



Pathogenic microorganisms carried by migratory birds passing through the territory of the island of Ustica, Sicily (Italy)

Maria Foti, Donatella Rinaldo, Annalisa Guercio, Cristina Giacobello, Aurora Aleo, Filomena De Leo, Vittorio Fisichella & Caterina Mammina

To cite this article: Maria Foti, Donatella Rinaldo, Annalisa Guercio, Cristina Giacobello, Aurora Aleo, Filomena De Leo, Vittorio Fisichella & Caterina Mammina (2011) Pathogenic microorganisms carried by migratory birds passing through the territory of the island of Ustica, Sicily (Italy), *Avian Pathology*, 40:4, 405-409, DOI: [10.1080/03079457.2011.588940](https://doi.org/10.1080/03079457.2011.588940)

To link to this article: <https://doi.org/10.1080/03079457.2011.588940>



Published online: 04 Aug 2011.



Submit your article to this journal [↗](#)



Article views: 3208



View related articles [↗](#)



Citing articles: 18 View citing articles [↗](#)

Pathogenic microorganisms carried by migratory birds passing through the territory of the island of Ustica, Sicily (Italy)

Maria Foti^{1*}, Donatella Rinaldo¹, Annalisa Guercio², Cristina Giacobello¹, Aurora Aleo³, Filomena De Leo¹, Vittorio Fisichella¹ and Caterina Mammina³

¹Department of Veterinary Public Health, University of Messina, Polo Universitario dell'Annunziata, 98168, Messina, Italy, ²Istituto Zooprofilattico Sperimentale, "A. Mirri", via G. Marinuzzi 3, 90129, Palermo, Italy, and ³Centre for Enteric Pathogens of Southern Italy (CEPIM), Department of Sciences for Health Promotion "G. D'Alessandro", University of Palermo, via del Vespro 133, I-90127 Palermo, Italy

Several studies have shown that migratory birds play an important role in the ecology, circulation and dissemination of pathogenic organisms. In October 2006, a health status evaluation was performed on a large population of migratory birds passing through the territory of Ustica (Italy), an island located on the migration route of many species of birds to Africa, and various laboratory tests were conducted. In total, 218 faecal swabs and the internal organs of 21 subjects found dead in nets were collected for bacteriological and virological examination, including avian influenza and Newcastle disease. In addition, 19 pooled fresh faecal samples were collected for mycological examination. The bacteriological analysis produced 183 strains belonging to 28 different species of the *Enterobacteriaceae* family. In particular, *Salmonella bongori*, *Yersinia enterocolitica* and *Klebsiella pneumonia* strains were isolated. Almost all of the isolates were susceptible to sulphamethoxazole/trimethoprim (99.4%), cefotaxime (98.9%), nalidixic acid (96.7%), chloramphenicol (95.6%), and tetracycline (93.4%). Alternatively, many strains were resistant to ampicillin (42.6%), amoxicillin-clavulanic acid (42.6%), and streptomycin (43.7%). According to reverse transcriptase-polymerase chain reaction analysis, all of the samples were negative for the M gene of avian influenza virus. Moreover, isolation tests conducted on specific pathogen free eggs were negative for avian influenza and Newcastle disease. Several hyphomycetes and yeasts belonging to different genera were present in the specimens, and *Cryptococcus neoformans* was observed in a pooled faecal sample. Antibiotic resistance in wildlife can be monitored to evaluate the impact of anthropic pressure. Furthermore, migratory birds are potential reservoirs of pathogenic agents; thus, they can be regarded as sentinel species and used as environmental health indicators.

Introduction

Ustica, an 8-km² island situated 36 marine miles north of Palermo, Sicily (Italy), is located on the migration route of many species of birds to Africa. Ustica is located between mainland Italy and Sicily, and becomes a refuge in spring and autumn for migratory birds that do not have sufficient strength to accomplish their entire journey or are opposed by contrary winds.

Over the past few years, the Ringing Station in Palermo has participated in the "Small Islands Project" of the National Wild Fauna Institute. Since 2000 a special protection area has been established under Birds Directive 409/79/EEC and Habitats Directive 43/92/EEC, and birds in transit through Ustica during the spring have been ringed.

The Regional District of Palermo, Managing body of the Natural Marine Reserve, "Island of Ustica" planned to use information about migrating birds for the

management of the Reserve, and collaborated with the Ringing Station.

Ustica possesses a rich and differentiated birdlife population, which is important for the sampling of bird migrations. Birds stop on the island for several days to feed on berries, seeds and small insects to regain the indispensable fat layer and essential energy that is necessary for longer journeys (Massa, 2003).

Owing to the considerable interest in the complex phenomenon of bird migration, systematic studies have been conducted. The crossing periods have been directly observed, and data obtained through the implementation of capture places have been analysed. To catch birds, trees and bushes can be used to channel birds into large net traps. Alternatively, large stretched nets called mist-nets can be employed (Barruel, 1959). The recapture of ringed birds and the discovery of deceased individuals

*To whom correspondence should be addressed. Tel: +39 90 3503720. Fax: +39 90 3503976. E-mail: malinvet@unime.it

Received 21 March 2011

ISSN 0307-9457 (print)/ISSN 1465-3338 (online)/11/040405-05 © 2011 Houghton Trust Ltd

DOI: 10.1080/03079457.2011.588940

(often shot by hunters) allow the distances involved in migration to be determined. The study of bird migrations may support surveillance programmes and contribute to the control of bird-borne infections. Several studies have shown that migratory wild birds play an important role in the ecology, circulation and dissemination of pathogenic organisms (Reed *et al.*, 2003), such as arbovirus, influenza A virus (Horimoto & Kawaoka, 2001; Reed *et al.*, 2003), Newcastle disease, duck plague, herpesvirus, *Chlamydophila psittaci*, *Anaplasma phagocytophilum*, *Mycobacterium avium*, *Candida* spp. (Smith *et al.*, 1996; Hubálek, 2004), *Borrelia burgdorferi* (Humair, 2002; Kurtenbach *et al.*, 2002), pathogenic enterobacteria such as *Salmonella* spp., *Campylobacter jejuni*, *Escherichia coli*, enterotoxigenic and verotoxin producers (O157-H7) (Hubálek, 1994; Wallace *et al.*, 1997; Hernandez *et al.*, 2003; Reed *et al.*, 2003), which act as biological and mechanical vectors of pathogens, and bloodsucking ectoparasite infections. These may also become carriers of enterobacteria strains that are resistant to antibiotics and could be responsible for the large-scale expansion of R plasmids (Kanai *et al.*, 1981).

The spread of pathogenic microorganisms depends on various biotic and abiotic factors that affect the survival of microorganisms in the ecosystem of the new geographic area. At rest sites, birds of different species often congregate, and the horizontal transmission of pathogens occurs due to interindividual and interspecies contact (Hubálek, 2004), including interaction with sedentary birds. Furthermore, due to heavy stress and immunosuppression, migration could promote the onset of infectious diseases and the spread of infectious agents. In previous studies, *Candida albicans* was isolated from the digestive tract and faeces of migratory aquatic birds (Kawakita & van Uden, 1965; Cragg & Clayton, 1971; Buck, 1990). In addition, other species of *Candida*, *Rhodotorula rubra*, *Cryptococcus albidus* and *Trichosporon cutaneum* (Cafarchia *et al.*, 2006a) were also identified.

Materials and Methods

In October 2006, the health status of a large population of migratory birds passing through the territory of Ustica was evaluated by conducting various laboratory tests.

In the present study, individuals belonging to the following orders were identified: *Passeriformes* (*Erithacus rubecula*, *Turdus philomelos*, *Hirundo rustica*, *Fringilla coelebs*, *Monticola solitarius*, *Alauda arvensis*, *Carduelis chloris chloris*, *Sylvia atricapilla*, *Sylvia cantillans*, *Phoenicurus phoenicurus*, *Hippolais icterina*, *Saxicola rubetra*, *Phylloscopus trochilus*, *Anthus trivialis*, *Sylvia borin*, *Saxicola torquata*, *Sylvia melanocephala*), and *Caprimulgiformes* (*Caprimulgus europaeus*).

The birds were caught using mist-nets placed at four different sites located in a restricted surveillance area. Mist-nets are often used by bird biologists to safely capture birds for research; however, birds must be removed from the nets as soon as they are captured to avoid stress, injury or death. Causes of mortality and ways to avoid or minimize the injury or death of birds during the use of mist-nets have been previously discussed by several authors (Recher *et al.*, 1985).

The nets were cast between sunrise and sunset, and were monitored every hour. Nevertheless, 21 birds perished in their struggle to escape from the net.

To transport captured birds to the ringing station, which was located 1 mile from the nets, the birds were placed in cardboard boxes. No more than four birds at a time were housed in the boxes.

In total, 218 faecal swabs and the internal organs of 21 subjects (19 *E. rubecula*, one *S. atricapilla* and one *S. borin*) found dead in the mist-nets were collected. Furthermore, 19 pooled fresh faecal samples

were collected from the boxes used to temporarily house the birds and were submitted to mycological examination. This sampling method was employed to expand the scope of the study and to limit further stress on the captured birds. Each pooled sample contained one to three faecal samples, which were obtained from each of the 19 boxes. The swabs were placed in Stuart's media (Meus, Piove di Sacco, Italy) and peptone water, and were immediately transported to the laboratory in an ice box for bacteriological investigation. All samples were subjected to bacteriological examination for the detection of enterobacteria. With a portion of the fresh faeces, mycological examination was performed, and pathogenic fungi were detected. In addition, 90 swabs were collected in duplicate from the same subjects and were subjected to virological examination, including the isolation of avian influenza virus and Newcastle disease. Moreover, the M gene of avian influenza virus was detected via molecular testing by reverse transcriptase-polymerase chain reaction (RT-PCR).

Bacteriological analysis. Swabs, internal organs and faeces samples were dipped in selenite broth (Oxoid, Milano, Italy), and the cultures were incubated at 37°C for 18 to 24 h. All samples showing bacterial growth were subcultured using brilliant green agar (Oxoid), *Salmonella-Shigella* agar (Oxoid) and Hektoen enteric agar (Liofilchem, Roseto degli Abruzzi, Italy).

Colonies showing morphological characteristics that were consistent with those of enterobacteria were subcultured on MacConkey agar (Oxoid).

All isolates were biochemically identified by the API 20 E system (Biomérieux, Marcy l'Etoile, France). Finally, *Salmonella* spp. and *Yersinia* spp. isolates were serotyped by slide agglutination with commercial antisera (Diagnostics Pasteur, Staten Serum Institut, Copenhagen, Denmark).

Antimicrobial susceptibility tests were performed on the isolated strains according to the disk diffusion method (Bauer *et al.*, 1966), and the following antibiotics were used: ampicillin (10 µg), amoxicillin-clavulanic acid (30 µg), cefotaxime (30 µg), chloramphenicol (30 µg), sulphamethoxazole/trimethoprim (25 µg), nalidixic acid (30 µg), streptomycin (25 µg) and tetracycline (30 µg).

Mycological analysis. Fresh faecal samples (0.5 g) were suspended in 4.5 ml sterile saline water, and the mixture was shaken for 30 min at 100 r.p.m. and allowed to stand for 15 min. One hundred microlitres of each dilution were plated in duplicate onto DRBC agar medium (Oxoid) for the determination of total fungal flora, *Guizotia abyssinica* creatinine agar supplemented with penicillin G (20 U/ml), streptomycin sulphate (40 U/ml) and biphenyl 0.1% (Staib *et al.*, 1987) and Pal's Agar for the selective isolation of *Cryptococcus* (*Cr. Neoformans*) (Criseo *et al.*, 1995).

The plates were incubated at 28°C for 15 days. At the end of the incubation period, the total number of colonies was counted, and the number of colonies with the characteristic dark colour (brown colour effect) of *Cr. neoformans* (Staib *et al.*, 1987) was determined.

Identification of hyphomycetes was performed on the basis of the macroscopic features of colonies grown on different cultural media and the micro-morphology of reproductive structures. Yeasts were identified with the ID32C system (Biomérieux). Presumptive colonies of *Cr. neoformans* were selected and subcultivated on Sabouraud dextrose agar (Difco, Milano, Italy).

Virological examination for the detection of avian influenza and Newcastle disease. Faecal swabs were homogenized to obtain a 10% w/v solution of phosphate-buffered saline supplemented with antibiotics, and the supernatants were inoculated into the chorioallantoic cavity of embryonated specific pathogen free chicken eggs at 8 to 11 days of incubation by performing two blind passages. After 6 days of incubation at 37°C, the eggs were chilled for 6 h at 4°C, etched above the air cell to obtain the allantoic liquid and tested by microplate haemagglutination using the red blood cells of chicken.

RT-PCR for the detection of the M gene of the avian influenza virus. Viral RNA extraction was performed according to the instructions of the SV Total RNA Extraction System kit (Promega Italia, Milan, Italy). Each sample was resuspended in phosphate-buffered saline, and 175 µl lysis buffer containing β-mercapto-ethanol and 350 µl dilution buffer were

added. After incubating for 3 min at 70°C, the samples were centrifuged at 10,000 r.p.m. for 10 min and were combined with 200 µl of 96 to 100% ethanol. After transferring the lysates to special spin columns and washing the material three times, the RNA was eluted in 100 µl RNase-free solution.

In a final volume of 50 µl, the first reaction mixture contained the following reagents: 5 µl RNA, 1 mM dNTP mix, 0.6 µM M25F and M12R primers, 10 mM DTT, 2.5 mM MgCl₂, 10 u RNasi (Promega Italia), 1x RT-PCR buffer and 1 µl enzyme mix (Titan One Tube RT-PCR System; Roche, Milano, Italy). The samples were amplified under the following conditions: 42°C for 20 min (reverse transcription), initial denaturation at 94°C for 30 min, 40 cycles of denaturation at 94°C for 1 min, annealing at 60°C for 1 min, extension at 72°C for 1 min and final extension at 72°C for 10 min (2720 Thermal Cycler; Applied Biosystems, Monza, Italy). PCR products of 100 base pairs were visualized on 3% agarose gel and were compared with a 50-base-pair ladder.

Results

The bacteriological analysis produced 183 strains belonging to 28 different species of the *Enterobacteriaceae* family (Table 1). The most common species were *E. coli* (53 strains, 28.9%) and *Enterobacter cloacae* (45 strains, 24.6%). Potentially pathogenic species including *S. bongori* and *Y. enterocolitica* were also identified.

Nine isolates could not be identified by API 20 E and were non-fermenting Gram-negative bacilli, which provide problematic results with conventional phenotypic tests. All of the isolates were susceptible to a large proportion of antimicrobial drugs. In particular, 182 (99.4%) proved to be susceptible to sulphamethoxazole/trimethoprim, 181 (98.9%) were susceptible to cefotaxime, 177 (96.7%) were susceptible to nalidixic acid, 175 (95.6%) were susceptible to chloramphenicol and 171 (93.4%) were susceptible to tetracycline. How-

ever, 103 (56.3%) isolates were resistant to ampicillin, 78 (42.6%) were resistant to amoxicillin-clavulanic acid and 80 (43.7%) were resistant to streptomycin.

Mycological analysis revealed that hyphomycetes were present in all of the samples, and species belonging to the genera *Rizhopus*, *Mucor*, *Aspergillus*, *Penicillium*, *Acremonium*, *Gliocladium*, *Stachybotrys*, *Curvularia* and *Cladosporium* were identified. Yeasts were present in eight (42.1%) of the samples, and species belonging to the genera *Cryptococcus* (five isolated), *Candida* (four isolated) and *Rhodotorula* (two isolated) were observed. The biochemical tests revealed that the prevalence of *Cr. albidus* (three isolated) colonies was greater than that of *Cryptococcus laurentii* (one isolated). One pooled faecal sample grew *Cr. neoformans*. *Candida* colonies belonging to the species *C. albicans* (two isolated) and *C. famata* (two isolated) were isolated. Both isolated *Rhodotorula* colonies were identified as *R. rubra*.

All of the samples tested negative for the M gene of avian influenza virus by RT-PCR. Isolation tests on specific pathogen free eggs were also negative for avian influenza virus and Newcastle disease.

Discussion

The results of the present study confirmed that migratory wild birds play an important role in the ecology and circulation of potential zoonotic pathogens.

In particular, *Y. enterocolitica* and *S. bongori*, which caused restricted outbreaks of serious enteric episodes in children in several areas of Sicily, were detected in the present investigation (Nastasi *et al.*, 1988; Pignato *et al.*, 1998). Research has shown that the prevalence of *S. bongori* 48:z35:- in the study area is low but sufficiently continuous to be indicative of the epidemiological characteristics of Sicily (Giammanco *et al.*, 2002). The two strains obtained in the present study were isolated from a male blackcap (*S. atricapilla*) (Foti *et al.*, 2009). Owing to the peculiar geographic and ecological distribution of this organism, our results are of interest and provide insight on the possible source and diffusion routes of *S. bongori* in urban areas.

Some of the hyphomycetes species isolated in the current investigation (such as *Aspergillus* spp.) are pathogenic to humans and animals, and some are associated with migratory birds (Hubálek, 2004). However, due to their cosmopolitan and ubiquitous nature, the role of migratory birds in their dispersal remains unclear.

All of the yeasts isolated in the present study were potential pathogenic fungi that can induce cutaneous and/or systemic animal and human diseases (Monga & Garg, 1980; Hubbard *et al.*, 1985; Thakur *et al.*, 2007; Castellá *et al.*, 2008; Perfect *et al.*, 2010; Ortega *et al.*, 2011).

Cr. neoformans, which is pathogenic to humans and animals, has some peculiar ecological and epidemiological characteristics. Therefore, due to the possibility of a clonal distribution of yeast that is dependent on the geographical area of origin, molecular studies on representative strains are in progress to determine the variety, serotype and the mating type of the yeast. Moreover, *Cr. albidus* and *Cr. laurentii* have been occasionally reported as potential pathogens for immunocompromised humans and animals (Kielstein *et al.*, 2000).

Table 1. Strains of *Enterobacteriaceae* isolated.

Species	Number of strains
<i>Buttiauxella agrestis</i>	2
<i>Citrobacter brackii</i>	1
<i>Citrobacter freundii</i>	4
<i>Citrobacter youngae</i>	3
<i>Enterobacter</i> spp.	2
<i>Enterobacter aerogenes</i>	5
<i>Enterobacter amnigenus</i>	3
<i>Enterobacter cancerogenus</i>	12
<i>Enterobacter cloacae</i>	45
<i>Enterobacter sakazakii</i>	6
<i>Escherichia coli</i>	53
<i>Hafnia alvei</i>	2
<i>Klebsiella pneumoniae</i>	2
<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	1
<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	2
<i>Klebsiella oxytoca</i>	4
<i>Khuyvera</i> spp.	1
<i>Pantoea</i> spp.	4
<i>Proteus mirabilis</i>	1
<i>Providencia alcalifaciens/rustigianii</i>	1
<i>Providencia rettgeri</i>	1
<i>Raoultella terrigena</i>	1
<i>Salmonella bongori</i> 48:z35:-	2
<i>Serratia liquefaciens</i>	2
<i>Serratia marcescens</i>	5
<i>Serratia odorifera</i>	1
<i>Yersinia enterocolitica</i>	8
Non-fermenting species	9
Total	183

For the most part, our results are in agreement with those of previous studies on the microflora of droppings of different kinds of birds (Cragg & Clayton, 1971; Criseo *et al.*, 1995) or resident microflora in the cloacae of migratory birds (Cafarchia *et al.*, 2006b). However, to our knowledge, this is the first report of the recovery of *Cr. neoformans* from the droppings of migratory birds.

According to previous studies, *Passeriformes* may play a minor role as a potential vector of avian influenza virus (Morishita *et al.*, 1999; Schnebel *et al.*, 2005) and Newcastle disease (Schnebel *et al.*, 2005). In the present study, avian influenza virus and Newcastle disease were not detected in any of the samples.

Aquatic birds are the most important avian vector of influenza (Stallknecht & Shane, 1988; Alexander, 2000); however, a recent study indicated that influenza prevalence is higher in *Passeriformes* than other orders of birds (Fuller *et al.*, 2010). Thus, in addition to water birds, *Passeriformes* should be monitored as a potential vector for the transmission of avian influenza virus to humans.

Although minimal exposure to antibiotics and anthropic pressure is expected in wildlife species, high proportions of resistance against ampicillin, amoxicillin-clavulanic acid and streptomycin were observed. Monitoring antibiotic resistance in wildlife is a useful method of evaluating the impact of anthropic pressure (Thaller *et al.*, 2010). Furthermore, because migratory birds are recognized as potential reservoirs of pathogenic agents, these birds can be regarded as sentinel species and used as environmental health indicators.

References

- Alexander, D.J. (2000). A review of avian influenza in different bird species. *Veterinary Microbiology*, 74, 3–13.
- Barruel, P. (1959). *Vita e costumi degli uccelli*. Torino, Italy: S.A.I.E. Editore.
- Bauer, A.W., Kirby, W.M.M., Sherris, J.C. & Turk, M. (1966). Antibiotic susceptibility testing by a standardised single disc method. *American Journal of Clinical Pathology*, 45, 493–496.
- Buck, J.D. (1990). Isolation of *Candida albicans* and halophilic *Vibrio* spp. from aquatic birds in Connecticut and Florida. *Applied and Environmental Microbiology*, 56, 826–828.
- Cafarchia, C., Camarda, A., Romito, D., Campolo, M., Quaglia, N.C., Tullio, D. & Otranto, D. (2006b). Occurrence of yeasts in cloacae of migratory birds. *Mycopathologia*, 161, 229–234.
- Cafarchia, C., Romito, D., Iatta, R., Camarda, A., Montagna, M.T. & Otranto, D. (2006a). Role of birds of prey as carriers and spreaders of *Cryptococcus neoformans* and other zoonotic yeasts. *Medical Mycology*, 44, 485–492.
- Castellá, G., Abarca, M.L. & Cabañes, F.J. (2008). Cryptococcosis and pets. *Revista Iberoamericana de Micología*, 25, 19–24.
- Cragg, J. & Clayton, Y.M. (1971). Bacterial and fungal flora of seagull droppings in Jersey. *Journal of Clinical Pathology*, 24, 317–319.
- Criseo, G., Bolignano, M.S., De Leo, F. & Staib, F. (1995). Evidence of canary droppings as an important reservoir of *Cryptococcus neoformans*. *Zentralblatt für Bakteriologie*, 282, 244–254.
- Foti, M., Daidone, A., Aleo, A., Pizzimenti, A., Giacopello, C. & Mammina, C. (2009). *Salmonella bongori* 48:z35:- in migratory birds, Italy. *Emerging Infectious Diseases*, 15, 502–503.
- Fuller, T.L., Saatchi, S.S., Curd, E.E., Toffelmier, E., Thomassen, H.A., Buermann, W., DeSante, D.F., Nott, M.P., Saracco, J.F., Ralph, C., Alexander, J.D., Pollinger, J.P. & Smith, T.B. (2010). Mapping the risk of avian influenza in wild birds in the US. *BMC Infectious Diseases*, 23, 10–187.
- Giammanco, G.M., Pignato, S., Mammina, C., Grimont, F., Grimont, P.A., Nastasi, A. & Giammanco, G. (2002). Persistent endemicity of *Salmonella bongori* 48:z35:- in Southern Italy: molecular characterization of human, animal, and environmental isolates. *Journal of Clinical Microbiology*, 40, 3502–3505.
- Hernandez, J., Bonnedahl, J., Waldenström, J., Palmgren, H. & Olsen, B. (2003). *Salmonella* in birds migrating through Sweden. *Emerging Infectious Diseases*, 9, 753–755.
- Horimoto, T. & Kawaoka, Y. (2001). Pandemic threat posed by avian influenza A viruses. *Clinical Microbiology Reviews*, 14, 129–149.
- Hubálek, Z. (1994). Pathogenic microorganisms associated with free-living birds (a review). *Acta Scientiarum Naturalium Brno*, 28, 1–74.
- Hubálek, Z. (2004). An annotated checklist of pathogenic microorganisms associated with migratory birds. *Journal of Wildlife Diseases*, 40, 639–659.
- Hubbard, G.B., Schmidt, R.E., Eisenbrandt, D.L., Witt, W.M. & Fletcher, K.C. (1985). *Journal of Wildlife Diseases*, 21, 25–28.
- Humair, P.F. (2002). Birds and *Borrelia*. *International Journal of Medical Microbiology*, 33, 70–74.
- Kanai, H., Hashimoto, H. & Mitsuhashi, S. (1981). Drug-resistance and conjugative R plasmids in *Escherichia coli* strains isolated from wild birds (Japanese tree sparrows, green pheasants and bamboo partridges). *Japanese Poultry Science*, 18, 234–239.
- Kawakita, S. & Van Uden, N. (1965). Occurrence and population densities of yeast species in the digestive tracts of gulls and terns. *Journal of General Microbiology*, 39, 125–129.
- Kielstein, P., Hotzel, H., Schmalreck, A., Khaschabi, D. & Glawischig, W. (2000). Occurrence of *Cryptococcus* spp. in excreta of pigeons and pet birds. *Mycoses*, 43, 7–15.
- Kurtenbach, K., De Michelis, S., Sewell, H.S., Etti, S., Schafer, S.M., Holmes, E., Hails, R., Collares-Pereira, M., Santos-Reis, M., Hanincová, K., Labuda, M., Bormane, A. & Donaghy, M. (2002). The key roles of selection and migration in the ecology of Lyme borreliosis. *International Journal of Medical Microbiology*, 33, 152–154.
- Massa, B. (2003). Importanza dell'isola di Ustica per gli Uccelli migratori. *Lettera del Centro Studi e Documentazione Isola di Ustica*, 5, 13–14.
- Monga, D.P. & Garg, D.N. (1980). Ovine pulmonary infection caused by *Rhodotorula rubra*. *Mycoses*, 23, 208–211.
- Morishita, T.Y., Aye, P.P., Ley, E.C. & Harr, B.S. (1999). Survey of pathogens and blood parasites in free-living passerines. *Avian Diseases*, 43, 549–552.
- Nastasi, A., Mammina, C., Villafrate, M.R., Massenti, M.F., Scarlata, G. & Diquattro, M. (1988). Multiple typing of strains of *Salmonella enterica* subsp. *bongori* ser.48:z35:- isolated in southern Italy. *Annales de l'Institut Pasteur Microbiologie*, 139, 605–612.
- Ortega, M., Marco, F., Soriano, A., Almela, M., Martínez, J.A., López, J. (2011). *Candida* species bloodstream infection: epidemiology and outcome in a single institution from 1991 to 2008. *Journal of Hospital Infection*, 77, 157–161.
- Perfect, J.R., Dismukes, W.E., Dromer, F., Goldman, D.L., Graybill, J.R., Hamill, R.J., Harrison, T.S., Larsen, R.A., Lortholary, O., Nguyen, M.-H., Pappas, P.G., Powderly, W.G., Singh, N., Sobel, J.D. & Sorrell, T.C. (2010). Clinical practice guidelines for the management of cryptococcal disease: 2010 update by the Infectious Diseases Society of America. *Clinical Infectious Diseases*, 50, 291–322.
- Pignato, S., Giammanco, G., Santangelo, C. & Giammanco, G.M. (1998). Endemic presence of *Salmonella bongori* 48:z35:- causing enteritis in children in Sicily. *Research in Microbiology*, 149, 429–431.
- Recher, H.F., Gowing, G. & Armstrong, T. (1985). Causes and frequency of deaths among birds mist-netted for banding studies at two localities. *Australian Wildlife Research*, 12, 321–326.
- Reed, K.D., Meece, J.K., Henkel, J.S. & Shukla, S.K. (2003). Birds, migration and emerging zoonoses: West Nile virus, Lyme disease, influenza A and enteropathogens. *Clinical Medicine & Research*, 1, 5–12.
- Schnebel, B., Dierschke, V., Rautenschlein, S. & Ryll, M. (2005). No detection of avian influenza A viruses of the subtypes H5 and H7 and isolation of lentogenic avian paramyxovirus serotype 1 in passerine birds during stopover in the year 2001 on the island Helgoland (North Sea). *Deutsche Tierärztliche Wochenschrift*, 112, 456–460.

- Smith, R.P., Jr, Rand, Lacombe, E.H., Morris, S.R., Holmes, D.W. & Caporale, D.A. (1996). Role of bird migration in the long-distance dispersal of *Ixodes dammini*, the vector of Lyme disease. *Journal of Infectious Diseases*, 174, 221–224.
- Staib, F., Seibold, M., Antweiler, E., Fröhlich, B., Weber, S. & Blisse, A. (1987). The brown colour effect (BCE) of *Cryptococcus neoformans* in the diagnosis, control and epidemiology of *C. neoformans* infections in AIDS patients. *Zentralblatt für Bakteriologie, Mikrobiologie und Hygiene A*, 266, 167–177.
- Stallknecht, D.E. & Shane, S.M. (1988). Host range of avian influenza virus in free-living birds. *Veterinary Research Communications*, 12, 125–141.
- Thakur, K., Singh, G., Agarwal, S. & Rani, L. (2007). Meningitis caused by *Rhodotorula rubra* in an human immunodeficiency virus infected patient. *Indian Journal of Medical Microbiology*, 25, 166–168.
- Thaller, M.C., Migliore, L., Marquez, C., Tapia, W., Cedeño, V., Rossolini, G.M. & Gentile, G. (2010). Tracking acquired antibiotic resistance in commensal bacteria of Galápagos land iguanas: no man, no resistance. *Public Library of Science One*, 5, e8989.
- Wallace, J.S., Cheasty, T. & Jones, K. (1997). Isolation of Vero cytotoxin-producing *Escherichia coli* O157:H7 from wild birds. *Journal of Applied Microbiology*, 82, 399–404.