



Emerging horizons for tick-borne pathogens: from the 'one pathogenone disease' vision to the pathobiome paradigm

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Shifting from pathogen to pathobiome: the example of tick-borne pathogens



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.... And Maria Kazimirova, Zdenek Hubalek, Sandor Hornok, Robert Farkas, Sarah Bonnet, Jean-François Cosson, Gwénaël Vourc'h, Andrei Mihalca, Olivier Plantard, Cornelia Silaghi and Annapaola Rizzoli







Common vision of pathogenic agents

- Old vision of microbe and infectious diseases : Since the 19th century: link between microbes to infectious diseases (Koch Postulate in 1884): One microbe – One disease
 - Today, the predominant vision of infectious disease is still
 One Microbe-One Disease
 - This vision is limited: Ex: association of different microbes may lead to infectious diseases
 - Pathogens are not isolated entities, they live in associations/interactions with other microbes which may influence their transmission, evolution or pathogenicity

Common vision of pathogenic agents

New vision of microbe and infectious diseases :

Integrate « pathogens » in their microbial environment (the so called **pathobiome)** to understand infection diseases

REVIEW ARTICLE

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Shifting the paradigm from pathogens to pathobiome: new concepts in the light of metaomics

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• Tick borne Pathogens or Tick Borne Pathobiome?

- A lot of tick borne pathogens
- Till recently, Lab were specialized on **one single pathogen** : few data with the all picture
- In the last few years, development of high throughput molecular techniques allow us to investigate tick borne pathogens as a whole : Beginning of the « Pathobiome » story



The questions the « Tick » community started to address were:

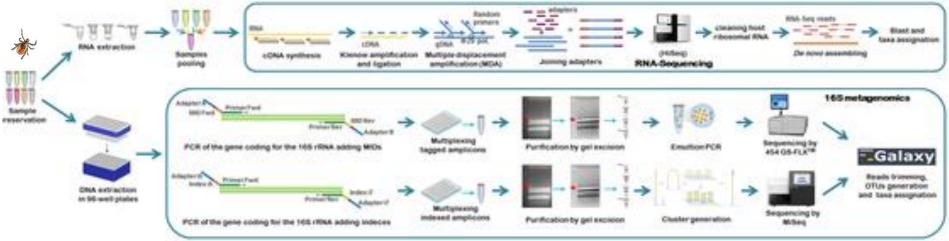
1- infection/co-infection at the individual tick level?
2- Interactions between pathogens and other microbes?
3- Effect on co-transmission?

4- Co-infection in hosts and effect on symptoms?

The first need: an inventory of the tick pathogens and other associated microbes



- Inventory of tick-borne pathogens
- Identification of microbial sequences in ticks
- Without a priori detection (16S and RNA sequencing)

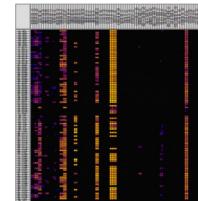


Razzauti et al. 2017, PNTD

• With a priori, targeting known tick-borne pathogens



Biomark[™] dynamic Assay

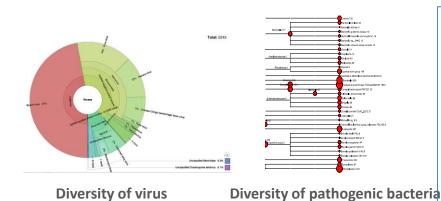


High throughput analysis of simultanously up to 48 pathogens in the same tick

Michelet et al. 2014, FCIM Moutailler et al., 2015 PNTD

• Inventory of tick-borne pathogens : Main results

• High diversity of bacterial, parasitic and viral sequences



Main results on european ticks:

- All the **known** Tick Borne Pathogens
- Known but unexpected pathogens (i.e., transmitted by other vectors, transmitted by ticks but never detected in France so far, forgotten pathogens)
- Unknwon micro-organisms

Ex. of known but unexpected or forgotten pathogens

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PLOS ONE

Next Generation Sequencing Uncovers Unexpected Bacterial Pathogens in Ticks in Western Europe

Muriel Vayssier-Taussat¹, Sara Moutailler¹, Lorraine Michelet¹, Elodie Devillers¹, Sarah Bonnet¹, Justine Cheval², Charles Hébert², Marc Eloit^{2,3,4}*

1 USC Bipar, INRA, Anses, Maisons-Alfort, France, 2 PathoQuest SAS, Paris, France, 3 Ecole Nationale Vétérinaire d'Alfort, UMR 1161 Virologie ENVA, INRA, ANSES, Maisons-Alfort, France, 4 Institut Pasteur, Laboratory of Pathogen Discovery, Paris, France

- *Borrelia miyamotoi:* firstly described in France (same strain as a pathogenic one isolated in The Netherland at the same time)
- Rickettsia felis: Human pathogen transmitted by fleas. Since other studies demonstrated it might also a TBP

GINAL ARTICLE

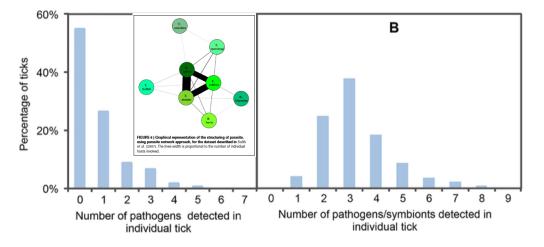
Diversity of viruses in *lxodes ricinus*, and characterization of a neurotropic strain of Eyach virus

S. Moutailler¹, L. Popovicl^{1,3}, E. Devillers¹, M. Vayssler-Taussat¹ and M. Eloit^{1,4}
1) UMR Bops, INRA, Anses, ENVA, Maissen-Affor, France, 2) Foculty of Veterinary Medicine, University of Agricultural Sciences and Veterinary Medicine, Deparament of Public Health, Iosi, Romania, 3) PathoQuest SAS and 4) Institut Patsaur, Biology of Infection Unit, Inserm U1117, Pathogen Discovery Laboratory, Pating, Irrance

Eyach virus: Described in the 70's

• Inventory of tick-borne pathogens : Main results





- Co-infection within ticks is the rule rather than the exception (*Moutailler et al. 2015*)
- Positive associations between some pathogens – different species of *Borrelia* sp. (Vaumourin et al., 2014)
- Negative associations (Borrelia and Anaplasma)
- Possible interactions

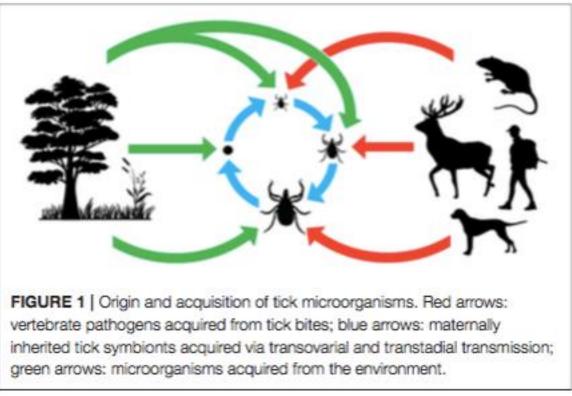


- What about co-infection in vertebrate hosts?
 - From our own preliminary data (OHTicks project) coinfections in humans and animals are detected when looked for (probable co-transmission?), impact on symptoms (ECDC Review in preparation – Cutler, Vayssier-Taussat et al.,)



What do we know about other tick associated microbes?

• Where do they come from?



Duron et al., 2017

- Acquired from Environment: commensals, other?
- Acquired during blood meals: commensals, pathogens
- Inheritated: symbionts (reproduction, nutrition, synthesis of major vitamins, etc...)

What do we know about other tick associated microbes?

• Inheritated bacteria/commensal/ pathogens: no clear frontier

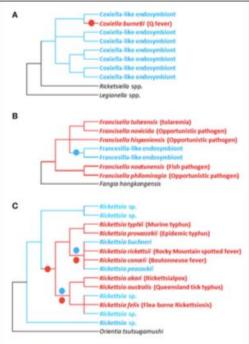
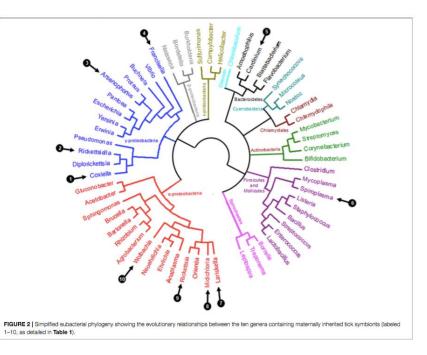


FIGURE 3 | Evolutionary relationships between pathogenic and non-pathogenic (symbiotic) forms within the Francisetle, Coxiella, and Rickettsia bacterial genera. (A-C) Simplified phylogenies of Coxielle, Francisetle, and Rickettsia, respectively, adapted from Periman et al. (2006), Weinert et al. (2009), Duron et al. (2015a), and Sjodin et al. (2012). Red: pathogenic forms; blue: endosymbiotic forms associated with arthropods (ticks for Francisetle and Coxiella; ticks and other arthropods frickettsia); black: bacterial outgroups. Colored circles on tree branches indicate major evolutionary transitions from symbiotic ancestors to pathogenic descendants (red circles) and from pathogenic ancestors to symbiotic descendants (blue circles).



- Symbionts are phylogentically closed to tick borne pathogens (that might have evolved to infect vertebrates)
- Some tick symbionts are also vertebrate pathogens

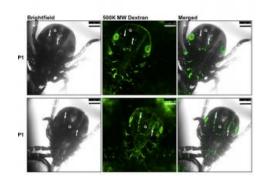
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- Interactions between gut microbiota and pathogens:
- The gut as a barrier pathogens have to disrupt: The ex. of *A.phagocytophilum*

Pathogen-mediated manipulation of arthropod microbiota to promote infection

Nabil M. Abraham^{a,b,1}, Lei Liu^{a,1,2}, Brandon Lyon Jutras^{b,c,d}, Akhilesh K. Yadav^e, Sukanya Narasimhan^a, Vissagan Gopalakrishnan^{a,b,f}, Juliana M. Ansari⁹, Kimberly K. Jefferson^h, Felipe Cava^e, Christine Jacobs-Wagner^{b,c,d,i}, and Erol Fikrig^{a,b,i,2}

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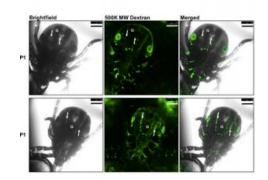


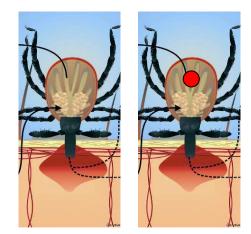
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A. phagocytophilum ingested with infected blood colonize the tick gut

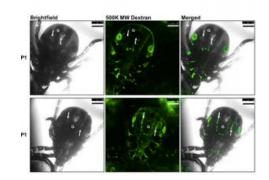
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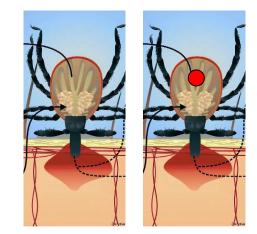
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• *A. phagocytophilum* ingested with infected blood colonize the tick gut

A. phagocytophilum induces the production of a tick anti-freeze glycoprot (iafgp) that alters bacterial biofilm and disrupt the gut barrier

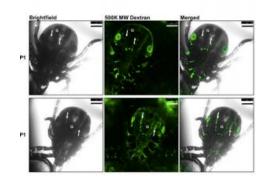
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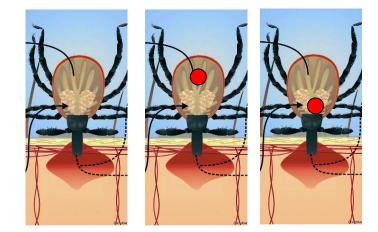
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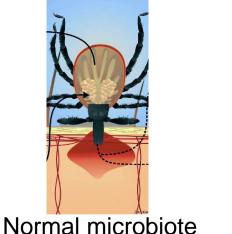
A. phagocytophilum can then cross the gut barrier and colonizes salivary gland from where it will be transmitted.

- Interactions between gut microbiota and pathogens:
- The gut microbiota as a helper of pathogen colonization: the ex. of *Borrelia burgdorferi*

Published in final edited form as: Cell Host Microbe. 2014 January 15; 15(1): 58-71. doi:10.1016/j.chom.2013.12.001.

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Sukanya Narasimhan^{1,¶}, Nallakkandi Rajeevan^{2,*}, Lei Liu^{1,*}, Yang O. Zhao^{1,*}, Julia Heisig¹, Jingyi Pan¹, Rebecca Eppler-Epstein¹, Kathleen DePonte¹, Durland Fish³, and Erol Fikrig^{1,4,¶}





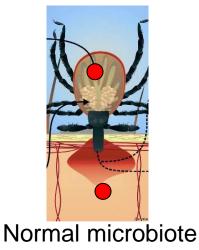
Dysbiosed ticks (Antibiotics)

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- Ticks were fed with *Borrelia* infected blood
- Surprinsingly, *Borrelia* did not survive in the gut of dysbiosed ticks

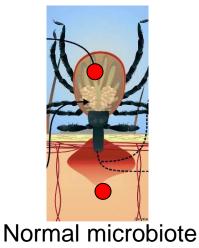
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In dysbiosed ticks: they obeserved a decrease of peritrophin that protect *Borrelia* from gut toxic compounds.

Dysbiosed ticks (Antibiotics)

• Summary of interactions between gut microbiota and pathogens:

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Antagonist effects of gut microbiota considering the pathogens: microbiota blocks *A. phagocytophilum* colonization while tick microbiota allows protection of *Borrelia* and its survival in the gut

These results may explain why *A. phagocytophilum* and *Borrelia* are not found associated in ticks.



- Interactions between symbionts and pathogens: symbionts seem to block pathogens colonization
 - First evidence of interaction was done by Burgdorfer in 1981: The presence of Rickettsial symbionts hampered multiplication of the highly pathogenic *R. rickettsii (Burgdorfer, 1981)*
 - *Rickettsia belli* (symbiont) is negatively associated with *A. marginale* in ticks (*Gall et al., 2016*)
 - Ticks infected with *Rickettsia buchneri* are less infected by *Borrelia burgdorferii*

Rickettsial symbionts might be a key factors to regulate tick borne pathogens abundance and diversity in ticks

Summary and conclusion

- ✓ Considering all these data, the tick pathobiome concept is not only a concept but a reality
- Ticks pathobiome is complex, with many interactions with implications in term of pathogens transmission and diseases
- ✓ For a better understanding of this very complex system , we need to combine our vision of traditionnal infectiology with microbial ecology adapted to pathogens



Many thanks to the european tick teams



MEM MP



- Partner 18 Institut Pasteur (IP), Paris, France.
- Partner 20 Institute of Vertebrate Biology (IVB), Brno, Czech Republic
- Partner 21 Sven Istvan University, Faculty of Veterinary Science (SZIE) Budapest, Hungary
- Partner 32 Institut National de Recherche Agronomique (INRA), Paris, France
- Partner 33 Slovak Academy of Sciences (SAS), Bratislava, Slovakia
- Partner 34 Ludwig Maximilians Universitaet Muenchen (LMU), Munchen, Germany

Partner 35 – Fondazione Edmund Mach (FEM), Trento, Italy

Partner 36 – Research Centre Borstel (RCB), Borstel, Germany

Partner 37 – Innovative Diagnostics-VET (ID-VET)

Partner 38 – Kafkas Universitesi (KAU), Kars, Turkey

Partner 40 – Friedrich Loeffler Institute (FLI), Riems, Germany

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