

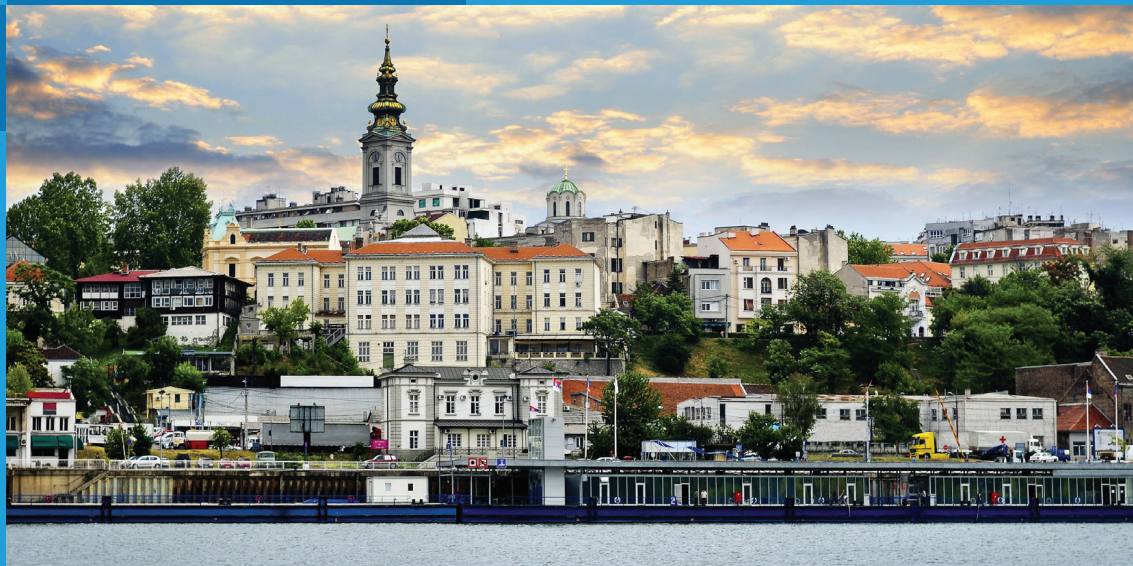
# 13<sup>th</sup> EUROPEAN MULTICOLLOQUIUM OF PARASITOLOGY


**emop** 20<sup>XIII</sup>  
21

changing climate  
changing parasites

Programme  
& Abstract  
Book

Belgrade, Serbia  
**October**  
**12-16, 2021**





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13<sup>th</sup> European Multicolloquium of Parasitology  
Belgrade, Serbia  
October 12-16, 2021

# PROGRAMME & ABSTRACT BOOK

IMPORTANT NOTICE:

The abstracts included in this book are the proceedings of the 13<sup>th</sup> European Multicolloquium of Parasitology, as provided by the authors. The Organizers of the EMOP2021 are not responsible for the scientific content of the abstracts.

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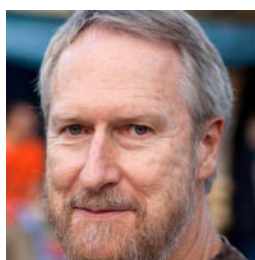


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# EDITORIAL



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Dear colleagues,

On behalf of the Organizing Committee, the Serbian Society for Parasitology and the European Federation of Parasitologists (EFP), it is our great pleasure to welcome you to the 13<sup>th</sup> European Multicolloquium of Parasitology (EMOP XIII, Belgrade, Serbia, 12-16 October 2021). Here, you will find the programme and the abstracts of all communications to be presented.

At the heart of this edition of the EMOP is CHANGE. Changes that the world is currently going through, including climate change, migrations of both people and animals, and changes in food habits, favour the persistence and contribute to the re-emergence of parasitic infections at the global level. We tried to capture this in the motto of EMOP 2021, back when it was supposed to be EMOP 2020. The mere fact that this is the first time in its 50-year long tradition that an EMOP has had to be postponed (for more than a year after the originally set dates), speaks even louder about the changes that we are living through. In this case, of course, changes caused by the covid-19 pandemic that has claimed more lives and disrupted life like no other peacetime event in a hundred years.

So, we should all be proud that there will be an EMOP at this time, and that we are meeting, whether on-site or online, to exchange knowledge and ideas, and even share some hugs, or smiles at least. And there is an exciting programme to benefit from, on the latest discoveries and technological developments, tackling major current global issues such as Climate change and parasite re-emergence, Migrations and parasites, Food and Water-borne parasitology, the One Health approach to combatting parasitic diseases, to mention just a few. In addition, because of the geographical position of the host country, developments in the field in the region of South East Europe are under the spotlight.

The number of papers submitted to EMOP 2021 that you can find in this volume may not be as large as would have been expected before the “new normal”. But it has been an endeavour to reach this point, both from us as organizers and from you as participants. Moreover, whatever the programme has lost in quantity may have been made up in quality, since the structure of the conference consists largely of symposia on particular topics organized by leaders in the field, with invited talks by top experts. This means our programme represents not only a rich learning experience, but also an excellent cross-section of current developments and perspectives in the broad field of parasitology in Europe and beyond.

We wish you all a stimulating and fulfilling congress.

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## INVITED LECTURES

### HORIZONTAL GENE TRANSFER PROVIDES INSIGHTS INTO THE EVOLUTIONARY HISTORY AND BIOLOGY OF *Trichinella*

Dante ZARLENGA

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**Background.** Deciphering processes that drive species diversity is key to understanding parasitism and help advance control strategies. Genomic and transcriptomic data on both parasitic and free living nematodes have been emerging at astonishing rates allowing more holistic investigations of evolution and the host:parasite interface. Sequencing has shed light on horizontal gene transfer (HGT) as a driving force in evolution and parasitism, a paradigm that has occurred independently many times among the Nematoda rather than as a single event.

**Results.** During the sequencing of the genome of *Trichinella spiralis*, we identified a cyanase gene which is typically found only in plants, bacteria and to a lesser extent fungi. In a database search, we identified a small subset of other Nematoda that also harbor this gene; however, the gene was not found in free-living worms or in organisms of the crown clade. The gene product from *T. spiralis* is biologically functional in recombinant form and resides naturally in the worm hypodermis. Phylogenetic analyses showed that cyanase proteins from the clade I nematodes *Trichinella* spp., *Trichuris* spp., and *Soboliphyme baturini*, (Subclass: Dorylaimia) formed a large, well-supported monophyletic clade with plant cyanases whereas all other cyanases within the Nematoda were monophyletic with those of bacterial origin.

**Conclusions** These results are consistent with: 1) independent HGT of the cyanase gene within parasitic nematodes but from multiple Kingdoms; 2) functional integration of the gene and encoded protein into the biology of *Trichinella*; 3) acquisition of the gene by members of the Dorylaimia over 400 million years ago prior to the divergence of the Trichinellida and Dioctophymatida, and; 4) early ancestors of the genus *Trichinella* having an association with plants or marine-derived nitrite-oxidizing bacteria given that cyanases from marine cyanobacteria and fungi clustered independent of the plant cyanases and *Trichinella*.

### HOW *Trichinella spiralis*-DERIVED EXTRACELLULAR VESICLES AFFECT DENDRITIC CELLS

Natasa ILIĆ, Maja KOSANOVIĆ, Alisa GRUDEN-MOVSESIJAN, Sergej TOMIĆ, Sofija GLAMOČLIJA, Marina BEKIĆ, Ljiljana SOFRONIĆ-MILOSAVLJEVIĆ

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*Trichinella spiralis* is a very promising candidate for modulation of immune response in sense of biasing the inflammatory towards anti-inflammatory type of response. This effect is achieved via its excretory secretory muscle larvae (ES L1) antigens which affect the maturation status and function of dendritic cells (DCs) as the most potent antigen presenting cells. ES L1 induces the tolerogenic status of DCs which leads to the mitigation of Th1 type of response and the activation of regulatory type of immune response both *in vitro* and *in vivo*. ES L1 treated DCs successfully alleviated the severity of experimental autoimmune encephalomyelitis, the animal model of human disease multiple sclerosis. Recent discovery of *T. spiralis* extracellular vesicles (TsEVs) suggested that the induction of a complex regulation of the immune response requires simultaneous delivery of different signals in nano-sized packages. This study aimed to explore whether TsEVs bare the similar potential as ES L1 to influence the status of DCs in initiation, progression and regulation of immune response. TsEVs were enriched from conditioned medium of *T. spiralis* muscle larvae by differential centrifugation and used for treatment of human monocyte derived DCs. TsEVs induced low expression of HLA DR and CD40, moderate CD83 and CD86 and increased expression of ILT3 and CCR7 on treated DCs, i.e. they induced tolerogenic DCs.

DCs generated this way possess the capacity to polarize T cell immune response towards regulatory type, with increased proportion of IL-10 and TGF- $\beta$  producing cells. These findings indicated that the ability of TsEVs to induce tolerogenic DCs favoring anti-inflammatory responses may be helpful in coping with diseases that involve Th1/Th17-, but also Th2-mediated inflammation, such as different autoimmune and allergic diseases, suggesting that potential TsEVs application could be a new therapeutic approach designed for treatment of inflammatory disorders.

**Funding source:** Institutional financing agreement №. 451-03-9/2021-14/ 200019

### WHAT DOES THE HUMORAL IMMUNE RESPONSE IN *Trichinella* INFECTIONS TELL US?

María Ángeles GÓMEZ-MORALES

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The diagnosis of *Trichinella* infections in the human host is based on the humoral immune response, in particular on the determination of the specific IgG. Moreover, the presence of such isotype in animals provides pivotal epidemiological information on parasite-host contacts. After infection, seroconversion most often occurs between the third- and fifth-weeks post infection (p.i.), although it can also take place earlier (12 days) or later (60 days) p.i., and the IgG responses can persist for years. Other isotypes such as IgM, IgE and IgA are known to be present, but their significance remains unclear. On the other hand, *Trichinella* antigens are heterogeneous, some epitopes are shared with other organisms and those highly specific maybe insufficiently sensitive due to their different expression in the developmental stages. The pleotropic immune response that accompanies trichinellosis is complicated and the data is still evolving on how best to diagnose infections. However, the actual tools for diagnosis and surveillance of these infections, as well as the knowledge on the biology of these parasites, might be exploited and combined to gather key information on the epidemiology of these infections. For example, in epidemiological investigations during a human outbreak, in which the source of infection could not be traced, and muscle biopsies were not available, the specific IgG pattern of recognition of sera from infected people on *Trichinella* proteins by western blot, showed to be an excellent tool for the identification of the aetiological agent. Furthermore, monitoring susceptible animals from different settings may provide evidences on the risk for *Trichinella* transmission or on the circulation of these parasites among those animals.

## ORAL PRESENTATIONS

### *Trichinella britovi* RECOMBINANT EXCRETORY-SECRETORY 21 kDa PROTEIN AND CHYMOTRYPSIN-LIKE PROTEIN FOR IgG ANTIBODIES LEVEL DETECTION IN TRICHINELLOSIS IN MICE AND PIGS

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**Background.** Trichinellosis occurs by consuming raw or inadequately cooked meat containing muscle larvae of the *Trichinella*. This parasite can infect a wide variety of hosts, including humans, causing a food-borne parasitic zoonosis. *Trichinella britovi* is the second most commonly identified species among infected animals and is one of the *Trichinella* spp. which may affect human health.

**Objectives.** Our study aimed to recognize *T. britovi*-specific proteins, obtain them in a recombinant form in the yeast expression system vector and verify its immunological properties, as a potential molecules for the *Trichinella* infection diagnosis.

**Material and Methods.** Proteomic analysis performed with *T. britovi* adult worm excretory-secretory antigen and muscle larvae crude extract revealed 21 kDa excretory-secretory (ES21) protein and chymotrypsin-like protein (CTRL). These proteins were chosen for expression in heterologous system. Muscle larvae from previously infected mice with *T. britovi* reference strain (ISS002) were used for total RNA isolation. cDNA