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RESEARCH ARTICLE

GENOMEWIDE SEQUENCING REVEALS PRESENCE OF RESISTANT GENES IN *E. COLI* ISOLATED FROM CHICKEN

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ABSTRACT

In this work, we report the whole genome sequence of the multiply antibiotic resistant Escherichia coli isolated from chicken in Nanded. Sequence analysis showed the assembled genome size to be 4,283,974 bp containing 4497 protein coding genes, 52961 single nucleotide polymorphism, 197 number of insertions and 181 number of deletions.

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INTRODUCTION

Escherichia coli is commonly found in human and animal intestinal tracts. This microbe is usefully harmless, but it is also a medically important bacterium causing a number of significant infections. Recently, many strains of *Escherichia coli* have been found to be resistant to multiple, structurally unrelated antimicrobial classes (H. Momtaz *et al*., 2012) A number of E. coli strains are recognized as important pathogen of colibacillosis in poultry and some of them can cause severe human disease such as haemorrhagic colitis and haemolytic uremic syndrome (Riley *et al.,* 1983; Chansiripornchai, 2009; Ferens and Hovde 2011). Various uses of antimicrobial agents in medicine, production of food animals, and crop protection are some of the reasons for increasing resistance to those agents (American Society of Microbiology, 2007). Today the development of antibiotic resistance and lack of discoveries of new antibiotics have created a serious public health concern.If bacteria come into contact with antibiotic but are not killed by antibiotic they may adapt their cell structure and/ or metabolism to make themselves resistant to that antibiotic. Once antibiotic resistance is acquired, they can share this information with other bacteria via vertical gene transfer. The veterinary practitioners have a limited choice of antibiotics for the treatment of animals, due to antimicrobial resistance issues and human health concerns. In view of this they use same antibiotics repeatedly, which leads to an increasing rate of antimicrobial resistance in bacteria (Mooljuntee *et al*. 2010). This resistance is not only limited to pathogenic bacteria but also spreads in the endogenous flora of exposed animals. There are several reports of the presence of antibiotic resistant bacteria in poultry and meat products. Researchers have reported high proportion of antibiotic resistant bacteria in the faecal flora of poultry (Piddock, 1996; Bogaard and Stobberingh 1999). Momtaz *et al.* (2012) had carried out a study to detect the distribution of antibiotic-resistant genes in *Escherichia coli* isolates from slaughtered commercial chickens in Iran. Similar studies have also been carried out in pigs during Metaphylactic Trimethoprim and Sulfamethoxazole treatment and in the Post-Exposure Period (Mazurek *et al* 2015). In some of the previous studies, transfer of antimicrobial-resistant bacteria from animal products to humans has been reported (Sanchez *et al*. 2002; Swartz 2002). In the last few years, many strains of *E.coli* have been reported to be resistant to multiple, structurally unrelated antimicrobial classes, like quinolones, cephalosporins, and aminoglycosides (Orden *et al*., 2001; Donaldson *et al*., 2006). Resistance among microorganisms can generally be detected either phenotypically or genotypically. The phenotypic approach is the usual method when testing bacteria for clinical purposes. However, in genotypic detection DNA based techniques are in use.

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MATERIALS AND METHODS

In this work, we studied the antibiotic resistance of Escherichia coli isolated from chicken using whole genome sequencing. So

far, to our knowledge, a genome sequence of a highly multidrug resistant E. coli strain isolated from chicken has not been available. It is therefore imperative to identify and characterize antimicrobial resistance genes of E. coli strains associated with chicken. The total genomic DNA was extracted using a Genomic DNA purification kit (Fermentas, germany) according to the manufactures instructions. The sequencing library was prepared with an TruSeq Nano DNA kit and run on the Illumina platform with paired end reads.

RESULT

In total 9,362,708 paired end sequence reads were obtained. The reads were de novo assembled using HiSeq2500. The genome size of E. coli 4, 283, 974 bp with a 50.47 mol% G+C content. The genome sequence was annotated using the Sequence Alignment/Map Tools (SAMTools) and NCBI servers. It contain 4497 protein coding genes, 52961 single nucleotide polymorphism, 197 number of insertions and 181 number of deletions. The isolates E. coli further antibiotic resistance genes , including those for choramphenicol (rarD), fosmidomycin (fsr), methlviologen (emrE), tellurite selenium resistance (tehB), bicylomycin resistance (bcr), chromate resistance (cysA), bacitracin resistance (bacA), acridine resistance (acrF) and penicillin resistance (ampC). The nucleotide sequence similarities of all antibiotic resistance genes were higher than 90% compared to the GenBank database.

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