BIOLOŠKI ODSJEK, PMF

HRVATSKO EKOLOŠKO DRUŠTVO

POZIV
na predavanje

15.6.2022. u **13:30** sati, u **Vijećnici Biološkog odsjeka**, Rooseveltov trg 6 (prizemlje desno), Zagreb, pod naslovom:

Exploring *Aphanomyces astaci*'s virulence: variability and genomic determinants

The causative agent of the crayfish plague, *Aphanomyces astaci*, is listed as one of the 100 most invasive species worldwide. Since its introduction into Europe in the 19th century caused mass mortalities among European freshwater crayfish populations, although not all strains of the pathogen are equally deadly for the host crayfish. Understanding the mechanisms of pathogen virulence could prove crucial to inform conservation actions. Therefore, in our lab we are working to characterize the virulence and genomic determinants of all major *A. astaci* strains occurring in Europe. A series of 15 standardized infection experiments with noble crayfish showed great variance of virulence among the different strains. This high virulence variability is not echoing the tentative virulence classification based on the currently used genetic markers, as some supposedly lowly virulent strains caused high mortality and vice versa. The results from the controlled infection experiments will be integrated with data on hyphal growth speed and spore production of the used strains, as additional factors to characterize virulence. In the meantime, we aim to sequence and assemble the genomes of all *A. astaci* strains, using a combination of Illumina short-reads and Oxford Nanopore long-reads. This will allow us to generate a representative pan-genome of *A. astaci*, to be used as reference for a genome-wide association study, to identify associations between genetic regions in the *A. astaci* genome with its respective phenotype (virulence), and to infer whether or not variation in strain virulence is coded within the pathogen´s genome.

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