Epidemiology of AMR in a rapidly urbanizing city

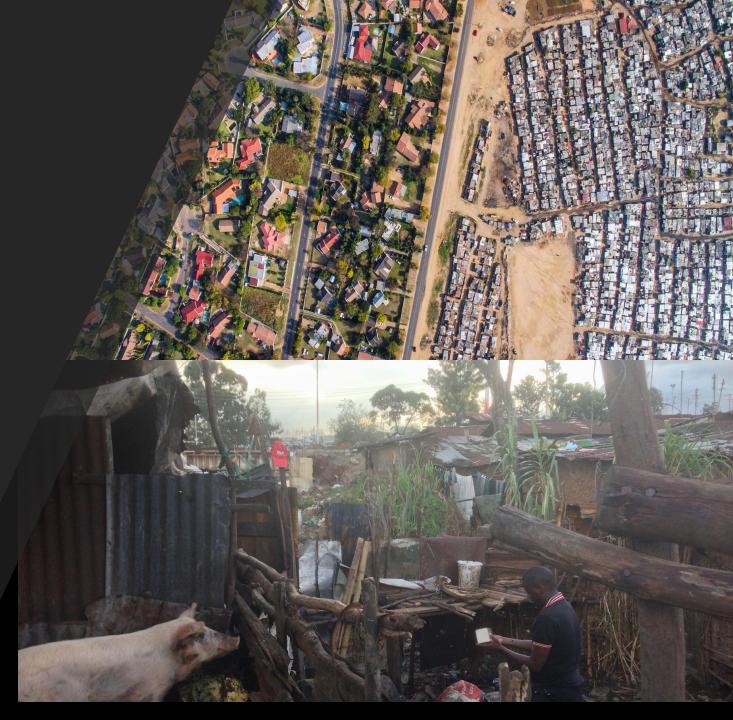
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URBAN ZOO

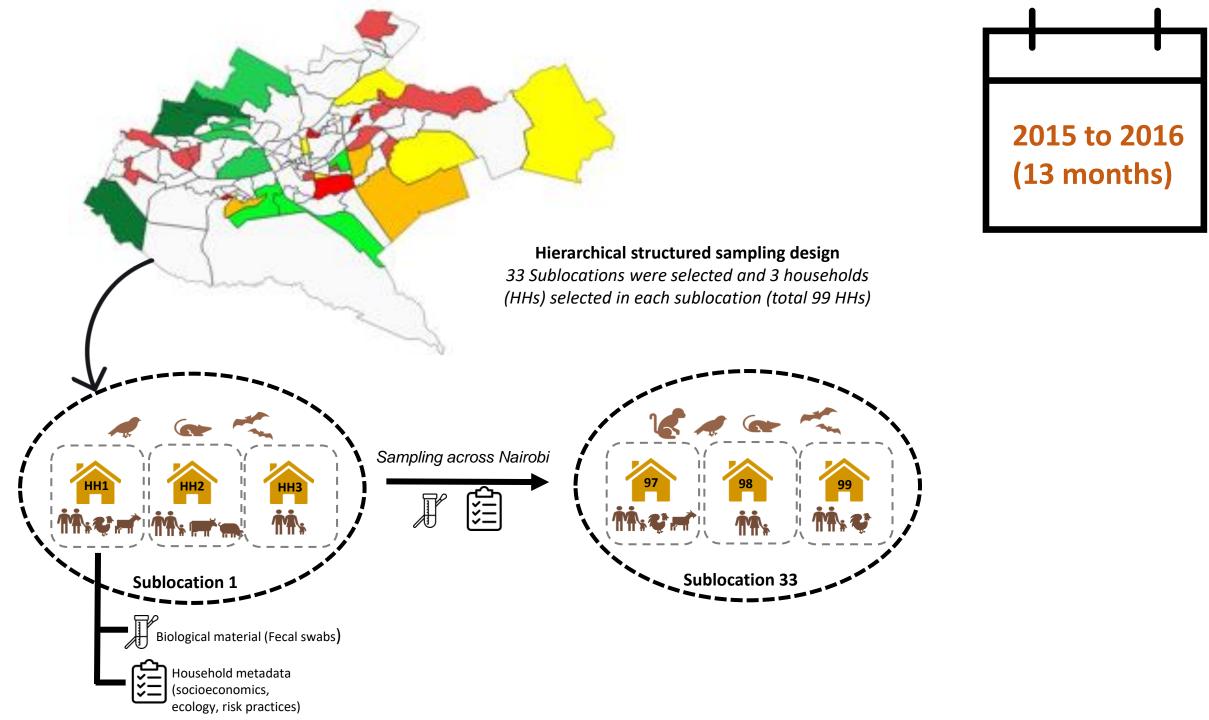
Introduction

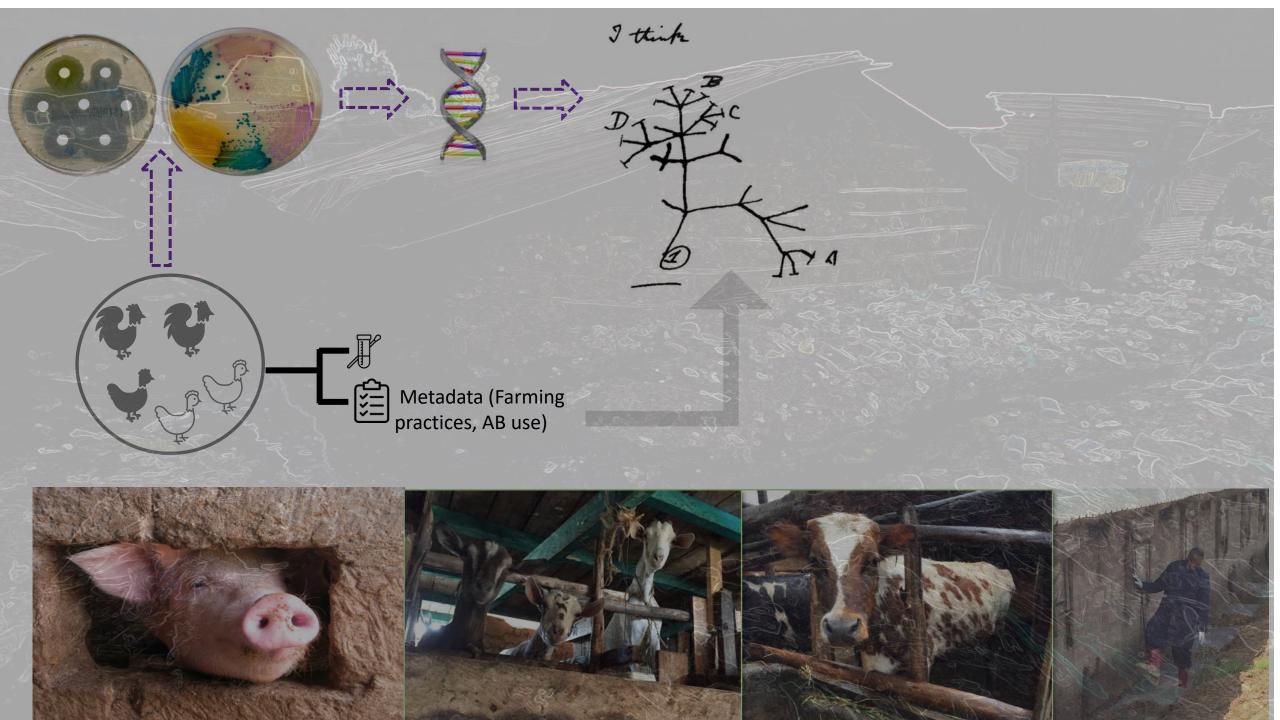
- The emergence and transmission of resistant bacteria and their AMR determinants is not well understood
- Nairobi, capital of Kenya (pop: 4 million), represents rapid urbanization in Sub-Saharan Africa
- Drivers of antibiotic use High burden of infectious diseases, increased antibiotic use with rising incomes, and ease of antibiotic purchase
- Urban agriculture and livestock keeping common (Household = interface)
- *Escherichia coli* is an ideal organism to study the spread of AMR in these complex interfaces



Investigate carriage and diversity of AMR bacteria and their resistant genes in humans and animal populations

H₀: ARGs have a cosmopilitan distribution H_{0:} Livestock keeping increases risk of human carraige of AMR genes





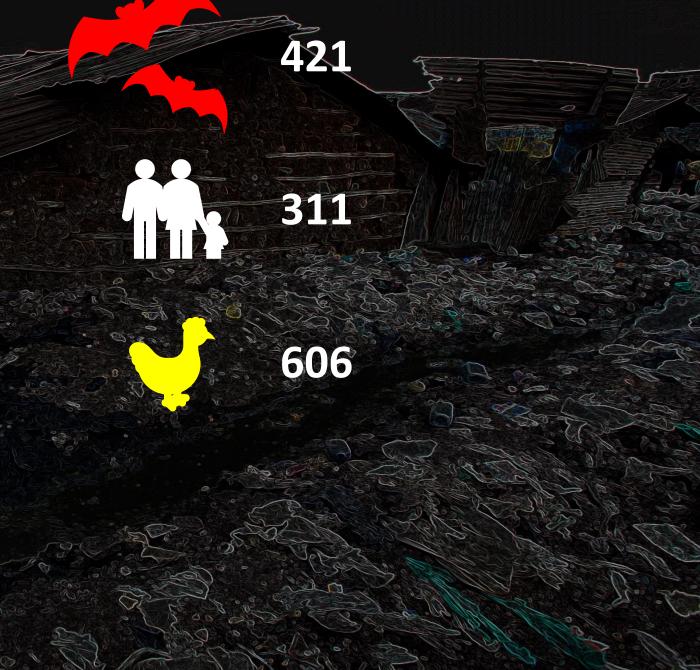
Summary of source categories

%

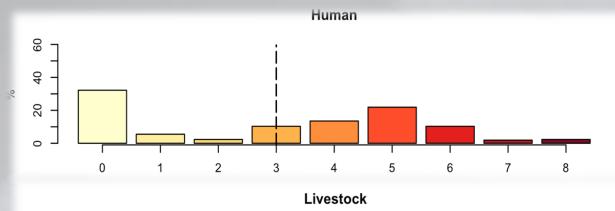
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0.2

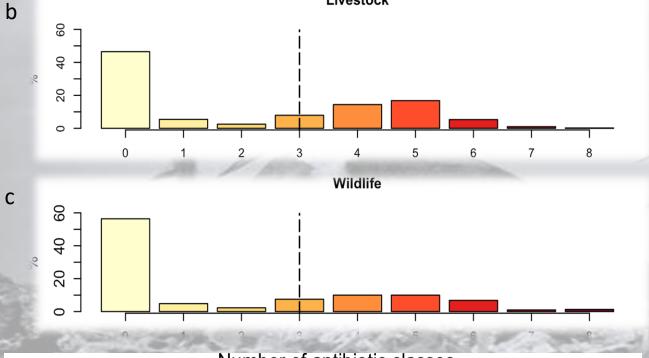
Source	Number	
Human	311	
Livestock:	606	
Poultry	324	
Goat	109	
Bovine	61	
Pig	49	
Rabbit	38	
Wildlife:	421	
Wild birds	245	
Rodents	130	
Primates	4	
Carnivore	3	
A State Stat		



- AMR genes are common
- parED475E · parEI529L Human parCE84G parCS80 parCA108\ Livestock parCS571 parCA56T parCE84V Wildlife parCE84A gyrAD87N gyrAS83A gyrAS83L Fluoroquinolones gyrAD87Y qnrS4 aac6lbcr gnrS2 gnrS1 qnrB7 qnrB66 gnrB2 gnrB19 qepA4 qepA1 tetB Tetracyclines tetA sul3 Sulphonamides sul2 sul1 Macrolides mphA fosA6 Fosfomycin fosA3 dfrB4 dfrA8 dfrA7 dfrA5 dfrA21 Trimethoprim dfrA17 dfrA16 dfrA15 dfrA14 dfrA12 dfrA1 floR cmIA1 Phenicols catB3 catA1 blaTEM70 blaTEM57 blaTEM34 blaTEM33 blaTEM30 blaTEM214 blaTEM1C blaTEM1B **Beta lactams** blaTEM176 blaTEM116 blaSHV1 blaOXA10 · blaOXA1 blaCTXM15 blaCTXM14 blaCMY4 blaCARB2 strB strA aph6lc aph3la aph3lla Aminoglycosides ant3la aadA5 aadA4 aadA2 aadA1 aac3lld aac3lla 20 40 60 %
- 56 ARGs + 13 points mutations detected = confer AMR to nine antibiotic classes
- Common ARGs sul2 (41.3%), strA (36.8%), strB (37.2%), tetA (35.6%), and blaTEM-1B
 - (23%)
- 365 (27%) isolates had at least one of the seventeen different ESBLs
- 8/69 genes commonly found in humans



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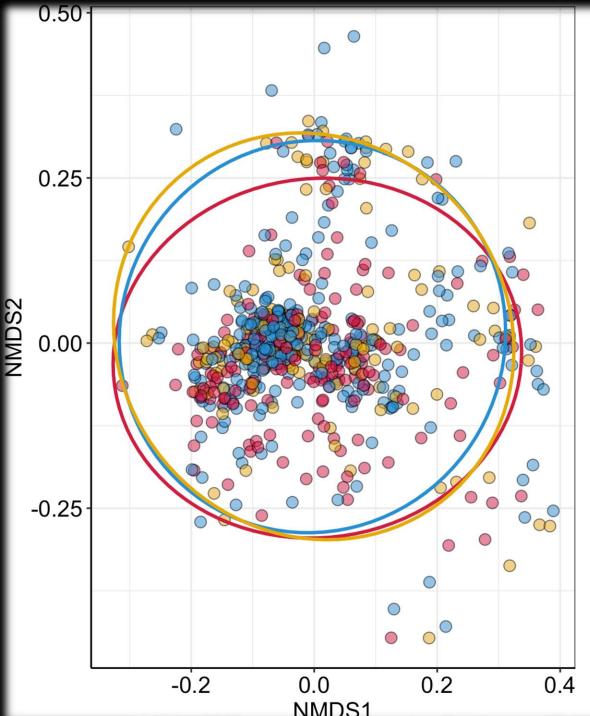
Number of antibiotic classes

25 < 0.001 < 0.001 20 ARG count 9 10-5 0 Human Livestock Wildlife Source

Human isolates had more acquired AMR

genes than livestock and wildlife isolates

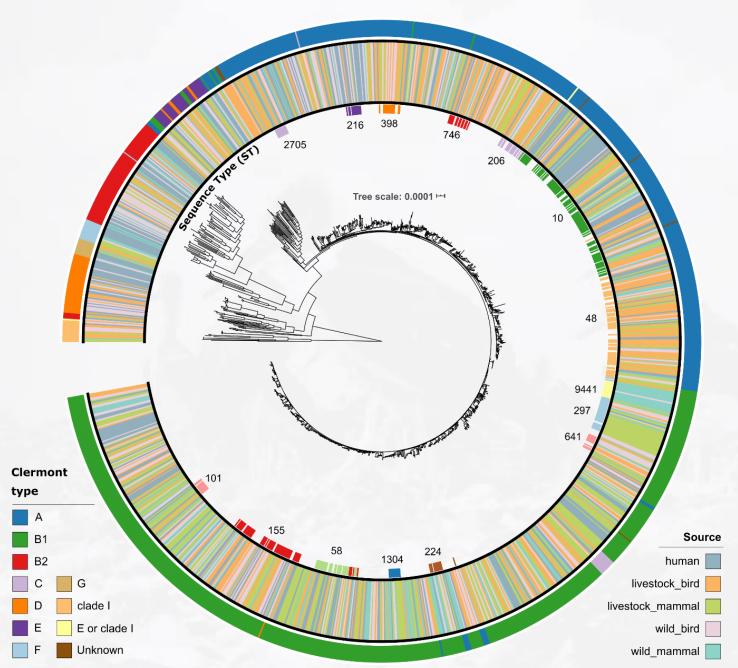
MDR carriage was common - Human 60.1%, Livestock 45.5% and wildlife 36.6



AMR gene communities are not structured by host

- source
- 🔶 human
- livestock
- 🔶 wildlife
- Non-metric multi-dimensional scaling (NMDS) of a Bray-Curtis distance matrix
- AMR gene assemblages in both human and animal were not statistically different

BUT

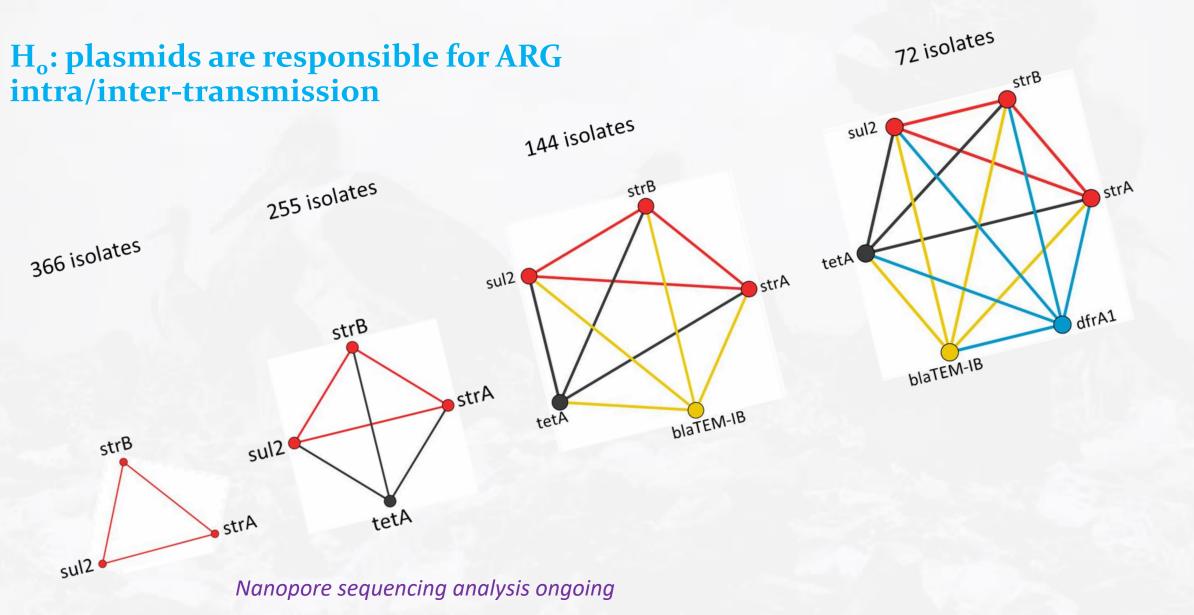


High inter-host ARG similarity BUT minimal strain sharing

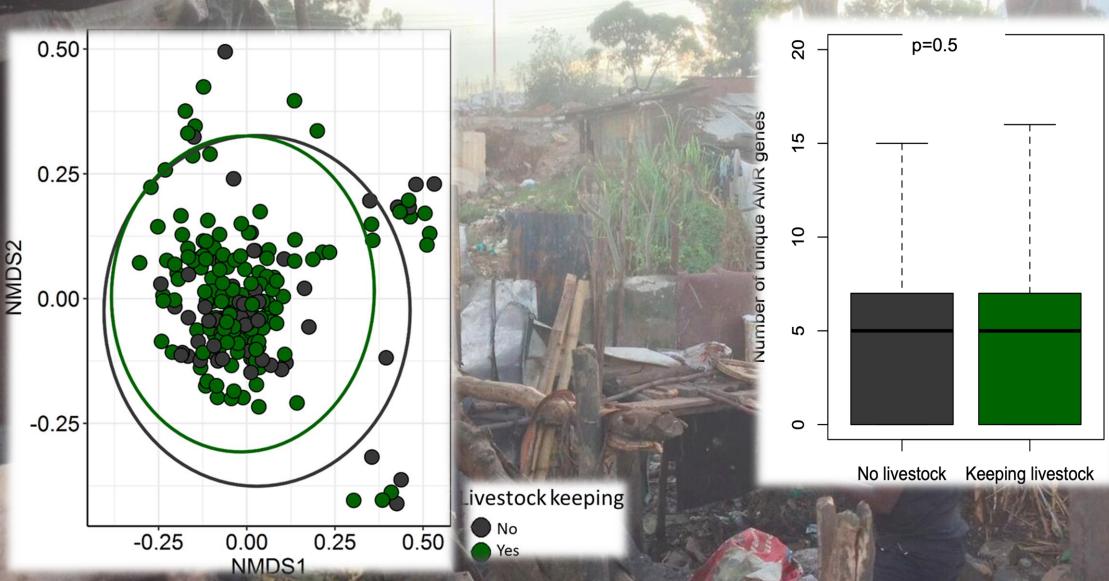
H₀: plasmids are responsible for ARG intra/inter-transmission

Muloi et al, under review

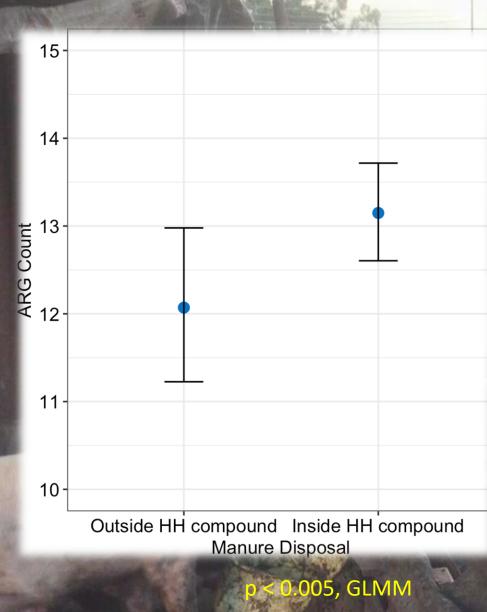
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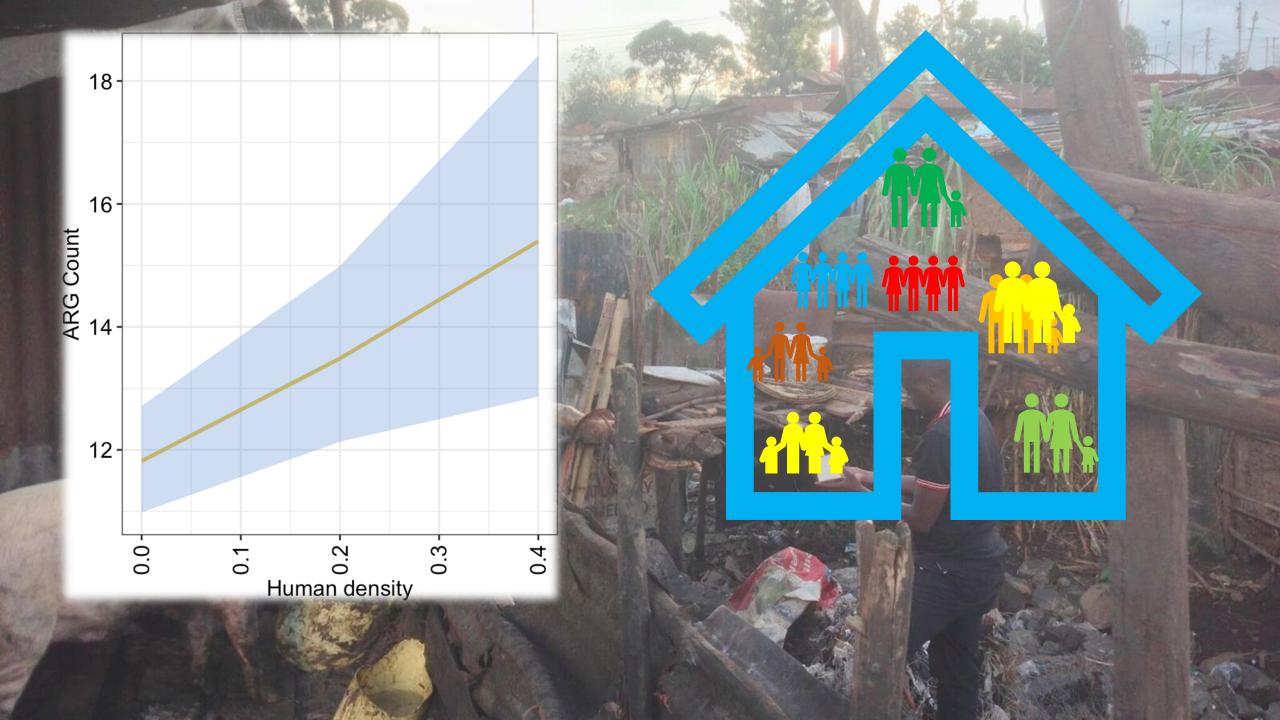


Does livestock keeping influence AMR carraige in humans?



Summary: Livestock keeping has little effect (if any) on carriage of different kind of AMR genes or number of AMR genes





CONCLUSIONS

Widespread AMR genes – common in both human and livestock Higher carriage (abundance and diversity) of AMR genes in humans vs livestock

imilarities in the resistome of the solates did not match the patterns of hared genomes – perhaps reflective of usage patterns or HGT mechanisms Livestock keeping has NO role on human AMR carriage but manure management and human density does! **International Livestock Research Institute**

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ILRI INTERNATIONAL LIVESTOCK RESEARCH IN STITUTE





Human – livestock pairs (n=10)

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Pair	Isolate ID	cgMLST	Source	ST	HHID	Wealth group	AMR	Livestock keeping	Liv_exposure	Edu	M/F	Occupation	Age
1	TMP022790	1 chie	chickens	10	NGN080	5		yes	moving handling housing manure milking eggs slaughter	1	М	domestic	37
	INT008356				GTN074	6							
2	PLQ2189	1	geese	538	KTS088	1		yes	moving handling housing manure eggs slaughter	2	М	farmhand	36
	PLQ2296				KTS088	1							
3	ALQ020141	3	chickens	23	UTH030	6	aph(3'')-Ib, aph(6)-Id, blaTEM-1B, dfrA8, mph(A), sul2	no	N/A	N/A	N/A	N/A	N/A
3	ALQ020449	5	CHICKEHS	23	UTH029	6	aph(3'')-Ib, aph(6)-Id, blaTEM-1B, dfrA8, mph(A), sul2						
А	INT004723	3 k	bovine	6178	KRR037	2		yes	handling milking eggs	6	М	public_sector	60
	INT004696	5	bovine	0178	KRR037	2							
5	INT007533	3	ducks	58	MWK056	6		yes	moving <mark>handling</mark> housing manure	3	М	domestic	36
	INT007394				MWK056	6	aph(3'')-Ib, aph(6)-Id, sul2, tet(A)						
6	ALQ023299	4	rabbit	9454	SPV064	2		yes	moving handling housing manure milking eggs slaughter	2	М	farmhand	31
	INT006051				SPV064	2							
7	ALQ023299	4 turkey	turkeys	9454	SPV064	2		yes	moving handling housing manure milking eggs slaughter	2	м	farmhand	31
	INT006147				SPV064	2							
8	TMP021689	4	chickens	206	KHW049	6	ant(3'')-la, aph(3'')-lb, aph(3')-la, aph(6)-ld, dfrA14, mph(A), sul2, tet(A)	yes	N/A	N/A	N/A	N/A	N/A
U	TMP021678	4 Chici	emekens	200	KHW049	6	ant(3'')-Ia, aph(3'')-Ib, aph(3')-Ia, aph(6)-Id, dfrA14, mph(A), sul2, tet(A)						
9	INT007648 INT005176	8	turkeys	1237	KOR058 EAS044	7 5		yes	N/A	N/A	N/A	N/A	N/A
	TMP024272				LOR099	1	blaTEM-1C,	no	none	6	м	manager	57
10	TMP024272	10 ch	chickens	48	LOR099	1	blaTEM-1C, tet(A)	no	none	0	141	manager	57
	101 024455				201057	-							