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E. coli is spreading by poor toilet hygiene, not through food

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Abstract:

Extended-spectrum β-lactamase-producing *Escherichia coli* (ESBL-*E coli*) is the most underlying cause of food poisoning in worldwide. The influence of the food chain to these infections is debated. We aimed to identify the most important reservoirs of ESBL-*E coli* that colonies and infect humans to identify the preventing point.

Introduction:

Escherichia coli is the most common cause of urinary tract infection and gram-negative rod sepsis, also cause food poisoning[(1)] , The most frequent of these are those which show Extended-spectrum beta-lactamases are enzymes that responsible for resistance to most beta-lactam antibiotics, including penicillins, monobactam, cephalosporins, and the, aztreonam, with ESBL-producing organisms have been associated with poor outcomes [(2)]. Food poisoning, is illness caused by eating contaminated food Infectious organisms including bacteria, viruses and parasites [(3)]. ESBL-*E coli*, isolated from, faeces, sewage, food, animals and slurry were received at PubIic Health England and looking for *bla*CTX-M, *bla*TEM, *bla*SHV and *bla*OXA by multiplex PCR. *bla*CTX-M-positive isolates were accepted as ESBL producers, whereas isolates that were positive for one of the other β-lactamase genes underwent double disc ESBL tests using amoxicillin–clavulanate (20 μg + 10 μg) discs about 20 mm apart (centre to centre) from cefotaxime (30 μg), ceftazidime (30 μg), and cefepime (30 μg) discs. Expansion of an oxyiminocephalosporin zone towards the amoxicillin–clavulanate disc suggested ESBL production. isolates flagged as shigella were confirmed as *E coli* based on *o*-nitrophenyl-β-D-galactosidase activity. Definitive confirmation as ESBL-*E coli* was done by whole-genome sequencing. ST131 isolates were assigned to organsim based on *fimH* sequences. Serotypes of ST10 isolates (which crossed among host species) were deduced from sequence data. The researchers found ESBL- *E. coli* in 11% of human fecal samples contained ESBL- *E. coli*, and 65% of retail chicken samples. No ESBL-*E. Coli* was found in fruits or vegetables and only a few other meat samples. [(2)]

Materials and Methods:

We examined ESBL-*E coli* from multiple sources, including human faeces, sewage, farm slurry, live food producing animals, and raw meat, fruit, and vegetables. Faecal specimens were submitted between Aug 12, 2013, and July 20, 2014, for detection of intestinal pathogens. Each laboratory was asked to randomly select and test 15–20 faecal specimens per day to a maximum of 100 per week. No information was given on how to select randomly. Faeces (about 0・5 g) was mixed with 1 mL of 0・85% saline, then 50-μL sample were spread on the two chromogenic agars and incubated for 18–24 h. ESBL-*E coli* must be visible as pink on CHROMagar ESBL or blue on CHROMagar CTX. Sewage samples analysis by centrifuge pelleting bacteria from about 30 mL sewage, re-suspended in 0·5 mL of freezing broth. ESBL-E coli were recovered, as red colonies, after plating 100 μL of defrosted material on UTI Brilliance Agar containing 10 mg/L of cefotaxime. We bought the following in many regions: beef, pork, and chicken (n=397 samples grapes (n=50), strawberries (n=38), raspberries (n=35), blueberries (n=27), celery (n=50), carrots (n=50), onions or spring onions (n=50), lettuce (n=50), coriander (n=43), and basil (n=7). Retailers included leading supermarkets, discount stores, convenience stores, and local butchers and greengrocers. Chromogenic agars used to recover ESBL-*E coli*. 97 slurry samples were collected and take it from dairy farms at many regions, after milking and before cleaning, Samples were taken from five different areas at each farm on the route that the cows followed when leaving the milking parlour. 1- g samples were incubated overnight at 37°C in 9 mL of buffered peptone water before plating 10-μL amounts on the two chromogenic agars. [(2)]

Result:

ESBL production was confirmed in 2157 (11%) of 20243 human faeces samples contained ESBL-E coli, ESBL-*E coli* also were frequent in sewage and retail chicken (104 [65%] of 159 meat samples), but were rare in other meats and absent from plant-based foods (0 of 400 fruit and vegetable samples). Sequence type (ST) 131 dominated among faeces (128 [36%] of 360), and sewage (14 [22%] of 65) with STs 38 and 648 also widespread; CTX-M-15 was the predominant ESBL in these lineages (319 [77%] of 416). STs 602, 23, and 117 mostly with CTX-M-1 ESBL dominated among food and veterinary isolates (68 [31%] of 218), with only two ST131 organisms recovered. ST10 occurred in both animals and humans, being frequent

in surveillance bovines (11 [22%] of 51 cattle) and representing 15 (4%) of 360 human faecal isolates however, both human and animal ST10 isolates were diverse in serotype [2]

Discussion:

We compared ESBL-E coli from human faeces, sewage, food, and slurry, animals, across many regions in the UK. Faecal ESBL-*E coli* were often linked to foreign travel (particularly to south or southeast Asia) or previous use of antibiotics Greater contamination of chicken than other meats concurs with previous findings. ESBL results showed commonality between faeces ESBL-E coli and those from sewage, with STs 131 (especially), 38, and 648 prominent in all these sources, largely with CTX-M-15 enzyme There was also commonality between the lineages from surveillance chickens and chicken meat, with STs 23 and 602 dominating, often with CTX-M-1 ESBL, and between cattle slurry, where ST10 (with CTX-M-14 or CTX-M-15) dominated. ST117 was widely found in isolates from both bovine and chickens. Little contamination was seen for foodstuffs other than chicken. Our findings do not support the assertion that invasive ESBL-E coli are disseminating via the food chain. Rather, they suggest that host-adapted ESBL-E coli lineages are circulating, with different interspecies transmission ST131, which dominated among human-related isolates, is well known multidrug resistant. Although ST131 occasionally occurs in food animals Among the major meat, ST23 was reported from an outbreak in a French hospital, with various further one-off reports but, as we report here, is mostly found in poultry. ST10, as the sole lineage to appear in the top ten of meat-associated groups has been repeatedly noted by other studies in both animals and humans.one of the regions we surveyed, which also found that these isolate groups and their resistance determinants are largely distinct. [2] Rather than the food chain, the human to human oral faecal route is likely to be the most frequent route of transmission for human-adapted ESBL-E coli. This route would account not only for the strain and enzyme distributions we have summarised, but also the regional variation in gut carriage of ESBL-E coli with higher rates in London than elsewhere, where sampling was solely from the Royal London Hospital, which predominantly serves poor, crowded areas and populations with frequent travel to and from south Asia A study in the WestMidlands, UK, similarly showed that human gut carriage of ESBL-E coli was more prevalent in inner city (ie, around Birmingham) than in rural .[4] We cannot exclude the possibility that some small minority of human infections might have a direct

origin from food, nor that local clusters can occur. Our findings suggest that efforts to stop the rise of ESBL-*E coli* in invasive infections should concentrate upon disrupting oral-faecal transmission by good post-toilet hygiene (eg, in care homes), on prevention of urinary tract infections by good hydration and catheter care, and on prompt effective treatment of preceding urinary tract infections. Vaccines could provide a solution in the future, with promising early results for cystitis in younger women.[(2)] Efforts to counter the spread of ESBL-*E coli* in food production seem unlikely to affect greatly the tally of invasive human infections but remain important in ensuring that veterinary infections remain tractable.

Conclusion:

Food is not the primary source of severe and spreading *E. coli* infection in humans, but rather the organism is spreading between human beings themselves. The most likely route is feco-oral, or in other words, the failure of humans to wash their hands properly after toilet functions leads to the organism lingering on the hands to be transmitted to the next object brought in contact with them.

References:

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