

# PCR for crypto-infections diagnosis in patients with PTLDS

**Comparison of matrices (venous blood, capillary blood, urine and saliva), effect of a biofilm breaker (serrapeptase)**

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# PCR for crypto-infections diagnosis in patients with PTLDS. Comparison of matrices (venous blood, capillary blood, urine and saliva).

## Pathotique 2 Study

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# Funding

- \* **Pathotique 2 study was funded by**
  - \* **Group Ramsay Santé (Dr Marie Mas)**  
Clinique Convert, Bourg-en Bresse, France
  - \* **Bionops, France** (which provided serrapeptase)

# PCR

- \* Various techniques, often home-made
- \* Various results
- \* Various matrices
  
- \* Frequent low sensitivity
  
- \* Need for comparative studies and standardization
- \* Need for a collaboration between human labs and vet labs

# Pathotique 2 Study Methods (1)

- \* PCR realized for 18 bacteria, 1 fungus (*Candida*), 2 parasites (*Babesia* & *Theileria*) and 13 viruses
- \* Patients with **SPPT** (persistent polymorphic syndrome after a possible tick bite, syndrome recognized by the French High Authority for Health, HAS), **close to PTLDS** (post-treatment Lyme disease syndrome)
- \* Not treated with anti-infective drugs for at least 2 months

# Pathotique 2 Study Methods (2)

- \* **PCR**
- \* **Two samples from each matrix, at Day 0 and Day 3**
  - \* Venous blood
  - \* Capillary blood
  - \* Urine
  - \* Saliva
- \* **After the first sample, intake per os of 480 000 IU of serrapeptase (biofilm breaker, *Bionops*) during 3 days**

# Pathotique 2 Study Methods (3)

- \* **PCR**

- \* **ADNucleis** extraction buffer (5M guanidium thiocyanate, 500 mM TrisHCL, 50 mM EDTA, 20% Tween 20, 20% Triton X-100, 750 µg proteinase K.
- \* Extraction on 300 µl of venous blood, capillary blood, saliva and urine pellet from 10 ml centrifuged urine

# Pathotique 2 Study Methods (4)

## \* Quantitative PCR

- \* 12 µl of extracted DNA or RNA
- \* Primers and probes from reference laboratories or articles (since 2000)
- \* ADNucleis PCR buffer (20mM Tris-HCl, 10 mM NH<sub>4</sub>SO<sub>4</sub>, 10mM KCl, 2 mM Mg<sup>2+</sup> +, 0.1% TritonX-100, pH 8.8 ), 2 mM of each dNTP, 600 nM of each primer, 1 µl of Evagreen and 5 units of *Taq* polymerase ADNucleis
- \* Taqman or Sybr Technology
- \* Synthetised DNA sequence insert in a plasmid is used as positive control
- \* PCR program : Initial denaturation step of 5 min at 95°C followed by 42 cycles of 15 s at 95°C and 40 s at 60°C (hybridization-elongation) and a last step of dissociation (10 min with temperature increments from 75°C to 95°C)
- \* Quantification with serial dilution of the positive control



# Pathotique 2 Study Methods (5)

- \* For ***Borrelia burgdorferi sensu lato*** species detection, three kits were used:
  - \* *B. burgdorferi s.l.*
  - \* *B. afzelii*
  - \* *B. garinii*
- \* These last two kits are more sensitive

# Babesia / Theileria

- \* In 2006 *Babesia microti* was renamed *Theileria microti*, thanks to the sequencing and the comparison of its ribosomal RNA.
  - \* Uilenberg, G. Goff, W.L. (2006). "Polyphasic Taxonomy". *Annals of the New York Academy of Sciences*. 1081 (1): 492–7.
  - \* Uilenberg, G (May 2006). "*Babesia*--a historical overview". *Veterinary Parasitology*. 138 (1–2): 3–10.
- \* In our study, *Theileria microti* was detected with *Theileria* spp primers, not with *Babesia* primers
- \* *Babesia* spp primers correspond to species of *Babesia* not yet identified (possibly *B. capreoli*, *B. duncani*, *B. divergens*, *B. venatorum* or *B. odocoilei*).

# Babesia / Theileria

\* **Current studies are trying to identify species.** With the following sequences:

B.spp ACCTGCTAACTAGTGTCCGTAAAAAGGTTCGTCC.GTTACGGTTTGCTTCTTAGAGGGACTTTGCGGCTCTAAGCCGCAAGGAAGTTTAAGGCAATAACAGGTCTGTG

B.div ACCTGCTAACTAGTGTCCGTAAAAAGGTTCGTCC.GTTACGGTTTGCTTCTTAGAGGGACTTTGCGGCTCTAAGCCGCAAGGAAGTTTAAGGCAATAACAGGTCTGTG

B.cap ACCTGCTAACTAGTGTCCGTAAAAAGGTTCGTCC.GTTACGGTTTGCTTCTTAGAGGGACTTTGCGGCTCTAAGCCGCAAGGAAGTTTAAGGCAATAACAGGTCTGTG

B.ven ACCTGCTAACTAGTGTCCGTAAAAAGGTTCGTCC.GTTACGGTTTGCTTCTTAGAGGGACTTTGCGGCTCTAAGCCGCAAGGAAGTTTAAGGCAATAACAGGTCTGTG

B.bov\* ACCT..TAACCTGCTATTTAGTCGCTCGGTCTCT.GTCCGTGCGCACTTCATAGAGGGACTCTGCGGCTCAAGCTGCGGTGAGGTTTAAGGCAATAACAGGTCTGTG

B.mic\* ACCT..TAACCTGCTAACTAGTTGCCGTTATTTTCAGTTTCGCCAGCTTCTTAGAGGGACTTTGGGGCTCTAAGCCACAAGGAAGTTTAAGGCAATAACAGGTCTGTG

T.equ\* ACCTGCTAAATAGGGT..GTTGG.A.GTTAT...GTTCTACACTGCTTCTTAGAGGGACTTTGCGGTCATAAATCGCAAGGAAGTTTAAGGCAATAACAGGTCTGTG

# Results of PCR in Pathotique 2 Study

- \* 105 patients
- \* PCR positive for at least one microbe
- \*
  - \* Venous blood: 20 (19%)
  - \* Capillary blood: 53 (50.5%)
  - \* Urine: 65 (61.9%)
  - \* Saliva: 60 (57.1%)

# Comparison of the results of PCR in Pathotique 1 and Pathotique 2 Studies

## \* PCR positive for at least one microbe:

	<i>Study 1</i>	<i>Study 2</i>
* Venous blood:	12/71 (17%)	20/105 (19%)
* Capillary blood:	15/34 (45%)	53/105 (50.5%)
* Urine:	34/71 (48%)	65/105 (61.9%)
* Saliva:	64/71 (90%)	60/105 (57.1%)

# Results of PCR for bacteria and *Candida*. All matrices (venous blood, capillary blood, urine & saliva)

## \* High frequency $\geq 29\%$

* <i>Mycoplasma spp</i>	97 (92.4%)
* <i>Candida spp</i>	33 (31.4%)
* <i>Rickettsia spp</i>	31 (29.5%)

## \* Moderate frequency between 6% and 12%

* <i>Bartonella spp</i>	12 (11.4%)
* <i>Bartonella henselae</i>	11 (10.5%)
* <i>Borrelia garinii</i>	7 (6.7%)
* <i>Ehrlichia spp</i>	7 (6.7%)
* <i>Chlamydia spp</i>	7 (6.7%)

# Results of PCR for bacteria. All matrices (venous blood, capillary blood, urine & saliva)

## \* Low frequency < 2%

* <i>Brucella spp</i>	2 (1.9%)
* <i>Bartonella quintana</i>	2 (1.9%)
* <i>Borrelia afzelii</i>	2 (1.9%)
* <i>Borrelia burgdorferi s.l.</i>	2 (1.9%)
* <i>Borrelia hermsii</i>	2 (1.9%)
* <i>Coxiella burnetii</i>	1 (1%)
* <i>Neoehrlichia mikurensis</i>	1 (1%)

## \* Not isolated in this series

- \* *Borrelia miyamotoi*
- \* *Francisella tularensis*
- \* *Anaplasma spp*

***Borrelia miyamotoi*: 43 cases diagnosed in France by real-time PCR in patients with persistent polymorphic signs and symptoms.**

**M. Franck et al. Front Med 2020.**

**[doi.org/10.3389/fmed.2020.00055](https://doi.org/10.3389/fmed.2020.00055)**

- \* **824 patients tested: 43 (5.22%) positive for *B. miyamotoi***
- \* **In the present study, 105 patients tested: no *Borrelia miyamotoi***
  - \* *This difference is not significant (frequency 0 is within the fluctuation interval which ranges from -0.05 to +0.15, with a threshold of 95%*



## Results of PCR for parasites. All matrices (venous blood, capillary blood, urine & saliva)

- \* *Theileria spp* 30 (28.6%)
- \* *Babesia spp* 3 (2.9%)

# Results of PCR for viruses. All matrices (venous blood, capillary blood, urine & saliva)

* CMV	3 (2.9%)
* HHV-6	3 (2.9%)
* Chikungunya	2 (1.9%)
* Zika	1 (1%)
* West Nile	1 (1%)
* TBEV	0
* EBV	0
* VZV	0
* Dengue	0
* Bourbon	0
* Powassan	0
* Eyach	0

# Results of PCR for bacteria and *Candida*. Positive matrices (venous blood, capillary blood, urine & saliva)

\* High frequency  $\geq 25\%$

		Venous blood	Capillary blood	Urine	Saliva
* <i>Mycoplasma spp</i>	97	3	17	50	96
* <i>Candida spp</i>	33	7	12	15	1
* <i>Rickettsia spp</i>	31	1	2	16	29

# Results of PCR for bacteria. Positive matrices (venous blood, capillary blood, urine & saliva)

- \* Moderate frequency between 5% and 24%

		Venous blood	Capillary blood	Urine	Saliva
* <i>Bartonella spp</i>	12	5	5	2	4
* <i>Bartonella henselae</i>	11	3	2	6	1
* <i>Borrelia garinii</i>	7			1	6
* <i>Ehrlichia spp</i>	7	2	4	1	2
* <i>Chlamydia spp</i>	7				8

# Results of PCR for bacteria. Positive matrices (venous blood, capillary blood, urine & saliva)

\* Low frequency < 5%

		Venous blood	Capillary blood	Urine	Saliva
* <i>Brucella spp</i>	2	1			1
* <i>Bartonella quintana</i>	2			1	1
* <i>Borrelia afzelii</i>	2		1	1	1
* <i>Borrelia burgdorferi s.l.</i>	2		1	1	
* <i>Borrelia hermsii</i>	2			1	1
* <i>Coxiella burnetii</i>	1			1	
* <i>Neoehrlichia mikurensis</i>	1		1		

# Results of PCR for parasites. Positive matrices (venous blood, capillary blood, urine & saliva)

		Venous blood	Capillary blood	Urine	Saliva
* <i>Theileria</i>	30	4	21	3	17
* <i>Babesia</i>	3	1		1	1

# Results of PCR for viruses. Positive matrices (venous blood, capillary blood, urine & saliva)

		<i>Venous blood</i>	<i>Capillary blood</i>	<i>Urine</i>	<i>Saliva</i>
* <b>CMV</b>	<b>3</b>		1	2	3
* <b>HHV-6</b>	<b>3</b>		1	1	1
* <b>West Nile</b>	<b>1</b>			1	
* <b>Chikungunya</b>	<b>2</b>			2	
* <b>Zika</b>	<b>1</b>			1	

# PCR: 1<sup>st</sup> sample negative, 2<sup>nd</sup> sample positive at day 3 after serrapeptase

	Patients
* Venous blood	9
* Capillary blood	16
* Urine	19
* Saliva	26



# PCR: Microbes only found in one matrix

* Venous blood	7
* Capillary blood	14
* Urine	24
* Saliva	71

# PCR: Microbes only found in venous blood

- \* **7 patients**

- \* *Bartonella spp* 2

- \* *Bartonella henselae* 2

- \* *Rickettsia* 1

- \* *Babesia* 1

- \* *Theileria* 1

# PCR: Microbes only found in capillary blood

- \* **14 patients**

- \* *Bartonella spp* 1

- \* *Ehrlichia* 1

- \* *B. burgdorferi s.l.* 1

- \* *Candida* 4

- \* *Theileria* 6

- \* HHV-6 1

# PCR: Microbes only found in urine

## \* 24 patients

* <i>Rickettsia</i>	4
* <i>Bartonella spp</i>	2
* <i>Bartonella henselae</i>	3
* <i>Bartonella quintana</i>	1
* <i>Ehrlichia</i>	1
* <i>Coxiella burnetii</i>	1
* <i>B. burgdorferi s.l.</i>	1
* <i>B. hermsii</i>	1
* <i>Candida</i>	6
* <i>Theileria</i>	1
* HHV-6	1
* Zika	1
* Chikungunya	1
* West Nile	1

# PCR: Microbes only found in saliva

## \* 71 patients

* <i>Rickettsia</i>	4
* <i>Bartonella spp</i>	2
* <i>Bartonella henselae</i>	3
* <i>Bartonella quintana</i>	1
* <i>Ehrlichia</i>	1
* <i>Coxiella burnetii</i>	1
* <i>B. burgdorferi s.l.</i>	1
* <i>B. hermsii</i>	1
* <i>Candida</i>	6
* <i>Theileria</i>	1
* HHV-6	1
* Zika	1
* Chikungunya	1
* West Nile	1

# Salivary infection

External colonization or secretion from salivary glands?

- \* Tropism of some micro-organisms for salivary glands
- \* Role of saliva for transmission of some infections (e.g. rabies, EBV).
- \* Salivary glands are holomerocrine: secretion needs disruption of the apex of the acini cells.
- \* Thus, these acini cells must multiply rapidly. This could enhance the tropism of some micro-organisms.

# PCRs: Comments

- \* ***Mycoplasma***. High level of carriage in saliva and infection or colonization in urine (from the genital tract?). Superiority of capillary blood.
- \* ***Candida***: Superiority of capillary blood. Saliva: probable colonization. Urine: possible contamination during urine collection
- \* ***Bartonella***: Interest of capillary blood. Saliva: source of transmission?
- \* ***Borrelia***: Low sensitivity
- \* ***Ehrlichia***: Interest of capillary blood
- \* ***Theileria***: Superiority of capillary blood, combined with venous blood. Interest of serrapeptase

# Conclusion

## SPPT / PTLDS

- \* **PCRs, interest to:**
  - \* *Search a wide range of micro-organisms*
  - \* *Take samples from several matrices (venous blood, capillary blood, urine and saliva)*
  - \* *Take samples twice (serrapeptase)*
- \* **An accurate microbial diagnosis may allow correlations with some signs and symptoms**