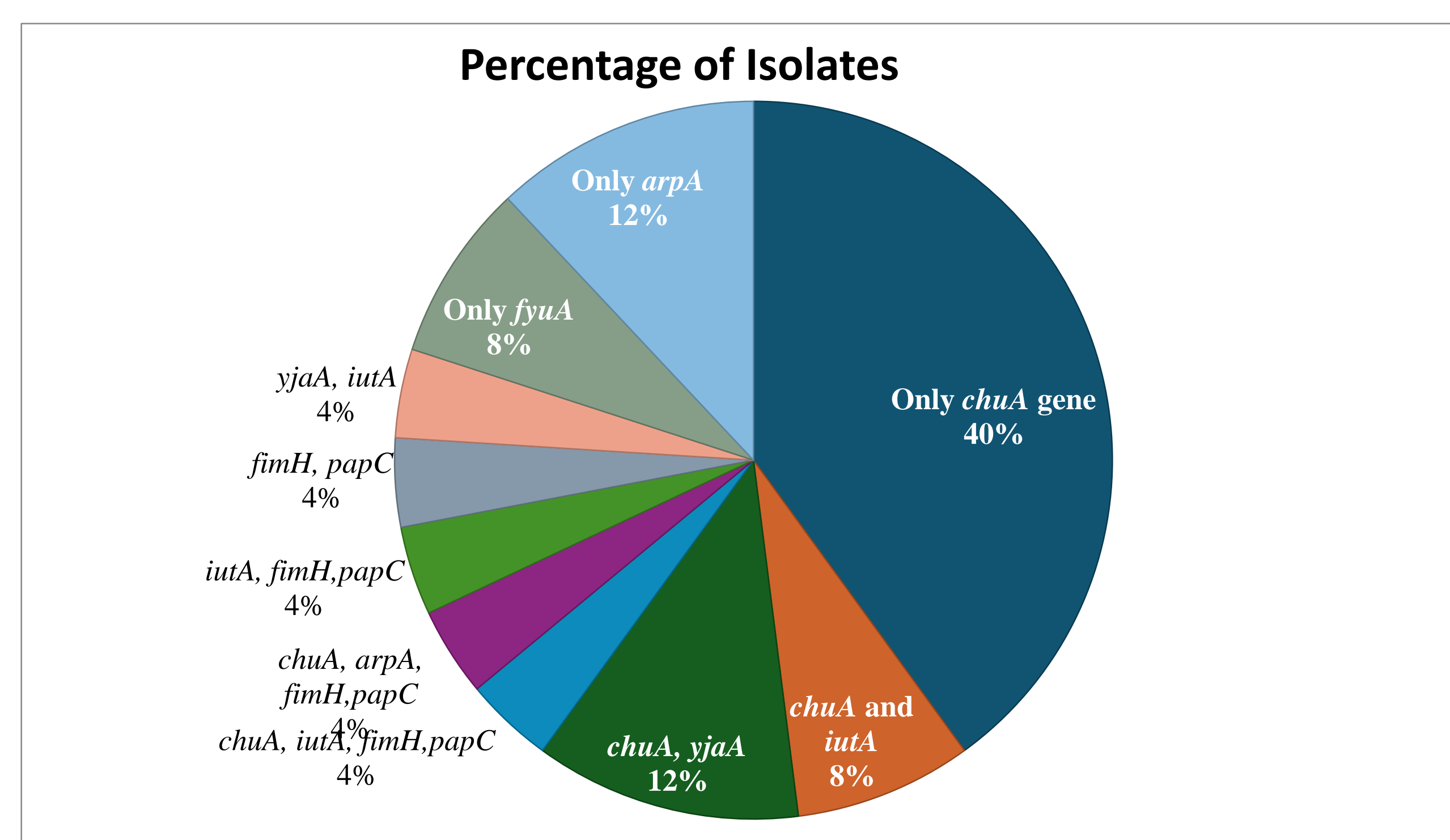


Figure 2: Percentage of isolates harbouring different virulence genes

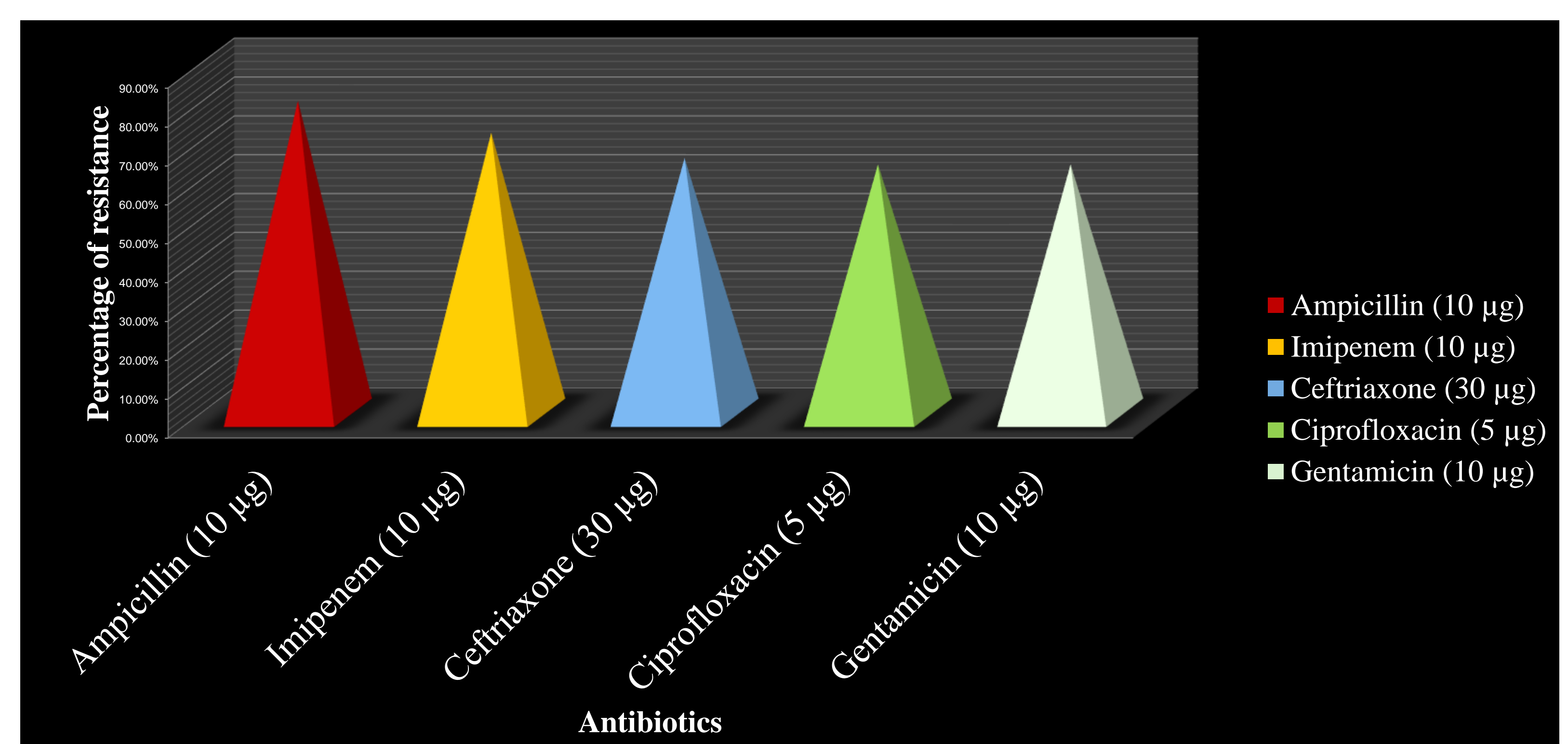


Figure 3: Resistance pattern of the isolates against different antibiotics

### CONCLUSIONS

This study revealed the presence of multidrug-resistant, multiple virulence gene harbouring *Escherichia coli* isolates highlighting the risk of dissemination of these virulence determinants causing a grave concern for infection control and prevention in the clinical settings.

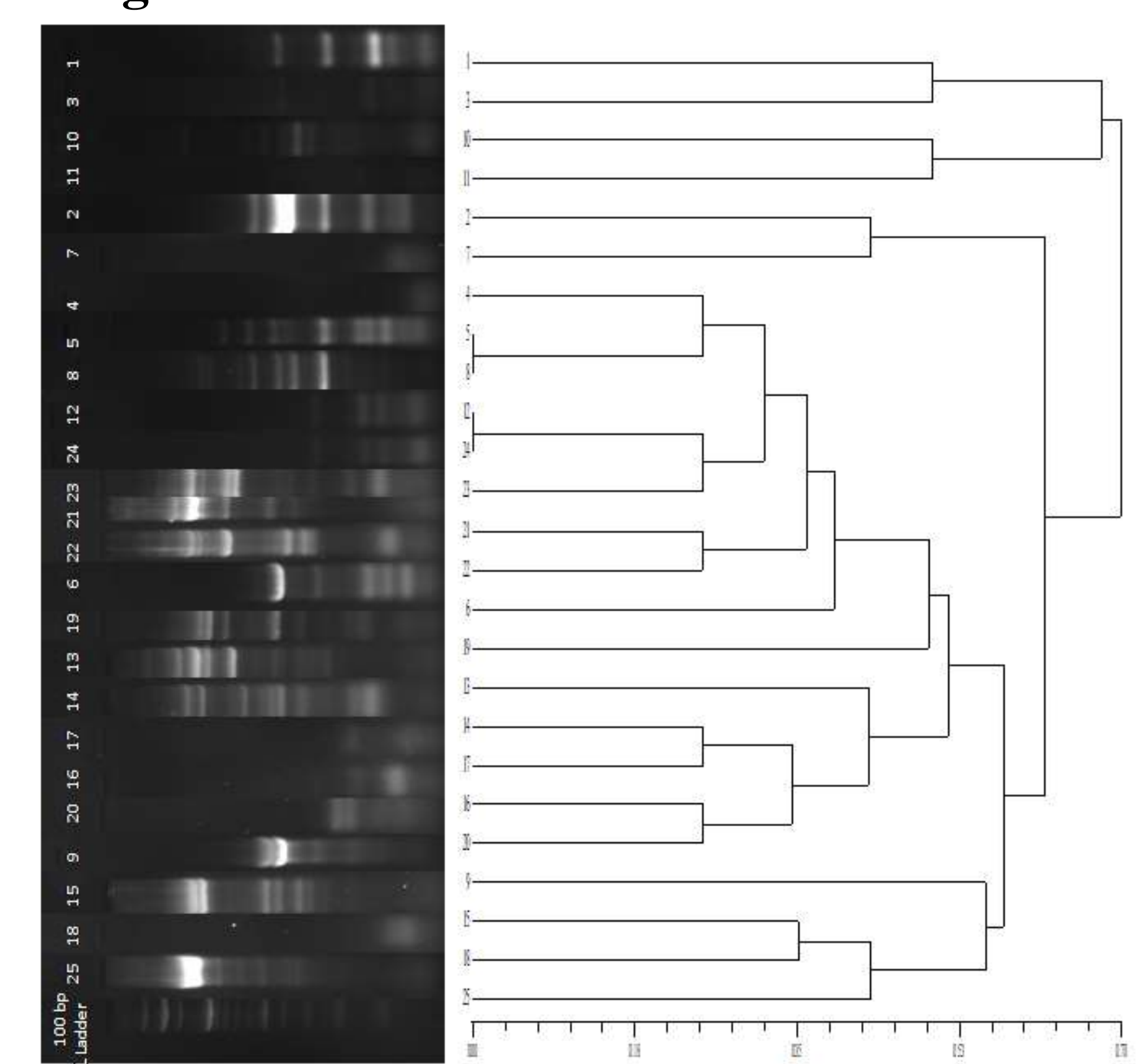


Figure 4: Dendrogram showing twenty-three different haplotypes of *E. coli*

### REFERENCES

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### ACKNOWLEDGEMENT

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