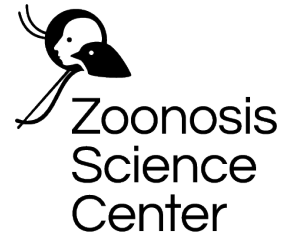




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## **Master level degree project at the Zoonosis Science Center (IMBIM, BMC) on arthropod viromics**

Next-Generation Sequencing (NGS), and in particular RNAseq, has showed that RNA viruses are common and abundant in all forms of life. It is clear that the knowledge concerning RNA viruses – their diversity, host-association, evolutionary history, interaction with other microbes, genome structure and function – is very limited (Shi, 2016).

In this very exciting project, we wish to (i) study and characterise novel viruses in arthropods; (ii) infer host-parasite evolutionary history; (iii) study microbe interactions and ecology of commensal and pathogenic microbes.

In this project, the student would work directly with NGS research data that needs to be analysed – from quality control of fastq-files to inferring evolutionary history. Lengthwise, this is suitable for a 45hp project (30hp at the very minimum).

The student will need to be (a bit) familiar with a Linux and bash-scripting environments. A background and interest in viruses, molecular evolution and phylogenetic analysis techniques and procedures is also good.

For more information, contact:

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References:

Shi et al. Redefining the invertebrate RNA virosphere. *Nature*. 2016 Nov 23. doi: 10.1038/nature20167. <https://www.ncbi.nlm.nih.gov/pubmed/27880757>

Pettersson et al. Characterizing the virome of Ixodes ricinus ticks from northern Europe. *Sci Rep*. 2017 Sep 7;7(1):10870. doi: 10.1038/s41598-017-11439-y. <https://www.ncbi.nlm.nih.gov/pubmed/28883464>