

# 13<sup>th</sup> EUROPEAN MULTICOLLOQUIUM OF PARASITOLOGY

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21




changing climate  
changing parasites




Programme  
& Abstract  
Book

Belgrade, Serbia  
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PROGRAMME  
&  
ABSTRACT BOOK

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## WILDP1

**MOLECULAR EPIDEMIOLOGY OF TRICHOMONADS IN WILD WETLAND BIRDS IN THE NETHERLANDS**W.J.M. LANDMAN<sup>1</sup>, M. SAWANT<sup>2</sup>, N. GANTOIS<sup>2</sup>, F.A. MAJOOR<sup>3</sup>, J.H.H. VAN ECK<sup>4</sup>, E. VISCOGLIOSI<sup>2</sup><sup>1</sup>Royal GD, Deventer, Netherlands; <sup>2</sup>manasi.sawant@pasteur-lille.fr, Institut Pasteur of Lille, Center for Infection and Immunity, Inserm U1019, UMR CNRS 9017, University of Lille, CHU of Lille, Lille, France; <sup>3</sup>SOVON Vogelonderzoek Nederland, Nijmegen, Netherlands; <sup>4</sup>Faculty of Veterinary Medicine, Utrecht University, Utrecht, Netherlands

**Background.** Severe granulomatosis in productive layers due to *Tetratrichomonas gallinarum* strain 13/16632 infection occurred in 2013 and 2017 on farms situated in a wetland area in the Netherlands. These outbreaks were mainly characterized by persistent increased mortality of hens and by a high within flock incidence of granulomas.

**Objectives.** Our aim was to evaluate the potential of wild wetland birds to act as a reservoir of virulent trichomonads such as *T. gallinarum* especially for chicken rearing farms.

**Material and Methods.** A prevalence survey on trichomonads was performed by analysing cloaca swabs of 526 birds belonging to 13 species of wetland birds. The number of birds sampled ranged from 1 to 275 per species. Birds were sampled at 15 locations, distributed over the Netherlands. DNA extracted from the cloaca swabs was subjected to a nested PCR assay using trichomonad specific primers targeting the ITS1 – 5.8S rRNA – ITS2 region. Positive nested PCR products were either cloned before sequencing or directly sequenced.

**Results.** Trichomonads were detected in nine bird species. The overall prevalence was 9% (47/526), while the prevalence in the five species of which a substantial number of birds were examined (at least 39 per species) ranged from 4 to 24%. Three trichomonad species were found: *T. gallinarum*, *Trichomonas tenax* and *Simplicimonas* sp. of which *T. gallinarum* dominated. The virulent *T. gallinarum* strain 13/16632 was not detected, but closely related strains were identified. Phylogenetic analysis revealed that all *T. gallinarum* isolates belonged to two clusters within lineage 15 of *Tetratrichomonas* lineages. All *T. tenax* isolates were identical and clustered with reference strains, while *Simplicimonas* sp. isolates showed large genetic diversity. Some isolates may represent a new species of the genus *Simplicimonas*.

**Conclusion.** We highlight that trichomonads are widespread and circulate abundantly amongst wetland birds, questioning, amongst others, its relevance for commercial poultry.

## WILDP2

**POSSIBLE INFLUENCE OF B CHROMOSOMES ON THE PREVALENCE AND ABUNDANCE OF INTESTINAL NEMATODE PARASITES OF THE YELLOW-NECKED MOUSE (*Apodemus flavicollis*)**Borislav ČABRILLO<sup>1</sup>, Jelena BLAGOJEVIĆ<sup>2</sup>, Mladen VUJOŠEVIĆ<sup>2</sup>, Milan MILJEVIĆ<sup>2</sup>, Božana TOŠIĆ<sup>1</sup>, Olivera BJELIĆ ČABRILLO<sup>1</sup><sup>1</sup>olivera.bjelic-cabrilo@dbe.uns.ac.rs, University of Novi Sad, Faculty of Sciences, Department of Biology and Ecology, Novi Sad, Serbia; <sup>2</sup>University of Belgrade, Institute for Biological Research “Siniša Stanković”, National Institute of Republic of Serbia, Belgrade, Serbia

**Background.** B chromosomes are supernumerary chromosomes that have been discovered in over 1000 eukaryote species. They show remarkable variation in structure and behaviour, their only common trait being their conditional dispensability. The influence of these genetic elements on their carriers is still debated, with the two most accepted models of their maintenance being the parasitic and the heterotic model.

**Objectives.** The purpose of this study was to investigate the possible influence of B chromosomes on quantitative characteristics of intestinal nematode infection in the yellow-necked mouse (*Apodemus flavicollis*).

**Material and Methods.** A total of 305 mice were sampled across 18 localities on the territory of Serbia over five years. Every individual with more than 48 chromosomes was considered to have Bs. After dissection, intestinal nematodes were extracted and identified. An analysis of Bs influence on parasite prevalence and

abundance was conducted, using the exact unconditional test and generalized linear modelling respectively. **Results.** Nine intestinal nematode species were detected in the host sample. In the total host sample, both prevalence and abundance of intestinal nematodes were greater in Bs carriers. Two nematode species, *Aspicularis tetraptera* and *Mastophorus muris*, had significantly higher prevalence in the B+ subset of the host sample. Similarly, B chromosomes explained a significant proportion of abundance variation of the nematode species *Syphacia frederici*, with its abundance greater in Bs carriers.

**Conclusion.** While the results of this study show a possible connection between Bs presence and higher prevalence and abundance of intestinal nematodes, this finding is purely correlational. Previously published data indicate a complex effect of B chromosomes on host characteristics and survival through various molecular pathways. Bs carriers may reap the benefits of increased survival prospects as a by-product of the selfish behaviour of the chromosomes themselves, blurring the line between the parasitic and heterotic model.

### WILDIP3

#### SYMBIONTS OF BIVALVE MOLLUSCS OF THE KANDALAKSHA GULF AND THE ONEGA BAY OF THE WHITE SEA

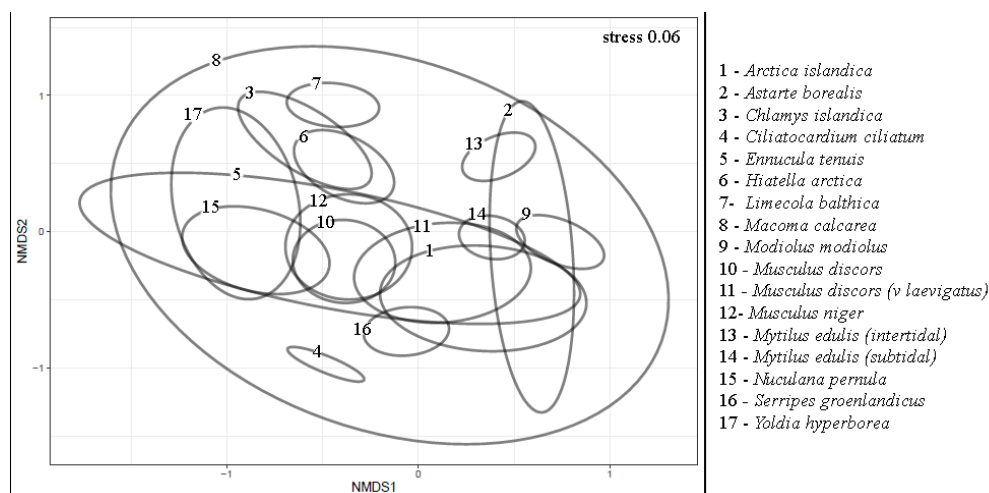
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**Background.** The parasitological examination of bivalves is necessary for understanding life cycles realized at a particular area. We studied the symbiofauna composition of mass species of bivalve molluscs in the southern and western parts of the White Sea.

**Material and Methods.** During years 2009-2021 we collected bivalves from subtidal and intertidal zones at three areas in the Kandalaksha Gulf and three areas in the Onega Bay (separated by tens to hundreds of kilometres) (1-20 sampling sites at each area). 2499 specimens of 24 bivalve species were collected (8 to 393 specimens of each species). Mainly we focused on metazoan symbionts (also noting the presence of Protista).

**Results.** The 17 taxa of metazoan symbionts included representatives of 4 phyla. All taxa excluding parasitic Digenea are considered commensals. Digenean sporocysts and most commensals (except for “turbellaria”) were host-specific, while digenean metacercaria used several species as hosts. Comparison of symbiofaunas of different bivalve species is represented as non-metric multidimensional scaling (Figure 1).



**Figure 1.** Non-metric multidimensional scaling (nMDS) ordination of the molluscs infected with turbellaria and trematoda based on the matrix of Bray-Curtis dissimilarities. Ellipses represent 95% confidence intervals of host species centroids.

**Conclusion.** The distribution of symbionts among the bivalve species was not uniform. The composition of symbiofauna of the studied bivalves was correlated with the host’s phylogenetic position and ecology.

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