Introduction
Food borne diseases are widespread and growing public health problem in both developed and developing countries. It has been estimated that 76 million cases of food borne illness occurred each year in the United States, costing between $6.5 and $34.9 billion in medical care and lost productivity. Among food borne disease, food borne gastroenteritis forms a major share (Van Fleet and Van Fleet, 2009). Above estimated food borne illnesses resulted hospitalization of 325,000 cases and approximately 5000 people died (Lister and Becker, 2010). In Canada, 2.2 million cases of food borne illness per year were estimated. On the other hand, in France, 750,000 food borne illnesses were reported, of which 113,000 people were hospitalized and about 400 died (CDPHE, 2010). According to an estimate, food borne illness may be under reported by as much as a factor of 30, thus the number of cases of gastroenteritis associated with food is estimated to be between 68 million and 275 million per year (Naravaneni and Jamil, 2005). According to the largest study of Infectious Intestinal Disease (IID) carried out in the UK to date estimated that 20% of the population of England (approximately 10 million persons) suffer from food poisoning (Abubakar et al., 2007). Reports are available on food borne outbreaks due to various bacterial pathogens in Europe (Bulletin, 2004; Anon, 2005a; Palchetti and Mascini, 2008; EFSA, 2012).

In developing countries including India, the magnitude of food borne illness is very high. The majority outbreaks of food borne disease are unreported, unrecognized or un-investigated. In such conditions, to estimate the exact scenario of food borne diseases is not possible. In India, an estimated 400,000 children below five years age die each year due to diarrhoea while millions of them suffer from multiple episodes of diarrhoea and still others fall ill on account of hepatitis A, enteric fever, etc. caused by poor hygiene (UNICEF, 2005). Common bacterial causative agents of food borne outbreaks includes members of *Campylobacter jejuni*, *S. aureus*, *C. perfringens*, *Y. enterocolitica* *Bacillus cereus*, *E. coli*, *Enterobacter spp.*, *Listeria spp.*, *Shigella spp.*, *S. aureus*, *S. Typhi*, *Streptococci spp.*, *Vibrio spp.* and *Yersinia spp.* etc. (Butool, 2004; Bansal and Kaul, 2004; Amruthasri and Devi, 2005; Chandrasekaran, 2005; CD Alert, 2009; Bhunia et al., 2009; Mandal et al., 2011).

Food safety has been recognized as major issue with international trade and public health implications globally. Countries from all over the world have increased
their efforts to improve food safety in response to the increasing number of food
borne illnesses. The World Health Assembly has adopted a resolution (WHA 53.15)
in which, the World Health Organization (WHO) emphasized on food safety issue
with the aim of developing suitable integrated food safety systems to trim down
health hazard along the entire food chain. In developing countries including India,
food safety has been recognized as an important component in protecting the health of
the people. Consumers have also become much more aware towards the food safety
issues. Therefore, food safety authorities are very strict towards HACCP to monitor
the quality of the food products for the presence of microbial pathogens (Sudershan et
al., 2009; Brankica et al., 2011).

As a consequence, the various international projects dedicated to the early
identification of hazards (SAFE FOODS sponsored by the European Commission
Directorate for Research’s Sixth Framework Program, EMRISK funded by the
European Food Safety Authority, etc.) were reviewed few years back. With the help
of these and other programmes, the indicators of the emergence of certain pathogens
based on trends towards increased incidences may be obtained by trends in data
generated from surveillance. An example of such a surveillance program is PulseNet,
a collaboration of US state public health laboratories which also cooperates with
several laboratory networks in Europe, Canada, Japan and other Asian and Latin
American countries in the research on outbreaks of several pathogen micro-
organisms. However, developing countries including India are not able to provide
accurate data on their incidence or prevalence, and surveillance programmes.
Furthermore, even when there is a reporting system, only a small proportion of
episodes of food borne diseases ever come to the attention of public health authorities
(Kleter and Marvin (2009). In India, National Centre for Disease Control (NCDC) has
also introduced Integrated Disease Surveillance Programme (IDSP) which is a
national surveillance programme and based on surveillance and early information of
various diseases including food borne illness (Murhekar et al., 2009). It is found that
many of the health problems resulting from food contaminants do not figure in
statistics of food borne diseases (ICEID, 2012). Therefore, there is serious concern
required about the communication of food borne diseases and early identification of
the pathogen with the aim of preventing these hazards from becoming real risks and causing diseases.

Antibiotic resistance is a well known phenomenon in nature that imparts role in public health. It becomes increase many folds due to human misuse and neglect (Kapil, 2005). The resistance reported among common food borne bacterial pathogens viz. Campylobacter, Salmonella, Listeria, Escherichia coli O157 and S. aureus is increasing regularly. The seriousness of food borne infections is reflected by increasing hospitalization rate. The health impact of these food borne infections is become more serious because of the growing rate of antimicrobial resistance among these food borne pathogens. In these days, threat has become global due to rapid dissemination of resistant organisms from one part of the world to another (Swartz, 2002). Several studies have been conducted to monitor the pattern of resistance among these food borne pathogens. In developed countries, several health agencies such as National Antibiotic Resistant Monitoring System (NARMS) in U.S. are monitoring the antibiotic resistance regularly (IDSA, 2011). However, in most of developing countries including India, no such systematic monitoring exists. Consequently, no exact information is available on antibiotic resistant strains of these food borne pathogens. This may lead further rise of more threatened infection due to these drug resistant food borne bacterial pathogens (Vila and Pal, 2010). Therefore there is a regular monitoring required among important food borne bacterial pathogens to avoid the further rise and spread of the antibiotic resistant strains.

Conventional bacterial identification methods to enumerate and isolate viable bacterial cells in foods were based on selective media and regarded as golden standards for the identification of bacterial pathogens. However, these cultural methods are time consuming and labor intensive. Another inherent problem in the detection of food pathogens is that they are generally present in very low numbers (less than 100 CFU per gram) in the myriad of up to a million or more other bacteria. Hence, these microbes may be lost among a background of indigenous microflora, and matrix substances present in the foods themselves may hinder recovery. There is also the problem of demonstrating that the strains recovered from a food sample are, indeed, pathogenic to human beings (Iyer and Kamosani, 2010; Mandal et al., 2011).
Therefore, molecular techniques based on PCR have been developed to detect various food borne pathogens. These methods are specific, faster and often more sensitive than conventional methods in testing for microbial contaminants in food. With the advent of 16S rRNA gene sequencing it is now generally accepted that species delineation may be based on 3% sequence divergence between a novel species and its closest relative provided and the corresponding phenotypic data allow differentiation from already recognized species of the genera in question. It is clear that an isolate if represents a new species, but shows less than 3% divergence with the nearest relative, DNA-DNA hybridization data is required along with phenotypic data. There are currently no specific guidelines with respect to subspecies delineation, only that there are recognizable phenotypic differences. Various genetic fingerprinting techniques, as well as genetic marking, have proven useful in subspecies discrimination or strain differentiation (McCartney, 2002). The advent of gene probe techniques has allowed the development of powerful assays by which particular bacterial strains can be rapidly identified without the need for isolating pure cultures (Hoorfar, 2011).

The polymerase chain reaction (PCR) based methods developed for the detection and identification of food borne bacteria is mainly based on 16S rRNA and virulence gene of specific group of bacteria which provide specific level of identification. The various virulence factors such as hippuricase, listeriolysin, invasion, enterotoxin and verotoxin have been recognized and used specifically for the detection of \textit{C. jejuni}, \textit{L. monocytogenes}, \textit{Salmonella spp.}, \textit{S. aureus} and VTEC respectively (Linton et al., 1997; Asma et al., 2009; Pourmand et al., 2009; Moussa et al., 2010; Navidinia et al., 2012). The detection based on virulent genes provides an advantage to direct information about the pathogenic potential of the organism (Alarcon et al., 2004; Blaiotta et al., 2004; Iyer and Kumosani, 2010; Lopez-Compez et al., 2012). The PCR based identification requires further standardization based on the nature of food, amount and type of contamination present. The development of standardized rapid techniques will be helpful to assess the local food borne contamination.

Some reports are also available in Indian context, however, systematic investigation of various foods in majority of Northern India hereunder studied has not
been conducted. Therefore, considering the global and National importance of food borne illness and the lack of concerted effort in India, the present study has planned with the following aims and objectives.

1. To study prevalence of common food borne bacterial pathogens in various foods collected locally, using cultural methods.

2. To assess the bacteriological load in selected food samples.

3. To characterize *Campylobacter jejuni*, *Listeria monocytogenes*, *Salmonella spp.*, *Staphylococcus aureus* and *Verotoxigenic E. coli* targeting specific gene by using standardized PCR methods.

4. Cultural and PCR method based detection of selected bacterial pathogens in spiked food samples.

5. To standardize multiplex PCR for simultaneous detection of *Listeria monocytogenes*, *Salmonella typhimurium* and *Staphylococcus aureus*.

6. To assess the antibiotic resistance profile of selected isolates of food borne bacterial pathogens.