Northwestern
McCORMICK SCHOOL
OF ENGINEERING

The built environment resistome:
potential of indoor dust microbial community for dissemination of antibiotic resistance genes

Sarah Ben Maamar[+], Adam J. Glawe[+], Taylor K. Brown[+], Ji-ping Wang[*], Erica M. Hartmann[+]

[+] Northwestern University, Dept. Of Civil and Environmental Engineering, 2145 Sheridan Road Evanston IL 60208
[*] Northwestern University, Dept. Of Statistics, 2006 Sheridan Road, Evanston IL 60208

Background

- Humans in urban environments spend near 90% of their time inside buildings.
- It is expected that 66% of the world population will be living in urban areas by 2050.
- Usage of antimicrobial chemicals is widespread.
- Antimicrobials are commonly found in dust and can trigger transfer of antibiotic resistance genes (ARG) in pathogenic bacteria, as seen in culture.
- The effects of antimicrobials on the transfer of ARG through mobile genetic elements (MGE) in the dust microbial community remains largely unknown.
- Research questions: *Is there evidence of transfer of ARG via MGE in dust? Does the rate of transfer increase in the presence of antimicrobials?*

Methods

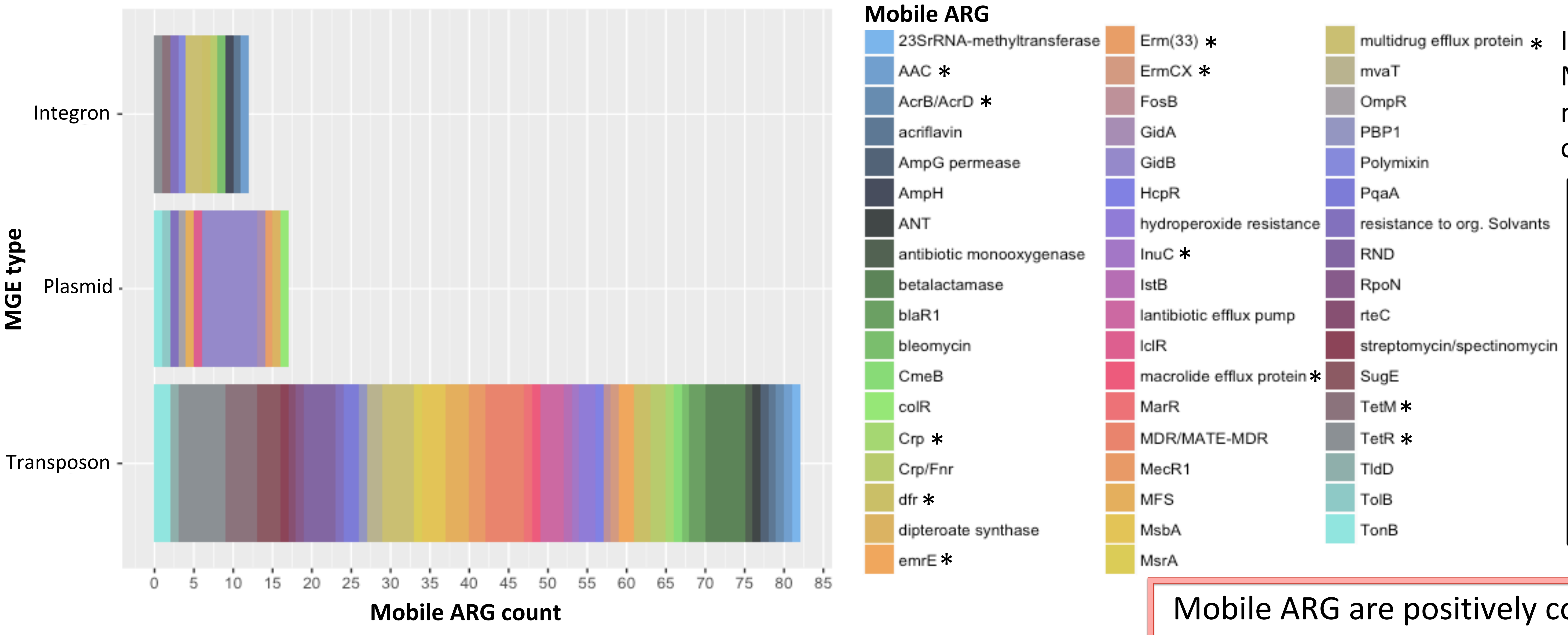
- Sample size: 167 samples from 63 distinct buildings
- Collected measurements: total microbial DNA and antimicrobial concentration (triclosan, triclocarban and parabens).

Data processing:

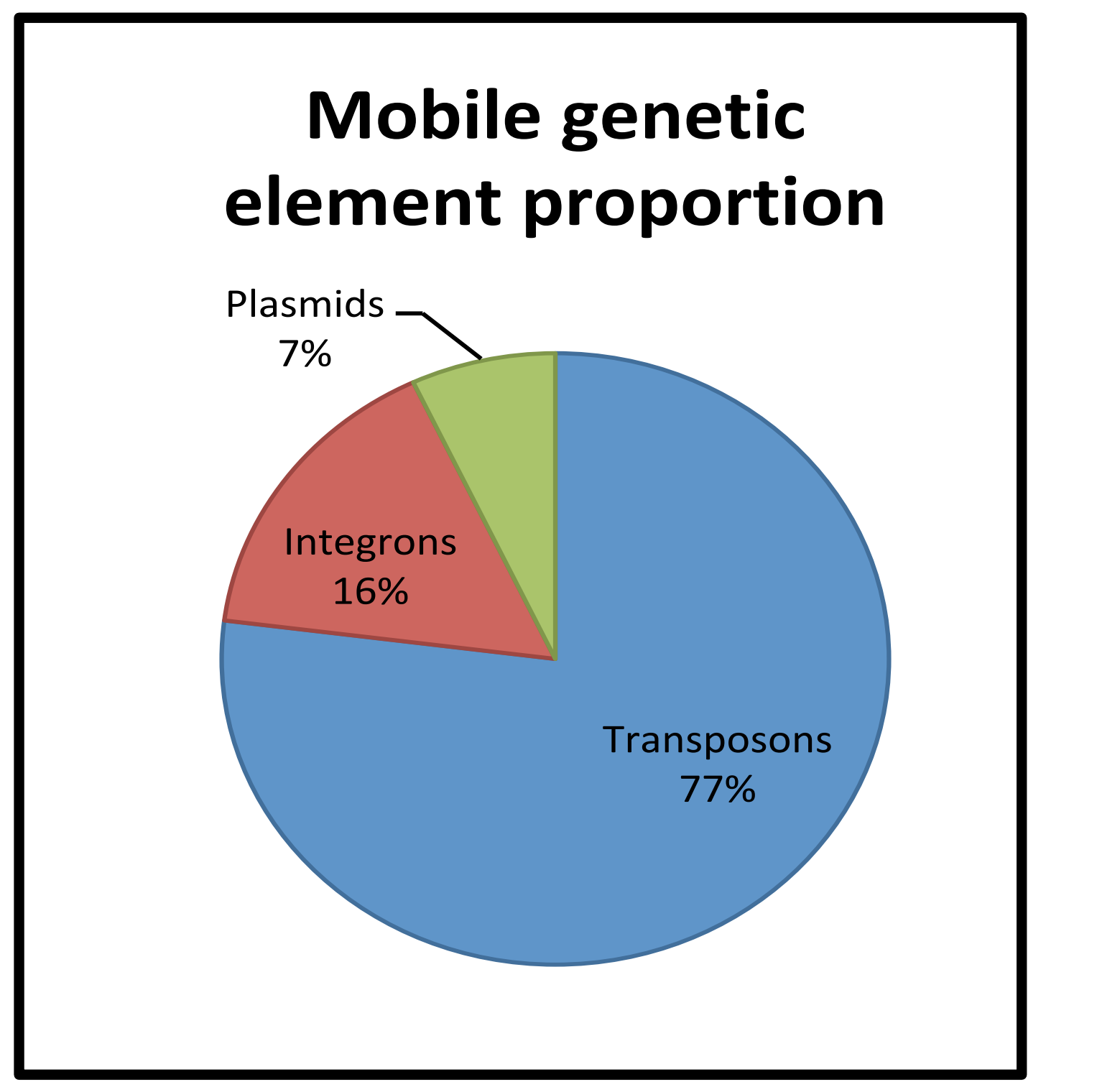
- Metagenomic sequences quality-controlled with Kneaddata.
- Antibiotic resistance profiles in each sample were determined with ShortBRED.
- MGE and associated mobile ARG were defined from assembled and annotated metagenomic contigs with Kiki and RAST respectively.
- Pearson correlations were calculated with R.

RESULTS

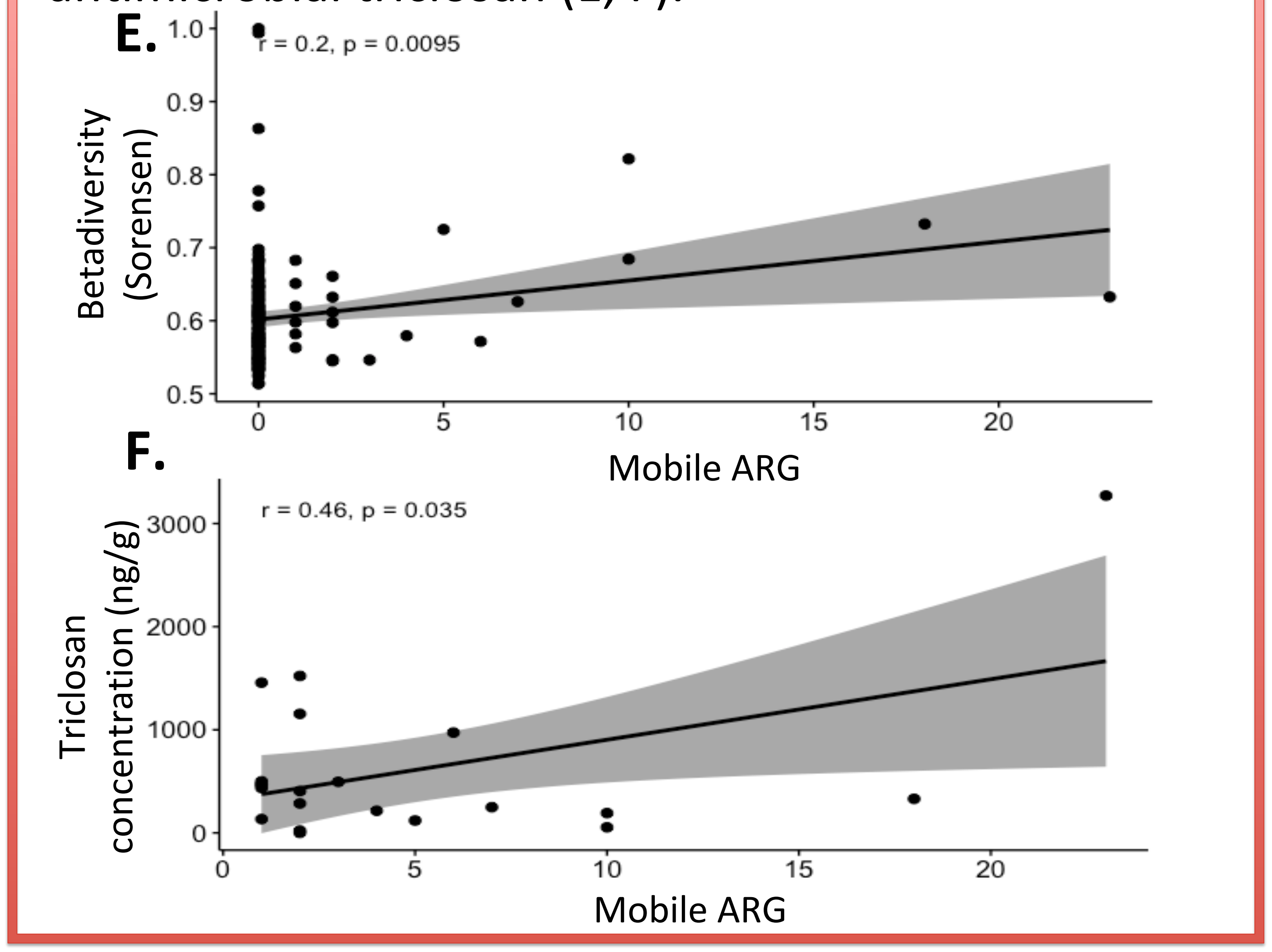
Top 20 ARG	Abundance (RPKM)	Antibiotic class
CRP	2.29	multidrug
AAC(3)-VIIIa	2.15	aminoglycosides
AAC(3)-VIIa	1.71	aminoglycosides
erm(33)	1.54	macrolides
mexT	1.37	multidrug
tetQ	1.26	tetracycline
emrR	1.16	multidrug
acrB	1.13	aminoglycosides
tetW	0.95	tetracycline
lnuA	0.81	lincosamides
cpxA	0.88	multidrug
tetO	0.87	tetracycline
qacA	0.76	multidrug
SRT-1	0.82	penicillin (betalactamase)
ermB	0.81	macrolides
dfrC	0.78	others (trimethoprim)
acrD	0.68	aminoglycosides
vanRO	0.62	glycopeptides
ErmO	0.61	macrolides
tet41	0.61	tetracylin



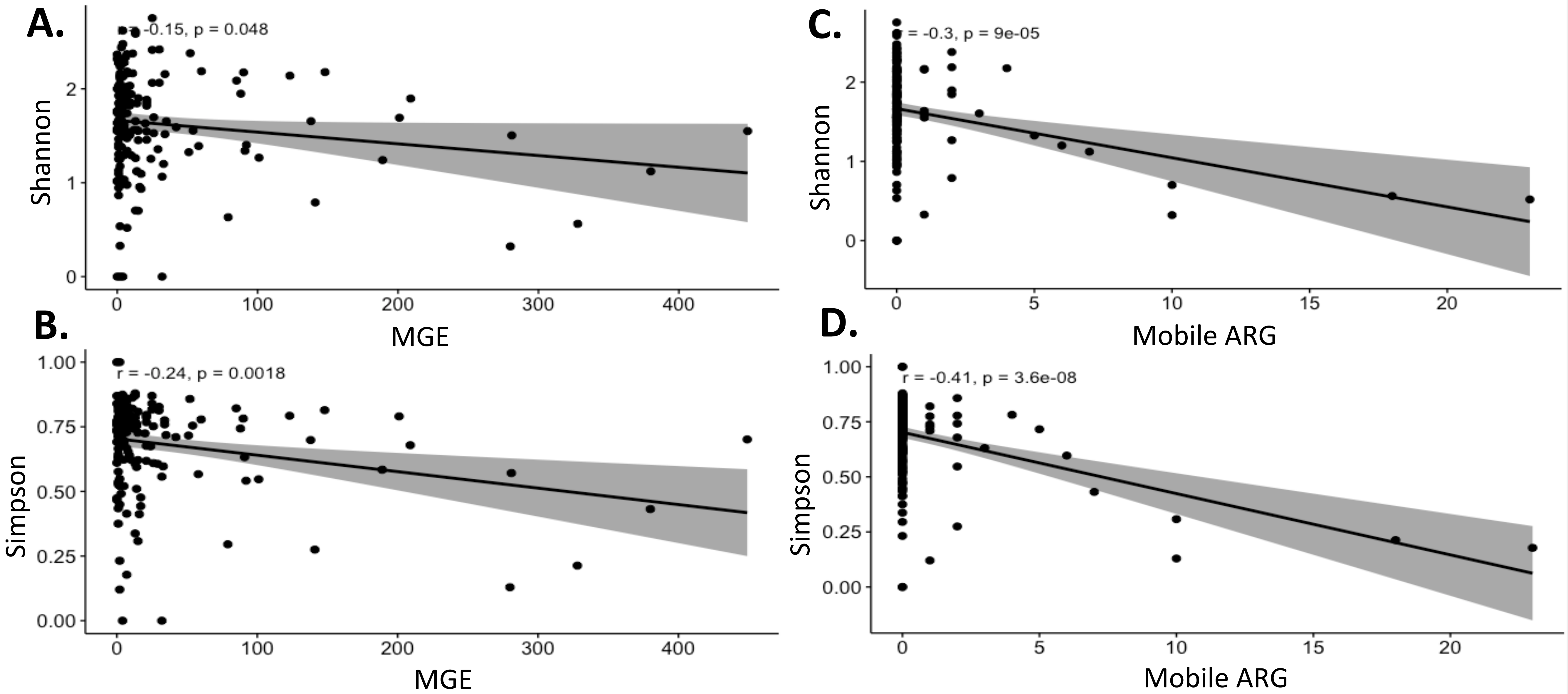
Identified mobile ARGs (i.e. in a MGE) are in the top 20 of the most abundant ARG detected over all dust samples.



Mobile ARG are positively correlated with ß-diversity (Sorensen index) and the concentration of the antimicrobial triclosan (E, F).



Both MGE and mobile ARG are negatively correlated with α-diversity (Shannon and Simpson indices; A-D).



OUTCOMES AND PERSPECTIVES

- Based on correlations with α-diversity, mobile ARG are likely carried by specific bacterial clades.
- Triclosan may foster ARG dissemination in dust.
- Assays on dust bacterial isolates for triclosan resistance and triclosan-related mobile ARG transfers (conjugation with plasmids carrying a *gidb* gene) are being performed to further confirm our results.

We thank the NU Data Science Initiative for funding and the Genomics Compute Cluster.