

Disease Risks Posed by Wild Birds Associated with Agricultural Landscapes

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Introduction

There are over 1,400 cataloged human pathogens, with approximately 62% classified as zoonotic (Taylor et al., 2001). While most evidence of direct transmission of pathogens to humans involves domestic and companion animals, the reservoir for most zoonoses is wildlife, yet there are relatively few well-documented cases for the direct involvement of transmission from wildlife to humans (Kruse et al., 2004). In part, this absence of evidence reflects the mobility of wildlife, the difficulty in accessing relevant samples, and the smaller number of studies focused on characterizing wildlife pathogens relative to the human and veterinary literature (McDiarmid, 1969; Davies et al., 1971; Hubalek, 2004). Because humans generally do not have direct contact with wild birds, exposure to pathogens is via indirect routes, i.e., environmental. This indirect exposure route (sapro-zoonotic) makes identifying the wild-bird source of the pathogen all the more difficult. Thus, most assessments implicating birds in carriage or transmission of pathogens of zoonotic importance are based on reasonable inference. The first step in this process is documentation that birds are hosts or can carry or transmit the pathogen. The second step involves a demonstration that the bird species involved is associated with agricultural food production. Usually the evidence provided is actual census information, behavioral observations, or evidence of the presence of feces. The third step involves demonstration that a pathogen or parasite that could originate from a bird associated with agricultural production or processing is the causative agent of human disease. The best evidence would be genetic, but even other diagnostic methods would suffice. Unfortunately this last step is rarely documented in the literature. However, with better diagnostic technologies and better understanding of the disease ecology, it is feasible that documenting the actual risks posed by wildlife to human health will become easier, and we will be better able to identify control points for pathogen management originating from wildlife.

Most of the evidence in the literature focuses on relatively few commensal wildlife species in urbanized environments, or at best, general wildlife surveillance and monitoring efforts (Tsiodras et al., 2008). In the absence of any compelling direct evidence, this review summarizes the circumstantial evidence, relying mostly on the characterization of host range of pathogens, similarities of virulence traits of animal and human pathogens, and habitat-use patterns of wild birds in agricultural and urban landscapes. Nonetheless, the material presented here does represent a solid circumstantial case for the potential of wild birds to contaminate field crops and act as agents for the transmission of pathogens to humans. More directed studies will be needed to form a more informed assessment as to what actual risks wild birds pose to field crop contamination with human pathogens, and by implication, to human health. Finally, this review also briefly covers mitigation efforts that might be undertaken to reduce risks of pathogen transmission by wild birds.

Bird species commonly associated with agriculture

There are two competing views regarding the value of birds to agriculture. The first view values the ecological services that birds may provide as consumers of pest insects and rodents (Mouysset et al., 2011; Power, 2011; Wenny et al., 2011; Benayas and Bullock, 2012). To capitalize on this service, a great deal of effort has been placed on research and management programs such as conservation reserves and other local habitat management to encourage beneficial species to associate themselves with agricultural production (Berges et al., 2010; Vickery et al., 2009). A full discussion of this topic is beyond the scope of this review. A competing view is the potential damage birds might cause to agriculture either from crop damage and depredation (Gebhardt et al., 2011; Kale et al., 2012; Merkens et al., 2012), or as an agent facilitating the contamination of production or processing of crops with pathogens (Bach and Delaquis, 2009). At the present time no bioeconomic or risk assessment models have comprehensively integrated these benefits and costs.

Wild birds, and especially migratory species, can become long-distance vectors for a wide range of microorganisms (Benskin et al., 2009; Hughes et al., 2009; Francesca et al., 2012; Crowder et al., 2013). Moreover, many bird species incorporate agricultural fields into their habitat use patterns. However, for the purpose of this review, focus is limited to only a few groups of birds: gulls (Charadriiformes), waterfowl (Anseriformes), pigeons and doves (Columbiformes), and selected passerine birds (Passeriformes) such as blackbirds, crows, starlings, and sparrows. These groups of birds tend to have high use patterns of agricultural habitats, they are abundant, and they have closer commensal relationships with human activity. These species also tend to be abundant and gregarious; hence they provide greater opportunity and capacity to contribute larger fecal loads to the environments they use.

Contamination of produce can occur via many routes, e.g., at the field level during the growing season, during harvesting, postharvest handling, processing, shipping, marketing, or in the home (Beuchat and Ryu, 1997). Wild birds are most likely to be involved in contamination while the crops are in the field, and perhaps at field-side processing and storage facilities. Moreover, the likelihood that birds are responsible for contamination of crops with human pathogens will largely depend on the birds' exposure to environmental sources of pathogens (Figure 7.1), their capacity to physically transport the pathogen, and perhaps, but not necessarily limited by, their ability to act as a reservoir of the pathogen (Kruse et al., 2004). However, in the end, it is the likelihood and magnitude for fecal contamination of soils, substrates, and water that is the most direct link for risk to human health (Mohapatra et al., 2008; Jokinen et al., 2011).

Pigeons

Pigeons (*Columba livia*) live in close association with humans (Johnston and Janiga, 1995). They are a gregarious species that feed in flocks, form large roosts, and visit habitats that have a high likelihood of harboring human pathogens, e.g., dairies and

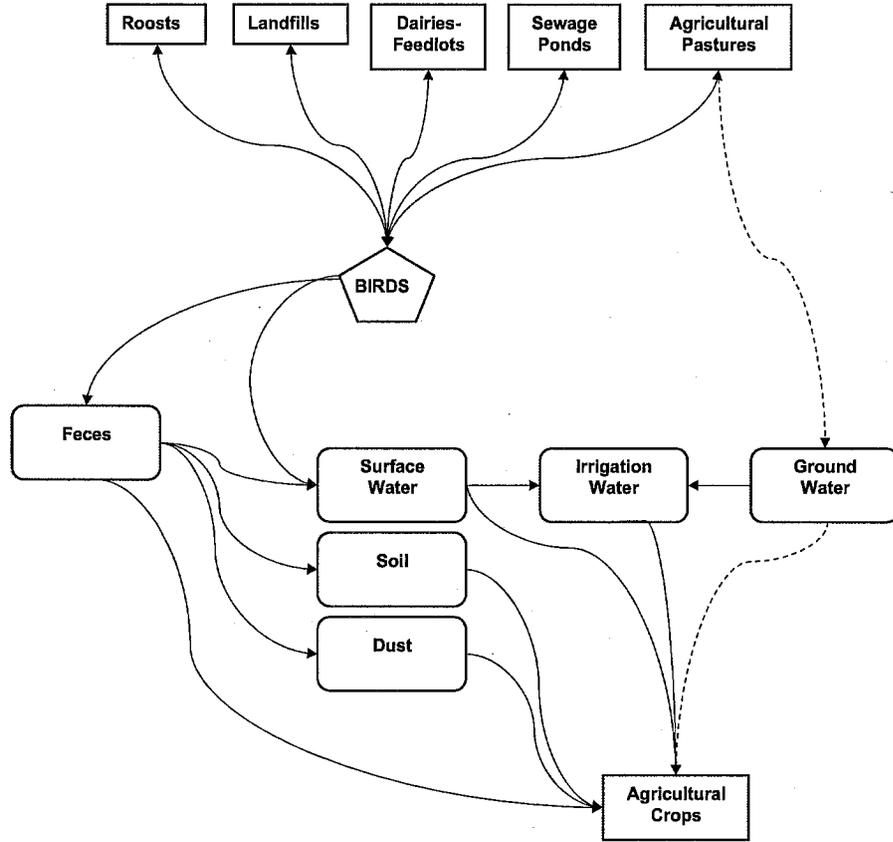


FIGURE 7.1

Possible routes of contamination of field or orchard crops by wild birds. Rectangles indicate environmental sources/habitats of pathogens. Pentagon represents various species of wild birds likely to visit both the source and agricultural landscapes. Rounded rectangles represent media pathogens may reside and be transported in.

feedlots. Pigeons will often flock to agricultural fields to pick up grit to aid in digestion, or to consume spilled grains. As with most commensal bird species considered to be high risk for transmission of human pathogens, pigeons have a prodigious capacity to produce feces. When occurring in large numbers, the fecal load for contamination of surface water and soils also can be large. Perhaps more importantly, is the propensity of pigeons to use architectural structures as day and night roosting sites. Open crop storage or processing sheds present an ideal circumstance for attracting pigeons, and in the absence of bird exclusionary mitigation measures, provide an opportunity for fecal accumulation. As with most species of birds, humans are not likely to come in direct contact with pigeons; rather, humans are likely to come in contact with feces or fecally contaminated substrates. Accumulation of feces

presents greater opportunities for contamination of produce or exposure *via* contaminated soils (Costa et al., 2010), dusts (Gage et al., 1970), and water sources (Graczyk, 2007b) (Figure 7.1).

Over 60 human pathogens have been isolated from pigeons; however, only five pathogens have been documented to routinely be transmitted to humans (Haag-Wackernagel and Moch, 2004): *Chlamydophila psittaci*, *Histoplasma capsulatum*, *Aspergillus spp.*, *Candida parapsilosis*, and *Cryptococcus neoformans*. Most cases of disease transmission are related to inhalation of dusts and aerosols (Anon, 2002), emphasizing the risk of accumulated feces at building structures to human health. Only one case of foodborne illness has been directly linked to pigeons; and that was attributed to lemon pudding made from the eggs of domestic pigeons (Clarenburg and Dornickx, 1933).

Gulls

A variety of species of gulls (Laridae) have been implicated in the carriage of human pathogens and contamination of watersheds, surface waters, and structures (Wither et al., 2005; Kinzelman et al., 2008). For the most part the number of gulls is increasing, largely owing to the availability of landfills, which provide a source of abundant food. Gulls are attracted to agricultural fields to forage on rodents, insects, and at times the crops themselves (O'Connor, 1992). Gulls can occur in large numbers, produce prodigious quantities of fecal material, and thus act as a source for contamination of soils and substrates. Gulls frequent landfills, dairies and feedlots, sewage ponds, other waste facilities, and agricultural pastures, all sources of human pathogens. Thus, they should be considered a major source of contamination risk to crops, produce, water easements, irrigation sources, and processing facilities (Coulson et al., 1983; Fricker, 1984; Yorio and Caille, 2004; Nelson et al., 2008; Ramos et al., 2010; Converse et al., 2012).

Waterfowl

Ducks and geese frequent agricultural fields to feed on crops, spilled grains, acquire grit, or loaf. Waterfowl are most likely to be a source of contamination of soils and surface waters, and indirectly, ground water (Somarelli et al., 2007; Graczyk et al., 2008). Large flocks are likely to begin use of agricultural fields in the fall and leave in the early spring (McKay et al., 2006; Amano et al., 2007). During this period the flocks may move across the landscape on a local, regional, or continental scale, thus increasing the opportunities for transporting pathogens from one site to another. Waterfowl are likely to use surface water areas, agricultural pastures, and sewage ponds, all of which can act as environmental sources of human pathogens (Conn et al., 2007).

Passerines

The number of passerine species that use agricultural fields is large, but those that travel in large flocks are more limited. Blackbirds (Ictaridae) and starlings (*Sturnus vulgaris*) will frequently use feedlots, dairies, and agricultural pastures, and thus, are

likely to encounter human pathogens at those sites (Odermatt et al., 1998; Kaleta, 2002; Nielsen et al., 2004). Both species are also likely to use agricultural crop fields as sources of food and grit, thereby providing an opportunity to contaminate soils and crops with their feces. Starlings may also use crop storage and processing facilities as roost sites, providing additional opportunities to contaminate produce. House sparrows (*Passer domesticus*) have a more restricted range. However, this species is commonly associated with poultry houses, feedlots, and dairies and are common roost and nesting inhabitants of crop storage and processing facilities (Craven et al., 2000, Kirk et al., 2002). Other species of passerines are more likely to use only the agricultural fields; thus the risk of their contaminating field crops will be based on their exposure to pathogens in the general environment (Boutin et al., 1999; Laiolo, 2005).

Bacterial diseases

Campylobacter

Campylobacter is widespread in wild birds (Luechtefeld et al., 1980). High isolation rates have been obtained in gulls (*Larus* spp., 15–50%), crows (*Corvus corone cornix*, *Corvus leuillanti* and *Corvus corone*, 34–89%), blue magpies (*Cyanopica cyanus*, 20%), gray starlings (*Sturnus cineraceus*, 14%), pigeons (4–26%), (Ito et al., 1988; Quessy and Messier, 1992; Casanovas et al., 1995; Ramos et al., 2010), and Canada geese (*Branta canadensis*, 5–40%) (Rutledge et al., 2013). In cases where stomach contents have been analyzed, it is evident that the birds have visited landfills, thus indicating the importance of food habits as a primary factor in the varying prevalence of *C. jejuni* (Kapperud and Rosef, 1983). *Campylobacters* are also widely distributed in aquatic environments and in sewage effluents and agricultural runoff, environments conducive to exposing waterfowl to the pathogen (Brown et al., 2004). *Campylobacter* species may survive, and remain potentially pathogenic, for long periods in aquatic environments, but less so on terrestrial substrates (Krampitz, and Hollander, 1999). *Campylobacter* has been found in water sources for human consumption and irrigation, and bird fecal material has been implicated in the contamination (Denis et al., 2011).

Campylobacters are one of the most significant causes of human gastrointestinal infections worldwide, and the role that terrestrial birds and waterfowl have in the spread of disease is beginning to be elucidated. For example, Starlings shed *Campylobacter* at high rates, suggesting that they may be a source of human and farm animal infection. However, based on genetic analysis Colles et al. (2008a) concluded that these bacteria were distinct from poultry or human disease isolates with the ST-177 and ST-682 clonal complexes, possibly representing starling-adapted genotypes. Thus, these authors concluded that there was no evidence that wild starlings represent a major source of *Campylobacter* infections of food animals or humans. Similarly, Colles et al. (2008b) investigated wild geese as a potential source of *Campylobacter* infection for humans and farm animals in waterborne disease outbreaks. The authors found that large numbers of wild geese carry *Campylobacter*; however,

there was limited mixing of *Campylobacter* populations among the different sources examined. Thus, they concluded that genotypes of *C. jejuni* isolated from geese are highly host specific, and geese are unlikely to be the source of the human disease outbreaks. In contrast, French et al. (2008) identified members of *Campylobacter* clonal complexes ST-45, ST-682, and ST-177 recovered from starling feces as being indistinguishable from those observed in human cases and concluded that wild birds could contribute to the burden of campylobacteriosis in preschool children at playgrounds.

Chlamydia

Avian chlamydiosis was originally called “parrot fever.” However, recent studies have shown that “parrot fever” and ornithosis are the same disease manifested in different species and are all caused by the bacterium, *Chlamydophila psittaci* (Andersen and Vanrompay, 2000). Chlamydial infections have been identified in over 150 species of wild birds (Brand, 1989). Generally, these wild birds are asymptomatic. Bacteria are shed sporadically in nasal secretions and feces. Although the natural host reservoir systems are unknown, its wide occurrence in wild bird populations and the intermittent infections of farm stock are consistent with exposure to wild birds. Sporadic shedding was seen in experimentally inoculated great-tailed grackles (*Cassidix mexicanus*) and cowbirds (*Molothrus ater*), indicating their potential as host-reservoir systems (Roberts and Grimes, 1978). The most probable risk to farm stock and poultry is when wild birds gain access to feed bins and contaminate the bins with their feces. Infection usually occurs through exposure to contaminated aerosol dusts (Page, 1959). Turkeys can become infected by exposure to starlings, common grackles (*Quiscalus quiscula*), and brown-headed cowbirds (Roberts and Grimes, 1978; Grimes et al., 1979). Serovars D and E can result in 50 to 80% morbidity and 5 to 30% mortality in turkeys (Andersen, 1997). In ducks the economic impact is also significant, with morbidity and mortality ranging from 10 to 80% and 0 to 30%, respectively (Andersen et al., 1997). The high morbidity and mortality in domestic fowl and waterfowl suggest that mortality events in the wild species occurring near agroecosystems may be a useful warning system for triggering enhanced field produce monitoring. Wild avian strains also can infect mammals, including humans, and can cause severe disease or death (Andersen and Vanrompay, 2000).

Escherichia coli

The most important reservoir for verocytotoxin-producing *Escherichia coli* (VTEC) is considered to be ruminants, particularly cattle, though VTEC can be isolated from many mammals and birds (Wallace et al., 1997; Rice et al., 2003). Infection of humans by STEC may result in combinations of watery diarrhea, bloody diarrhea, and hemolytic uremic syndrome. Severe disease in the form of bloody diarrhea and the hemolytic uremic syndrome is attributable to Shiga toxin (Stx), which exists as two major types, Stx1 and Stx2 (Gyles, 2007). Humans can become infected through contamination of food and water, as well as through direct contact. Given the propensity of certain species of birds to frequent facilities or pastures used by ruminants,

there remains a distinct possibility that wild birds may play a role in the transmission of VTEC to field crops and fruits.

Several studies have implicated wild birds in the transmission of VTEC, based on the similar characterizations between avian and human isolates (Asakura et al., 2001; Kobayashi et al., 2002). Numerous studies have documented the presence of *Stx*-producing *E. coli* (STEC) in pigeons (Morabito et al., 2001), gulls (Makino et al., 2000), waterfowl (Feare et al., 1999; Kullas et al., 2002), and passerines (Nielsen et al., 2004; Kobayashi et al., 2008). Other human virulence factors have also been identified in these species, including *eae*, *cldt*, CNF-1, CNF2, K1, LT, *hlyA*, SLT-I, SLT-II, STa, and STb, (Morabito et al., 2001; Kullas et al., 2002; Fukuyama et al., 2003; Pedersen et al., 2006). In addition, phylogenetic studies have illustrated the similarity of VTEC based on a number of measures (Makino et al., 2000). Though less common, a few studies have shown direct linkages and phylogenetic relatedness between avian VTEC and isolates causing human illness (Sonntage et al., 2005; Ejidokun et al., 2006).

Though VTEC are widely reported in the species groups discussed above, Canada geese have been implicated as the most likely source of non-point source pollution of inland waters. Molecular fingerprints of *E. coli* isolated from regional populations showed an unexpectedly high percentage of isolates identified as having a wildlife origin (geese and deer). Geese were the dominant source of *E. coli* (44.7–73.7% of the total sources) in four sub-watersheds followed by cows (10.5–21.1%), deer (10.5–18.4%), humans (5.3–12.9%), and unidentifiable sources (0.0–11.8%) (Somarelli et al., 2007).

Public pressure is mounting to reduce or eliminate antimicrobials as ingredients of feed for poultry and other agricultural animals, primarily due to the fear of multidrug-resistant bacteria in clinical infections in both animals and humans. Wild birds have been implicated as reservoirs and as vectors for the spread of antibiotic resistant strains of *E. coli*. Gibbs et al. (2007) found drug-resistant strains of *E. coli* in feces of yellow-headed blackbird (*Xanthocephalus xanthocephalus*). Dolejska et al. (2008) reported *E. coli* resistant to 12 antimicrobials in 9% (n=54) of isolates from house sparrows (*Passer domesticus*). Greater than 95% of *E. coli* isolates from Canada geese in agricultural environments were resistant to penicillin G, ampicillin, cephalothin, erythromycin, lincomycin, sulfathiazole, and vancomycin; no *E. coli* were resistant to bacitracin or ciprofloxacin (Fallacara et al., 2001; Cole et al., 2005; Middleton and Ambrose, 2005).

Most studies have only focused on the serotype O157:H7/H–, however, there are suggestions that wild birds may be involved in the transmission of other pathogenic serotypes (Kullas et al., 2002). Morabito et al. (2001) described widespread, clonally-related isolates of *E. coli* O45, O18ab, and O75 serotypes in several pigeon flocks. The overall prevalence was similar between three flocks (10.8%), with evidence of *Stx*-producing *E. coli* (STEC).

Listeria

Listeriosis in humans is caused by infection by *Listeria monocytogenes*. While all serovars of *L. monocytogenes* are considered human pathogens, the most potentially virulent are 4b, 1/2b, and 1/2a. *L. monocytogenes* is commonly associated with soils

and feces in the environment and may be one of the most ubiquitous microorganisms in the soil. Human exposure is most likely through ingestion of contaminated food, but hand–oral contact or inhalation may also occur. Approximately 1 to 10% of the human population is thought to carry *L. monocytogenes* asymptomatically in the intestines. Healthy people rarely become ill after exposure. Serious cases almost always occur in the elderly, pregnant women, newborns, and those who are debilitated or immunocompromised (Acha and Szyfres, 2003).

Listeria spp. are commonly found in birds (Harkin et al., 1986; Fenlon, 1985). Overall, the prevalence detected across species lies within the same range. On the lower end Quessy and Messier (1992) found a prevalence of 9.5% in fecal samples of ring-billed gulls (*Larus delawarensis*). Clark and Sullivan (unpublished data) found prevalence ranging from 8 to 12% from Canada goose (*Branta canadensis*) fecal samples from five states (Colorado, New York, Pennsylvania, Washington, and Wisconsin) collected throughout the year. On the higher end, investigators have found prevalence of 43.2% in crows and 36% in gulls (Helstrom et al., 2008). Wild birds may pose a risk to human health. The magnitude of prevalence may reflect local environmental conditions that birds may visit, e.g., landfills, sewage treatment facilities, or livestock facilities. Visitation of such environments may also impact exposure and carriage of virulent strains of *Listeria*. The serovars 1/2a and 4b predominated in the eight serotyped *L. monocytogenes* isolates in the Yoshida et al. (2000) study. Similar genotypes have been found in wild birds and local fresh food markets as well (Zhang et al., 2007; Mosupye and von Holy, 2000; Hellstrom et al., 2007).

Salmonella

Various *Salmonella* strains have been isolated from a range of wild bird species. Given the ubiquitous nature of the host range, and the pathogenicity of the organism to humans, caution should be exercised anytime there is exposure to fecally contaminated surfaces or soils. When sapro-zoonotic infections do occur, 99% of the documented cases appear to have resulted from aerosol exposure (Haag-Wackernagel and Moch, 2004).

Gulls appear to pose the greatest risk of infection and carriage. This is perhaps owing to their greater propensity to visit sewage treatment ponds and thus acquire pathogens. *Salmonella* prevalence in gulls ranges between 1 to 55% (Butterfield et al., 1983; Fenlon, 1981, 1983; Sixl et al., 1997; Casanova, 1995). Several genetic and epidemiological studies have linked transport of pathogens from the site of acquisition to distant sites, including food-processing facilities and stockyards (Coulson et al., 1983; Nesse et al., 2005). Persistence in marked free-ranging gulls was shown to be limited to about 10 days (Snoeyenbos et al., 1967; Palmgren et al., 2006). Other genetic studies have shown that strains carried by gulls are similar to human pathogens.

Pigeons are generally characterized by low prevalence (3–4%) of *Salmonella* (Pasmans et al., 2004; Tanaka et al., 2005; González-Acuña et al., 2007). Despite the low prevalence, studies have implicated pigeons and sparrows in the maintenance of the pathogen at feedlots and dairies (Quevedo et al., 1973; Connolly et al., 2006; Pedersen et al., 2006).

Fungal diseases

Aspergillus

Aspergillus spp. are rapidly growing molds most commonly associated with decaying matter and the feces of waterfowl and raptors, though a variety of wild birds and domestic poultry are also known to become infected with *Aspergillus* spp. (Buxton and Sommer, 1980; Friend, 2006). In animals, greater than 90% of infections are caused by *A. fumigatus* (Quinn, 1994). The highest prevalence of *A. fumigatus* in waterfowl is in winter. The most susceptible people in populations for the respiratory and allergic complications of infection are those who are immunocompromised or on extended regimens of medication (Latge, 2001).

Cryptococcus

Cryptococcus neoformans is a fungus typically associated with bird feces (Blaschke-Hellmessen, 2000). *C. neoformans* typically only affects the immunocompromised. Cryptococcal infection may cause a pneumonia-like illness, with shortness of breath, coughing, and fever. Skin lesions may also occur. Another common form of cryptococcosis is central nervous system infection, such as meningoencephalitis. The primary risk for infection is inhaling dusts containing contaminated feces. Pigeons appear to be the primary wild bird involved in transmission to humans, though *C. neoformans* has been detected in a variety of other species (Pollock, 2003; Cafarchia et al., 2006; Rosario et al., 2008). Prevalence in pigeons may range between 9–19% (Weber and Shafer, 1991; Soogarun et al., 2006). Unlike *Histoplasma*, *C. neoformans* viability in the environment is limited. Ruiz et al. (1982) showed that viability of *C. neoformans* decreased from 50 to 86% over the course of a year, once pigeons were excluded from a roost. They attributed this decrease in viability to desiccation.

Histoplasma

Histoplasma capsulatum is a zoonotic fungal pathogen, commonly found in soils and bird feces, that affects the respiratory system (Ajello, 1964). In endemic areas of the United States as much as 80 to 90% of the human population is infected (Rubin et al., 1959). Fewer than 10% of those who inhale airborne spores develop a pulmonary infection. However, the pulmonary form can disseminate and is potentially fatal if not treated. Acute pulmonary histoplasmosis is the most dramatic form of the disease and occurs in people who have inhaled massive doses of spores. Chronic infection in humans can result in permanent lung damage. People with HIV are most susceptible to the disseminated form of the illness. People at highest risk are those working in agriculture, particularly poultry operations, or those people coming in contact with bird feces associated with bird roosts (Dodge et al., 1965; Tosh et al., 1966). Such roosts are likely to be associated with dense vegetation (i.e., agricultural wind breaks), trees, or storage or processing sheds. Because transmission is through breathing dust particles containing spores, any disturbance of contaminated soil can

cause infection (Storch et al., 1980; Stobierski et al., 1996). Soil studies have shown that the viable spores persist in contaminated soils over many years (9–13+ years, DiSalvo and Johnson, 1979), at times long after bird activity at a site has ceased (Gustafson et al., 1981). Moreover, residents downwind from disturbed contaminated soils can become infected (Latham et al., 1980; Chick et al., 1981). Formalin has been used to sterilize soils contaminated with *Histoplasma* and deemed to be a high risk of further infection to local human populations (Smith et al., 1964; Tosh et al., 1967; Bartlett et al., 1982). Though *Histoplasma* has been detected in the feces of many bird species, pigeons, blackbirds, and starlings are the most likely wild birds to be a source of soil contamination, and the species of wild birds most likely to be associated with roosts near agriculture production or processing (Schwarz et al., 1957; Pollack, 2003; Cermeno et al., 2006).

Parasitic diseases

Cryptosporidia

Cryptosporidium parvum is an important gastrointestinal parasite of humans and other animals that can be transmitted via contamination of food and water (Mackenzie et al., 1994; Millar et al., 2002). Symptoms may be long lasting and include diarrhea, loose or watery stools, stomach cramps, upset stomach, and a slight fever (Fayer et al., 1998). Some people have no symptoms. In persons with average immune systems, symptoms usually last about 2 weeks. Waterfowl in general, but Canada geese in particular, have been implicated in the contamination of water (Hatch, 1996; Smith et al., 1993; Graczyk et al., 1997; Fallacara et al., 2004), and oocytes recovered from feces have been demonstrated to be infectious Graczyk et al. (1998). Starlings and other birds have also been implicated as carriers of *Cryptosporidium parvum* near farms (McCarthy et al., 2008; Lord et al., 2010).

Microsporidia

Microsporidians (*Encephalitozoon intestinalis*, *E. hellem*, *E. cuniculi*, *E. bienewsi*) are obligate intracellular parasites that increasingly are involved in opportunistic infections of immunocompromised and immunocompetent people (Weber et al., 1994). *E. hellem* has been the species most commonly associated with avian hosts (Slodkiewicz-Kowalska et al., 2006). Epidemiological evidence strongly supports contaminated water, including water used for crop production, as a significant risk factor for human disease (Dowd et al., 1998; Fournier et al., 2000; Mathis et al., 2005; Thurston-Enriquez et al., 2002), and avian contamination of surface water via defecation as an important contributory risk factor for pathogen transmission (Slodkiewicz-Kowalska et al., 2006). Although waterborne transmission is the most likely avenue for opportunistic infection of humans, a study by Haro et al. (2005) showed that pigeon feces was positive for *E. bienewsi* (9.7% prevalence), *E. intestinalis* (4% prevalence), and *E. hellem*

(1% prevalence) and 4.8% of pigeons were co-infected. Bart et al. (2008) found similar prevalence. The authors concluded that there was no barrier to transmission from pigeons to humans.

Toxoplasma

Toxoplasma gondii is a common single-celled parasite responsible for infection of more than 60 million people in the United States each year (Dubey, 2002). Infection can be acquired via hand to mouth contact with feces, contaminated soil, water, or raw meat. In most cases, the hosts' natural immune system clears the disease, and most healthy humans are rarely aware that they are infected. Symptoms are flu-like and include swollen joints and fatigue. However, people with impaired immune systems, embryos, and neonates are particularly vulnerable to severe consequences of infection, e.g., eye and brain damage. Birds are included in the extensive list of wildlife species implicated as carriers of this parasite (Coutelen et al., 1953; Drobeck et al., 1953; Siim et al., 1963; Dubey, 2002). The prevalence of *T. gondii* in wild birds likely to be associated with agricultural landscapes is moderately high (Table 7.1). This is of some concern because *T. gondii* is readily transmitted through the fecal-water route and represents a risk for contaminating crops or water sources used by humans for consumption or food processing (Bahiea-Oliverira et al., 2003). Finally, human populations can be affected by exposure to feces associated with roosts (Peach et al., 1989).

Table 7.1 Prevalence of *Toxoplasma gondii* in Selected Species of Birds Commonly Associated with Agricultural Production or Processing

Order	Common Group Name	Prevalence Range (%)	Reference
Charadriiformes	gulls	6–16	Dubey, 2002; BurrIDGE et al., 1979
Anseriformes	duck, geese	1–28	Dubey, 2002; Pak, 1976
Galliformes	pheasants, quail, turkey	2–19	Dubey, 2002
Columbiformes	pigeons, doves	5–12	Dubey, 2002; Gibson and Eyles, 1957; Jacobs et al., 1952; Catar, 1974
Passeriformes	house sparrow <i>Passer domesticus</i>	1–18	Hejlícek et al., 1981; Ruiz and Frenkel, 1980; Dubey, 2002; Pak, 1976
	starling <i>Sturnus vulgaris</i>	1	Dubey, 2002; Pak, 1976
	crow <i>Corvus brachyrhynchos</i>	1	Finlay and Manwell, 1956

Determinating risk and control points

The first step in developing cost-effective contamination management is to develop robust risk analyses. Carefully constructed, such analyses will identify the important control points. For example, Duffy and Schaffner (2002) developed a Monte Carlo simulation that showed contamination with *E. coli* was higher in dropped apples owing to higher probability of fecal contamination by gulls, and increased site risks when orchards were near sewage ponds or landfills. Because gulls have a high association with landfills and sewage ponds, and those associations can result in higher carriage rates for pathogens (Ferns and Mudge, 2000; Nelson et al., 2008; Ramos et al., 2010), the risk to the orchard becomes higher either because it is an attractive foraging site, or merely by being en route when gulls fly over and drop feces. In this case the practical solution is to avoid using dropped apples in production of unpasteurized foods and drinks. Alternatively, management of contamination sources for *E. coli* may also be effective, though beyond the control of the orchardist. Such land-use patterns, as part of the risk assessment, are emerging as part of a developing field for aviation safety as it relates to birds and could equally be applied to agricultural landscapes.

The current emphasis of the agricultural and microbiological community is in the refinement of the risk analysis process. Improved genetic and biochemical methodologies are resulting in better quantification in drawing the linkage between wildlife as vectors and carriers, wildlife use patterns of agricultural production and processing facilities, and the contamination of agricultural products and processes (Table 7.2). The next step in developing cost-effective contamination management is to better integrate existing bird control and management technologies and methodologies that have been used in mitigating crop damage towards a focus on preventing pathogen and parasite contamination (see below). In doing so, incorporation of bioeconomic modeling into the management simulations for the evaluation of risk mitigation strategies will be a critical step for managers. Such fully integrated simulation models generally have not been applied. The discipline is still largely in the empirical descriptive and univariate management mode. As food safety issues become increasingly important and more diverse technical collaborative teams are assembled, this constraint on management will dissipate.

Mitigation options

Several excellent reviews exist on the general practices of excluding and repelling birds from preharvest agricultural landscapes (Hyngstom et al., 1994; Mason, 1997; Conover, 2002; Linz, 2003). Other venues for research and methods for animal damage control can be found in the *Proceedings of the Vertebrate Pest Conference*, *Proceedings of Animal Damage Management Conference*, and the following journals: *Human-Wildlife Conflict*, *Journal of Wildlife Management*, and *Wildlife Society Bulletin*, and *Wildlife Research*.

Table 7.2 Selected Examples of Microbiological Risks Associated with Wild Birds and Agricultural Production and Processing

Bird Species	Pathogen	Contamination Circumstance	Risk	Reference
Gulls	Fecal coliforms, <i>Salmonella</i> spp., <i>Aeromonas</i> spp.	Beach water quality degraded as a function of visitation of site by gulls.	A	Levesque et al., 1993
birds	<i>Salmonella</i>	Mango processing	A	Sivapalasingam et al., 2003
birds	<i>E. coli</i>	Pecked apples	A	Riordan et al., 2010
birds	<i>E. coli</i>	Watershed	I	Jiang et al., 2007
Canada goose	<i>Cryptosporidium parva</i>	Detected in feces of geese that had rested in agricultural fields.	CC	Fayer et al., 2000
birds	<i>Salmonella</i>	Droppings associated with orange juice production	CC	Cook et al., 1998
Magpies	<i>Campylobacter jejuni</i>	Magpies pecking milk bottle tops contaminated milk. Children drinking milk from compromised containers became ill.	SC	Riordani et al., 1993
birds	<i>Mycobacterium</i> spp., <i>Salmonella</i> spp., <i>Cryptosporidia</i> spp.	Livestock food storage contamination. Model developed showing that fecal contamination was good predictor of disease outbreak in livestock.	SC	Daniels et al., 2003
birds	<i>E. coli</i>	<i>E. coli</i> strains were common in sweet cherry orchard environment and birds. <i>E. coli</i> was not commonly found on fruit still on the tree. However, <i>E. coli</i> was found on pickers' and processors' hands and could be related to environmental and bird sources. Cherries increasingly became contaminated from picking to processing. The implication is that hand-picking cherries also provided opportunity to pick up environmental contaminants thus transferring contamination.	SC, DE	Bach and Delaquis, 2009
Sandhill Cranes	<i>Campylobacter jejuni</i>	Cranes feeding on peas at farm-side contaminated peas with feces and a human outbreak ensued from consuming raw peas. Pathogens linked by PFGE.	SC, DE	Gardner et al., 2011

Table 7.2 Selected Examples of Microbiological Risks Associated with Wild Birds and Agricultural Production and Processing—cont'd

Bird Species	Pathogen	Contamination Circumstance	Risk	Reference
Gulls, pigeons, sparrows, crows	<i>Listeria monocytogenes</i>	A variety of birds using municipal landfills also visited food processing plants (fish, meat). <i>L. monocytogenes</i> strains at contaminated food processing sites and birds were similar by PFGE.	SC, DE	Hellstrom et al., 2007 Neese et al., 2010
European Starling birds	<i>E. coli</i> O157:H7	Dairy	DE	LeJeune et al., 2008
birds	<i>E. coli</i> : (stx1, stx2, hlyA, ehxA, LT1, ST1 cdtB, east 1, cnfl, cvaC)	Contamination of rainwater storage tanks from birds showed biochemical homology to contaminated water samples.	DE	Ahmed et al., 2013
birds	fungi	Damage to fruit allows fungal infection of wound, leading to rot of stored fruit.	E	Creemers, 1989
birds	<i>Aspergillus</i> spp.	Damage to pistachio allowing <i>Aspergillus</i> contamination	E	Doster and Michailides, 1994

(I) Implicated. Genetic evidence of pathogen being same strain as found on produce or human infection.
(A) Associated. Concordant evidence of animal feces and pathogen contamination. Animal known carrier of pathogen.
(CC) Casual circumstantial evidence, avian fecal contamination found along with other risk factors.
(SC) Strong circumstantial evidence, avian fecal contamination identified as most likely risk factor.
(DE) Direct genetic evidence linking animal, pathogen, and product/substrate.
(E) Enabling. Physical activity of bird allows opportunistic infection or contamination.

Lethal control generally is not an option for bird control, owing to federal and state statutes and prohibitions, except as allowed under permit. It is also not practical or economical to exclude birds from large agricultural fields. The exception is for bird netting for high value fruits such as grapes (Tracey and Saunders, 2010; Baldwin et al., 2013). Non-lethal methods to scare birds off fields are the only recourse available to growers. However, in reality, it is not practical to exclude all wild birds from large agro-ecosystems, though it is feasible using integrated pest management approaches to limit populations for smaller areas (Avery, 1989; Mason and Clark, 1992, 1996; Clark, 1998). Methods can include the use of frightening devices, such as visual deterrents, pyrotechniques, propane exploders, or alarm calls, but it is important to avoid presenting cues on a systematic or regular basis so as to avoid habituation. A review of each of these methods

and the successes and failures can be found in the handbook, *The Prevention and Control of Wildlife Damage* (Hyingstrom et al., 1994). The difficulty with the approaches outlined in the handbook is one of expense and human vigilance, both of which are at the root cause of failure. Stevens et al. (2000) explored the use of demand performance systems using radar technologies to activate a variety of bird-scaring devices. The method was successful at keeping migratory birds off hazardous waste ponds of 180 and 90 acres for over a year. The principal drawback of the system was expense. Most agricultural operations could not afford such protection.

Chemical repellents have been tried, but not all crops are amenable to their use owing to expense and regulatory restrictions (Clark, 1997). Nonetheless, several products have been developed, e.g., methyl anthranilate and anthraquinone-based products, and several other investigatory repellents have been evaluated (Avery and Mason, 1997; Cummings et al., 2002; Avery et al., 2005; Werner et al., 2008).

As mentioned, preharvest exclusion of birds from agriculture production may not be realistic either from an efficacy point of view, or where feasible, from an economic point of view. The scale of the areas to be protected in agricultural landscapes are simply too large, and the attractiveness of the resource to birds (i.e., food) is too compelling for repellents and other non-lethal technologies to work towards a goal of total exclusion. The solutions at the preharvest level need to be more carefully thought out. The first assessment should be one of risk. The literature appears to indicate that fecal contamination of water sources and not direct contamination of crop is the control point that should be addressed (Bach and Delaquis, 2009; Slifko et al., 2000; Riordan et al., 2010; Steele and Odumeru, 2004; Ijabadeniyi et al., 2011; Table 7.2). If this is the case, then irrigation practices and water storage and access can be addressed from a resource protection perspective toward bird control, using management strategies that are more temporally and spatially focused, hence practical and economically feasible using existing technologies.

It is becoming increasingly evident that an important control point is prevention of irrigation water contamination (McCarthy et al., 2008; Jokinen et al., 2010; Ijabadeniyi et al., 2011). While there is not much that can be done at the watershed scale, changes in irrigation pattern, water treatment prior to processing, and protection of farm-side water sources may be manageable. For example, drip-irrigation reduces splashing, which can distribute contaminated water on plant surfaces (Forslund et al., 2012). Passing water through a central treated and protected holding facility prior to drip irrigation or processing may further reduce risk of contamination from birds. Postharvest risk of contamination from birds can be addressed by physical exclusion of birds from processing areas, e.g., use of netting. The goal is to prevent fecal contamination of produce, grains, or water sources. Several investigators have studied the efficacy of water treatments and other chemical treatments to make sure that water used for washing becomes decontaminated.

SUMMARY

Wild birds are capable of pathogen carriage, acting as reservoirs, and becoming infected with a wide variety of pathogens, some of which are zoonoses. This review did not attempt to provide an exhaustive list. Rather its intent was to focus on the avian species and pathogens that represented the greatest likelihood to be of concern at the agricultural production and processing level. Unfortunately, little direct evidence bears on this issue; hence risk was assessed using information derived from urban human health, water quality, poultry, livestock production, wildlife health, and the veterinary literature. Despite the lack of direct evidence available relating to birds and the risks to farm-side production and processing of produce, it appears there is ample evidence to support the notion that birds can pose a human health risk by serving as a source of contamination of produce and crops. Nonetheless, more detailed empirical and risk modeling studies are needed. Moreover, such studies should be integrated into a larger ecological perspective of the values of birds to agro-ecosystems balanced against the risks they pose. Finally, studies and analyses should also incorporate assessments of mitigation management strategies in the context of economic, ecological, and public health valuations. These approaches are clearly beyond the scope of this review, but should be seriously considered over a simplistic interpretation of disease risk posed by wild birds and measures needed to eliminate them from agro-ecosystems.

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