

Antibiotic resistance is the ability of some microorganisms to survive and multiply in the presence of various antimicrobials and represents a health problem that has afflicted the world population for years. Various bacterial species are naturally resistant, while others acquire, through vertical and horizontal transfer, characteristics that make them resistant to the action of some antibiotics. Antimicrobial resistance is a serious global problem in the 21st century, strictly due to several factors linked with the growth and lifestyle of the population, the excretion of incompletely metabolized antibiotics by humans and animals, the disposal of unused drugs, and waste from pharmaceutical processes. The livestock sector constitutes one of many focal points for the evolution and dissemination of antibiotic-resistant bacteria.

Antibiotics are widely used in food-producing animals for therapeutic, prophylactic, and growth-promoting purposes. In addition, the global sale of antimicrobials is continuously increasing. Antimicrobial resistance represents a problem of worldwide interest, which includes animals and humans. In particular, a study found a resistance to two or more antimicrobials of 85% in food and animal strains and 77.4% in human strains.

Therefore, the tracking of this phenomenon is of fundamental importance to countering its spread, and the monitoring of antibiotic resistance in Salmonella is considered to be of high priority by various global health organizations. Although poultry meat and eggs represent one of the principal sources of *S. enterica* infection in the food supply chain, other animal species could represent a means of spreading this zoonosis.

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Salmonella are the main pathogens responsible for food zoonoses in both industrialized and developing countries. About 95% of salmonellosis affecting humans is attributable to the food vehicle; the spread is favored by the wide variety of infection reservoirs and the complexity of the agri-food production chains, both of animal and vegetable origin. Livestock has been implicated as a reservoir for antibiotic-resistant bacteria, and foods of animal origin can be vectors of transmission to humans. The antibiotic resistance in *Salmonella* spp. isolated from animal sources and from their meat has been widely demonstrated, even beyond the serovariates on which the attention of microbiologists and clinicians is focused.

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Awareness of the consequences of the indiscriminate and unnecessary use of antimicrobials is slowly growing, but numerous studies still report highly virulent and resistant bacteria in areas of human activity. This study reported the results on the antibiotic resistance profiles of 10 different serotypes of *Salmonella* spp. in circulation in livestock-related samples in Italy. The results gathered in the current study confirm the scientific evidence available in the literature, according to which the resistance towards antibiotics is continuously increasing. This represents a worrying perspective since they should be usually used as a last option for therapy against bacterial infections. As a matter of fact, the current study highlights the need for the consolidation of surveillance activities for public health.

Leptospirosis is an important zoonotic disease caused by infection with pathogenic spirochaete, bacteria belonging to *Leptospira* genus. Traditionally, the classification of Leptospire was based on their antigenic phenotype: more than 250 pathogenic *Leptospira* serovars are known. These are classified into 25 different sero groups. More recently, the biomolecular approach based on DNA homology has permitted us to identify 17 pathogenic species of *Leptospira* spp., seven of which are the most common agents causing disease in human and a wide variety of wild and domestic animals. The infection is spread worldwide, particularly in Tropical areas, where many environmental and cultural conditions favorable for its transmission occur, such as the close coexistence between people and wild or domestic animals and a predominantly warm humid climate.

Leptospirosis can also occur in urban environments of industrialized countries or in temperate rural contexts with a seasonal trend characterized by a maximum incidence in warm and rainy months. Reservoir animals harbor *Leptospire*s in their kidneys for a long time, often without symptoms, shedding them in the environment through urinary elimination and playing an important role as a source of infection. Animals can develop variable clinical signs such as fever, renal and hepatic failure, and reproductive disorders. As concerning the association of serovar reservoir, many epidemiological studies reported specific animal species might act as the reservoir for particular *Leptospira* serovars. Rodents are the main reservoir hosts of pathogenic *Leptospira* serovar *Icterohaemorrhagiae*, along with other marsupial and mammalian species.



Dogs are susceptible to a wide range of *Leptospira* serovars. Infection with one of these serovars more virulent frequently leads to severe clinical symptoms. However, it is difficult to determine if susceptibility in dogs can be related to age, breed, or sex. Among the main serovars detected in dogs, Canicola recognizes the dog as a reservoir host, representing a major concern in a One Health vision. On the other hand, mass vaccination of dogs has contributed to the decrease of infection by *Leptospira interrogans* serogroup Canicola serovar Canicola in Europe. Different kinds of dog vaccine are available in Italy: bivalent vaccines containing two antigen strains, belonging respectively to two serovars (Canicola and Icterohaemorrhagiae), a trivalent vaccine containing three antigen strains, belonging to three serovars (Canicola, Icterohaemorrhagiae, and Grippotyphosa), and tetravalent vaccines containing four antigen strains, belonging to four serovars (Canicola, Icterohaemorrhagiae, Grippotyphosa, and Bratislava). In cats, clinical signs are rare. Moreover, both infected dogs and cats can shed *Leptospire*s in the environment through their urine, potentially contributing to the infection spreading.

Canine parvovirus type 2 is a non-enveloped single-stranded DNA virus, taxonomically included by the International Committee on Taxonomy of Viruses in the species *Protoparvovirus carnivora* 1. It is the causative agent of an acute and often fatal disease of domestic dogs and wild carnivorans, characterized by severe gastroenteritis and lymphopenia. Nowadays, it is considered one of the main viral canine pathogens, threatening particularly young or non-immunised dogs. The original type of Canine parvovirus type 2, to date no longer circulating in the field and present only in some vaccines, was first identified as a canine pathogen in the late 1970s and has been soon replaced by three antigenic and genetic variants, namely CPV-2a, CPV-2b, an CPV-2c currently distributed worldwide.

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Canine parvovirus type 2 is a non-enveloped single-stranded DNA virus, taxonomically included by the International Committee on Taxonomy of Viruses in the species *Protoparvovirus carnivora* 1. Soon after its first evidence in the late 1970s, CPV-2 rapidly spread worldwide and is still considered the main viral cause of Gastroenteric infection in canine species, particularly in younger dogs, although the wide use of vaccines has substantially contributed to the control of this infection. During the last four decades, an increasing number of studies investigated its spread, epidemiology, and evolution, leading to a more in-depth characterization of CPV-2 genomic heterogeneity. In Italy, a considerable amount of literature has contributed during the years to outline the evolution and spread of CPV-2 in domestic dogs. Overall, several pieces of evidence suggested a continuous change in the occurrence and distribution of classical and new CPV-2 lineages, that need to be constantly monitored.

Over the last decades several pestiviruses, which are genetically distinct from bovine viral diarrhea virus type 1, BVDV-2 (Pestivirus B), classical swine fever virus (Pestivirus C), and border disease virus (Pestivirus D) were discovered in ruminants, pigs, and more recently also in non-ungulate hosts. Consequently, the nomenclature and taxonomy of pestiviruses, which belong to the family Flaviviridae, were updated and currently, the genus Pestivirus comprises eleven established virus species. Pestiviruses of cloven-hoofed animals are widely distributed pathogens and are responsible for economically important diseases affecting domestic and wild animal species worldwide. The consequences of pestivirus infections in bats, rodents, whales and pangolins are unknown and the association with a disease still needs to be established.

Natural infections of pigs with from Bovine Viral Diarrhea Virus or Border disease virus occur in countries where pigs and ruminants are housed in close contact. In contrast to Classical Swine Fever Virus, postnatal infections with these pestiviruses frequently do not result in clinical disease and are mainly associated with reproductive disorders. After trans-placental infection of sows the degree of clinical disease depends on the stage of gestation. In particular, the occurrence of persistently infected piglets have a major impact on the epidemiology of the disease since these animals are viremic, antibody negative and constantly excrete virus.

Due to antigenic relatedness of classical swine fever and ruminant pestiviruses, infection of pigs with ruminant pestiviruses can result in the production of cross-reacting antibodies, which may interfere with serological diagnosis of classical swine fever.

The Tunisian sheep-like virus (TSV), which was first isolated from batches of a contaminated sheep pox vaccine in Tunisia, represents an additional ovine pestivirus that is genetically closely related to Classical Swine Fever Virus. Subsequently, Tunisian sheep-like virus was also detected in sheep in France as well as in goats and sheep in Italy. Analyses of pestivirus evolution resulted in the hypothesis that Classical Swine Fever Virus emerged from Tunisian sheep-like virus by a host switch from sheep to pig around 225 years ago and that TSV represents not only an ancestor for CSFV but also for the novel ovine pestivirus from Italy. So far, TSV has not been found in pigs and it is unknown whether it has the capacity to cause disease in pigs.

Viruses are recognized as a cause of foodborne and waterborne disease transmitted by faecal–oral cycle. Among the main foods involved in the transmission of human enteric viruses are molluscs and fruits and vegetables irrigated with wastewater and/or washed with non-potable water or contaminated by contact with surfaces or the hands of infected personnel during preparation. Also, viral waterborne disease outbreaks associated with contaminated drinking water or recreational water are reported worldwide. The last decade has seen a succession of health alarms regarding ‘foodborne diseases’ and ‘waterborne diseases’, increasing attention to food and water safety. However, data on viral contamination of food and water in Sicily are scarce and fragmentary. This is the first study to analyze both matrices for a panel of enteric viruses.

Hepatitis E virus (HEV) represents one of the principal causative agents of hepatitis transmitted by the fecal-oral route and an ongoing internationally challenging issue for public health. Among the five HEV genotypes affecting humans, 3 and 4 are zoonotic.

Domestic pigs and wild boars are the main animal reservoir of these genotypes; serological and virological evidence of HEV infection was also documented in other animal species including cattle. The epidemiological role of these domestic species is uncertain. Dairy cattle could act as a potential HEV reservoir. Thus further complementary studies focusing on molecular detection of virus RNA should be carried out, to investigate about the possible role of cattle in HEV transmission. Also consumption of undercooked beef, as well as pork, might contribute to the transmission of HEV to humans.