Incidence of *Bartonella* sp. bacteremia in patients with cutaneous T cell lymphomas and healthy subjects: a pilot study

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Introduction

Bartonella spp. are fastidious Gram-negative bacilli, capable of infecting and surviving inside erythrocytes and endothelial cells. They are transmitted from infected humans or animals to new hosts through blood-sucking arthropod vectors. While transmission through animal scratches has been reported, it remains uncertain. Recent studies suggest that transmission can also occur through blood transfusion. Many species are pathogenic to humans, but three are responsible for most clinical symptoms: *Bartonella bacilliformis*, *Bartonella quintana*, and *Bartonella henselae*. The most common types of bartonellosis include vascular proliferative tumors, such as *verruga Peruana* and bacillary angiomatosis, as well as acute or chronic lymphadenopathy, such as cat scratch disease. However, non-classic manifestations are also described, such as fever of unknown origin, splenic and hepatic manifestations, encephalopathies, ocular diseases, and endocarditis[4].

The relationship between *Bartonella* sp. and skin cancer is still unknown. Ericson *et al*. successfully detected *B. henselae* inside melanoma cells in a co-culture containing both bacteria and melanoma cells. In these *B. henselae*-infected melanoma cells, there was a notable increase in the expression of VEGF and interleukin-8 compared to melanoma cells cultured alone[5]. It has also been described to infect myeloid angiogenic cells, promoting tumor vascularization and progression through the release of angiogenic cytokines, immunomodulation, and matrix remodeling[6].

Methods

The objective was to evaluate the incidence of *Bartonella* sp. bacteremia in patients with CTCL and healthy subjects (HS) using conventional and nested PCR from blood samples. Conventional PCR targets the genus-specific ITS region, while nested PCR is specific to *Bartonella henselae* and targets the *FtsZ* gene.

The inclusion criteria comprised adult patients with CTCL or HS, while exclusion criteria included antibiotic treatment within 1 month prior to enrollment or refusal to participate.

Laboratory analyses were conducted in accordance with the methods outlined in this research[7].

Results

Cutaneous lymphomas subjects with detection of *Bartonella* sp in blood samples			
	Conventional PCR	**Nested PCR**	**DNA sequencing**
LC 1	(-)	(+)	100% *B. henselae*
LC 26	(-)	(+)	100% *B. henselae*
LC 27	(-)	(+)	Unavailable
Healthy subjects with detection of *Bartonella* sp in blood samples			
	Conventional PCR	**Nested PCR**	**DNA sequencing**
C 10	(+)	(+)	100% *B. henselae*
C 12	(-)	(+)	99% *B. henselae*
C 13	(-)	(+)	100% *B. henselae*
C 20	(-)	(+)	100% *B. henselae*
C 25	(-)	(+)	Unavailable

Table 1. Participants in whom *Bartonella henselae* ´s DNA was found. (-) undetectable; (+) detectable; Conventional PCR: genus specific PCR for the ITS region; Nested PCR: species specific PCR for the *FtsZ* gene

After signing the consented term, 27 patients with CTCL and 27 HS were enrolled.

CTLC group included 21 initial MF, 5 advanced MF and 1 SS; 14 were female, median age of 57.18 years. Control group included 14 women, median age of 34.92 years. *Bartonella* sp. bacteremia was detected in 3 patients and 5 HS.

Statistical analyses were made with Fisher exact test, alpha level=.05. No significant difference was found between the groups in the incidence of bacteremia ($p = 0.70$) and risk factors, such as dogs or cats as pets ($p = 1$ and $p = 0.58$), dog bites ($p = 0.41$), cat scratches ($p = 1$), flea bites ($p = 0.42$), tick bites ($p = 0.16$) and blood transfusions ($p = 0.11$).

Discussion

We could not find other studies evaluating the detection of *Bartonella* sp. DNA in CTCL. In this research, there was no statistical difference between the groups, which may be related to the number of subjects enrolled or even the choice of biological sample. *Bartonella* sp. bacteremia is low in healthy individuals (10-100 genomic equivalents/ml) and may be lower than the detection limit of the PCRs used[8]. The initial niche of these bacteria is unknown; it could be the endothelial cells, skin, or lymph nodes[9]. Therefore, these materials may be more suitable for research.

In this study, two different PCR methods were used to enhance sensitivity. Nested PCR demonstrated better sensitivity than conventional PCR, consistent with other published research[10].

Conclusion

In conclusion, no significant difference was found in the incidence of *Bartonella* sp bacteremia between CTCL patients and HS. This study represents the first analysis of *Bartonella* sp. in CTCL patients. Further investigations, including the evaluation of its presence in skin tissue or larger studies, may help elucidate this relationship.

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