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Abstract book



Result: Leptospire were detected in 11 of the (MDA) samples from both ovine and bovine processing areas at the splitting saw, evisceration, exsanguination and pelt removal. There was no evidence of leptospire in samples taken in the boning or meat cutting areas, or in the five blanks taken. Two of the original DNA samples, both from the ovine pelt removal area, also tested positive for leptospire.

Discussion: This is the first study to show that leptospire can be detected in a bioaerosol within an abattoir, suggesting a possible route of transmission to meat workers. The organism was detected at locations adjacent to slaughter, pelt removal and evisceration, with the strongest evidence near ovine pelt removal. This distribution directly mirrors the pattern of risk shown in serological testing of meat workers.

Keywords: Leptospirosis, bioaerosol, slaughterhouse

P8. Toward the definition of *Aedes albopictus* and *Aedes koreicus* pathobioma from an area of recent invasion in northern Italy.

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Aedes mosquitoes are considered highly successful invasive species globally. They are also vectors of several viruses of medical importance. As other species, they host a community of bacteria in their midgut, which can play an important role in affecting their fitness, physiology, food digestion, metabolism, immunity, adaptation to new environmental conditions including the capacity to transmit pathogens. Using a metagenomic approach we characterized the microbial community of two mosquito species of medical relevance: *Aedes albopictus* and *Aedes koreicus*. Using high-throughput sequencing we analysed the v3-v4 hypervariable region of 16S rRNA of the midgut from 30 non-fed *Ae. albopictus* females and 30 non-fed *Ae. koreicus* females from the Province of Trento. Alpha and beta diversity indices were used to assess the diversity and richness of bacterial communities in both mosquito species and the differences among countries. The two species showed a large core microbiota, including 75.98% of the identified Operational Taxonomic Units, largely composed by species of the genus *Pseudomonas*, suggesting a common developmental environment. Notably Wolbachia, an intracellular endosymbiont of mosquitoes known to modulate their ability to transmit many pathogens, was present in *Ae. albopictus* (0.1%) but not in *Ae. koreicus*, while *Asaia* spp. was found mainly in *Ae. koreicus* (14.42%) and in very low proportions in *Ae. albopictus* (0.07%). In conclusion, assessing the composition and diversity of invasive mosquito species gut microbiota provides the basis for the development of further research studies aimed at characterizing the effect of environmental conditions on vectorial capacity and therefore the actual disease hazard within a new habitat.

Keywords: *Aedes albopictus*, *Aedes koreicus*, pathobioma, northern Italy.

P9. The transcriptional factor sigma H as a virulence regulator in *Corynebacterium pseudotuberculosis*.

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