

MHC genes regulate host gut microbiome in bats with acute coronavirus infections

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Genes of the exceptionally polymorphic Major Histocompatibility Complex (MHC) region play a critical role in pathogen defence and the cross-talk with host commensals. Yet, it remains unclear how the gut microbiota response to infection and to what extent this response is influenced by host immunogenetics. Here, we aimed to disentangle their interplay in roughly 600 African hipposiderid bats, which harbour the most recent coronavirus ancestors to HCoV-229E and SARS-like CoVs, both of which replicate enterically, where MHC class II expression is densest and gut microbiota flourishes. We previously linked host MHC diversity and certain MHC supertypes to CoV infections. Now we uncovered that gut microbial alpha-diversity differed between CoV infections, and microbial network structure varied decisively between uninfected, singly and co-infected bats with potentially pathogenic bacteria taking the role of hub taxa in CoV infected bats. Joint species distribution model underscores that several mutualistic and potentially pathogenic taxa differ between infection status. When host immunogenetic information in form of MHC diversity and supertypes was added, several interactions emerged in prominent bacterial genera. Our work suggests that host immune genes and CoV infection influence gut microbiota independently, but also highlights that their interaction shapes host susceptibility to CoV infections and the establishment and persistence of a pathobiome.

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Microbiome, MHC, Coronavirus, Ghana, co-infections

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No, I am not a Junior Scientist.

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