

Insect/Bacteria Association and Nosocomial Infection

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1. Introduction

The genus *Salmonella* belongs to the family Enterobacteriaceae, a group of bacteria normally found in the intestine of the hosts. More than 2,500 serotypes have been identified in the *Salmonella enterica* complex (Popoff et al., 2004). *Salmonella* species are classified as Gram-negative, rod-shaped, facultatively aerobic bacteria that have mobility in liquid environments and reproduce at temperatures ranging from 5°C to 47°C and pH from 4.5 to 9.0 (Varnan & Evans, 1991). *Salmonella* species produce hydrogen sulfide, are oxidase, indol, and Voges-Proskauer negative, catalase, citrate, lysine-ornithine, decarboxylase, and glucose positive, also presenting other carbohydrates fermentation with acid and gas liberation (Le Minor, 1984). Although the dispersion of these microorganisms is limited due to their incapacity to sporulate and sensitivity within the pasteurization temperature range (Varnan & Evans, 1991; D'Aoust, 2000), they are resistant to desiccation and freezing and are able to survive in the environment for several years (Tortora et al., 2005).

A variety of human foods of plant and animal origin have been identified as vectors of transmission of *Salmonella*. A study with inoculation of *Salmonella* in a tomato plantation soil evidences the risk of human contamination through ingestion of plant foods (Barak & Liang, 2008). According to Hirsh (2003), apparently healthy animals can develop diseases caused by *Salmonella* because of stress factors, such as sudden alterations of the environment temperature, water and food deprivation, overpopulation, gathering animals of different lots, and inappropriate antimicrobial use. As contaminated meat is the most frequent source of human disease caused by *Salmonella*, this type of food is of particular interest concerning epidemiological studies (Gatto et al., 2006). The genus *Salmonella* was found in 20% of the commercialized chicken samples in Malaysia (Rusul et al., 1996). Human disease outbreaks caused by *Salmonella* are generally associated to egg, chicken, and pork consumption (Castagna et al., 2004). Inappropriate food storage also represents an important cause of proliferation and dissemination of these microorganisms (Murmman et al., 2005). *Salmonella enteritidis* and *Salmonella typhimurium* were the most prevalent serotypes involved in foodborne infections registered in the world (Van Der Wolf et al., 2001).

2. Epidemiology

The acute symptoms of the infection caused by *Salmonella* are fever, migraine, nausea, and dysentery. Depending on the patient profile, the extraintestinal chronic form can evolve into sepsis (CDC, 1999; Wilson & Whitehead, 2004; Loureiro et al., 2010). *S. enterica* serotype Blockley is related to up to 29% of the cases of arthritis described in the literature (Dworkin et al., 2001). An aggravating factor in diseases caused by *Salmonella* is the evolution of resistant types due to uncontrolled antibiotic use both in domesticated animals and humans. Antibiotics and chemotherapies are chemical compounds that can inhibit bacterial growth (Cromwell, 1991), but can result in microorganism resistance if used indiscriminately, disregarding bacterial specificity or the minimum inhibitory concentration (Wannmacher, 2004). Therefore, Silva et al. (2004) consider that the use of antimicrobials in bird diets is of great importance to break the cycle of bird disease caused by *Salmonella*. In cases of continuous or prolonged treatment with high-dose antibiotic in humans, instead of curing the patient the infection rates can increase (Barza & Travers, 2002; Wannmacher, 2004). Studies demonstrated that the rates of *Salmonella* multi-drug resistance have increased considerably in recent years (Haneda et al., 2004; Chiu et al., 2006; Carneiro et al., 2008; Pesquero et al., 2008). Bacterial resistance can lead to increased virulence and consequently increased morbidity and mortality of infected people (Mølbak, 2005).

Salmonella resistance to antibiotics has been related to the presence of plasmids. Approximately 30 low-molecular-weight plasmids have been identified in *S. enteritidis* (Rychlik et al., 2001). Plasmids described in *S. enterica* serovar typhi isolates (Boyd et al., 2003) confer pathogenicity to these bacteria (Baker & Dougan, 2007). Some plasmids simultaneously confer resistance and virulence to *Salmonella*. This bacteria-plasmid association presents epidemiological relevance, because a process of recombination with *Salmonella* provides it with advantages to survive in a hostile environment and chances to evolve a new genetic lineage (Majtan et al., 2006).

Antibiotic resistance genes are frequently located within transposons, but they can also be found in the form of gene cassettes captured and clustered in integrons and thereafter mobilized to spread resistance among other organisms (Fluit, 2005). In *S. typhimurium*, antibiotic resistance depends on integrons more frequently associated to a genomic island located on the bacterial chromosome (Tosini et al., 1998). There are two categories of integrons, one represented by repeated direct sequences (IS) and the other represented by inverted sequences (IR). The first integron category, widely distributed in *Salmonella*, consists of two conserved sequences, regions 50 Cs and 30 Cs, which carry the gene *int I* to the integrase protein and the gene *sul I* of resistance to the sulfonamide, respectively (Guerra et al., 2002).

Some plasmids are responsible for the phage conversion, which permits bacteria to resist phage infection. For example, the pOG670 plasmid of 54 kb, belonging to the group of incompatibility X (IncX), present in *S. enteritidis*, is capable of converting phages types 1 and 4 into type 6a, and phage 8 into type 13 (Ridley et al., 1996). In *S. abortus-equi*, a plasmid of 85 kb that codifies resistance to toxic heavy metals (chromium, arsenic, cadmium, and mercury) was described. This plasmid was also proven to encode genes that allowed the use of citrate and conferred β -lactam antibiotic resistance (Ghosh et al., 2000).

Guiney et al. (1995) and Roudier et al. (1992) found serotypes of non-typhoid *Salmonella*, associated with extraintestinal disease, possessing virulent plasmids (spvC) that contain virulence genes (spvC), important for the induction of a systemic and lethal infection. Fierer et al. (1992) reported plasmids in *Salmonella* in 76% of 79 samples of human blood and in 42% of 33 human stool samples. Both in animals and humans, bacteria of the genus *Salmonella* are more frequently found in systemic infections compared with enteric ones. According to Fierer et al. (1993), non-typhoid *Salmonella* pathogenicity is related to the presence of plasmids.

The high susceptibility of hospitalized children to nosocomial infections was attributed to antimicrobial resistance of *S. enterica* (Fonseca et al., 2006). Some disease outbreaks caused by *Salmonella* serotypes resistant to antibiotics have been registered in pediatric settings worldwide and can provoke the death of newborn babies (Pessoa-Silva et al., 2002; Bouallègue-Godet et al., 2005). Diseases caused by *Salmonella* represent 10% to 15% of the acute gastroenteritis cases all over the world (Jay, 2005). Of the 4,012 disease outbreaks of enteric infections that occurred in England and Wales, *Salmonella* was the most frequent microorganism, responsible for 22% of the cases (Guard-Petter, 2001). Estimates indicate that *Salmonella* is responsible for one third of the cases of foodborne illnesses in the US, corresponding to 2-4 million cases a year (Andrews et al., 1992), causing economic losses of about 4 billion dollars annually (Mead et al., 1999). In South American countries, the prevalence of *Salmonella* infections is low (2.5%) compared with the US, although considered one of most important epidemiological illnesses (Franco, 2003).

3. Insect vectors

The transformation of natural ecosystems into urban areas and crop fields results in changes in animal, plant, and microorganism biodiversity and dynamics. In a broad sense, the simplification of the environment reduces biological diversity but, on the other hand, it favors the population growth of other species of bacteria (Fowler, 1983). Opportunistic animals that benefit from human presence are called synanthropic and considered pests if they cause damages to human health and the economy. The current context of worldwide social economic development contributes to environmental deterioration, facilitating horizontal and vertical transmission of illnesses through vectors, mainly insects (Pongsiri & Roman, 2007).

Vectors are organisms that contribute to the dispersion of pathogens by carrying and transmitting them (Purcell & Almeida, 2005), and are known as intermediate or definitive hosts, respectively when the pathogenic organism is carried externally or internally to the vector body. Transmission between hosts can occur indirectly by pathogen spread in the environment, normally through feces and/or secretions, and also due to physical contact, when the pathogen is adhered to the surface of the vector body, or directly by inoculation of the pathogen in the host body through the vector bite. Triatomine species (Hemiptera: Reduviidae) increase human transmission rate of the protozoan *Trypanosoma cruzi* by depositing feces contaminated with infecting metacyclic trypomastigotes on the host face skin near the insect bite.

Insects are among the most diversified, abundant, and widely dispersed animals in the world. They represent more than 50% of all species living on the planet, 71% of animal

species, 74% of invertebrates, and 87% of arthropods (Lewinson & Prado, 2002). This success is mainly due to their morphologic characteristics, such as locomotion appendices (legs and wings), exoskeleton, small body size, and metamorphosis. Insects can use specialized types of sexual and asexual reproduction, such as parthenogenesis, pedogenesis, and neoteny, as reproductive strategies (Gullan & Cranston, 2008). The most representative insect orders regarding species richness and abundance are Coleoptera (beetles), Diptera (flies and mosquitoes), Hymenoptera (bees, wasps, and ants), Lepidoptera (butterflies and moths), and Hemiptera (chinch bugs, aphids, whiteflies, mealybugs, and cicadas).

Some species of blood-feeding insects found a direct food source in humans, and many of them are vectors of microorganisms that cause important diseases in tropical and subtropical countries, such as malaria, yellow fever, typhoid fever, dengue fever, filariasis, leishmaniasis, chagas disease, and sleeping sickness. Another group of synanthropic insects indirectly benefits from human foods found in crop fields, or stored, industrialized, and prepared in households, or rejected food waste in landfills and sewage. These insects are known as phytophagous, granivorous, parasites, saprophagous, coprophagous, and generalists, constituting the great majority of insects associated with humans in urban centers and rural areas. Among these insects, the species that are carriers of pathogenic microorganisms from contaminated environments to human food, medical instruments, and kitchen utensils deserve special attention of public health authorities. Therefore, the participation of insects in the transmission of bacteria has been investigated aiming to reduce the occurrence of enteric disease outbreaks in hospitals.

Arthropods are common in hospital environment (Gazeta et al., 2007) and the main vectors of pathogenic microorganisms that infect humans are cockroaches, ants, and flies because of their contact with human feces and other contaminated materials. Sewage and landfills are major sources of pathogenic microorganisms and lack of investments in basic sanitation is a serious public health problem (Andreoli & Bonnet, 2000; Bastos et al., 2003). Cockroaches (Blattodea) are dorsoventrally flattened body insects that eat preferentially decayed vegetable substances. They have specific enzymes and endosymbiotic microorganisms that assist them in cellulose digestion and essential amino acid synthesis (Hirose & Panizzi, 2009; Louzada, 2009). *Blattella germanica* and *Periplaneta americana* are cosmopolite cockroach species adapted to urban environments, specially sewage, bathroom, and kitchen, where they find abundant food and absence of predators. Microbiological analyses of cockroaches captured in hospitals and residences have identified these insects as vectors of more than 80 recognized bacteria species belonging to 51 genera, many of them resistant to antimicrobials, posing health risk to the already weakened interns (Table 1). *Salmonella* was found in nine out of twelve studies with cockroaches in hospitals and residences in the world. Although *Salmonella* multiplication might occur in the intestines of the insects (Klowden & Greenberg, 1977), Gram-negative bacteria are more commonly found in their cuticle, facilitating the dispersion of pathogens (Mpuchane et al., 2006).

Ants are eusocial insects that live in colonies with one or more queens and thousands of workers. The latter need to collect food for their own maintenance and to feed both the immature and adult individuals of the colony, including the queen. Through chemical orientation, workers can cover great distances searching for food and return to the nest indicating the way for the other members of the colony. Their feeding habit is varied (Brandão et al., 2009), but the species adapted to urban environments are characterized by the

consumption of a generalist diet, mobility of colonies, polygeny, monomorphism, and reduced body size (Passera, 1994). *Monomorium pharaonis*, *Paratrechina longicornis*, *Tapinoma melanocephalum*, and species of *Pheidole* and *Solenopsis* are the main ants already found in hospital environments (Fig. 1), and the literature registered 50 bacteria species belonging to 31 genera associated to these and other ant species (Table 2, Fig. 2). Species of the genus *Staphylococcus*, *Escherichia*, *Pseudomonas*, *Enterobacter*, *Bacillus*, *Streptococcus*, and *Klebsiella* are the most frequent bacteria associated with ants in Brazilian hospitals (Fig. 3). *Salmonella* was found associated only with *Monomorium pharaonis* (Beatson, 1972) and a species of *Pheidole* (Pesquero et al., 2008) carries bacteria presenting antimicrobial resistance (Carneiro et al., 2008).

Diptera constitutes a great order of insects that present small body size, fly fast, and have a variety of feeding habits, including necrophagy and coprophagy, during the immature phase. When walking over feces and corpses to deposit eggs, female flies acquire and carry pathogenic bacteria to the interior part of residences, restaurants, and hospitals, contaminating mainly foods and kitchen utensils. *Musca domestica* (Muscidae) is a very common cosmopolite and synanthropic species in urban zones, and together with five other species of flies, is associated to 12 bacteria species belonging to 11 genera (Table 3). *Musca domestica* is the most studied fly considered a vector of *Salmonella* that occurs in some countries (Bolaños-Herrera, 1959; Bidawid et al., 1978; Arnold, 1999; Olsen & Hammack, 2000; Mian et al., 2002; Oliveira et al., 2006; Cardozo et al., 2009; Prakash & Tikar, 2009; Butler et al., 2010; Choo et al., 2011).

Cockroaches	Bacteria	Reference
<i>Blattella germanica</i>	<i>Enterobacter</i> <i>Enterococcus</i> <i>Escherichia coli</i> <i>Haemophilus</i> <i>Klebsiella</i> <i>Pseudomonas</i> <i>Shigella</i> <i>Staphylococcus</i> <i>Streptococcus</i>	Salehzadeh et al. (2007)
<i>Periplaneta</i> <i>Blatta</i>	<i>Salmonella bovis</i> <i>Salmonella morbitans</i> <i>Salmonella oslo</i> <i>Salmonella typhimurium</i>	Devi & Murray (1991)
<i>Blattella germanica</i>	<i>Salmonella enteritidis</i>	Ash & Greenberg (1980).
<i>Periplaneta americana</i> <i>Blattella germanica</i> <i>Supella longipalpa</i> <i>Blatta lateralis</i> <i>Polyphaga aegyptiaca</i> <i>Arenivaga roseni</i> <i>Parcoblatta</i>	<i>Salmonella</i>	Fathpour et al. (2003)

Cockroaches	Bacteria	Reference
cockroaches	<i>Aeromonas</i>	Tatfeng et al. (2005)
	<i>Escherichia coli</i>	
	<i>Citrobacter freundii</i>	
	<i>Enterobacter cloacae</i>	
	<i>Klebsiella pneumoniae</i>	
	<i>Proteus mirabilis</i>	
	<i>Proteus vulgaris</i>	
	<i>Pseudomonas aeruginosa</i>	
	<i>Salmonella</i>	
	<i>Serratia marcescens</i>	
<i>Staphylococcus aureus</i>		
<i>Staphylococcus faecalis</i>		
<i>Staphylococcus epidermidis</i>		
<i>Periplaneta americana</i>	<i>Enterobacter</i>	Lamiaa et al. (2007)
	<i>Escherichia coli</i>	
	<i>Klebsiella</i>	
	<i>Proteus vulgaris</i>	
	<i>Salmonella</i>	
	<i>Serratia</i>	
	<i>Shigella</i>	
	<i>Staphylococcus aureus</i>	
<i>Staphylococcus epidermidis</i>		
<i>Blattella germanica</i>	<i>Streptococcus</i>	Tachbele et al. (2006)
	<i>Bacillus cereus</i>	
	<i>Escherichia coli</i>	
	<i>Salmonella</i>	
	<i>Shigella flexneri</i>	
<i>Staphylococcus aureus</i>		
<i>Periplaneta americana</i> <i>Blattella germanica</i>	<i>Acinetobacter</i>	Fakoorziba et al. (1910)
	<i>Alcaligenes faecalis</i>	
	<i>Arizona</i>	
	<i>Bacillus</i>	
	<i>Citrobacter freundii</i>	
	<i>Enterobacter aerogenes</i>	
	<i>Enterobacter agglomerans</i>	
	<i>Enterococcus</i>	
	<i>Escherichia coli</i>	
	<i>Hafnia alvei</i>	
	<i>Klebsiella pneumoniae</i>	
	<i>Proteus mirabilis</i>	
	<i>Proteus vulgaris</i>	
	<i>Providencia rettgeri</i>	
	<i>Pseudomonas</i>	
	<i>Salmonella typhimurium</i>	
<i>Shigella</i>		
<i>Staphylococcus</i>		
<i>Yersinia</i>		

Cockroaches	Bacteria	Reference
<i>Periplaneta americana</i>	<i>Enterobacter aerogenes</i>	Miranda & Silva (2008)
	<i>Escherichia coli</i>	
	<i>Citrobacter freundii</i>	
	<i>Hafnia alvei</i>	
	<i>Salmonella</i>	
	<i>Serratia liquefaciens</i>	
<i>Periplaneta americana</i> <i>Blatta orientalis</i>	<i>Staphylococcus</i>	Chaichanawongsaroj et al. (2004)
	<i>Cedecea davisae</i>	
	<i>Cedecea lopaiei</i>	
	<i>Cedecea neteri</i>	
	<i>Citrobacter diversus</i>	
	<i>Citrobacter freundii</i>	
	<i>Edwardsiella ictaluri</i>	
	<i>Edwardsiella tarda</i>	
	<i>Enterobacter aerogenes</i>	
	<i>Enterobacter agglomerans</i>	
	<i>Enterobacter asburiae</i>	
	<i>Enterobacter cloacae</i>	
	<i>Enterobacter gergoviae</i>	
	<i>Enterobacter sakasakii</i>	
	<i>Escherichia balttae</i>	
	<i>Escherichia coli</i>	
	<i>Escherichia hermannii</i>	
	<i>Escherichia vulneris</i>	
	<i>Ewingella americana</i>	
	<i>Hafnia alvei</i>	
	<i>Klebsiella oxytoca</i>	
	<i>Klebsiella ozanae</i>	
	<i>Klebsiella pneumoniae</i>	
	<i>Klebsiella rhinoscleromatis</i>	
	<i>Klebsiella terrigena</i>	
	<i>Kluyvera ascorbata</i>	
	<i>Moraxella urethralis</i>	
	<i>Morganella morganii</i>	
	<i>Obesumbacterium</i>	
	<i>Proteus mirabilis</i>	
	<i>Proteus myxofeaceus</i>	
	<i>Proteus penneri</i>	
	<i>Proteus vulgaris</i>	
	<i>Providencia rustigianii</i>	
	<i>Pseudomonas aeruginosa</i>	
	<i>Pseudomonas maltophilia</i>	
<i>Pseudomonas pseudoalkaligenes</i>		
<i>Rahnella aquatilis</i>		
<i>Salmonella</i>		
<i>Serratia liquefaciens</i>		
<i>Serratia marcescens</i>		
<i>Serratia odotifera</i>		

Cockroaches	Bacteria	Reference
	<i>Achromobacter</i>	
	<i>Acinetobacter calcoaceticus</i>	
	<i>Aeromonas hydrophila</i>	
	<i>Alcaligenes faecalis</i>	
	<i>Buttiauxella agrestis</i>	
	<i>Cedecea</i>	
	<i>Citrobacter diversus</i>	
	<i>Citrobacter freundii</i>	
	<i>Enterobacter aerogenes</i>	
	<i>Enterobacter agglomerans</i>	
	<i>Enterobacter amnigenus</i>	
	<i>Enterobacter cloacae</i>	
	<i>Enterobacter sakazakii</i>	
<i>Supella supellectilium</i>	<i>Escherichia adecarboxylata</i>	Le Guyader et al. (1989)
	<i>Escherichia coli</i>	
	<i>Klebsiella oxytoca</i>	
	<i>Klebsiella pneumoniae</i>	
	<i>Kluyvera</i>	
	<i>Proteus mirabilis</i>	
	<i>Pseudomonas aeruginosa</i>	
	<i>Pseudomonas cepacia</i>	
	<i>Pseudomonas paucimobilis</i>	
	<i>Pseudomonas fluorescens</i>	
	<i>Pseudomonas maltophilia</i>	
	<i>Pseudomonas stutzeri</i>	
	<i>Serratia marcescens</i>	
	<i>Serratia liquefaciens</i>	
	<i>Staphylococcus aureus</i>	
	<i>Actinomyces randingae</i>	
	<i>Alcaligenes faecalis</i>	
	<i>Arthrobacter cummingsii</i>	
	<i>Aureobacterium</i>	
	<i>Bacillus</i>	
	<i>Brevibacterium</i>	
	<i>Burkholderia vietnamiensis</i>	
	<i>Buttiauxella</i>	
cockroaches	<i>Citrobacter</i>	Mpuchane et al., (2006)
	<i>Corynebacterium</i>	
	<i>Enterobacter</i>	
	<i>Erwinia</i>	
	<i>Escherichia coli</i>	
	<i>Hafnia</i>	
	<i>Kauri rosea</i>	
	<i>Kigali</i>	
	<i>Klebsiella</i>	
	<i>Kluyvera</i>	

Cockroaches	Bacteria	Reference
	<i>Leuconostoc</i>	
	<i>Microbacterium</i>	
	<i>Micrococcus</i>	
	<i>Proteus</i>	
	<i>Providencia ruttier</i>	
	<i>Pseudomonas</i>	
	<i>Rhodococcus australis</i>	
	<i>Rhodococcus rhodochrous</i>	
	<i>Salmonella typhimurium</i>	
	<i>Serratia</i>	
	<i>Shigella</i>	
	<i>Spingobacterium thalpophilum</i>	
	<i>Staphylococcus</i>	
	<i>Stenotrophomonas maltophililla</i>	
	<i>Streptococcus</i>	
	<i>Tsakamurella inchonensis</i>	
	<i>Vibrio metschnikovii</i>	
	<i>Xanthomonas</i>	

Table 1. Registry of occurrences of vector species of the order Blattaria and types of transported bacteria.

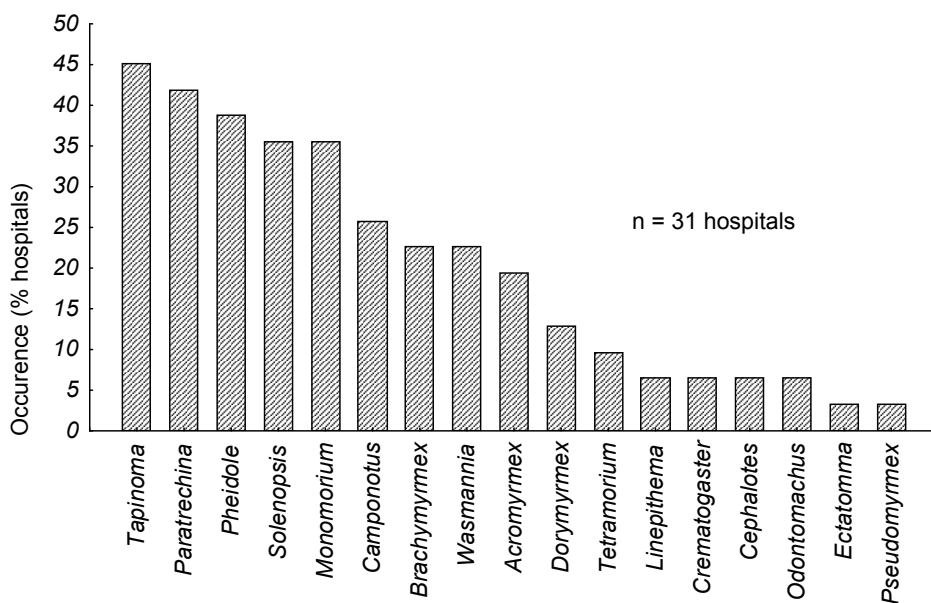


Fig. 1. Occurrence of ants in hospitals.

Ant	Bacteria	Reference
<i>Acromyrmex</i>	<i>Pseudomonas aeruginosa</i> <i>Staphylococcus</i> <i>Streptococcus faecalis</i>	Santos et al. (2009)
<i>Brachymyrmex</i>	<i>Enterococcus</i> <i>Streptococcus agalactiae</i>	Lise et al. (2006)
<i>Camponotus</i>	<i>Corynebacterium diphtheria</i> <i>Corynebacterium jeikeium</i> <i>Streptococcus</i>	Lise et al. (2006); Santos et al. (2009)
<i>Camponotus vittatus</i>	<i>Bacillus</i> <i>Staphylococcus</i>	Rodvalho et al. (2007)
<i>Linepithema humile</i>	<i>Escherichia coli</i> <i>Streptococcus</i>	Santos et al. (2009)
<i>Monomorium pharaonis</i>	<i>Acinetobacter haemolyticus</i> <i>Aeskovia</i> <i>Clostridium</i> <i>Corynebacterium</i> <i>Listeria monocytogenes</i> <i>Planococcus</i> <i>Pseudomonas aeruginosa</i> <i>Pseudomonas luteola</i> <i>Salmonella</i> <i>Sphingobacterium</i> <i>Sphingomonas paucimobilis</i> <i>Staphylococcus intermedius</i> <i>Stenotrophomonas maltophilia</i> <i>Streptococcus bovis</i> <i>Enterobacter agglomerans</i> <i>Enterococcus faecalis</i> <i>Enterococcus faecium</i> <i>Gemella haemolysans</i> <i>Klebsiella pneumoniae</i> <i>Streptococcus acidominimus</i> <i>Staphylococcus lugdunensis</i>	Lise et al. (2006); Moreira et al. (2005); Beatson (1972)
<i>Odontomachus</i>	<i>Enterococcus</i> <i>Escherichia coli</i> <i>Pseudomonas aeruginosa</i> <i>Staphylococcus</i> <i>Streptococcus</i>	Santos et al. (2009)

Ant	Bacteria	Reference
<i>Paratrechina longicornis</i>	<i>Acinetobacter haemolyticus</i>	Lise et al. (2006); Moreira et al. (2005); Fontana et al. (2010); Tanaka et al. (2007)
	<i>Alcaligenes faecalis</i>	
	<i>Alcaligenes sylosidans</i>	
	<i>Bacillus</i>	
	<i>Burkholderia cepacia</i>	
	<i>Citrobacter diversus</i>	
	<i>Comomonas acidoverans</i>	
	<i>Corinebacterium</i>	
	<i>Enterobacter aerogenes</i>	
	<i>Enterobacter agglomerans</i>	
	<i>Enterobacter cloacae</i>	
	<i>Escherichia coli</i>	
	<i>Gemella haemolysans</i>	
	<i>Gemella morbillorum</i>	
	<i>Klebsiella pneumoniae</i>	
	<i>Proteus mirabilis</i>	
	<i>Providencia alcalifaciens</i>	
	<i>Pseudomonas fluorescens</i>	
	<i>Pseudomonas putida</i>	
<i>Pseudomonas stutzeri</i>		
<i>Serratia marcescens</i>		
<i>Serratia rubidae</i>		
<i>Staphylococcus aureus</i>		
<i>Staphylococcus cohnii</i>		
<i>Stenotrophomonas altophilia</i>		
<i>Pheidole</i>	<i>Aeromonas</i>	Santos et al. (2009); Pesquero et al. (2008); Carneiro et al., (2008)
	<i>Enterococcus</i>	
	<i>Escherichia coli</i>	
	<i>Klebsiella</i>	
	<i>Pseudomonas aeruginosa</i>	
	<i>Salmonella</i>	
<i>Staphylococcus</i>		
<i>Streptococcus</i>		
<i>Pheidole megacephala</i>	<i>Acinetobacter baumannii</i>	Fontana et al. (2010)
	<i>Bacillus</i>	
	<i>Escherichia coli</i>	
	<i>Pseudomonas aeruginosa</i>	
	<i>Serratia liquefaciens</i>	
<i>Shigella sonnei</i>		
<i>Staphylococcus aureus</i>		

Ant	Bacteria	Reference
<i>Solenopsis</i>	<i>Enterococcus</i> <i>Staphylococcus</i> <i>Streptococcus</i>	Santos et al. (2009)
<i>Solenopsis globularia</i>	<i>Bacillus</i> <i>Staphylococcus</i>	Fontana et al. (2010)
<i>Solenopsis saevissima</i>	<i>Corynebacterium</i> <i>Enterococcus</i> <i>Neisseria</i> <i>Pseudomonas luteola</i> <i>Staphylococcus saprophyticus</i> <i>Stenotrophomonas maltophilia</i>	Lise et al. (2006)
<i>Tapinoma melanocephalum</i>	<i>Acinetobacter baumannii</i> <i>Alcaligenes faecalis</i> <i>Bacillus</i> <i>Burkholderia cepacia</i> <i>Corinebacterium</i> <i>Enterobacter aerogenes</i> <i>Enterobacter amnigenus</i> <i>Enterobacter cloacae</i> <i>Enterococcus faecalis</i> <i>Escherichia coli</i> <i>Gemella morbillorum</i> <i>Hafnia alvei</i> <i>Klebsiella oxytoca</i> <i>Klebsiella pneumoniae</i> <i>Pseudomonas aeruginosa</i> <i>Pseudomonas fluorescens</i> <i>Staphylococcus saprophyticus</i> <i>Sphingomonas paucimobilis</i> <i>Staphylococcus aureus</i> <i>Staphylococcus epidermidis</i> <i>Staphylococcus equorum</i> <i>Staphylococcus saprophyticus</i> <i>Staphylococcus simulans</i> <i>Staphylococcus warneri</i> <i>Streptococcus viridans</i>	Lise et al. (2006); Moreira et al. (2005); Fontana et al. (2010); Tanaka et al. (2007); Teixeira et al. (2009); Rodovalho et al. (2007); Santos et al. (2009)
<i>Wasmannia auropunctata</i>	<i>Pseudomonas aeruginosa</i> <i>Staphylococcus</i> <i>Streptococcus</i>	Santos et al. (2009)

Table 2. Registry of occurrences of vector species of the family Formicidae (Hymenoptera) and types of transported bacteria.

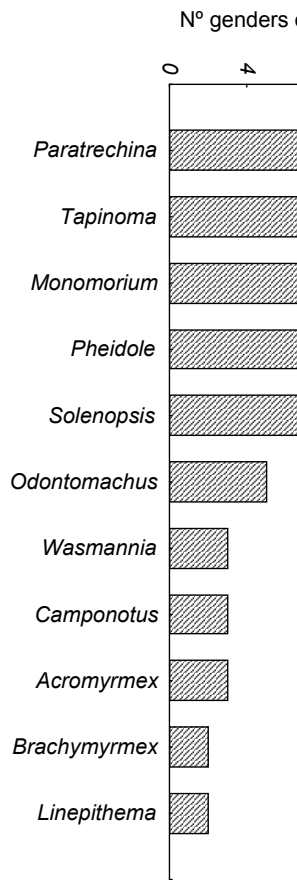


Fig. 2. Occurrence of bacteria genera per ant genus in hospitals.

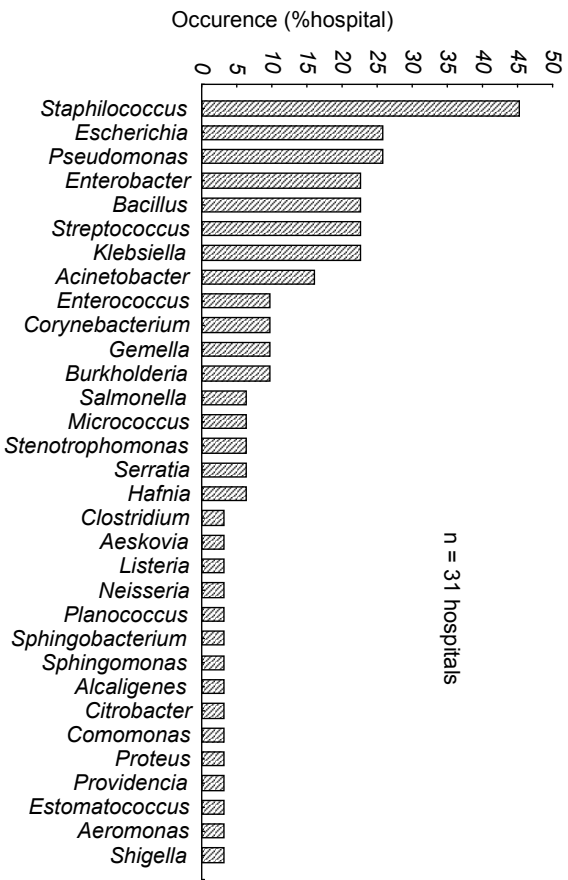


Fig. 3. Occurrence of bacteria genera in hospitals.

Fly	Bacteria	Reference
<i>Hydrotaea aenescens</i> <i>Musca domestica</i>	<i>Salmonella</i>	Olsen & Hammack (2000)
<i>Chrysomya megacephala</i> <i>Musca domestica</i>	<i>Citrobacter</i> <i>Enterobacter</i> <i>Escherichia coli</i> <i>Klebsiella</i> <i>Morganella</i> <i>Proteus mirabilis</i> <i>Pseudomonas</i> <i>Salmonella agona</i>	Oliveira et al. (2006)
<i>Musca domestica</i>	<i>Salmonella</i> <i>Shigella</i>	Bolaños-Herrera (1959)
<i>Musca domestica</i> <i>Fannia canicularis</i> <i>Muscina stabulans</i> <i>Phaenicia sericata</i>	<i>Salmonella</i> <i>Shigella</i>	Bidawid et al. (1978)
<i>Musca domestica</i>	<i>Salmonella enteritidis</i>	Mian et al. (2002)
<i>Musca domestica</i>	<i>Escherichia coli</i> <i>Salmonella typhi</i> <i>Shigella flexneri</i> <i>Yersinia enterocolitica</i>	Béjar et al. (2006)
<i>Musca domestica</i>	<i>Campylobacter</i> <i>Salmonella</i>	Choo et al. (2011)

Table 3. Registry of occurrences of vector species of the Order Diptera and types of transported bacteria.

4. Conclusion

The presence of any serotypes of *Salmonella* in any types of food is a reason to classify them as improper for consumption in the international market. Animals contaminated with *Salmonella* destined to human feeding cannot show clinical signals of the illness (Castagna et al., 2004). Therefore, industries that deal with products of animal origin must implement quality control strategies with the purpose of guaranteeing food safety. The main insect vectors of *Salmonella* are cockroaches and flies, but ants also represent a potential risk. Therefore, governments must invest in the construction of modern hospitals equipped with some devices capable of avoiding the entrance and permanence of vectors, particularly these three types of insects.

5. References

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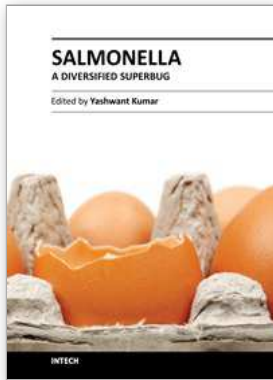
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Salmonella is an extremely diversified genus, infecting a range of hosts, and comprised of two species: enterica and bongori. This group is made up of 2579 serovars, making it versatile and fascinating for researchers drawing their attention towards different properties of this microorganism. Salmonella related diseases are a major problem in developed and developing countries resulting in economic losses, as well as problems of zoonoses and food borne illness. Moreover, the emergence of an ever increasing problem of antimicrobial resistance in salmonella makes it prudent to unveil different mechanisms involved. This book is the outcome of a collaboration between various researchers from all over the world. The recent advancements in the field of salmonella research are compiled and presented.

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