Methods of Determining Antimicrobial Resistance in Bacteria Collected from Farm Soil

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Background

Why antibiotic resistance (AR)?
- Major Public Health threat[1,2]
- Antibiotics are frequently used in livestock and in health care settings[1]
- Bacteria grow quickly and can rapidly evolve to develop AR[3,4]
- New antibiotics not being developed [1]

Purpose

Can we predict antibiotic susceptibility with genomic techniques?

Questions

- Is metagenomic sequencing of a bacterial community sufficient to determine antibiotic resistance?
- How does human traffic and antibiotic use affect the diversity of soil-borne bacteria and their resistance to antibiotics?

References

1. Davies J, Davies D. Origins and Evolution of Antibiotic Resistance. *MMBR*. 2010;74(3):417-433. doi:10.1128/MMBR.00016-10
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3. Arhin RE, Hackman HK, Whyte BK, Sa-eed A. Microbial Diversity and Antibiotic Resistance of Bacteria on Washroom Fomites in a Public University. *EJHS*. 2020;5(1):1-11.
4. Gupta, Lee, Bisesi, Lee. Indoor Microbiome and Antibiotic Resistance on Floor Surfaces: An Exploratory Study in Three Different Building Types. *IJERPH*. 2019;16(21):4160. doi:10.3390/ijerph16214160
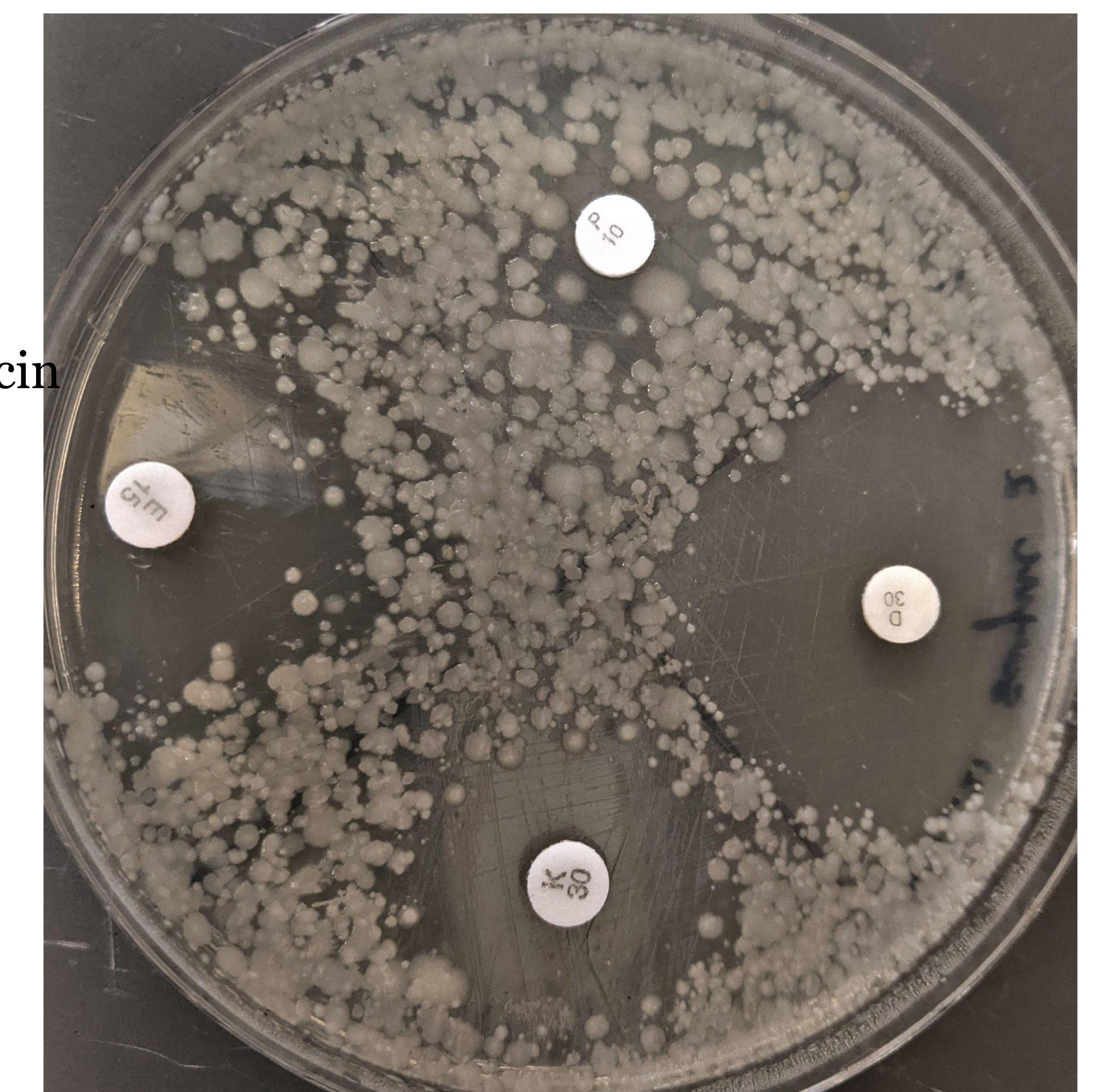
Results

	high traffic farm w/antibiotics	low traffic farm w/o antibiotics	high traffic non farm
Penicillin	0*	0*	0*
Doxycycline	1.0	0.92	1.0
Kanamycin	0.47*	0.67	0.68*
Erythromycin	0.25	0.45	0.92

Table 1. Average radius (cm) for each sample in the respective antibiotic. * indicates resistance

Figure 1 (right). high traffic farm w/antibiotics plated with four antibiotics: penicillin (top), erythromycin (left), kanamycin (bottom) and doxycycline (right).

What bacteria species are present? Are they the same as the cultured approach?

Methods

Genomic
- Soil DNA Extraction using kit
- Nanodrop to determine [DNA]
- sequence DNA
- determine presence of AR gene with Muthur

Culturomic
- Plate with antibiotic discs: penicillin, kanamycin, doxycycline, erythromycin
- determine AR by disk diffusion
- Count and plate satellite colonies

How many distinguishable bacteria are in each sample? are they susceptible to antibiotics?

Discussion

- there is a correlation between human traffic levels in AR , but more data is needed to determine if traffic plays a role development in AR bacteria
- more information needed to determine if genomic analysis can identify novel AR genes

Future Directions

- Can bioinformatics techniques alone identify novel antimicrobial resistance genes?
- Are there soil bacteria that can't be cultured in the lab?