

# Impact of host genetics in the house mouse hybrid zone on microbiome composition and antimicrobial resistance

*Tuesday, 10 October 2023 15:03 (1 minute)*

Antibiotic resistance (AR) is a priority public health problem. Selection mechanisms for AR are well understood, while the transmission of antibiotic resistance genes (ARGs) is a comparatively under-researched topic. Particularly, the links between molecular, genomic, bacterial community, and host community level are rarely analysed in an overarching manner. Given the importance of understanding how bacteria carrying ARGs interact in the microbiome and with the environment of their hosts, here we used an amplicon sequencing approach, to simultaneously study bacteria and predict ARGs composition in natural populations from house mice (*Mus musculus*). We compared gastrointestinal bacterial diversity, composition and abundance across a gradient of pure and hybrid genotypes in the European house mouse hybrid zone between the subspecies *M. m. musculus* and *M. m. domesticus* at different geographical and temporal scales. We detected extreme phenotypes of bacterial abundance with the hybridisation of mice. Some bacteria and overall ARGs have elevated abundance in hybrid genotypes. In contrast, the abundance of other bacteria, but not of any ARGs, are reduced in hybrids compared to parental mice. Our results confirm that host genotype drives the abundance of gastrointestinal bacteria and raises the question whether environmental covariates of the hybrid zone or host genotypes influence the occurrence of ARGs in natural populations of house mice.

## Keywords

ARG, Mice, Genetics, Microbiome

## Registration-ID code

622

## Professional Status of the Speaker

Postdoc

## Junior Scientist Status

Yes, I am a Junior Scientist.

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**Session Classification:** Lunch & Poster Viewing (P2)

**Track Classification:** Environmental factors & Ecology of Zoonotic Infections