

Daily occupational exposure in swine farm alters human skin microbiota and antibiotic resistome

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Introduction

- ◆ Antimicrobial resistance (AMR) is widespread in humans, animals and the environments.
- ◆ The farming environment has received considerable attention for its role in Antibiotic resistance genes (ARGs) and Antibiotic resistance bacteria (ARB) transmission.



The European Medicines Agency (EMA) advocates the prudent and responsible use of veterinary antibiotics

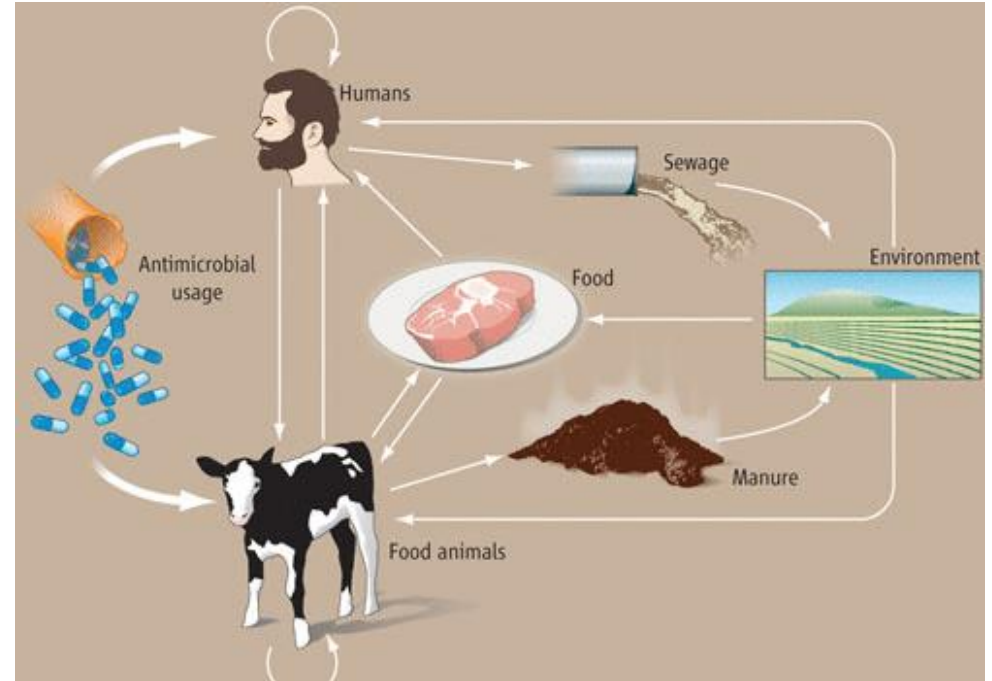


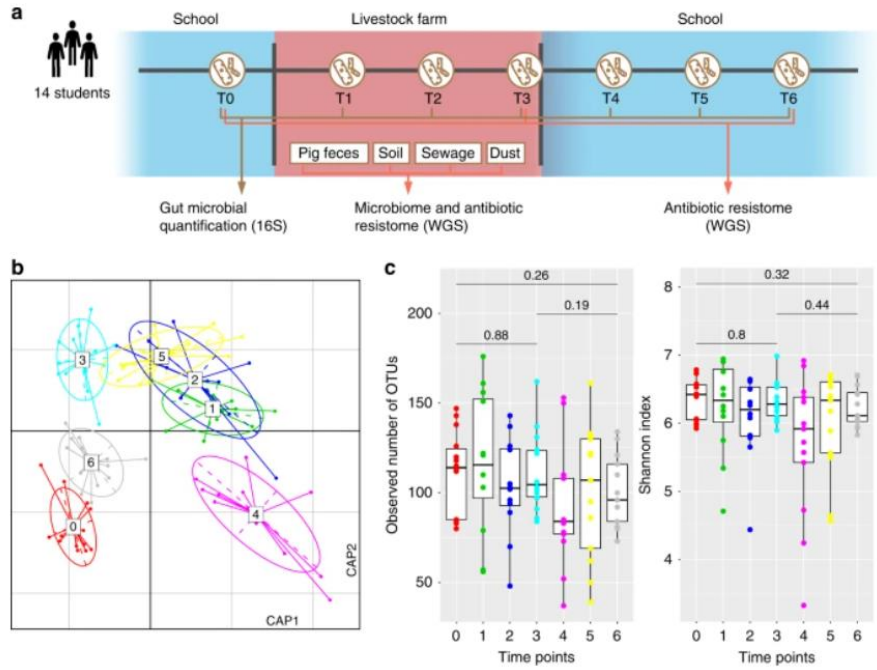
Diagram of transmission routes of AMR among the farm animals, environments, and humans

McEwen et al. *Microbiology Spectrum*, 2018

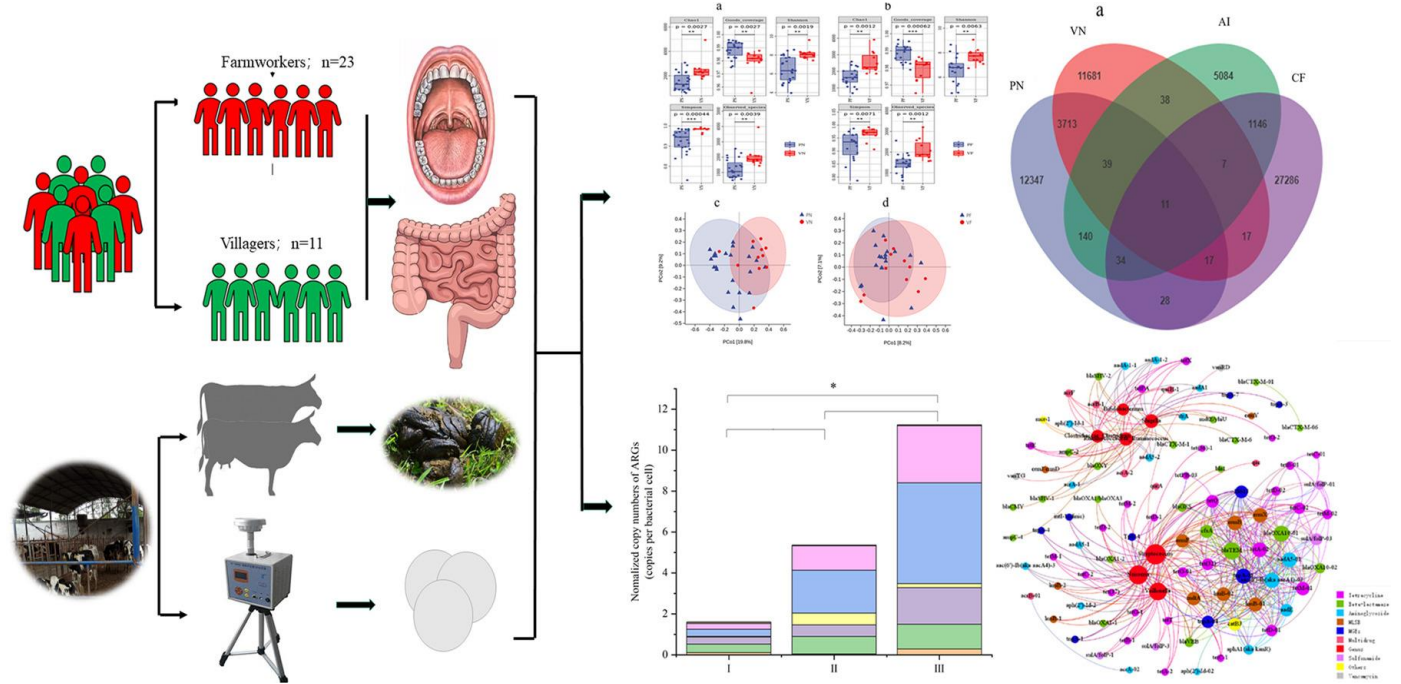


Introduction

- ◆ Environmental exposure remodels human gut microbiota and antibiotic resistome in swine farms.
- ◆ ARGs can be transmitted by host bacteria among farm environments, animals, and the human oral cavity.



Sun et al. *Nature Communications*, 2020

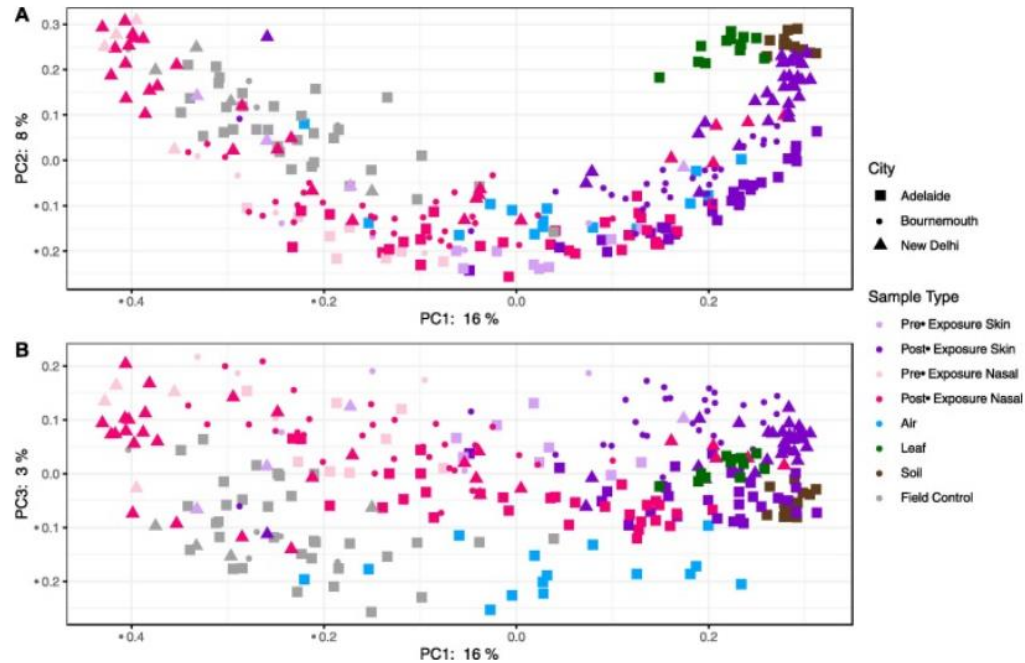


Ding et al. *Sci Total Environ*, 2021

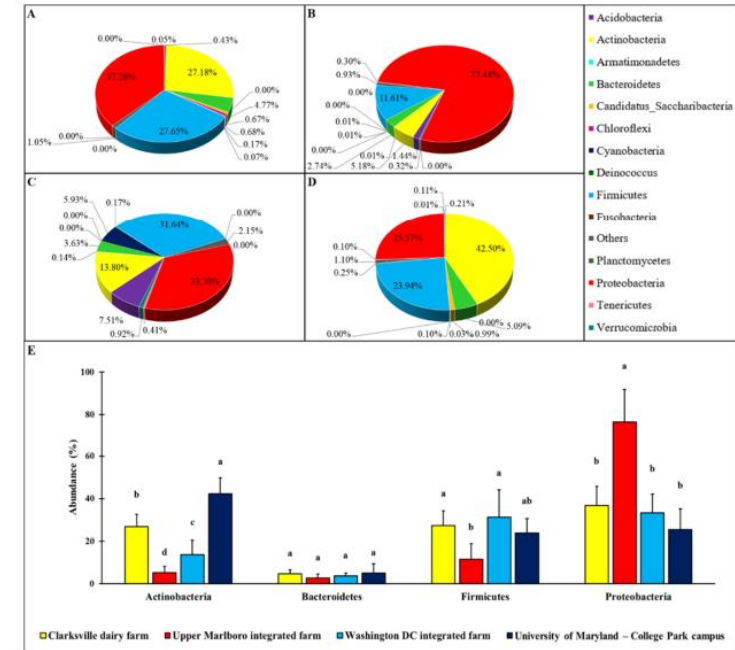


Introduction

- ◆ Human skin microbiome altered in response to environmental and occupational exposure.
- ◆ Frequent interactions with farm animals reshape human skin microbiome and increase the risk of skin infections in livestock workers.



Selway et al. *Environment International*, 2020

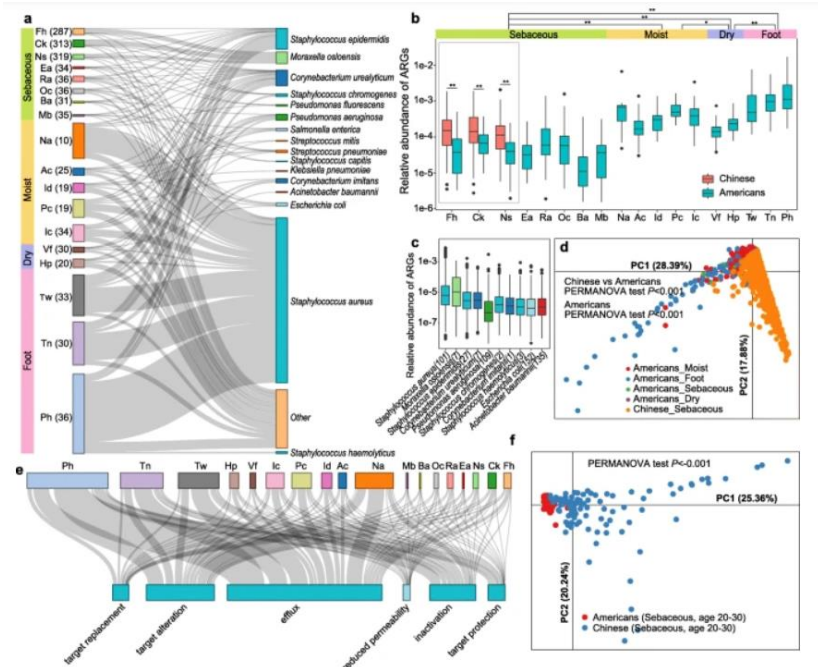


Peng et al. *Microorganisms*, 2019

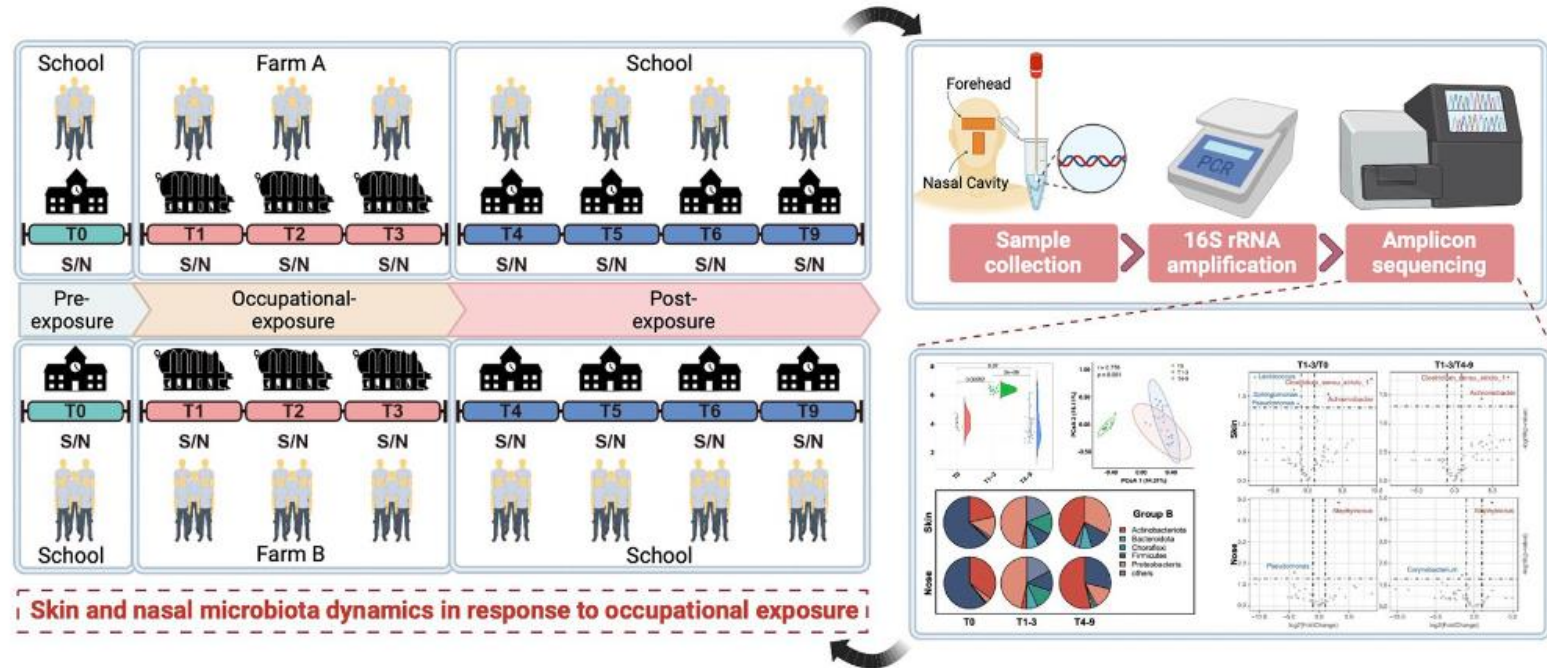


Introduction

- ◆ Skin microbiota is considered as one important reservoir of both ARGs and ARB.
- ◆ Previous studies have found that long-term occupational exposure in swine farms alters human skin microbiota.



Li et al. *Microbiome*, 2021



Wang et al. *Frontiers in Microbiology*, 2023



Results

- Exposure to livestock-associated environment, which is with more microbially enriched than school environment, can remodel the human skin microbiome.
- 5-hour exposure is sufficient to alter the structure of human skin microbiome.

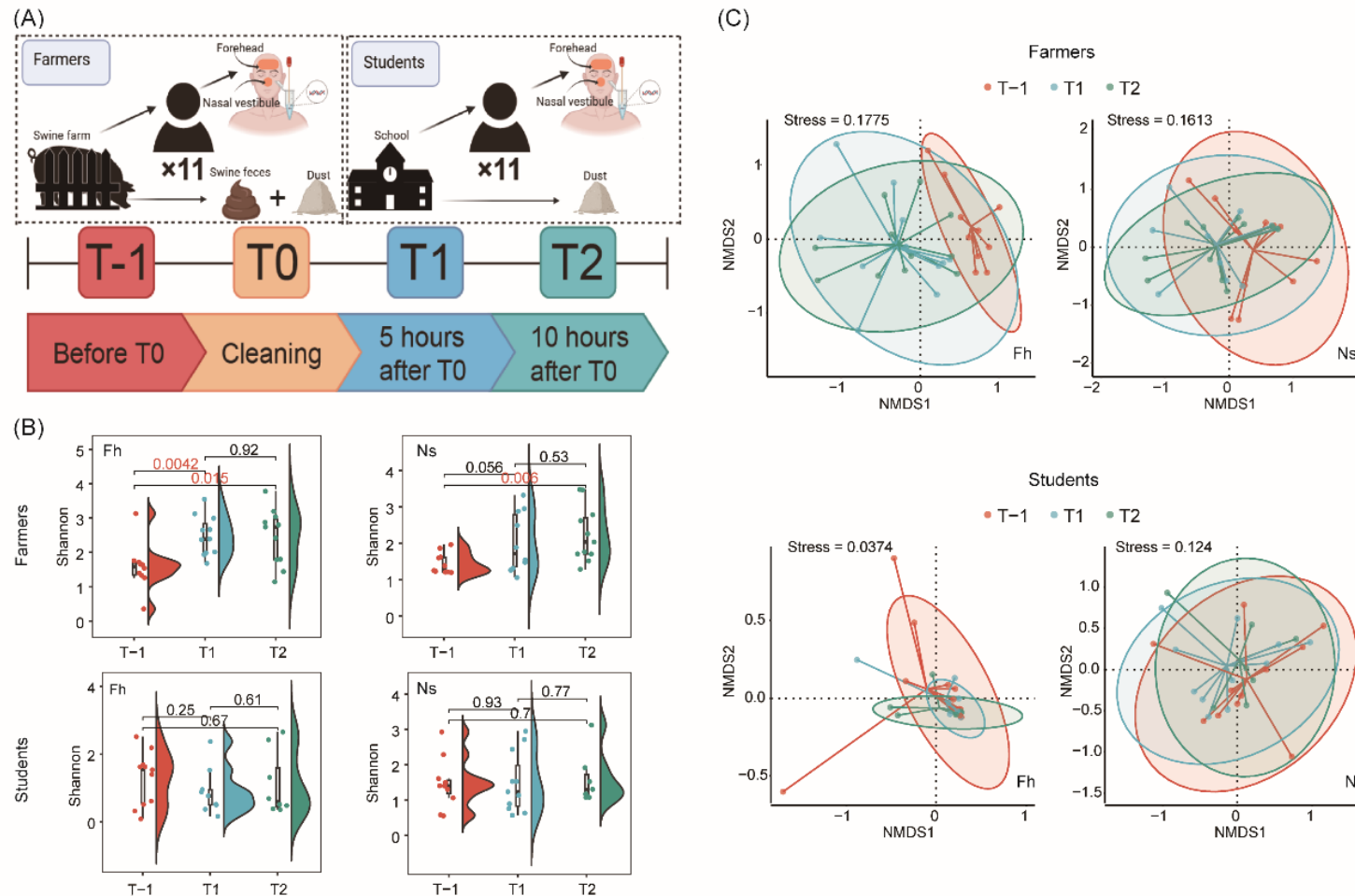


Figure 1 Changes in skin microbiota diversity following environmental exposure.



Results

- Phyla: Dominant phyla did not change; Genera: The genera with the most significant changes were *Lactobacillus*, *Brevibacterium* and *Enterococcus*. Species: The low abundance species changed significantly, while the high abundance dominant species remained relatively stable.
- A total of 42 distinct microorganisms were found, most of which belonged to *Staphylococcus* and *Corynebacterium*.

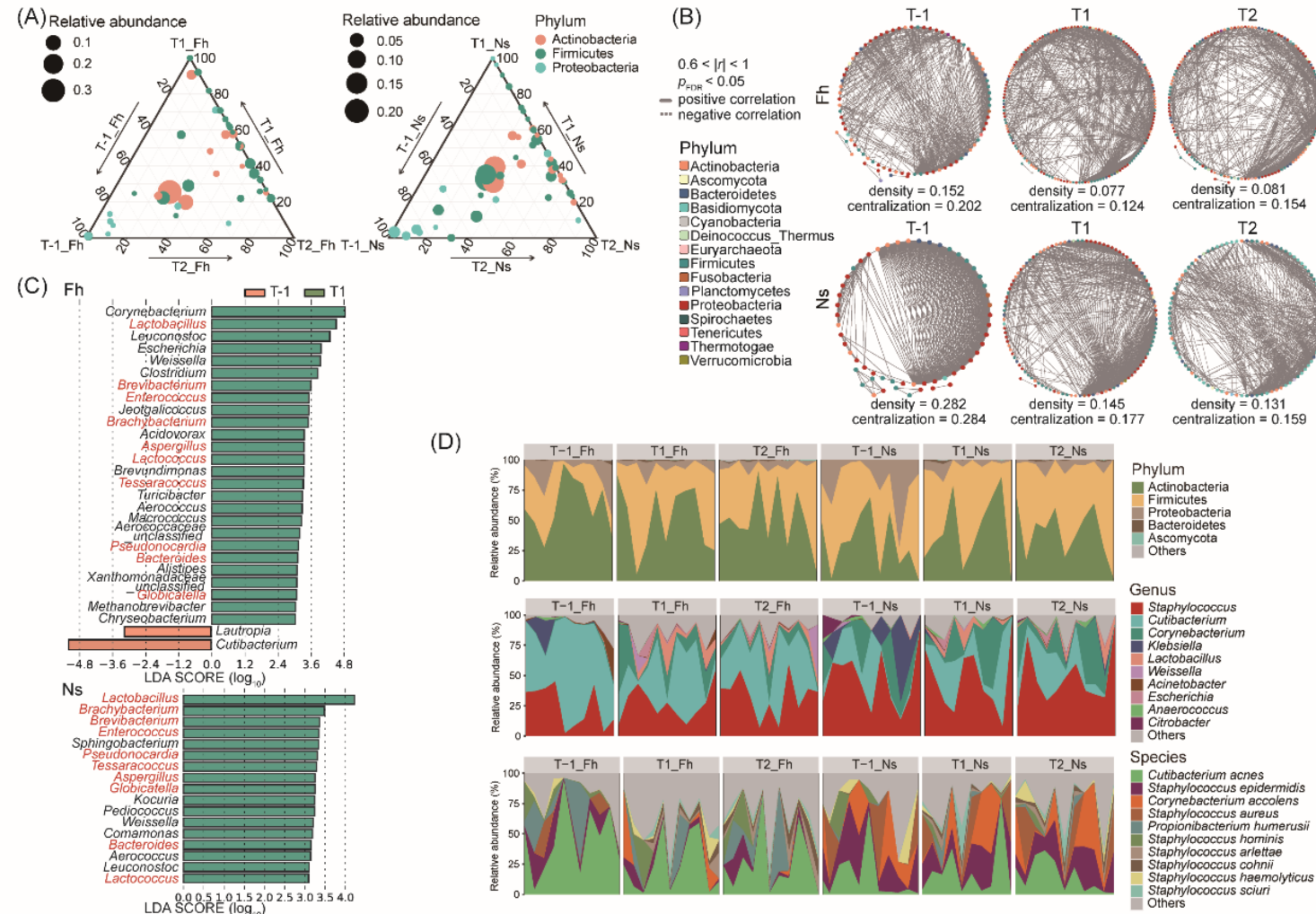


Figure 2 The variation of workers' skin microbiota composition across time points.

Results

- Environmental dusts were the main drivers of skin microbiome alteration after occupational exposure.
- The significantly altered species demonstrated close phylogenetic relationships to environmental microbiome.

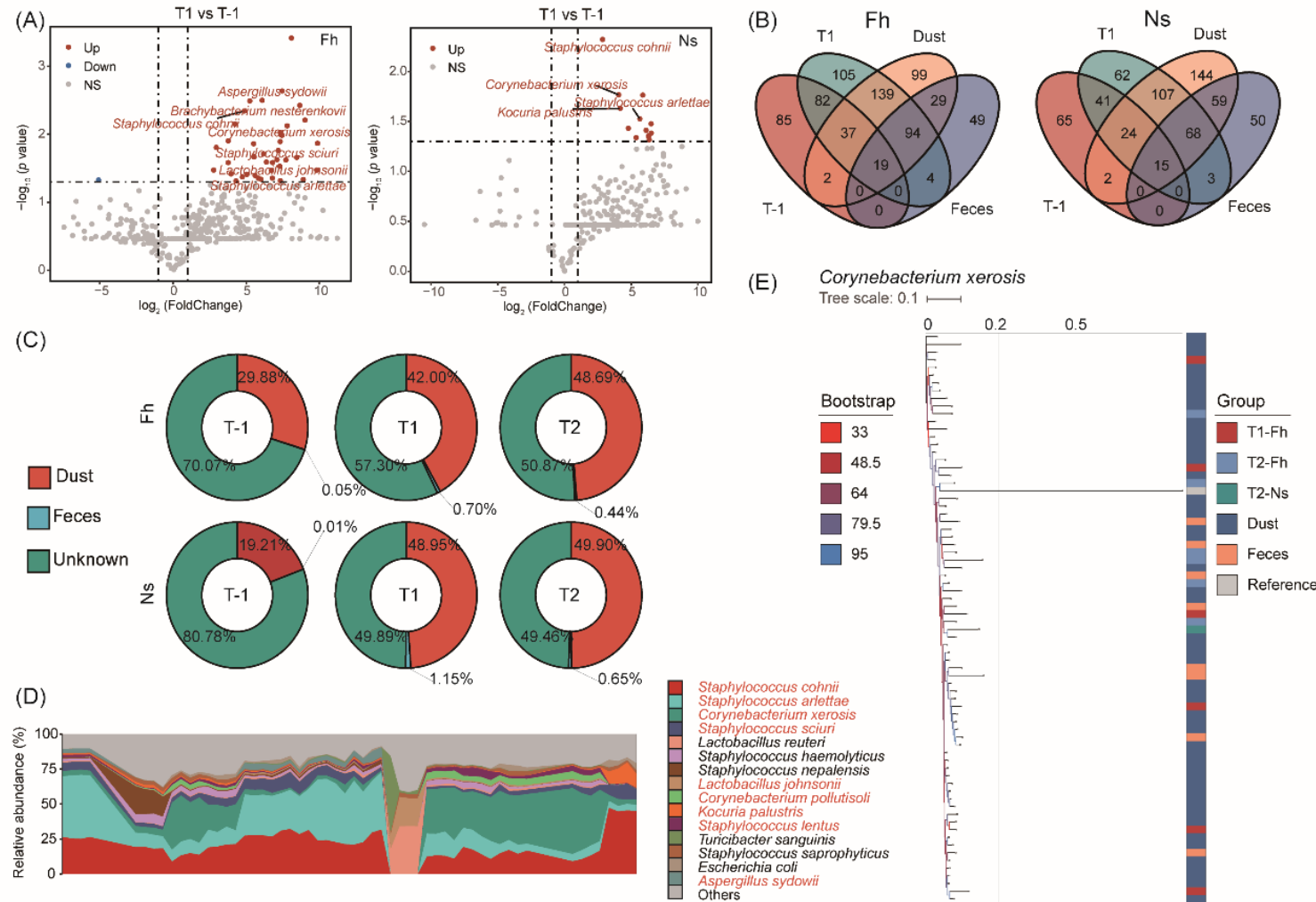


Figure 3 Transmission of microbes from the swine farm environment to workers' skin.



Results

- Diversity and abundance of human skin resistome significantly increased in response to exposure in farm.
- The structure of human skin resistomes displayed similar patterns to that of dust yet differed from that of swine feces.
- The most significantly elevated ARG type was the lincosamide resistance gene.

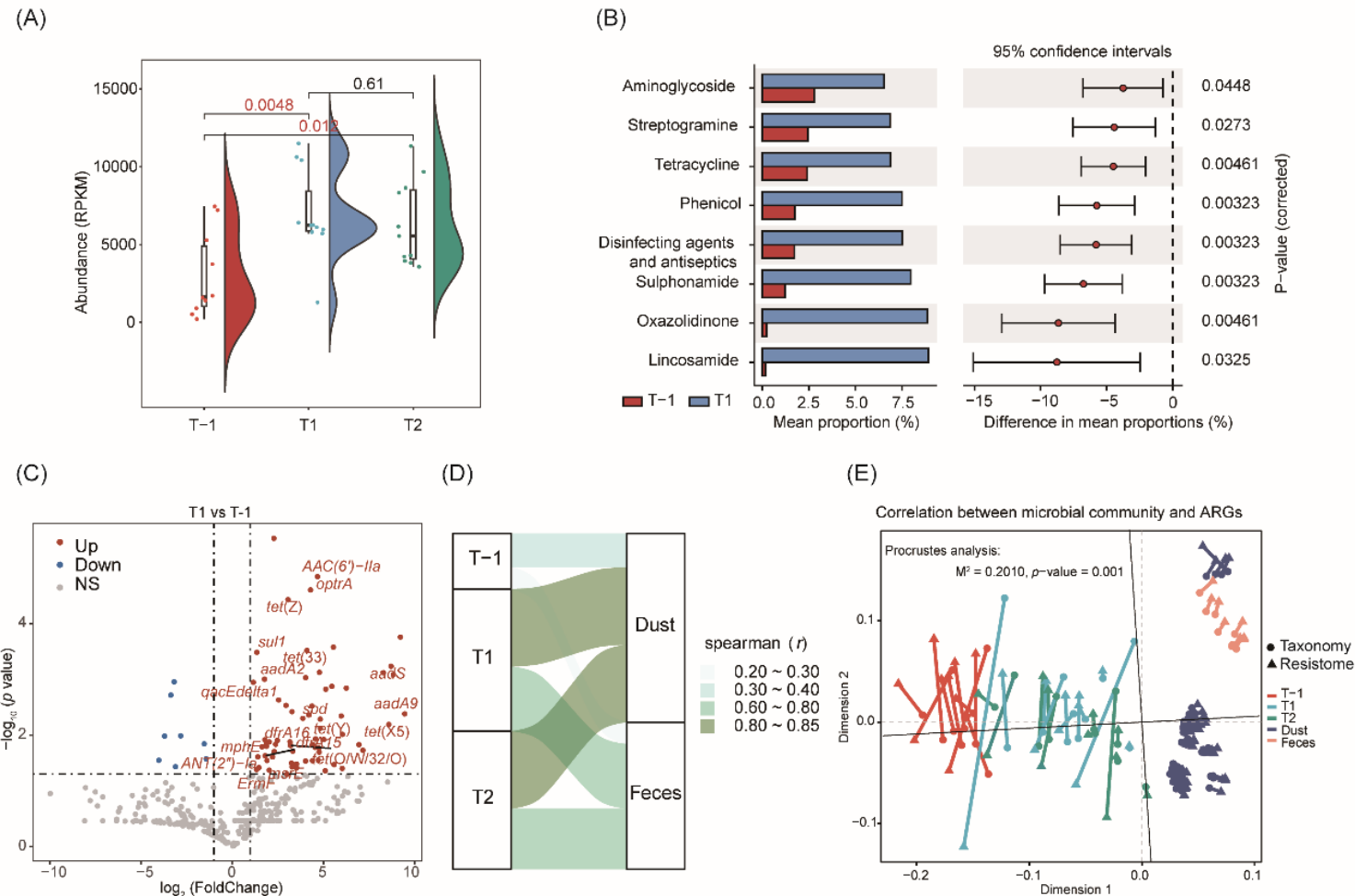


Figure 4 Antibiotic resistome structure was influenced by occupational exposure.



Summary

(1) 5 hours of exposure is sufficient to alter the microbiota and ARG structure of skin and these changes were retained once formed, wherein the environmental dust is a major driver of the change.

(2) Acquired ARB from swine farm are able to stably persist on human skin, indicating the potential risk of transmission of such ARGs among ecologies.

(3) It is necessary to take corresponding intervention measures in the production process to reduce the possibility of ARGs and ARB transmission.

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