TECHNICAL BULLETIN

No. 41, 2023

Zoonotic Diseases of Pets and Their Management

Pets are lovely things, but they can also transmit diseases. In Bangladesh, pet keeping is becoming popular, especially in the urban areas, and the commonest pets are dogs, cats and rabbits with some guinea pigs, birds and fish, and with this, the risk of infections with zoonotic diseases is rising. Pathogens of these diseases can be transmitted from animals to humans through direct contact and through fomite, aerosol, blood, saliva, urine, feces, food, water, scratches including different vectors. It has been reported that there are about 1415 pathogens affecting humans of which 61% are zoonotic, and it has been estimated that approximately 75% of recently emerging infectious diseases affecting humans are diseases of animal origin. The direct impact of zoonoses can be considerable with illness, monetary loss, and adverse effect on morale of the affected persons etc. Indirect effects are barriers to livestock trade, added costs associated with control programs, ensuring safety for human consumption and the loss of market owing to reduced consumer confidence.

Several diseases/disease conditions/symptoms of pets, many of these with zoonotic potentials, have also been reported from Bangladesh. However, these reports are mostly based on clinical signs, symptoms and presumptive diagnosis, laboratory confirmation based on either serological and/or molecular diagnosis as well as pathogen isolation is important for proper identification of causal agents for the management of the diseases caused by them. This study was conducted to identify zoonotic diseases arising from pets, assess the risk factors associated with zoonoses and raise awareness among pet owners.

Methodology

The study was conducted in selected veterinary hospitals and pet clinics in the Dhaka and Chattogram cities. The samples were initially screened at the collection sites and confirmatory diagnosis was done at the Animal Biotechnology Division of the National Institute of Biotechnology (NIB). Information was collected through a questionnaire. Based on the findings of this project, leaflets were printed and distributed for raising awareness.

A retrospective study was conducted in different veterinary hospitals of Dhaka and Chattogram metropolitan areas of Bangladesh. Previous two years' data (years 2017 and 2018) were collected for retrospective analysis of pet diseases and disease conditions recorded in selected veterinary hospitals. In all, 583 samples were collected from different pet animals brought to the veterinary hospitals and pet clinics involved in this study. Different types of tests such as quick screening by a quick diagnostic kit, culture and biochemical tests, antimicrobial sensitivity tests, PCR, RT-PCR, partial gene sequencing, whole genome sequencing, matrix-assisted laser desorption/ionization-time of flight (MALDI-TOF) were used for

KRISHI GOBESHONA FOUNDATION
A non-profit foundation for sustainable support to agricultural research and development

confirmatory diagnosis of microorganisms. For sequencing the dideoxy chain termination method using the Dye Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystems) was used. The multiple sequence alignment was performed with the MEGA software and the evolutionary history was inferred using the Neighbor-Joining method. Whole genome sequencing of bacteria was done using the MiniSeq sequencer (Illumina).

The service was taken from Invent Technologies. Annotation was done using RAST, PROKKA platform. Antimicrobial profiling (AMR) of some isolates was performed by with commonly used antibiotics in Mueller Hinton Agar (MHA) according to standard method. The microbiome study of pet animals was conducted to get a better insight into microorganisms. Fifty-seven samples (dog=15, cat=15, ornamental birds=12, pigeon=15) were collected aseptically and analyzed.

Results and Outputs

Retrospective analysis

Cases of pet diseases/disease conditions/others obtained numbered 3775 in total. The recorded cases were derived from dogs (20.93%), cats (30.75%), birds (37.46%) and rabbits (10.86%). Among the causal agents (Fig. 1) viral cases (17.32%) were the highest followed by parasitic (13.32%), bacterial (5.72%), fungal (2.33%), protozoal (0.93%) and mycoplasma (0.37%) cases. Injury was recorded in about 9.72% cases. Non-specific cases including diarrhea, fever, pneumonia, etc. were found in 28.87% and others namely wound dressing, stitch cutting, deworming, vaccination, etc. were 20.11%.

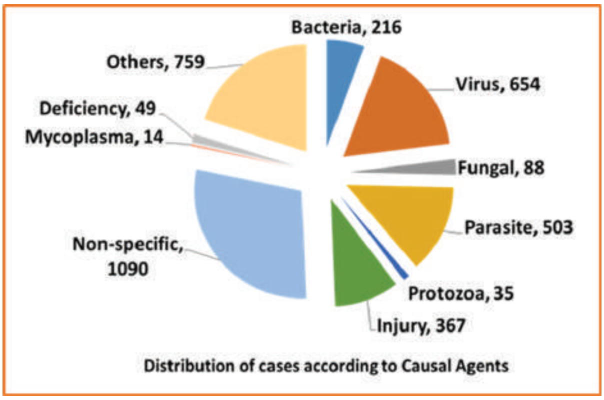

Fig. 1. Distribution of zoonotic cases on the basis of causal agents

Prospective analysis

Quick screening

Out of 583 samples, the majority (51.63%) were derived from cats followed by dogs (25.04%), birds (20.93%) and rabbits (2.40%). Initially 400 samples were randomly tested with different quick diagnostic kits for preliminary detection of disease which indicated feline panleukopenia virus (FPV) (20.0%), feline calicivirus (FCV) (10.0%), canine parvovirus (CPV) (44.0%), and canine distemper virus (CDV) (20.0%). Besides, pittacosis (2.0%), giardiasis (1.5%) were also detected.

Molecular tests

About 500 samples were analyzed in the laboratory. Based on their colony characteristics and biochemical tests different bacteria such as, *E. coli, Salmonella spp, Streptococcus spp., Lactobacillus spp., Staphylococcus spp., Campylobacter spp., Raoultella ornithinolytica, Raoultella planticola, Citrobacter freundii, Citrobacter amalonaticus, Citrobacter farmeri, Aeromonal hydrophila* and viruses like, canine parvovirus and canine distemper virus, feline panleukopenia virus, feline calicivirus, feline immune deficiency virus, etc, were detected. Representative images are shown in the Figure 5. Phylogenetic analysis revealed that closest organisms were derived from different countries of the world.

Antimicrobial profiles

Antimicrobial profiles of isolated bacteria were done (Fig. 2). Many bacteria showed resistance to commonly used antibiotics. Even they became multidrug resistant.

Microbiome study

A microbiome study of pet animals was done (Fig. 3) to derive better information regarding the gut microbiota. One hundred and twenty-two bacteria having zoonotic potentials were identified for the time being.

Whole genome analysis

Whole genome sequencing of *Raoultella ornithinolytica* was done. The genome length was foundn to be 53,76,960 bp with 55.9% G+C content. It carries genes associated with resistance to heavy metals and antibiotics. It is an emerging pathogen with the potential to cause human infections. This is the first isolation and identification of this organism in Bangladesh.

Fig. 2. Antimicrobial profiles of E. coli from cat

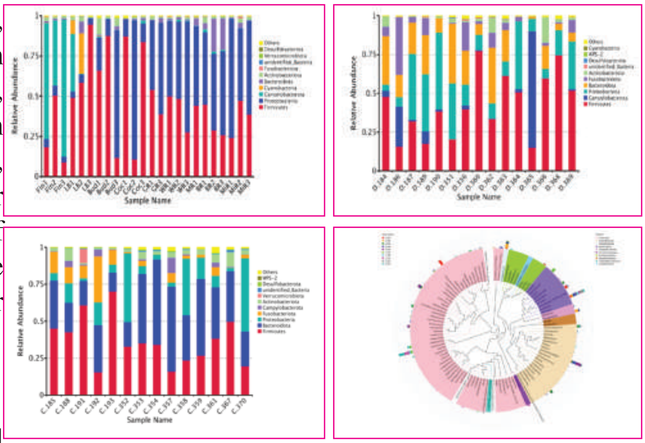

Fig. 3. Gut microbiome analysis of pet birds (upper left), dogs (upper right), cats (lower left) and evolutionary analysis of dog originated bacteria (lower right) at phylum level

Risk perception

Among the 800 pet owners surveyed for assessing risk perception 90.75% were found to be aware that pets could spread diseases like rabies, anthrax, cat scratches, influenza etc. Some 90% Pet of the pet owners surveyed appeared to know that physical contact with affected pets may transmit zoonotic diseases to humans.

Risk factors assessment

Risks of infection with zoonotic diseases were found to be 64.75%, 18.25%, 15.25% and 1.75% from rearing of cats, dogs, birds and rabbits, respectively. Touching of pets in pets in different ways such as, licking, kissing, sleeping with pets, and improper cleaning of pets utensils, no non-use of hand gloves, disinfectants, etc. may be major contribute risk factors for common zoonosis of humans.

Expected Impact

The findings of this project will contribute directly or indirectly to the safety different sections of the people, especially the pet owners. Public awareness regarding zoonotic disease and risks of their transmission to humans Willm get a boost. The diagnostic protocols established will be helpful for future researchers in the fields of pathology and animal diseases. Information on pet diseases and AMR can be used by veterinarians in prescribing suitable antimicrobial drugs, and can also contribute significantly to national AMR surveillance and policy making to combat AMR.

Recommendations

- Facilities for the identification of causal agents of zoonotic diseases and diagnosis of pet diseases need to be developed and strengthened veterinary hospitals
- Skill development and expansion of facilities for the application of modern tools like next generation sequencing and data analysis need to be taken care of urgently
- Two emerging bacteria viz. *Raoultella ornithinolytica* and *Raoultella planticola* were isolated and identified from oral swabs of cat. Raoultella spp. was also detected by metagenomic analysis. They intensify the zoonotic disease risk factors, so pet owners need to be extra vigilant in day to day management of their pets
- Pet owners know about zoonotic diseases but they do not follow proper hygienic practices properly. An awareness raising campaign should be started and continued
- Close consultation with veterinarians needed to be maintained for proper management of pets.

This Technical Bulletin has been prepared on the basis of technical information available from a completed BKGET-KGF Funded CGP Project, the details of which are given below:

Project Code and Title: TF 46-L/17. Study on Zoonotic Diseases of Pets and Assessment of Risk Factors of Commonly Occurred Zoonoses for better Management

Principal Investigator: Dr. Jahangir Alam, Chief Scientific Officer (CSO), Animal Biotechnology Division, National Institute of Biotechnology, Ganakbari, Ashulia, Savar, Dhaka-1349, Cell: 01712819098, e-mail: alamjahan2003@yahoo.com;

Project duration: January 2018- December 2023

Edited by:
Nasrin Akter, GM Panaullah and Nathu Ram Sarker
Krishi Gobeshona Foundation (KGF)

Published by:
Krishi Gobeshona Foundation, AIC Building, 3rd Floor, BARC Campus, Farmgate, Dhaka-1215, Bangladesh, Cell: 01729 480988, Website: www.kgf.org.bd, e-mail: kgf-bd@kgf.org.bd