Whole-genome characterization of Shiga toxin-producing *Escherichia coli* isolated from Ghanaian livestock

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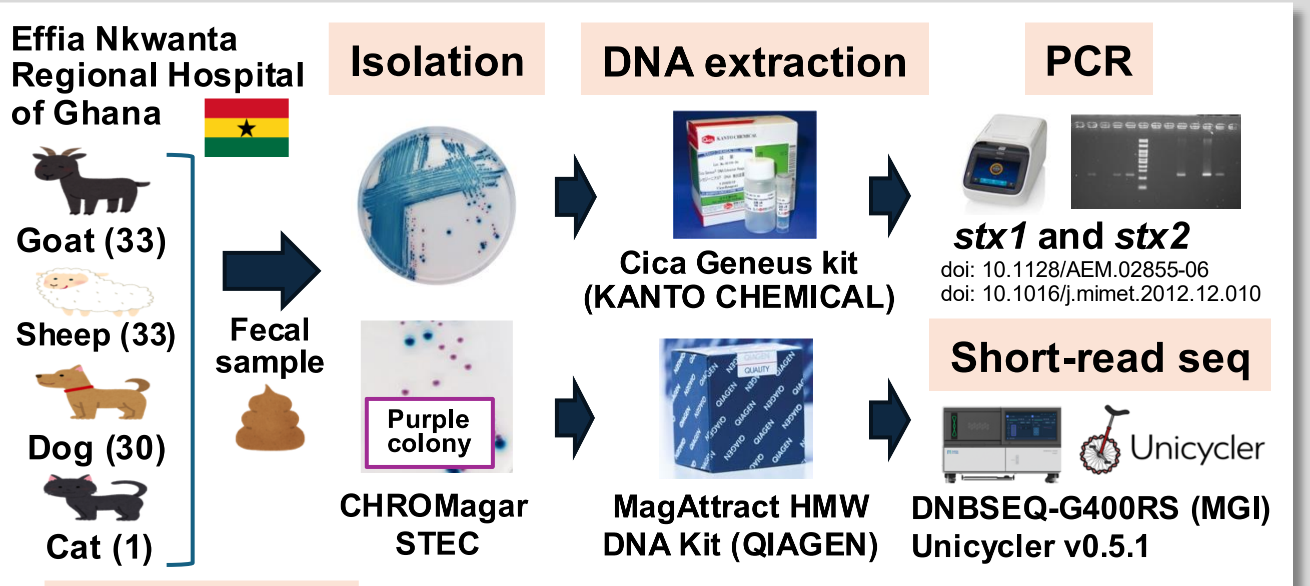
BACKGROUND

Shiga toxin-producing *Escherichia coli* (STEC) is a zoonotic pathogen with notable public health implications, and a One Health approach is required to understand its distribution and potential transmission. However, its prevalence and characteristics in livestock and companion animals remain underexplored in low-income countries. In this study, we investigated the prevalence and genomic characteristics of STEC in these animals in the western region of Ghana and this is the first genomic report in the country.

MATERIALS AND METHODS



Effia Nkwanta Regional Hospital of Ghana

Goat (33)
Sheep (33)
Dog (30)
Cat (1)

Fecal sample

Isolation

Purple colony

CHROMagar STEC

DNA extraction

Cica Geneus kit (KANTO CHEMICAL)

MagAttract HMW DNA Kit (QIAGEN)

PCR

stx1 and *stx2*
doi: 10.1128/AEM.02855-06
doi: 10.1016/j.mimet.2012.12.010

Short-read seq

DNBSEQ-G400RS (MGI)
Unicycler v0.5.1

Data analysis

- **SeroTypeFinder v2.0** (serotype)
- **ResFinder v4.6.0** (resistance genes)
- **VirulenceFinder v2.0.** (virulence genes)
- **MLST v2.0** (sequence type: ST)
- **Roary v3.13.0** and **IQ-TREE v2.3.0** (Maximum likelihood phylogenetic tree)

RESULTS

Table 1. Positive rates of STEC from animals.

Species	STEC agar	*stx1*(+)/ *stx2*(+)	*stx1*(+)/ *stx2*(-)	*stx1*(-)/ *stx2*(+)
Goat (n=33)	6 (18.2%)	1 (3.0%)	1 (3.0%)	2 (6.1%)
Sheep (n=33)	9 (27.3%)	4 (12.1%)	0	0
Dog (n=30)	2 (6.7%)	0	0	0
Cat (n=1)	0	0	0	0
All (n=97)	17 (17.5%)	5 (5.2%)	1 (1.0%)	2 (2.1%)

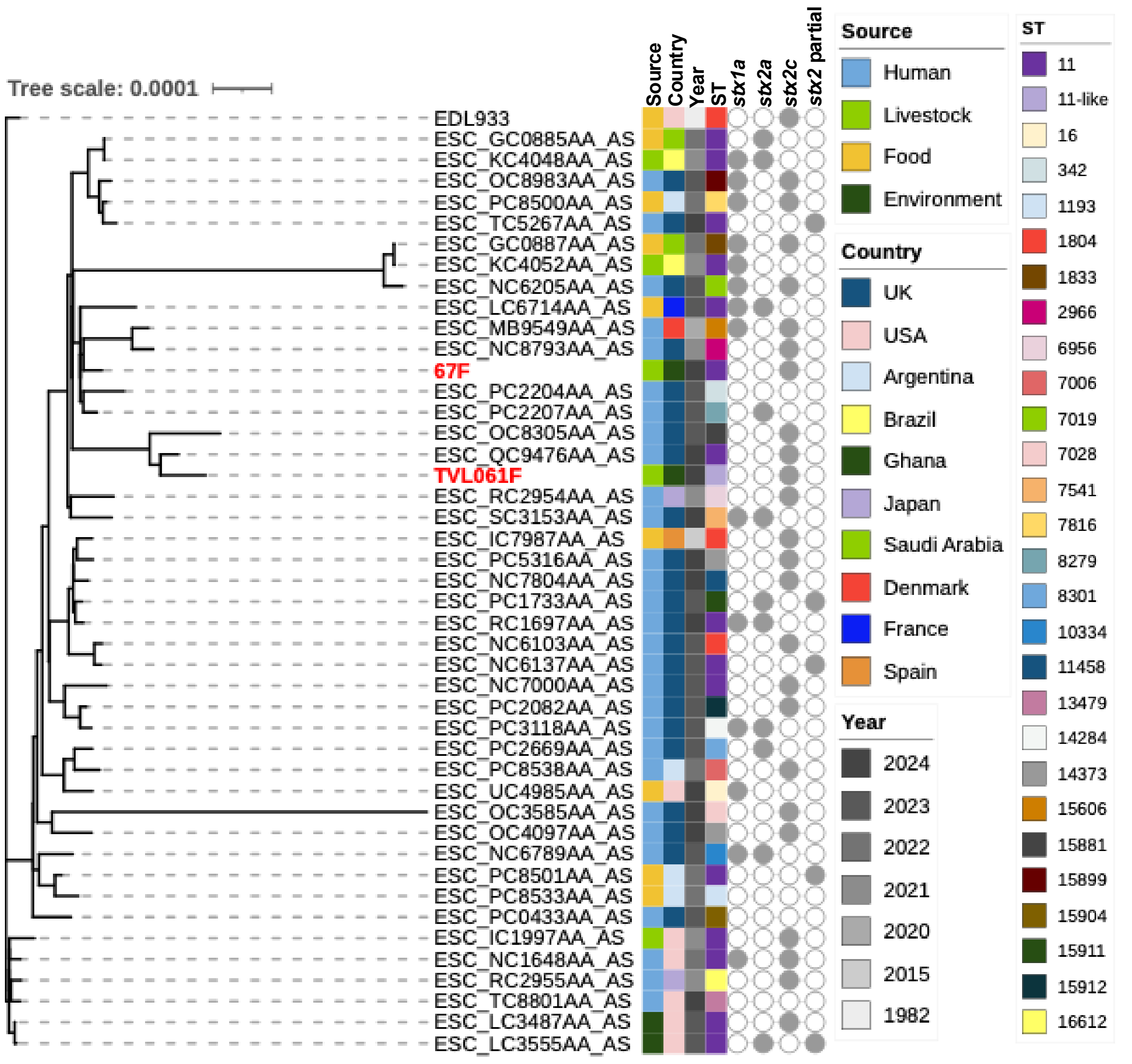
- ✓ 17 (17.5%) tested positive for STEC agar and only samples from goats (12.1%) and sheep (12.1%) tested positive for *stx*.

Table 2. Serotype and virulence profile of STEC.

Sample	TVL041F	TVL044F	TVL050F	TVL052F	TVL053F	TVL060F	TVL061F	67F
Species	Sheep	Goat	Goat	Sheep	Sheep	Sheep	Goat	Goat
Serotype	O38:H26	O43:H2	O43:H2	O43:H2	O38:H26	O38:H26	O157:H7	O157:H7
ST	ST10	ST937	ST937	ST937	ST10	ST10	ST11	ST11-like
Virulence genes linked to enterohemorrhagic *E. coli*								
chuA	-	-	-	-	-	-	+	+
eae	-	-	-	-	-	-	+	+
espA	-	-	-	-	-	-	+	+
espB	-	-	-	-	-	-	+	+
espI	+	-	-	-	+	+	-	-
espJ	-	-	-	-	-	-	+	+
espP	-	-	-	-	-	-	+	+
espY2	-	-	-	-	-	-	+	+
nleA	-	-	-	-	-	-	+	+
nleB	-	-	-	-	-	-	+	+
nleC	-	-	-	-	-	-	+	+
stx1c	+	+	+	+	+	+	-	-
stx2b	+	+	-	+	+	+	-	-
stx2c	-	-	-	-	-	-	+	+
tir	-	-	-	-	-	-	+	+
toxB	-	-	-	-	-	-	+	+

- ✓ STEC were classified into O38:H26, O43:H2, and O157:H7.
- ✓ No antimicrobial resistance genes were detected.
- ✓ *stx2c* and various virulence genes were exclusively detected in the O157:H7 serotype.

Figure 1. Maximum-likelihood phylogenetic tree of STEC serotype O157:H7.



- ✓ A wide range of STs has been reported among O157:H7, with *stx2c* gene being identified across diverse strains.
- ✓ Our isolates were related to clinical and food-derived strains from Europe, suggesting a potential for human infections and foodborne transmission.

CONCLUSION

This study provides the first whole-genome analysis of STEC including O157:H7 serotype from livestock animals in Ghana. Our findings highlight the need for continued STEC surveillance and control under the One Health framework to inform public health in Ghana.

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