Mini Review

Public health significance of companion animals in emergence and re-emergence of bacterial zoonoses

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regarding infectious zoonotic diseases.

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ABSTRACT

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Companion animals especially cats and dogs can provide a bridge for transmission of emerging bacterial diseases that are zoonotic in nature. Zoonotic diseases had posed numerous risk to ownership of companion animals by human either through direct or indirect contact especially in recent years where livestock species are being used as pets. Furthermore, companion animals could play a significant role in zoonosis as a potential reservoirs of various infections. These diseases have impacted greatly to the definition of new paradigms posed by emerging and re-emerging infectious diseases particularly relating to biosecurity policies and broadly to the protection of public health. Multi-sectorial collaboration for disease containment should be emphasized towards curtailing and managing health risks

KEYWORDS

Bacterial zoonoses; Companion animals; Pet; Public health

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INTRODUCTION

Over the recent years, there are numerous cases of emergence of new infectious diseases and re-emergence of existing ones across different geographical region with changes in their epidemiology almost yearly (Bloom et al., 2017). These have attracted great public health concern at national and international levels from both developing and developed countries (Cantas and Suer, 2014). Majority of emerging diseases are zoonotic in nature and they are becoming widely used to refer to the manifestation of a presently obscured disease or an earlier known disease that has broadened in a different population or geographical region and oftentimes appended by a distinct alteration in virulence and increase in incidence (Gortazar et al., 2014). Similarly, these infections are often associated with emergence of antimicrobial resistance against chemotherapeutic agents which is also a major public health problem (Abatcha, 2017). Emerging diseases which could be due to changes or evolution of an existing pathogens has no limit of its spread across national boundaries (Machalaba et al., 2018).

Companion animals encompass a wide array of species that are kept as part of a household or other useful purposes which includes dogs, cats, horses, ferrets, guinea pigs, reptiles, rodents, rabbits, birds and ornamental fish, as well as food production animal species, such as domestic pigs and wild-caught animals (Damborg et al., 2016; Reperant et al., 2016). However, cats and dogs appeared to be the most frequently kept of all the companion animals with an estimated population of 185 millions in Europe followed by pet birds (39 million) (FEDIAF, 2016). Moreover, among the estimated population of 71 million and 74 million for dogs and cats respectively in the US, 50% of households have these as pets. (AVMA, 2012). Companion animals are potential source of emerging and re-emerging infectious diseases for man and have a great public health significance (Rijks et al., 2016).

Issues regarding the emergence of diseases such as antibiotic resistance, influenza, tuberculosis are a multifaceted and all-encompassing efforts with the Centers for Disease Control and Prevention (CDC) of the United States being at the forefront of tackling challenges posed by them. Its represents CDC's effort in addressing scientific publications towards the menace of emerging infections. These publications are continues and evolving across the globe, they present elusive views and reports from wide authorship base and extensive independent peer-reviewing (Drotman and Hughes, 2015). The Organization for Animal Health (OIE) and the World Trade Organization's (WTO) further strengthened and reinforced the protocols and guidelines provided by the source organization for global models on animal health and zoonoses. Based on this, between the year 2012 and 2014, the European Union (EU) established a structure 7-funded blueprint known as Companion Animal multi-sectorial inter-professional and Interdisciplinary Strategic Think tank On zoonoses (CALLISTO) including researched on zoonotic infections spread among companion pets and human and food-producing animals (Cito et al., 2016).

However, in contrast to man and animal diseases, no any international health organization are authorized to regulate monitoring of infections in pets with the exception of the surveillance systems for a few small animal zoonosis which basically comprises the bulk of companion animals. Therefore companion animals can as well be at risk of contracting the infections from these animals species (Day, 2011). Recently, human and animal health suffered great consequences from diseases linked with outbreaks of emerging or re-emerging infections (NIH, 2007). The zoonotic infections could be transmitted either through direct animals to humans transmission in which an animal or human is infected. It can also be attributed to diseases in which companion animals serve as a source of spreading infections, including possessing the potential for infecting source of food and water for human consumption. To achieve optimum prevention and control strategy in developed countries, basic enforcement of existing rules to enhance responsible pet-ownership. Similarly, the rules should be enacted in some countries that they are lacking (van Knapen and Overgaauw, 2015).

A major focus now is on the concept of "One Health" which has attracted greater attention in the field of emerging and re-emerging infectious diseases. This concept entails seamless interaction between veterinarians and medical practitioner toward infections transmitted by humans, livestock, pets, and wildlife in particular relation to the environment (Day, 2011). However, their are paucity of data on the role of companion animals in the emergence and spread of infectious diseases in man both in research and in surveillance.

Factors in the emergence of infectious zoonoses

Most emerging infectious diseases of bacterial origin are due to their persistent presence in the environment and are known to have included some of the most scourge of

the previous epidemic (NIH, 2007). Disease emergence is primarily due to a change in the ecology of host, pathogen, or both ordinarily induced by anthropogenic determinants, such as worldwide trade and high humanwildlife contact frequency via increasing human population density and encroachment into wildlife habitat and phylogeny or the change of an infectious agent or a current parasite. Numerous factors that have been identified and associated as risk factors for the emergence of zoonotic diseases include the continuous booming of international travel and trade across the world, high rate of mingling among human, wildlife, exotic, domesticated and companion animals, production of novel diagnostic instruments, rise in individual susceptibility to bacterial agents as well as emergence of more virulent bacterial strains and opportunistic infections (Vouga and Greub, <u>2016</u>).

Similarly, other factors such as human behavior, rapid microbial adaptation, changes in climates and ecosystems as well as changes in livestock management methods (Cleaveland et al., 2001). Raise in the true incidence of emerging pathogens can also be related to the pathogenicity of the strain or vector. Furthermore, the emergence of a bacterial disease is contributed by factors such as precise social, ecological, climatic, environmental or demographic determinants, however, the mechanism and ranking of causes of infections remain unachievable. (Weiss and McMichael, 2004). Moreover, pathogens that persist in the environment, therefore, have a more selective affinity and the potential to infect a higher number of host and taxonomic order that makes them more prone to emergence when compared with pathogens of restricted host (Cleaveland et al., 2001). Technology and industrial development has resulted in high-volume rapid urbanization and movement characterized by travel across different borders (Morse, 2001).

Recent use of biological food processing production has greatly potentiate the productivity and chances of accidental contamination with zoonotic organisms in the line of food production. These processes or application results of genetically modified origin, modern production techniques result in higher efficiency and decreased finances but can raise the likelihood of unintentional infection and increase the effects of such disease (Economou and Gousia, 2015). Globalization further compound this effect through the introduction of agents that are new from a far or entirely different region. An infectious agent existent in any of these new bodies may gain its access inside a huge group of the final result (<u>Wu</u> et al., 2016). Opportunistic host plays a role in the re-emergence of diseases as major source of spreading diseases to human. Improved and efficient surveillance is a key strategy in the public health sector focused on the locations with high chances of disease outbreak (emergence). These strategies comprises of effective reporting of diseases and detection of microbes, rapid outbreak detection, elaborate research to identify factors that favour re-emergence, and effective preventive measures (Fraser et al., 2004).

Campylobacteriosis

The genus *Campylobacter* is a diverse and large group with numerous species and sub-species. Majority of Campylobacter species are considered as emerging human and animal pathogens across the globe and they are the preeminent etiology of gastroenteritis in developed countries (Humphrey et al., 2007; Man, 2011). They are very vital infectious emerging bacterial zoonotic agent that are known to be foodborne pathogens that causes gastrointestinal illness in humans (Humphrey et al., 2007). However, they have been shown to be isolated from companion animals such as cats, dogs, and birds; and are known to be shed in the feces which in turn may contaminate and spread in the environment. This could be associated with the high incidence in stray dogs and cats due to their exposure to environmental sources of Campylobacter infection. A high prevalence (up to 97%) of Campylobacter in companion animals are known to have published from research conducted in Malaysia, Spain, Nigeria and North America (Chaban et al., 2010; Goni et al., 2017a). In some cases, companion animals are fed infected meat from livestock animals as well as association with pets poses a vital hazard for the sharing of Campylobacter species (de Perio et al., 2013). However, the prevalence of Campylobacter species in pets posed a major public health concern due to there closeness with humans and therefore they act as a potential reservoir and risk factor for human infections (Goni et al., 2017b).

Leptospirosis

Leptospirosis is a bacterial and a common zoonotic disease with etiological agents by microbes of the genus *Leptospira* which is a distinct branch of gram-negative bacteria that can affect both man and animal. It is generally regarded as an emerging disease across the world and is endemic in most companion animals particularly dogs and often under reported, with rodents being the major reservoirs of the pathogen (<u>littapalapong</u>

et al., 2009). Although curable if treated early, it is often misdiagnosed and can be fatal if left untreated. However, the re-emergence of Leptospira species in companion animals populations has been a great concern across different geographical zones due its severity (Damborg et al., 2016). The incidence in human is reported to be low in different countries and are mild and asymptomatic although is associated with kidney failure especially in risk individuals (Dupouev et al., 2014). Leptospira species can be transmitted by oral administration or close contact of mucous membranes or damaged skin with the pathogen, however, the majority of infections are contracted from water and environmental sources that are contaminated with urine (Adler and de la Peña Moctezuma, 2010). of Leptospirosis vary from Symptoms fever. nonproductive cough, headache, musculoskeletal pain, diarrhea, nausea, vomiting, alveolar hemorrhage, and even meningitis (Terpstra, 2003).

Salmonellosis

Salmonella is a gram-negative bacteria that can withstand warm and most environmental condition for months (Abatcha et al., 2014a). Companion animals such as dogs, cats and especially reptiles species are important reservoirs of the pathogen (Mistry 2013). They are major public health concern in both developed and developing countries (Abatcha et al., 2014b). However, figures on the prevalence of Salmonella species in household pets are relatively low. Data from some studies showed the prevalence rate in dogs, cats and other companion animals ranging from as low as 0 to 9% (Marks et al., 2011; Abatcha et al., 2014b). The incidence and intestinal occurrence of Salmonella species among companion animals is of public health interest across the globe. Several studies have confirmed the shedding and spreading of Salmonella to humans (Wright et al., 2005; Lowden et al., 2015; van Knapen and Overgaauw, 2015). Similarly, a study reported Salmonella prevalence among pedigree dogs and shown 43.5% of pets were colonized with it, however, a study elsewhere showed the prevalence rate among racing Alaskan dogs at 60% (Hoelzer et al., 2011).

The emergence of antimicrobial-resistant *Salmonella* and other enteric pathogens has become a major public concern worldwide. However the role of other companion animals in transmission of *Salmonella* spp. to humans is unclear and probably of less concern. Some companion animals are potentially at greater risk of infection by *Salmonella* due to their indiscriminate feeding character mainly related to scavenging and hunting. Human Salmonellosis have been attributed to contact with infected dogs or cats at home or in veterinary premises (<u>Hoelzer et al., 2011</u>). Therefore constitute a risk of cycling infection by *Salmonella* which is mainly harbored in the small intestine from where it can excreted into the environment via feces (<u>Mistry, 2013</u>).

Methicillin-resistant Staphylococcus aureus (MRSA)

Methicillin-resistant Staphylococcus aureus (MRSA) is considered as an emerging nosocomial pathogen that is zoonotic in nature and was first reported in the United Kingdom. It was isolated as when semi-synthetic beta lactams antibiotics that were used for therapeutics of infection by strain S. aureus became resistant (Chen et al., 2014; Asinamai et al., 2016). Currently, substantial strains of S. aureus have developed resistance to most penicillin derivatives and other common antibiotics (Chen et al., 2014). The epidemic potentials of MRSA according to some studies have showed that the rapid emergence of novel MRSA clones is at a rapid pace which has redefined the knowledge of its clonality (Saleha and Zunita, 2010; Graveland et al., 2011). Recently, new strains of MRSA were initially coined to cause human diseases but it was later found out to be associated with a clone of MRSA related to farm animals (Asinamai et al., 2016). Due to the similarities of the strains of pets and human isolates of MRSA, it is reported that pets could serve as source of infection of humans and vice versa (Bramble et al., 2011). The occurrence of MRSA and cross infection and transmission between horse, cats, dogs, and man as well as animals hospital were extensively demonstrated in several studies which were reviewed by Rendle and Page (2018).

MRSA were isolated at 1.5% occurrence rate from samples of companion animals across the UK with dogs and cats being the most infected/colonized (Loeffler et al., 2005). However, risk factors that could predisposed risk groups as potential reservoirs of infection are associated with ownership of companion animals, veterinary practice and farmers. Therefore, human stands a great possibility of occurrence or infection with MRSA (Mustapha et al., 2014). The rapid changes linked with emergence of numerous global attention MRSA clones generated worldwide, the epidemiologic variation is on a major scale and could affect the patient, health care workers and pharmaceutical companies. For these reasons, new clones harbors various determinants for virulence and antibiotic resistance and dissemination in the environment (Grema et al., 2015).

Arcobacter

Arcobacter belongs to the family Campylobacteriaceae and it was initially referred to as aerotolerant Campylobacter due to the fact that its organisms could thrive aerobically before it was later moved to genus Arcobacter (Shah et al., 2012). Recently, Arcobacter species are now regarded as an emerging food-borne zoonotic pathogen across the world and categorized to be of serious hazard to human health. (Ramees et al., 2017). Several studies have elaborated the carriage of Arcobacter species in pets and their role in transmission to human (Goni et al., 2016). The most common species of this genus is A. butzleri and have gained popularity from researchers in different parts of the world as an important foodborne organism linked with diseases in man such as severe diarrhea, enteritis, bacteremia, and septicemia. They are also been associated in the etiology causative organism of traveler's diarrhea with Campylobacter, E. coli, Shigella, and Salmonella (Collado et al., 2014). But recently, studies on carriage rate in various animals across the world reported 54.4% (dogs), 78.8% (cats) (Fera et al., 2009; Goni et al., 2016). However, their occurrence in companion animals are vital due to the fact that the presence of these emerging foodborne pathogens pose a risk to the human population and constitutes a public health concern (Goni et al., 2017c). The prevalence of Arcobacter species in companion animals may be deprecated possibly due to its misidentification in the past years.

Listeriosis

The genus Listeria consists of species that are the etiological agent for Listeriosis which comprises 17 different species that are presently marked as an emerging food-borne zoonosis which posed a great threat to the public health. (Dhama et al., 2013; Weller et al., 2015). Among these species, only L. monocytogenes is known to cause infections in human and numerous animal species, while L. ivanovii is rarely caused a disease to humans. Listeriosis is characterized with meningo-encephalitis, septicaemia, resulting in abortion in animals and humans (Dhama et al., 2015). The organisms are well disseminated in the environment and can be isolated from soil, silage, and sewage. Listeria monocytogenes is also found in the faecal culture of healthy pets and man (Kocabiyik et al., 2006). Listeria infections was reported to be responsible for 47% of the deaths recorded in 2011 foodborne pathogens (Abatcha, among 2017). Companion animals especially infected birds are regarded as a major source of human infection through contact and ingestion of contaminated poultry products with

pregnant women, immunocompromised individuals, aged persons and new born being at high risk of infections (Popovic et al., 2014).

Escherichia coli

The enterohaemorrhagic Escherichia coli (EHEC) species are a subgroup of Shiga toxin-producing E. coli species that have usually resulted in human and animals diseases. As a result of contamination from faeces, it is often found in soil, water and food. One of the rich sources of the spread and emergence of antibiotic resistance is the commensal E. coli flora (da Costa et al., 2013). However, extended-spectrum β-lactamases (ESBLs) can be considered as a rapidly emerging set of β -lactamases which that partake the capability to hydrolyze thirdgeneration cephalosporins and aztreonam but are hindered with clavulanic acid (Bitrus et al., 2018). They represent the prime instance that β-lactamase-mediated resistance to β -lactam antibiotics produced from basic variations in the substrate spectra of the enzymes (King et al., 2012). Recently, there is an emergence of Multidrug drug resistant E. coli ST131 across the globe in human as a pandemic clone. Numerous strains of ST131 E. coli species from pet animals are comparable to human strains ST131 E. coli confirmed based on their pathogen genotype, resistance properties, plasmid content and PFGE characterization (Pomba et al., 2017).

The risk group of developing a severe infection are the children and the and therefore a particularly important concern in public health and traverse the food and agricultural productions. (CDC, 2001). Several species of animals such as sheep, goats, heifer, birds, deer, geese, turkey, seabirds, dogs, cat, gull, chicken, pig, monkey, reptiles, llama, and horses, as well as on flies serves as reservoir for verotoxin-producing E. coli O157 with cattle being the major one (Johnsen et al., 2001; Lenahan et al., 2009). Isolates of variety of strains of E. coli around the world were reported to be closely related to each other based on genotypic analysis. This suggests the roles played by rapid and global dissemination. Several factors contributed to the globalization of the pathogens such as direct human-to-human transmission, international travel, environmental dissemination, fecal carriage in livestock and carriage by companion pets which apparently aid in the spread of strains of human importance (Platell et al., 2011). The re-emergence of antimicrobial resistance may hinder the therapy of E. coli infections in pet animals. Thus the treatment options of humans infections with E. coli from their pets may be limited (Shaheen et al., 2013).

Tuberculosis

Tuberculosis is regarded as an important disease both man and animals which results in morbidity, mortality and economic loss worldwide (Thoen et al., 2009). The genus Mycobacterium consists of diverse species that are the etiological agents of tuberculosis in humans and other The Mycobacterium tuberculosis animals. complex comprises of M. tuberculosis, M. cannettii, M. africanum, M. bovis, M. pinnipedii, M. caprae and M. microti and they constitute a great public health concern especially in developing countries due to the presence of comorbidities. (LoBue et al., 2010). Its re-emergence in parts of the United Kingdom had led to it occurrence which has been documented in broad range of animals including companion animals hence its zoonotic nature (Chomel, 2014). Tuberculosis due to M. bovis in human is rare, however the pathogen is of high economic importance in domestic animals around the globe (De Kantor and Ritacco, 2006; Jajere et al., 2018).

It is widely regarded that the dogs can harbor *M. bovis* and *M. tuberculosis* similar to the case of transmitting human infection (Monies et al., 2006). However, infection with *M. tuberculosis* in cats is rare due to resistance of cat to the infection. Although ingestion of contaminated food materials in presence of infected cattle has been reported to be the reserviour of infection for cats (Ramdas et al., 2015).

CONCLUSION

This review demonstrated the importance and role of companion animals in the zoonotic potential of bacterial infections that are emerging and re-emerging. Emerging disease posed an enormous risk, therefore in order to reduce the related risk an enhanced robust surveillance, diagnostic and preventive measures is required especially in developing countries where veterinary settings and facilities remain inadequate and hindered by lack of resources. In recent years, sophisticated control measures such as advanced animal health care have remained frequently applied together with surveillance and standard control practices, which involve stamping out (culling) and movement confinements (including zoning, compartmentalization, isolation, and quarantine). Similarly, antimicrobial resistance in companion animals has increased as a result of the rise in number of reports of companion animals colonized with important multidrug resistant organisms of public health importance such as methicillin-resistant Staphylococcus aureus (MRSA). The concept of One health and enlightenment of pet

owners would provide the impetus required for public health improvement and prevention of numerous zoonotic pathogens among companion animals and possible transmission to humans. These will also ensure proper surveillance and monitoring system for determining the occurrence of these zoonotic pathogens.

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CONFLICT OF INTEREST

There is no conflict of interest to declare.

AUTHORS' CONTRIBUTION

MDG, IJM and AAB conceived and drafted the manuscript, SMJ, KMS, AA and MG reviewed the manuscript. MDG and AAB approved the final draft of this review article.

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