

Profiling the agricultural labor-OME: Showering disrupts work-related shifts in swine worker skin microbiomes, resistome, and mobilomes

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Objective

Workers in swine facilities have frequent and varied contact with pigs during their workday and may harbor a higher prevalence of some bacteria (e.g., *Staphylococcus aureus*) compared to the general public. Close contact with swine is a risk factor for this increased prevalence. However, it is unknown whether frequent exposure to swine results in detectable and sustained impacts to worker microbiomes and critical genes within microbiomes responsible for antimicrobial resistance (i.e. the 'resistome') as well as horizontal gene transfer potential via mobile genetic elements (i.e. the 'mobilome'). We aimed to profile the microbiome-resistome-mobilome of swine workers of a commercial farm, and to determine whether this profile changes throughout the course of a typical workday.

Methods

Workers in a commercial Minnesota farrowing unit were enrolled into a cross-sectional study, involving taking composite skin-swab samples from four loci (hands, antecubital and popliteal fossae, and axillae), at three intervals during their workday (i.e. pre-showering in, end of work, and immediately post-showering out just prior to exiting the facility). Dorsal swabs of sows or piglets in pens were collected and matched to each worker directly contacting pigs in each pen. Resulting gDNA samples were subjected to enrichment for ARGs, mobile genetic elements, and virulence genes using custom probes and shotgun metagenomic sequencing. Microbiome profiling was performed via 16S rRNA V3-V4 sequencing. Custom bioinformatic pipelines were used to quantitate the microbiome, resistome, and mobilome composition; and to compare these compositions between pigs and workers; and between samples collected throughout the workday.

Results

Initial results show a shift in the overall worker skin microbial composition at phylum, family, and genus levels in samples collected prior to the start of the workday (i.e. 'pre-showering-in') vs end of work (PERMANOVA $P < 0.001$). Samples collected post-showering out indicated a reversion from a swine-like skin microbiome at the end of work, to that of the composition observed at the start of the workday (PERMANOVA

$P < 0.001$). These statistical results correlate with microbial network models predicting highly dynamic shifts in community organization and dominance of keystone species following swine exposure and again after showering. While group-level AMR genes and type-specific MGE mechanism richness differs across sampling timepoints, the overall resistome and mobilome composition remains stable throughout the course of the workday.

Conclusions

Though human skin microbiome composition of healthy adults is known for its remarkable stability over time scales and daily perturbations, our results demonstrate that occupational exposures significantly impact swine worker skin microbiomes. However, showering as an intervention that is historically used to control entry and dissemination of swine pathogens, may inadvertently dampen the impacts of work exposures on worker skin microbiomes.

Keywords: Antimicrobial resistance, Mobile Genetic Elements, Metagenomics, Worker, Biosecurity

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