Introduction

Antibiotics are used in human and veterinary medicine to treat and prevent infectious diseases, as well as for other purposes, including growth promotion in food animals. It is well documented that all antibiotics can select for spontaneous resistant mutants and bacteria that have acquired resistance factors through various gene transfer mechanisms. Typically, the more an antibiotic is used, the more likely resistant populations will develop among pathogens and commensal bacteria in animals exposed to the antibiotic(s) (Phillips et al., 2005). The occurrence of antimicrobial resistance in bacteria harbored by animals is likely to become an increasingly important threat to sustainable methods of agriculture. There is concern that the commensal flora of animals may act as a reservoir of resistance genes that can be transferred to pathogenic bacteria in both animals and man. Currently, published data indicate that *E. coli* isolated from food animals are often multidrug-resistant (Guerra et al., 2003, Kijima-Tanaka et al., 2003, Sφrum and L'Abée-Lund, 2002). Additionally, integrons appear to play an important role in the transfer of antibiotic resistance in *E. coli* from food animals (Barlow et al., 2004, Lanz et al., 2003, Maynard et al., 2003) and humans (Ahmed and Shimamoto, 2004, Hall and Collis, 1995, Heir et al., 2004, Mathai et al., 2004, Nijsten et al., 1996, Skurnik et al., 2005,) because they are able to capture, integrate, and express gene cassettes encoding antibiotic resistance (Hall and Collis, 1995). The prevalence of integrons has been reported to range from 49% to 60 % in diarrheal pigs (Lanz et al., 2003, Maynard et al., 2003). Ebner et al. (2004) reported that the integrons were common among non-hemolytic *E. coli* isolated from apparently healthy swine. At least one other study noted that microflora from younger pigs had a higher prevalence of integrons than that of older groups of swine (Campbell et al., 2005). Our objective for this study was to determine the prevalence of resistance factors, including integrons, in commensal bacteria from a wider range of swine in Thailand, including healthy swine and diarrheal piglets, and determine if such resistance factors might impact the microflora of humans who have direct contact with those animals. We therefore examined integrons and antimicrobial susceptibility in *E. coli* isolated from healthy and diarrheal piglets, market hogs and sows, pig farmers, and humans without contact with hog farms in southern Thailand. *E. coli* isolates from raw pork loins were also included in this study.