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The resistance mechanism of *Escherichia coli* induced by ampicillin in laboratory

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Pathogenic *Escherichia coli* often causes diarrhea, sepsis and other clinical symptoms, and is still one of the main intestinal pathogens affecting human and animal health. The aim of this study was to compare the differences in non-synonymous single nucleotide polymorphisms (non-SNP) between drug-resistant strains and sensitive strains, and to understand the function of related genes and the metabolic pathways involved. We simulated the process of clinical antibiotics in organisms by using the method of ampicillin laboratory induction and explored the relationship between the degree of drug resistance and the mutation site. This study provides a basis for the early detection of drug-resistant strains, the rational and effective application of antibiotics and a new idea for solving the problem of E.coli resistance. Combined mutations of *ftsI* and *envZ* genes were found to induce higher resistance. Mutations in the *frdD*, *OmpD*, *acrB* and *VgrG* genes may also be linked to antibiotic resistance in β -lactamide antibiotic.

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