Chapter: 1

Introduction
1.1. General introduction

In a recent annual report on global risks, the World Economic Forum (WEF) concluded that “arguably the greatest risk to human health comes in the form of antibiotic-resistant (ART) bacteria (Spellberg et al., 2013). The main reason for the rapid development of antibiotic resistance (AR) development is due to indiscriminate use of antibiotics in the treatment of infections, as prophylactic agents and as growth promoters (Florez et al., 2008). The great current concern is the use of antibiotics in the food chain, mainly in food-producing animals which has contributed to the development and spread of resistant bacteria in the environment (Egervarn et al., 2007). Antibiotics for human use belong to the same pharmacological classes as those employed in agriculture (animal husbandry, poultry and aquaculture). Thus selection of ART bacteria by exposure to a specific drug, therefore, leads to cross-resistance to against all antibiotics that belong to the same class (Devirgiliis et al., 2011).

Over 1,000 bacterial species are represented within the human and animal intestinal microbiota (Bik, 2009). These include the lactic acid bacteria (LAB) and even the opportunistic pathogens such as enterococci as natural members of the gut microflora that are capable of acquiring genes (Ogier and Serror, 2008). Among the intestinal microflora, LAB have a long history of safe use as food processing aids, such as starter cultures and as probiotics with health benefits (Egervarn et al., 2007). Because of their broad environmental
distribution, LAB may function as reservoirs of AR genes (Teuber et al., 1999). The main threat associated with these non-pathogenic commensal and food-associated bacteria is the risk of horizontal transfer of resistant determinants to other bacteria including the human intestinal pathogens (Devirgiliis et al., 2011).

Among the various clinically important antibiotics, macrolides, lincosamides and streptogramin B (MLS\textsubscript{B}) antibiotics are currently used in human and veterinary medicine due to their proven record of excellence to cure illness. Their widespread usage has also resulted in the development of strains resistant to these life-saving antibiotics (Bailey et al., 2008). Recent updates indicated that at least 66 genes are responsible for bacterial resistance to MLS\textsubscript{B} antibiotics through three different mechanisms (Roberts, 2008). Several of the recent investigations also showed that erythromycin resistance genes in food-borne LAB are similar to those detected in clinically important pathogens.

1.2 Scope of investigation

Untill recently, published reports on selection and dissemination of AR genes within the complex community of the human gut focused mainly on clinically important pathogens. However, studies on AR in LAB cautions that these bacteria may play a major role as AR gene reservoirs and may disseminate to pathogens.
With the mounting of reports on AR among LAB in developed countries (Europe in particular), precautionary principle in preventing potential risks to human health, antibiotics as growth promoters have been banned. However, in many developing countries, antibiotics are available without any prescription and there are no government regulations on the use of antibiotics in agriculture. In addition, due to the lack of published studies and awareness in countries like India, the idea of extent of prevalence of AR in food chain is absent. Among the several ART determinants, erythromycin resistance (ER<sup>r</sup>) has been found common in bacteria of both clinical settings and in food chain. In addition, it is possible for ER<sup>r</sup> genes could be linked to tetracycline resistance (TC<sup>r</sup>) genes as observed in many pathogens. In order to evaluate the prevalence of AR in food chain and to gain better insights in the role of LAB as reservoirs of antibiotics resistance (ER<sup>r</sup> and TC<sup>r</sup>) genes, the work was undertaken with the following framed objectives.

1.3. Objectives of the study

- Screening lactic acid bacteria isolated from food for erythromycin resistance
- Genetic and molecular evidences for erythromycin resistance in lactic acid bacteria
- Studies on the modes of transmission of erythromycin resistance genes among lactic acid bacteria