Abstract

The enterotoxigenic and porcine enteropathogenic Escherichia coli (ETEC and PEPEC) strains are agents associated with swine neonatal diarrhea, causing economic losses in swine production. The main goal of this study was to identify virulence genes of ETEC, verotoxigenic (VTEC) and PEPEC in intestinal strains responsible for swine diseases, by molecular typing using PCR in newborn piglets from an intensive farm system. Two hundred and sixty seven rectal swabbings from 7-15 days- old Landrace x Large White crossbred piglets were taken, and 123 randomly selected samples, biochemically compatible with E. coli, were tested for E. coli virulence genes by PCR. A frequency (%) compatible with: 68 ETEC, 24 VTEC, and 8 EPEC were found. Of all E. coli strains studied, 19.51 % carried at least one virulence gene. These data showed conclusively that, in spite of the application of strict sanitary measures in the intensive farm, genes encoding virulence factors of intestinal pathogens compatible with ETEC are still detected; therefore these strains will probably keep circulating among animals.

Keywords

Virulence genes, Escherichia coli, piglets, intensive farm.