Microbial Ornithology?

Two traditional disciplines are coming together to chart the movements and roles of wild birds in disseminating agents of infectious disease in humans

Bernard Dixon

One of the most illuminating applications of citation analysis is its use in demonstrating the evolving landscape of science—the ways in which different specialties can come together for the first time, while others mutate or shift their center of gravity. I recall my friends at the Institute for Scientific Information in Philadelphia showing me how the new discipline of psychoneuroimmunology, which explores the influence of the mind on susceptibility to infection, emerged during the 1980s and 90s. Gradually, the totally disparate literatures of psychology and medical microbiology forged links, as microbiologists began to cite papers in experimental psychology journals, while psychologists referenced medical microbiology papers. Publishers have even adopted this type of approach to identify areas for potential new journals.

I suspect that citation analysis in much more recent times would reveal another area of interdisciplinary activity, centered on the roles played by wild birds in disseminating agents of communicable disease. Triggered by the emergence of the Asiatic H5N1 highly pathogenic A1 virus in 2005, virologists and epidemiologists have had to interest themselves in aspects of ornithology that would previously have escaped their attention entirely. These include the migration patterns and feeding habits of wild birds responsible for carrying avian influenza and other viruses. Ornithologists, likewise, have discovered that their expertise has attracted offers of professional collaboration from microbiologists.

These thoughts were fostered by my reading a recent paper on vancomycin-resistant enterococci in rooks wintering in Europe, published in Environmental Microbiology (15:548, 2013) and written by Veronika Oravcova and colleagues at the University of Veterinary and Pharmaceutical Sciences at Brno in the Czech Republic, and elsewhere. The bibliography at the end of their paper contains not only references to the Journal of Bacteriology but also to the Handbook of the Birds of the World (J. del Hoyo et al., ed., Lynx Edicions, Barcelona, 2009). Another paper is entitled “Involving Ornithologists in the Surveillance of Vancomycin-Resistant Enterococci.”

Oravcova and her collaborators began their work because of concern in Europe over the declining sensitivity of enterococci to glycopeptides, especially vancomycin. In the past, such resistance has been associated with the use of avoparcin (a glycopeptide related to vancomycin) to promote the growth of farm animals. Although its use was banned in the European Union in 1997, leading to a decline in resistance, a significant problem remains. And previous evidence has established that wild birds in areas with a high density of livestock are often colonized by antibiotic-insensitive strains of Escherichia coli, presumably as a consequence of the use of the drugs in animal husbandry.

The focus of attention for the new investigation was the rook (Corvus frugilegus), an omnivorous, medium-sized corvid with Palearctic distribution, which travels long distances when migrating and spends its winters mostly in lowlands. Roosting overnight, the birds fly off to search for food each day. Because of the scavenging diet and lengthy flights, Oravcova and her coworkers argued that rooks could be important vectors for the distribution of drug-resistant enterococci throughout Europe.

The investigators recovered 1,073 samples of rook feces from eight different European countries, including Spain, Italy, Germany, and Poland. Of these, 62 samples (6%) yielded vancomycin-resistant enterococci—the first demonstration of this organism in rooks. The bacteria were often insensitive to other antimicrobials as well, especially gentamicin, tetracycline, and erythromycin. Despite the low isolation rate, the
findings are disquieting. “In the past two decades, multidrug-resistant [Enterococcus] faecium has emerged as a serious nosocomial pathogen in human hospitals,” the authors of the paper write, citing previous evidence of intra- as well as interspecies transfer of the vancomycin traits from E. faecium. “We detected low transfer frequency in filter mating, thus indicating the potential for horizontal transfer of vanA and ermB among E. faecium.”

Last year, another interdisciplinary project, based in Portugal, highlighted the common buzzard as a hitherto unrecognized reservoir of drug-resistant organisms. It is a medium to large bird of prey whose geographic distribution covers most of Europe and extends into Asia. Buzzards eat rabbits, pheasants, and other small mammals, and can often be seen walking over recently ploughed fields scavenging for worms and insects. Hajer Radhouani and collaborators at the University of Tras-os-Montes and Alto Douro, Vila Real, and other centers in Portugal launched their study in order to determine the prevalence of antimicrobial resistance and the mechanisms implicated in fecal E. coli isolates and Enterococcus species in common buzzards in their country. They focussed on various natural areas in the north and center of the country, where buzzards build their nests.

As reported in the Journal of Medical Microbiology (61:837, 2012), the Portugese team recovered 36 isolates of E. coli and 31 isolates of enterococci from 42 samples of the birds’ feces. The former showed high levels of resistance to streptomycin and tetracycline, while the enterococci had very low sensitivity to kanamycin, gentamicin, and streptomycin. “Common buzzards seem to represent an important reservoir, or at least a source, of multi-resistant E. coli and enterococci isolates,” the authors conclude, “and consequently may represent a considerable hazard to human and animal health by transmission of these isolates to waterways and other environmental sources via their fecal deposits.” The teams suggests that one reason for the high rates of resistance is that common buzzards are large, predatory birds at the top of the food chain.

It’s odd that, while international travel by humans has long been recognized as contributing to the dissemination of pathogens, interest in its role in spreading drug-insensitive organisms has attracted attention only over the past few years. One recent key paper (G. Peirano et al, J. Travel Med. 18:299, 2011) provides evidence that travellers returning home from other parts of the world may be colonized by E. coli producing CTX-M β-lactamases. Even more surprising, given that an estimated 5 billion birds migrate each year, is the neglect of avian migration as a vehicle for the global dissemination of resistance.

A research collaboration based at the Free University of Berlin and other centers in Germany and elsewhere has extended our knowledge of this phenomenon by analyzing E. coli in fecal samples from 281 birds of prey in two very different areas. These were Saxony-Anhalt in Germany and the much more remote Gobi Desert in Mongolia. Sebastian Guenther and his co-workers report in PLoS One (7:12, e53039, 2012) that extended-spectrum β-lactamase producers from wild birds originating from the two areas differed in their resistance genes. This was not unexpected since the avian species examined do not migrate between Mongolia and Central Europe. “Nevertheless,” they write, “all Mongolian avian hosts sampled in this study undergo southward migration, namely on the Korea Peninsula (Black Vulture), to China (buzzards) and to India (Demoiselle Crane), connecting remote areas to the globalised world with high frequencies of ESBL-E. coli in humans and livestock.”

Meanwhile, researchers in Portugal and Switzerland have been investigating wild birds as reservoirs of Borrelia burgdorferi sensu lato, the aetiological agent of Lyme borreliosis. Their work in enzootic areas of Portugal led them to discover 23 birds (2.3% of their sample) harboring infected ticks, and to report Borrelia turdi for the first time in Western Europe. “Concerning the epidemiologic relevance of birds as reservoirs of B. burgdorferi s.l., we detected a B. garinii genetic variant in birds identical to one isolate from human skin in Taiwan,” A. C. Norte and colleagues write in Environmental Microbiology (15:386, 2013).

Although all of these studies reflect very recent new lines of research, this is a saga that will, I believe, run and run.