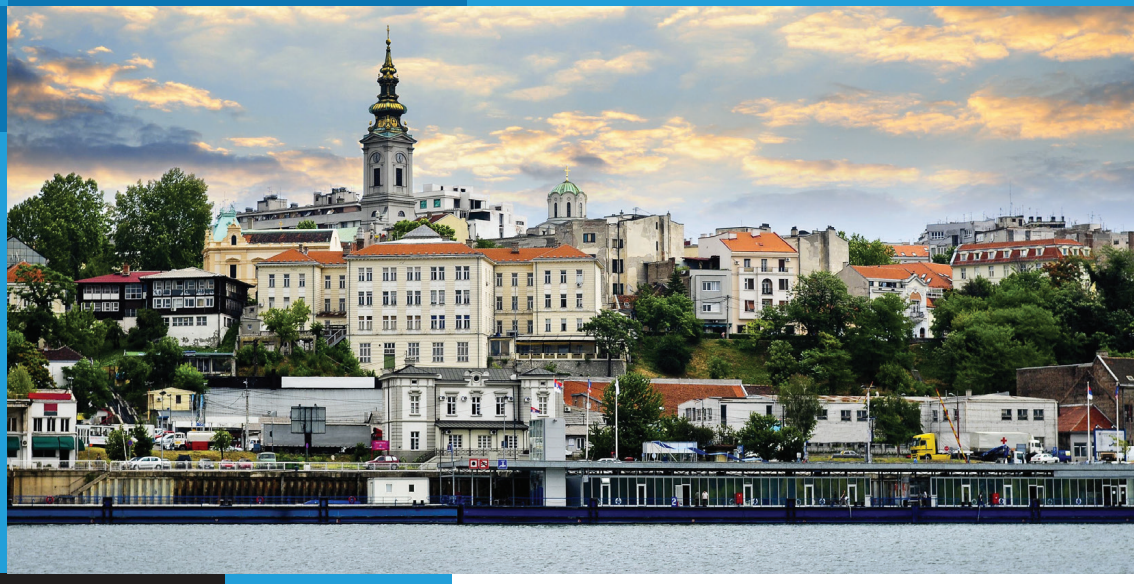
13th EUROPEAN MULTICOLLOQUIUM OF PARASITOLOGY

emop 2021 XIII

changing climate
changing parasites

Programme
& Abstract
Book



Belgrade, Serbia
October
12-16, 2021

13th 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 13th European Multicolloquium of Parasitology, as provided by the authors. The Organizers of the EMOP2021 are not responsible for the scientific content of the abstracts.

Editors:
Ivana Klun & Olgica Djurković-Djaković

Layout and prepress:
Olivera Popović

Organizer:
SERBIAN SOCIETY OF PARASITOLOGY
Belgrade, Serbia, Bulevar oslobodjenja 18/I, rm. 111
E: dps@imi.bg.ac.rs, T: +381 11 2685 788, ext. 106, W: www.parazit.org.rs

EMOP2021 Secretariat:
CONGREXPO d.o.o.
Belgrade, Serbia, Svetozara Markovića 81/5
W: www.congrexpo.co.rs

TOXOPLASMA GENETIC DIVERSITY
Organizer / Moderator: Marie-Laure Dardé

INVITED LECTURES

ANALYSING THE GENETIC DIVERSITY OF *Toxoplasma gondii* IN AN EUROPEAN COUNTRY VIA HUMAN SAMPLES

Marie-Laure DARDE[1,2,3], Karine PASSEBOSC[1,2], Marie-Fleur DURIEUX[2,3], Farid BOUMEDIENE[3], Lokman GALAL[3], Aurélien MERCIER[3], and the Network of the French National Reference Center for Toxoplasmosis
[1]CNR Toxoplasmose, pôle souches, Limoges, France; [2]CHU Limoges, Department of Parasitology, Limoges, France; [3]INSERM, Univ. Limoges, IRD, U1094 Tropical Neuroepidemiology, Institute of Epidemiology and Tropical Neurology, GEIST, Limoges, France; marie-laure.darde@unilim.fr

Toxoplasma gondii is now well known for having a spatial structure of its population. France is a cosmopolitan country with multiple origins of migrating populations. It also covers a large geographical area due to the overseas departments, from the Americas to the Indian and Pacific Oceans. The French National Reference Center for Toxoplasmosis, that receives strains or DNA samples for genotyping, has made it possible to capture the diversity of isolates circulating in patients in France, and to show how this survey can contribute to the knowledge of both local and global geographical distribution of strains. Out of a total of 2124 samples (2006-2019), a full 15-microsatellite (MS) genotype was obtained for 1344 samples (63.3%). Nine hundred and twenty nine corresponded to unique genotypes and 236 were distributed among 83 genotypes using 15-MS (2 to 12 isolates per clone). Clones were more frequent in insular environments, but we also detected Type II epidemiological clones in France circulating over a few months. This large collection has made it possible to detect new genotypes or new clonal lineages in regions where the *Toxoplasma* genetic diversity was previously unexplored, such as the French Polynesian or La Réunion islands. The diversity of countries of origin of African patients has broadened our knowledge of the population structure on this continent, despite the uncertainties about the exact locations of their infection. In a number of cases, the presence of an unusual genotype in France (i.e. different from Type II) can be explained by the consumption of imported food, but this is not always the case, raising the question of the circulation in France of uncommon native genotypes, such as HG16 or HG12 usually found in North America. The associated clinical data are used to try finding an association with genotypes.

Funding source: The National Reference Center for Toxoplasmosis is funded by Santé Publique France.

MASSIVE INTROGRESSIONS OF *Toxoplasma gondii* DOMESTIC ALLELES IN THE AMERICAS COINCIDE WITH THE RECENT INTRODUCTION OF THE DOMESTIC CAT

Lokman GALAL[1], Franck PRUGNOLLE[2,3], Meriadeg LE GOUIL[4,5], Marie-Laure DARDE[1,6], Azra HAMIDOVIC[1], Frédéric ARIEY[7], Aurélien MERCIER[1]
[1]lokmanmagalal@gmail.com INSERM, Univ. Limoges, CHU Limoges, IRD, U1094 Tropical Neuroepidemiology, Institute of Epidemiology and Tropical Neurology, GEIST, Limoges, France; [2]Laboratoire MIVEGEC (Université de Montpellier-CNRS-IRD), 34394 Montpellier, France; [3]Centre of Research in Ecology and Evolution of Diseases (CREES), Montpellier, France; [4]Groupe de Recherche sur l'Adaptation Microbienne, EA2656 Université de Caen Normandie, Caen, France; [5]Virology Lab, Department of Biology, Centre Hospitalier Universitaire de Caen, 14000 Caen, France; [6]Centre National de Référence (CNR) Toxoplasmose/Toxoplasma Biological Center (BRC), Centre Hospitalier-Universitaire Dupuytren, Limoges, France; [7]INSERM 1016, Institut Cochin, Service de Parasitologie-Mycologie, Hôpital Cochin, Université de Paris, Paris, France

Toxoplasma gondii, a cyst-forming apicomplexan parasite of virtually all warm-blooded species, is the etiologic agent of toxoplasmosis, a disease causing substantial public health burden worldwide. Its wide range of host species and its global occurrence probably complicate the study of its evolutionary history, and conflicting scenarios have been proposed to explain its global spread. By analysis a global set of 156 genomes and by providing the first direct estimate of *T. gondii* mutation rate, we show that major Old World domestic clonal

lineages have spread from Europe and Africa to the Americas in the last few centuries and hybridized with New World specific clades. These events coincide with the recent expansion in the New World of the domestic cat and of a number of rodent species, the main hosts of *T. gondii* in the domestic environment. By combining environmental and functional data to selection inference tools, we identify the top candidate genes under selection in these hybrid populations of North and South America. We show that a unique domestic allele inherited from the recently introduced Old World lineages has been selected in these emergent domestic populations in the New World. The selection of this domestic allele is most parsimoniously explained by local adaptation to the domestic ecotype and to transmission by domestic cats.

ORAL PRESENTATIONS

GENOME-WIDE SINGLE NUCLEOTIDE VARIATION IN *Toxoplasma gondii* TYPE II ISOLATES FROM EUROPE

Pavlo MAKSIMOV[1], Simone CACCIO[5], Maike JOERES[1], Franz J. CONRATHS[1], Bretislav KOUDELA[2,3], Radu BLAGA[4], Mercedes FERNÁNDEZ-ESCOBAR[6], Rafael CALERO-BERNAL[6], M. Luis ORTEGA-MORA[6], Pikka JOKELAINEN[7], Gereon SCHARES[1]

[1]pavlo.maksimov@fli.de, Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health, Institute of Epidemiology, Greifswald-Insel Riems, Germany, [5]Italian National Institute of Health (ISS), Rome, Italy; [2]Central European Institute of Technology (CEITEC), University of Veterinary Sciences, Brno, Czech Republic; [3]Faculty of Veterinary Medicine, University of Veterinary and Pharmaceutical Sciences, Brno, Czech Republic; [4]ANSES, INRAE, Ecole Nationale Vétérinaire d'Alfort, UMR BIPAR, Laboratoire de Santé Animale, Maisons-Alfort, F-94700, France; [6]SALUVET, Animal Health Department, Faculty of Veterinary Sciences, Complutense University of Madrid, Spain; [7]Statens Serum Institut (SSI), Copenhagen, Denmark

Background. *Toxoplasma gondii* is a highly prevalent protozoan parasite that globally infects a broad range of animals, including humans. A better knowledge of the genetic diversity and population structure of *T. gondii* may help to understand the many transmission routes and sources of infection. There are limited data on genome-wide comparisons of field isolates belonging to the same genotype or lineage. Therefore, the aim of the present study was to assess genome-wide genetic diversity among *T. gondii* type II isolates from Europe, where this lineage appears predominant.

Material and Methods. Whole genome sequences of 4 European type II field isolates were assessed by whole genome sequencing (WGS) and highly polymorphic regions identified. These regions showed a considerable number of single nucleotide polymorphisms (SNPs), insertions and deletions (INDELS) relative to a T. gondii reference genome (strain ME49), available in a public data base (ToxoDB).

Results. At least 95% of the reads for each *T. gondii* European field isolate were mapped to the reference genome. The mapped reads covered over 99% of the type II reference genome with a read depth of > 20 per base. The total number of SNPs varied between ~4000 and ~11000.

Conclusion. This study demonstrates considerable genetic variation among European type II isolates and provides new insights into the population structure of *T. gondii* in Europe.

Funding source: This work was part of TOXOSOURCES project, funded by the European Union's Horizon 2020 Research and Innovation programme under grant agreement № 773830: One Health European Joint Programme.

VIRULENCE AND UNDERLYING MECHANISMS OF FOUR DISTINCT LINEAGE III VARIANT GENOTYPES OF *Toxoplasma gondii*

Aleksandra UZELAC, Ivana KLUN, Vladimir ĆIRKOVIĆ, Olgica DJURKOVIĆ-DJAKOVIĆ

aleksandra.uzelac@imi.bg.ac.rs, National Reference Laboratory for Toxoplasmosis, Centre of Excellence for Parasitic Zoonoses, Institute for Medical Research, University of Belgrade, Belgrade, Serbia

Background. Strains of *Toxoplasma gondii* lineage III circulate globally and tend to occur more frequently in animals. The archetype (ToxoDB#3) has been extensively used as an experimental model and has been shown to be of low to intermediate virulence, yet the virulence of variant strains is largely unknown as are the underlying mechanisms.