

Table S1. Prevalence of *E. coli* in meat samples sold at the Tamale Metropolis.

Sample	No. of samples examined	^a No. samples positive	^b No. <i>E. coli</i>
Beef	45	39	39
Chevon	45	34	34
Mutton	45	40	40
Local chicken	45	36	36
Guinea fowl	45	40	40
Overall	225	189	189

^aNumber of samples positive for *E. coli*.

^bOne *E. Coli* isolate was selected from each positive sample.

Table S2. A table showing the eBURST (Based Upon Related Sequence Types) analyses of the study sequence types with global curated STs in *Escherichia* PubMLST database.

MLST (Isolate)	Type of clone	Closest global ancestry sequence type (ST)	Source
ST69 (SG6)	Similar ^a	ST69	Animal (Food), Human
ST155 (SLC2, TLC13, CM4)	Similar	ST155	Animal (Food), Human, Environment
ST297 (TLC1)	Similar	ST297	Human
ST1727 (NC3)	Similar	ST1727	Human
ST44 (AC1)	Single-Locus Variant (SLV) ^b	ST10, ST752	Animal (Food), Human
ST469 (CC6)	Single-Locus Variant (SLV)	ST162	Food
ST540 (AB1, TG1)	Single-Locus Variant (SLV)	ST4093	Human
ST1141 (NM11)	Single-Locus Variant (SLV)	ST10, ST744	Animal (Food), Human
ST7473 (NB12)	Single-Locus Variant (SLV)	ST10	Animal (Food), Human
ST6646 (CB1)	Satellite ^c	None	-
ST7483 (NB12)	Satellite	None	-

^a Similar: study isolate was similar to a global curated known sequence type.

^b Single-Locus Variant (SLV): study isolate only shared similarity with global curated known sequence types that differed in one allelic gene.

^c Satellite: study isolate as a distantly related and did not shared any similarity with global curated known sequence types.

Table S3. In silico identification and characterization of conserved stress response mechanisms in the *E. coli* strains.

Type of Mechanisms	Associated Proteins/Enzymes/Genes
Osmotic stress (n=14)	
a. Osmoregulation (4)	Outer membrane protein A precursor
	Aquaporin Z
	Osmotically inducible protein (<i>OsmY</i>)
	Glycerol uptake facilitator protein
b. Osmoprotectant ABC transporter (4)	Permease protein (<i>YehY</i>)
	Inner membrane protein (<i>YehW</i>)
	Binding protein (<i>YehZ</i>)
	ATP-binding subunit (<i>YehX</i>)
c. Synthesis of osmoregulated periplasmic glucans (3)	Glucans biosynthesis protein C
	Glucans biosynthesis protein D precursor
	Glucans biosynthesis protein G precursor
d. Choline and Betaine Uptake and Betaine Biosynthesis (3)	High-affinity choline uptake protein (<i>BetT</i>)
	Choline dehydrogenase
	Betaine aldehyde dehydrogenase
Oxidative stress (n=38)	
a. Protection from Reactive Oxygen Species (3)	Superoxide dismutase [Cu-Zn] precursor
	Cytochrome <i>c551</i> peroxidase
	Superoxide dismutase [Fe]
b. Oxidative stress (9)	Redox-sensitive transcriptional activator (<i>SoxR</i>)
	Superoxide dismutase [Cu-Zn] precursor
	Paraquat-inducible protein B
	Superoxide dismutase [Fe]
	Ferric uptake regulation protein FUR
	Superoxide dismutase [Mn]
	Nitrite-sensitive transcriptional repressor (<i>NsrR</i>)
	Paraquat-inducible protein A
	Fumarate and nitrate reduction regulatory protein
c. Glutathione: Biosynthesis and gamma-glutamyl cycle (3)	Gamma-glutamyltranspeptidase
	Glutathione synthetase
	Glutamate--cysteine ligase
d. Glutathione: Non-redox reactions (10)	Glutathione S-transferase
	Uncharacterized glutathione S-transferase-like protein
	Lactoylglutathione lyase
	FIG005121: SAM-dependent methyltransferase
	Glutathione S-transferase, omega
	Uncharacterized GST-like protein (<i>yncG</i>)
	Uncharacterized GST-like protein <i>yghU</i> associated with glutathionylspermidine synthetase/amidase
	Hydroxyacylglutathione hydrolase
	Probable glutathione S-transferase, <i>YfcF</i> homolog
	Probable glutathione S-transferase, <i>YfcG</i> homolog

	Glutathione S-transferase (EC 2.5.1.18)
e. Glutathione: Redox cycle (6)	Glutathione reductase
	Glutaredoxin-like protein (<i>NrdH</i>), required for reduction of Ribonucleotide reductase class Ib
	Glutathione peroxidase
	Glutaredoxin 3 (<i>Grx3</i>)
	Glutaredoxin 1
	Glutaredoxin 2
f. Glutaredoxins (4)	Glutaredoxin-like protein (<i>NrdH</i>), required for reduction of Ribonucleotide reductase class Ib
	Glutaredoxin 3 (<i>Grx3</i>)
	Glutaredoxin 1
	Glutaredoxin 2
g. Glutathionylspermidine and Trypanothione (3)	Glutathionylspermidine amidohydrolase
	Uncharacterized GST-like protein <i>yghU</i> associated with glutathionylspermidine synthetase/amidase
	Glutathionylspermidine synthase
Periplasmic stress (n=11)	
a. Periplasmic Acid Stress Response in Enterobacteria (4)	Transcriptional activator (<i>GadE</i>)
	Membrane transporter (<i>HdeD</i>), H-NS repressed
	Chaperone (<i>HdeA</i>)
	Chaperone (<i>HdeB</i>)
b. Periplasmic Stress Response (7)	Sigma factor <i>RpoE</i> negative regulatory protein <i>RseA</i>
	Outer membrane stress sensor protease (<i>DegS</i>)
	Outer membrane protein H precursor
	Intramembrane protease (<i>RasP/YluC</i>)
	Sigma factor <i>RpoE</i> negative regulatory protein <i>RseB</i> precursor
	Outer membrane stress sensor protease <i>DegQ</i> , serine protease
	<i>HtrA</i> protease/chaperone protein
Detoxification (n=9)	
a. Uptake of selenate and selenite (3)	Inner membrane transport protein (<i>YbaT</i>)
	Sulfate and thiosulfate import ATP-binding protein (<i>CysA</i>)
	<i>DedA</i> protein
b. Tellurite resistance (Chromosomal determinants) (3)	Uncharacterized membrane lipoprotein clustered with tellurite resistance proteins (<i>TehA/TehB</i>)
	FIG005189: putative transferase clustered with tellurite resistance proteins (<i>TehA/TehB</i>)
	Tellurite resistance protein (<i>TehA</i>)
c. Glutathione-dependent pathway of formaldehyde detoxification (3)	S-formylglutathione hydrolase
	S-(hydroxymethyl)glutathione dehydrogenase
	<i>FrmR</i> : Negative transcriptional regulator of formaldehyde detoxification operon