

## **Programme & Abstracts**

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hosted by: **Micah Dunthorn & Nadine Graupner Eukaryotic Microbiology University of Duisburg-Essen** 

## Inheritance of mating types in Paramecium calkinsi

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The system of mating types (MT) has appeared multiple times in evolution of eukaryotes. MT form a sexual compatibility system in ciliates which is used to prevent self-fertilization and to increase genetic exchange within a population. Various kinds of MT systems, different numbers of MT, and diverse mating type genes are present in different groups of Ciliophora. Ciliates are a perfect example for MT investigation because they easily proceed through mating under laboratory conditions. However, mechanisms of mating type determination and inheritance are highly diverse even among closely related species. Paramecium (Oligohymenophorea) is the best-known model ciliate. MT determination and expression patterns for some species were described recently (Singh et al. 2014; Orias et al. 2017; Sawka-Gadek et al. 2020). For instance, three different types of MT inheritance (mendelian, maternal, and stochastic) are known in 16 sibling species of the P. aurelia complex. Paramecium bursaria and P. putrinum have a system of multiple MT. At the same time, the MT systems of many Paramecium species have not been sufficiently studied yet. The less known group - the species of *Cypriostomum* subgenus. *Paramecium polycaryum* was even thought to be incapable of mating, while data on other species remain fragmentary. We manage to figure out the mode of MT inheritance for *Paramecium* calkinsi. We established the synchronization protocol allowing to obtain sexually reactive *P. calkinsi* cultures. The cells become capable of mating after mild starvation at 25°C. Several rounds of conjugation revealed that *P. calkinsi* is characterized by maternally inherited determination of MT. It is the first case of maternal inheritance outside of Paramecium subgenus. This type of inheritance was previously described only for some species of the *P. aurelia* complex which are not closely related to *P.* calkinsi. Thus, our finding is important to understand the MT evolution within Paramecium genus. Supported by RFBR 19-04-00710a.