

Genome Sequence of a Porcine Extraintestinal Pathogenic *Escherichia coli* Strain[∇]

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Extraintestinal pathogenic *Escherichia coli* (ExPEC) is an important pathogen which can infect humans and animals and cause many diseases outside the intestine. Here, we report the first draft genome sequence of a porcine ExPEC strain, PCN033, isolated from a pig with meningitis.

Escherichia coli strains can be classified into three major groups according to genetic and clinical criteria (5): commensal, intestinal pathogenic, and extraintestinal pathogenic *E. coli* (ExPEC). ExPEC strains are an important group of pathogens which can infect many organs outside the intestine; they mainly include uropathogenic *E. coli* (UPEC), newborn meningitis-causing *E. coli* (NMEC), and avian pathogenic *E. coli* (APEC) (2, 3, 4). From 2003 onward, many pig ExPEC strains with extensive multidrug resistance were isolated in China (6). These strains cause several diseases, including meningitis, septicemia, and pneumonia, and there have been few studies on pig ExPEC. Because of the high risk for food safety and public health security, greater focus on pig ExPEC is needed. The genome sequence of this microbe will enhance the study of its pathogenic mechanism and benefit disease control efforts.

We sequenced the genome of ExPEC strain PCN033, a pathogenic strain isolated from the brain of swine. Whole-genome sequencing was performed by Illumina/Solexa paired-end sequencing technologies at the Chinese National Human Genome Center in Shanghai. Assembly of short reads was carried out using the software Velvet (9). The number of large contigs (>500 bp) was 174, and the maximum contig length was appropriately 377.5 kb. The total length of the assembled contigs for strain PCN033 was 5,060,931 nucleotides, with a sequencing depth of 120-fold coverage. The overall G+C content of the PCN033 genome assemblies was 50.7%, which is close to the expected value based upon the other sequenced *E. coli* genomes. The draft assemblies of strain PCN033 contained 4,901 potential protein-coding sequences (CDSs); 2,920 proteins were assigned to the functional COG categories (7), 554 proteins had general function predictions only, and the remaining proteins had unknown functions. In comparison with the commensal *E. coli* strain K-12 MG1655 (1) and the uropathogenic *E. coli* strain CFT073 (8), 1,223 and 1,156 genes, respectively, unique to strain PCN033 were identified.

These may include candidate genes involved in the virulence and adaptation of this porcine pathogenic strain.

Bacterial drug resistance is an important worldwide problem. As shown in a previous study, ExPEC strain PCN033 is a multidrug-resistant strain (6). In our sequence, there are at least 50 multidrug resistance-associated genes, including 11 ABC-type multidrug transport system genes, 15 multidrug resistance efflux pump genes, and nine genes similar to arabinose efflux permease genes. In addition to these genes, the sequence also contains other resistance genes: one trimethoprim resistance gene, two acriflavine resistance genes, one fosmidomycin resistance gene, one bleomycin resistance gene, one tetracycline resistance gene, and one bicyclomycin resistance gene.

This is the first genome sequence of pig ExPEC, and its availability will provide a better-defined genetic background for future studies and promote the study of its pathogenesis and mechanisms of multidrug resistance.

Nucleotide sequence accession number. The genome shotgun project of ExPEC strain PCN033 has been deposited at GenBank under the accession number AFAT00000000.

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