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**Isolation, identification and genome-wide analysis of diarrhea-derived Escherichia coli in Donkey**

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**Abstract:**

**Background/Objective:** Pathogenic *Escherichia coli* is the main factor causing diarrhea and death of donkey, which seriously affects the development of the donkey farm.

**Methods:** [Describe the methodology used in the research. Include information about the design, setting, participants, data collection, and analysis methods.]To identify the biological features and influence factors of pathogenic donkey *Escherichia coli* isolates associated with severe diarrhea in Northern China, 332 diarrhea foal samples were collected for bacterial separation culture, biochemical identification, mice pathogenic test and main virulence factors identification used PCR.In addition, representative strain p*E.coil*La18 were selected for whole genome sequencing and comparative analysis.

**Results:** The results showed that 196 *E. coli* were identified from the samples, and they carried multiple virulence genes and had high pathogenicity. The p*E.coil*La18 strain carried multiple virulence genes and resistant genes. The p*E.coil*La18 strain was closest to *Escherichia\_coli\_O15\_H18\_str.\_K1516:1446601*,and the evolution direction was similar to that of the *Escherichia\_coli\_UMEA\_3151\_1 strain.*

**Conclusion:** These results indicated that donkey diarrhea foal was mainly caused by diarrhea-derived *E. coli*,and the isolated strains have high pathogenicity. Moreover, in large-scale donkey farms, donkey foal diarrhea may be caused by a combination of multiple *E. coli* strains.

**Keywords:**donkey diarrhea; Escherichia coli; virulence gene; pathogenic; Whole genome sequencing