Avian and differential media. these procedure are

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Aviansalmonellosis is an economically important bacterial disease ailment inflictingserious difficulty to the growth of poultry industry (Rajagopal & Mini, 2013). It is caused by Salmonella, a member of the family Enterobacteriaceae, a Gram- negative facultative intracellular pathogen that is able to causedifferent disease syndromes in a broad range of hosts. It constitutes twospecies Salmonellabongori (S. bongori) and Salmonellaenterica (S. enterica) (Reeves, et al., 1989). Although there are greaterthan 2, 600 Salmonellaserovars (Rainier, et al.

,, 2013), relatively fewserovar cause infection in most animal (Saeki, et al., 2013; Zhu et al., 2015). Hence, Salmonellaentericasubsp. enterica serovar Enteritidis (S.

Enteritidis), serovar Gallinarumbiovars Gallinarum and pullorum and S. Typhimurium are generally isolated from poultry. Among theseserovar Salmonellaentericaserovar Gallinarum (S. Gallinarum) consists of two biovars, Gallinarum and Pullorum that cause fowl typhoid and pullorum disease in adultand young , respectively (Hossain, et al.

, 2006). Salmonellosis is one of themajor challenge of poultry farming that hinder its growth and development. Therefore, it is necessary to screen virulence gene of Salmonellaat molecularlevel for development of rapid and fast disease diagnosing technique. Poultry industry isuplifting as profitable sector in Nepal. Since, 1974 the remarkable improvement ofcommercial poultry in Nepal. And had results in tremendous development of thissector over the recent period of time.

Since, 1974 the remarkable improvement ofcommercial poultry in Nepal had been started (FAO, 2012). In ourcountry, 50 – 55 % of poultry birds arecommercially managed. And, poultry industry contributes about 3. 5% in GDP.

Aditionally, provides an employmentopportunity creating an income along with improving the nutritional level ofthe country. This also provides fulltime employment to about nine thousand andpartial employment to about ninety nine thousand people (CBS, 2015). Usually bacterialculture methods are used to identify Salmonellaand require at least 3-11days. The standard protocol for isolating Salmonellaspecies includenon-selective pre-enrichment followed by selective enrichment and plating onselective and differential media. These procedure are time consuming and labourintensive (Menghistu, Rathore, Dhama, & Agarwal, 2011). In recentyears, particularly in developed countries, several methods such as EnzymeLinked Immunosorbent Assay (ELISA), latex agglutination , immunodiffusion, Polymerasechain reaction (PCR), and real time PCR (RT PCR) had been introduced.

In comparision to other method, polymerase chain reaction (PCR)technology and real time PCR (RT PCR) have allowed the specificamplification of particular target portion of DNA, which can be used for the diagnosisof pathogen of veterinary importance. PCR tests havedemonstrated their utility as screening tools for Salmonellabroiler andlayer samples to reduce workloads and shorten time for Salmonellaevaluation(Bautista et al., 2011). S.

enterica consistof several virulence genes which encode products that help the organisms toexpress its virulence in the host. Among the virulence genes, 16srna encodefor the confirmation of Salmonellaat genus level whereas invA for adhesionand invasion of the pathogen in the host system, spv for systemicdisease state in the host cells, speffor ornithine decarboxylase of Salmonellagallinarum, sdi and hilA encode for protein belonging to the transcriptionalregulators, fim H for fimbrin like protein, avrA tomodulate host cellular functions, agf for diagnosis of Salmonellaarrayed on hydrophic grid membranefilters, sivh gene for outer membrane protein and Stn forenterotoxin genes of host pathogenic processes . While spvA, spvB, and Spvc virulencegene codes for plasmid of pathogenic organism. Thus, precise and systematic method should be adopted for screeningvirulence genes from S.

enterica isolates originated from the infectedsamples (Murugkar et al., 2003). Similarly, Polymerase chain reaction (PCR) had been discovered as ahigh-throughput approach with a high degree of sensitivity and specificity for pathogen detection. Therefore, this research was undertaken in the clinical cases of broilers to screen thevirulence gene responsible for salmonellosis along with the antibioticresistance pattern of these sample. Salmonellaisolates will be screenedbased on virulence gene profiling, focusing on virulence determinantsassociated with SPIs, plasmids, toxins, fimbriae, and flagella that werepositive for the infection by Salmonellaas an intracellular pathogen