

# Population Structure and Antimicrobial Resistance in *Campylobacter jejuni* and *C. coli* Isolated from Humans with Diarrhea and from Poultry, East Africa

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Campylobacteriosis and antimicrobial resistance (AMR) are global public health concerns. Africa is estimated to have the world's highest incidence of campylobacteriosis and a relatively high prevalence of AMR in *Campylobacter* spp. from humans and animals. Few studies have compared *Campylobacter* spp. isolated from humans and poultry in Africa using whole-genome sequencing and antimicrobial susceptibility testing. We explored the population structure and AMR of 178 *Campylobacter* isolates from East Africa, 81 from patients with diarrhea

in Kenya and 97 from 56 poultry samples in Tanzania, collected during 2006–2017. Sequence type diversity was high in both poultry and human isolates, with some sequence types in common. The estimated prevalence of multidrug resistance, defined as resistance to  $\geq 3$  antimicrobial classes, was higher in poultry isolates (40.9%, 95% credible interval 23.6%–59.4%) than in human isolates (2.5%, 95% credible interval 0.3%–6.8%), underlining the importance of antimicrobial stewardship in livestock systems.

*Campylobacter jejuni* and *C. coli* are causes of food-borne enteric infection worldwide (1). *Campylobacter* spp. are among the most frequent pathogens identified in diarrheal samples from persons in Africa, particularly in children (2), and among World Health Organization regions, the highest burden of campylobacteriosis is observed in the Africa Region (1). Lack of surveillance data hinders attempts to

assess the actual burden in this setting (2), however, and determining whether *Campylobacter* is the causal agent of diarrhea can be difficult (3). *Campylobacter* spp. are increasingly recognized as associated with other conditions, including stunting (4).

Animals and foods of animal origin make an increasing contribution to human nutrition in low- and middle-income countries as sources of high-quality

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protein and micronutrients (5). Food of animal origin is also a source of zoonotic pathogens, including *Campylobacter* spp.; 3 systematic reviews identified poultry (6–8) as a source of *Campylobacter* spp. in Africa. In Tanzania, consumption of chicken meat was the only animal-related risk factor for human campylobacteriosis (9), and genetic studies demonstrate the possibility of transmission between poultry and children (10).

Molecular epidemiologic approaches have improved our understanding of sources of human *Campylobacter* infection and contributed to campylobacteriosis control programs in high-income countries (11,12). Earlier molecular studies used low-resolution techniques such as 7-gene multilocus sequence typing (MLST) (11,12), whereas in recent years, whole-genome sequencing (WGS) has played an increasing role in informing control strategies (13). To date, few studies of *Campylobacter* spp. in Africa using WGS exist (14,15), and even fewer have been conducted comparing human and poultry isolates (16).

The prevalence of antimicrobial resistance (AMR) is high among *C. jejuni* and *C. coli* isolated from humans (9,16), poultry (16–18), and other animals (7) in sub-Saharan Africa. Examining the genomic epidemiology of *Campylobacter* spp. and evidence for AMR in isolates from poultry and humans in this region is necessary. To this end, we integrated food safety research in northern Tanzania (19) with an established diarrheal disease etiology surveillance system in neighboring Kenya to provide detailed WGS and AMR data on *Campylobacter* spp. isolated from persons with diarrhea and from poultry in East Africa and to explore similarities and differences between isolates from humans and from chickens reared in different farming systems.

## Materials and Methods

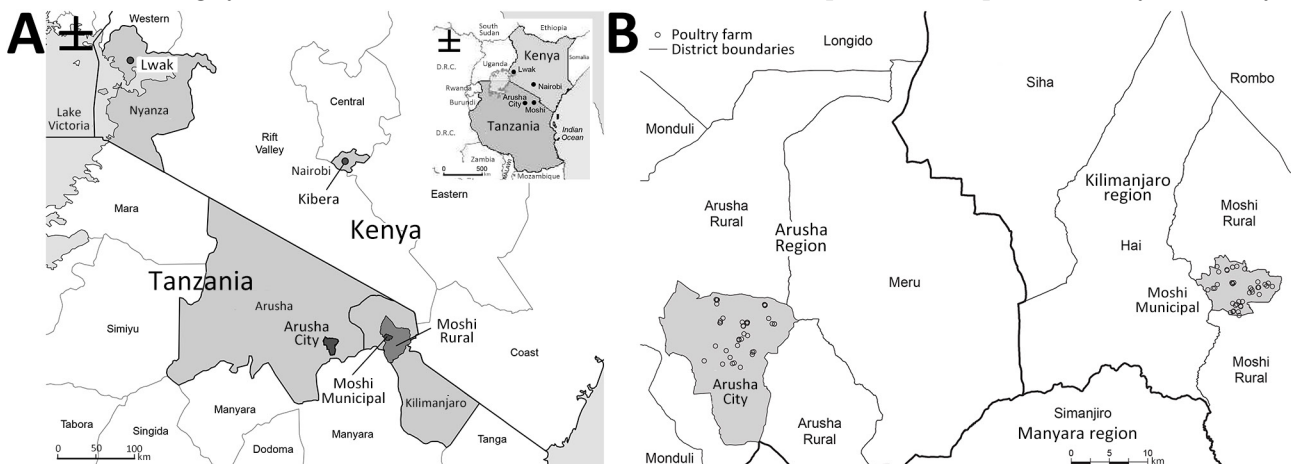
### Study Setting and Sampling

#### Chicken Isolates from Tanzania

We conducted sampling during October 10, 2016–July 24, 2017, at 66 poultry farms in Arusha City and Moshi Municipal Districts, Tanzania (Figure 1). We collected cloacal swab specimens from  $\leq 10$  visually healthy chickens per farm in 8 randomly selected wards in Arusha City District and 10 randomly selected wards in Moshi Municipal District. Per ward, we included up to 1 farm per production system; production systems were classified as extensive (not housed, indigenous breeds), semi-intensive (partly housed, indigenous breeds), intensive (fully housed, indigenous breeds), and broiler (fully housed, exotic breeds) (20). We collected cloacal swab specimens from live animals using Amies charcoal transport swabs (Sterilin Ltd, <http://www.sterilin.co.uk>) and transported samples in a cooler box with freezer packs to Kilimanjaro Clinical Research Institute Biotechnology Laboratory in Moshi for processing on the day of sampling. We isolated and identified *Campylobacter* as described by Sindiyo et al. (20) (Appendix, <https://wwwnc.cdc.gov/EID/article/30/10/23-1399-App1.pdf>).

#### Human Isolates from Kenya

We requested *Campylobacter* isolates collected from human stool ( $n = 81$ ) from Tabitha Clinic, Kibera, Nairobi (urban informal settlement), and St. Elizabeth Lwak Mission Hospital, Asembo, western Kenya (rural site), during December 14, 2006–March 22, 2016, from the Population-Based Infectious Disease Surveillance platform, implemented by the Kenya



**Figure 1.** Location of sampling sites in study of population structure and antimicrobial resistance in *Campylobacter jejuni* and *C. coli* isolated from humans with diarrhea and from poultry, East Africa, 2006–2017. A) Data collection sites in Lwak and Kibera in Kenya and Arusha and Kilimanjaro in northern Tanzania. Inset shows location of Kenya and Tanzania in East Africa. B) Poultry farm locations sampled in Arusha and Kilimanjaro regions, northern Tanzania.

Medical Research Institute in collaboration with the US Centers for Disease Control and Prevention (CDC) as described in Crump et al. (19). Isolates were shipped to Kilimanjaro Clinical Research Institute in Trypticase Soya Broth with 20% glycerol (BD Diagnostics, <https://www.bd.com>) and stored at  $-80^{\circ}\text{C}$  (Appendix).

### Molecular Confirmation and WGS Analysis of *Campylobacter* Isolates

We sent *Campylobacter* isolates in brain-heart infusion plus glycerol on dry ice to mEpiLab, Hopkirk Research Institute, Massey University (Palmerston North, New Zealand), for WGS and analysis. Isolates were subcultured on Columbia horse blood agar (Fort Richard Laboratories, <https://www.fortrichard.com>) at  $42^{\circ}\text{C}$  in a microaerobic atmosphere (5%  $\text{O}_2$ , 10%  $\text{CO}_2$ , 85%  $\text{N}_2$ ) provided by a MACS VA500 incubator (Don Whitley Scientific, <https://www.dwscientific.com>). We extracted DNA using the QiaAmp DNA minikit (QIAGEN, <https://www.qiagen.com>) and confirmed *Campylobacter* isolates by PCR using *hipO* (21) and *ceuE* primers (22). We performed library preparation using an Illumina NexteraXT library preparation kit (Illumina, <https://www.illumina.com>) according to the manufacturer's instructions. We submitted prepared libraries to New Zealand Genomics Limited (University of Otago, Dunedin, New Zealand), which performed sequencing using Illumina HiSeq 2  $\times$  125-bp PE v4 instrument. We submitted raw sequence data to the National Center for Biotechnology Information (NCBI) (<https://www.ncbi.nlm.nih.gov/bio-project>) under BioProject no. PRJNA1026168, and we use accession numbers to refer to the sequences.

### Antimicrobial Susceptibility Testing and Analysis

We performed antimicrobial susceptibility testing (AST) against gentamicin, ampicillin, ciprofloxacin, nalidixic acid, erythromycin, trimethoprim/sulfamethoxazole, and tetracycline on all human and poultry isolates as described by the EUCAST disk diffusion method (23,24). We used horse blood Mueller-Hinton agar supplemented with  $\beta$ -nicotinamide adenine dinucleotide (Fort Richard Laboratories) with microaerobic atmosphere (MACS VA500) at  $41^{\circ}\text{C}$  for 24  $\pm$  2 hours. We interpreted data according to EUCAST guidelines for *Campylobacter* for ciprofloxacin, erythromycin, and tetracycline; EUCAST guidelines for Enterobacterales for ampicillin, gentamicin, and trimethoprim/sulfamethoxazole; and Clinical and Laboratory Standards Institute guidelines for Enterobacterales for nalidixic acid (25). We displayed the frequencies of AMR phenotypes using UpSet plots in

R (The R Project for Statistical Computing, <https://www.r-project.com>) using the packages ComplexUpset and ComplexHeatmap (<https://github.com/krassowski/complex-upset>).

We evaluated estimates of the prevalence of AMR in human and poultry isolates, where the outcome of interest was defined as resistance to  $\geq 1$  (AMR) or  $\geq 3$  (multidrug resistance [MDR]) classes, using intercept-only Bayesian regression models with AMR and MDR as Bernoulli distributed response variables. We assumed isolates from humans were statistically independent. To account for nonindependence between multiple isolates from the same flock or bird, we randomly selected 1 isolate from each farm. We repeated this random selection to create 500 random datasets, then used those datasets to create a combined posterior distribution using the outputation method (26). We fitted models using the R package brms (27) using 4 chains with 2,000 iterations per chain for each of the 500 poultry datasets and  $1 \times 10^6$  iterations for the human dataset and a 50% burn in. To improve convergence and avoid overfitting, we specified mildly informative, conservative priors on the fixed effects (Normal [0, 5]). We describe results as mean prevalence estimates and mean differences in prevalence between poultry and human isolates with 95% credible intervals (CrIs).

### Genetic and Phylogenetic Analyses

We characterized all isolates according to their 7-gene sequence type (ST) and clonal complex (CC) by uploading contig fasta files to the PubMLST *Campylobacter* website (28). In addition, we identified genes and alleles associated with resistance using the Comprehensive Antibiotic Resistance Database (29) and customized scripts for extracting and aligning individual genes and detecting mutations associated with resistance.

We established cgMLST allele profiles by using the 1343 gene cgMLST scheme (30) and plotted them as a minimum spanning tree using the MSTree V2 algorithm in GrapeTree (31). We created a circular dendrogram based on single linkage clustering of isolates and their cgMLST profiles with metadata on the host, farm type, *Campylobacter* species, resistome, and AST using the Interactive Tree of Life online tool (32).

### Ethics Statement

This study was approved by the Tanzania National Institutes for Medical Research National Research Ethics Coordinating Committee, Kilimanjaro Christian Medical University College Research Ethics Committee, the Kenya Medical Research Institute

Scientific and Ethics Review Unit, the University of Otago Human Ethics Committee, and the University of Glasgow School of Veterinary Medicine Research Ethics Committee. The protocol for the source of the human isolates was approved by the Kenya Medical Research Institute Scientific and Ethics Review Committee (SSC protocol nos. 1899 and 2761). This activity was reviewed by CDC and was conducted consistent with applicable federal law and CDC policy as provided for in the Code of Federal Regulations (45 C.F.R part 46 and 21 C.F.R. part 56). Written informed consent was obtained from participants (or parent or guardian) before stool specimen collection.

## Results

### *Campylobacter* spp. Prevalence and Population Structure

We isolated *Campylobacter* spp. from 56 (8.6%) of 649 chicken cloacal swab specimens (Table). Differences in prevalence between farm types were not significant ( $\chi^2$  test at farm level  $p > 0.05$ ).

All isolates ( $n = 178$ ) were confirmed as *C. jejuni* or *C. coli* and used for WGS and AST, including 81 from patients with diarrhea (44 from Lwak and 37 from Kibera) and 97 from 56 poultry samples (15 singletons and 82 pairs of isolates from 41 birds from 33 farms). *C. coli* made up 6 (7.4%) of 81 human isolates and 18 (18.6%) of 97 poultry isolates. The remaining isolates were *C. jejuni*.

We identified 11 *C. coli* STs and 67 *C. jejuni* STs, including 57 STs from patients with diarrhea and 29 STs in poultry samples. The most common STs were *C. jejuni* ST353 (4 human and 10 poultry isolates from 6 farms), ST2122 (10 poultry isolates from 4 farms), and ST1932 (9 poultry isolates from 5 farms), and *C. coli* ST8043 (11 poultry isolates from 5 farms), each of which comprised  $< 6.2\%$  of the isolate collection. The most common CCs were CC353 (7 human and 20 poultry isolates), CC354 (7 human and 4 poultry

isolates), and CC828 (6 human and 5 poultry isolates). Human and poultry isolates were distributed around the minimum spanning tree showing the population structure according to cgMLST (Figure 2); some clusters represented 7-gene CC or ST derived from mixed host populations and others associated with a single host (e.g., CC257, CC460/ST1932, ST2122, and ST8043 in poultry; CC45 and CC403 in humans).

By cgMLST, isolates were largely clustered according to their STs and CCs, with some exceptions. For example, *C. jejuni* CC49 isolates clustered in 2 distinct clades; 1 included ST479 and ST10922 and 1 included ST3720 and ST4624. Further, most isolates belonging to *C. jejuni* CC353 clustered together, with the exception of 1 isolate belonging to ST1036. The most closely related human and poultry isolates differed by 53 alleles on the basis of cgMLST; all were identified as ST362 based on 7-gene MLST.

At the time of writing, 22 (12.4%) isolates belonged to STs that were unique to this study (ST numbers 10893 and above). Three (1.7%) were *C. coli* isolates from CC828 and the remainder were *C. jejuni* (Appendix Tables 1, 2).

Of the 29 STs from poultry samples, 9 (31%) were identified on multiple farms (e.g., ST353 on 6 [9.1%] farms, ST1932 and ST8043 on 5 [7.6%] farms each, and ST2122 on 4 [4.5%] farms) (Figure 3). ST353, ST1932, and ST2122 were identified in Arusha and Moshi, whereas ST8043 was only identified in Moshi. For isolates belonging to the same ST, the median pairwise allele difference between isolates from the same farm on the basis of cgMLST was 46 (interquartile range [IQR] 38–59.75, range 15–230), whereas the median pairwise allele difference between isolates from different farms was 167 (IQR 102.5–245, range 24–497).

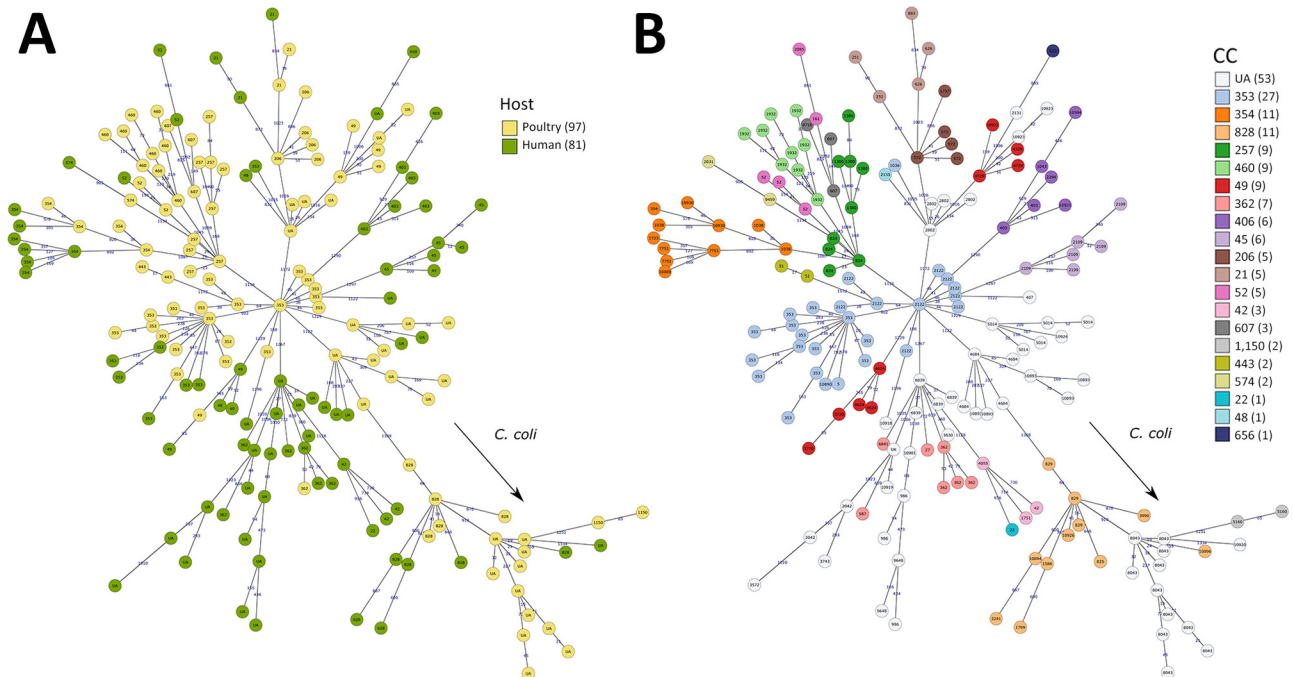
### Antimicrobial Resistance

AMR was detected in 75.3% (95% CrI 65.4–83.9%) and MDR was detected in 2.5% (95% CrI 0.3–6.8%) of 81 human isolates, and the point estimates of prevalence were similar in both regions (75.7% in Kibera and 75.0% in Lwak for AMR and 2.7% in Kibera and 2.3% in Lwak for MDR). No evidence of a trend in resistance in human isolates over the period of collection was seen. In poultry, the crude estimate of AMR prevalence was 85.7% of 97 poultry isolates from 87.5% of 56 poultry samples. The crude estimate of MDR prevalence was 40.2% of 97 poultry isolates from 44.6% of 56 poultry samples. After allowing for clustering of isolates within farms, the estimated prevalence in poultry was 85.4% (95% CrI 70.6–95.8%) for AMR and 43.1% (95% CrI 25.6%–61.4%) for MDR. The estimated difference between poultry and humans was

**Table.** Prevalence of *Campylobacter* spp. in poultry by region and production type, Tanzania, 2016–2017\*

Characteristic	Farm-level prevalence		
	Prevalence, %	No. positive	No. sampled
Region			
Arusha City	42.3	11	26
Moshi Municipal	55.0	22	40
Production type			
Extensive	37.5	6	16
Semi-intensive	43.8	7	16
Intensive indigenous	72.2	13	18
Intensive broiler	43.8	7	16

\*There were no significant differences in prevalence between regions and production types ( $\chi^2$  test  $p > 0.6$  for both contingency tables).



**Figure 2.** Minimum spanning tree population structure of *Campylobacter jejuni* and *C. coli* isolated from humans with diarrhea and from poultry from Kenya and Tanzania, 2006–2017 (human) or 2016–2017 (poultry), based on core genome multilocus sequence types profiles. A) Plot colored by host (human or poultry) with CC indicated in each node; B) plot colored by CC with sequence type indicated in each node. Core-genome multilocus sequence type allele differences are indicated on each branch. CC, clonal complex; UA, unassigned.

nonsignificant for AMR (10.1% [95% CrI –7.0% to 24.8%, including 0]), but significant for MDR (40.6% [95% CrI 22.7%–59.1%, excluding 0]).

The most resistant isolates were resistant to 5 of the 6 classes of antimicrobial drugs tested. That phenotype was observed in 5 isolates from 3 birds from 2 farms, an intensive indigenous farm and a broiler farm, and all were *C. coli* belonging to ST8043.

The distribution of AST profiles differed between human and poultry isolates; 6 of the 9 MDR profiles were only found in poultry, and of the 5 most common resistance profiles among poultry isolates, only 1 was also detected in human isolates (Figure 4). The most common AMR profile in human isolates was resistance to trimethoprim/sulfamethoxazole, whereas the most common profile in poultry isolates was resistance to ciprofloxacin, nalidixic acid, trimethoprim/sulfamethoxazole, and tetracycline. Of the 41 birds with 2 isolates, 36 (87.8%) had pairs of isolates with identical AST profiles (Figure 5). All isolates were susceptible to gentamicin.

#### Relationship among AST, Genotype, and Host

The relationship among the population structure, as determined by single linkage clustering of cgMLST profiles, and other epidemiologic, genotypic, and phenotypic variables was displayed as a circular

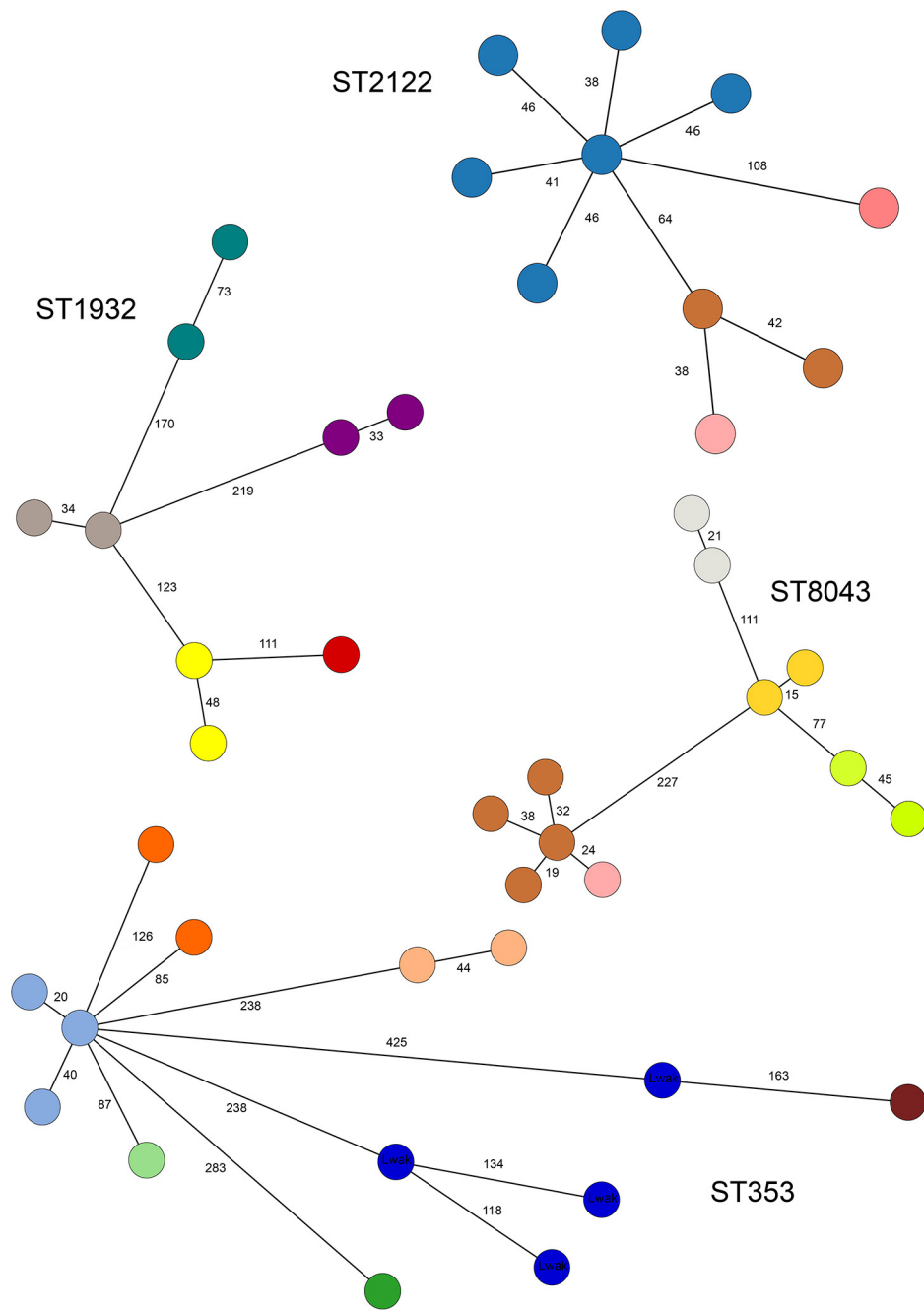
dendrogram (Figure 5). We observed near-complete concordance between the genomically derived resistome and AST phenotypes associated with fluoroquinolone, macrolide, and tetracycline resistance. All isolates that were resistant to ciprofloxacin and nalidixic acid carried the C257T mutation, associated with fluoroquinolone resistance in the *gyrA* gene. Similarly, we observed complete concordance between the presence of the A2075G mutation in the 23S rRNA gene, associated with macrolide resistance and resistance to erythromycin. Tetracycline resistance was found in all isolates with the *tetO* gene, with the exception of isolate ZLB391b. In contrast, agreement was relatively poor between the presence of the  $\beta$ -lactamase-encoding gene *bla*<sub>OXA</sub> and ampicillin resistance, and no isolates with genes associated with aminoglycoside resistance were resistant to gentamicin.

#### Discussion

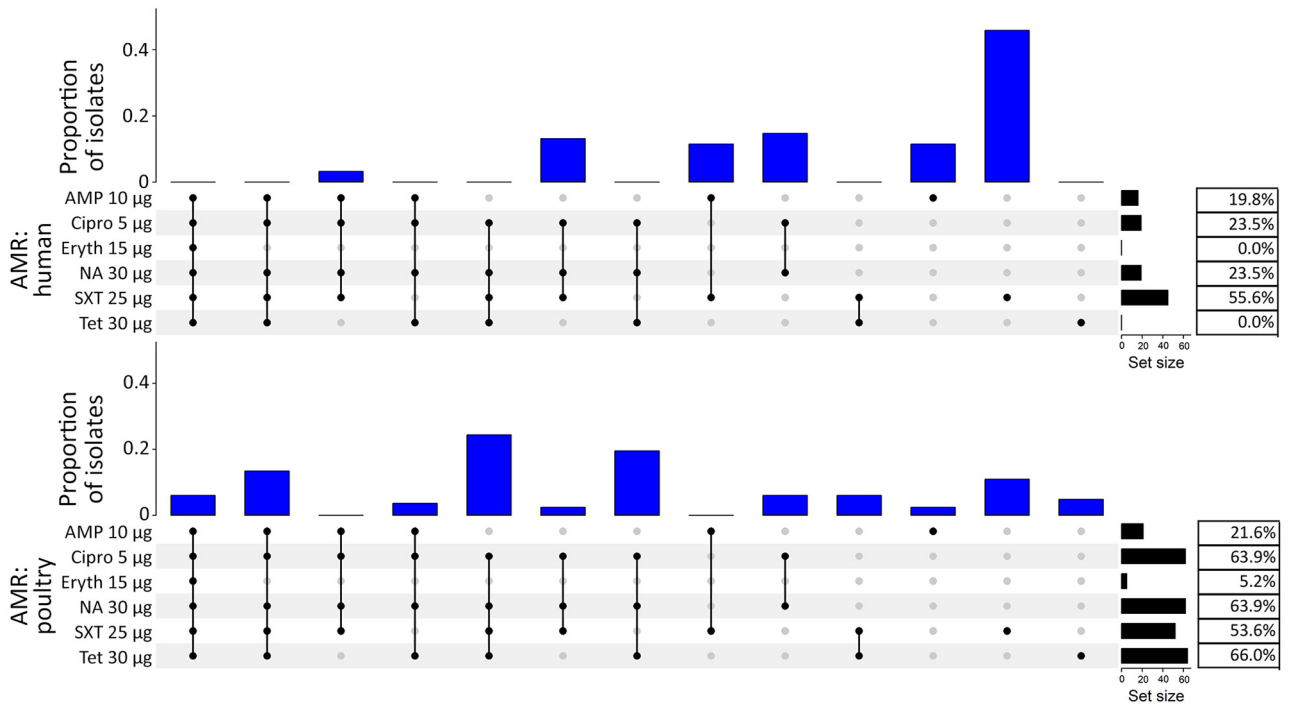
This study provides a detailed description of the population structure of *Campylobacter* spp. isolated from clinically healthy poultry and persons with diarrhea in East Africa and associations with AMR phenotypes, genes, and alleles. Key findings include evidence of a relatively high prevalence of AMR (>75%) in both human and poultry isolates and a higher prevalence of MDR in isolates from poultry

than in those from humans. Further, considerable genetic heterogeneity within and between human and poultry *Campylobacter* isolates and many previously unreported STs were observed. The absence of dominant STs is in contrast to findings for nontyphoidal *Salmonella* collected from the same region over the same time period where 2 STs include almost two thirds of human diarrhea-derived isolates and 4 STs account for more than three quarters of poultry-derived isolates (19).

Earlier studies conducted in Tanzania estimated a similarly high farm-level prevalence of *Campylobacter* in poultry and also provided evidence of a higher prevalence of *C. jejuni* than *C. coli* and a higher prevalence in free-range chicken than in broilers (10,33). Those Tanzania studies did not examine AMR or sequence data. In contrast, a study conducted in Botswana showed evidence of a relatively higher prevalence of *C. coli* than *C. jejuni* in broilers compared with free-range poultry (16), and a higher



**Figure 3.** Minimum spanning tree of core-genome multilocus sequence types profiles from the 4 most prevalent 7-gene multilocus sequence type–based ST isolated from poultry in Tanzania, 2016–2017, in a study of *Campylobacter jejuni* and *C. coli*, East Africa. Each color represents a different farm, with the exception of 4 ST353 isolates from human cases (dark blue). Core genome multilocus sequence type allele differences are indicated on each branch. The 2 pairs of isolates from different farms with the lowest number of allele differences, belonging to ST8043 (24 allele differences) and ST2122 (38 allele differences) (shown in brown and light pink) were from 2 farms in the same location in Luongo, Moshi. One was an intensive indigenous farm (light pink isolates), and the other was an intensive broiler farm (brown isolates). ST, sequence type.



**Figure 4.** Distribution of different combinations of AMR in *Campylobacter jejuni* and *C. coli* human isolates from Kenya (top, n = 81) and poultry isolates from Tanzania (bottom, n = 97) in study of population structure and AMR in *C. jejuni* and *C. coli* isolated from humans with diarrhea and from poultry, East Africa, 2006–2017. The percentage of isolates resistant to each antimicrobial is given in the table to the right of each plot. All isolates were susceptible to gentamicin. The histogram represents proportion of isolates by antimicrobial resistance pattern. Black dots represent AMR and gray dots represent absence of AMR to the specific antimicrobial agent listed. Black lines join black dots to visualize patterns of AMR. AMP, ampicillin; AMR, antimicrobial resistance; Cipro, ciprofloxacin; Eryth, erythromycin; NA, nalidixic acid; SXT, trimethoprim/sulfamethoxazole; Tet, tetracycline.

prevalence of AMR was observed in *C. coli* than in *C. jejuni*. In common with our Tanzania study, the Botswana study used WGS and included 3 isolates belonging to *C. coli* ST8043, all of which carried *tetO* and *bla<sub>OXA</sub>* genes; 1 had the *gyrA* C257T mutation encoding for quinolone resistance. Both in our study and in the study from Botswana, some STs were shared between humans and poultry, suggesting the possibility of interspecies transmission as also observed for certain types of nontyphoidal *Salmonella* (19). However, both studies were population-level studies, and analysis of epidemiologically linked isolates (e.g., from humans and animals within the same household or farm, or from poultry meat and its handlers and consumers) would be needed to generate direct evidence of interspecies transmission.

Comparison of the cgMLST allele differences within and between poultry farms showed greater similarity of isolates within farms compared with between farms, consistent with lower between-farm transmission than within-farm transmission. However, the 2 pairs of isolates from different farms with the lowest number of allele differences, belonging to ST8043 (24 allele differences) and ST2122 (38

allele differences) (Figure 3), were from 2 farms in the same location in Luongo, Moshi. Of those farms, 1 was an intensive indigenous farm and the other an intensive broiler farm. This finding is consistent with local spread or spread from a common source, such as shared equipment, inputs, or the environment (34), underlining the importance of biosecurity for preventing the spread of foodborne pathogens and AMR within the poultry sector.

Other studies of potential sources of human campylobacteriosis in Tanzania include *C. jejuni* and *C. coli* in duck intestinal contents (35), pig fecal samples (36), and beef carcasses and raw milk (37). In the study of beef carcasses and raw milk, prevalence of AMR was similar to that observed in poultry in our study.

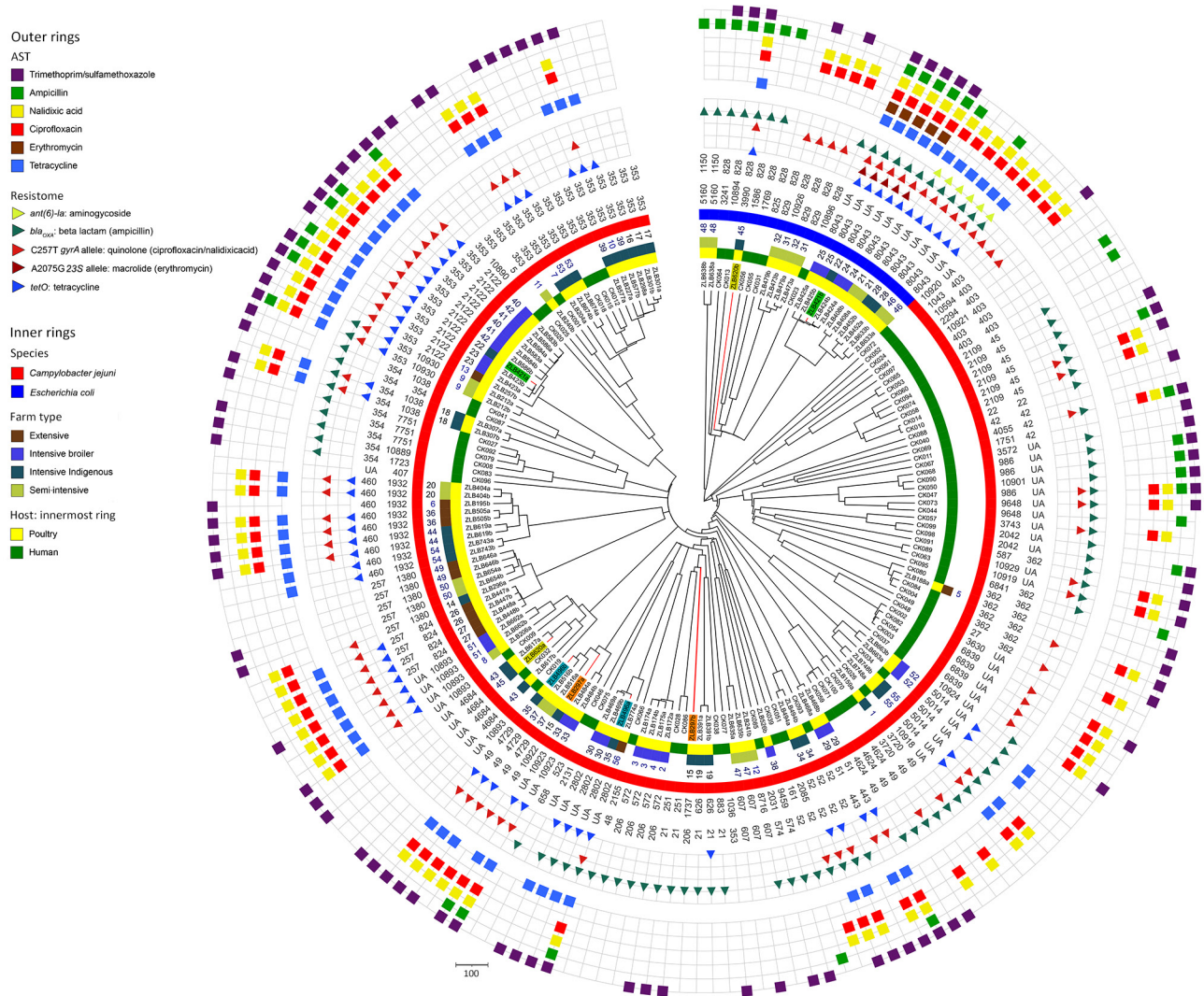
Few studies have reported MDR prevalence estimates in human isolates in Kenya. However, 1 review (6) indicates a low prevalence of AMR in human isolates across multiple antimicrobials, similar to other countries in Africa and this study. By inference from individual AMR prevalence estimates, MDR in *C. jejuni* in Kenya was at most ≈10% (6).

Of the 78 STs identified in this study, 27 have been isolated from other countries in Africa and

recorded on PubMLST. Those isolates include the most prevalent STs: ST353, which has also been isolated from Malawi, and ST1932 and ST8043, which have been isolated from Botswana (Appendix Table 2).

With the exception of  $\beta$ -lactams and aminoglycosides, the resistome was strongly correlated with the AST results; the *tetO* gene was associated with tetracycline resistance (38), the C257T mutation in *gyrA* was associated with fluoroquinolone resistance (39), and the A2075G mutation in the 23S rRNA was associated

with macrolide resistance (40). The A2075G mutation in the 23S rRNA (*E. coli* equivalent base 2058) was observed only in *C. coli* isolates in this study, which is consistent with other international studies (40). The relatively high prevalence of tetracycline and fluoroquinolone resistance in human or poultry isolates might be the result of selection pressure resulting from the widespread use of these antimicrobials in humans, food production, or both. A recent study in Dar es Salaam, Tanzania, indicated widespread use



**Figure 5.** Circular dendrogram showing, from outer to inner rings, AST in study of population structure and antimicrobial resistance in *Campylobacter jejuni* and *C. coli* isolated from humans with diarrhea and from poultry, East Africa, 2006–2017. Colored blocks indicate resistance (all isolates were susceptible to gentamicin so this ring is not included), resistome, clonal complex (CC), sequence type (ST), *Campylobacter* species, poultry sample number, farm type, host and isolate ID for isolates from Kenya and Tanzania, 2006–2017 (human) or 2016–2017 (poultry). Isolates from the same poultry sample that belonged to a different ST are highlighted (samples 15, 22, 35, and 45) using colored isolate identification labels. The resistome indicates detection of resistance genes (encoding for resistance to some aminoglycosides,  $\beta$ -lactam antimicrobials and tetracyclines) and alleles (encoding for resistance for fluoroquinolones in the gyrase A gene, and macrolides in the 23S rRNA gene). Clustering of antimicrobial resistance phenotypes and the resistome with some CCs and STs is evident. For example, multidrug resistance is observed in *C. jejuni* ST2122 and *C. coli* ST8043 isolates. Scale bar indicates number of core-genome multilocus-sequence typing allele differences. AST, antimicrobial sensitivity.

of both tetracyclines and fluoroquinolones in poultry and cattle production; >40% of farmers surveyed were not compliant with drug withdrawal periods (41). Evidence of noncompliance with withdrawal periods was also reported in a study of commercial small-holder egg producers in Morogoro, Tanzania (42). In human medicine, evidence exists of wide availability and sale of fluoroquinolones in authorized and unauthorized drug outlets. More than 70% of pharmacists surveyed reported dispensing antimicrobial drugs without a prescription, including penicillins, macrolides, and fluoroquinolones (43).

Our study had relatively low power to detect associations between epidemiologic variables and AMR and did not assess all transmission pathways. In addition, human diarrheal isolates were sourced from a wider temporal range (2006–2016) than poultry isolates (2016–2017), and isolates were co-located at regional rather than village or household level. However, although the human isolates were from a different country to the poultry isolates, it is worth noting that Nairobi is 272 km by road from Arusha and 326 km from Moshi, closer than other locations in Tanzania with human *Campylobacter* isolates potentially available for sequencing. Chicken production systems are largely similar across East Africa, including flock sizes and extensive, semi-intensive and intensive management systems between Kenya and Tanzania (44).

In conclusion, this study provides a detailed examination of the population structure of isolates of *C. jejuni* and *C. coli* in a region of East Africa. Although this study was smaller than similar studies conducted in high-income countries (13), it is one of the largest studies using WGS to characterize *Campylobacter* spp. isolates in Africa and has generated several valuable insights. The study showed a striking diversity of *Campylobacter* in both humans and poultry, with some STs common to multiple farms or to humans and poultry. AMR was highly prevalent, particularly to tetracyclines, fluoroquinolones, or sulphonamides, and MDR was prevalent in a high proportion of poultry compared with human isolates. The high prevalence of MDR and the identification of previously undescribed STs highlights the need for ongoing investigation of enteric pathogens, such as *Campylobacter* spp., in low-resource settings. That effort would require genomic tools to be embedded within formal and transparent surveillance systems, in addition to a greater understanding of the role of antimicrobial use and biosecurity measures as drivers of the emergence of resistance in human health and food production and improved governance of antimicrobial use in both sectors.

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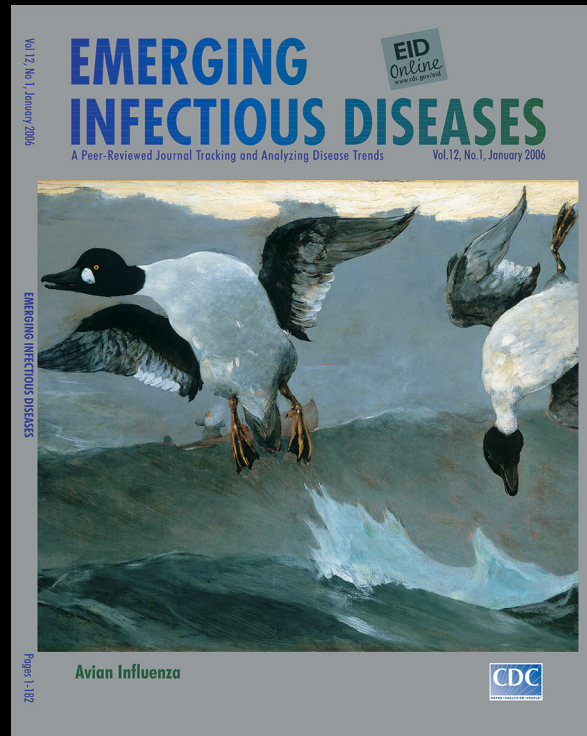
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# Population Structure and Antimicrobial Resistance in *Campylobacter jejuni* and *C. coli* Isolated from Humans with Diarrhea and from Poultry, East Africa

## Appendix

### **Further details of the methods used for culture and isolation.**

For poultry samples swab tips were enriched in 20mL Bolton broth, supplemented with 5% horse blood (TCS Biosciences, Botolph Claydon, UK) and selective supplement SR0208E (Oxoid, Basingstoke, UK). After 48 h incubation in a micro-aerophilic atmosphere (CampyGen; Oxoid), enrichments were plated on modified charcoal cefoperazone deoxycholate agar (mCCDA; Oxoid) and incubated for 48 h micro-aerophilically.

For human samples whole stool samples were swabbed and transported to the Enterics laboratory in Caryblair Transport media. In the lab, the swabs were inoculated on *Campylobacter* agar medium plates (CM0935, Oxoid) with supplement (SR0167, Oxoid) using standard microbiology procedures and incubated at 42°C for 48 hours under microaerophilic conditions. Colonies with typical morphology of *Campylobacter* were examined microscopically and confirmed biochemically by oxidase and hippurate hydrolysis tests.

**Appendix Table 1.** Isolate details showing the sample date, *Campylobacter* species, host, 7-gene MLST Sequence Type (ST) and Clonal Complex (CC), poultry sample number, poultry farm type and location. UA indicates the ST has not been assigned to a Clonal Complex.

ID no.	Sample date	species	Host	ST	CC	Poultry sample no.	Poultry farm type	Location	Accession
CK001	11/05/2011	<i>C. jejuni</i>	Human	353	353	NA	NA	Lwak	SRX22036608
CK002	29/05/2012	<i>C. jejuni</i>	Human	6839	UA	NA	NA	Lwak	SRX22036609
CK003	19/08/2011	<i>C. jejuni</i>	Human	6839	UA	NA	NA	Lwak	SRX22036762
CK004	9/08/2011	<i>C. jejuni</i>	Human	362	362	NA	NA	Lwak	SRX22036613
CK008	14/11/2013	<i>C. jejuni</i>	Human	10889	354	NA	NA	Lwak	SRX22036624
CK009	20/11/2013	<i>C. jejuni</i>	Human	10893	UA	NA	NA	Lwak	SRX22036635
CK010	10/10/2013	<i>C. jejuni</i>	Human	2109	45	NA	NA	Lwak	SRX22036710
CK011	17/02/2014	<i>C. jejuni</i>	Human	1751	42	NA	NA	Lwak	SRX22036721
CK012	10/03/2014	<i>C. jejuni</i>	Human	353	353	NA	NA	Lwak	SRX22036732
CK013	17/03/2014	<i>C. coli</i>	Human	10894	828	NA	NA	Lwak	SRX22036775
CK014	18/03/2014	<i>C. jejuni</i>	Human	2109	45	NA	NA	Lwak	SRX22036610
CK015	27/11/2014	<i>C. jejuni</i>	Human	353	353	NA	NA	Lwak	SRX22036653
CK018	14/04/2010	<i>C. jejuni</i>	Human	353	353	NA	NA	Lwak	SRX22036664
CK019	27/01/2016	<i>C. jejuni</i>	Human	10893	UA	NA	NA	Lwak	SRX22036675
CK020	14/09/2015	<i>C. jejuni</i>	Human	10890	353	NA	NA	Lwak	SRX22036686
CK023	10/06/2014	<i>C. coli</i>	Human	10896	828	NA	NA	Lwak	SRX22036697
CK024	7/11/2014	<i>C. jejuni</i>	Human	10594	403	NA	NA	Lwak	SRX22036740
CK025	27/11/2012	<i>C. jejuni</i>	Human	5	353	NA	NA	Lwak	SRX22036751
CK026	16/01/2014	<i>C. jejuni</i>	Human	10918	UA	NA	NA	Lwak	SRX22036760
CK027	6/12/2013	<i>C. jejuni</i>	Human	7751	354	NA	NA	Lwak	SRX22036761
CK028	26/11/2012	<i>C. jejuni</i>	Human	251	21	NA	NA	Lwak	SRX22036763
CK031	6/11/2012	<i>C. coli</i>	Human	825	828	NA	NA	Lwak	SRX22036764
CK032	6/06/2012	<i>C. jejuni</i>	Human	4684	UA	NA	NA	Lwak	SRX22036765
CK034	23/10/2014	<i>C. jejuni</i>	Human	5014	UA	NA	NA	Lwak	SRX22036766
CK037	21/01/2016	<i>C. jejuni</i>	Human	10924	UA	NA	NA	Lwak	SRX22036767
CK038	22/01/2016	<i>C. jejuni</i>	Human	883	21	NA	NA	Lwak	SRX22036768
CK039	21/03/2016	<i>C. jejuni</i>	Human	161	52	NA	NA	Lwak	SRX22036769
CK040	19/10/2012	<i>C. jejuni</i>	Human	42	42	NA	NA	Lwak	SRX22036770
CK041	22/03/2016	<i>C. jejuni</i>	Human	1038	354	NA	NA	Lwak	SRX22036771
CK044	27/06/2013	<i>C. jejuni</i>	Human	9648	UA	NA	NA	Lwak	SRX22036612
CK046	1/12/2014	<i>C. jejuni</i>	Human	523	658	NA	NA	Lwak	SRX22036614
CK047	9/12/2013	<i>C. jejuni</i>	Human	986	UA	NA	NA	Kibera	SRX22036615
CK048	15/01/2014	<i>C. jejuni</i>	Human	3630	UA	NA	NA	Kibera	SRX22036616
CK049	5/05/2014	<i>C. jejuni</i>	Human	27	362	NA	NA	Kibera	SRX22036617
CK050	3/06/2014	<i>C. jejuni</i>	Human	10901	UA	NA	NA	Kibera	SRX22036618
CK051	3/06/2014	<i>C. jejuni</i>	Human	2085	52	NA	NA	Kibera	SRX22036619
CK052	24/05/2014	<i>C. jejuni</i>	Human	1043	403	NA	NA	Kibera	SRX22036620
CK053	7/05/2008	<i>C. jejuni</i>	Human	403	403	NA	NA	Kibera	SRX22036621
CK054	24/07/2008	<i>C. jejuni</i>	Human	6839	UA	NA	NA	Kibera	SRX22036622
CK055	14/01/2011	<i>C. coli</i>	Human	1769	828	NA	NA	Kibera	SRX22036623
CK056	8/09/2010	<i>C. coli</i>	Human	1586	828	NA	NA	Lwak	SRX22036625
CK057	3/07/2007	<i>C. jejuni</i>	Human	3743	UA	NA	NA	Kibera	SRX22036626
CK058	10/03/2009	<i>C. jejuni</i>	Human	2109	45	NA	NA	Kibera	SRX22036627
CK059	30/01/2009	<i>C. jejuni</i>	Human	4624	49	NA	NA	Kibera	SRX22036628
CK060		<i>C. jejuni</i>	Human	2109	45	NA	NA	Kibera	SRX22036629
CK061	20/06/2008	<i>C. jejuni</i>	Human	2294	403	NA	NA	Kibera	SRX22036630
CK063	19/11/2008	<i>C. jejuni</i>	Human	10919	UA	NA	NA	Kibera	SRX22036631
CK064	27/01/2009	<i>C. coli</i>	Human	3241	828	NA	NA	Kibera	SRX22036632
CK065	6/02/2009	<i>C. jejuni</i>	Human	403	403	NA	NA	Kibera	SRX22036633
CK066	14/01/2009	<i>C. jejuni</i>	Human	2155	48	NA	NA	Lwak	SRX22036634
CK067	8/07/2008	<i>C. jejuni</i>	Human	3572	UA	NA	NA	Kibera	SRX22036636
CK068	27/09/2008	<i>C. jejuni</i>	Human	986	UA	NA	NA	Kibera	SRX22036637
CK069	1/08/2008	<i>C. jejuni</i>	Human	4055	42	NA	NA	Lwak	SRX22036638
CK070	11/11/2008	<i>C. jejuni</i>	Human	3720	49	NA	NA	Kibera	SRX22036639
CK071	18/03/2009	<i>C. jejuni</i>	Human	4624	49	NA	NA	Kibera	SRX22036640
CK072	18/03/2009	<i>C. jejuni</i>	Human	10920	UA	NA	NA	Kibera	SRX22036641
CK073	11/03/2008	<i>C. jejuni</i>	Human	9648	UA	NA	NA	Kibera	SRX22036642
CK074	21/01/2009	<i>C. jejuni</i>	Human	2109	45	NA	NA	Kibera	SRX22036643
CK075	3/03/2009	<i>C. jejuni</i>	Human	2131	UA	NA	NA	Kibera	SRX22036708
CK077	21/03/2011	<i>C. jejuni</i>	Human	1036	353	NA	NA	Lwak	SRX22036709
CK079	11/08/2010	<i>C. jejuni</i>	Human	7751	354	NA	NA	Lwak	SRX22036711

ID no.	Sample date	species	Host	ST	CC	Poultry sample no.	Poultry farm type	Location	Accession
CK080	6/08/2010	<i>C. jejuni</i>	Human	362	362	NA	NA	Lwak	SRX22036712
CK082	16/03/2011	<i>C. jejuni</i>	Human	6839	UA	NA	NA	Lwak	SRX22036713
CK083		<i>C. jejuni</i>	Human	1723	354	NA	NA	Kibera	SRX22036714
CK084	5/01/2011	<i>C. jejuni</i>	Human	362	362	NA	NA	Lwak	SRX22036715
CK085	8/06/2010	<i>C. jejuni</i>	Human	2031	574	NA	NA	Lwak	SRX22036716
CK086	18/02/2011	<i>C. jejuni</i>	Human	251	21	NA	NA	Lwak	SRX22036717
CK087	8/06/2010	<i>C. jejuni</i>	Human	354	354	NA	NA	Lwak	SRX22036718
CK088	22/06/2010	<i>C. jejuni</i>	Human	22	22	NA	NA	Lwak	SRX22036719
CK089	1/12/2008	<i>C. jejuni</i>	Human	10929	UA	NA	NA	Kibera	SRX22036720
CK090	17/09/2008	<i>C. jejuni</i>	Human	986	UA	NA	NA	Kibera	SRX22036722
CK091	25/11/2008	<i>C. jejuni</i>	Human	587	362	NA	NA	Kibera	SRX22036723
CK092	10/03/2009	<i>C. jejuni</i>	Human	7751	354	NA	NA	Lwak	SRX22036724
CK093	14/12/2006	<i>C. jejuni</i>	Human	52	52	NA	NA	Kibera	SRX22036725
CK094	16/02/2007	<i>C. jejuni</i>	Human	2109	45	NA	NA	Kibera	SRX22036726
CK095	14/03/2009	<i>C. jejuni</i>	Human	6841	362	NA	NA	Kibera	SRX22036727
CK096	13/03/2009	<i>C. jejuni</i>	Human	407	UA	NA	NA	Kibera	SRX22036728
CK097	26/01/2010	<i>C. jejuni</i>	Human	10921	403	NA	NA	Kibera	SRX22036729
CK098	8/10/2008	<i>C. jejuni</i>	Human	2042	UA	NA	NA	Kibera	SRX22036730
CK099	24/05/2007	<i>C. jejuni</i>	Human	2042	UA	NA	NA	Kibera	SRX22036731
CK100	16/10/2008	<i>C. jejuni</i>	Human	4624	49	NA	NA	Kibera	SRX22036733
ZLB159a	10/10/2016	<i>C. jejuni</i>	Poultry	3720	49	1	Intensive Indigenous	Arusha	SRX22036734
ZLB172a	10/10/2016	<i>C. jejuni</i>	Poultry	572	206	2	Intensive broiler	Arusha	SRX22036735
ZLB174a	10/10/2016	<i>C. jejuni</i>	Poultry	572	206	3	Intensive broiler	Arusha	SRX22036736
ZLB174b	10/10/2016	<i>C. jejuni</i>	Poultry	572	206	3	Intensive broiler	Arusha	SRX22036737
ZLB175a	10/10/2016	<i>C. jejuni</i>	Poultry	572	206	4	Intensive broiler	Arusha	SRX22036738
ZLB188a	17/10/2016	<i>C. jejuni</i>	Poultry	362	362	5	Extensive	Arusha	SRX22036739
ZLB195b	17/10/2016	<i>C. jejuni</i>	Poultry	1932	460	6	Extensive	Arusha	SRX22036772
ZLB204a	17/10/2016	<i>C. jejuni</i>	Poultry	353	353	7	Intensive Indigenous	Arusha	SRX22036773
ZLB206a	17/10/2016	<i>C. jejuni</i>	Poultry	10893	UA	8	Semi intensive	Arusha	SRX22036774
ZLB212a	17/10/2016	<i>C. jejuni</i>	Poultry	10930	354	9	Semi intensive	Arusha	SRX22036776
ZLB212b	17/10/2016	<i>C. jejuni</i>	Poultry	10930	354	9	Semi intensive	Arusha	SRX22036777
ZLB227a	24/10/2016	<i>C. jejuni</i>	Poultry	353	353	10	Intensive Indigenous	Arusha	SRX22036778
ZLB240b	24/10/2016	<i>C. jejuni</i>	Poultry	353	353	11	Semi intensive	Arusha	SRX22036779
ZLB241b	24/10/2016	<i>C. jejuni</i>	Poultry	8716	607	12	Semi intensive	Arusha	SRX22036780
ZLB257b	24/10/2016	<i>C. jejuni</i>	Poultry	2122	353	13	Extensive	Arusha	SRX22036781
ZLB296a	14/11/2016	<i>C. jejuni</i>	Poultry	1380	257	14	Intensive Indigenous	Arusha	SRX22036782
ZLB297a	14/11/2016	<i>C. jejuni</i>	Poultry	10922	49	15	Intensive Indigenous	Arusha	SRX22036783
ZLB297b	14/11/2016	<i>C. jejuni</i>	Poultry	1737	206	15	Intensive Indigenous	Arusha	SRX22036784
ZLB298a	14/11/2016	<i>C. jejuni</i>	Poultry	353	353	16	Intensive Indigenous	Arusha	SRX22036785
ZLB301a	14/11/2016	<i>C. jejuni</i>	Poultry	353	353	17	Intensive Indigenous	Arusha	SRX22036611
ZLB301b	14/11/2016	<i>C. jejuni</i>	Poultry	353	353	17	Intensive Indigenous	Arusha	SRX22036644
ZLB307a	21/11/2016	<i>C. jejuni</i>	Poultry	1038	354	18	Intensive Indigenous	Arusha	SRX22036645
ZLB307b	21/11/2016	<i>C. jejuni</i>	Poultry	1038	354	18	Intensive Indigenous	Arusha	SRX22036646
ZLB391a	5/12/2016	<i>C. jejuni</i>	Poultry	626	21	19	Intensive Indigenous	Arusha	SRX22036647
ZLB391b	5/12/2016	<i>C. jejuni</i>	Poultry	626	21	19	Intensive Indigenous	Arusha	SRX22036648
ZLB404a	9/04/2017	<i>C. jejuni</i>	Poultry	1932	460	20	Semi intensive	Moshi	SRX22036649
ZLB404b	9/04/2017	<i>C. jejuni</i>	Poultry	1932	460	20	Semi intensive	Moshi	SRX22036650
ZLB408a	9/04/2017	<i>C. coli</i>	Poultry	8043	UA	21	Semi intensive	Moshi	SRX22036651
ZLB408b	9/04/2017	<i>C. coli</i>	Poultry	8043	UA	21	Semi intensive	Moshi	SRX22036652
ZLB421a	9/04/2017	<i>C. jejuni</i>	Poultry	2122	353	22	Intensive Indigenous	Moshi	SRX22036654

ID no.	Sample date	species	Host	ST	CC	Poultry sample no.	Poultry farm type	Location	Accession
ZLB421b	9/04/2017	<i>C. coli</i>	Poultry	8043	UA	22	Intensive Indigenous	Moshi	SRX22036655
ZLB423a	9/04/2017	<i>C. jejuni</i>	Poultry	2122	353	23	Intensive broiler	Moshi	SRX22036656
ZLB423b	9/04/2017	<i>C. jejuni</i>	Poultry	2122	353	23	Intensive broiler	Moshi	SRX22036657
ZLB424a	9/04/2017	<i>C. coli</i>	Poultry	8043	UA	24	Intensive broiler	Moshi	SRX22036658
ZLB424b	9/04/2017	<i>C. coli</i>	Poultry	8043	UA	24	Intensive broiler	Moshi	SRX22036659
ZLB425a	9/04/2017	<i>C. coli</i>	Poultry	8043	UA	25	Intensive broiler	Moshi	SRX22036660
ZLB425b	9/04/2017	<i>C. coli</i>	Poultry	8043	UA	25	Intensive broiler	Moshi	SRX22036661
ZLB447a	15/05/2017	<i>C. jejuni</i>	Poultry	824	257	26	Extensive	Moshi	SRX22036662
ZLB447b	15/05/2017	<i>C. jejuni</i>	Poultry	824	257	26	Extensive	Moshi	SRX22036663
ZLB448a	15/05/2017	<i>C. jejuni</i>	Poultry	824	257	27	Extensive	Moshi	SRX22036665
ZLB448b	15/05/2017	<i>C. jejuni</i>	Poultry	824	257	27	Extensive	Moshi	SRX22036666
ZLB452a	15/05/2017	<i>C. coli</i>	Poultry	8043	UA	28	Intensive Indigenous	Moshi	SRX22036667
ZLB452b	15/05/2017	<i>C. coli</i>	Poultry	8043	UA	28	Intensive Indigenous	Moshi	SRX22036668
ZLB468a	15/05/2017	<i>C. jejuni</i>	Poultry	51	443	29	Intensive broiler	Moshi	SRX22036669
ZLB468b	15/05/2017	<i>C. jejuni</i>	Poultry	51	443	29	Intensive broiler	Moshi	SRX22036670
ZLB469a	15/05/2017	<i>C. jejuni</i>	Poultry	2802	UA	30	Intensive broiler	Moshi	SRX22036671
ZLB469b	15/05/2017	<i>C. jejuni</i>	Poultry	2802	UA	30	Intensive broiler	Moshi	SRX22036672
ZLB473a	15/05/2017	<i>C. coli</i>	Poultry	829	828	31	Semi intensive	Moshi	SRX22036673
ZLB473b	15/05/2017	<i>C. coli</i>	Poultry	10926	828	31	Semi intensive	Moshi	SRX22036674
ZLB479a	15/05/2017	<i>C. coli</i>	Poultry	829	828	32	Semi intensive	Moshi	SRX22036676
ZLB479b	15/05/2017	<i>C. coli</i>	Poultry	829	828	32	Semi intensive	Moshi	SRX22036677
ZLB484a	22/05/2017	<i>C. jejuni</i>	Poultry	10923	UA	33	Intensive broiler	Moshi	SRX22036678
ZLB484b	22/05/2017	<i>C. jejuni</i>	Poultry	10923	UA	33	Intensive broiler	Moshi	SRX22036679
ZLB494a	22/05/2017	<i>C. jejuni</i>	Poultry	52	52	34	Intensive Indigenous	Moshi	SRX22036680
ZLB494b	22/05/2017	<i>C. jejuni</i>	Poultry	52	52	34	Intensive Indigenous	Moshi	SRX22036681
ZLB496a	22/05/2017	<i>C. jejuni</i>	Poultry	2802	UA	35	Intensive Indigenous	Moshi	SRX22036682
ZLB496b	22/05/2017	<i>C. jejuni</i>	Poultry	4729	49	35	Intensive Indigenous	Moshi	SRX22036683
ZLB505a	22/05/2017	<i>C. jejuni</i>	Poultry	1932	460	36	Extensive	Moshi	SRX22036684
ZLB505b	22/05/2017	<i>C. jejuni</i>	Poultry	1932	460	36	Extensive	Moshi	SRX22036685
ZLB516a	22/05/2017	<i>C. jejuni</i>	Poultry	4729	49	37	Semi intensive	Moshi	SRX22036687
ZLB516b	22/05/2017	<i>C. jejuni</i>	Poultry	4729	49	37	Semi intensive	Moshi	SRX22036688
ZLB526b	29/05/2017	<i>C. jejuni</i>	Poultry	9459	574	38	Intensive broiler	Moshi	SRX22036689
ZLB577a	22/06/2017	<i>C. jejuni</i>	Poultry	353	353	39	Intensive Indigenous	Moshi	SRX22036690
ZLB577b	22/06/2017	<i>C. jejuni</i>	Poultry	353	353	39	Intensive Indigenous	Moshi	SRX22036691
ZLB583a	22/06/2017	<i>C. jejuni</i>	Poultry	2122	353	40	Intensive broiler	Moshi	SRX22036692
ZLB583b	22/06/2017	<i>C. jejuni</i>	Poultry	2122	353	40	Intensive broiler	Moshi	SRX22036693
ZLB584a	22/06/2017	<i>C. jejuni</i>	Poultry	2122	353	41	Intensive broiler	Moshi	SRX22036694
ZLB584b	22/06/2017	<i>C. jejuni</i>	Poultry	2122	353	41	Intensive broiler	Moshi	SRX22036695
ZLB586a	22/06/2017	<i>C. jejuni</i>	Poultry	2122	353	42	Intensive broiler	Moshi	SRX22036696
ZLB586b	22/06/2017	<i>C. jejuni</i>	Poultry	2122	353	42	Intensive broiler	Moshi	SRX22036698
ZLB617a	28/06/2017	<i>C. jejuni</i>	Poultry	4684	UA	43	Intensive Indigenous	Moshi	SRX22036699
ZLB617b	28/06/2017	<i>C. jejuni</i>	Poultry	4684	UA	43	Intensive Indigenous	Moshi	SRX22036700
ZLB619a	28/06/2017	<i>C. jejuni</i>	Poultry	1932	460	44	Intensive Indigenous	Moshi	SRX22036701
ZLB619b	28/06/2017	<i>C. jejuni</i>	Poultry	1932	460	44	Intensive Indigenous	Moshi	SRX22036702
ZLB620a	28/06/2017	<i>C. jejuni</i>	Poultry	4684	UA	45	Intensive Indigenous	Moshi	SRX22036703
ZLB620b	28/06/2017	<i>C. coli</i>	Poultry	3990	828	45	Intensive Indigenous	Moshi	SRX22036704
ZLB633a	28/06/2017	<i>C. coli</i>	Poultry	8043	UA	46	Semi intensive	Moshi	SRX22036705
ZLB633b	28/06/2017	<i>C. coli</i>	Poultry	8043	UA	46	Semi intensive	Moshi	SRX22036706
ZLB635a	28/06/2017	<i>C. jejuni</i>	Poultry	607	607	47	Semi intensive	Moshi	SRX22036707
ZLB635b	28/06/2017	<i>C. jejuni</i>	Poultry	607	607	47	Semi intensive	Moshi	SRX22036741

ID no.	Sample date	species	Host	ST	CC	Poultry sample no.	Poultry farm type	Location	Accession
ZLB638a	28/06/2017	<i>C. coli</i>	Poultry	5160	1150	48	Semi intensive	Moshi	SRX22036742
ZLB638b	28/06/2017	<i>C. coli</i>	Poultry	5160	1150	48	Semi intensive	Moshi	SRX22036743
ZLB646a	3/07/2017	<i>C. jejuni</i>	Poultry	1380	257	49	Extensive	Moshi	SRX22036744
ZLB646b	3/07/2017	<i>C. jejuni</i>	Poultry	1380	257	49	Extensive	Moshi	SRX22036745
ZLB654a	3/07/2017	<i>C. jejuni</i>	Poultry	1380	257	50	Semi intensive	Moshi	SRX22036746
ZLB654b	3/07/2017	<i>C. jejuni</i>	Poultry	1380	257	50	Semi intensive	Moshi	SRX22036747
ZLB662a	3/07/2017	<i>C. jejuni</i>	Poultry	10893	UA	51	Intensive broiler	Moshi	SRX22036748
ZLB662b	3/07/2017	<i>C. jejuni</i>	Poultry	10893	UA	51	Intensive broiler	Moshi	SRX22036749
ZLB663a	3/07/2017	<i>C. jejuni</i>	Poultry	5014	UA	52	Intensive broiler	Moshi	SRX22036750
ZLB663b	3/07/2017	<i>C. jejuni</i>	Poultry	5014	UA	52	Intensive broiler	Moshi	SRX22036752
ZLB674a	3/07/2017	<i>C. jejuni</i>	Poultry	353	353	53	Intensive Indigenous	Moshi	SRX22036753
ZLB674b	3/07/2017	<i>C. jejuni</i>	Poultry	353	353	53	Intensive Indigenous	Moshi	SRX22036754
ZLB743a	17/07/2017	<i>C. jejuni</i>	Poultry	1932	460	54	Intensive Indigenous	Moshi	SRX22036755
ZLB743b	17/07/2017	<i>C. jejuni</i>	Poultry	1932	460	54	Intensive Indigenous	Moshi	SRX22036756
ZLB748a	17/07/2017	<i>C. jejuni</i>	Poultry	5014	UA	55	Intensive Indigenous	Moshi	SRX22036757
ZLB748b	17/07/2017	<i>C. jejuni</i>	Poultry	5014	UA	55	Intensive Indigenous	Moshi	SRX22036758
ZLB774a	24/07/2017	<i>C. jejuni</i>	Poultry	2802	UA	56	Extensive	Moshi	SRX22036759

Sequence data are available in BioProject PRJNA1026168.

**Appendix Table 2.** Table showing which of the sequence types (ST) identified in the present study have also been isolated from other countries in the African continent. Data were extracted from PubMLST (27) on 1 December 2021; numbers refer to the number of isolates.

ST	Kenya and Tanzania, this study			Africa, other studies							
	Human	Poultry	Total	Africa total	Botswana	Burkina Faso	Egypt	Malawi	Nigeria	Senegal	South Africa
5	1		1								
22	1		1	4				1		1	2
27	1		1								
42	1		1	1			1				
51		2	2	1	1						
52	1	2	3	7	3					4	
161	1		1								
251	2		2								
353	4	10	14	3				3			
354	1		1	6			4		2		
362	3	1	4	25		1		1			23
403	2		2								
407	1		1								
523	1		1	4		2			2		
572		4	4	2			2				
587	1		1								
607		2	2	3					3		
626		2	2								
824		4	4	2			1			1	
825	1		1	2			1		1		
829		3	3	3		3					
883	1		1	3	3						
986	3		3								
1036	1		1	14					3	11	
1038	1	2	3	4				1		3	
1043	1		1								
1380		5	5								
1586	1		1								
1723	1		1	3	3						
1737		1	1								
1751	1		1								

ST	Kenya and Tanzania, this study			Africa, other studies							
	Human	Poultry	Total	Africa total	Botswana	Burkina Faso	Egypt	Malawi	Nigeria	Senegal	South Africa
1769	1		1	1	1						
1932		9	9	7	1				6		
2031	1		1								
2042	2		2	2	1	1					
2085	1		1								
2109	6		6								
2122		10	10								
2131	1		1	3	3						
2155	1		1								
2294	1		1	1				1			
2802		4	4								
3241	1		1	4	3		1				
3572	1		1								
3630	1		1								
3720	1	1	2								
3743	1		1								
3990		1	1								
4055	1		1								
4624	3		3								
4684	1	3	4								
4729		3	3								
5014	1	4	5								
5160		2	2								
6839	4		4	1				1			
6841	1		1	1				1			
7751	3		3								
8043		11	11	3	3						
8716		1	1	2	2						
9459		1	1								
9648	2		2								
10594	1		1								
10889	1		1								
10890	1		1								
10893	2	3	5								
10894	1		1								
10896	1		1								
10901	1		1								
10918	1		1								
10919	1		1								
10920	1		1								
10921	1		1								
10922		1	1								
10923		2	2								
10924	1		1								
10926		1	1								
10929	1		1								