ICP8

8TH INTERNATIONAL CONFERENCE ON PHTHIRAPTERA

June 10-13, 2025
Marseille - France

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LOCATION

IHU Méditerranée Infection, Marseille, France
19-21 boulevard Jean Moulin, 13005 Marseille
https://icp8.org

MÉDITERRANÉE INFECTION

EDITO

Dear colleagues, Dear friends,

I am extremely pleased and honored to welcome you in Marseille for the 8th International Conference on Phthiraptera 2025. The adventure began with a first meeting in United States of America in 1972 (ICP1) and the rhythm of meetings from 2002 (ICP2) increased to its current pace of one congress every four years. The 2025 meeting gathers 100 participants from throughout the world, and the program is equally balanced between oral and poster presentations. I would like to acknowledge the precious help of the members of the ICP8 Organizing and Scientific Committees who have enabled us to build an attractive program.

I hope that you will enjoy your time in Marseille and wish you a fruitful conference.

Pierre-Edouard Fournier
Director of the IHU
Mediterranee Infection

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ARMÉE DU SALUT

General overview

	Tue. June 10	Wed. June 11	Thur. June12	Fri. June 13
Time				
9:00		Opening remarks	Annoncements nominations	Annoncements nominees
9:15		Keynote : Bret (T1)	Keynote : Dale (T23) (RDP memorial) (T23)	IHU Méditerranée Infection (T31-32)
9:30				
9:45				
10:00		Epidemiology & control of lice in humans & domesticated animals (T2-T5)	Morphology, Systematics, Diversity – Part I (T18 - T22)	
10:15				Human lice: Genetics, Geography & Relationships with Symbionts (T33-T35)
10:30				
10:45				
11:00		Coffee Break	Coffee Break	Coffee Break
11:15				
11:30		Continued	Population genetics, genomics & evolution (T28 - T30)	Continued (T36-T39)
11:45				
12:00				
12:15				
12:30		Lunch	Lunch	Lunch
13:45				
14:00		Continued (T10 - T11)	Local excursions	Ecology & Evolution (T40 - T47)
14:15				
14:30		Population genetics, genomics & evolution (T12 - T17)		
14:45				
15:00				
15:15				
15:30				
15:45				
16:00		Coffee Break		Coffee Break
16:15				
16:30		Morphology, Systematics, Diversity – Part I (T18 - T22)		Concurrent Roundtables Futur of human head lice control or Updating host-parasite checklists
16:45				
17:00				
17:15				
17:30				
17:45		Break		
18:00	Welcome Reception	Poster Session	Gala Dinner	Closing and Farewell
19:00				
20:00				

Scientific Program

June 10th

18:00-20:00
Welcome ceremony

June 11th

9:00-9:15
Opening Remarks

Keynote

Chair: Sarah E. Bush

T1. *9:15-10:00*

Bret Boyd
Assistant Professor, Center for Biological Data Science, Virginia Commonwealth University
Untangling nature's hidden experiment with lice and bacteria provides insights into the evolution of symbiosis.

Epidemiology & control of lice in humans & domesticated animals

T2. *10:00-10:15*
Mattéo Dorvillé, Berthine Toubaté, Foteini Koutroumpa, Claudio Lazzari, Catherine Dupuy, Joël Meunier and Françoise Debierre-Grockiego – Effect of ivermectin on olfactory receptor expression and behaviour towards repellent molecule of human lice.

T3. *10:15-10:30*
Marina Eremeeva, Lance A. Durden, Jonathan Eisenstat, Brian C. Hargrove and Edward B. Mondor – Severe *Pediculus humanus capitis* infestation and neglect: pathology, morphological and genetic features.

T4. *10:30-10:45*
Carl Boodman – The changing epidemiology of louse-borne diseases in Canada.

T5. *10:45-11:00*
Ian Burgess – Innovations and failures of treatments for head lice in the 21st century.

11:00-11:30 **Break**

T6. *11:30-11:45*
Ian Burgess – The long view of Covid-19 and head lice.

T7. *11.45-12:00*
Birgit Habedank – Control of head louse infestations: Updated recommendations in Germany.

T8. *12:00-12:15*
Joanna Shu – Novel mechanical approaches to head lice: Clinical and lab data from a medical device startup.

T9. *12:15-12:30*
Nambininiavo Marianne Ranorohasimanana, Mohammad Akhoundi, Sedera Radoniaina Rakotondrasoa, Masy Nasandratra Razafindrakotosoa, Yannick Sonjah Raveloarisaona, Ourida Chebbah, Sophie Brun, Philippe Parola, Arezki Izri, and Lala Rasoamialy-Soa Razanakolona – A cross-sectional study of human lice infestations in Antananarivo, Madagascar: Epidemiological and clinical insights.

12:30-14:00 **Lunch**

T10. *14:00-14:15*
Merel Jacobs, Jennifer Ketzis, Andreea Iani, Clara Camargo, Christian-Olimpiu Martonos, Bart Rossel and Laurens De Schepper – The efficacy of a novel lice product was assessed based on its ability to reduce lice infestation, using chickens as a model.

T11. *14:15-14:30*
Camille Gamblin – Efficacy of (es)afoxolaner (NexGard®/NexGard® Combo) against natural infestations with lice in dogs and cats under field conditions.

Population genetics, genomics & evolution

Chair: Jan Štefka

T12. *14:30-14:45*
Andrew Sweet, Kevin Johnson, Tomas Najer and Stephen Cameron – Extreme variation in the structure and organization of mitochondrial genomes in parasitic lice.

T13. *14:45-15:00*
Renfu Shao and Nan Song – Loss of mitochondrial single stranded DNA-binding protein (mtSSB) gene is associated with mitochondrial genome fragmentation in Psocodea (bark lice, book lice and parasitic lice).

T14. *15:00-15:15*
Jana Martinů, Lenka Kotěborská and Jan Štefka – Different patterns of admixture in mitochondrial and nuclear DNA across *Polyplax serrata* hybrid zone in central Europe.

T15. *15:15-15:30*
Tomas Najer, Jorge Doña, Aleš Buček, Andrew D. Sweet, Oldřich Sychra and Kevin P. Johnson – High-throughput sequencing reveals the timescale of evolution in Amblycera.

T16. *15:30-15:45*
Juliana Soto-Patiño, Jorge Doña and Kevin P. Johnson – Tracking host evolution through parasites: Myrsidea lice in suboscines and the puzzling case of *Sapayoa aenigma*.

T17. *15:45-16:00*
Andrew Sweet, and Kevin P. Johnson, Stephany Virrueta Herrera, and Jorge Doria. Estimating effective population size from a single louse genome: Case studies.

16:00-16:30 **Break**

Morphology, Systematics, Diversity – Part I

T18. *16:30-16:45*
Kayce C. Bell, Priscilla A. San Juan, Jana Martin Říhová, Lance A. Durden, Jessica E. Light and Julie M. Allen – New insights into sucking louse (Anoplura) relationships.

T19. *16:45-17:00*
Lance A. Durden, Kayce C. Bell, Priscilla A. San Juan, Julie M. Allen and Jessica E. Light – Systematics of sucking lice (Phthiraptera: Anoplura): morphological or molecular classification?

T20. *17:00-17:15*
Priscilla A. San Juan, Lance A. Durden, Julie M. Allen, Anna J. Phillips and Kayce C. Bell – Combining morphology with genomics to shed light on chipmunk sucking louse systematics (genus *Hoplopleura*).

T21. *17:15-17:30*
Marek Schneider, Stanislav Kolencik, Kevin P. Johnson, Jason D. Weckstein, Mohamed F. Sallam, Julie M. Allen and Oldrich Sychra – Diversity, host associations and geographical distribution of lice of the genus *Myrsidea* (Amblycera: Menoponidae).

T22. *17:30-17:45*
Therese ("Rese") A. Catanach, Kiana Habersham, Kevin P. Johnson, Jason D. Weckstein – Integrating legacy data and whole genome sequencing on both sides of the tanglegram uncovers unexpected cospeciation in *Degeeriella*.

18:00-20:00 **Poster Session *(cover page 12)***

June 12th

9:00-9:15 **Announcements**

Keynote

Chair: Kosta Y. Mumcuoglu

T23. *9:15-10:00*

Dale H. Clayton
Professor, School of Biological Sciences, University of Utah - **Mighty oaks from humble acorns grow: Roger Price and the emergence of coevolutionary biology.**

Chairs: Jason D. Weckstein, Alexandra Grossi

T24. *10:00-10:15*
Jason D. Weckstein, Therese A. Catanatch, Michel P. Valim, Matthew Soesanto, Lukas Musher, Sarah E. Bush, Matthew E. Kinney, Armand M. Kuris, Chelsea L. Wood and Kamila M. D. Kuabara – Parasites lost no more: rediscovery, description, and comparative genomic diversity of California Condor lice.

T25. *10:15-10:30*
Daniel R. Gustafsson, Alexandra A. Grossi, Leshon Lee and Fasheng Zou – Biodiversity and biogeography of Asian and Australo-Papuan Guimaraesiella Eichler, 1949 (Phthiraptera: Ischnocera).

T26. *10:30-10:45*
Oldrich Sychra, Marek Schneider, Kevin P. Johnson, Jason D. Weckstein, Mohamed F. Sallam, Julie M. Allen and Stanislav Kolencik – The parasitic louse genus *Myrsidea* (Amblycera: Menoponidae): a comprehensive review.

T27. *10:45-11:00*
Annabella Maria Schmiedová, Oldřich Sychra, Miroslav Capek and Ivan Literák – Morphometric study of the genera *Trochiliphagus* and *Trochiloecetes* in hummingbirds.

11:00-11:30 Break

T28. *11:30-11:45*
Alexandra A. Grossi, Daniel R Gustafsson, Wenyi Zhou and Fasheng Zou – Diversity of chewing lice infesting birds in Western Yunnan, China.

T29. *11.45-12:00*
Julie M. Allen, Masoud A. Rostami, Behnaz Balmaki, Stanislav Kolencik, Daniel R. Gustafsson, Jason D. Weckstein, John Gausas, Ricardo L. Palma, Oldrich Sychra, Andrew D. Sweet, Kamila M. D. Kuabara, Katja Seltman, Nicolas J. Dowdy, Jennifer M. Zaspel, Jessica E. Light, Rob Guralnick and Sarah E. Bush – The promise and impediments of artificial intelligence for species identification in Phthiraptera.

T30. *12:00-12:30*
Ricardo Palma. Collecting lice in “Las Islas Encantadas”

12:45-18:30 **Local excursions**

From 19:00 **Gala Dinner**

June 13th

9:00-9:15 **Announcements**

Highlights of Research at IHU Méditerranée Infection

Chair: Olivier Chosidow

T31. *9:15-9:45*
Pierre-Edouard Fournier – Louse-borne infections in the 21st century: Forgotten diseases but current threats.

T32. *9:45-10:15*
Oleg Mediannikov, Alissa Hammoud, Florence Fenollar and Pierre-Edouard Fournier – Human head lice as vectors of *Bartonella quintana*.

Human lice: Genetics, Geography & Relationships with Symbionts

Chair: Ariel Toloza

T33. *10:15-10:30*
Marina S. Ascunce, Ariel C. Toloza, Angélica González-Oliver and David L. Reed – Genetic footprints of the treks of human lice around the globe.

T34. *10:30-10:45*
Parisa Sharafi, Ayca Ozsipahi, Bengu Akgok, Fatma Gufran Suleyman, Kosta Y. Mumcuoglu and Aysegul Taylan-Ozkan – Detection of human louse DNA in different soil samples.

T35. *10:45-11:00*
Kosta Y. Mumcuoglu, Parisa Sharafi and Aysegul Taylan-Ozkan – Microbiota of the human head louse, *Pediculus humanus capitis*, and the human body louse, *Pediculus humanus humanus* (Anoplura: Pediculidae) in Israel.

***11:00-11:30* Break**

T36. *11:30-11:45*
Emily Dunn and Renfu Shao – Transcription of the fragmented mitochondrial genomes of human head and body lice.

T37. *11.45-12:00*
Saima Naz, Maria Rebecca, Nazir Ahmed Brohi, Aziz Ahmed Ujjan, Shaila Khaskheli and Farooque Ali Hattar - First report of crab louse, *Pthirus pubis* (L. 1758) and the fungal association of head louse, *Pediculus humanus capitis* De Geer, 1767 in people of low socioeconomic status of Hyderabad, Sindh, Pakistan.

T38. 12:00-12:15
Gholizadeh Saber – Molecular detection of novel glutamate channel mutations in field collected human head lice (Phthiraptera: Pediculidae) from Iran.

T39. 12:15-12:30
Anthony Marteau, Sophie Brun, Arezki Izri and Mohammad Akhoundi - Prevalence and genetic diversity of heritable bacterial symbionts in human lice.

***12:30-14:00* Lunch**

Ecology & Evolution

Chair: Saima Naz and Matthew Waler

T40. 14:00-14:15
Jana Martinů and Jan Štefka – Prevalence differences between closely related louse species occurring in sympatry: specialist and 'generalist' lineages of *Polyplax serrata.*

T41. 14:15-14:30
Sarah E. Bush, Matthew M. Waller, Kyle M. Davis, Sonora F. Clayton and Dale H. Clayton – Birds in arid regions have depauperate louse communities: Climate change implications?

T42. 14:30-14:45
Stephany Virrueta Herrera and Kevin P. Johnson – Extensive host switching between orders of birds by *Rallicola* lice.

T43. 14:45-15:00
Matthew M. Waller, Sarah E. Bush, Nicole A. Amedee and Dale H. Clayton – Does the length of the bill overhang correlate with the abundance of lice on birds?

T44. 15:00-15:15
Yoshika Oniki-Willis, Edwin O. Willis, Oldrich Sychra, Terry Galloway and Lajos Rozsa – Adaptive sex-ratio patterns in hummingbird lice (Ricinidae: Trochiloecetes, Trochiliphagus).

T45. 15:15-15:30
Jessica E. Light, Conrad A. Matthee, Nina du Toit-Heunis, Sonja Matthee and Lance A. Durden – Host associations, host switching, geographic location and potential reticulate evolution shape the systematics of sucking lice (Psocodea: Anoplura) belonging to the genera *Hoplopleura* and *Polyplax*.

T46. 15:30-15:45
Saima Naz, Ahmed Madani, Oldrich Sychra, Shaila Khaskheli, Mohammad Awais Memon, Farooque Ali Hattar and Aziz Ahmed Ujjan – New data on genus *Colocera*s (Ischnocera: Philoperidae) infesting birds of Family Columbidae (Columbiformes) with an updated list of columbid chewing lice from Pakistan.

T47. 15:45-16:00
Kristýna Plšková, Stanislav Kolenčík, Mario A. Loaiza-Muñoz, Gustavo A. Londono, Julie M. Allen and Oldřich Sychra – Understanding the life history characteristics of bird lice: Amblycera versus Ischnocera.

16:00-16:30 Break

16:30-18:00 **Round Table Discussions**

- **Updating host-parasite checklists**
  Chairs: Sarah E. Bush, Daniel Gustafsson
- **Future of human head lice control**
  Chairs: Pierre-Edouard Fournier, Kosta Y. Mumcuoglu

18:00-19:30 **Closing and Farewell**

Poster Presentations

Human lice

P1. Sandra Leverenz, Anikó Fuhrmann, Lana Sawicki, Hans Dautel and Kerstin Büchel - Artificial membrane feeding for in vitro rearing of body lice *Pediculus humanus humanus* and development of a rapid lice repellent screening assay.

P2. Bouthaina Hasnaoui, Zaina Amirat, Noelle Masotii, Dikra Hamadouche, Rim Bouledroua, Basma Ouarti and Philippe Parola - Unlocking lice science: Breeding *Pediculus humanus humanus* on rabbits for research.

P3. Basma Ouarti, Maureen Laroche, Ahmed Benakhla, Khaoula Ouarti and Philippe Parola - The introduction of mass spectrometry in medical entomology and its application in lice identification.

P4. Berthine Toubate, Françoise Debierre-Grockiego and Isabelle Dimier-Poisson - Repellent effects of essential oils on human lice.

P5. Ariel C. Toloza, Eunice Sosa-Quiroga, Agustina Fañani, Ana Puente-Santamaria, Eduardo Guzmán, Emilia Martínez and Alejandro Lucia - Chemical interaction and pediculicidal activity of binary nanomicelles loaded with monoterpenes against head lice.

P6. Ariel C. Toloza, Marina Ascunce and David Reed - Understanding the movements of permethrin-resistant head lice in schools from a genetic perspective.

P7. Joshua Kamani, Shimon Harrus, Bukar Laminu, Yaarit Nachum-Biala, Mike Shand, Gonzalo Roca-Acevedo and Ariel C. Toloza - First report of kdr alleles T917I and L920F in head and body lice from Nigeria.

P8A. Elisabeth Yawa Diawara, Alpha Kabinet Keita, Alissa Hammoud, Adama Zan Diarra, Basma Ouarti, Coralie L'ollivier and, Stéphane Ranque - Pediculosis: an epidemiological survey of schoolchildren in the Republic of Guinea.

P8B. Elisabeth Yawa Diawara, Alpha Kabinet Keita, Adama Chérif Camara, Stéphane Ranque, Marc-Karim Bendiane - Differences in gender perception of psychological and social consequences of human pediculosis in Guinee: results of an exploratory epidemiological study.

P9. Noureddine Rabah Sidhoum, Mehdi Boucheikhchoukh, Bouthaina Hasnaoui, Noureddine Mechouk, Lobna Dib, Hamza Leulmi, Ahmed Benakhla and Philippe Parola - Synopsis of lice species associated with humans, domestic, and wild animals in Algeria.

P10. Boukehila Chahinez, Dib Loubna, Philippe Parola and Basma Ouarti - Human lice control: Morphological characterization of *Pediculus humanus capitis* populations.

P11. Younes Laidoudi, Samia Bedjaoui, Sébastien Meige, Julien Renaud, Nicolas Grelaud and Bernard Davoust - Spatio-temporal and economic analysis of pediculosis in France (2021–2024): Prevalence, seasonality, and public health burden.

P12. Rym Bouledroua, Adama Zan Diarra, Remy Amalvict, Jean-Michel Berenger, Ahmed Benakhla, Philippe Parola and Lionel Almeras - Assessment of MALDI-TOF MS for arthropod identification based on exuviae spectra analysis.

Ecology, evolution & diversity

P13. Younes Laidoudi, Samia Bedjaoui, Stéphanie Watier-Grillot, Anthony Levasseur and Bernard Davoust - Microbial community and zoonotic potential of wild boar lice (*Haematopinus apri*) in France.

P14. Austin R. Clayton, Sarah E. Bush, Matthew M. Waller and Dale H. Clayton - Galápagos mockingbirds that groom more have fewer lice.

P15. Alexandra A. Grossi, Daniel R. Gustafsson and Oldrich Sychra - How many endangered species of chewing lice are there?

P16. Jake Jacobsen, Ethan X. Kahn, Amanda Leyel, Mia C. Rosati, Graham A. Montgomery, Jessie F. Salter and Morgan W. Tingley - Island of lice: Comparing range competition of chewing lice across three avian hosts.

P17. Noureddine Rabal Sidhoum - Epidemiological and ecological patterns of lice (Phthiraptera) populations in Algeria.

P18. Abir Adjroud, Habiba Saadi-Idouhar, Bouthaina Hasnaoui, Diarra Zan Adama, Faiza Marniche and Philippe Parola - Contribution to the knowledge of chewing lice of the wild Gambra partridge in Algeria.

P19. Olga St-Onge (in absentia) - Hangers-on: An overview of the current state of Phthiraptera conservation.

P20. Chahinez Boukehila, Dib Loubna, Philippe Parola and Basma Ouarti - Prevalence of lice infestation in domestic mammals in northeastern Algeria.

P21. Alex Sutherland and Colin Dale - Going deeper: In-depth sequencing of the endosymbiont of *Columbicola columbae.*

P22. Chaoqun Yao - Molecular characterization of *Heterodoxus spiniger* from dogs on St. Kitts.

P23. Oldřich Sychra, Lajos Rózsa, János Podani, Vojtěch Sychra, Ivan Literák, Annabella Maria Schmiedová and Miroslav Capek - Multivariate study of lice (Insecta: Psocodea: Phthiraptera) assemblages hosted by hummingbirds (Aves: Trochilidae).

P24. Oldřich Sychra, Annabella Maria Schmiedová, Lajos Rózsa and Leonor Guardia Claps - Occurence of chewing lice (Phthiraptera: Ricinidae) on Red-tailed comet (*Sappho sparganurus*).

P25. Saima Naz, Farooque Ali Hattar, Aziz Ahmed Ujjan, Shaila Khaskheli and Sajid Siyal - Epidemiology of the goat louse, *Linognathus africanus* Kellogg and Paine, 1911 (Anoplura: Linognathidae) and its new association with fungal flora.

P26. Saima Naz, Mohammad Awais Memon, Oldrich Sychra, Aziz Ahmed Ujjan, Shaila Khaskheli, Ahmed Madani and Sajid Siyal - New data on chewing lice (Psocodea: Phthiraptera) of *Corvus splendens* Vieillot (Corvidae) from Pakistan.

P27. Daniel R. Gustafsson, Fasheng Zou, Zhu Li and Xiuling Sun – Descriptions of five new genera in Goniodidae (Ischnocera).

P28. Daniel R. Gustafsson, Zhengzhen Wang, Alexandra A. Grossi and Fasheng Zou - New species in the Resartor-group complicate genus limits further.

P29. Daniel R. Gustafsson - Host association patterns of *Brueelia*-complex lice (Phthiraptera: Ischnocera) parasitizing starlings (Passeriformes: Sturnidae).

P30. Noureddine Mechouk, Bouthaina Hasnaoui, Noureddine Rabah sidhoum, Mehdi Boucheikhchoukh, Andrei Daniel Milhalca, Philippe Parola - MaxEnt model-based prediction of potential distributions of Pidiculus human capitus in Algeria.

ABSTRACTS

Oral Abstracts

Poster Abstracts

Oral présentations

KEYNOTE

Chair: Sarah E. Bush

T1. Bret Boyd – **Untangling nature's hidden experiment with lice and bacteria provides insights into the evolution of symbiosis**

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Author Affiliation: Center for Biological Data Science, Life Sciences, Virginia Commonwealth University.

Over their 480-million-year history, insects have repeatedly forged beneficial relationships with heritable bacteria. These relationships have, in tum, influenced insect evolution and diversification, including the evolution of parasitism by lice. Studies of lice and their bacterial partners over the last century have provided insights into the biology and evolution of insect-bacterial symbiosis. Recently, research has capitalized on the close relationships between lice and their vertebrate hosts to examine the sources of bacterial symbionts, the trajectory of bacterial genome evolution in symbiosis, and the impact of humans on insect-bacterial symbiosis. This talk will focus on findings of these recent studies and discuss their broader implications for entomology, microbiology, and evolutionary biology. Studies of lice and their bacterial partners will continue to support new discoveries. The talk will also highlight gaps in our knowledge of louse-bacterial symbiosis and future directions for research.
Keywords: Evolution, symbiosis

Epidemiology & control of lice in humans & domesticated animals

Chairs: Renfu Shao, Marina Eremeeva, Arezki Izri.

T2. Mattéo Dorvillé, Berthine Toubaté, Foteini Koutroumpa, Claudio Lazzari, Catherine Dupuy, Joël Meunier and Françoise Debierre-Grockiego – **Effect of ivermectin on olfactory receptor expression and behaviour towards repellent molecule of human lice**

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Author Affiliation: University of Tours - UMR 1282 ISP

Ivermectin is a macrocyclic lactone that is sometimes prescribed to treat pediculosis systemically. Lotions containing 0.5% or 1% ivermectin can also be applied topically. Ivermectin targets post-synaptic receptors for γ-aminobutyric acid and glutamate present at the neuromuscular junction of arthropods. However, there is growing evidence that this type of receptors is also present in the antennal lobe of insects. We have previously shown that ivermectin causes death of the human body louse *Pediculus humanus humanus*. In the present work, we focused on the effect of ivermectin on the olfactory system and the behavior of body lice. The results show that lice treated for 24 hours with a sublethal dose of ivermectin had the tendency to spend less time in the area impregnated with the repellent molecule 2,3-dimethylphenol than untreated lice. In parallel, expression of the *P. humanus* Olfactory Receptor 2, Olfactory coReceptor and Ionotropic Receptor 25 in the head of lice was quantified by RT-qPCR and the three genes were upregulated 24h after treatment. Taken together, these results suggest that ivermectin could increase receptor expression in the olfactory system of lice, leading to increased sensitivity to repellent volatile molecules.

Keywords: Human louse, ivermectin, olfactory receptors, behaviour, repellent molecule

T3. Marina Eremeeva, Lance A. Durden, Jonathan Eisenstat, Brian C. Hargrove and Edward B. Mondor – **Severe *Pediculus humanus capitis* infestation and neglect: pathology, morphological and genetic features.**

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Author Affiliation: Georgia Southern University

Head louse pediculosis is prevalent among school-age children. From a public health perspective, head lice are often not viewed as a significant health hazard because they can be controlled using topical treatments combined with improved personal hygiene. However, the associations between pediculosis and neglect or abuse of children have numerous legal precedents; consequently, lice are assuming increasing importance in forensic investigations. Prolonged and chronic louse infestations may result in serious health outcomes including severe iron deficiency anemia. Herein, we provide a review of published records of louse-associated cases of iron deficiency anemia and analyze this information in the context of our forensic investigation of a severe case of pediculosis that possibly led to severe anemia and subsequent death. Numerous lice were found postmortem on the head, face, and neck of a 12-year-old child, as well as on bedding and clothing. Nits were found only on head hairs and none on the clothing. Analysis of the distribution of nits along individual hairs determined that the infestation occurred at least 5 months before medical evaluation. The lice had anomalous morphological traits characteristic of both body lice and head lice. However, genotyping based on cytB, cox1, and 12S rRNA gene placed these lice in clade B, comprising the most common haplotypes and genotypes of head lice from the Americas, including the US. All lice were heterozygous for the T917I kdr marker of permethrin resistance. Nineteen (79.2%, 95%CI 59.5-90.8%) louse DNA samples tested TaqMan positive for *Acinetobacter* sp., but no *Bartonella* was detected. In conclusion, severe head louse infestations should be included as a part of the differential diagnosis of causes of severe anemia. Children with limited parental attention should be screened routinely for lice because the diagnosis of pediculosis may provide indications about a child's poor well-being and need for timely medical and social intervention.

Keywords: Pediculosis, head lice, genotyping, morphology, neglect

T4. Carl Boodman – The changing epidemiology of louse-borne diseases in Canada

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Background: Body lice are traditionally known to transmit 3 pathogens: *B. quintana* (trench fever/ endocarditis), *Rickettsia prowazekii* (epidemic typhus), and *Borrelia recurrentis* (louse-borne relapsing fever). *B. quintana* is the only human louse-borne disease acquired in Canada in modern times and the only pathogen to be identified in Canadian body lice. The epidemiology of Canadian *B. quintana* differs from other jurisdictions as transmission occurs in remote Indigenous communities with limited access to water, in addition to homeless populations. This presentation summarizes the epidemiologic trends of *B. quintana* in Canada by combining vector and human data, including a recent outbreak of transplant donor-derived infection. *Methods:* This study combined an analysis of laboratory data from Canada's National Microbiology Laboratory (NML) with a systematic review of the literature and a prospective body lice study. Laboratory data included quantitative polymerase chain reaction (qPCR) cycle threshold values and indirect immunofluorescent antibody titers with the year and province of the sample acquisition. For the systematic review, we searched PubMed, Scopus, Embase, and Web of Science for articles published before 15 July 2024, with terms related to *B. quintana* in Canada. *Results:* Thirty-three individuals with qPCR-positive *B.quintana* were documented in seven provinces and one territory. The number of cases increased over time (p-value = 0.005), with the greatest number of cases being reported in 2022 and 2023. The percent positivity for the *B. quintana* qPCR performed at the NML increased over time (p-value = 0.036). The systematic review identified fourteen individuals with qPCR-positive *B. quintana* and seven probable cases of *B. quintana* disease. Four of these twenty-one individuals from the systematic review died (19%). All fatalities were attributed to endocarditis. A cluster of transplant donor-derived *B. quintana* infection occurred in Alberta from 2021-2023. Of 32 transplanted organs from 11 *Bartonella* seropositive donors, 6 recipients developed *B. quintana* disease. Only one human body louse study has occurred in Canada: 556 body lice were analyzed from 7 individuals. 17 louse pools (218 lice) from 1 person were positive for *B. quintana*. *Conclusions:* The detection of *B. quintana* disease in seven provinces and one territory suggests that *B. quintana* has a national distribution in Canada with dozens of urban and rural foci of transmission. *B. quintana* disease is increasingly diagnosed in Canada with novel routes of transmission from solid organ transplant donors and concealed transmission from body lice.

Keywords: Body lice, *Bartonella quintana*, endocarditis, transplant

T5. Ian Burgess – **Innovations and failures of treatments for head lice in the 21st century**

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As the 20th century drew towards a close treatment of head louse infestation became more difficult worldwide as a result of the increased prevalence of resistance to current treatments. The problem was partially exacerbated by the almost universal dependence upon pyrethroid insecticides and permethrin in particular. As a result, it was necessary to rethink the way lice should be killed, leading to several innovative concepts based on synthetic mineral oils. However, the underlying premise of this type of treatment was not only widely misunderstood but also misused so that among the plethora of products based on these "physically acting" principles many products were sub-optimally effective. The concept of "physically acting" has been applied mainly to occlusive preparations but also to various other mechanisms such as cuticular lipid dissolution and misapplied to materials such as essential oils, which have been clearly demonstrated to have pharmacological activity. These conditions have only arisen because regulators have allowed head louse treatments with minimal or no pharmacological effect in humans to be classified as the least risk medical devices, a category that in many jurisdictions permits manufacturers to self-certify and thus make claims for the products that are not based on either evidence or logic, with the mistaken belief that these types of products are "resistance proofed" because they act "physically". The result has been inefficient louse management in the community leading to a developing resistance to a range of chemical groups.

Keywords: Physically acting chemicals, essential oils, resistance

T6. Ian Burgess – The long view of Covid-19 and head lice

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Abstract: The pandemic caused by Covid-19 had many consequences and disrupted numerous aspects of society in ways that have still not fully recovered. Closure of schools and restricting the social and play contacts between children have altered the longer-term behaviour and ways in which children interact even now. The immediate impact of the lockdown process was to remove or minimise the possibility that children could come into contact so that transmission of contagious conditions, including head louse infestation, were effectively terminated. Various studies from around the world have shown that head louse infestation decreased during the lockdowns, either by showing reduction of sales of pediculicides or reduced reporting or diminished prevalence during screening of children. Some of these effects were demonstrably real but it is possible that others were as a result of misinterpretation of observations because overall there has been no long term effect beyond trends that were present before the pandemic and are unrelated to the lockdown processes, for example a reduction in louse prevalence as a result of a reduction in the numbers of children in a community due to declining birth rates. However, Covid-19 has provided information that could not be learned otherwise and, if similar circumstances arise, could be used positively to have an impact on lice in the future.

Keywords: School closures, pediculicide sales, reduced prevalence

T7. Birgit Habedank – Control of head louse infestations: Updated recommendations in Germany

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The human head louse is spread worldwide and more frequently among children. For a more effective control of the head louse, the international recommendations for head louse control were published that include recommendations for health authorities, health providers, research institutions, producers of pediculicides and general recommendations (Mumcuoglu et al., 2021).

There are a variety of products to control head lice on the market, including approved medicinal products, an increasing number of products registered as medical devices, and other products. At the German Environment Agency products to control head lice are tested and evaluated according to Section 18 of the German Infection Protection Act. Products that are effective to eradicate lice populations are published in a list according to section 18 Infection Protection act. Our investigations showed that the efficacy of products for topical treatment of head louse infestations can be very different, e.g. depending on the active ingredient, formulation, applied dose, application of the product and exposure time. The instructions for use often lack important information that would enable users to improve product application and to check the treatment success. To quickly recognize treatment errors or failures by products with less or insufficient efficacy, a more intense monitoring for potentially surviving lice stages is necessary. The consistent lice control is essential to prevent spreading of lice. Thus, in the updated recommendations in Germany (main target groups: medical doctors, medical professionals and public health service) we recommend for an effective head louse control combining the treatment with anti-louse remedies and wet combing for active removal of surviving lice or newly hatched lice instars, and an additional continued monitoring period after the last treatment to ensure the overall success of the treatment. Furthermore, measures on infestation management and prevention issues important for community facilities and public health are addressed.

Keywords: topical head louse treatments, recommendations for control

T8. Joanna Shu – **Novel mechanical approaches to head lice: Clinical and lab data from a medical device startup.**

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As the founder and CEO of a medical device and OTC health startup, I approach head lice not from the lab bench, but from a product innovation lens that is grounded in extensive customer research and prioritizes accessibility and efficacy for real-world use. Our team has been developing OTC lice treatments that leverage physical rather than chemical mechanisms: controlled temperature, CO_2 gas exposure, and mechanical abrasion.

In this presentation, I'll share results from our initial clinical trial, where our topical lice treatment gel formulated with plant-derived abrasives achieved a 95.8% kill rate without neurotoxic agents. I'll also present internal bench data from early-stage testing of our temperature-controlled CO_2 bonnet prototype, which appears to kill both lice and nits while remaining comfortable and non-toxic to the user.

I will also discuss our extensive customer discovery and initial discussions with FDA. While I don't represent academia, I believe our findings offer a complementary perspective to the clinical and scientific literature, particularly in the area of mechanical treatment modalities. I welcome discussion and feedback, and hope our data can contribute to ongoing efforts to improve patient outcomes in lice management.

T9. Nambininiavo Marianne Ranorohasimanana[1,2], Mohammad Akhoundi[1,3], Sedera Radoniaina Rakotondrasoa[3], Masy Nasandratra Razafindrakotosoa[4], Yannick Sonjah Raveloarisaona[1], Ourida Chebbah[5], Sophie Brun[1], Philippe Parola[2], Arezki Izri[1] and Lala Rasoamialy-Soa Razanakolona[6] – **A cross-sectional study of human lice infestations in Antananarivo, Madagascar: Epidemiological and clinical insights**

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Human lice have long been parasites of humans and have played a significant role in epidemics throughout medical history. Head lice (*Pediculus humanus capitis*) infestation remains common worldwide. Most studies, especially those conducted in schools, report a prevalence of around 20% among children. Transmission occurs primarily through direct hair-to-hair contact, and their role in disease transmission remains unconfirmed. Body lice (*Pediculus humanus humanus*), associated with poor hygiene, live and lay eggs on clothing. They are known vectors of *Rickettsia prowazekii* (typhus), *Borrelia recurrenti*s (relapsing fever), and *Bartonella quintana* (trench fever). In Madagascar, human lice infestations are a neglected public health issue, with limited epidemiological data available. To address this gap, a cross-sectional survey was conducted from Sept. to Nov. 2024 in four regions of the Antananarivo province. Participants were selected using a cluster sampling design. Epidemiological and clinical data were recorded via a questionnaire. A total of 651 individuals (351 females and 300 males) from 181 families living across 20 districts were examined. Among them, 92 individuals from 32 families were infested with head and/or body lice, resulting in 14.1% overall prevalence. Of those infested, 67,4% were female. The prevalence of head lice infestation was 9.1% (n=59/651) against 9.4% (n=61/651) for body lice. Among those with head lice, 40.7% were adults over 18 years old, predominantly women (83.3%). Rural areas were more affected, accounting for over half of the cases (55.2%), and 15.3% were reported in the urban Antananarivo district. Clinical symptoms were dominated by scalp pruritus (56.9%), often associated with insomnia (22,4%), followed by macular/papular erythematous lesions on the scalp (25.4%). Regarding body lice infestations, 47.5% of the affected population were children and adolescents under 18 years old, with females representing 62.1%. Urban areas were more affected, representing 52.5% of the cases, with Arivonimamo district being the most impacted (23%). Symptoms primarily included pruritus with insomnia (41%), and papular-erythematous lesions were observed in 42.6% of cases. Co-infestation with both head and body lice was found in 31.5% (n=29/92) of the infested individuals, representing 4.5% of the general population. Household density ($p<0.001$) and bed-sharing practices ($p<0.001$) were significantly associated with lice infestations. This study shows that head lice infest adults as much as children, whereas body lice infestations are notably higher among children. These findings highlight the impact of household overcrowding and bed-sharing on lice transmission.

Keywords: Human lice, epidemiological survey, prevalence, clinical features, Madagascar

T10. Merel Jacobs[1], Jennifer Ketzis[2], Andreea Iani[2], Clara Camargo[2], Christian-Olimpiu Martonos[2], Bart Rossel[1] and Laurens De Schepper[1] - **The efficacy of a novel lice product was assessed based on its ability to reduce lice infestation, using chickens as a model**

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Background: Head lice infestations are very common; about 0.48% to 22.4% of the European population being affected. Managing infestations can be a significant burden on families, requiring time-consuming treatments and repeated care. In recent years, growing concerns over resistance and safety have emphasized the need for alternative treatments including silicone- or mineral oil-based head lice products that act through physical mechanisms. However, these treatments are al??? liquid-based, requiring extensive washing and combing protocols, which not only add to the inconvenience for patients and caregivers but also lead to poor adherence and high treatment dropout rates. There is a clear need for a dry, effective, and safe method for treating head lice that minimizes disruption to daily life. In response to this, we have developed a novel dry hair formula with a physical mode of action. This study evaluates its efficacy in an animal model.

Methods: The efficacy of a novel lice product was assessed based on its ability to reduce lice infestation in chickens with natural infestation of *Menopon* spp. and *Menacanthus* spp., using chickens as a model for human head lice infestation. In group 1 (n=8), chickens were treated with a single application of formula X92001919. In group 2 (n=8), chickens were treated twice, three days apart, using formula X92001919. Group 3 (n=8) was a placebo group, where treatment was mimicked using an empty bottle twice, three days apart. The chickens were then followed up for 6 days after the last treatment to assess the impact of nit hatching, with hatching typically occurring at days 4–5. Statistical differences between groups were assessed using ANOVA testing.

Results: The chicken model was effective, and no chickens had adverse events due to the application. Both a single treatment and two treatments significantly decreased the number of lice compared to the placebo group (group 3) at each time point. Moreover, group 1 and group 2 differed significantly on day 9.

Conclusions: The treatments showed a strong and prolonged reduction in the number of lice. Towards the end of the study, lice were not completely eradicated in groups 2 and 3. However, as no nits were observed after the treatment and the lice seen at these time points were fully mature, this suggests transfer of lice from group 3 (the untreated placebo group), as these chickens were kept in the same pen. These data indicate that we have developed a unique formula with a physical mode of action inside a novel galenic format, which demonstrates good efficacy in vivo compared to a placebo control.

Keywords: Head lice infestation, pediculosis capitis, *Menopon* sp., *Menacanthus* sp.

T11. Camille Gamblin – Efficacy of (es)afoxolaner (NexGard®/NexGard® Combo) against natural infestations with lice in dogs and cats under field conditions

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Felicola subrostratus and *Trichodectes canis* (Trichodectidae) are chewing lice affecting cats and dogs, respectively. In tropical regions (Asia, Pacific, Australia, America, Africa), dogs can be infested with another chewing louse, *Heterodoxus spiniger* (Boopiidae), which exhibits hematophagous behavior. The presence of these lice is associated with moderate to intense pruritus and can serve as an intermediate host of the zoonotic tapeworm *Dipylidium caninum*. Recently, three distinct field studies were conducted to demonstrate the efficacy of a single dose of two isoxazoline formulations, i.e. afoxolaner (NexGard®, Boehringer Ingelheim) and esafoxolaner (the active enantiomer of afoxolaner, NexGard® Combo, Boehringer Ingelheim) in treating naturally infested dogs and cats. In each of the three studies, the systemic acting isoxazoline treatment was compared to a positive control group treated topically with fipronil (Frontline Combo®, Boehringer Ingelheim) registered against dog and cat chewing lice. Isoxazolines act as inhibitors of the helical subunits of Gamma-aminobutyric acid (GABA), a neurotransmitter found in the peripheral nervous system of invertebrates, resulting in paralysis and mortality. Afoxolaner is bound to plasma protein and acts after its ingestion by arthropods. Here we hypothesized that the skin inflammatory process would allow chewing lice to ingest the insecticidal compound. The studies included 43 dogs infested with *T. canis*, 31 cats infested with *F. subrostratus*, and 36 dogs infested with *H. spiniger*. All animals were treated on day 0. By day 30, no lice were found in any of the *T. canis* infested groups, with eggs still present in one dog in the fipronil treated group. By day 30, all cats infested with *F. subrostratus* in both groups scored 0 for the presence of live lice, demonstrating 100% efficacy. Clinical scores significantly improved from day 0 to day 30. In the third study, by day 15, all dogs infested with *H. spiniger* scored 0 for lice, with no living lice or nits detected. Significant improvements in pruritus, hair loss, and skin lesions were observed. These studies demonstrate that (es)afoxolaner formulations are highly effective against the most common lice species infesting dogs and cats. The efficacy of fipronil spot-on formulations was also confirmed. All treatments showed a 100% efficacy in eliminating lice and significantly improved clinical symptoms, with no observed reinfestations for a month following a single dose. These results support the use of these products for treating lice infestations in pets.

Keywords: Pets, Chewing Lice, Afoxolaner, Fipronil, Efficacy assessment.

Population genetics, genomics & evolution

Chair: Jan Štefka

T12. Andrew Sweet[1], Kevin Johnson[2], Tomas Najer[3] and Stephen Cameron[4] – **Extreme variation in the structure and organization of mitochondrial genomes in parasitic lice**

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Mitochondrial genomes (mitogenomes) are remarkably variable in parasitic lice, which contrasts with the highly conserved mitogenome structures found across most other bilaterian animals. Many species of lice have fragmented mitogenomes, where the mitochondrial genes are separated onto multiple circular chromosomes. Fragmentation has evolved repeatedly across parasitic lice. Many lice also have mitogenomes with highly rearranged gene orders. The extreme diversity of mitogenome structure and gene arrangements have been repeatedly demonstrated at broad taxonomic scales, but focusing on mitogenome structure within specific clades of lice is likely the key to understanding both proximate (how) and ultimate (why) explanations for this unusual variation. Here, we present results from comparative studies of mitogenomes in several clades of bird lice. We show that the structure and gene order of mitogenomes are variable even among closely related lice, although patterns of fragmentation tend to be more consistent at lower taxonomic levels. We also found evidence that variation in mitogenomes is linked with selection, nucleotide composition, and loss of certain nuclear genes involved in mitochondrial function, but these factors are not consistent across all clades of lice. Together, our results reinforce the complex nature of mitogenome variation in lice and further show the utility of dense taxon sampling within clades for comparative genomics.

Keywords: Mitochondria, genomes, fragmentation, genomics

T13. Renfu Shao and Nan Song – **Loss of mitochondrial single stranded DNA-binding protein (mtSSB) gene is associated with mitochondrial genome fragmentation in Psocodea (bark lice, book lice and parasitic lice)**

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Organelle genome fragmentation is a drastic large-scale chromosomal mutation. Why and how organelle genomes become fragmented is still poorly understood. An early study based on whole genome comparison between human body louse and fruit fly suggested that the loss of mtSSB gene (for mitochondrial single-stranded DNA-binding protein) might be associated with mitochondrial (mt) genome fragmentation. Whether this association is valid has not been investigated due to the lack of data on mt genome fragmentation. In the past few decades, fragmented mt genomes have been found in 87 species of parasitic lice from all of the five parvorders of Phthiraptera while the single-chromosome mt genome organization is retained in the other 81 species of parasitic lice in the parvorders Amblycera and Ischnocera. Fragmented mt genomes were also found in three species of book lice in the genus Liposcelis, which is the sister group of parasitic lice. Mitochondrial genome fragmentation has occurred numerous times repeatedly in these lice, providing a large data set for validating the association between mtSSB gene and mt genome fragmentation. In the current study, we investigated this association by exploring the genomic and transcriptomic data of 190 species of parasitic lice, book lice, bark lice and other closely related hemipteroid insects. We show that the loss of mtSSB gene is correlated significantly with mt genome fragmentation in bark lice, book lice and parasitic lice (Psocodea). Absence of mtSSB is more frequent than expected in the species with fragmented mt genomes whereas presence of mtSSB is more frequent than expected in the species with single-chromosome mt genome organization. Nevertheless, our results reject a cause-and-effect association between the loss of mtSSB gene and mt genome fragmentation because mtSSB is present in 28 species of parasitic lice that have fragmented mt genomes. A plausible explanation to the observed association is that fragmented mt genomes with multiple small-sized minichromosomes may make mtSSB gene and mtSSB protein less critical or unnecessary, which may eventually lead to their loss in the species with fragmented mt genomes.

Keywords: Psocodea, lice, mitochondrial genome fragmentation, mtSSB

T14. Jana Martinů, Lenka Kotěborská and Jan Štefka – **Different patterns of admixture in mitochondrial and nuclear DNA across *Polyplax serrata* hybrid zone in central Europe**

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Hosts and parasites possess different generation times, reflected by different tempos of molecular evolution. Therefore, during geographic fragmentation of their populations (e.g., in glacial refugia), hosts and parasites may reach different degrees of genetic differentiation. Upon secondary contact, the host populations can re-establish a single panmictic population across the area of contact, while the parasite populations stop their dispersal at the secondary contact zone and create a narrow hybrid zone (HZ). Using whole genome (WG) and mitochondrial (mtDNA) information we characterise clinal transition of genetic content in one such area of contact in central Europe. There, western and eastern clades of a host-specific louse *Polyplax serrata* create a HZ, while the *Apodemus flavicollis* host population is panmictic. We obtained WG data for 114 lice from an 88 km transect across the HZ and supplemented them with 18 individuals from other sites of distribution. MtDNA data were obtained for 151 individuals across the transect. WG data produced over 4 million Single Nucleotide Polymorphisms (SNPs), which were filtered to 4,500 independent loci. Clinal analysis of the transect showed different widths of the HZ for mtDNA and nuclear data. Furthermore, mtDNA showed less steep cline and the centre of the HZ shifted towards the west. Differences in the cline steepness may reflect less strict natural selection in mtDNA genes. Relative shift in the centre of the HZ requires additional analyses, but it could be explained by mito-nuclear incompatibility in hybrids, asymmetric back-crossing preferences of the lice, or other evolutionary processes producing asymmetrical introgression of genes across the HZ. We also studied clines of individual genome scaffolds (representing possible chromosomes) showing slight variation in the steepness. In future, when supplemented with functional gene annotation, the *Polyplax* HZ may serve as a useful model for studies of interspecific genetic introgression in parasites.

Keywords: Population genetics, hybrid zone, genomics, evolution

T15. Tomas Najer, Jorge Doña, Aleš Buček, Andrew D. Sweet, Oldřich Sychra and Kevin P. Johnson – **High-throughput sequencing reveals the timescale of evolution in Amblycera**

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In recent decades, whole-genome sequencing has helped resolve the higher-level phylogenies of many different organisms, including parasitic lice (Insecta: Phthiraptera). In lice, phylogenomic studies inferred from thousands of genes were gradually published for most parvorders, with only the highly diverse Amblycera remaining unexplored. To fill this gap, we performed several phylogenomic

analyses to resolve the relationships within and among the families of Amblycera. Our phylogenomic trees support the monophyly of the families Ricinidae and Laemobothriidae. Trimenoponidae and Gyropidae are not monophyletic, and we suggest merging them into a single family, Gyropidae. The position of *Trinoton* is highly unstable across different trees, and we suggest recognizing Trinotonidae as a separate family. Several of our trees indicate that the family Boopiidae might be sister to all other Amblycera. However, this result remains obscured by the instability of Trinotonidae; denser sampling is required to confirm the placement of Boopiidae. At the genus level, our trees strongly support the genera *Colpocephalum*, *Hohorstiella*, *Menacanthus* and *Ricinus* as paraphyletic. Regarding complexes of genera, the trees revealed that the *Menacanthus* complex is monophyletic, but the *Colpocephalum* complex is paraphyletic, and includes different genera than previously thought. Dating analysis suggests that Amblycera diverged from other parasitic lice in the Late Cretaceous (103–75 Mya), and most families of Amblycera diversified shortly after the Cretaceous-Paleogene boundary 66 Mya. This diversification was then followed by the massive divergence of genera within the family Menoponidae in the early Tertiary. Cophylogenetic analyses revealed that during the evolution of Amblycera, host switching was more common than cospeciation, indicating that the evolutionary history of Amblycera does not mirror that of its hosts as tightly as previously thought. Ancestral host reconstructions revealed that the ancestral host of Amblycera was most likely a bird, and Amblycera switched to mammals twice. Combining the results of phylogenomics, molecular dating, and cophylogenetic analyses provides the first large-scale picture of the evolution of Amblycera, which supports the Southern Hemisphere origin of Amblycera and can be used as a robust basis for further investigation

Keywords: High-throughput sequencing, Amblycera, coevolution, host switching

T16. Juliana Soto-Patiño, Jorge Doña and Kevin P. Johnson – **Tracking host evolution through parasites: *Myrsidea* lice in suboscines and the puzzling case of *Sapayoa aenigma***

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Parasites can serve as independent tracers of host evolution, offering insight into historical biogeographic patterns and evolutionary processes. *Myrsidea*, the most diverse genus of avian lice (Menoponidae), primarily parasitizes Passerines, with lesser representation in Piciformes and Apodiformes. Its presence on suboscines—an evolutionary distinctive lineage within Passeriformes—offers a unique opportunity to investigate parasite-host associations, dispersal, and host-switching events. This study examines the phylogenetic placement of *Myrsidea* from suboscine hosts, with a particular focus on the enigmatic *Sapayoa aenigma*, a

Neotropical species whose evolutionary relationships have been an enigma, but is likely most closely related to Old World suboscines. We hypothesize that *Myrsidea* on *Sapayoa* either retain an ancestral Old World lineage through cospeciation, cluster with New World suboscines through host-switching, or reflect a lineage that was initially Old World but later donated to Neotropical suboscines. Using whole-genome sequencing, we analyzed *Myrsidea* from a broad range of avian hosts, including both Old and New World suboscines, and reconstructed their evolutionary history based on 2,395 single-copy gene orthologs. We incorporated cophylogenetic and biogeographic analyses to examine host-parasite relationships, cospeciation, and historical dispersal patterns. Our preliminary results show that suboscines generally acquired *Myrsidea* through multiple host-switching events from oscine passerines. However, the *Myrsidea* species found on *Sapayoa aenigma* is embedded among an Old World oscine-associated lineage, reinforcing the hypothesis of Sapayoa's Old World origin and its subsequent dispersal into the Neotropics. These findings provide parasite-based evidence that complements host biogeographic history, highlighting the potential of parasites as evolutionary markers to validate host dispersal events and evolutionary transitions between continents.

Keywords: Avian lice, biogeography, host-parasite coevolution, phylogenetics, phylogenomics

T17. Andrew Sweet[1], Kevin P. Johnson[2], Stephany Virrueta Herrera[3] and Jorge Doña[4]. **Estimating effective population size from a single louse genome: Case studies**

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Effective population size impacts the relative contributions of genetic drift and natural selection in determining the trajectory of genetic change in a population or species. Considerable attention has been given to this metric in free-living populations, but much less so for parasites. Lice provide a good model for studies of effective population size, because their populations can be readily defined given they spend their entire lifecycle on a host. New techniques have emerged to estimate effective population size using genome wide data from a single individual. These techniques have been applied to several studies of lice, in which estimates have been made from genome sequence datasets of single individual lice. Results have indicated that not only is louse effective population size related to host population size, but host body size also plays an important role, with lice from larger bodied hosts having higher effective population sizes. In addition, different louse ecomorphs from the same host species can differ in their effective

population sizes, related to differences in dispersal ability. These studies have revealed considerable promise for this approach, providing biological insights into aspects of louse populations that would otherwise be difficult to estimate without genomic data.

Keywords: Effective population size, genomics, host body size, inbreeding

Morphology, systematics & diversity – Part I

Chair: Therese ("Rese") A. Catanach.

T18. Kayce C. Bell[1], Priscilla A. San Juan[1], Jana Martin Říhová[2], Lance A. Durden[3], Jessica E. Light[4] and Julie M. Allen[5] – **New insights into sucking louse (Anoplura) relationships**

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Parasitism is one of the most common forms of life on the planet. However, the factors that affect parasite adaptations to their hosts, and shape host associations are poorly understood. Sucking lice (Anoplura) infest many species across nine mammalian orders and multiple louse species can be recovered from the same host species. This provides an excellent framework for exploring whether the diversification of lice and their associations with hosts are mainly influenced by historical factors and host adaptations, or if lice have the potential to parasitize a wide range of hosts but are confined to one or a few species due to limited dispersal. The first step in understanding Anoplura diversification and host associations is to build a comprehensive phylogenomic tree for mammalian sucking lice. This phylogeny will shed new light on louse relationships, permit testing of morphological evolutionary hypotheses, and serve as the basis for determining the role of adaptations in louse-host associations. Our preliminary phylogeny sampled 70 louse species representing 11 louse families at 1,107 loci across the genome. This research resulted in the first genetic data for some families and the phylogenetic relationships suggest our current understanding of sucking louse systematics needs revision. This framework will guide future investigations of host-parasite relationships.

Keywords: Anoplura, phylogenomics, systematics

T19. Lance A. Durden[1], Kayce C. Bell[2], Priscilla A. San Juan[2], Julie M. Allen[3] and Jessica E. Light[4] – **Systematics of sucking lice (Phthiraptera: Anoplura): morphological or molecular classification?**

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Ever since Linnaeus described the first sucking lice in 1758, the classification of this group of obligate ectoparasites has been based on morphological characters. Following that classification, 16 families, 52 genera and 601 species of sucking lice are currently recognized. The most speciose genera are *Hoplopleura* (178 species) (family Hoplopleuridae), *Polyplax* (81 species) (Polyplacidae), *Linognathus* (53 species) (Linognathidae), *Enderleinellus* (46 species) (Enderleinellidae) and *Neohaematopinus* (31 species) (Polyplacidae). Four monotypic families (Pecaroecidae, Hybophthiridae, Hamophthiridae, Mirophthiridae) and 19 monotypic genera (*Cuyana, Ctenophthirus, Docophthirus, Echinophthirius, Galeophthirus, Haematopinoides, Hamophthirus, Hybophthirus, Hylophthirus, Lagidiophthirus, Latagophthirus, Microphthirus, Mirophthirus, Paradoxophthirus, Pecaroecus, Phthirunculus, Proenderleinellus, Sathrax, Typhlomyophthirus*) of Anoplura are currently recognized. However, the recognition of some of these genera (e.g., *Pardoxophthirus, Cuyana, Galeophthirus* and *Lagidiophthirus*), based on morphology, is tenuous, and could benefit from other datasets such as those based on molecular/genetic information. Also, whether geographically widespread and speciose genera, such as *Hoplopleura, Eulinognathus*, and *Polyplax*, should be split into additional genera is unclear, based solely on morphology. Finally, the family Polyplacidae as currently treated, includes 20 genera and appears to represent an unwieldy group of morphologically diverse lice. Molecular/genetic data can aid in these taxonomic decisions and will be discussed for published molecular data as part of a morphological overview of the Anoplura. Molecular datasets are currently available for only a small subset of the Anoplura but new initiatives are underway and will help to resolve these and other issues.

Keywords: Anoplura, systematics, morphology, molecular data

T20. Priscilla A. San Juan[1], Lance A. Durden[2], Julie M. Allen[3], Anna J. Phillips[4] and Kayce C. Bell[4] – **Combining morphology with genomics to shed light on chipmunk sucking louse systematics (genus *Hoplopleura*)**

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Western chipmunks (23 species of *Tamias*, subgenus *Neotamias*) and the eastern chipmunk (*Tamias striatus*) are infested by two different species of *Hoplopleura* sucking lice, *H. arboricola* and *H. erratica*. *Hoplopleura arboricola* has been found on 19 of 23 western chipmunk species, while *H. erratica* has only been described as a parasite of *T. striatus*. The two groups of chipmunks diverged approximately 17 million years ago, so different species of louse parasites are not unexpected. We aimed to investigate the relationships between the two species and their morphological traits, which the original descriptions characterized as unique. We combined published genomic data with additional samples of sucking lice and morphological examinations. Sucking lice (n=47) were collected from wild-caught chipmunks or combed from chipmunk museum study skins, then preserved in 80% ethanol. We estimated phylogenetic relationships using 1107 coding loci in a Maximum Likelihood framework and a species tree approach. Both phylogenetic approaches recovered two well-supported clades of *H. arboricola*, one of which included *H. erratica*, suggesting that the two louse species are not distinct and challenging prior species classification. Further, examination of louse specimens did not find morphological traits that could distinguish lice from any of the lineages, including differentiating *H. erratica* from *H. arboricola*. Based on the genetic similarities and phylogenetic relationships of the lice, it appears that an ancestral louse was associated with western chipmunks, diverged into two major lineages and was then transferred to the eastern chipmunk, from one of those lineages. This work illustrates the importance of genomic approaches and phylogenetic analyses to study species interactions, the history of interspecific associations, and validating taxonomy. Additionally, our findings challenge the approach of assuming strict host-parasite associations and that sucking lice co-diverge with their hosts.

Keywords: Host–parasite associations, Anoplura, Tamias, North America

T21. Marek Schneider, Stanislav Kolencik, Kevin P. Johnson, Jason D. Weckstein, Mohamed F. Sallam, Julie M. Allen and Oldrich Sychra – **Diversity, host associations and geographical distribution of lice of the genus *Myrsidea* (Amblycera: Menoponidae)**

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With a total of 382 described species, *Myrsidea* Waterston, 1915 represents the most diverse genus of avian chewing lice. *Myrsidea* has a global distribution, is thought to be highly host-specific, and parasitizes mostly passerine birds (366 species on a total of 488 passeriform host species from 57 families). The 16 remaining species of *Myrsidea* parasitize 13 species of toucans (Ramphastidae) and 3 species of hummingbirds (Trochilidae). In general, species of *Myrsidea* are highly host-specific, with 78% of *Myrsidea* species restricted to a single host species. The remaining species are known to occur on 2–11 closely related host species. The only extreme case of a generalist *Myrsidea* seems to be the *M. quadrifasciata* species complex, which has been reported from 35 host species belonging to 8 passerine families (Calcariidae, Emberizidae, Fringillidae, Icteridae, Passeridae, Ploceidae, Thraupidae, and Viduidae). Of the 488 bird species known to be parasitized by *Myrsidea*, 88.5% (n = 432) harbor only one species of *Myrsidea*. Synoxenic distribution of *Myrsidea*, i.e., the presence of more than one *Myrsidea* species on the same host species, has been reported for 58 bird species, with 43 host species are known to harbor only 2 *Myrsidea* species, while the other 13 host species harbor 3–9 *Myrsidea* species. Based on the type of genital sac sclerite we divided *Myrsidea* species into 63 morphotype groups. The highest diversity of morphotype groups was found in Indomalaya, where *Myrsidea* belonging to 37 (58%, n = 63) morphotype groups occur. A total of 39 (62%) morphotype groups are found in only one biogeographic region. On the other hand, 3 morphotype groups - rustica, thoracica, and quadrifasciata - have cosmopolitan distributions, occuring in 6 regions. The highest numbers of *Myrsidea* from different morphotype groups were found infesting species in the following bird families: Leiothrichidae (10), Estrildidae (8), Corvidae (8), Sturnidae (7), Thraupidae (6), Icteridae, Ploceidae, Turdidae, Tityridae, and Tyrannidae (4), suggesting some level of host-switching among host families.
This work was supported by VETUNI grant number 2025ITA23
Keywords: Birds, lice, morphotypes, passeriformes

T22. Therese A. Catanach[1], Kiana Habersham[1,2], Kevin P. Johnson[3], and Jason D. Weckstein[1,4] – **Integrating legacy data and whole genome sequencing on both sides of the tanglegram uncovers unexpected cospeciation in *Degeeriella***

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Historically, the louse genus *Degeeriella* was considered a parasite of diurnal birds of prey, including hawks, eagles, and falcons, which were believed to be a single related lineage of hosts. However, molecular phylogenetic analyses have shown that falcons are not closely related to hawks, eagles, or their relatives. Furthermore, the respective species of *Degeeriella* on these two groups are also not closely related. Previously published cophylogenetic studies of the genus *Degeeriella* from hawks and eagles more specifically have indicated that the louse phylogeny is not congruent with the host phylogeny, and that phoresy has likely played a major role in explaining the parasite distribution on these hosts. However, using whole genome sequencing to produce a more taxonomically complete hawk phylogeny indicates that many aspects of the trees of hosts and parasites are congruent, implying codiversification events between hawks and their lice in the genus *Degeeriella*. Thus, previously published cophylogenetic studies that relied on incomplete host phylogenies erroneously interpreted the coevolutionary history of these hosts and parasites. In particular, the *Degeeriella* parasitizing *Buteo* and related genera are structured based on host geography and not host relationships, whereas *Degeeriella* parasitizing *Accipiter* and *Circus* show evidence of cospeciation.

Key Words: Cospeciation, genomics, phylogenetics, systematics

Keynote

Chair: Kosta Y. Mumcuoglu

T23. Dale H. Clayton - **Mighty oaks from humble acorns grow: Roger Price and the emergence of coevolutionary biology**

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Dr. Roger Price (1929 – 2024) was one of the most influential taxonomists ever to work on lice (Insecta: Phthiraptera). He was a brilliant, unassuming researcher and wonderful mentor. He published more than 250 papers on lice, including descriptions of over 600 new species/subspecies and 25 higher taxa, as well as 625 new synonymies. His taxonomic descriptions and the illustrations accompanying them are among the best in the history of work on this order of insects. Over several decades he amassed the database used to create *The Chewing Lice: World Checklist and Biological Overview*, coauthored with R. Hellenthal, R. Palma, K. Johnson and D. Clayton. Most active researchers studying the biology of lice depend on the foundation created by Roger, whose work forms the basis of many important contributions to coevolutionary biology. Roger's taxonomic work on the lice of pocket gophers set the stage for classic studies of the co-diversification of these two groups. His taxonomic work on different groups of bird lice also set the stage for textbook studies of the co-diversification and co-adaptation of birds, their lice, and endosymbiotic bacteria in the lice of birds and mammals. Roger's work also catalyzed serendipitous work on the control of head lice in humans. In this talk I will provide an overview of Roger Price, his career, and the central role of his work in coevolutionary biology.

Keywords: Cophylogeny, cospeciation, coadaptation, bird, mammal, human, lice

Morphology, systematics & diversity – Part II

Chairs: Jason D. Weckstein, Alexandra Grossi.

T24. Jason D. Weckstein[1,2], Therese A. Catanatch[1], Michel P. Valim[3], Matthew Soesanto[1], Lukas Musher[1], Sarah E. Bush[4], Matthew E. Kinney[5], Armand M. Kuris[6], Chelsea L. Wood[7] and Kamila M. D. Kuabara[1] – **Parasites lost no more: rediscovery, description, and comparative genomic diversity of California Condor lice**

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In 1987, the extinction of California Condor (*Gymnogyps californianus*) was thwarted when all 27 remaining wild individuals were captured, given veterinary care, treated for parasites, and placed in a breeding program. This program was extremely successful and there are now more than 300 wild condors distributed across California, Utah, Arizona, and Baja California. In some areas, recruitment in the wild is now approaching the level required to maintain a stable population. Ironically, one unfortunate side effect of this process was the supposed extermination of the host specific louse, *Colpocephalum californici*. *Colpocephalum californici* has been touted as the poster child for parasite extinction – a key example of how human activities can inadvertently drive parasites extinct. However, in 2018 veterinarians at the San Diego Zoo Safari Park found lice on several California Condors being readied for release in the wild. A combination of morphological examination and analysis of DNA sequence data revealed that these specimens are in fact the "lost" California Condor louse, *Colpocephalum californici*. Since the initial records, additional sampling of birds by San Diego Zoo Safari Park, Santa Barbara Zoo, The Peregrine Fund, and U.S. Fish and Wildlife Service have found more *C. californici* and an undescribed *Falcolipeurus* species that was first noted by Kellogg (1910), which we have now confirmed is specific to California Condor. Fortunately, two species of California Condor lice survived the conservation practices of the 1980's. Unfortunately, however, our recent surveys have not found any *Cuculiphilus alternatus*, a species known to infest California Condors (Kellogg 1910; Scharf & Price 1965). In addition to morphological and phylogenetic analysis, we have sequenced whole genomes from these lice and several other congeners from other New World Vultures to test the hypothesis that genomic variation due to population bottlenecks in the lice can tell us about historical population fluctuations in the endangered avian hosts. This "use" of parasite data underscores an additional value of conserving parasites not only for their own existence but to provide better understanding of their endangered hosts. As expected, comparisons between California Condor lice and other New World Vulture lice in the genera *Colpocephalum* and *Falcolipeurus* demonstrate the expected signatures of population bottlenecks of condors with respect to other more abundant vulture species.

Keywords: Parasite coextinction, systematics, morphology, biodiversity, phylogenetics, population genomics

T25. Daniel R. Gustafsson[1], Alexandra A. Grossi[1], Leshon Lee[2] and Fasheng Zou[1] – **Biodiversity and biogeography of Asian and Australo-Papuan *Guimaraesiella* Eichler, 1949 (Phthiraptera: Ischnocera).**

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The genus *Guimaraesiella* comprises a taxonomically diverse, but morphologically homogeneous, genus of lice in the *Brueelia*-complex, parasitizing mainly songbirds (Passeriformes) worldwide. Presently, 110 species of *Guimaraesiella* have been described in five subgenera, but the diversity of this genus is poorly explored. For instance, almost half of the species (N = 46 species; 41.8%) have been described since 2017, and phylogenetic analyses of *Guimaraesiella* regularly include large numbers of undescribed species. A recent estimate suggested that the true diversity of *Guimaraesiella* may be over 2600 species, most of which are found in the tropics. Genetic data from mainly South China indicate that several additional groups deserve recognition as distinct subgenera; in all cases there is also morphological support for these divisions, which is discussed here. This includes at least two groups that are known exclusively from babblers (Leiothrichidae, Pellorneidae, Timaliidae). In addition, the subgenus *Guimaraesiella* (*Cicchinella*) and the sister-group of *Guimaraesiella*, the genus *Priceiella*, are both almost exclusively known from babblers. We found no evidence for significant co-speciation between *Guimaraesiella*, *Priceiella* and their hosts. Together, this suggests that babblers may have been colonized by *Guimaraesiella* several times independently, which may be correlated with their frequent role as core members of mixed-species feeding flocks in Southeast Asia. Participation of hosts in such flocks may also underlie the existence of several clades of morphologically cryptic species of *Guimaraesiella* with very wide host ranges. Genetic data has revealed that one such species, *Guimaraesiella impiger* sp. nov. is found on over 30 host species across the Old-World tropics, and several other species of *Guimaraesiella* have similarly wide host ranges. In at least some cases, these cryptic host generalists overlap geographically and occur on closely related hosts, meaning that DNA data may be necessary for accurate identification. DNA data has also revealed that some host generalist *Guimaraesiella* may occur over very large geographical areas, and may have ranges that span multiple biogeographical regions, including cases where the hosts do not overlap in range.

Keywords: *Brueelia*-complex, cryptic species, subgenera, host specificity

T26. Oldrich Sychra, Marek Schneider, Kevin P. Johnson, Jason D. Weckstein, Mohamed F. Sallam, Julie M. Allen and Stanislav Kolencik – **The parasitic louse genus *Myrsidea* (Amblycera: Menoponidae): a comprehensive review**

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Myrsidea Waterston, 1915 is the most diverse genus of avian chewing lice. The rate of taxonomic studies describing new species is still relatively low, and it is thought that much of the diversity of *Myrsidea* is yet to be discovered. This low rate of taxonomic description for this genus, and many others, may be related to the time-consuming nature of morphological species description and a lack of comprehensive review of characters important for its taxonomy. Furthermore, most of the revisions have focused on specific host families, and no comprehensive review of the morphology combined with results of molecular work. We reviewed the taxonomy and systematics of *Myrsidea* and described and summarized all morphological characteristics important for species descriptions, and provided a comprehensive checklist of a total of 382 known and recognized *Myrsidea* species described to date (updated dataset: https://github.com/StanleeKol/MyrsideaReview). According to the type of genital sac sclerite we divided these species into 63 morphotype groups. More research on comparative morphometric and molecular analysis is needed to evaluate the level of intraspecific and interspecific variability among male genital sac sclerite characters and its taxonomic importance within the genus *Myrsidea*. This work was supported by VETUNI grant number 2025ITA23.

Keywords: Diversity, morphometry, taxonomy

T27. Annabella Maria Schmiedová[1], Oldřich Sychra[1], Miroslav Capek[2] and Ivan Literák[1] – **Morphometric study of the genera *Trochiliphagus* and *Trochiloecetes* in hummingbirds**

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Trochiliphagus and *Trochiloecetes* (Amblycera: Ricinidae) are genera of ectoparasitic lice described from hummingbirds, yet their taxonomy remains unclear due to poorly described species, often based on single specimens. Despite being parasites of one of the smallest birds, lice from these genera are among the largest ectoparasitic lice and almost exclusively blood-feeding, raising questions about their potential impact on their hosts. This study aims to revise the taxonomy of *Trochiliphagus* and *Trochiloecetes* through an integrative approach, analyzing 1,085 specimens (238 *Trochiliphagus* and 847 *Trochiloecetes*) from museum collections, including the United States National Museum of Natural History and more.This research aims to revise the taxonomy of *Trochiliphagus* and *Trochiloecetes* through morphometrical analysis. Metric analysis included measuring 8–10 body parts (depending on genus and sex) to assess intra- and interspecific variability. A statistical analysis (PCA) was performed. Over 130 morphological characteristics, originally established

for species identification in the genus *Ricinus*, were evaluated for *Trochiliphagus*, 92,3 % proving applicable, while the rest were excluded due to morphological differences or specimen quality. Some traits exhibited morphological differences, particularly in head and prothorax shape, while others showed no significant variability. Variability in the number of setae (e.g., on the gulla and vulva) was observed, potentially reflecting natural intraspecific variation. Abnormalities, such as broken setae, highlighted challenges in reliable identification based on single specimens. Preliminary results indicate that *Trochiliphagus* may include only 1–3 species, rather than 13 as previously described. Some characteristics show similarities with the genus *Ricinus*, some not. To clarify the genetic diversity, molecular data are essential. A field expedition to Argentina is planned to collect fresh lice samples for DNA analysis, which is expected to provide more definitive insights into the taxonomy of these genera. This work was supported by VETUNI grant number 2025ITA23.

Keywords: Ricinidae, ectoparasites, taxonomy, variability

T28. Alexandra A. Grossi[1], Daniel R Gustafsson[1], Wenyi Zhou[2] and Fasheng Zou[1] – **Diversity of chewing lice infesting birds in Western Yunnan, China**

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Western Yunnan, China, is a hot spot for bird biodiversity, combining elements of Himalayan, Indian, and Southeast Asian bird faunas. The area is among the most diverse in China, yet the chewing louse fauna of Yunnan is poorly known. Over the course of two collecting trips a total of 909 birds, representing 112 species (97% of which belonged to the Passeriformes) were fumigated for chewing lice. The overall infestation prevalence of lice (Amblycera + Ischnocera) was 23% (210 birds). A region of the COI gene was sequenced from one louse of each unique genus per infested bird. Based on an operational taxonomic unit (OTU) analysis, the collected lice represented 70 OTUs, of which 20% (14 species) could be tentatively identified through BLAST searches on GenBank. The most prevalent louse genera were *Guimaraesiella* (10 OTUs), *Myrsidea* (19 OTUs), and *Menacanthus* (7 OTUs); in total 22 genera of lice were obtained. Our OTU analysis allowed us to estimate the host specificity of these lice. Overall, 45 OTUs (64.3%) were recovered from only a single host species; 25 of these OTUs were recovered from a single host individual, whereas 19 were collected from multiple conspecific host individuals. Another 25 OTUs (35.7%) comprised specimens collected from 2–5 host species. In some cases, these may represent stragglers, but several species were recovered

multiple times from multiple host species, and thus likely represent species that are established on more than one host species. This includes OTUs identified as *Menacanthus eurysternus*, *Guimaraesiella* (*Cicchinella*) *mcgrewi*, *Guimaraesiella* (*Cicchinella*) *yuhinae*, *Priceiella* (*Thescelovora*) *austini*, and an undescribed species of *Guimaraesiella* s. str. from two species of flycatchers. Notably, the recently described and widely distributed *Guimaraesiella impiger* was found only from 3 samples, despite known host species of this louse species being examined, and this species having been collected more broadly in this region of Yunnan in previous years. Dense, repeated sampling of the same area over multiple field seasons may thus reveal that some lice are less host specific than commonly thought. Notably, babbler species that are common participants in mixed-species feeding flocks had diverse louse faunas, with 7 louse species recovered from *Alcippe fratercula*, 7 from *Leiothrix argentauris* and 5 from *Stachyris nigriceps*. Further work in identifying and describing these lice will be necessary to make identification by barcoding more feasible.

Keywords: Diversity, prevalence, species identification.

T29. Julie Allen[1], Masoud A. Rostami[2], Behnaz Balmaki[1,3], Stanislav Kolencik[4], Daniel R. Gustafsson[5], Jason D. Weckstein[6,7], John Gausas[7], Ricardo L. Palma[8], Oldrich Sychra[9], Andrew D. Sweet[10], Kamila M. D. Kuabara[6,7], Katja Seltman[11], Nicolas J. Dowdy[12], Jennifer M. Zaspel[12], Jessica E. Light[13], Rob Guralnick[14] and Sarah E. Bush[15] - The promise and impediments of artificial intelligence for species identification in Phthiraptera

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Artificial Intelligence (AI) applications have become ubiquitous in the field of biology. For example, phone applications are widely used by non-experts to identify species of plants and animals through images (e.g., "seek", "iNaturalist", "BugFinder"). These methods require large amounts of known data to train a model appropriately. However, many species have few available images, often not enough to properly train a model. One potential way to circumvent this knowledge gap is to use "transfer learning", where a model pre-trained on a large general dataset (e.g., ImageNet, a database containing millions of labeled images across thousands of categories) is further fine-tuned using fewer images of the target species. This method requires fewer images of the target species and may help to bypass the need for large collections of images. Here, we discuss a recent study in which we built a model to identify species of poultry lice using a transfer learning approach. Poultry lice are encountered frequently by non-experts and are often misidentified. We collected images of known poultry louse genera, and trained several available models. We then ran novel images through the best model to determine how well the model could identify species. We discuss areas where the model performed well and issues that need to be addressed to develop models that can be widely used for species identification in Phthiraptera.
Keywords: Artificial Intelligence, species identification, Phthiraptera

T30. Ricardo Palma - Collecting lice in "Las Islas Encantadas"

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During March–May 1992, I participated in an entomological expedition to the Galápagos Islands to collect lice from as many host species as possible. The purpose was to establish which were the natural and regular host-louse associations, considering that earlier louse collections had been cross contaminated giving a completely wrong pattern of host-louse associations. This mainly pictorial presentation shows how and where we collected lice, and some of the hosts caught during the three months spent on the islands.
Keywords: Galápagos, field biology, host-parasite associations, louse diversity

Chair: Olivier Chosidow

T31. Pierre-Edouard Fournier – Louse-borne infections in the 21st century: forgotten diseases but current threats

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Louse-borne infections, historically associated with poverty, war, and displacement, continue to pose a significant public health threat in the 21st century. Of the three primary diseases transmitted by the human body louse (*Pediculus humanus humanus*), trench fever (*Bartonella quintana*), louse-borne relapsing fever (*Borrelia recurrentis*) and epidemic typhus (*Rickettsia prowazekii*), the former two have increasingly been reported in both endemic regions and high-income countries. Current risk factors fueling this resurgence include growing global displacement, urban homelessness, inadequate access to hygiene, and climate-related disasters. Recent outbreaks in East Africa and cases among migrant and homeless populations in Europe and North America underscore the vulnerability of marginalized communities and the ease with which these infections can spread under conditions of social instability. Diagnosis often remains challenging due to non-specific symptoms and underreporting, while prevention relies on improved hygiene, access to clean clothing, and targeted public health interventions. Despite their preventability and the availability of effective treatments, louse-borne infections remain neglected due to limited surveillance and public health prioritization, non-specific symptoms and underreporting. This reemergence highlights an urgent need for integrated interventions that combine medical care with social support, improved sanitation infrastructure, and enhanced monitoring to mitigate the growing risk of louse-borne disease outbreaks.

Keywords: Body louse, epidemic typhus, trench fever, louse-borne relapsing fever

T32. Oleg Mediannikov[1,2], Alissa Hammoud[1,2], Florence Fenollar[1,3] and Pierre-Edouard Fournier [1,2] – Human head lice as vectors of *Bartonella quintana*

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Bartonella quintana is a louse-borne, Gram-negative bacillus that remains a poorly characterized etiological agent of trench fever, as well as bacteremia, prolonged fever, and infective endocarditis. Its transmission, intrinsically linked to body louse (*Pediculus humanus humanus*) infestation, is favored by conditions of poverty, armed conflict, overcrowding, and limited access to hygiene facilities.

To date, *B. quintana* and *Bartonella bacilliformis* are the only known Bartonella species strictly associated with primate hosts. The role of the body louse in *B. quintana* transmission was first elucidated during the First World War, establishing that trench fever is propagated through contamination with infected louse feces introduced via scratching. Following Charles Nicolle's 1912 discovery of the body louse as a vector of epidemic typhus, subsequent microbiological and epidemiological studies concentrated on the role of body lice in transmitting the three major louse-borne infections: epidemic typhus, relapsing fever, and trench fever. Although early experimental evidence (1912) demonstrated that head lice could excrete viable *Rickettsia prowazekii*, the etiologic agent of epidemic typhus, a prevailing paradigm quickly developed asserting that only body lice served as competent vectors for all three major louse-borne diseases. However, recent advances in molecular screening and point-of-care diagnostics of infectious diseases in tropical regions have begun to challenge this view, revealing a potential, previously overlooked role for head lice in the transmission of certain pathogens, particularly *B. quintana*. In our recent investigation conducted in Senegal, we employed a combination of culture-based methods, molecular diagnostics, and genomic analyses to document an outbreak of trench fever associated with head lice. In 2014, ongoing surveillance of febrile patients in the village identified an outbreak affecting 9 individuals among approximately 400 residents. Two *B. quintana* strains were isolated—one from a patient's blood sample and the other from head lice collected from a different patient. Whole-genome sequencing revealed a 99.98% genetic identity between the two isolates. Coupled with multiple reports of the detection of *B. quintana* in headlice from all over the world, these findings strongly support the hypothesis that head lice are capable of serving as vectors for *B. quintana*. Absence of body lice in a village, isolation of viable *B. quintana* from head lice, combined with the genomic identity between strains from human blood and lice during a localized outbreak, provides compelling evidence of the vectorial capacity of head lice, warranting further investigation.

Keywords: *Bartonella quintana*, vector, human head lice, human body lice

Human lice: Genetics, geography & relationships with symbionts

Chairs: Olivier Chosidow, Ariel Toloza.

T33. Marina S. Ascunce[1,2], Ariel C. Toloza[3], Angélica González-Oliver[4] and David L. Reed[5] – **Genetic footprints of the treks of human lice around the globe**

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The human louse, *Pediculus humanus*, is an obligate blood-sucking ectoparasite that has coevolved with humans for millennia. Because of the intimate relationship between this parasite and the human host, the study of human lice has the potential to shed light on aspects of human evolution that are difficult to interpret using other biological evidence. In this study, we analyzed the genetic variation in 274 human lice from 25 geographic sites around the world by using nuclear microsatellite loci and female-inherited mitochondrial DNA sequences. Nuclear genetic diversity analysis revealed the presence of two distinct genetic clusters I and II, which are subdivided into subclusters: Ia-Ib and IIa-IIb, respectively. Our results showed these two divergent nuclear louse genetic clusters have very limited and recent admixture, mostly in the New World. We suggested that this pattern is reflective of human dispersal to the Americas, with an early wave of louse-human co-migration during the population of the New World represented by cluster I and the most recent European migration represented by cluster II. We also hypothesized that there is a potential mechanism that is preventing admixture between these two divergent nuclear clusters, most likely epigenetic in origin. Due to the use of microsatellites that are known to be fast-evolving markers, our analyses are more suited to recent events, and slower evolving markers could provide insights into more ancient events. Further studies in human lice including more samples, whole genomic, and epigenomic approaches could provide new knowledge about louse evolution as well as their human host.

Keywords: Human lice, human migration, nuclear genetic diversity, microsatellites, admixture

T34. Parisa Sharafi[1], Ayca Ozsipahi[2], Bengu Akgok[2], Fatma Gufran Suleyman[2], Kosta Y. Mumcuoglu[3] and Aysegul Taylan-Ozkan[4] - **Detection of human louse DNA in different soil samples**

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The recovery and molecular identification of arthropod DNA from soil samples pose significant challenges due to the complex nature of soil matrices. This study optimized a DNA isolation protocol to extract *Pediculus humanus humanus* (body louse) DNA from different soil types, including clay, calcareous, humus, and sandy soils. To achieve this, Sheather's sugar flotation method was used to separate louse fragments from the soil before DNA extraction. Using the *cytochrome c oxidase subunit 1* (*COX1*) gene, louse DNA was detectable in clay, calcareous, and sandy soils, with optimal performance observed in clay and calcareous samples. However, humus soil proved unsuitable due to the flotation of low-density particles, which interfered with the separation process. Louse DNA was detectable in calcareous soil in a dilution of 1:1,000. These findings highlight the feasibility of using a modified flotation-based approach to molecularly detect *P. h. humanus* DNA in soil samples. This method has potential applications in forensic entomology, archaeological investigations, and epidemiological studies involving ectoparasite-borne diseases.

Keywords: *Pediculus humanus humanus*, DNA extraction, Sheather's sugar solution, forensic entomology, soil matrix, PCR detection

T35. Kosta Y. Mumcuoglu[1], Parisa Sharafi[2] and Aysegul Taylan Ozkan[3] - **Microbiota of the human head louse, *Pediculus humanus capitis*, and the human body louse, *Pediculus humanus humanus* (Anoplura: Pediculidae) in Israel**

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The microbiota of the head louse (*Pediculus humanus capitis*), collected from the head of infested individuals, and that of the body louse (*Pediculus humanus humanus*), reared in the laboratory on rabbit blood, were compared. A total of 84,988 operational taxonomic units were detected in head lice and 63,608 in body lice. The bacterial phyla Bacillota, Pseudomonadota, Bacteroidota, and Actinomycetota were dominant in both louse ecotypes. A total of 69 bacterial orders were detected in head lice and 63 orders in body lice, the most abundant being Bacillales, Lactobacillales, Bacteroidales, Enterobacterales, Eubacteriales, and Legionellales. Out of 139 bacterial families present in head lice and 120 families present in body lice, Bacillaceae, Lactobacillaceae, Enterobacteriaceae,

Streptococcaceae, Staphylococcaceae, Bacteroidaceae, and Prevotellaceae were the most abundant in both lice. A total of 320 bacterial genera were identified in head lice and 251 in body lice; the most abundant were *Bacillus, Prevotella, Lactococcus, Lactiplantibacillus*, and *Phocaeicola*, while the genera *Pseudomonas* and *Macrococcus* were present only in the head louse group. A total of 566 bacterial species were identified in head lice and 429 bacterial species in body lice. The differences observed between the two ecotypes could be partially explained by different blood sources (human versus rabbit), different environmental conditions (human skin temperature and humidity versus 25°C and 50-60% relative humidity), and exposure to various skin and/or fur microorganisms. It is also possible that some members of the body louse microbiota have been lost due to laboratory rearing over the past 75 years.

Keywords: *Pediculus humanus*, microbiota, Israel, head louse, body louse

T36. Emily Dunn and Renfu Shao – **Transcription of the fragmented mitochondrial genomes of human head and body lice**

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Typical mitochondrial genomes of eukaryotes comprise a single circular chromosome. Gene transcription in typical mitochondrial genomes of eukaryotes has been well studied in several model organisms. In a number of eukaryotic lineages, the single-chromosome mitochondrial genome has fragmented into multiple to numerous mini-chromosomes. For instance, the mitochondrial genomes of human head and body lice each comprise 20 mini-chromosomes. How genes are transcribed in fragmented mitochondrial genomes is still poorly known. We analysed the RNA-seq data of human head and body lice generated in the past few years to understand how genes are transcribed in fragmented mitochondrial genomes. RNA-seq data of human lice were obtained from the NCBI Sequence Read Archive database and mapped to their mitochondrial genomes. The coverage of each gene, each mini-chromosome and non-coding region was determined using Geneious Prime and compared statistically. The transcription of two specific GC-rich and AT-rich motifs in the non-coding regions were obtained and compared with the immediate downstream and upstream regions respectively. In both head and body lice, mitochondrial mini-chromosomes are transcribed entirely with genes transcribed at much higher levels than non-coding regions. The 37 mitochondrial genes are transcribed unevenly with several genes including *rrnL* transcribed at significantly higher levels than other genes. Most genes were expressed at a similar level between head and body lice. Most transcription events terminate near a GC-rich motif in the non-coding regions; however, some transcription events can pass this motif, leading to the transcription of the entire non-coding regions. No

distinct initiation sites of transcription could be located, indicating the possibility of multiple initiation sites on each mini-chromosome. The high *rrnL* transcription is expected due to the high demand for ribosomes in mitochondria; however, the comparatively much low transcription of *rrnS* was unexpected. The transcription patterns observed in the human lice differ substantially from those in the animals with the typical single-chromosome mitochondrial genomes. Further study is necessary to show whether the transcription patterns observed in human lice are common in other animals and eukaryotes with fragmented organelle genomes.

Keywords: Human lice, fragmented mitochondrial genome, mini-chromosomes, gene transcription, RNA-seq

T37. Saima Naz[1], Maria Rebecca[1], Nazir Ahmed Brohi[2], Aziz Ahmed Ujjan[3], Shaila Khaskheli[1] andFarooque Ali Hattar[1] - **First report of crab louse, *Pthirus pubis* (L. 1758) and the fungal association of head louse, *Pediculus humanus capitis* De Geer, 1767 in people of low socioeconomic status of Hyderabad, Sindh, Pakistan**

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In the lower-socioeconomic community of Hyderabad in Sindh province, the living conditions are very difficult and a major portion of the population suffers from poverty, poor healthcare facilities, and inadequate sanitation, hence contributing to higher health risks. Due to poor hygiene and overcrowding, most people have a higher incidence of skin infections, including scabies, pediculosis, onychomycosis and other fungal and dermatological infections. By surveying these communities, we found 93.6% of individuals were infested with *Pediculus humanus capitis* (Head louse), among which six individuals (0.6%) were infested with *Pthirus pubis* (Crab louse) as well. It was the first report of crab louse infesting humans in the country. The association of pediculosis and fungal infection was also studied in the present survey. The head lice specimens were collected from individuals with any skin and hair infection and were kept in SDA for the culture of fungus species associated with them. The human head louse was found associated with 12 species of fungi including *Aspergillus flavus* Link, 1809, *A. fumigatus* Fresenius 1863, *A. niger* van Tieghem, 1867, *A. terreus* Thom, 1918, *Apophysomyces* sp., *Microsporum canis* (Bodin, 1902), *Microsporum ferrugineum* Ota, 1921, *Penicillium verrucosum* (Dierckx, 1901), *Trichoderma* sp., and three species of the genus *Trichophyton* with one new species were reported in association with head louse, *P. humanus capitis* for the first time in Pakistan.

Keywords: Crab louse, *Pediculus,* fungal association, low-SES, Pakistan

T38. Gholizadeh Saber – Molecular detection of novel glutamate channel mutations in field collected human head lice (Phthiraptera: Pediculidae) from Iran

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Introduction: Insecticides are a primary strategy for eliminating head louse infestations. Recently, new insecticides, such as ivermectin, which target glutamate chloride (GluCl) channels in the nervous system of invertebrates, have garnered attention for head louse treatment. However, resistance to this insecticide threatens the effectiveness of control programs. To address this issue, implementing insecticide resistance management systems and conducting resistance monitoring in head lice we used molecular sequence analysis. *Materials and Methods:* In the current study, to identify mutations in the GluCl gene of head louse populations collected from seven provinces in Iran, louse DNA was extracted, and PCR was conducted. The products were sequenced, and the resulting sequences were analyzed for GluCl gene possible mutations. *Results:* Five non-synonymous amino acid mutations were identified, resulting in the following substitutions: arginine to lysine (R37K), glutamic acid to lysine (E50K), aspartic acid to asparagine (D93N), arginine to glutamine (R100Q), and methionine to arginine (M101R). The most frequent substitutions were R37K and E50K (85.71%), followed by D93N (64.28%), M101R (35.71%), and R100Q (28.57%). These mutations are reported here for the first time. The identification of these novel mutations raises concerns about the potential emergence of ivermectin resistance. Further research is required to explore the functional implications of these mutations and their impact on insecticide efficacy. *Discussion:* The smart utilization of insecticides and comprehensive resistance management strategies are crucial to combating the spread of resistance. The identification of novel GluCl gene mutations highlights the potential emergence of ivermectin resistance. Future experiments should investigate these potential links to develop effective control measures. Staying updated with research findings and implementing appropriate strategies are vital to addressing insecticide resistance in head louse populations.

Keywords: Head louse, Iran, ivermectin, glutamate chloride channel, GluCl gene

T39. Anthony Marteau[1], Sophie Brun[1,2], Arezki Izri[3] and Mohammad Akhoundi[1,4] - Prevalence and genetic diversity of heritable bacterial symbionts in human lice

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Human lice are obligate bloodsucking ectoparasites harboring endosymbiotic bacteria essential for their survival. Despite the medical significance of human lice, their endosymbionts remain understudied, and knowledge about their species identity, prevalence and genetic diversity is largely limited. Head, body and pubic lice specimens' collection from infested patients of various origins, consulting at the Avicenne Hospital in Bobigny, between 2019 and 2023 enabled molecular screening for prevalence and genetic diversity of bacterial endosymbionts through conventional PCR targeting two fragments of 16S-rDNA. A total of 209 louse specimens isolated from patients of 18 geographical origins, including 186 head lice, 11 body lice and 12 pubic lice were examined with 77.5%, 41.7% and 94.3% of the specimens found to be infested with *Candidatus* Riesia pediculicola, *Candidatus* Riesia pthiripubis and *Wolbachia*, respectively. Inferred phylogenetic analysis of *Candidatus* and *Wolbachia* sequences revealed heterogeneity clustering into four and three clades, respectively. No specific correlation was observed between these endosymbionts and lice species or geographical origin demonstrating that head, body and pubic lice share the same *Candidatus* and *Wolbachia* strains with independent adaptation and coevolution, except *Candidatus* Riesia pthiripubis which was identified exclusively in pubic lice. These phylogenetic results were confirmed by Network analysis. These findings could be helpful in evolutionary and biological control investigations.

Keywords: Human lice, *Candidatus* Riesia pediculicola, *Candidatus* Riesia pthiripubis, *Wolbachia*, endosymbionts

Ecology & Evolution

Chair: Saima Naz and Matthew Waler

T40. Jana Martinů and Jan Štefka – **Prevalence differences between closely related louse species occurring in sympatry: specialist and 'generalist' lineages of *Polyplax serrata***

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Host generalist and specialist strategies in parasites entail specific trade-offs in host-parasite co-evolution. For example, specialists may optimize fitness by maximising their potential to infect a single host, which is offset by the

fragmented distribution of the parasite if the host population is not dense. In contrast, oligoxenous or polyxenous parasites may be less successful in infecting individual hosts, but their quantity can be increased by a continuous distribution over multiple hosts. Using prevalence and intensity as proxies of parasite fitness, we investigated possible trade-offs in populations of single-host and two-host lineages of *Polyplax serrata*, representing specialist (specific, S) and 'generalist' (non-specific, N) parasite strategies, respectively. The S lineage is found only on *Apodemus flavicollis* and forms two mitochondrial DNA sublineages that collide in a narrow hybrid zone (HZ) in central Europe. The less specific N lineage is found on both *A. flavicollis* and *A. sylvaticus*. By sampling 1234 mice from 103 locations, we found significant differences in the prevalence of lice on the shared *A. flavicollis*, with the S lineage reaching a higher prevalence (12.2%) than the N lineage (2.6%). However, the N lineage occurred at a high prevalence (12.2%) on non-shared *A. sylvaticus* hosts and showed a tendency to utilise *A. flavicollis* when the louse populations became too dense. Therefore, we argue that parasite's 'choice', not the accessibility of the host or interspecific competition on the shared host, is the main factor affecting the louse prevalence. We suggest that historical differences in the geographical distribution of both lice and mice could provide a possible explanation for the observed differences in life history strategies. We also analysed hybridising sublines of the S lineage, where a decrease in the prevalence of lice in the HZ centre (hybrids) would be expected if intrinsic genetic incompatibilities led to a decrease in fitness. Contrary to expectations, we did not find a decrease in the hybrids, but in one of the parental lineages. We consider instability of the hybrid zone or local changes in host abundance as possible explanations for this result.

Keywords: host-parasite co-evolution, specialization, host-parasite specificity, geographic specificity

T41. Sarah E. Bush, Matthew M. Waller, Kyle M. Davis, Sonora F. Clayton and Dale H. Clayton – **Birds in arid regions have depauperate louse communities: Climate change implications?**

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Environmental factors such as temperature and humidity influence the distribution of free-living organisms. As climates change, the distributions of these organisms change along with their associated parasites, mutualists and commensals. Less studied, how- ever, is the possibility that environmental conditions may directly influence the distribution of these symbionts even if the hosts are able to persist in altered environments. Here, we investigate the diversity of parasitic lice (Insecta: Phthiraptera) on birds in arid Utah compared to the humid Bahamas. We quantified the parasite loads of 500 birds. We found that the prevalence, abundance and richness of lice was considerably lower among birds in Utah, compared to the Bahamas, despite sampling greater host taxonomic richness in Utah. Our data suggest that as climates change, birds in arid regions will have less diverse louse communities over time, potentially relieving birds of some of the cost of controlling these ectoparasites. Conversely, birds in more humid regions will see an increase in louse diversity, which may require them to invest more time and energy in anti-parasite defense. Additional research with other ectoparasites of birds and mammals across different environmental conditions is needed to more fully understand how climate change may reshape parasite communities, and how these changes could influence their hosts.

Keywords: Host–parasite ecology, humidity, lice, parasite diversity, birds

T42. Stephany Virrueta Herrera and Kevin P. Johnson – **Extensive host switching between orders of birds by *Rallicola* lice**

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While most genera of lice are restricted to a single order of family of birds, the feather louse genus *Rallicola* is found across 14 avian families in 6 orders with a worldwide distribution. We sampled lice of this genus across all six avian orders on which it is found and estimated the phylogeny of these feather lice using data from whole genome sequencing. A phylogenomic data set from 1,107 targeted gene assemblies was analyzed using concatenated and coalescent methods and we also compared the resulting phylogenetic tree to that of their avian hosts. In the cophylogenetic analyses we found some evidence of cospeciation, but also several host-switching events which have occurred across these parasites. The host switching events point to an origin of *Rallicola* in South America, which may have then gained worldwide distribution through the dispersal of rails out of South America.

Keywords: *Rallicola*, host switching, phylogenetics

T43. Matthew M. Waller, Sarah E. Bush, Nicole A. Amedee and Dale H. Clayton – **Does the length of the bill overhang correlate with the abundance of lice on birds?**

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Preening is the main behavioral defense used by birds to combat harmful lice. Most birds have a small overhang at the tip of their bills that is used to generate shearing forces which damage the tough exoskeletons of lice. This overhang increases the effectiveness of preening. Previous work shows that species of Peruvian songbirds with longer overhangs have more lice than species with shorter overhangs. Experimental work demonstrates that removal of the overhang in captive rock pigeons triggers a large increase in the number of lice on birds. Woodhouse's Scrub Jays with intermediate overhang lengths had fewer lice than jays with longer or shorter overhangs. We quantified the length of the bill overhang and the number of lice on each of 6 species of birds to further explore the relationship between overhang length and louse number. We tested for a relationship within each species with negative binomial generalized linear models. We found no relationship between the relative length of the overhang and louse intensity for 5 of the 6 species tested. We did find a significant relationship for Woodhouse's Scrub Jays; jays with longer overhangs had more lice. Our data suggest that while the presence of the overhang is important, the relative length of the overhang does not appear to influence the ability of most species of birds to control their louse infestations in the wild.

Keywords: Anti-louse morphology, bird, louse control

T44. Yoshika Oniki-Willis[1], Edwin O. Willis[2]†, [3]Oldrich Sychra, [4]Terry Galloway and [5]Lajos Rozsa – **Adaptive sex-ratio patterns in hummingbird lice (Ricinidae: Trochiloecetes, Trochiliphagus)**

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Evolutionary theory predicts that highly inbred populations should exhibit female-biased sex ratios. In the case of lice, this hypothesis yields two predictions. First, it is reasonable to expect that multiple infestations lead to more outbred louse subpopulations (inhabiting host individuals) and are also associated with higher infestation intensities than single infestations. Consequently, when comparing conspecific subpopulations, infestation intensity is predicted to correlate positively with sex ratio (the proportion of males). Second, when compared across different louse species, multiple infestations are expected to be more frequent in species with higher prevalence. Thus, in interspecific comparisons, parasite prevalence should be positively correlated with sex ratio. These patterns are expected to be particularly pronounced in lice with relatively large body sizes and, consequently, small subpopulation sizes (i.e., low infestation intensities). Relative to their hummingbird (Trochilidae) hosts, *Trochiloecetes* and *Trochiliphagus* species are exceptionally large-bodied lice. Therefore, we analyzed the sex-ratio patterns

of South-, Central- and North American hummingbird lice to test the above two predictions. Our results unanimously support the first but not the second prediction.

Keywords: Evolution, sex ratio, inbreeding

T45. Jessica E. Light[1], Conrad A. Matthee[2], Nina du Toit-Heunis[1,2], Sonja Matthee[2] and Lance A. Durden[3] – **Host associations, host switching, geographic location and potential reticulate evolution shape the systematics of sucking lice (Psocodea: Anoplura) belonging to the genera *Hoplopleura* and *Polyplax***

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Sucking lice (Psocodea: Anoplura) represent a species rich parasite group that shares an intimate evolutionary relationship with their mammalian hosts. Two anopluran genera, *Polyplax* and *Hoplopleura*, primarily parasitize rodents and the taxonomy of these lice is mainly based on morphological characters with some inferences derived from host associations. To shed more light on the systematics and the evolutionary mechanisms that gave rise to *Polyplax* and *Hoplopleura* species diversity, data derived from the 16S rRNA, COI, 18S rRNA and EF-1γ genes were used to generate a phylogeny for 105 individuals representing ~56 morphologically identified species. Concatenated data analyses found significant nodal support for five higher level monophyletic clades among *Hoplopleura* and four higher level clades and 15 subclades among *Polyplax* species. The monophyly of neither *Polyplax* nor *Hoplopleura* was supported and topological conflict among individual gene trees resulted in a non-tested hypothesis that ancestral hybridization and/or independent lineage sorting may have shaped the evolution of some *Polyplax* species. Several species complexes or cryptic divergences were detected specifically within the hoplopleurid species *H. acanthopus, H. arizonensis, H. hesperomydis, H. oryzomydis, H. pacifica,* and *H. sciuricola,* and the polyplacid species *P. arvicanthis P. auricularis, P. biseriata, P. myotomydis, P. otomydis, P. reclinata,* and *P. spinulosa.* Four morphological and genetically distinct taxa were sampled from Gerbillinae or Deomyinae and these probably represent new species. The taxonomy of *Polyplax* and *Hoplopleura* needs a thorough revision, and the species diversity of these lice can be attributed to an interplay between host associations, host switching and geographic locations of host species.

Keywords: Anoplura, molecular data, systematics

T46. Saima Naz[1,] Ahmed Madani[1], Oldrich Sychra[2], Shaila Khaskheli[1], Mohammad Awais Memon[1], Farooque Ali Hattar[1] and Aziz Ahmed Ujjan[3] - **New data on genus *Coloceras* (Ischnocera: Philoperidae) infesting birds of family Columbidae (Columbiformes) with an updated list of columbid chewing lice from Pakistan**

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The present study contributes knowledge towards updated fauna of chewing lice, infesting birds of Pakistan, mainly pigeons and doves (Columbiformes: Columbidae). According to present studies, there were 17 species of chewing lice enlisted, infesting six species of pigeons and doves from different areas of Sindh and Punjab, including *Columba livia* Gmelin, *Streptopelia capicola* (Sundevall), *S. decaocto* (Frivaldszyka), *S. senegalensis* (L.), *S. tranquebarica* (Hermann), and *Treron phoenicopterus* (Latham). Among chewing lice, four species of the genus *Coloceras* namely, *C. damicorne* (Nitzsch, 1866), *C. piageti* (Johnston and Harrison, 1912), *C. theresae* Tendeiro, 1973 and *C. truncatum* Tendeiro, 1973, with one new species of *Coloceras* from *Streptopelia decaocto* were described for the first time. The fauna of columbid chewing lice was updated with ten previously known species *viz. Campanulotes compar* (Burmeister, 1838), *C. bidentatus* (Scopoli, 1763), *Colpocephalum afrozeae* Naz et al., 2012, *C. turbinatum* Denny, 1842, *Columbicola columbae* (L., 1758), *C. theresae* Ansari, 1955, *C. tschulyschman* Eichler, 1942, *Hohorstiella lata* (Piaget, 1880), *H. modesta* (Ansari, 1951) and *H. streptopeliae* Eichler, 1953, and three new records namely, *Bonomiella columbae* Emerson, 1957, *Columbicola bacillus* (Giebel, 1866) and *C. joudiae* Adly et al., 2019 were updated.
Keywords: Columbidae, chewing lice, *Coloceras,* checklist, Pakistan

T47. Kristýna Plšková, Stanislav Kolenčík, Mario A. Loaiza-Muñoz, Gustavo A. Londono, Julie M. Allen and Oldřich Sychra – **Understanding the life history characteristics of bird lice: Amblycera versus Ischnocera**

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The samples for study survivorship rates were collected during fieldwork conducted in the Anchicayá region, Buenaventura, Valle del Cauca in Colombia, in 2019. The survivorship rates of bird lice reveal significant differences between the two groups, Amblycera and Ischnocera. The results indicate that rapidly moving amblyceran lice have a shorter survival time when off their host compared to ischnoceran lice and feather supplementation does not significantly improve their survival. Amblyceran lice tend to feed on blood more frequently than ischnoceran lice, as blood provides richer nutrients than a feather-based diet, which could enhance their mobility. Additionally, observations suggest that amblyceran lice are more inclined to move on the skin of their hosts, while ischnoceran lice prefer to navigate along feathers. For evaluation of diet preference, we examined a total of 4,587 chewing lice specimens from Dr. Frantisek Balát's collection of slide-mounted louse specimens, comprising 1,418 amblyceran lice and 3,169 ischnoceran lice, to assess their diet preferences and survival capabilities off their avian hosts. Samples were collected from wild birds from former Czechoslovakia. In amblyceran lice was blood detected in 36% of the cases, encompassing 43 species from 14 genera within the families Menoponidae and Ricinidae. The presence of host blood in the digestive tract of lice from specific genera varied significantly, with some genera showing a blood presence ranging from 4% to 100%. Notably, a strictly blood-based diet was recorded for the genera *Hohorstiella* and *Machaerilaemus*. For ten other genera, including *Amyrsidea, Austromenopon, Ciconiphilus, Colpocephalum, Kurodaia, Menacanthus, Meromenopon, Myrsidea, Pseudomenopon*, and *Ricinus*, both blood and feathers were observed in their diets. Supported by the project 2024ITA23 from the University of Veterinary Sciences, Brno.

Keywords: Diet, ecology, ectoparasites, environment, survival

Poster Presentations

Posters: Human lice

P1. Sandra Leverenz, Anikó Fuhrmann, Lana Sawicki, Hans Dautel and Kerstin Büchel - **Artificial membrane feeding for in vitro rearing of body lice *Pediculus humanus humanus* and development of a rapid lice repellent screening assay**

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Several lice rearing in vivo and in vitro methods have been developed. Also, rabbits have long been used as hosts and blood suppliers for in vivo rearing of body lice (*Pediculus humanus humanus*, Orlando strain adapted to rabbit blood since the 1940s). As lice depend on frequent blood meals, colony maintenance is very time consuming and also stressful for the rabbits. In accordance with the 3R principle, we have replaced the use of rabbits with an artificial feeding method and established the first commercial body lice breeding colony based on in vitro feeding in Europe. This allows us to test regularly insecticides and repellents against body lice in the laboratory. We have also established a screening pipeline in a joint project to discover novel repellents against various arthropod pests including body lice. Since 2021, our Artificial Lice Feeding System (ALFS) with a Hemothek apparatus has allowed us to continuously maintain a lice colony that produces sufficient lice to conduct efficacy studies. The generation time is approximately 21 days (15 feedings) and the colony can be ramped up or down as required. Lice mortality during one generation (L1-Ad) depends mainly on the quality of the rabbit blood that we obtain from a commercial supplier in Germany. Increasing the lice feeding frequency (daily versus every two or three days) significantly improves the number and quality of eggs as determined by the hatching rate. We have also developed a rapid lice repellent screening assay that takes into account the specific biological behaviour of the lice. The test system is called the Static Object Bioassay (SOB) and studies the upward movement of lice on a static cylinder impregnated with test repellent. The use of an in vitro rearing system allows the testing of various systemic and topical pediculicides of both synthetic and natural origin. It also provides many opportunities to study the biology of the body louse and its potential to transmit pathogens. We are confident that the continued development and validation of our SOB will lead to the introduction of innovative repellents to the market, providing new solutions for arthropod control and protection.

Keywords: *Pediculus humanus humans*, artificial feeding system, repellents, screening tests

P2. Bouthaina Hasnaoui[1,2], Zaina Amirat[1,2], Noelle Masotii[1,2], Dikra Hamadouche[1,3], Rim Bouledroua, Basma Ouarti[1,2] and Philippe Parola[1,2] - **Unlocking lice science: Breeding *Pediculus humanus humanus* on rabbits for research**

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The recent epidemics of trench fever, typhus epidemic and relapsing fever - diseases transmitted by the human body louse *Pediculus humanus* - have highlighted the crucial importance of studying the biology of lice, In particular, understanding the louse's vectorial capacity and vector competence such as *Bartonella quintana*. Although several studies have demonstrated the potential of in vitro lice rearing methods, these techniques have proved insufficient to maintain several consecutive generations on artificial membranes, highlighting a major limitation of current research methodologies. Initial efforts to maintain body lice for research purposes relied on human volunteers.

However, this approach proved problematic, often causing discomfort and leading to allergic reactions such as pruritus, inflammation and secondary infections. Because of these ethical and practical concerns, researchers set out to identify a suitable animal host that could sustain lice colonies under laboratory conditions. that was first successfully achieved by Culpepper in the 1940s in his Orlando, Florida laboratory. The development of the rabbit model has since provided a reliable alternative, enabling researchers around the world to maintain body lice colonies for experimental studies. Currently, the use of a laboratory reared *Pediculus humanus humanus* -lice maintained on female New Zealand White rabbits, remains the standard method for producing synchronized cohorts of lice at different life stages for research. In our laboratory, *P. h. humanus* rearing began in 1995. Lice are kept in ventilated plastic jars on pieces of black cotton cloth under controlled conditions (29–30°C and 70–80% relative humidity). Feeding is provided every 48 hours. Eggs are collected and transferred to new plastic jars. The newly hatched larvae are monitored for sex, morbidity, and vitality throughout the experiment.

In a global health landscape where vector-borne diseases are re-emerging and evolving, the ability to maintain and study human body lice under controlled laboratory conditions is more critical than ever. Our work contributes to bridging the gap between in vitro limitations and ethical constraints of human-based models by refining and sustaining a reliable rabbit-based rearing system. This approach

supports deeper investigations into the vectorial competence of *Pediculus humanus*, particularly in relation to pathogens such as *Bartonella quintana*.
Keywords: Lice, rabbits, feeding, rearing, France

P3. Basma Ouarti[1], Maureen Laroche[2], Ahmed Benakhla[3], Khaoula Ouarti[3] and Philippe Parola[1] - **The introduction of mass spectrometry in medical entomology and its application in lice identification**

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The advent of matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) has revolutionized medical entomology by providing a rapid, cost-effective, and accurate method for arthropod identification. In this study, MALDI-TOF MS was utilized to identify lice collected from livestock and poultry in Algeria. Mass spectrometry (MS) spectra were obtained for 408 adult specimens representing 14 species, including *Bovicola bovis*, *Bovicola ovis*, *Bovicola caprae*, *Haematopinus eurysternus*, *Linognathus africanus*, *Linognathus vituli*, and *Solenopotes capillatus*, as well as laboratory-reared lice species like *Menacanthus stramineus*, *Menopon gallinae*, *Chelopistes meleagridis*, *Goniocotes gallinae*, *Goniodes gigas*, *Lipeurus caponis*, and *Pediculus humanus corporis*. Out of the 305 MS profiles analyzed, most were of high quality. The spectral analysis demonstrated strong intra-species reproducibility and clear inter-species specificity, aligning with both morphological and molecular classifications. A blind test of 248 specimens from species included in a spectral database confirmed that MALDI-TOF MS is an effective tool for discriminating lice species, achieving identification rates between 76% and 100% and high identification scores (mean LSV: 2.115). These findings highlight the reliability of MALDI-TOF MS as a valuable tool for lice identification.
Keywords: Identification, mass spectrometry, tools for morphological identification

P4. Berthine Toubate, Françoise Debierre-Grockiego, Dimier-Poisson Isabelle - **Repellent effects of essential oils on human lice**

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The transmission of head lice is facilitated by direct head-to-head contact or

indirectly by sharing clothing or hairbrushes. The development of effective repellents against human lice remains an area of research of interest, both for product developers and families regularly affected by the infestations. To address this public health concern, manufacturers are exploring innovative delivery formats such as pre-impregnated supports (hair scrunchies, tiaras, headbands, clips) and topical hair lotions containing repellent agents. Among the active ingredients under investigation, essential oils—natural extracts derived from various parts of aromatic plants—are particularly attractive due to their broad-spectrum biological activities. Essential oils are not always applicable in their pure form and are contraindicated in young children, but may be incorporated into carefully formulated products to enhance their repellent potential. In this work, different essential oils have been tested for their repellent properties against body lice. A total of 33 lice at all developmental stages (larvae and adults) were placed around a droplet of the pure product. After 15 minutes, the distance each louse had moved away from the application point was measured. The farther the lice moved, the stronger the repellent activity. These results offer new insights into the differential efficacy of essential oils, providing useful guidance to healthcare professionals responding to questions from concerned parents and caregivers. Furthermore, these results can assist manufacturers in selecting appropriate plant-based ingredients for the development of effective and user-friendly lice repellent products.

Keywords: Human louse, essential oils, repellent

P5. Ariel C. Toloza[1], Eunice Sosa-Quiroga[1], Agustina Fañani[2,3], Ana Puente-Santamaria[4], Eduardo Guzmán[4,5], Emilia Martínez[2] and Alejandro Lucia[2] - **Chemical interaction and pediculicidal activity of binary nanomicelles loaded with monoterpenes against head lice**

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Argentina has the highest infestation level in the Americas, with an overall value of 51%. In Argentina, over –the -counter (OTC) products containing permethrin or silicones are the most commonly used pediculicides to control head lice infestation. However, the excessive use of permethrin has led to the development of insecticide resistance in most of the populations of Argentina. The bioactive components of essential oils possess varying physicochemical properties and are

effective against head lice. The combination of monoterpenoids with an adjuvant can increase efficacy and the environmentally friendly character of insecticidal formulations. This study evaluates the pediculicidal activity of nanoformulations containing various binary mixtures of essential oil components: eugenol and linalool; 1,8-cineole and linalool; and eugenol and thymol. Immersion bioassays were conducted to assess the knockdown time that affects 50% of the individuals (KT_{50}). Additionally, we analyzed the type of interaction between the components in each mixture using the combination index (IC). The KT_{50} values obtained were 6.07 hours for linalool, 8.83 hours for 1,8-cineole, 7.17 hours for eugenol, and 27.23 hours for thymol. When examining the eugenol and linalool mixtures, the effectiveness was equal to or lower than that of the pure compound nanoformulations, with KT_{50} values of 13.33, 8.16, and 6.71 hours for ratios of 3:1, 1:1, and 1:3, respectively. These mixtures displayed an IC greater than 1, indicating an antagonistic interaction that increases with higher eugenol content. For the binary mixtures of 1,8-cineole and linalool, the KT_{50} values were similar to those observed in the eugenol and linalool mixtures with comparable ratios. In this case, the IC values approached unity, suggesting additive interactions regardless of the mixture composition. Conversely, the eugenol and thymol mixtures with 1:1 and 1:3 ratios yielded KT_{50} values of 9.40 and 32.93 hours, while the mixture with a 3:1 ratio demonstrated the highest efficacy with a KT_{50} of 4.42 hours. The eugenol and thymol mixtures exhibited synergistic interactions ($IC < 1$) for the 3:1 and 1:1 combinations, whereas no interaction was detected for the 1:3 ratio. This indicates that eugenol enhances the activity of thymol. These findings represent an important advancement in the development of effective pediculicidal nanoformulations based on botanical compounds.

Keywords: Head lice, monoterpenes, chemical interactions, polymer-based nanomicelles, botanical products

P6. Ariel C. Toloza[1], Marina Ascunce[2] and David Reed[3] - **Understanding the movements of permethrin-resistant head lice in schools from a genetic perspective**

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The cosmopolitan ectoparasite, the human head louse *Pediculus humanus capitis* (De Geer) (Phthiraptera: Pediculidae), primarily affects school-aged children. Infestations are reported annually, largely due to the louse's resistance to pyrethroids. One of the main mechanisms of this resistance is target site insensitivity (known as kdr), caused by single nucleotide polymorphisms (SNPs) located within the voltage-sensitive sodium channel gene. In this study, we analyzed individual head lice both toxicologically, by assessing their susceptibility to permethrin, and genetically, by genotyping their kdr alleles and nuclear microsatellite loci. Lice were collected from four schools in Buenos Aires, Argentina. The resistance ratios ranged from 33.3% to 71.4%, with the frequency of the kdr mutation being 87.31%. Additionally, 83% of the head lice samples were found to be homozygous resistant to pyrethroids. Microsatellite data indicated that the genotype proportions in all school louse populations deviated from Hardy-Weinberg expectations, with an FIS >0 reflecting a deficit of heterozygotes. Bottleneck analysis suggested that all louse populations experienced a recent reduction in size. Furthermore, most of the schools exhibited gene flow values around 1, indicating ongoing gene flow among those schools. Our study suggests that head louse populations in Buenos Aires represent a metapopulation, where each school represents a small population undergoing cycles of extinction and recolonization under strong selection pressure from permethrin. This is the first multilevel analysis integrating toxicological data, kdr genotyping, and microsatellite data in human louse populations.

Keywords: Human head lice, insecticide resistance, kdr, population genetic structure, Argentina

P7. Joshua Kamani[1], Shimon Harrus[2], Bukar Laminu[1], Yaarit Nachum-Biala[2], Mike Shand[3], Gonzalo Roca-Acevedo[4] and Ariel Ceferino Toloza[4] - **First report of kdr alleles T917I and L920F in head and body lice from Nigeria**

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Pediculosis is a neglected tropical disease (NTD) produced by the presence of the human head louse (*Pediculus humanus capitis* De Geer) and the body louse (*Pediculus humanus humanus* L.). Although less common than head lice, body lice are vectors of serious diseases, namely epidemic typhus, trench fever, and louse-borne relapsing fever. In Nigeria, pediculicides containing permethrin are the first line of treatment but there is currently no evidence regarding the insecticide resistance status of head and body lice. Knockdown resistance (kdr) is the main pyrethroid resistance mechanism which arises from two-point mutations within the voltage-sensitive sodium channel gene (VSSC). Genomic DNA was extracted from 85 head and body lice collected in the localities of Yunusari and Maiduguri. The kdr mutation T917I detected in head lice ranged from 0.21 to 0.76, while in body lice, it ranged from 0.10 to 0.95. Notably, all examined lice exhibited the resistant genotype L920F, indicating that, regardless of the genotype for mutation

T917I, mutation L920F was present. There were significant differences in the frequency of resistance alleles between head and body lice across the two study sites. This is the first report of kdr mutations T917I and L920F in human lice from Nigeria.

Keywords: Human lice, pyrethroid resistance, kdr, Nigeria.

P8A. Elisabeth Yawa Diawara[1,2,3], Alpha Kabinet Keita[4,5], Alissa Hammoud[2], Adama Zan Diarra[2,3,6], Basma Ouarti[2], Coralie L'ollivier[2,3] and Stéphane Ranque[2,3] - **Pediculosis: an epidemiological survey of schoolchildren in the Republic of Guinea**

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The human head louse, *Pediculus humanus capitis*, is a globally distributed blood-sucking ectoparasite, particularly endemic among school-aged children that is considered as a significant public health concern. Infestation rates vary by region, with a notable impact in low-income countries, where lice serve as potential vectors of pathogens. This study aimed to assess the prevalence of pediculosis and lice-borne pathogens among primary school children in the Republic of Guinea. A descriptive cross-sectional study was conducted in March 2023 across eight schools in the Boké, Labé, Kankan and Nzérékoré. A total of 497 children aged from 5 to 12 years were randomly selected, and their hair was visually examined for lice infestation. Among the 497 children clinically examined, 33 (8%) had head lice. In the Boké and Kankan regions, 81 head lice were collected from 18 schoolgirls. Molecular analyses revealed that 97% (77/79) of the samples belonged to clade E, while 3% (2/79) belonged to clade A. Three distinct haplotypes were identified within clade E, including one previously unreported. Pathogen screening detected *Acinetobacter* spp. DNA in 46% (37/81) of the samples, with *Acinetobacter baumannii* confirmed in 8% (3/37) through a specific qPCR analysis. This study provides the first epidemiological data on head lice prevalence, genetic diversity, and associated pathogens in Guinean schoolchildren. Pediculosis remains a serious health issue in Guinea, particularly in the Boké and Kankan regions Further studies focused on pediculosis are required to assess its endemicity in the Republic of Guinea, and the vectorial capacity of clades A and E lice.

Keywords: Pediculosis, schoolchildren, haplotypes, *Acinetobacter* spp., Republic of Guinea

P8B. Elisabeth Yawa Diawara[1,2,3], Alpha Kabinet Keita[4,5], Adama Chérif Camara[6], Stéphane Ranque[2,3], Marc-Karim Bendiane[7] - Differences in gender perception of psychological and social consequences of human pediculosis in Guinee: results of an exploratory epidemiological study

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Background: Skin diseases or epidermal parasites such as human pediculosis are very common and have a considerable impact on people's quality of life, particularly in low-income countries such as the Republic of Guinea, where access to healthcare remains limited. These conditions pose serious public health problems for prepubertal children.

Objective: The present study aimed to analyze gender differences in terms of perceptions, beliefs, and knowledge of skin disorders including human pediculosis among the Guinean adult population.

Methods: In March 2023, in parallel with an epidemiological study of superficial mycoses and parasitosis in schools including human pediculosis, we conducted a socio-behavioral study to examine gender disparity in the perception of these conditions. A cross-sectional survey was conducted in eight localities, covering four regions of Guinea.

Results: A total of 432 questionnaires were completed by volunteers aged between 15 and 76 years, giving an overall response rate of 89%, varying between 80% and 90% depending on the site. Men accounted for 60.4% of respondents (261). Most participants (74%) were under 46 years of age. Of the 497 children surveyed, 433 (87%) had a skin disorder. Human pediculosis accounted for 8%. Assessment of participants' knowledge showed that only 31% about human pediculosis, recognizing the impact of these conditions on children's quality of life.

Conclusions: The results showed that men were more sensitive to the external image of the sick child, whereas women were more concerned about the psychological aspect. Most of the respondents used modern treatments. Finally, this study underlines the importance of raising public awareness through adapted programs that consider different perceptions of men and women.

Keywords: Guinea, KABP, Gender disparity, Psychosocial impact, Schoolchildren

P9. Mehdi Boucheikhchoukh[2,3], Noureddine Rabah Sidhoum[2,3], Bouthaina Hasnaoui[1]Noureddine Mechouk[4,5], Lobna Dib[2,3], Hamza Leulmi[6], Ahmed Benakhla[2] and Philippe Parola[1] **- Synopsis of lice species associated with humans, domestic, and wild animals in Algeria**

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Traditional living conditions in Algeria expose ruminants, domestic birds, and humans to various ectoparasites, including lice (Phthiraptera), which can cause discomfort, disease, and economic losses. This five-year study investigated lice diversity in northeastern and central northern Algeria, assessing their epidemiological importance. Lice were manually collected from cattle, sheep, goats, backyard chickens, turkeys, pigeons, rats, and children across ten regions and identified morphologically. Among collected lice, 18 species were identified, with common species including *Bovicola caprae* (goats), *Haematopinus eurysternus* (cattle), *Menacanthus stramineus* (chickens), and *Pediculus humanus capitis* (children). The findings highlight the widespread nature of lice infestations in both animals and humans, underscoring the need for further research on their impact on public and animal health.
Keywords: Lice, biodiversity, checklist, Algeria, veterinary

P10. Chahinez Boukehila[1], Dib Loubna[1], Philippe Parola[2] and Basma Ouarti[2] **- Human lice control: Morphological characterization of *Pediculus humanus capitis* populations**

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Human lice infestations, primarily caused by *Pediculus humanus capitis*, remain a significant public health concern, especially in school settings where close

contact between students facilitates transmission. This study aims to support the improvement of lice control measures through detailed morphological characterization of head lice populations. Specimens were collected over a one-year period from several primary schools in the Annaba region, eastern Algeria. Morphological identification was meticulously performed using standard taxonomic keys at the Laboratory of Biodiversity and Ecosystem Pollution, Chadli Bendjedid University, El-Tarf, and further confirmed at the RITMES Laboratory, IHU Méditerranée Infection, Marseille, France. The analysis confirmed the identification of all specimens as Pediculus humanus capitis and provided detailed descriptions of their key morphological traits. These findings establish a foundation for subsequent studies on the susceptibility of lice populations to available pediculicidal treatments. Additionally, this work emphasizes the importance of continuous local surveillance as a cornerstone for effective and sustainable lice control programs, particularly in school environments. The morphological approach applied represents a fundamental tool in the development of targeted strategies to combat this persistent public health issue.

Keywords: *Pediculus humanus capitis*, human lice control, primary schools, pediculicides, morphological identification

P11. Younes Laidoudi[1,2], Samia Bedjaoui[1,2], Sébastien Meige[3], Julien Renaud[3], Nicolas Grelaud[3] and Bernard Davoust[1,2] - **Spatio-temporal and economic analysis of pediculosis in France (2021–2024): prevalence, seasonality, and public health burden**

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In France, human lice are mainly responsible for pediculosis of the scalp caused by *Pediculus humanus capitis*. Its prevalence in school-aged children (especially among 6–8-year-olds) varies from 0.5 to 20%. To treat affected children, we can distinguish three groups of products sold commercially: chemical insecticides, phytotherapeutic treatments and anti-lice combs. We analyzed from an epidemiological, economic, and socio-demographic dynamics point of view the variations in sales of anti-lice products in the 95 departments of metropolitan France (except Corsica) over four years from 2021 to 2024. Our data comes from the panel of OpenHealth Company: 13,598 dispensing pharmacies. We conducted a multi-dimensional analysis combining over product purchase records with child population statistics across departments. Seasonality was assessed via time series decomposition and cost dynamics over 48 months. Prevalence was estimated per 100,000 population and correlated with socio-economic factors such as poverty rate, income, and population density. Geographic

and product category trends were also explored. The estimated annual national expenditure on anti-lice treatment reaches approximately 70 million euros in 2024 with an increase of 35% from 2021. Seasonal trends indicate a marked increase in summer and autumn, aligning with school return periods. The highest prevalence per 100,000 was observed in departments with strong association to elevated poverty rates: Cantal, Corrèze, Creuse and Lozère. A clear inverse correlation was observed between total population size and prevalence, suggesting higher burden in rural or lower-density areas. Products belonging to the chemical category dominate the market with highest units sold and estimated cost of ~56 million euros/year, suggesting market centralization. In France, the most used product is based on the dimeticone which has a physical action on lice of different developmental stages. Pediculosis is not only a recurring seasonal condition but also disproportionately affects children in socio-economically disadvantaged departments. The high economic burden and strong seasonal signature emphasize the need for targeted public health strategies, including prevention campaigns during peak periods and subsidies or centralized policies in vulnerable regions. Future efforts should integrate digital surveillance with school-based prevention to reduce cost and prevalence at national scale.

Keywords: Human lice, anti-lice treatment, prevalence, France

P12. Rym Bouledroua[1,2], Adama Zan Diarra[2,3], Remy Amalvict[1,2,4], Jean-Michel Berenger[1,2], Ahmed Benakhla[5], Philippe Parola[1,2] and Lionel Almeras[6,7,8] - Assessment of MALDI-TOF MS for arthropod identification based on exuviae spectra analysis

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MALDI-TOF MS is an innovative tool for identifying hematophagous and non-hematophagous arthropods at various life stages. However, identification by MALDI-TOF MS currently requires euthanizing of the specimen, hindering further phenotypic tests. All arthropods have a common factor, molting of their exoskeletons leaving a remaining structure known as the exuviae. This phenomenon is indispensable for their growth and can evidence past arthropod presence. This study assessed the performance of MALDI-TOF MS biotyping for arthropod identification using exuviae from nine distinct laboratory-reared species (*Aedes aegypti, Anopheles coluzzii, Cimex lectularius, C. hemipterus, Pediculus humanus humanus, Triatoma infestans, Rhodnius prolixus, Supella longipalpa and Blattella germanica*) compared its efficiency with a molecular identification approach using DNA sequencing. Molecular analysis showed low DNA quantity in exuviae (n = 108) across species, resulting in low success of COI, 16s, and 18s amplification (50.0%), depending on the species and sequencing (10.2%). The establishment of an exuviae protocol for MS submission yielded spectra of high reproducibility and specificity per species. After upgrading a homemade reference MS database with exuviae spectra, a query with remaining spectra revealed that 100% of samples were correctly identified, with 85.8% (278/324) exceeding the threshold score value for reliable identification. MALDI-TOF MS showed high efficiency in identifying various arthropod species based on their exuviae. This approach is a groundbreaking development in the field of entomology underlining that MALDI-TOF outperformed traditional methods of exuviae identification, including morphological and molecular tools. It also prevents specimen sacrifice which could be used for complementary analyses.

Keywords: Arthropods, biotyping, exuviae, MALDI-TOF MS, species identification.

Posters: Ecology, evolution & diversity

P13. Younes Laidoudi[1,2], Samia Bedjaoui[1,2], Stéphanie Watier-Grillot[3], Anthony Levasseur[1,2] and Bernard Davoust[1,2,3] - **Microbial community and zoonotic potential of wild boar lice (*Haematopinus apri*) in France**

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In France, the wild boar (*Sus scrofa*) population has been continuously increasing. These animals often harbour ticks, and some are also infested with lice. In late 2024, we collected lice from a wild boar in the Var department. Wild boar lice (i.e., *Haematopinus suis* and *Haematopinus apri*) are host-specific ectoparasites with potential roles in pathogen transmission, however their microbial communities remain poorly characterized. This study employed shotgun metagenomic sequencing to investigate the microbiota of nine individually collected lice specimens, assessing both taxonomic composition and the presence of vector-borne pathogens. Total DNA was extracted and sequenced on the Illumina NovaSeq 6000® platform, yielding ~50 Gb of paired-end data. Quality control (fastp) confirmed high sequencing integrity (Q30 > 93%), minimal adapter contamination (<0.05%), and consistent GC content (~54%), supporting robust downstream analyses. Mitochondrial genome reconstruction revealed that the lice species possess seven distinct mini-mitogenomes, exhibiting high query coverage (85–100%) and moderate identity (75.9–80.6%) to reference *H. apri* sequences previously isolated from wild boars in China. Taxonomic profiling revealed the microbiota was dominated by *Achromobacter* (77.3%), *Pseudomonas* (17%), and *Ewingella* (2.4%), with substantial inter-individual variation in microbial composition. Alpha-diversity metrics (Shannon index range: 0.43–0.90) and principal component analysis (PCA) indicated no significant clustering by individual louse (Kruskal–Wallis *p-value* = 0.4335), despite the identification of 200 distinct genera across samples. Notably, several pathogenic bacterial genera with known zoonotic potential were detected, including *Coxiella* (Q fever), *Mycobacterium* (tuberculosis), *Bordetella* (whooping cough), *Burkholderia* (melioidosis), and *Clostridium* (enterotoxemias). While the presence of microbial DNA does not confirm active transmission, these findings suggest that wild boar lice may act as cryptic reservoirs or mechanical vectors of pathogens relevant to veterinary and public health. Ectoparasites such as *Haematopinus* lice are increasingly recognized as reservoirs of microbial diversity, with previous studies detecting *Anaplasma*, *Rickettsia*, and *Bartonella* in related species. Our results expand this understanding by revealing a taxonomically rich and functionally diverse microbiome in wild boar lice, highlighting potential ecological overlap with other arthropod vectors. These findings provide foundational insights into the microbiota of an understudied ectoparasite and highlight the need for expanded surveillance under a One Health framework. Future research should incorporate pathogen-specific assays (e.g., PCR, culture) and functional analyses to evaluate transmission risks. Given the close interactions among wild boars, livestock, and humans, further studies are needed to assess the role of lice in zoonotic disease dynamics and to inform integrated control strategies.

Keywords: Wild boar, lice, *Haematopinus apri*, microbiota, France

P14. Austin R. Clayton, Sarah E. Bush, Matthew M. Waller and Dale H. Clayton - **Galápagos mockingbirds that groom more have fewer lice**

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Grooming behaviors (i.e., preening with the bill and scratching with the feet) are the principal way in which birds defend themselves from ectoparasites like feather lice. In captivity, birds experimentally infested with lice increase their grooming rates by 50% because they are well fed and have few other demands on their time. In the wild, however, birds are presumably more limited in the amount of time and energy they can devote to grooming. Given these constraints, birds with limited time for grooming may not be able to control their lice as well as birds that can spend more time grooming. Here we investigate the relationship between grooming behavior and ectoparasite abundance by monitoring the behavior and parasite populations of Galápagos mockingbirds (*Mimus parvulus*) in the wild. Galápagos mockingbirds provide a unique opportunity to study this relationship because they are relatively tame. Consequently, it is possible to capture mockingbirds, quantify their ectoparasites, and observe them closely with binoculars to make detailed recordings of behavior. We examined 27 mockingbirds, and found that most (77.8%) were infested with parasitic feather lice (*Brueelia galapagensis*). Nearly all of the birds (92.9%) were also infested with feather mites (*Analges* sp.). Over the course of one month, we collected at least 30 minutes of behavioral data for 16 individual mockingbirds. Birds spent a mean of 12.7% of their time grooming (range = 1.5% – 31.0%. Birds that groomed more had significantly fewer lice ($P = 0.05$), but there was no significant relationship between grooming time and the number of mites ($P = 0.77$). These data underscore the importance of grooming for controlling feather lice, which are parasites that reduce host fitness. The data further show that grooming does not control feather mites, which are generally considered commensals rather than parasites.

Keywords: Ecology, anti-parasite behavior, bird, lice

P15. Alexandra A. Grossi[1], Daniel R Gustafsson[1], Oldrich Sychra[2] - **How many endangered species of chewing lice are there?**

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Currently 651 bird species are listed by the IUCN red list in the three highest threat categories: Endangered, Critically Endangered or Extinct in the Wild. Of these, chewing lice (Amblycera + Ischnocera) are known from only 134 (21%) host species; this number comprises 108 louse species that are known from only a single highly threatened host species, and another 10 that are known from more than one host species, all of which are in the three highest threat categories. However, none of these 118 louse species are presently listed in the IUCN red list at any threat category. Moreover, a large percentage of the true louse fauna is presently unknown, presumably including lice from highly threatened host species. Based

on Indices of Specificity calculated for each host family/louse genus association separately, we estimate that the true diversity of avian lice is 41,627–42,410, of which only 4535 species (~11.0%) are presently described. Our estimations also indicate that as many as 2237 louse species could occur on highly threatened bird hosts, of which 1162 (52%) belong to host family/louse genus associations with an Index of Specificity ⩾1.0, indicating that they would be found only on that highly threatened host species. Thus, the number of unknown louse diversity on highly threatened bird species appears to greatly outnumber the known diversity by an order of magnitude. More work is needed to discover and document this diversity, and preserve it alongside their hosts, before they are lost.
Keywords: Biodiversity assessment, parasite conservation, louse estimate

P16. Jake Jacobsen, Ethan X. Kahn, Amanda Leyel, Mia C. Rosati, Graham A. Montgomery, Jessie F. Salter and Morgan W. Tingley - **Island of lice: Comparing range competition of chewing lice across three avian hosts**

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Ectoparasites on host organisms provide a unique opportunity to study key ecological questions regarding competition, coexistence, range shifts, niches, and island biogeography. Hosts can be viewed as islands – their ectoparasite occupants can adapt to microhabitats and compete with one another. Multiple species of lice can occur on single host islands, and the drivers of competitive outcomes (e.g., competitive displacement, stability) between these species remains unclear. There have also not yet been studies bringing together multiple ectoparasite species on multiple host species to study variation of those outcomes. Avian chewing lice on preserved museum specimens provide an accessible but greatly underutilized system for studying these questions. We compared louse distributions across three avian taxa with markedly different natural histories – House Finch (*Haemorhous mexicanus*), Northern Bobwhite (*Colinus virginianus*) and Hairy Woodpecker (*Dryobates villosus*) – to investigate factors influencing competitive release, such as whether ground-living species are susceptible to more ectoparasites than arboreal species. We collected lice and nits from specimens in six museum collections including 133 House Finches, 65 Hairy Woodpeckers and 210 Bobwhites, and digitized lice location using ImageJ. We found evidence of varying degrees of niche separation between the louse species on each host, and no evidence of current competitive displacement on any host. This may suggest that factors other than resource competition primarily shape ectoparasite interactions, and that these vary between host species. Studying ectoparasites though a “host island” lens can have implications for both ectoparasitic and geographic systems, and better understanding ectoparasite niches on avian hosts may also aid veterinary

practitioners and rehabbers in managing ectoparasites on their subjects.

Keywords: Host biogeography, niche, *Haemorhous mexicanus*, *Colinus virginianus*, *Dryobates villosus*

P17. Noureddine Rabah Sidhoum[2,3], Mehdi Boucheikhchoukh[2,3], Bouthaina Hasnaoui[1], Noureddine Mechouk[4,5], Lobna Dib[2,3], Hamza Leulmi[6], Ahmed Benakhla[2] and Philippe Parola[1] - Epidemiological and ecological patterns of lice (Phthiraptera) populations in Algeria

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Lice (Phthiraptera) are permanent ectoparasites that infest mammals, birds, and humans. However, large-scale studies on their diversity and ecological dynamics remain limited in Algeria. This study represents the most extensive survey of lice in the country to date. Over four years, lice were collected from domestic animals, wildlife, and humans across ten governorates: Algiers, Blida, Boumerdes, M'sila, Bordj Bou Arreridj, Mila, Setif, Oum El Bouaghi, Guelma, and El Tarf. A total of 5,991 lice were recovered, representing 18 species. *Polyplax spinulosa* was the most dominant species in rats, followed by *Menacanthus stramineus* in backyard chickens and *Bovicola caprae* in goats. The studied population exhibited a high Shannon-Wiener diversity index and strong host specificity, except for *M. stramineus*, which infested both backyard chickens and turkeys. Further molecular analyses are needed to assess the distribution of lice-borne diseases in Algeria.

Keywords: Lice, dynamics, wildlife, Algeria, biodiversity

P18. Abir Adjroud[1] , Habiba Saadi-Idouhar[1], Bouthaina Hasnaoui[2], Diarra Zan Adama[2], Faiza Marniche[1], Philippe Parola[2] - **Contribution to the knowledge of chewing lice of the wild Gambra partridge in Algeria**

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Through its way of life, survival conditions, and defense mechanisms, each living organism can coexist, benefit from the same environment, and protect themselves from one another to ensure the survival of their offspring. This concept is summarized by the term biodiversity. The persistence of certain organisms strictly depends on the temporary or permanent benefit they gain from other organisms, with or without harm to the host. This study focuses on the identification of ectoparasites of game birds, aiming to understand the interactions between ectoparasites and birds, as well as to assess their role in pathogen transmission and their impact on the health of game birds, particularly the wild Gambra partridge. To our knowledge, this is the first study to investigate ectoparasites in this species. The research was conducted for the very first time in the forested areas of the Batna and Bordj Bou Arreridj regions in Algeria. Various methods were used to collect and identify ectoparasites. Samples were preserved in 70% ethanol. Lice were mounted between a slide and a coverslip for initial morphological identification using dichotomous keys (Nitzsch, 1866; Clay, 1949). Species confirmation and detection of associated pathogens were performed using molecular biology techniques and MALDI-TOF spectrometry at the IHU Méditerranée Infection in Marseille, France. The identified ectoparasites include chewing lice such as *Goniodes securiger*, *Menopon pallens*, and *Cuclutogaster barbara*. None of the targeted pathogens (*Borrelia, Coxiella, Anaplasma, Bartonella, Rickettsia*) were detected in the analyzed ectoparasites. In conclusion, this study provides important preliminary data on the diversity of ectoparasites of game birds. It contributes to improving health management strategies for birds by deepening the understanding of ectoparasite impacts. Future research should focus on developing prevention and control measures to reduce the effects of these ectoparasites on bird health and animal production.

Keywords: Phthiraptera, chewing lice, animal health, game birds, Gambra partridge, lice of veterinary importance.

P19. Olga St-Onge (in absentia) - **Hangers-on: An overview of the current state of Phthiraptera conservation**

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Parasite conservationists aim to conserve wildlife parasite species based on the wide variety of ecosystem services they provide and the intrinsic ethical value of preserving species diversity. In order to evaluate the progress made in applying conservation principles to Phthiraptera, the published literature on parasite conservation and wild louse biodiversity was reviewed for mentions of conservation or threatened status. Despite being highly diverse, reliant on contact between host individuals for dispersal, and prone to host-specificity, few louse species have been evaluated for extinction risk globally or regionally. At present, only one louse species has been assessed on the IUCN Red List, and no conservation efforts directed towards threatened lice currently exist. However, a growing number of papers are addressing extinction risk among lice, and some recent species descriptions recommend listing lice as co-threatened with their hosts. Although there is still much work to be done in order to ascertain global extinction risk for the Phthiraptera, some key threats can be identified. The decline of threatened host species can cause risk to lice populations by limiting or eliminating opportunities to spread between host individuals, resulting in an increase in inbreeding and the eventual extinction of the louse alongside its host, referred to as co-extinction. Additionally, lice species may be threatened by efforts to conserve their host species, such as through translocations or the use of medications to eliminate ectoparasites, referred to as conservation-induced extinction. There have already been documented and suspected extinctions among the Phthiraptera through both co-extinction and conservation-induced extinction. Despite the lack of conservation efforts deliberately targeted towards lice, however, there have been cases where lice have been unintentionally conserved by conservation efforts targeted towards their hosts. A priority among wildlife phthirapterists and conservationists should be to assess the extinction risk of lice species and conserve lice alongside their threatened hosts.

Keywords: Conservation, co-threatened, co-extinction, wildlife

P20. Boukehila Chahinez[1], Dib Loubna[1], Philippe Parola[2], Basma Ouarti[2] - **Prevalence of lice infestation in domestic mammals in northeastern Algeria**

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Lice (Phthiraptera) are highly host-specific ectoparasites known for their role in the transmission of infectious diseases in both animals and humans. They represent a major concern in both public and veterinary health due to their ability to transmit pathogens and induce skin disorders. As part of a doctoral thesis, this study was conducted between September 2022 and December 2024 to assess the prevalence and diversity of lice infestations among domestic mammals in northeastern Algeria.

Sampling was performed on cattle, sheep, goats, and humans in collaboration with local farmers and veterinary services. Morphological identification was initially carried out at the Laboratory of Biodiversity and Ecosystem Pollution at Chadli Bendjedid University, El Tarf, and confirmed through advanced analysis at the RITMES laboratory, IHU Méditerranée Infection, Marseille. The identified species included *Linognathus africanus, Bovicola bovis, Bovicola caprae, Bovicola ovis,* and *Pediculus humanus capitis*. Close monitoring of these infestations is essential to detect any potential shifts in parasitic behavior and to assess their evolving impact. The presence of these lice represents a significant risk of contamination for both livestock and nearby human populations. These preliminary findings emphasize the importance of sustained surveillance and the implementation of integrated management strategies to mitigate the broader health and economic impacts of lice infestations in both veterinary and public health contexts.

Keywords: Phthiraptera, lice, domestic animals, contamination, identification.

P21. Alex Sutherland and Colin Dale - **Going deeper: In-depth sequencing of the endosymbiont of *Columbicola columbae***

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Endosymbiosis is a vital component of the development of many eukaryotes, particularly insects. The feather louse *Columbicola columbae* relies on its endosymbiont to compensate for its nutritionally incomplete diet of feather keratin. *C. columbae*'s endosymbiont belongs to the Sodalis-allied clade of endosymbionts, which commonly forms mutualistic associations with a wide variety of insects, including feather lice, weevils and parasitoid wasps, among others. Over evolutionary time, endosymbionts undergo genome degeneration, making culturing or laboratory manipulation of the endosymbiont difficult or impossible. Genome degeneration has also made traditional sequencing approaches such as Illumina difficult due to the large amounts of genomic repeats, causing fragmented assemblies. However, there remains a significant need to sequence and analyze endosymbiont genomes to ascertain their genetic composition. The development of two novel sequencing platforms, Aviti and Nanopore, paired with endosymbiont-directed tissue dissection, will be leveraged for more accurate genome assembly using Aviti's high-quality reads to polish Nanopore's extremely long reads. This approach will allow for a polished, complete genome sequence to be assembled and published. Once the endosymbiont genome is assembled, transcriptomics will be performed to ascertain what endosymbiont genes are upregulated in symbiotic tissues, such as the louse ovaries. Subsequent analyses can be performed with a complete genome assembly using comparative genomics to determine genes universally retained in feather louse symbionts and symbionts of other insects within the Sodalis endosymbiont clade. Transcriptomics of symbionts in ovarian tissues will help generate a framework for genes that potentially play a role in endosymbiont transmission and germline establishment.

Keywords: Endosymbiont, *Columbicola columbae*, genomics

P22. Chaoqun Yao - **Molecular characterization of *Heterodoxus spiniger* from dogs on St. Kitts**

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Chewing lice are common ectoparasites of mammal and avian hosts including pet dogs. *Heterodoxus spiniger* has been found on dogs in different geographical locations including Africa (Egypt, Ethiopia, Nigeria), Asia (India, Iran, Lao PDR, Malaysia, Thailand), and America (Brazil, Cost Rico, Mexico). However, there is a great paucity of its location in the Caribbean and its DNA sequence. In the current study, *H. spiniger* was collected from two client-owned dogs. Total genomic DNAs were individually extracted from two male and two female adult lice that originated from each dog. Duplex PCR was performed to simultaneously amplify cox1 and 18S rRNA using genomic DNA as templates followed by simplex PCR for individual targets using duplex PCR products as templates. PCR products were directly sequenced in both directions. cox1 and 18S rRNA were 1,539 bp and 2,077 bp, respectively. There were 99.03% and 99.71% identity among the six DNA sequences for each sequence. Six sequences we generated for each gene were the largest data set for *H. spiniger* deposited into the GenBank so far. Phylogenetic analyses showed all six cox1 sequences formed a clade along with an additional one from India and the other one of unknown location. Unexpectedly, the Thai isolate was in the same clade as *Trinoton querquedulae*, which was used as an outgroup. Similarly, all six 18S rRNA sequences formed a clade along with an additional entry of *H. spiniger* whereas the three sequences of *Trinoton* spp. formed a separated clade. These data should serve as a springboard for studying this important ectoparasite of pet dogs.

Keywords: *Heterodoxus spiniger*, chewing louse, dog, St. Kitts

P23. Oldřich Sychra[1], Lajos Rózsa[2,3,4], János Podani[2,5], Vojtěch Sychra[1], Ivan Literák[1], Annabella Maria Schmiedová[1] and Miroslav Capek[6] - **Multivariate study of lice (Insecta: Psocodea: Phthiraptera) assemblages hosted by hummingbirds (Aves: Trochilidae)**

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Lice were collected from 579 hummingbirds, representing 49 species, in 19 locations in Brazil, Costa Rica, Honduras, Paraguay and Peru, at elevations 0–3000m above sea level. The following variables were included in an ecological analysis (1) host species' mean body mass, sexual size dimorphism, sexual dichromatism, migratory behaviour and dominance behaviour; (2) mean elevation, mean and predictability of temperature, mean and predictability of precipitation of the host species' geographic area; (3) prevalence and mean abundance of species of lice as measures of infestation. Ordination methods were applied to evaluate data structure. Since the traits are expressed at different scales (nominal, interval and ratio), a principal component analysis based on d-correlations for the traits and a principal coordinates analysis based on the Gower index for species were applied. Lice or louse eggs were found on 80 (13.8%) birds of 22 species. A total of 267 lice of 4 genera, *Trochiloecetes*, *Trochiliphagus*, *Myrsidea* and *Leremenopon*, were collected, with a total mean intensity of 4.6. There were positive interactions between migration behaviour and infestation indices, with elevational migrants having a higher prevalence and abundance of lice than resident birds. Further, we found weak negative correlations between host body mass and infestation indices and positive correlations between mean elevation and prevalence and abundance of *Trochiliphagus*. Thus, formerly unknown differences in the ecological characteristics and infestation measures of *Trochiliphagus* and *Trochiloecetes* lice were revealed, which allows a better understanding of these associations and their potential impacts on hummingbirds. This work was supported by the National Research, Development, and Innovation Fund of Hungary (K143622).

Keywords: Host-parasite associations, ecology, migration, environment

P24. Oldřich Sychra[1], Annabella Maria Schmiedová[1], Lajos Rózsa[2,3,4] and Leonor Guardia Claps[5]- **Occurrence of chewing lice (Phthiraptera: Ricinidae) on Red-tailed comet (*Sappho sparganurus*)**

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To evaluate the occurrence of chewing lice on Red-tailed comet (*Sappho sparganurus*) we looked for chewing lice and their nits on museum skins of this species, which are deposited in the Ornithological Collection, Vertebrate Institute, Zoology Area, Fundación Miguel Lillo, Tucumán, Argentina. We examined a total of 88 skins: 59 males, 27 females, 1 immature. and 1 undetermined. These hummingbirds were collected from 1899 to 2004 in Argentina. In addition, we examined 3 alive birds in September 2024 near the Rio Las Piedras, Yerba Buena, Tucumán, Argentina. We found a total of 191 eggs of lice on 48 (55%) birds: 33 (56%) males and 15 (56%) females. We found 1–18 eggs per bird: mostly 1–2 eggs (in 54% cases), 3–5 (27%), 6–10 (15%) and the highest number of eggs were found in two males with 16 and 18 eggs. In males, younger males had higher prevalence of egg occurrence (77%; n=30) than adult males (36%; n= 28). Eggs were found mostly on ventral side: on throat (55% eggs; n=191), breast (12%) and belly (2%); then on sides of the head - on the base of bill or near the ears (15%); and less on dorsal side - forehead and crown (3%), nape (5%), mantle (4%) and back (4%). We found also 10 lice of the genus *Trochiloecetes* and 1 louse of the genus *Philopterus* s.l., that most likely represents a straggler. We evaluated also the effect of season and altitude on the occurrence of nits. This work was supported by VETUNI grant number 2025ITA23.
Keywords: Red-tailed comet, *Sappho sparganurus*, *Trochiloecetes, Philopterus*

P25. Saima Naz[1], Farooque Ali Hattar[1], Aziz Ahmed Ujjan[2], Shaila Khaskheli[1] and Sajid Siyal[3] **- Epidemiology of Goat louse, *Linognathus africanus* Kellogg and Paine, 1911 (Anoplura: Linognathidae) and its new association with fungal flora**

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The goat louse, *Linognathus africanus* Kellogg and Paine, 1911 (Anoplura: Linognathidae) is the most common species of goat worldwide, causing serious damage to goat skin and hair loss. In Pakistan, there are 36 breeds of goats, among which 13 are found in Sindh. In the present study, goat lice were collected from various breeds in different districts of Sindh province, considering the intrinsic and extrinsic factors in the data collection. Among 13, only four commonest breeds were found to be highly prevalent in lice infestation. It was observed that the highest prevalence of *Linognathus africanus* was recorded in the Kamori breed (26.66), followed by Kachan and Pateri (23.33 and 16.66), whereas the lowest prevalence was found in Jattan (6.66). The intensity of lice was also higher in Kamori (95.5), followed by Jattan (52) and Kachan (43). In these goat breeds, the hair quality and skin infections were also observed hence, the lice were kept in SDA media for the isolation of fungal flora. A potential synergistic interaction between goat louse and fungus was studied for the first time in the country with the isolation of three fungal species, cultured in 40% samples of lice. The isolates of fungus were examined carefully and identified as *Aspergillus niger* van Tieghem, *A. terreus* Thom, and *Microsporum* spp. It is the first study of its kind in Pakistan and documents the new association of sucking lice with mycoflora in goats.

Keywords: Goat louse, Anoplura, epidemiology, fungal association, Pakistan

P26. Saima Naz[1], Mohammad Awais Memon[1], Oldrich Sychra[2], Aziz Ahmed Ujjan[3], Shaila Khaskheli[1], Ahmed Madani[1] and Sajid Siyal[4] - **New data on chewing lice (Psocodea: Phthiraptera) of *Corvus splendens* Vieillot (Corvidae) from Pakistan**

Email: dr.symanaz@outlook.com

Author Affiliations: [1]Advanced Parasitology Research Laboratory (APRL), Department of Zoology, University of Sindh, Pakistan. [2]Department of Biology and Wildlife Diseases, University of Veterinary Sciences, Brno. Czech Republic. [3]Plant's Pathogens, Pests and Protection Lab (PPPPL), Institute of Plant Sciences, University of Sindh, Pakistan. [4]Department of Wildlife Management, Shaheed Benazir Bhutto University of Veterinary and Animal Sciences, Sakrand. Sindh, Pakistan.

It is the first study of chewing lice (Psocodea: Phthiraptera) infesting house crows, *Corvus splendens* Vieillot (Corvidae) in Pakistan. The house crow is a common but antagonistic bird found mostly near human habitation and is considered an important source of pathogen transmission in the community. However, its ectoparasitic studies have yet been negligible in the region. In the present study, eight species of chewing lice have been collected from *C. splendens,* with two species of Philopteridae, and six species of Menoponidae. Among these species, *Corvonirmus saliemi* (Ansari, 1957), *Philopterus lahorensis* Ansari, 1955, *Colpocephalum fregili* Denny, 1842, and *Myrsidea bakttitar* (Ansari, 1951) were previously reported by Ansari (1951; 1955; 1957); *Colpocephalum tristis* Price and Beer, 1965, *Menacanthus eurysternus* (Burmeister, 1838), *Menacanthus gonophaeus* (Burmeister, 1838), and *Myrsidea splendenticola* Klockenhoff, 1973 were additionally reported for the first time on this host with new record from Pakistan.

Keywords: *Corvus splendens,* chewing lice, new records, Pakistan

P27. Daniel R. Gustafsson[1], Fasheng Zou[1], Zhu Li[2], Xiuling Sun[3] – **Descriptions of five new genera in Goniodidae (Ischnocera)**

Email: kotatsu@fripost.org

Author Affiliations: [1]Guangdong Key Laboratory of Animal Conservation and Resource Utilization, Guangdong Public Laboratory of Wild Animal Conservation and Utilization, Institute of Zoology, Guangdong Academy of Sciences, Guangdong, China. [2]Department of Life Sciences, National Natural History Museum of China, China. [3]Collections Department, National Natural History Museum of China, Beijing, China.

The Goniodidae comprises a wide variety of morphological groups, presently placed in a handful of genera, most of which are highly polytypic. Above all, the division between two of the largest genera – *Goniodes* and *Goniocotes* – has never been well defined morphologically. As presently circumscribed, no single morphological character proposed to define *Goniocotes* cannot also be found in at least some *Goniodes*, and vice versa. As part of an ongoing revision of the Goniodidae of galliform hosts, we here summarize recently proposed genera within the Goniodidae, as well as propose five new genera based on species presently placed in *Goniodes*. These new genera are: *Arborophilicola* n. gen. for *Goniodes indicus* Kellogg & Paine, 1914; *Rhopaloncus* n. gen. for *Goniodes megaceros* Kellogg & Paine, 1914, and related species; *Sulciferides* n. gen. for *Goniodes meinertzhageni* Clay, 1940; *Tragoniodes* n. gen. for *Goniocotes spinicornis* Nitzsch [in Giebel], 1866) and related species; and *Sikongia* n. gen. for *Goniodes tetraophasis* Chou & Liu, 1986. As several of these are presumably closest to *Goniodes* s. str., the type species of this genus is here redescribed for clarity. We also list a number of previously proposed genera that should be recognized as valid based on morphological data, and provide an updated checklist to the proposed classification of the Goniodidae on galliform hosts.

Keywords: Goniodidae, new genera, China

P28. Daniel R. Gustafsson, Zhengzhen Wang, Alexandra A. Grossi, and Fasheng Zou - **New species in the *Resartor*-group complicate genus limits further**

Email: kotatsu@fripost.org
Author affiliations: Guangdong Key Laboratory of Animal Conservation and Resource Utilization, Guangdong Public Laboratory of Wild Animal Conservation and Utilization, Institute of Zoology, Guangdong Academy of Sciences, Guangdong, China.

The *Resartor*-group of genera within the *Brueelia*-complex comprises ten genera and subgenera of lice parasitizing a broad range of hosts mainly in the Old World tropics. Within this group, the genera *Resartor* Gustafsson & Bush, 2017, *Timalinirmus* Mey, 2017, and *Turdinirmoides* Gustafsson & Bush, 2017, are morphologically similar. Members of all three genera are long and slender, with often reduced abdominal chaetotaxy, and similar male genitalia. Morphological differences between these genera are mainly found in the fusion or division of the subgenital plates of both sexes, as well as the presence or absence of *sternal setae* on male abdominal segment VII. Moreover, from a gross morphology perspective members of the genus *Resartor* have elongated heads, *Turdinirmoides* have short, rounded heads, and *Timalinirmus* are intermediate between the two. *Resartor* and *Timalinirmus* are presently known exclusively from "babblers" (Leiothrichidae, Pellorneidae, Timaliidae, Zosteropidae), whereas *Turdinirmoides* is more widely distributed, mainly among high-altitude hosts. During recent fieldwork in Hubei Province, China, two new species in this complex were collected, one each from *Erythrogenys gravivox* (David, 1873) and *Sinosuthora webbiana* Gould, 1852. Both these species are short-headed, but with subgenital plates in both sexes as expected from *Resartor*, making their placement difficult from a morphological point. COI data were extracted from these two species, a range of *Resartor* species and one of two known *Timalinirmus* species. This data suggests that both Hubei species and *Timalinirmus curvus* Gustafsson *et al.*, 2022, are nested inside *Resartor*, and should be placed in that genus. No sequences were available from the type species of *Timalinirmus* [*Brueelia hrabali* Najer & Sychra (in Najer *et al.*), 2012], nor from any species of *Turdinirmoides*. We suggest that *Timalinirmus* should be considered a synonym of *Resartor*, accepting that the head shape and structure of the female subgenital plate of this genus can evidently vary. Whether *Turdinirmoides* should also be considered a synonym of *Resartor* will have to await future collections of species in this genus.

Keywords: *Brueelia*-complex, genus limits, new species, China

P29. Daniel R. Gustafsson - **Host association patterns of *Brueelia*-complex lice (Phthiraptera: Ischnocera) parasitizing starlings (Passeriformes: Sturnidae)**

Email: kotatsu@fripost.org
Author affiliation: Guangdong Key Laboratory of Animal Conservation and Resource Utilization, Guangdong Public Laboratory of Wild Animal Conservation and Utilization, Institute of Zoology, Guangdong Academy of Sciences, Guangdong, China.

Starlings comprise a diverse group of mainly medium-sized songbirds distributed across Africa, Eurasia, and parts of the Australo-Papuan region. Collectively, they are associated with three radiations within the *Brueelia*-complex: *Brueelia* Kéler, 1936, and the head louse genera *Sturnidoecus* Eichler, 1944, and *Schizosairhynchus* Gustafsson & Bush, 2017. Presently, 12 species of *Brueelia*, 25 species of *Sturnidoecus*, and 3 species of *Schizosairhynchus* are known from sturnid hosts; however, lice are unknown from a large number of starling species, and the true diversity is likely much higher. As a case in point, we have examined material representing 16 undescribed species of *Brueelia* and 4 undescribed species of *Schizosairhynchus*. Together with the known species, the outlines of some host association patterns among *Brueelia*-complex lice on starlings can be discerned. First, in several cases host associations appear to be strongly influenced by host phylogeny. The genus *Schizosairhynchus* and two species group of *Brueelia* (*acutangulata* and *museiberolinensis*) are known exclusively from hosts in the Australo-Papuan radiation of starlings from Thailand to the Solomon Islands, but no specimens from these louse groups have been seen from starlings in other radiations in this region. Conversely, no lice belonging to the *Brueelia fuscopleura* and *Sturnidoecus pastoris* species groups have been seen from the Australo-Papua radiation of starlings, despite these species groups being widely distributed across Eurasia, including in Southeast Asia. Secondly, both the *Brueelia clara* and *Sturnidoecus senegalensis* species groups contain louse species that parasitize distantly related starling hosts in Africa. Several other species groups appear to be limited to African hosts, but as many African starling species are not known to be associated with *Brueelia*-complex lice, the distribution of these groups may be only partially known. Notably, the two largest African radiations of starlings (genera *Lamprotornis* and *Onychognathus*) appear to be collectively parasitized by a variety of *Brueelia*-complex lice, including both otherwise African and otherwise Eurasian louse radiations. As many of the lice from these hosts have only been collected a few times, more data are needed before possible patterns in the host associations among lice parasitizing *Onychognathus* and *Lamprotornis* hosts can be discerned.

Keywords: *Brueelia*-complex, genus limits, new species, China

P30. Noureddine Mechouk[1,2], Bouthaina Hasnaoui[3], Noureddine Rabah sidhoum[4], Mehdi Boucheikhchoukh[4], Andrei Daniel Milhalca[1], Philippe Parola[3] - **MaxEnt model-based prediction of potential distributions of Pidiculus human capitus in Algeria.**

Email: noureddine.mechouk@usamvcluj.ro
Author affiliation: Department of Parasitology and Parasitic Diseases, University of Agricultural Sciences and Veterinary Medicine of Cluj-Napoca, Calea Mănăștur 3-5, 400372, Cluj Napoca, Romania, Department of Biology, Faculty of Science, Badji Mokhtar University, Annaba 23200, Algeria, Unité de Recherche en Maladies Infectieuses et Tropicales Emergentes (URMITE), AP-HM Institut Hospitalo-Universitaire Méditerranée Infection, Marseille, France, Université Chadli Bendjedid, Département des Sciences Vétérinaires, El Tarf, Algérie

The MaxEnt model, widely used in ecological and biological studies, utilizes presence-only occurrence data and environmental variables to predict the potential suitable habitats of species. *Pediculus humanus capitis*, commonly known as the head louse, is an obligate ectoparasite that infests the scalp and hair of humans, feeding on blood several times a day. It is primarily transmitted through direct head-to-head contact and is most prevalent among children. While it causes itching and discomfort, it is not a proven vector of human disease.

This study compiled a dataset on the distribution of *Pediculus humanus capitis* in Algeria, drawing from literature databases and historical records. The data underwent extraction, cleaning, and removal of duplicate entries. Analysis using the MaxEnt model identified the north-central and northeastern regions of the country as the most suitable habitats for *P. h. capitis*. The model demonstrated high predictive performance with an accuracy rate of 99%. Notably, Annual Precipitation (BIO12) showed the highest permutation importance (63.4%), followed by Temperature Seasonality (BIO4), indicating these factors most strongly influence the distribution of this louse species.

Epidemiological surveillance of *Pediculus humanus capitis* infestations remains important as a public health concern, particularly in high-risk populations such as school-aged children and communities with limited access to hygiene resources. The MaxEnt model provides a valuable tool for predicting suitable habitats and guiding targeted control efforts.

Keywords: *Pediculus humanus capitis,* Head lice, MaxEnt model, Species distribution modeling, Bioclimatic variables, Algeria.

Author Index

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Pouxit
FLASH
N°1
EN PHARMACIE¹
TUÉ EN 5 MINUTES*
SCENE DE CRIME - ZONE INTERDITE - SCENE DE CRIME - ZONE I
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Cooper
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TRAITEMENT
5 min
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Protéger la peau découverte

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Les insectes piqueurs apprécient particulièrement votre sang car ils y puisent les nutriments essentiels à leur survie ou à leur reproduction. Certains peuvent alors vous transmettre de graves maladies.

La gamme **Insect Ecran Peau** « repousse » les moustiques.

***Attention**, il est fortement recommandé de ne pas utiliser les bracelets, la vitamine B1, les huiles essentielles ou les ultrasons, pour se protéger efficacement des piqûres de moustiques.*[1]

COMMENT FAIRE ?

Appliquer les produits Insect Ecran à usage cutané sur la peau découverte de façon généreuse, homogène, sélective et répétée. Avec Insect Ecran Zones Infestées et Insect Ecran Spécial Enfants, éviter tout contact avec les plastiques, fibres synthétiques, cuirs, vernis, lunettes et verres de montres. Respecter la posologie et les recommandations indiquées au dos des flacons. En cas d'application d'une protection solaire, attendre 20 minutes pour appliquer le répulsif.

Trouvez le produit Insect Ecran adapté pour votre voyage[2]

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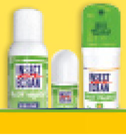
Flashez moi !

Quels produits Insect Ecran choisi

MOUSTIQUES MALADIES TRANSMISES	AEDES : MOUSTIQUE TIGRE ZIKA, DENGUE, CHIKUNGUNYA	ANOPI PALUDI
Entre 1 an et 24 mois		
Dès 24 mois		
Femme enceinte [4]		
Dès 6 mois Protection d'origine végétale		

Insect Ecran Peau

Nouvelle formule

Idéal pour les voyages

ZONES TROPICALES

DEET 50%
Extrait d'eucalyptus citriodora 1%
Spray 75 ml

Dès 24 mois — Efficace jusqu'à 16H (6)

AMM biocide

Bords de lacs et rivières, forêts, marais

ZONES INFESTÉES

DEET : 50 %
Spray 100 ml & 50 ml

Dès 24 mois — (4) — Efficace jusqu'à 16H (7)

Activités de la vie courante

FAMILLES

Icaridine : 20 %
Spray 100 ml & 200 ml

Dès 24 mois — (4) — Efficace jusqu'à 12H (9)

AMM biocide

Formule destinée aux enfants dès 1 an

ENFANTS

DEET : 10%
Spray 100 ml

Dès 1 an — Efficace jusqu'à 6H

Spray à base d'actif végétal pour une protection en zones tropicales et tempérées

Brume et roll-on anti-moustiques Application facilitée et plus ciblée

ACTIF VÉGÉTAL

Extrait d'eucalyptus citriodora :

30%
Spray 100 ml

Dès 36 mois — Efficace jusqu'à 12H (10)

20%
Aérosol 100ml & roll-on

Dès 6 mois — Efficace jusqu'à 10H (11)

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(1) Recommandations sanitaires aux voyageurs, HCSP, 2024. (2) Uniquement pour les produits à usage cutané. (3) Valable pour la gamme peau et vêtements. (4) En zones à risque de transmission de maladie vectorielle. (5) J Econ Entomo en zones tempérées, à raison de 2 applications par jour. Durée d'efficacité pour 1 application : 8h contre les moustiques et phlébotomes, 7h contre les tiques en zones tempérées. (8) Sans odeur après séchage. (9) sur moustiques, et jusqu par jour. Durée d'efficacité pour 1 application, jusqu'à 8h en zones tropicales sur moustiques et jusqu'à 6h en zones tempérées, jusqu'à 6.5h sur tiques . Efficacité variables selon les individus et conditions d'environnements. (11) Efficace + PBO 0,222g/L + d-Tétraméthrine 0,078g/L. (13) Données sell-out pharmacie – GERS – CAM 12/23. Utilisez les biocides avec précaution. Avant toute utilisation, lisez l'étiquette et les informations concernant le produit. Visuels non contra

r ?

HÈLE ISME	ANOPHÈLE + AEDES PALUDISME, ZIKA, DENGUE, CHIKUNGUNYA	CULEX NUISANCE SANS RISQUE

Traiter ses vêtements

POUR QUOI FAIRE ?

40% des piqûres de moustiques surviennent à travers les vêtements 5.

Le spray Vêtements & Tissus repousse les moustiques avant qu'ils ne se posent sur les vêtements.

Un flacon de 100 ml qui permet de traiter 15 vêtements environ. Pulvériser uniformément le produit à une distance de 10 à 20 cm en direction de la surface à traiter. Renouveler l'application après chaque lavage ou utilisation des vêtements traités.

Pour une protection complète en zones tropicales, opter pour la double protection peau + vêtements :

Efficacité renforcée Tropiques : sur l'anophèle, vecteur du paludisme

ZI : sur Aedes, vecteur du Zika, de la Dengue, du Chikungunya

OU

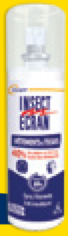
SPRAY 75 ml
SPRAY 100 ml

Dès 24 mois | Jusqu'à 16h (6) | Dès 24 mois | (4) | Jusqu'à 16h (7)

+

Efficace 8h même après 30 jours de stockage.

Un flacon de 100 ml permet de traiter 15 vêtements environ.



SPRAY 100 ml

Dès 1 an | Jusqu'à 8h | Sans odeur (8)

Vêtements

Environnement

Les produits cosmétiques après - piqûres

50ml

Efficace 8h même après 30 jours de stockage.

Un flacon de 100 ml permet de traiter 15 vêtements environ.

VÊTEMENTS & TISSUS

IR3535
Spray 100ml

Dès 1 an | Efficace jusqu'à 8H | Sans odeur (8)

HABITAT

Aérosol 250ml

Dès 12 mois

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Sensation de douceur

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Gel apaisant
Soulage rapidement
Stoppe le gonflement
Format pocket

GEL APRÈS-PIQÛRE

Tube de 20g

Dès 3 ans

l 1945 ; 38 : 671-675. (6) sur moustiques en zones tropicales à raison de 2 applications par jour. Durée de protection pour 1 application : 6h sur moustiques en zones tropicales. (7) sur moustiques et phlébotomes, et jusqu'à 14h sur tiques u'à 10h sur tiques en zones tempérées, à raison de 2 applications par jour. Durée de protection pour 1 application : 6h sur moustiques, 5h sur tiques en zones tempérées. (10) sur moustiques en zones tropicales, à raison de 1 application jusqu'à 10h sur moustiques, et jusqu'à 12h sur tiques en zones tempérées, à raison de 2 applications par jour. Durée d'efficacité pour une application : 5h sur moustiques, 6h sur tiques en zones tempérées. (12) Cyperméthrine 0,556g/L ctuels.

Les risques des voyageurs

Quand l'eau se fait menace

L'eau est une évidence naturelle. Mais pas sa qualité pour la boisson. En voyage, l'eau devient un problème. Eau de boisson, brossage des dents, lavage des fruits et des légumes, autant de gestes quotidiens rendus inquiétants, voire dangereux. Comment être sûr d'une eau non contrôlée ? Comment la désinfecter ? Quels sont les risques encourus ? Quelles sont les précautions à prendre ?

Les risques de contamination

Les voyageurs sont principalement exposés aux risques de diarrhée, la classique diarrhée du voyageur.

Cette infection se fait par l'ingestion d'eau ou d'aliments contaminés par des micro-organismes et par les mains sales. Les voyageurs ne disposent d'aucun moyen pour apprécier la salubrité d'une eau. La limpidité, le goût ou la saveur d'une eau n'apportent aucune garantie sur sa qualité microbiologique.

La désinfection de l'eau

La désinfection de l'eau est une n
méthodes sont disponibles.

■ **L' ébullition** (au moins 10 minut
plus difficile à mettre en œuvre.

■ **Les filtres portables.** Ils exig
initiale conséquente et leur comme
d'aucune obligation d'évaluation.

■ **Pailles.** Elles sont inefficaces con

■ **La désinfection chimique.**

- Le tosylchloramide (Hydroclonazo
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- Le chlorure d'argent a été inte
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pour permettre la désinfection de l'e
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- L'hypochlorite de sodium sous fo
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- En revanche, **Aquatabs**® seule
sodique (DCCNa) à détenir l'autori
Santé pour le traitement de l'e
désinfectant le plus performant,
à utiliser sous sa forme de compri
- **Aquatabs**® est conforme aux
Recommandations sanitaires aux v

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(1) - Unicef Ireland, July 2006.

(2) - BAYLAC (P.) et coll.-Comparaison du pouvoir désinfectant de la chloramine T et du dichloroisocyanurate de sodium sur une eau de rivière. ***Rec. Méd. Vét*, 1996, 173** (7/8), 391-399.

(3) - SCHLOSSER (O.) et coll.-Assessment of bacterial removal from inexpensive portable systems of water treatment for travelers. 6th Conference of the International Society of Travel Medicine, Montréal, 6-10 juin 1999. Résumé dans SCHLOSSER (O.) - Efficacité des systèmes de traitement de l'eau. ***La lettre de la Société de Médecine des Voyages***. Sept 1999, 3.

(4) - PRESCRIRE RÉDACTION - La qualité de l'eau de boisson du voyageur. ***La revue prescrire*** Mai 2000 ; Tome 20 (n°206) : 363-369.

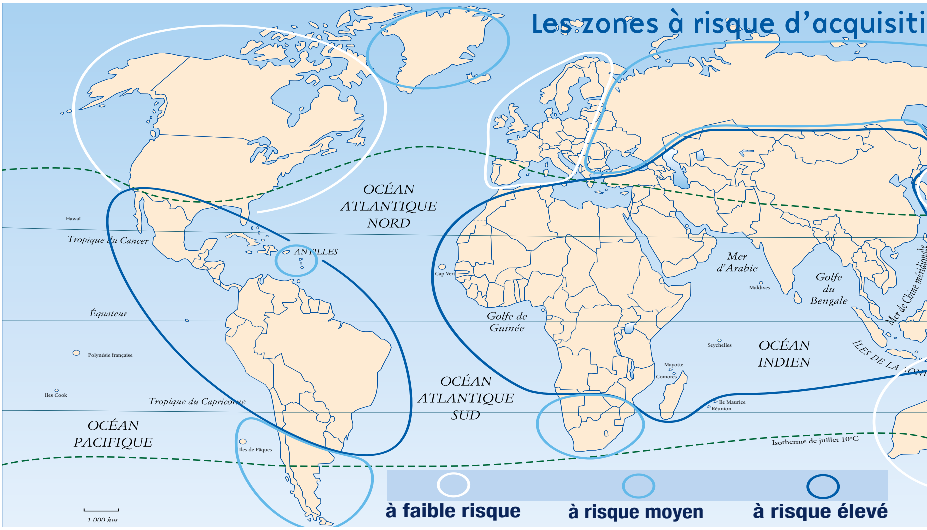
(5) - ***JO de l'Union européenne***, L 124 du 24.4.2014, p. 29.

(6) - Haut Conseil de la Santé Publique - mai 2023.

(7) - MARCHOU (B.) - Diarrhées du voyageur : épidémiologie, prévention et conduite à tenir. ***La Presse Médicale*** tome 42 > n°1 > janvier 2013 ; 76-81.

(8) - WHO International Scheme to Evaluate Household Water Treatment Technologies, 2015 p. 3.

(9) - Effect of in-line drinking water chlorination at the point of collection on child diarrhoea in urban Bangladesh: a double-blind, cluster-randomised controlled trial. www.thelancet.com/lancetgh Vol 7 September 2019


Les zones à risque d'acquisiti

"Qu'il s'agisse de choléra ou d'autre chose, la sécurisation de l'eau de boisson ne peut fai
*Pr PIARROUX (R.). CHOLÉRA Haïti 2010 - 2018, Histoire d'un désastre. **CNRS Éditions**, Par*

écessité absolue. Pour cela, plusieurs

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tre les virus.

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recommandations de l'OMS et aux
voyageurs(6) (8).

on d'une diarrhée

re que du bien".
is, 2022. p.229

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À l'usage des voyageurs - Désinfection de l'eau de qualité inconnue ou douteuse

Une formulation innovante pour la désinfection de l'eau d'alimentation. **Aquatabs®**, premier comprimé effervescent à base de Troclosène sodique (DCCNa)***, prévient les diarrhées en éliminant les bactéries et les virus présents dans l'eau contaminée.

Une utilisation pratique. Des comprimés effervescents pour une libération rapide du principe actif. **AQUATABS® 1 LITRE :** 1 comprimé pour 1 litre d'eau traité seulement en 30 minutes. Boîte de 60 comprimés qui permet d'obtenir 60 litres d'eau potable. **AQUATABS® 10 LITRES :** 1 comprimé pour 10 litres d'eau traités seulement en 30 minutes. Boîte de 40 comprimés qui permet d'obtenir 400 litres d'eau potable.

Une action rapide et efficace. **Aquatabs®** libère très rapidement dans l'eau son désinfectant. Dans l'eau traitée, une partie du désinfectant disponible est sous forme libre, le reste est combiné et assure un effet de rémanence qui protège contre une recontamination pendant 3 jours.

Une eau potable, sans goût et sans conservateur. **Aquatabs®** permet d'obtenir une eau potable, plate, sans goût et sans conservateur. C'est idéal pour les vacances et les voyages à l'étranger, la navigation de plaisance, la randonnée.

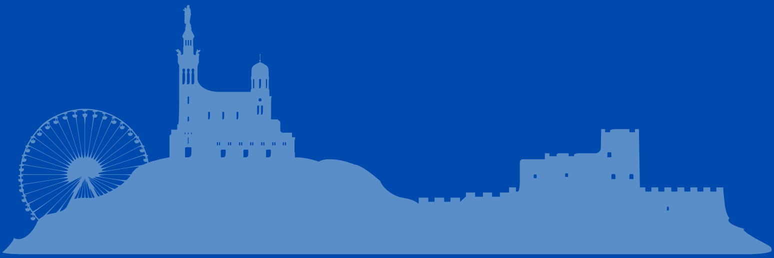
1 litre : Code EAN : 3401575790261

10 litres : Code EAN : 3401577319361

AQUATABS®1 LITRE Forme et présentation : boîte de 60 comprimés conditionnés individuellement dans un complexe aluminium/PE/papier de 10 comprimés. Une boîte ne pèse que 14 g et permet de traiter 60 litres d'eau. **Composition** : préparation contenant 3,5 mg par comprimé de sel de sodium de 1,3 - dichloro-s-triazine 2,4,6, - trione (DCCNa). Excipients : qsp un comprimé de 50 mg. **Conservation** : 5 ans. **Indications** : désinfection de l'eau pour la boisson, le brossage des dents, le lavage des fruits et légumes. **Mode d'emploi** : **ajouter 1 comprimé dans 1 litre d'eau claire**, laisser agir 30 minutes avant de consommer l'eau. Si l'eau contient des sédiments, sa décantation ou sa filtration est nécessaire préalablement à l'ajout du comprimé. **Précautions d'emploi** : ne pas avaler les comprimés. TENIR HORS DE PORTÉE DES ENFANTS.
AQUATABS®10 LITRES Forme et présentation : boîte de 40 comprimés conditionnés individuellement dans un complexe aluminium/PE/papier de 10 comprimés. Une boîte ne pèse que 12 g et permet de traiter 400 litres d'eau. **Composition** : préparation contenant 33 mg par comprimé de sel de sodium de 1,3 - dichloro-s-triazine 2,4,6, - trione (DCCNa). Excipients : qsp un comprimé de 55 mg. **Conservation** : 5 ans. **Indications** : désinfection de l'eau pour la boisson, le brossage des dents, le lavage des fruits et légumes. **Mode d'emploi** : **ajouter 1 comprimé dans 10 litres d'eau claire**, laisser agir 30 minutes avant de consommer l'eau. Si l'eau contient des sédiments, sa décantation ou sa filtration est nécessaire préalablement à l'ajout du comprimé. **Précautions d'emploi** : ne pas avaler les comprimés. TENIR HORS DE PORTÉE DES ENFANTS.

Fabricant : Aquatabs® est une marque déposée et une formule brevetée de Medentech Ltd, Irlande. ■ **Aquatabs® 1 litre - Autorisation** : Direction Générale de la Santé du 3 mai 1999. Dossier 980119 ■ **Aquatabs® 10 litres - Autorisation** : Direction Générale de la Santé du 17 octobre 2001. Dossier 010014. ■ **Aquatabs®** a reçu l'accord de l'Office Fédéral de la Santé Publique (Suisse) N° 103901 du 3 juillet 2003, la certification N.S.F du 9 avril 2007, et l'autorisation de l'Agence pour la Protection de l'Environnement Américaine du 2 avril 2011 (US E.P.A.).

*** Le Troclosène sodique (DCCNa) agit principalement sous forme de chlore libre, hautement efficace.



ICP8

8th International Conference on Phthiraptera

ICP1 - *1972* - Washington D.C., United States of America
ICP2 - *2002* - Brisbane, Australia
ICP3 - *2006* - Buenos Aires, Argentina
ICP4 - *2010* - Cappadocia, Turkey
ICP5 - *2014* - Park City, United States of America
ICP6 - *2018* - Brno, Czech Republic
ICP7 - *2023* - Guangzhou, China (virtual)
ICP8 - *2025* - Marseille, France