**CHAPTER: 1**

 **INTRODUCTION**

Increased prevalence of antimicrobials resistance of pathogenic bacteria is a growing world wide concern. Its major risk factor has been generally considered as a consequence of the wide use of antimicrobials leading to the emergence and dissemination of resistant bacteria and resistance genes (Bogaard *et al*., 2000).

Antibiotics are used prophylactically to treat microbial infections in humans and animals & also given in low doses to food animals to advance their growth rate (Helmuth *et al*., 2000). The approximation of antimicrobials usage in feed leads to modification of intestinal flora by creating a selective pressure in favor of resistant bacterial pathogens that get transferred into humans through the environment and food chains (Diarra *et al*., 2007). Similarly, the genetic modifications, receptor insensitivity and decreased drug uptake and R factors contribute significantly in the spread of resistance to antimicrobials (O’Brien, 2002). Dogs are probably pets to which most antimicrobial agents are administered. The antimicrobial substances used in dogs are often similar, or identical, to those used in human medicine (Sternbuerg, 1999). Heavy use of antibiotics in settings such as hospitals and farms, where drugs are often given to animals to enhance growth, may increase the level of resistant bacteria (Levy, 1998). Hospitalized animals are frequently exposed to an environment laden with antimicrobial substances which may facilitate the transmission of resistance genes (Sternbuerg, 1999). Pets are, by definition, in close contact with people, and there is ample opportunity for exchange of resistance genes between bacteria from these different host species. This resistance can be disseminated by the spread of the bacteria or by transfer of genes to other bacteria (ANONYMOUS, 1998). It is well recognized today that resistance genes can be exchanged among bacteria populations (Davies, 1998).

To our knowledge, however, there has been no previous study on antimicrobial resistance

in fecal indicator bacteria from healthy or sick dogs in Bangladesh. *Escherichia coli* is an inhabitant of normal flora of the gastrointestinal tract of humans and animals, and is believed to facilitate food digestion through enzyme synthesis, however, few of them are potentially pathogenic and known to be a very good indicator for selection pressure by antimicrobial use and for resistance problems to be expected in pathogens (Levine, 1987).

The objective of this study was, therefore,

1. To assess the prevalence of E. coli in fecal isolates recovered from rectal swab samples of companion dogs that have been submitted to SAQTVH.
2. To determine the antimicrobial susceptibility patterns of *E. coli* isolates to 9 antimicrobial agents, to verify their multidrug resistance patterns, and to assess their significance as sources of infection.