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REVIEW

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Salmonella and the chicken: reflections on salmonellosis and its control in the United Kingdom

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Abstract

The association between *Salmonella* with chicken meat and eggs is the best-known source of a foodborne infection and its livestock reservoir. Whilst expansion of intensive farming and globalisation of the industry have facilitated its spread, *Salmonella* has an impressive toolkit that allows its colonisation and survival in the harsh environment of both the gut and egg. After infection in chickens *Salmonella* can pass through the pH of the stomach and, through adhesins such as fimbriae, are able to attach to the gut wall. Within the intestines, diverse metabolic pathways mean *Salmonella* can utilise a range of nutrients and elicit inflammation that releases oxygen to help its colonisation process through competition with the strict anaerobes in the gut. Certain *Salmonella* are also able to colonise the reproductive tract and pass into developing eggs in the ovary or oviduct prior to the addition of the egg-shell. *Salmonella* is also able to withstand high levels of antimicrobial peptides and antibody within eggs.

A range of controls including vaccination, microbial-based products, coupled with improvements to hygiene and biosecurity, have all played a role in reducing *Salmonella*-foodborne illness associated with chicken consumption in Europe, though no single method is a 'magic bullet' of complete control. New variants, including antimicrobial resistant variants, such as *Salmonella* Typhimurium ST34 and its monophasic variants, pose a constant threat. In addition, serovars such as *Salmonella* Kentucky, associated with feed contamination but not protected by current vaccines, pose specific difficulties for control.

A clear understanding of the infection biology of *Salmonella* can help underpin the development and application of controls, while areas of new understanding, such as the role and potential exploitation of the microbiome, offer up potentially novel controls. This all requires maintenance of surveillance systems and risk-based approaches to keep effective control of the *Salmonella* in chicken production.

Keywords Salmonella, Chicken, Foodborne infection, Virulence, Colonisation, Transmission, Vaccination, Metabolism, Microbiome, Eggs

Background

Although *Salmonella* has multiple livestock sources the link between *Salmonella*, the chicken and foodborne illness is understood by the public far more than other sources and risks of other foodborne pathogens. The relationship between poultry meat and eggs and foodborne gastroenteritis caused by *Salmonella* is well established. Even though *Campylobacter* is a more frequent cause of poultry-associated foodborne infection in the UK and

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many other countries, it has not become embedded in the public's psyche in the same way.

Chicken meat and egg production intensified from the 1950s which led to more frequent contacts between larger numbers of birds and their faeces facilitating spread within flocks. Moreover, the move to a global industry and the development of modern genetic hybrid layer and broiler breeds and the distribution of infected breeding stock across the world facilitated the spread of *Salmonella* strains internationally. Our awareness of poultry meat and eggs as a source of salmonellosis became apparent through the 1970s and 1980s and eventually consumer pressure driving a range of controls that in Europe have been successful in reducing the burden of human salmonellosis.

So why is *Salmonella* so associated with chicken? After more than a quarter of a century researching avian salmonellosis, in this review I reflect on the biology of *Salmonella* infection of the chicken, success in control focussed on the approaches used in the UK and perspective on current and future issues that mean avian salmonellosis remains a major headache for public health professionals. The aim is not to focus on a specific aspect of infection, but to give a 'big picture' viewpoint of avian salmonellosis as a whole.

Salmonella and the chicken-historical perspectives

The genus *Salmonella* was first described by Theobald Smith in 1882 as the putative cause of "Hog Cholera". Smith was mistaken, as "Hog Cholera" was in fact Classical Swine Fever, a viral infection. But what Smith had found in the Gram-negative bacillus associated with severe disease in pigs was what we now know as *Salmonella enterica* serovar Choleraesuis. Smith named this new bacterial genus *Salmonella* in honour of Daniel Salmon, another pioneering veterinary microbiologist, and his superior at the USDA. Current *Salmonella* classification is based on the Kaufman-White scheme of serotyping by the 'O' or somatic antigen, based on lipopolysaccharide structure, and the 'H' flagellar antigen. Although the genus has only two species in *Salmonella enterica* and *Salmonella bongori*, *S. enterica* has several subspecies and over 2500 serological variants termed serovars. For ease *Salmonella enterica* serovars are usually referred to short form such as *Salmonella* Dublin or *S.* Dublin with the serovar in Roman script and, although an informal arrangement, is widely used.

As in other livestock species the initial recognition of *Salmonella* in chickens came through high mortality and morbidity infections caused by the avian adapted serovars *Salmonella* Gallinarum (Fowl Typhoid), originally termed *Bacillus gallinarum* by Klein in 1889, and *Salmonella* Pullorum (Pullorum Disease) as the cause of 'white diarrhea' in chickens by Gage in 1914 [1]. Whilst these diseases remain important worldwide, they were largely controlled in developed poultry industries in the 1950s and 1960s through 'test and cull' policies [2]. Although epidemiological links of zoonotic S*almonella* transmission between poultry and humans were made as early as the 1930s [3] and an association with poultry was found in the major 1953 *Salmonella* Typhimurium outbreak in Sweden [4], the clear role the chicken plays as a major source for human salmonellosis only became more widely apparent in the 1970s-80s. Indeed *Salmonella* surveillance reports in the UK between 1941 and 1972 do not show any clear link between poultry and human cases and more reflect the incidence of disease in livestock rather than as a zoonotic source of infection [5]. However, by the 1980s a clear link between *Salmonella,* the chicken and the egg became apparent with the rise of *Salmonella* Enteritidis in the US [6] and in Europe [7]. Although, as we discuss below, effective control measures including the use of vaccines have successfully reduced the incidence of human salmonellosis associated with poultry in Europe, the carriage of *Salmonella*, antimicrobial resistance and emerging serovars remain a significant public health issue for the poultry industry worldwide.

Salmonella Enteritidis in the UK: an exemplar of effective interventions to reduce zoonotic burden

On December 3rd 1988, the then-Junior Health Minister and member of United Kingdom Parliament, Mrs. Edwina Currie made the statement "Most of the egg production in this country, sadly, is now affected with *Salmonella*". Mrs. Currie's statement was remarkably honest and led to what became the first in a series of food microbial safety scares in the UK in the late 1980s and 1990s ranging from 'Listeria hysteria' to Mad Cow Disease [8] Unsurprisingly the initial reaction of the poultry industry was hostile but over time public and retailer pressure led to legislation to improve hatchery hygiene, followed by a voluntary scheme in 1998 (Lion Mark) that included flock surveillance, improvements to biosecurity and, crucially, vaccination of laying hens that had a large impact in reducing the frequency of *Salmonella* isolation from flocks and in reducing cases of human salmonellosis. These approaches were largely adopted into European Union legislation for *Salmonella* control as defined by National Control Plans (NCP). NCPs for layer, breeder and broiler chickens set down standards for hygiene, biosecurity and surveillance across all commercial poultry production and requirements for vaccination in layer and breeder flocks as a consequence of which not only S. Enteritidis levels fall, but so did human cases associated with chicken caused by other serovars [9].

Salmonella and the chicken-factors around infection and transmission

Most *Salmonella* serovars can colonise the intestinal tract of chickens with limited disease in the host but have the potential to contaminate meat and meat products [10]. Indeed, both intestinal and reproductive tract infection rarely manifest as overt clinical disease. Most human cases are caused by serovars Typhimurium and Enteritidis. Infection via eggs is most commonly seen with *S.* Enteritidis which, along with host-adapted *S.* Gallinaum and *S.* Pullorum, is considered to have specifically evolved to colonise the reproductive tract of chickens and allow vertical transmission as a consequence of domestication of the Red Jungle Fowl for sport and food [11]. Whilst other serovars can contaminate the egg surface after laying they very rarely display transovarian transmission, though some strains of *S.* Typhimurium and adapted strains of *S.* Heidelberg have been shown to colonise the reproductive tract in a similar way [12]. The washing of eggs to remove any faecal contamination is very much a double-edged sword as this eliminates the protective cuticle from the egg surface allowing bacterial entry.

Infection and survival in the chicken gut

Whether infection is via meat or eggs, *Salmonella* must be able to survive within one or the host niches of the gut, reproductive tract or egg to cause zoonotic transmission. These may all be considered as hostile environments. The main site of *Salmonella* colonisation in the gut is within the two large, blind caeca that sit at the junction between the small intestine and short colon. Maintaining colonisation at this site requires any bacterial species to overcome low oxygen tension, avoid being flushed away by intestinal flow, be nutritionally flexible as well as having the capacity to overcome any host response (Fig. 1).

As a facultative anaerobe *Salmonell*a will survive and replicate both in the presence and absence of oxygen, though more recent evidence suggests it may favour a more aerobic environment in the gut. A range of factors associated with motility, attachment and host cell invasion have been shown to be involved in colonisation and attachment including flagella and lipopolysaccharide [13, 14]. In both *S.* Enteritidis and S. Typhimurium a range of fimbrial types are associated with colonisation of the gut [15, 16]. The *Salmonella* pathogenicity island (SPI) encoded Type III secretion systems (T3SS) have also been shown to have involvement in colonisation of *S.* Typhimurium in the chicken gut [17, 18], though perhaps unsurprisingly the SPI1 encoded T3SS usually associated

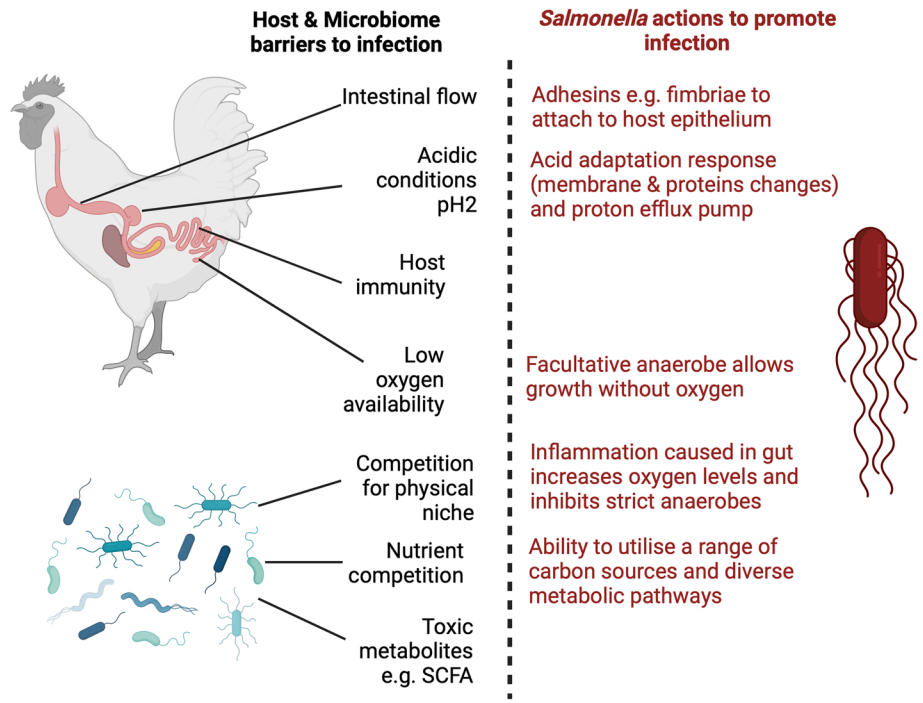

Fig. 1 Overview of pathogen-host-microbiome interactions during intestinal *Salmonella* infection of the chicken. Major features of host and microbiome (black) that act to inhibit infection and *Salmonella* (red) virulence factors and functions that act to colonise and survive within the gastrointestinal tract of the chicken. Created with BioRender.com

with intestinal invasion plays the more significant role in colonisation of both *S.* Typhimurium [19] and *S.* Enteritidis [20].

The intestinal tract environment provides a diverse range of physical and chemical challenges to any colonising bacteria along with a complex ecosystem of host and microbiome which varies substantially through the gut. Therefore, *S. enterica* has developed an array of receptor and regulatory systems, including two component signal transduction systems (TCS) including PhoP/PhoQ that are able to recognise and respond to receptors and a range of alternative sigma factors that allow rapid transcriptional response to stress [21]. Mutation in either TCS (PhoQ) or in Sigma factors (RpoS) genes of *S.* Typhimurium attenuate colonisation of the chicken [22]. As in any monogastric system, passage into the stomach exposes *Salmonella* to a highly acidic environment. In response to acid shock, some 51 inducible proteins have been found in *S.* Typhimurium including pathways involved in DNA repair, iron uptake and fatty acid metabolism [23], though it has been suggested that passage through the mildly acidic crop may help a more efficient acid adaptation than in monogastric mammals such as the pig [24]. Colonisation of the intestinal tract requires significant metabolic and nutritional diversity. One of the key genomic signatures of host adaptation of *Salmonella* towards causing a systemic infection rather than intestinal colonisation is the loss of certain metabolic pathways. *S.* Gallinarum has pseudogenes that disrupt metabolic pathways that utilise allantoin, tetrathionate and propanediol in colonisation of the chicken gut that are present in *S.* Enteritidis [11]. Similar functional loss of metabolic pathways associated with reduced intestinal colonisation is seen in S. Typhimurium genotypes including DT2 associated with systemic disease in pigeons and ST313 associated with invasive non-typhoidal salmonellosis in humans [25, 26]. It is clear that *Salmonella* has diverse nutritional and metabolic capacity to survive and grow within the chicken gut with multiple and alternative metabolic pathways [27]. However, the reality of gut colonisation is one of establishing an infection within a complex ecosystem of the microbiome, host metabolites and host immune response along with the pathogen itself. The immune response to *Salmonella* is the most studied of all bacterial infections in the chicken [28], though there are still significant gaps in key areas of the intestinal response especially around regulatory T cell and Th17 functions. Whilst there is an initial inflammatory response to infection, this rarely causes overt disease, and usually leads to transient infection of the liver and spleen, colonisation of the caeca and resolution of any inflammatory damage [26, 29]. More recently the idea of an immunometabolic response in the gut has been suggested and that inflammatory and metabolic signals are recognised together in the gut which leads to an anti-inflammatory state that allows colonisation [30, 31].

The intestinal microbiome will exert effects on *Salmonella* both directly and via the immune systems and equally *Salmonella* infection will modify the microbiome [32]. As such it is more appropriate to consider the relationship of pathogen, host response and microbiome as a complex ecosystem rather than a simple one or two-way interaction. That the microbiome or microflora can inhibit *Salmonella* colonisation has long been established with the work of Nurmi and Rantala laying down the concept of competitive exclusion [33, 34]. The key idea is that the members of the microflora and pathogenic bacteria compete for nutritional resources and a physical niche, and that metabolites of members of the microflora may be inhibitory for the colonising pathogen. Competitive exclusion has formed the basis of probiotic, prebiotic and microflora products utilised to reduce *Salmonella* colonisation in chicken production [35, 36]. Whilst some of the interactions within the gut are straightforward to explain, such as short chain fatty acids produced as metabolites by anaerobes butyrate being directly inhibitory to *Salmonella*, or low oxygen levels at the gut epithelium favouring strict anaerobes, others may be more complex. Recent evidence of *Salmonella* colonisation in mammals, reviewed by Rogers et al. [37] show that other Enterobacterales such as *Escherichia coli* may outcompete *Salmonella* for the available oxygen, but that *Salmonella*-mediated inflammation acts to release oxygen from the host response and also releases host derived nutrient sources such as lactate and tetrathionate. It is tempting to speculate that the chicken provides further support to this theory with the consideration that *S.* Gallinarum does not elicit an inflammatory response in the gut [38], lacks functional metabolic pathways to utilise tetrathionate [11] and is a poor coloniser of the chicken gut, whereas serovars that elicit inflammation such as *S.* Typhimurium and *S.* Enteritidis have a full complement of metabolic pathways. Indeed, experimental evidence that *S.* Enteritidis infection elicits the release of oxygen in the chick gut and that commensal *E. coli* competes for this oxygen to inhibit *Salmonella* supports the theory that the ability to compete for oxygen is a key for *Salmonella* and likely *Campylobacter* colonisation of the chicken caeca [39].

Infection and survival in the reproductive tract and eggs

S. Enteritidis and *S.* Pullorum are the most efficient serovars in terms of reproductive tract infection and transovarian transmission to eggs, though certain S. Typhimurium and S. Heidelberg strains can also rarely transmit through this route. The main host and pathogen

factors effecting reproductive tract and egg infection are summarised in Fig. 2.

Egg infection associated with other serovars is more usually associated with faecal contamination after laying [40]. The chicken female reproductive tract consists of a functional left ovary and oviduct with vestigial organs on the right side [41]. The ovary consists of a central cortex surrounded by a follicular medulla of developing oocytes. As these develop into a mature oocyte, or yolk, with a membrane. Mature oocytes, both fertilised and non-fertilised, are released into the oviduct. The oviduct is a structure with an extended length of 70-80cm in mature hens. The oocyte is released into the funnel-like infundibulum and moves on to the magnum where the albumen is deposited onto the yolk. The egg then moves on to the isthmus where the membrane is added before moving onto the uterus where the egg is calcified by the shell-duct forming the shell. Finally, a protective cuticle is added prior to the egg being laid. The process from release from the ovary takes around 20 h. Whilst the reproductive tract does not pose the same challenges of a highly complex microbiome, availability of oxygen and the need for metabolic diversity as the gut, there is a functional immune system with considerable secretion of antimicrobial peptides into the oviduct. Moreover, motility down the oviduct with highly ciliated epithelial cells make colonisation of the reproductive tract by bacteria very challenging. The egg itself constitutes a barrier to penetration by bacteria and a hostile environment for bacterial survival and growth. The cuticle is a proteinaceous layer added to the shelled egg in the uterus [42]. The intact cuticle acts as a physical barrier to contamination of the egg including acting as a pore plug for respiratory pores in the egg and contains antimicrobial peptides [43]. The effect of washing eggs on penetration by *Salmonella* and other bacterial species remains controversial, whilst washing reduces surface contamination and is widely practiced in North America and Japan [43], it is illegal in the European Union as it is considered to risk damage to the cuticle and used to cover bad hygiene practice [44]. However, there is also evidence that washing makes limited difference to the ability of a range of *Salmonella* serovars to penetrate the egg and that the pore plug function of the cuticle remains intact, though there appears to be a reduction in its antimicrobial activity following washing [43].

Egg white is a challenging environment for bacterial survival, as it contains a number of antimicrobial proteins including ovotransferrin and lysozyme [45] and antimicrobial peptides including ovodefensins, a family of beta defensins secreted into the egg in the oviduct [46]. Specific and natural IgY antibody is also found in the yolk, often at high titres, along with IgA and IgM antibodies secreted into the egg white during development in the oviduct [41]. Specific antibodies have been shown to inhibit *Salmonella* growth in vitro [47]. High titres of

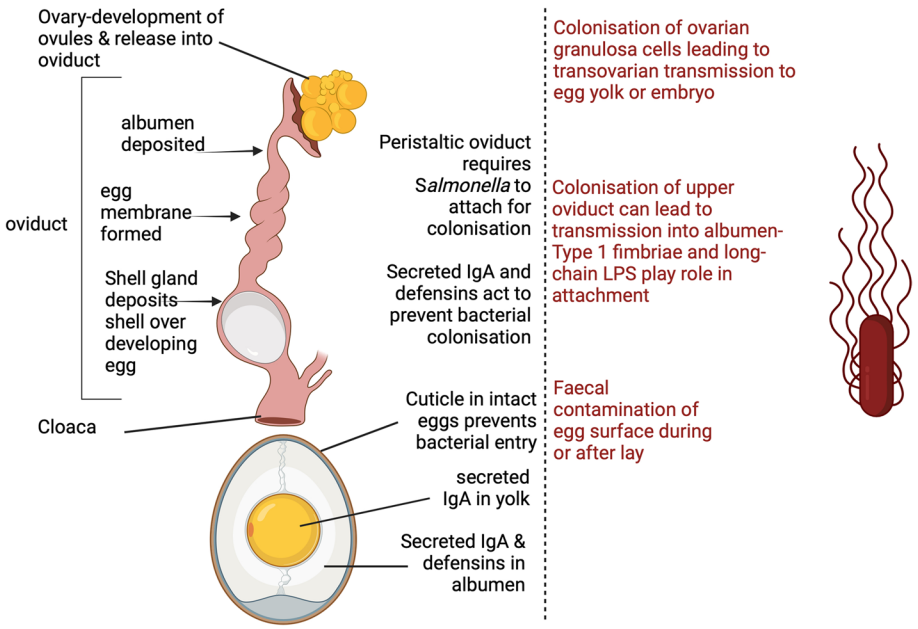

Fig. 2 *Salmonella* infection of the reproductive tract and eggs-main host and pathogen features. Main features of the chicken reproductive tract highlighting host factors that inhibit infection in both the tract and eggs (black). The main areas targeted by *Salmonella* and mechanisms employed to achieve colonisation are in red. Colonisation of the ovaries or upper oviduct leads to 'true' transovarian transmission. Faecal contamination during lay or hatch rarely enters eggs unless cracked or protective cuticle is removed. Created with BioRender.com

antibody found in the eggs of *S.* Pullorum infected hens, are considered to prevent excessive growth of bacteria in fertilised eggs killing the developing embryo [48].

As such, *S.* Enteritidis has a number of key features which allow it to colonise the reproductive tract and infect the developing egg.

Salmonella is able to colonise the reproductive tract through attachment to the oviduct or ovarian epithelium [49, 50]. Type 1 fimbriae and long 'O' chain lipopolysaccharide, both surface expressed adhesins, have been consistently identified as factors in colonisation [51–53]. A genome-wide microarray-based approach identified some 81 genes upregulated in colonisation including SPI1 and SPI2 T3SS effectors and genes found on four *Salmonella* genomic islands (SGI) which were found to play a key role in the reproductive tract in an earlier study [54, 55].

Vaccination provides strong protection to infection of the reproductive tract via a combination of antibody and cellular responses. *Salmonella*, however, can exploit a chink in the armour of immunity. Hens undergo a significant local and systemic immunosuppression event at point-of-lay [56]. In birds persistently infected with *S.* Pullorum, this drop in immune function allows bacterial numbers to increase and spread to the reproductive tract [57]. In *S.* Enteritidis infection this allows a window of opportunity, as even in vaccinated birds, there is a decrease in specific immunity and increased susceptibility to challenge, albeit vaccination still provides increased protection over naïve animals [56].

Transmission within flocks

Shedding of *Salmonella* in faecal and caecal droppings and subsequent faecal-oral transmission are considered the main transmission route within farms and this can be modelled using seeder bird infection experiments [58, 59]. Obviously, larger sheds allow greater capacity to transmit via this route. The initial source of *Salmonella* can be from the hatchery, via vertical transmission to chicks, from contaminated feed or litter, via workers and tools or via wild birds, vermin, and invertebrates. The hatchery as a source of *Salmonella* has long been established with faecal contamination of the egg surface, penetration into the egg, vertical transmission or contamination of hatchery equipment such as incubators and brooders [60]. Measures to improve hatchery management and hygiene were amongst the earliest controls for *Salmonella* put in the place in the UK and Europe and remain a vital cog in controls. Recent studies in the UK show that although many hatcheries have little or no problem with *Salmonella* contamination, the bacterium can persist within hatcheries and that high levels of hygiene, disinfection and biosecurity are needed to control *Salmonella* from this source [61].

Both feed and litter, the substrate that broiler and many layer chickens are reared on, can become contaminated with *Salmonella,* which has the long-term capacity for survival in dry materials. Whilst chickens are naturally foragers and scavengers, in the commercial sector birds are fed grain-based diets (usually maize or wheat), supplemented with protein (mainly vegetable based proteins such as soya), and micronutrients formulated into mash, crumb or pelleted feeds. Contamination may potentially come from raw ingredients, contamination of the feed mill or contamination of stored feeds such as through vermin [62]. Although manufacturers are likely to test raw ingredients for microbial safety and presence of mycotoxins the multiple points by which *Salmonella* may enter feed production mean that recent surveys of S*almonella* in UK and US feed mills showed contamination to remain a significant problem [63, 64]. Both chemical and heat treatment of feed can successfully reduce the risk of contamination [65, 66]. Such treatments have included formaldehyde-based disinfectants and organic acids, though tighter controls on the use of the former in the EU mean increased use of non-formaldehyde-based compounds [67].

On farm, breakdowns in biosecurity can result from poor training, poor maintenance of the fabric of buildings, wild bird and animal ingression, but equally from reduced vigilance and a degree of complacency or even 'cutting corners' to meet the demands of the job. A study on broiler 'catchers' around biosecurity in relation to *Campylobacter* revealed that although those trained in biosecurity were more aware of potential breaches, the pressures of time and the lack of equipment provided meant that biosecurity procedures were frequently ignored [68]. In the UK egg sector, approaches and understanding of biosecurity are generally good though this may be at least in part to the relative vigour of enforcement via national control plans [69]. The recent avian influenza outbreaks are a stark reminder of the need for effective biosecurity in disease control. These have also highlighted the massive increase in hobbyist and backyard production, that may act as a reservoir of pathogens including *Salmonella*. Indeed, the understanding of the risks of infection from backyard production is mixed amongst poultry keepers in the UK and the US with some owners treating animals as pets including cuddling and kissing of hens and a lack of acceptance that infection is not restricted to commercial production [70–72].

Current and emerging trends in *Salmonella*

As with any microbial pathogen we see the emergence of new variants with *Salmonella* evolution. On top of this we see changes and trends in how we rear chickens with an increased emphasis on cage-free and free-range production and in the reduction of antimicrobials used in production either through legislation or successful voluntary stewardship schemes. Perhaps the clearest examples are in the evolution *of Salmonella* Typhimurium Sequence Type (ST) 313, associated with human invasive disease in Africa [73] and the emergence of ST34 *S.* Typhimurium and Typhimurium-like monophasic variants in pigs [74]. Whilst ST313 can colonise chickens, there is little evidence of an animal reservoir, suggesting human-to-human transmission is the main route of infection [75]. In contrast, frequently multi-drug resistant pandemic ST34 strains are associated with food production animals around the world, most frequently in pigs but also in other species including chickens and turkeys [76]. Evolution of ST34 is considered to be driven by acquisition of a chromosomally encoded genomic island (SGI-4), as was a previous drug resistant multispecies pandemic *Salmonella* Typhimurium DT104 in the 1990s [77]. Indeed, the last decade has revealed a wider range of genotypes and host range or infection phenotype in both *Salmonella* Typhimurium and Enteritidis ([25, 78–80].

Whilst it is clear that in Europe the targeted approach to *Salmonella* control has been successful in poultry and in reducing human cases, such gains have slowed in pace, and 2021 showed an upturn in human cases of salmonellosis [81]. Cases of human foodborne salmonellosis are predominantly still caused by *S.* Enteritidis, *S.* Typhimurium and its monophasic variants, while other serovars are considered as substantive threats including *S.* Infantis, *S.* Agona, *S.* Derby and *S.* Kentucky [82]. Increased prevalence of *S.* Derby in pigs, along with S. Typhimurium and monophasic variants have driven more frequent disease-associated with pork products but *S.* Infantis and *S.* Kentucky have greater association with poultry. One of the likely issues why certain *Salmonella* have merged is the limited levels of vaccine protection in breeding birds against serovars outside of Group B and Group D. Previously we have shown that *S.* Typhimurium (serogroup B) provides no protection to *Salmonella* Virchow (Group C) [83], and it is likely that individual or bivalent vaccines offer little protection to emergent or re-emergent Group C serovars such as *S.* Infantis or *S.* Kentucky nor to the array of *Salmonella* from Group C and E found in UK chicken production but rarely associated with human disease.

In the case of *S.* Kentucky there has been emergence of a worldwide multi-drug resistant ST198 strain resistant to ciprofloxacin [84]. ST198 is found in both human cases and isolated regularly from poultry and the production environment in North America, Asia, Europe and Africa [85–87]. One key reason for the emergence of *S.* Kentucky is its ability to survive well in feed [88] which may help explain its worldwide prevalence. In contrast *S.* Infantis is more resilient to chilling which may also explain its success in more developed industries with chilled supply lines.

Future needs and controls: a perspective

Complete eradication of *Salmonella* from food production is unrealistic, given the multiple potential animal and environmental reservoirs. As such, an integrated, risk-based approach to control, informed by strong surveillance data from farm-to-fork, remains the best way to minimise foodborne salmonellosis. Within poultry the continued use of vaccines and ideally multivalent vaccines remains central to any control. Vaccination only works well when supported by good biosecurity and hygiene through the production cycle. Surveillance is needed not only to understand the main risks associated with production, but also the potential emergence of multi-drug resistant strains and of serovars not protected via vaccines.

Our enhanced understanding of the role of the microbiome in infection and gut health also opens new possibilities of microbial-based controls including probiotics. These interventions are of particular value in broiler production, where vaccination is rarely used for reasons of cost, safety and efficacy. Added to this is the drive for reductions or even cessation of antimicrobial use, which reduce the tools available for infection control, though rarely used directly against salmonellosis. A new generation of vaccines is arguably needed to strengthen protection, offer protection across all serogroups and potentially offer better protection in newly-hatched chicks and have a shorter withdrawal period that could allow routine use in broiler production as well as in broiler breeders.

Salmonella remains a public health problem for poultry production. The UK has used a risk-based approach to control based around surveillance, biosecurity and vaccination now specified in legislation. This has successfully lowered the cases of human salmonellosis for close to 30 years. Slight increases in numbers of isolations from flocks and in human cases in recent years in the EU and UK are a clear warning that we should avoid the complacency that the problem has 'gone'. We need to retain surveillance and have the flexibility to identify emerging serovars and minimise the risk of rising cases. *Salmonella* has the metabolic flexibility and diversity that allow a range of serovars to colonise the bird in its production life and is undergoing constant evolution leading to a constant threat with many potential reservoirs. In recent

decades the UK poultry industry has been at the forefront of public health partnerships both through legislation and perhaps more importantly voluntary schemes such as 'Lion Mark' and more recently in antimicrobial stewardship which has resulted in around 65% reduction of antimicrobial use in egg production and over 75% in broiler chickens [89]. Maintaining such partnership is key to the long-term control of *Salmonella*.

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