because of the poor surveillance systems for recording animal casualties. Most of the reported animal cases were in domestic goats and only a lesser number were in domestic cows and dogs. In addition, two cases of deaths in humans and eight cases of deaths in animals, which were attributed to rabies virus infection had history of stray dog bites. Among the animal deaths due to rabies, there were five goats, two cows and one domestic dog.

**Conclusion:** Unless the local civic bodies undertake adequate measures to control the numbers of stray dogs, changing the public perception as well as opinion against the mass killings will remain an uphill task.

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**Predominance of “atypical” enteroaggregative Escherichia coli among human, animal, foods and associated environmental sources**

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**Background:** Infectious diarrhoea particularly due to pathogenic bacteria is a major health problem in developing countries, including India. Despite significant reports of diarrhoeagenic *Escherichia coli* (DEC) pathotypes across the globe, there is paucity of studies which reveal their relatedness with respect to their isolation from different sources. This present study determines isolation and identification of DEC pathotypes from different sources, their genetic characterization and antibiogram sensitivity profiling.

**Methods & Materials:** A total of 336 samples comprising of diarrhoeic stool samples from infants (n = 103), young animals (n = 106), foods and associated environmental sources (n = 127) were screened for *E. coli*. The identified *E. coli* were confirmed as DEC pathotypes by using PCR based assays. These isolates were further studied for their genetic diversity using Pulse Field Gel Electrophoresis (PFGE) subtyping tool and their antibiogram profile was determined against seven commonly used drugs.

**Results:** Of the four DEC pathotypes investigated, Enteroaggregative *E. coli* (EAEC) was found to be the predominant pathogen with an isolation rate of 16.50% from infants, 17.92% from young animals and 10.24% from foods and environmental sources. These EAEC isolates, on further characterization revealed predominance of ‘atypical’ EAEC, with an isolation rate of 10.68% from infants, 15.09% from young animals and 10.24% from foods and associated environmental sources. On PFGE analysis, discrimination was also evident within DEC pathotypes, as only closely related EAEC isolates clustered together irrespective of their source of isolation. Further, higher antibiotic resistance pattern was observed among the isolated DEC pathotypes as almost 86.44% of isolates were found to be resistant against ≥ 3 tested drugs.

**Conclusion:** EAEC pathotype in particular ‘atypical’ strains were found to be the predominant pathogen. On PFGE analysis, sharing and circulation of EAEC isolates between human and animal, including foods and associated environmental sources was evident. Besides this, an alarming antimicrobial resistance profile was observed for majority of the recovered DEC pathotype isolates.

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**Development of safe, effective and immunogenic vaccine candidate for diarrheagenic Escherichia coli main pathotypes in mouse model**

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**Background:** Glanders is a highly contagious and fatal zoonotic disease primarily of horses, mules and may occur in fields in wild fields. At once time, *B. mallei* infection occurred worldwide, but over last 100 years occurrence decreased and many parts of world has been eradicated. However, sporadic cases of glanders are still registering in Far East, South America, North Africa, Middle East and Asia. In Mongolia, major glanders outbreaks were reported during the middle of last Century and due to specific measures, the prevalence was decreased to 0.05% by the end of 1980s. During the last decade, has been detecting sporadic cases and glanders likely re-emerging in Mongolia. The present study aimed to conduct the risk-based survey and identify *B. mallei* by conventional and molecular methods and identify a course of re-introduction of *B. mallei*.

**Methods & Materials:** Risk-based survey was conducted in Central part of Mongolia from 2014 to 2015. A total of 809 horses were tested by mallein test and CFT. Tissue samples from positive reactors were subjected for bacteriological examination and isolates were characterized by conventional and molecular methods, such as PCR, immunohistochemistry and etc. PCR performed using primers based on nucleotide difference in the 23S rDNA between *B. mallei* and *B. pseudomallei*, described previously elsewhere.

**Results:** Several cases of glanders, with clinical symptoms were reported and were conducted risk based surveys in outbreak areas. Of the 809 horses, 9 were positive by mallein test and 12 by CFT. From pathological samples were isolated 6 Gram negative, non-motile rods suspicious for *B. mallei*. These isolates, by PCR with primers specific for *B. mallei* and *B. pseudomallei* were positive, and with *B. mallei* specific antisense primer, sense primer specific for *B. cepacia*, *B. vietnemese*, *B. mallei* and *B. pseudomallei* and competitive oligonucleotide probe for other Burkholderia, except *B. mallei* were