

# NEW BACTERIAL ZOOONOTIC PATHOGENS

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## Summary

The article presents the problem of new zoonotic bacterial pathogens posing a threat to humans. Currently, 11 pathogens responsible for causing human zoonotic diseases are being monitored by the European Union epidemiological authorities, 7 of which are bacteria: *Salmonella* spp., *Campylobacter* spp., *Listeria monocytogenes*, *Mycobacterium bovis*, *Brucella* spp., *Escherichia coli* VTEC/STEC and *Coxiella burnetii*. Nonetheless, many new emerging zoonotic bacteria, which are not currently monitored by ECDC might also pose a serious epidemiological problem in the foreseeable future: *Streptococcus iniae*, *S. suis*, *S. dysgalactiae* subsp. *equisimilis* and staphylococci: *Staphylococcus intermedius* and *S. pseudintermedius*. These species have just crossed the animal-human interspecies barrier. The mechanism of this phenomenon remains unknown. It is connected, however, with genetic variability and capability to survive in changing environment, which are the result of DNA rearrangement and horizontal gene transfer between bacterial cells. The recent substantial increase in the number of scientific publications on this subject testifies to the importance of the problem.

Keywords: zoonoses, disease reservoirs, epidemiology, crossing interspecies barriers, pathogen evolution

There are approximately 1400 pathogens which currently pose a threat to humans. Most of these pathogens are of zoonotic origin. Among them, there are the most dangerous pathogens, which broke the animal-human interspecies barrier in recent times. E.g. viruses like: HIV, H5N1 and H1N1 influenza, coronaviruses or Ebola have become a serious epidemiological problem during the last 50 years. The number of pathogenic viruses increases by approximately 25 every 10 years. Among bacteria, *Helicobacter pylori*, pathogenic serotypes of *Escherichia coli* (VTEC, EIEC, EPEC, EAaggEC, DAEC, O104:H4) and *Borrelia burgdorferi* have emerged during last 50 years.

The primary reservoir of many species is the environment (e.g. *Legionella pneumophila*, *Bacillus anthracis*) but most of them (nearly 1000 species and varieties) originate from animal pathogens. Only about 3.5% of all etiological factors are exclusive to humans and nowadays do not have any animal or environmental reservoir. This group comprises e.g. *Streptococcus pyogenes*, *Neisseria gonorrhoeae* and *Treponema pallidum* (1). The notion “zoonoses” is usually used to describe infections that can be transmitted directly from animals to humans. Sometimes, when a pathogen gains the ability of human-to-human transmission, we forget about its animal origin. However, it is still able to infect its primary hosts and might be transported by them. Some zoonotic bacteria have over the years achieved the ability to cause epidemic diseases,

like plague (caused by *Yersinia pestis*) and typhoid fever (caused by *Rickettsia prowazekii*). New zoonotic human RNA viruses are the most frequently noted, due to their spectacular epidemics, e.g. HIV (transmitted from apes), SARS (from civets), H5N1 influenza (from birds), H1N1 influenza (from pigs) and, last but not least, the most current – Ebola virus (from bats). According to Woolhouse and Gaunt (2), the danger of new zoonotic pathogens emergence (or new varieties of already known pathogens) is one of the biggest challenges of XXI century. Taylor et al. (1) proved that animal pathogens (bacteria and fungi) pose a three-fold higher danger of becoming new etiological factor of human diseases than bacteria and fungi of other origin.

The process of evolutionary changes in the transformation of an animal pathogen into a specialized pathogen of humans has already been described by Wolfe et al. (3). Five steps constituting this process are shown in figure 1. It also demonstrates the current location of the emerging pathogens described in the article. The bases of this evolutionary process usually remain unknown but it is connected with genetic variability and obtaining new features which allow bacteria to survive and spread in a new environment. This ability mainly results from horizontal gene transfer (HGT) and DNA rearrangements (4).

European Union epidemiological authorities collect data on zoonoses from all Member States. Their annual

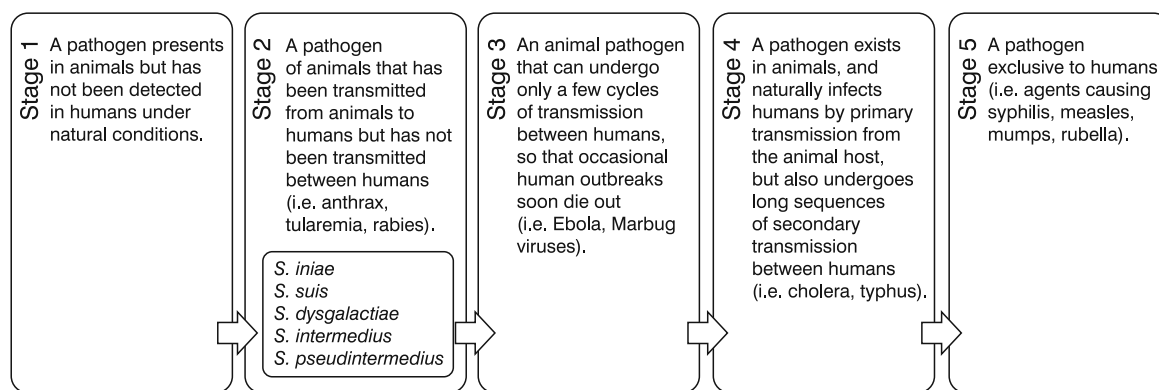


Fig. 1. Scheme presenting evolutionary transformation of zoonotic pathogens, including emerging zoonotic bacterial pathogens described in this article (3 – modified).

reports describe 11 most important zoonotic etiological factors, 7 of which are bacterial pathogens. European Union summary reports on zoonoses include following bacterial pathogens: *Salmonella* spp., *Campylobacter* spp., *Escherichia coli* O104:H4 (VTEC/STEC), *Listeria monocytogenes*, *Mycobacterium bovis*, *Brucella* spp. and *Coxiella burnetii* (5). These bacteria are well-known and described. However, the abovementioned list includes only some of zoonotic pathogens, selected arbitrarily by the epidemiological authorities, mainly connected with foodborne diseases. Over the last years many other animal pathogens have gained the ability to infect humans. Highlighting the presence of these new bacterial pathogens, as well as the fact that the EU list of monitored pathogens is no longer up-to-date, seems to be of vital importance.

A prevalent genus actively adapting to human environment is *Streptococcus*. *Streptococcus iniae* used to be regarded as a significant fish and dolphin pathogen. In the late nineties human infections were also noticed with a large variety of severe symptoms like cellulitis (6), endocarditis (7), meningitis and sometimes sepsis with streptococcal toxic shock syndrome (7). Recent data show that during the past few years over 2000 human *S. iniae* infections have been noted in Australia and Canada (8, 9). Other *Streptococcus* species – for instance *S. suis*, was regarded as an important swine pathogen, connected with high mortality infections. In 2005 the first outbreak of epidemic in humans took place in China. According to the official data 39 people died. Since then, hundreds of cases have been documented, also in many countries in Europe, including Poland. 72.5% of infections led to meningitis, 73.0% of which ended in deafness. 24.2% of patients suffered from sepsis with streptococcal toxic shock syndrome. These statistics show that the frequency of severe infections was significantly higher than the one connected with well-described human streptococci (4, 10, 11). However, the infections of both *S. iniae* and *S. suis* are still regarded

as primary infections, which cannot transmit between humans (stage 2 according to Wolfe et al.) (9). Usually the route of infection is a direct contact with an infected animal or its meat when a pathogen penetrates the human organism through wounds (12).

Not only pigs or fish might be the reservoir of zoonotic pathogens. Also pets, such as cats and dogs frequently transmit various streptococci and staphylococci. For instance, until recently *Streptococcus dysgalactiae* had been reported as a typical animal pathogen, not found in clinical samples from humans. In the past few years, more and more frequently, *S. dysgalactiae* subsp. *equisimilis* has been isolated from purulent infections in humans, like pharyngitis, pneumonia and necrotizing fasciitis. *S. dysgalactiae* subsp. *equisimilis* has also appeared to have the potential to cause focal infections such as sepsis, endocarditis or meningitis (13, 14). Bacteria are usually transmitted by direct contact with an animal or its secretions. Similarly to *S. iniae* and *S. suis*, the human-to-human transmission has not been proven yet.

*Staphylococcus intermedius* frequently colonizes skin and mucosal membranes of dogs and might cause deep pyoderma. The first case of human infection as a result of a dog bite was reported in 1989 (15). Furthermore, Guardabassi et al. (16) demonstrated that multi-resistant *S. intermedius* strains, infective for dogs, were simultaneously isolated from the oral and nasal cavities of their owners. Human infections are usually mild. However, in patients with compromised immunity they might lead to endocarditis (17), pneumonia (18), brain abscess (19) and acute meningitis (20). The human-to-human transmission of *S. intermedius* has not been observed yet.

*Staphylococcus pseudintermedius* also colonizes animal skin and mucosal membranes and might cause opportunistic diseases, like superficial and deep pyoderma or otitis media (21). According to Kadlec et al. (22). *Staphylococcus pseudintermedius* might also cause

septicemia, nephritis, rhinitis and wound infections in cats. The animal-to-human transmission usually results from an animal bite or close contact with a cat or a dog. Similarly to *S. intermedius*, the colonization of dog owners' nasal cavity by *S. pseudintermedius* strains isolated also from their dogs, has been proven (23). This pathogen may cause mild opportunistic infections in humans. However, single cases of sinusitis (24), endocarditis (25) and pneumonia (26) have also been described. As the human-to-human transfer has not been proven yet, *S. pseudintermedius* is currently on stage 2 according to Wolfe et al.

The abovementioned examples demonstrate that the list of zoonotic pathogens being monitored by the European Union epidemiological authorities should remain open, because evolutionary changes of many different pathogens occur incessantly. In the foreseeable future, particularly because potential animal reservoirs live close to humans, next animal pathogens might break the animal-human interspecies barrier and pose a substantial epidemiological risk. The importance of this problem is illustrated by the notable increase in the number of scientific publications on this subject. □

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