**Characterizing the Antibiotic Resistance of Clinical *Acinetobacter baumannii* Strains through Analysis of RND Efflux Pump Genes**

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**Background and aims.** The enhanced activity of efflux pumps, particularly the AdeABC (RND family) efflux system, plays a crucial role in the increasing multidrug resistance (MDR) of *A. baumannii*. This study was conducted to develop a rapid and reliable method for screening MDR *A. baumannii* strains.

**Methods.** The presence of *ade*ABC genes in *A. baumannii* isolated from clinical specimens was identified by colony multiplex PCR. Antibiotic susceptibility testing for twelve antibiotics was performed using the disk diffusion method. Statistical differences in antibiotic sensitivity between strains possessing efflux pump genes and those lacking them were analyzed using either the Chi-square test or Fisher’s exact test.

**Results.** A total of 80 *A. baumannii* strains were collected. The resistance rate to 9 of 12 antibiotics was 77%, except for piperacillin/tazobactam (66.25%), tigecycline (8.75%), and ampicillin/sulbactam (5.00%). Among these, 67, 64, and 68 strains carried the *ade*A, *ade*B, and *ade*C genes, respectively. Strains with *ade*B or *ade*C showed significantly lower susceptibility to ceftazidime, meropenem, amikacin, piperacillin/tazobactam, sulfamethoxazole/trimethoprim, imipenem, tobramycin, levofloxacin, ciprofloxacin, and ceftriaxone than those without. Strains carrying *ade*AB (58/80) or *ade*AC (60/80) or *ade*ABC (60/80) showed significantly lower susceptibility to all antibiotics tested. All *ade*B-positive strains were MDR; this rate was 94.03% for *ade*A and 98.53% for *ade*C. Strains harboring two or more *ade* genes were MDR.

**Conclusion/Discussion.** In summary, identifying genes encoding the efflux pump in *A. baumannii* strains isolated from clinical samples helps clarify their antibiotic resistance mechanisms in hospital. Moreover, colony multiplex PCR enabled simultaneous bacterial identification and detection of specific antibiotic resistance genes, thereby reducing the time required for microbiological testing.

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