Hepatitis E virus infection dynamics in endemically infected pig farms

Results from longitudinal and genetic data



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Aim: Compare infection dynamics of HEV in fattening pig farms with a high vs. low seroprevalence of HEV

Methods

Farms

- Farm 1: Seroprevalence slaughter pigs 75%
- Farm 2: Seroprevalence slaughter pigs 40%
- 3 fattening compartments
- 36 pens (8-12 pigs/pen)
- Pens as unit of observation
- Last weeks batch A, and batch B and C followed: ~38 weeks



Sampling and Twice blood sampling (4/pen)

lab analysis

- RT-PCR on feces & antibody ELISA on serum
 - Illumina sequencing each batch: 2/pen

Analyses

- Alignment to reference (HEV3, human, 2017)
- Sequences with max. 5% gaps
- Phylogenetic tree (RAxML-NG)
 - Maximum likelihood
 - Substitutions GTR+
 - 1000 bootstraps •
- Visualizations: R (longCatEDA, ggTree)

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