

L2

Module "Agents Infectieux, Hygiène"

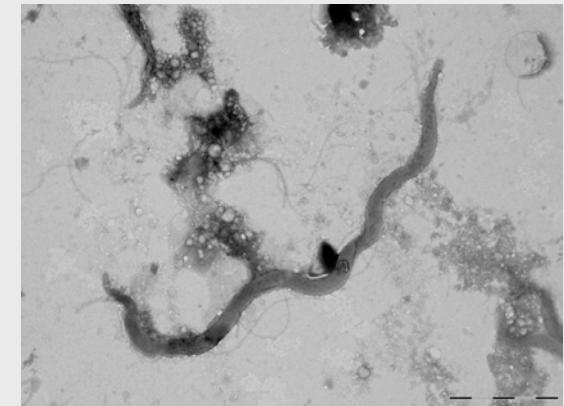
Infections à spirochètes

Michel DRANCOURT

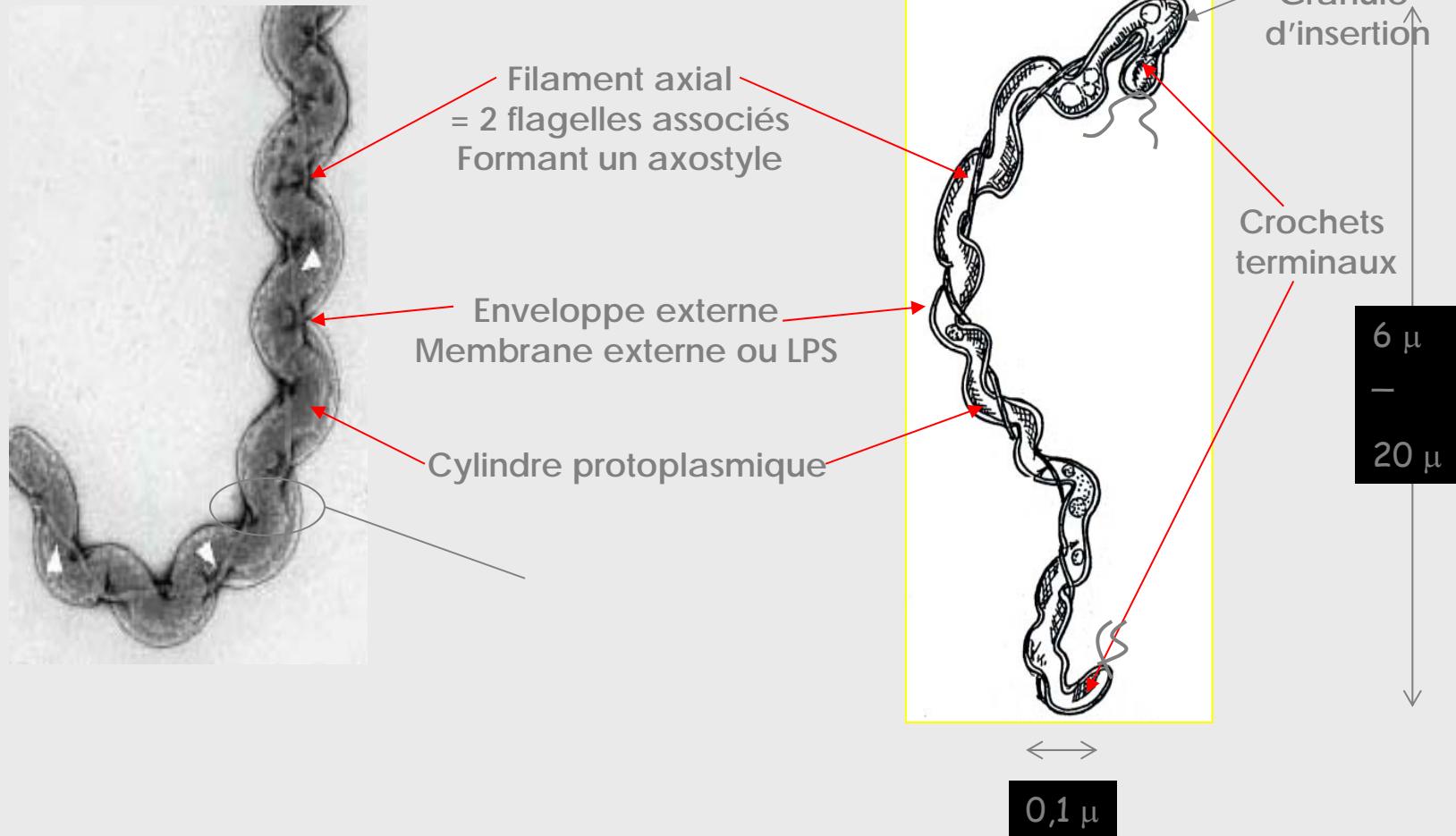
Aix Marseille Université – IHU Méditerranée Infection
MEPHI

Spirochète

- Bactéries
- Gram « zéro »
- Très mobiles
- 3 genres pathogènes pour l'homme
 - Treponema: syphilis
 - Leptospira: leptospirose
 - Borrelia: maladie de Lyme et Fièvres récurrentes
- Fastidieuses



Morphologie - Structure



Genome Architecture



Green colour: region common between *B. duttonii* and *B. recurrentis*

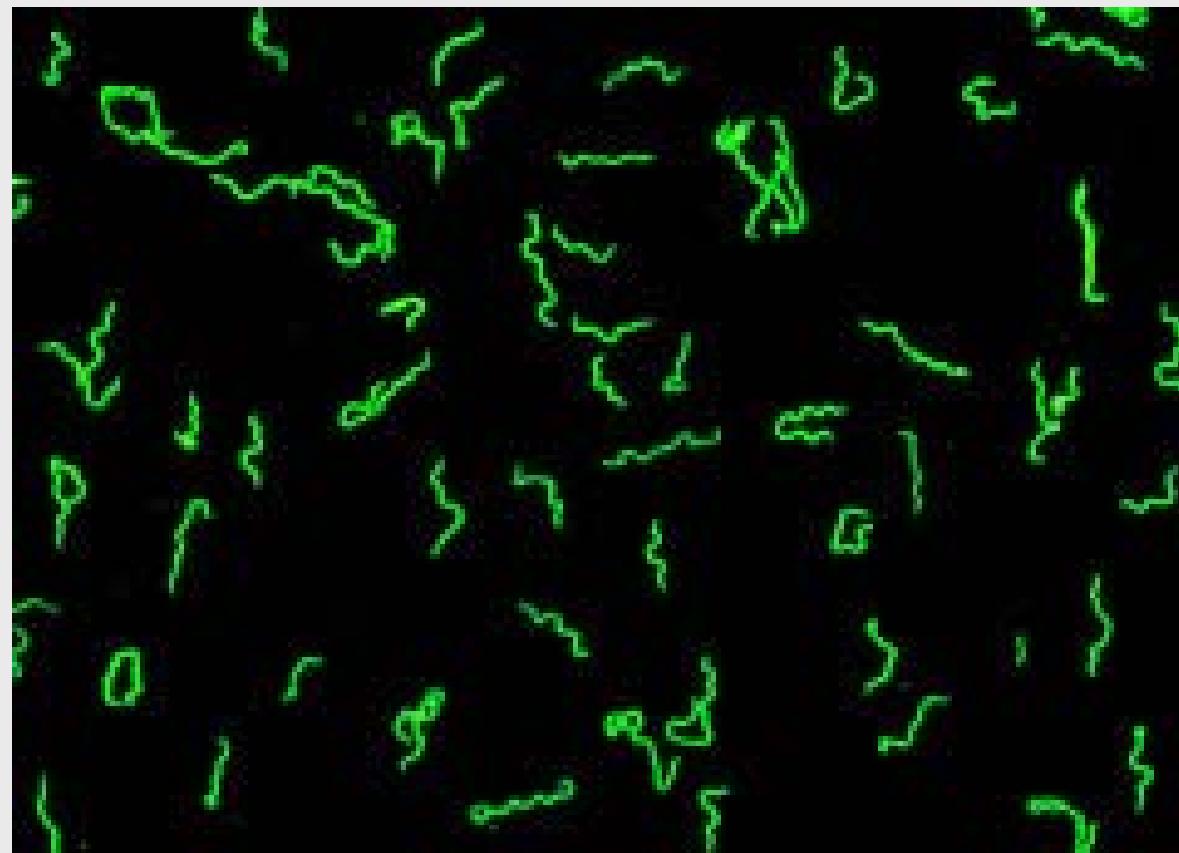
Brown colour: region common between *B. crocidurae* and *B. duttonii*

Genome alignment of *B. duttonii*, *B. recurrentis* and *B. crocidurae*

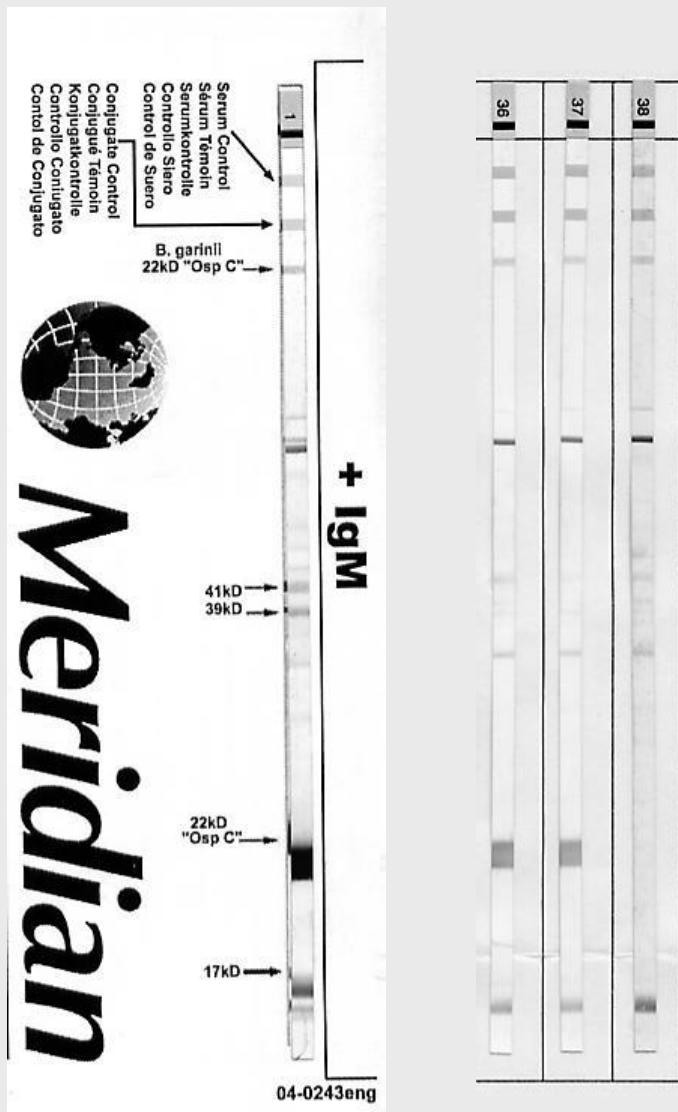
Diagnostic direct par PCR en temps réel



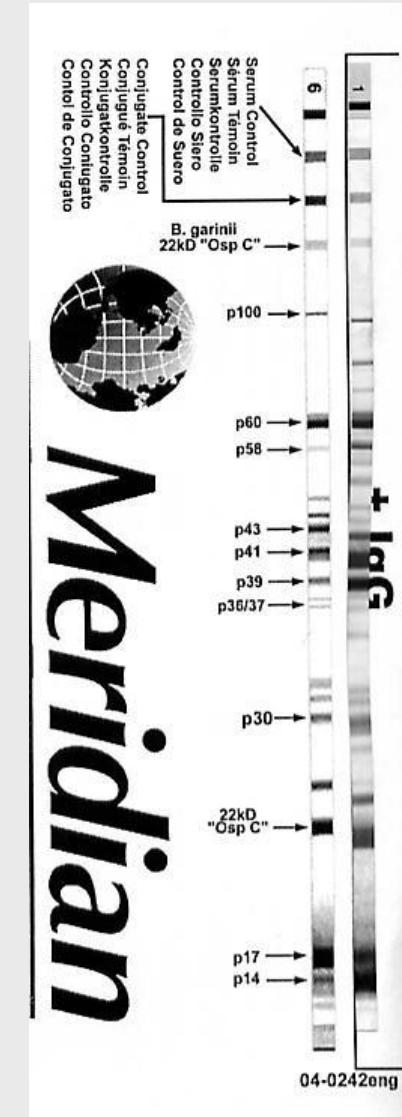
Sérologie par immunofluorescence: *Treponema pallidum*



Sérologie par Western Blot: *Borrelia burgdorferi*

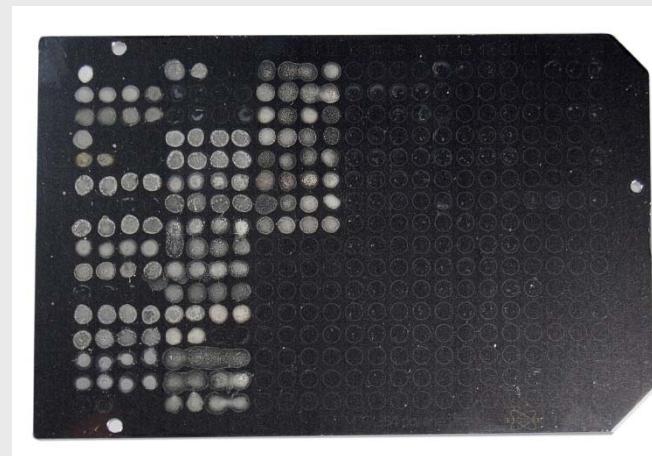


Meridian

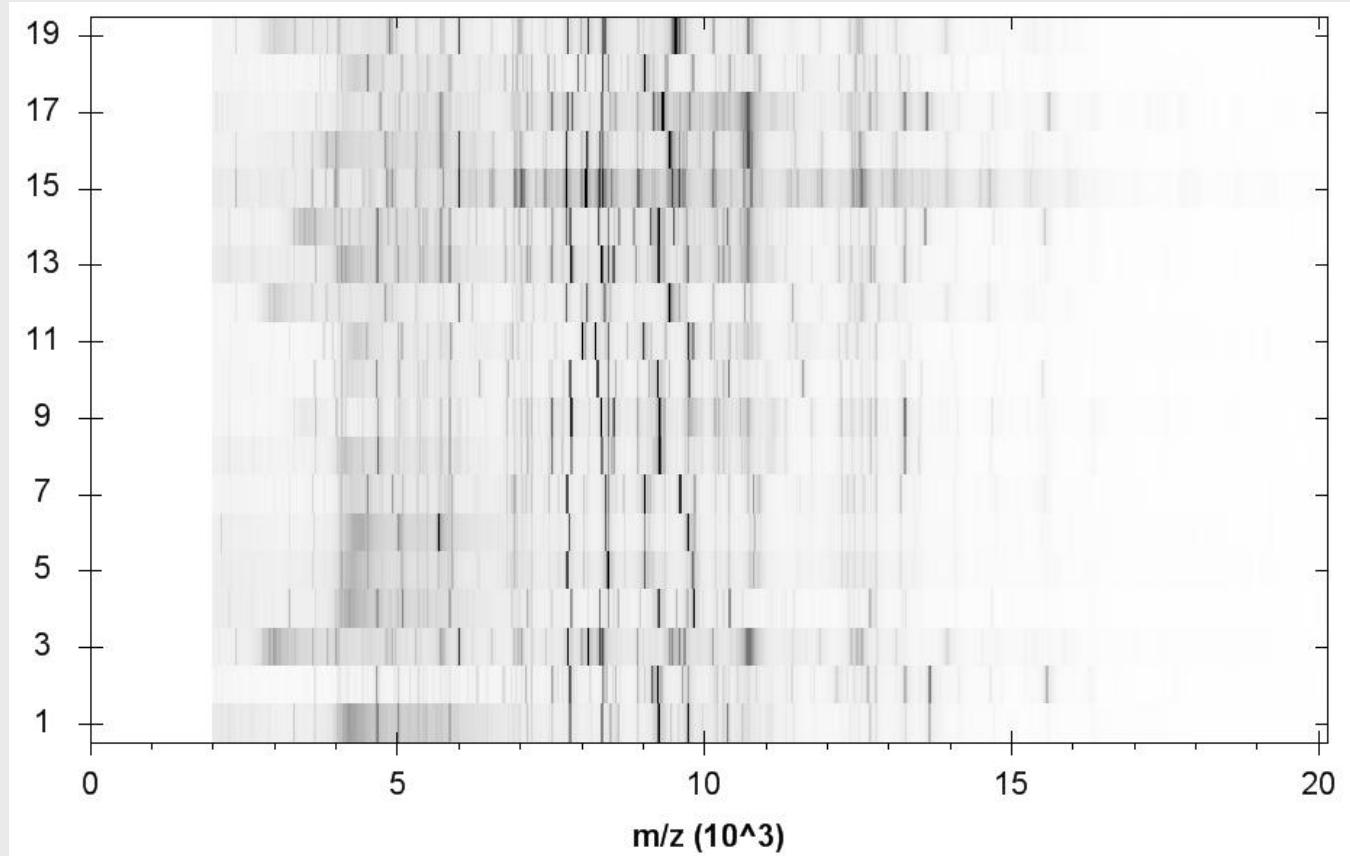


Meridian

Identification rapide par MALDI-TOF



Identification rapide par MALDI-TOF: *Leptospira* sp.



Syphilis

CONCISE COMMUNICATIONS

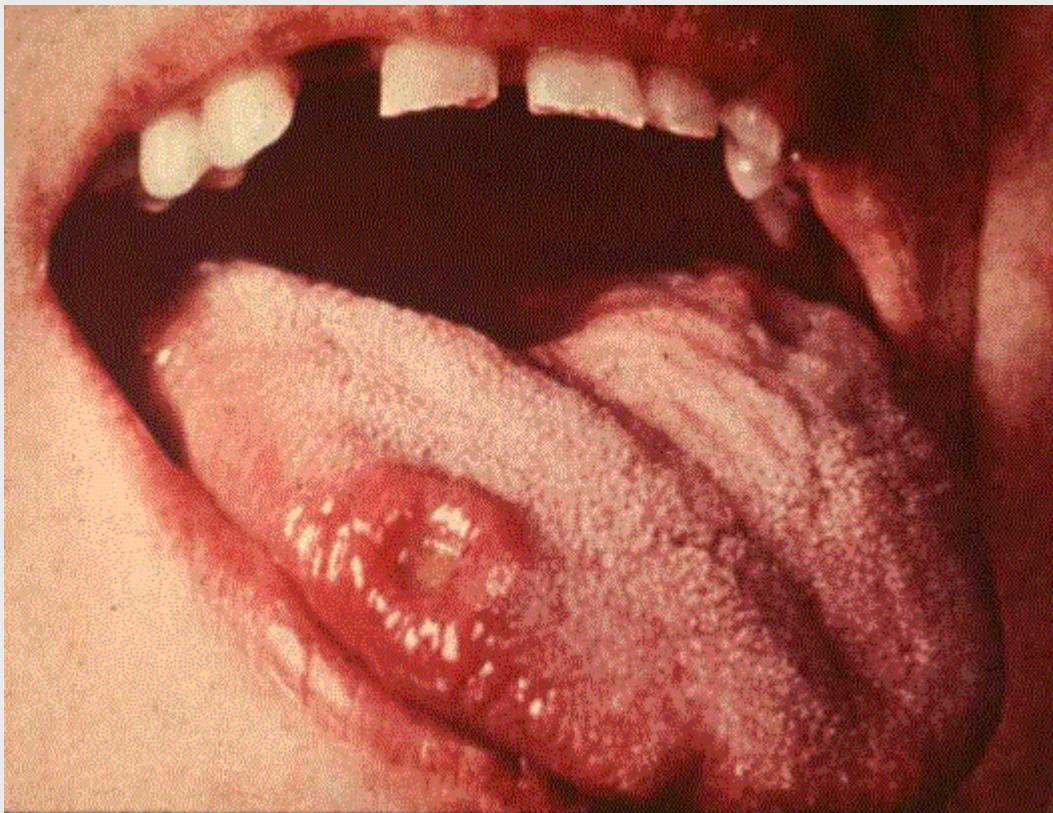
Identification of *Treponema pallidum* Subspecies *pallidum* in a 200-Year-Old Skeletal Specimen

Connie J. Kolman,^{1,a} Arturo Centurion-Lara,²
Sheila A. Lukehart,² Douglas W. Owsley,³
and Noreen Tuross¹

¹Smithsonian Center for Materials Research and Education,
Suitland, Maryland; ²Department of Medicine, University
of Washington, Seattle; ³Department of Anthropology, Smithsonian
Institution, Washington, DC

Treponema pallidum subsp. *pallidum*, the causative agent of venereal syphilis, was detected in a 200-year-old skeletal specimen from Easter Island. An initial diagnosis of treponemal infection was confirmed by extensive purification of immunoglobulin that reacted strongly with *T. pallidum* antigen. Extracted DNA exhibited a single-base polymorphism that distinguished *T.p.* subsp. *pallidum* from 4 other human and nonhuman treponemes. Extensive precautions against contamination of the subject matter with modern treponemal DNA were employed, including analysis of archaeological and modern specimens in 2 geographically separate laboratories. Molecular determination of historical disease states by using skeletal material can significantly enhance our understanding of the pathology and spread of infectious diseases.

**Syphilis: transmission inter-humaine
directe: IST**

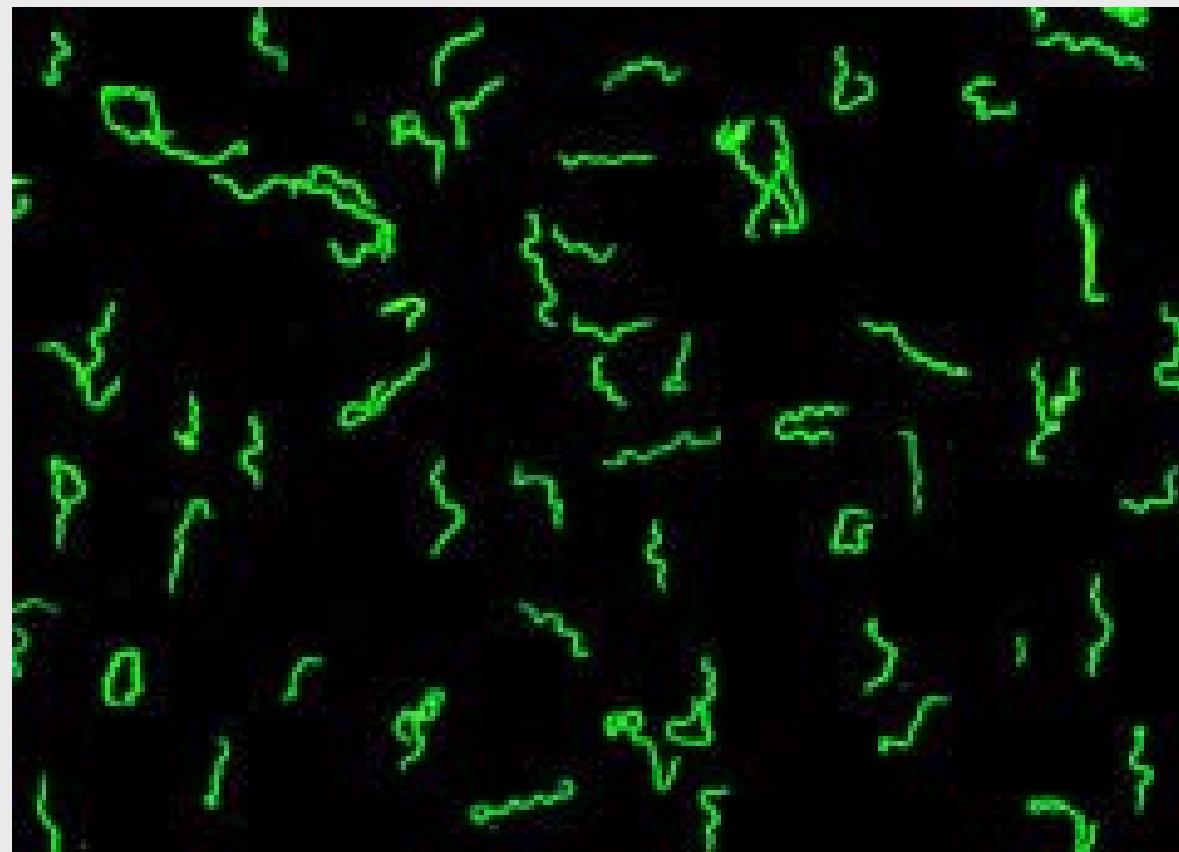


Syphilis: transmission inter-humaine directe: IST



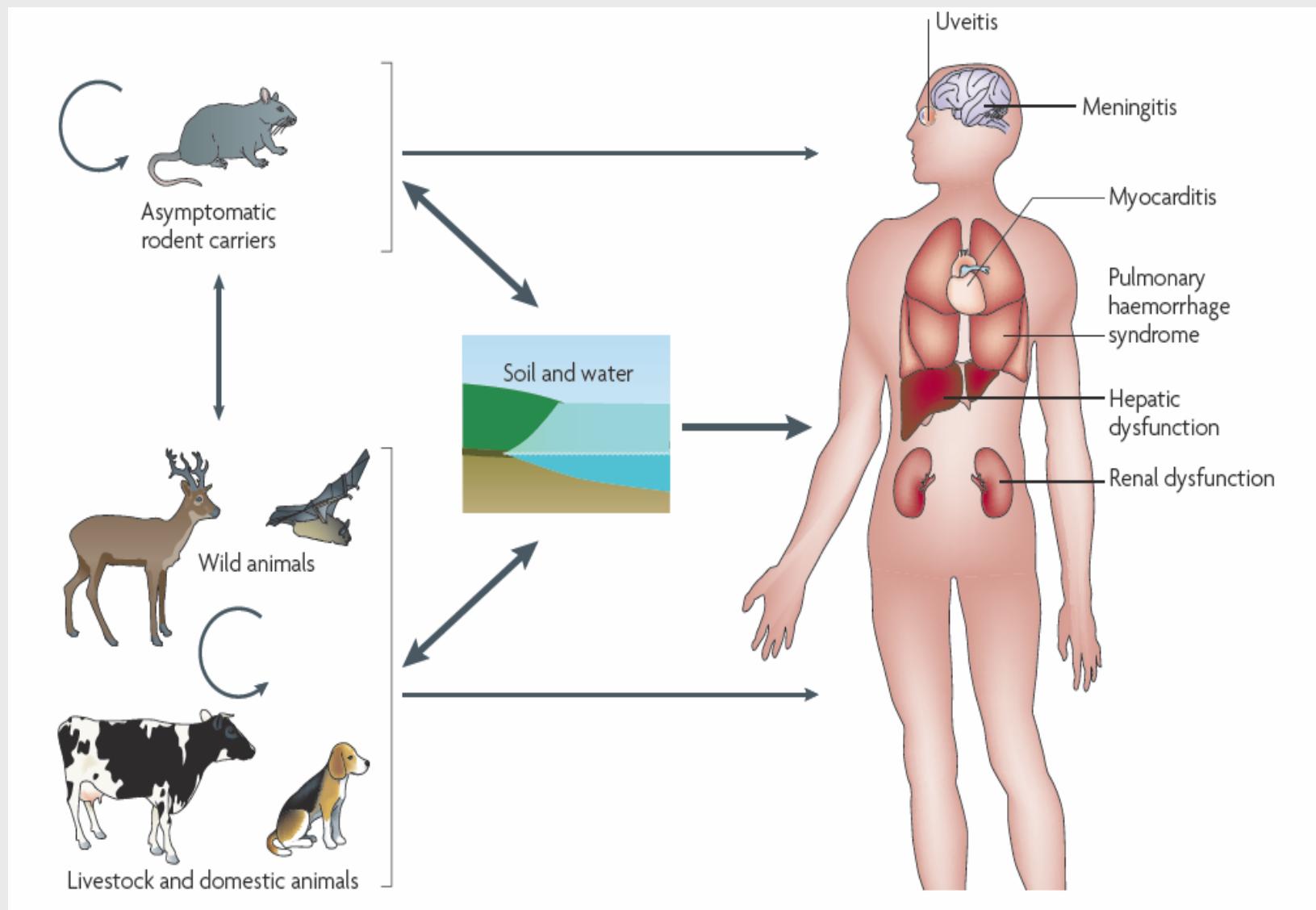
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Sérologie par immunofluorescence: *Treponema pallidum*



Leptospirose

Cycle épidémiologique



(Albert I. Ko, 2009. *Nature Reviews Microbiology* 7, 736-747)

Epidémiologie

Epidémiologie synthétique

* Bactérie à répartition mondiale

Endémique dans les pays à climat chaud et humide

→ Persistance annuelle du germe

→ Occurrence annuelle des leptospiroses

Occurrence saisonnière dans les pays à climat tempéré

→ Maladie du printemps, de l'été et de l'automne

* Nombreuses espèces animales sont réceptives

- Rôle des animaux sauvages = réservoirs notamment rongeurs: rats - Icterohaemorragiae)

- Rôle des animaux domestiques (bovins, porcins - Pomona; Chien - Canicola)



Fig. 1. Leptospirosis incidence in Europe in 2010 (cases/100,000 inhabitants) [ND = presence of leptospirosis, but lack of comprehensive data]

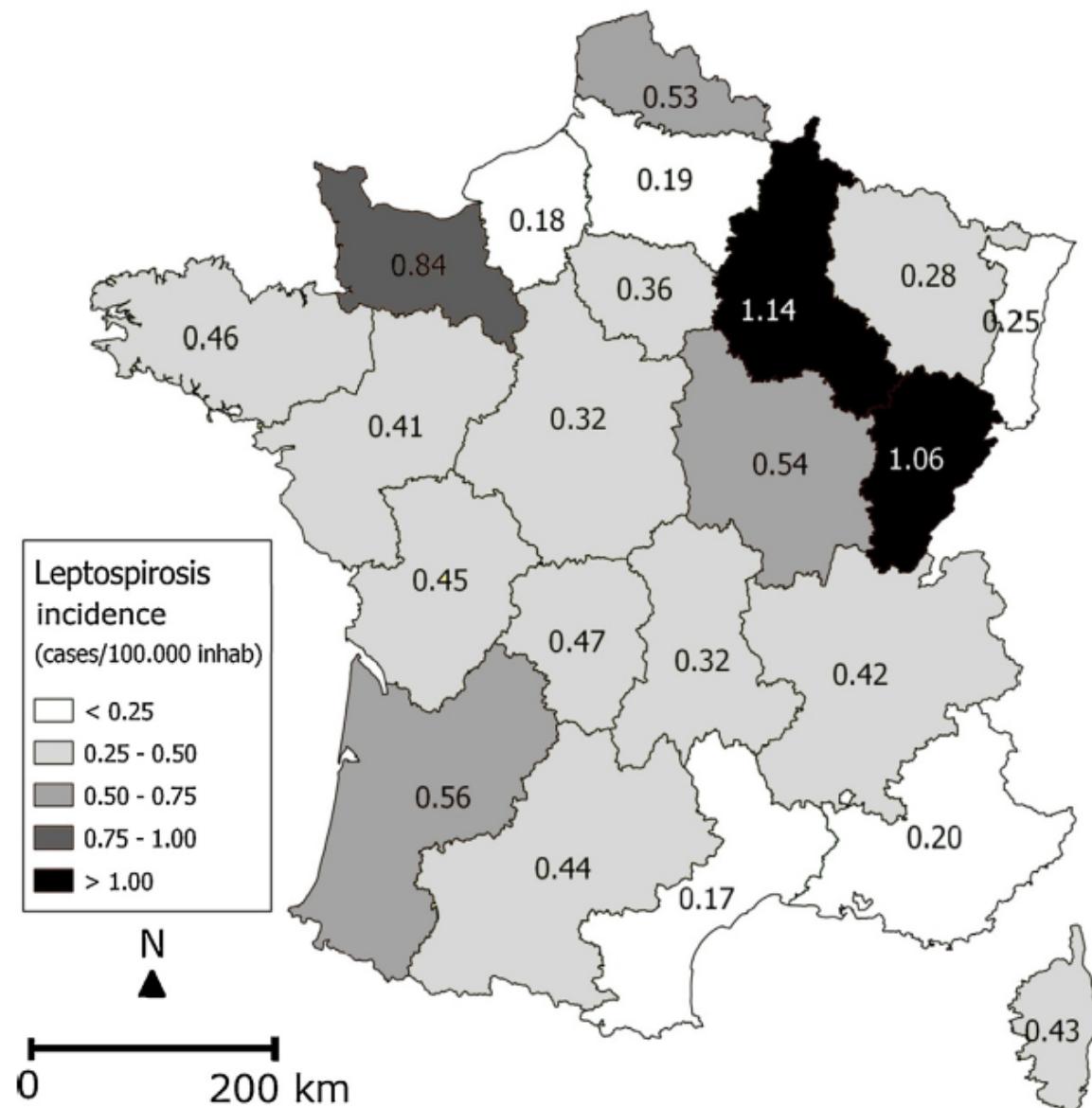


Fig. 3. Global leptospirosis incidence in France, 2006–2010 (cases/100,000 inhabitants) [11].

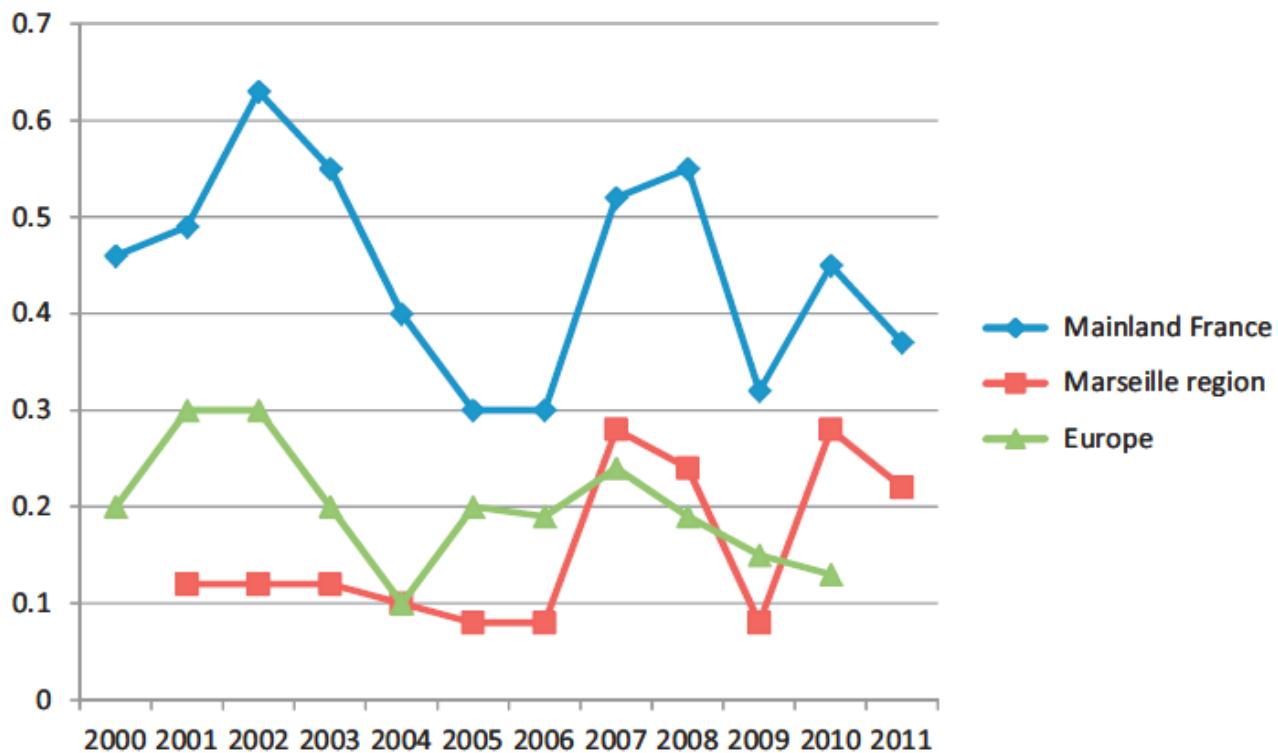
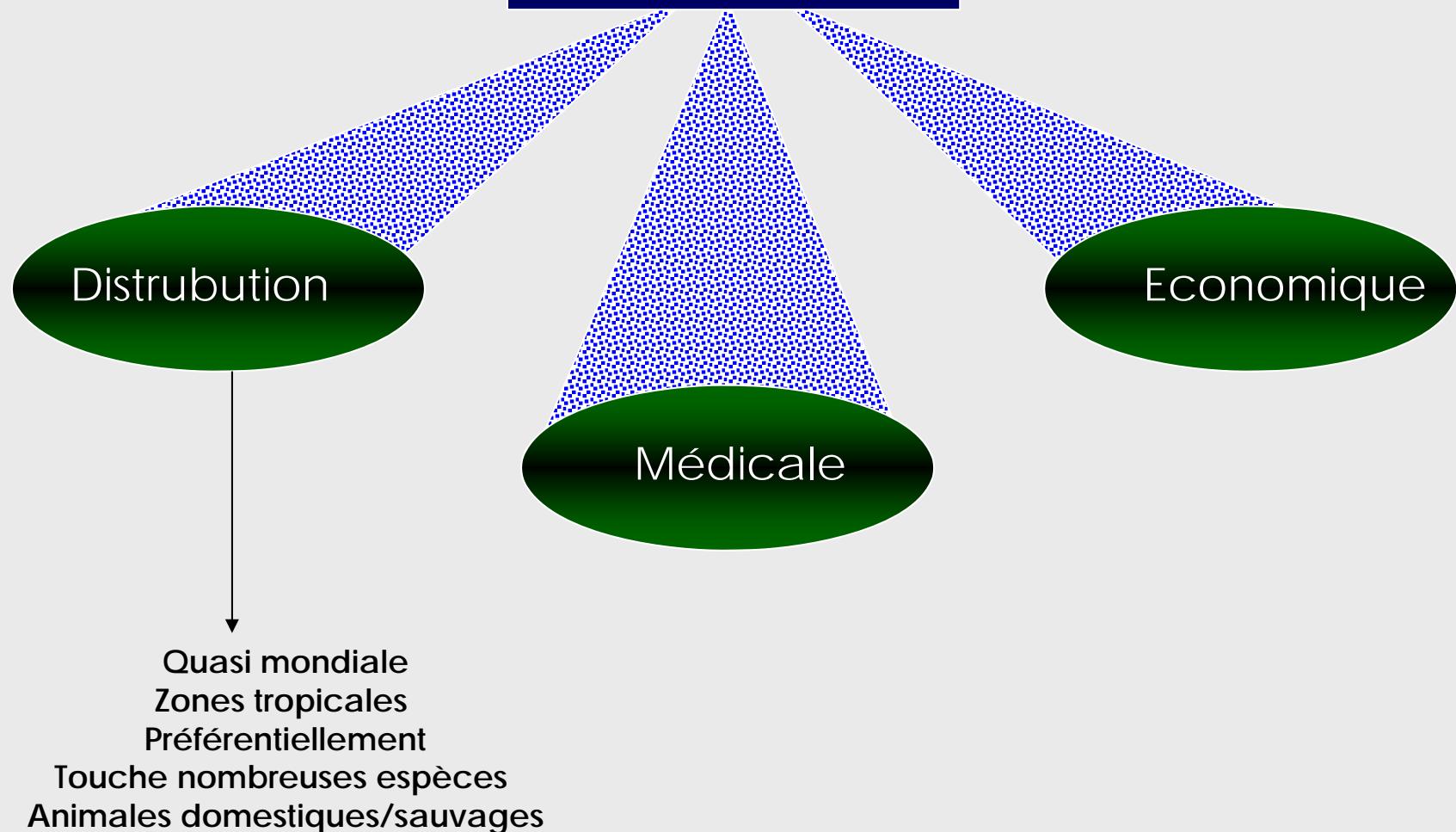
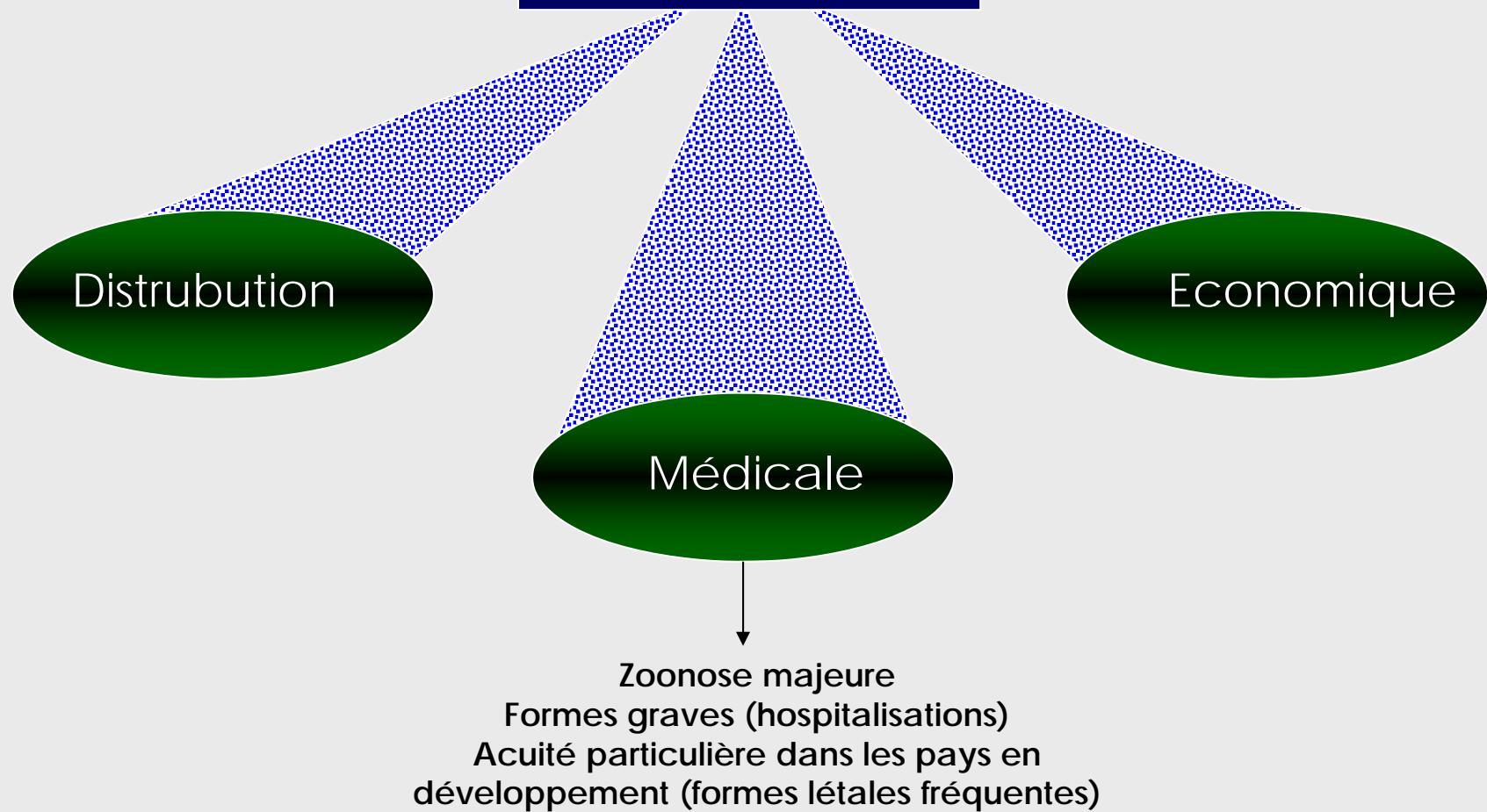


Fig. 2. Evolution of leptospirosis incidence in mainland France, the Marseille region, and Europe, 2000–2011 [9,11, personal communications].

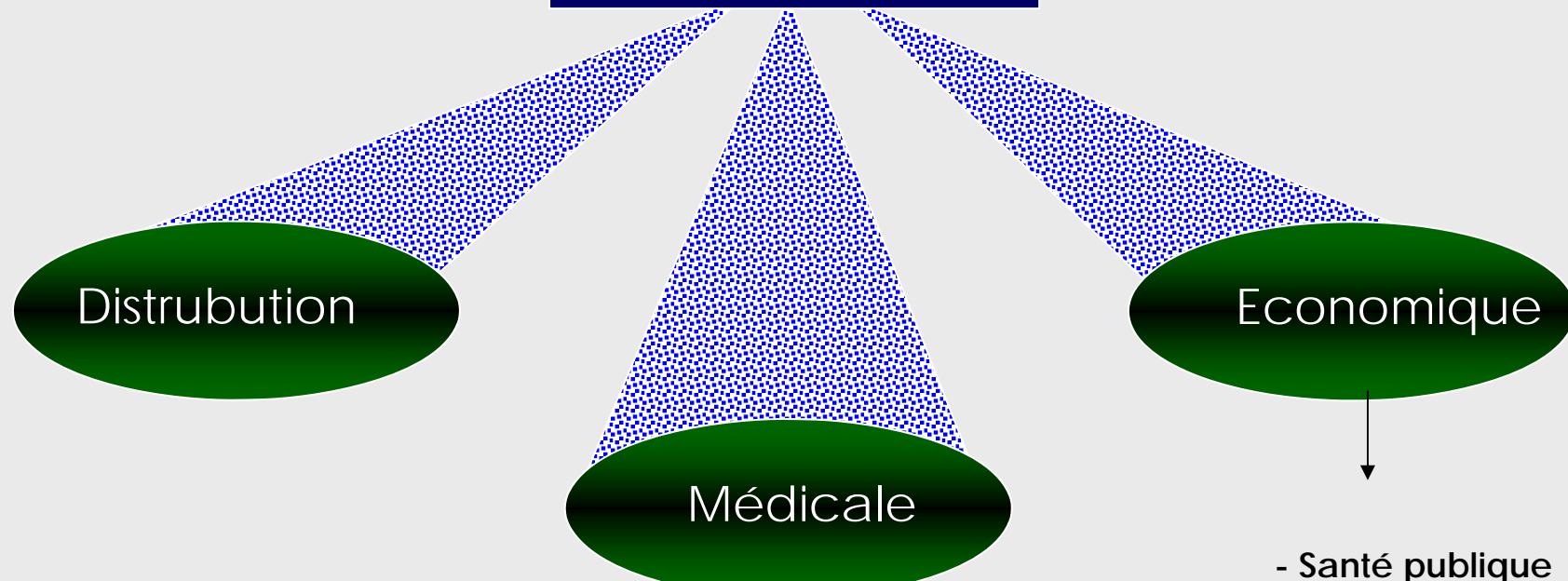
Importance



Importance



Importance

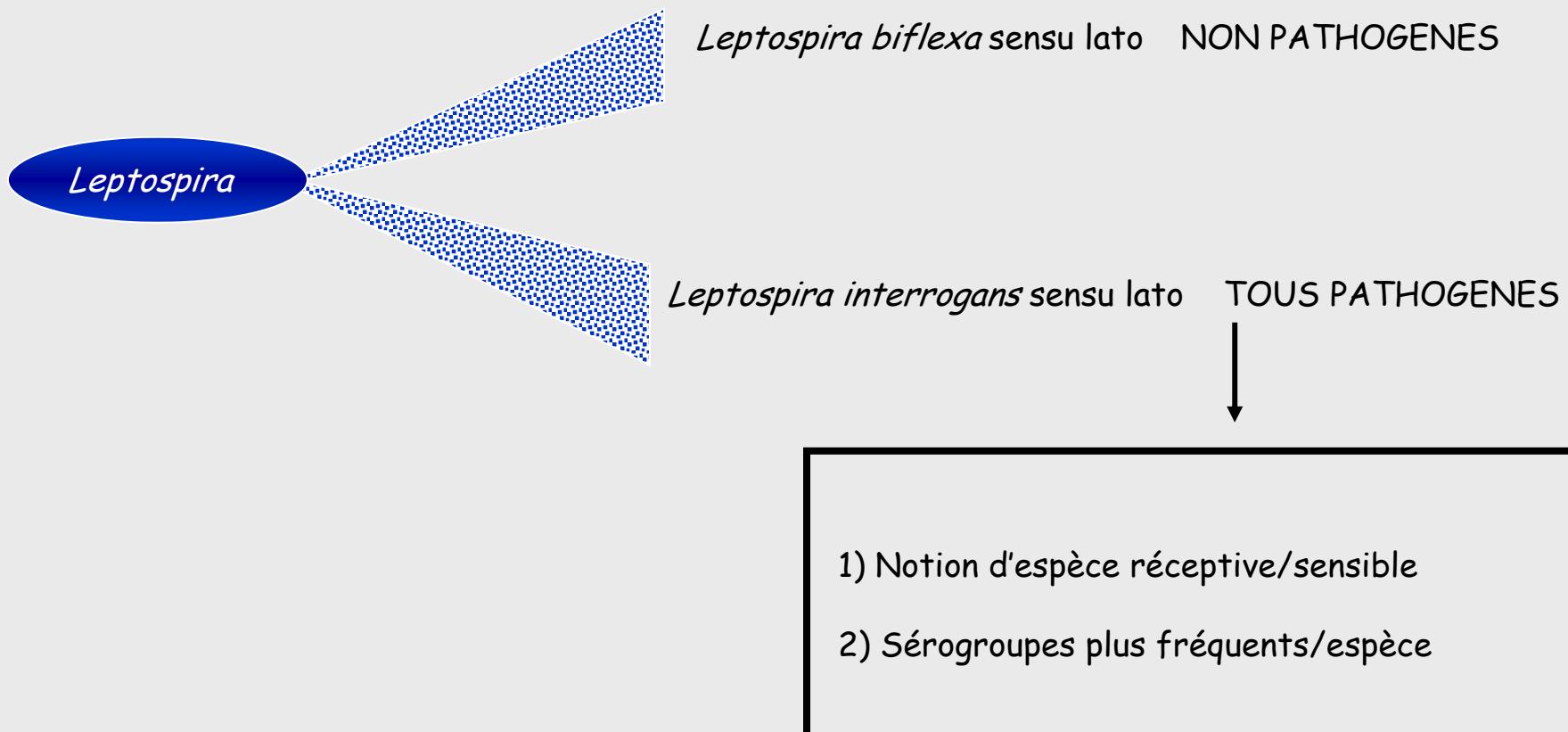


- Santé publique
coûts des hospitalisations)

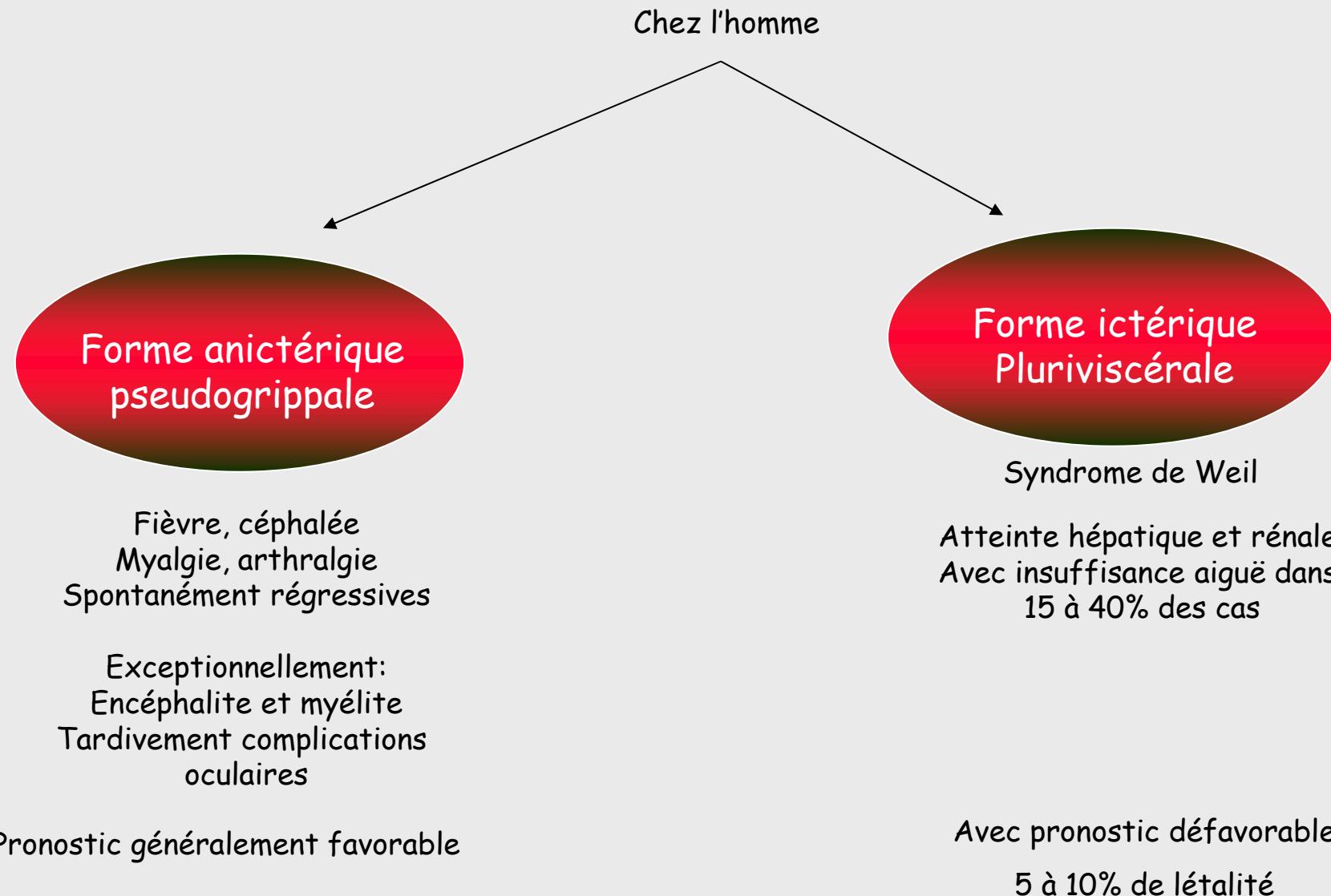
Impacts sur les productions
animales [Ruminants – Suidés]

Pouvoir pathogène

Caractéristiques générales



Pouvoir pathogène naturel



Prélèvements utiles au diagnostic de leptospirose

- Diagnostic direct
 - Urines
 - Sang
 - L.C.R.
- Diagnostic indirect: sérologie:
 - Serum

Maladie de Lyme

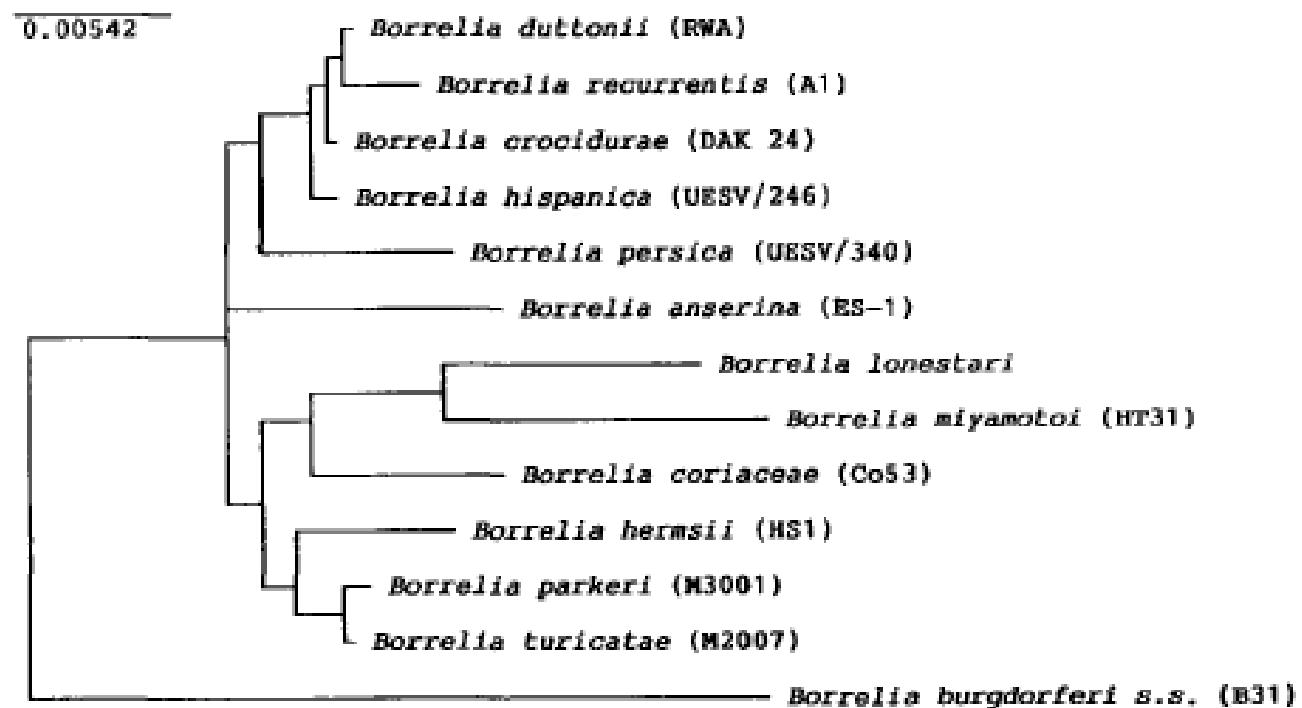


FIG. 1. Phylogenetic tree based on a comparison of the 16S rRNA sequences of RF *Borrelia* species. The branching pattern was generated by the neighbor-joining method.

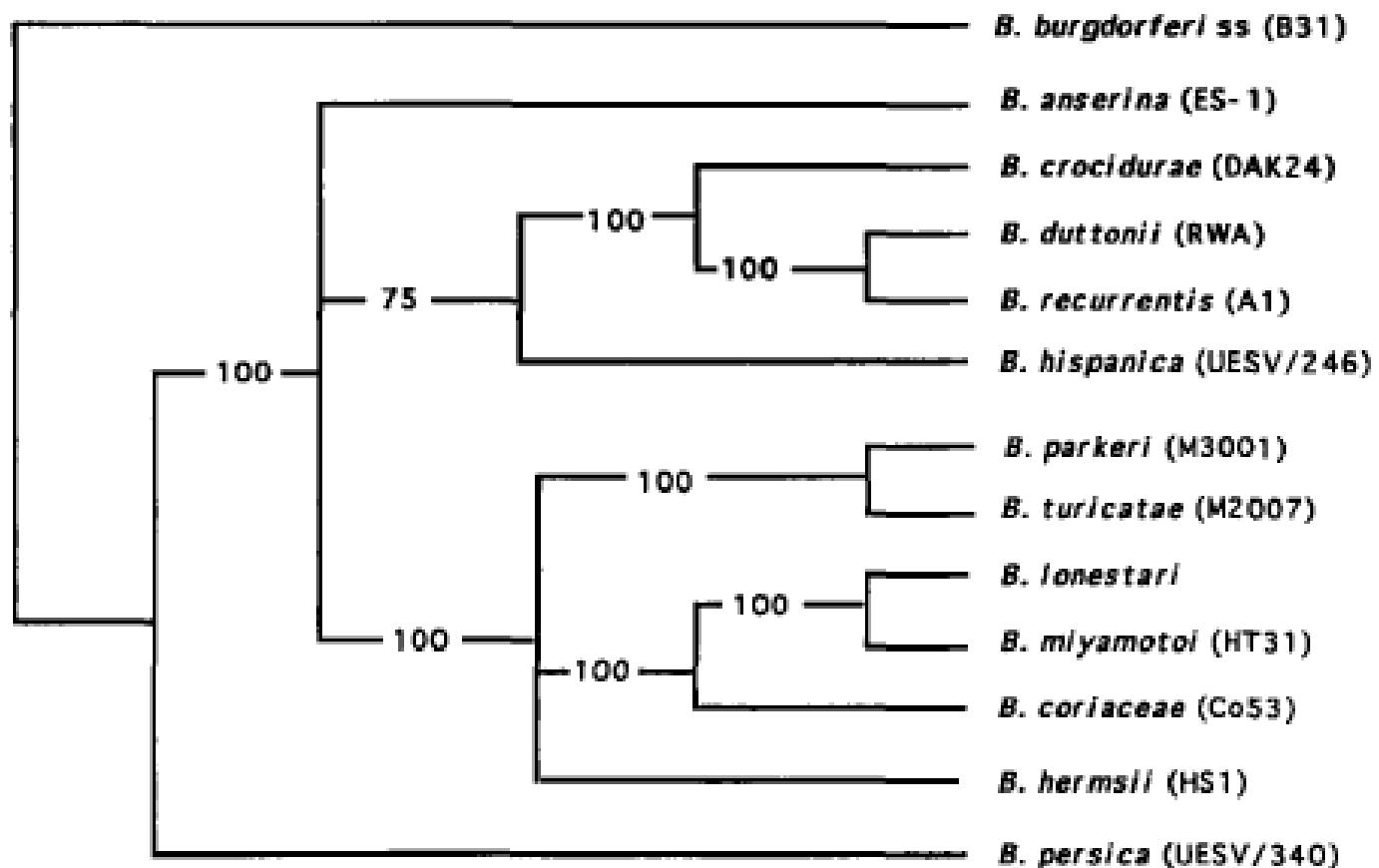


FIG. 2. Phylogenetic tree based on a comparison of the 16S rRNA sequences of RF *Borrelia* species. This 50% majority rule consensus tree based on 12 trees was obtained by using a maximum-parsimony method.

Maladie de Lyme: Erythème migrant



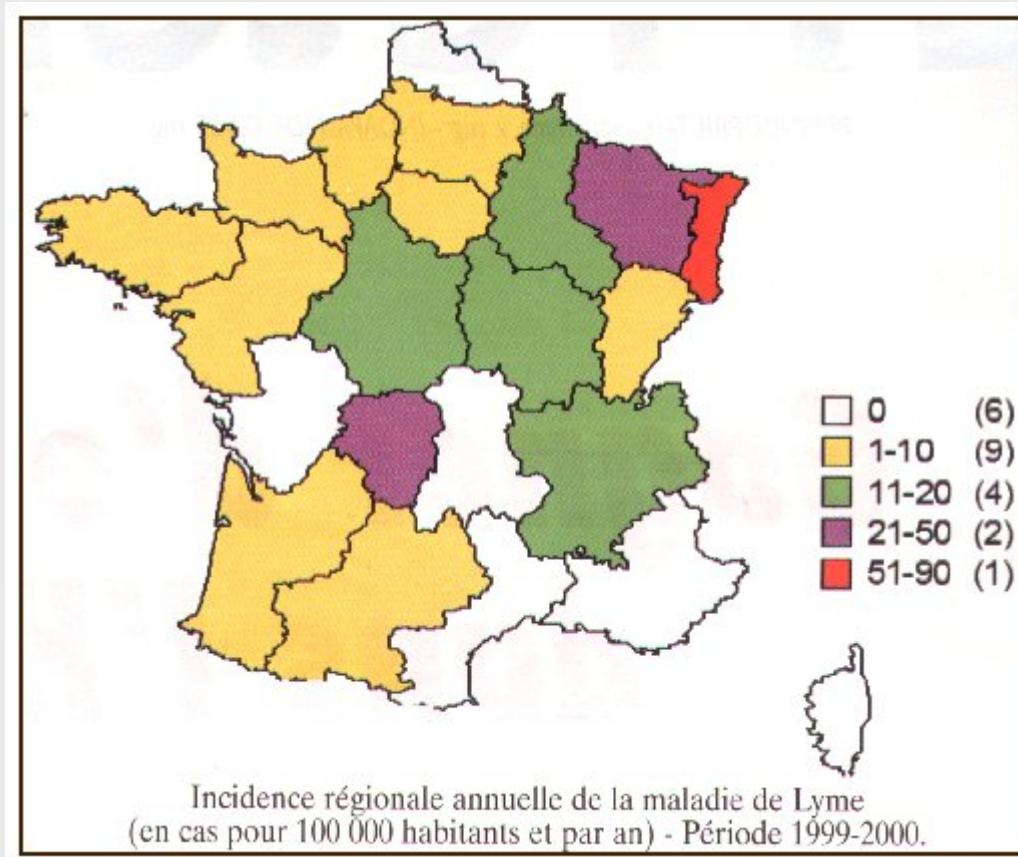
Maladie de Lyme: une infection véctorisée



Maladie de Lyme: USA



Maladie de Lyme: France



Borrélioses récurrentes

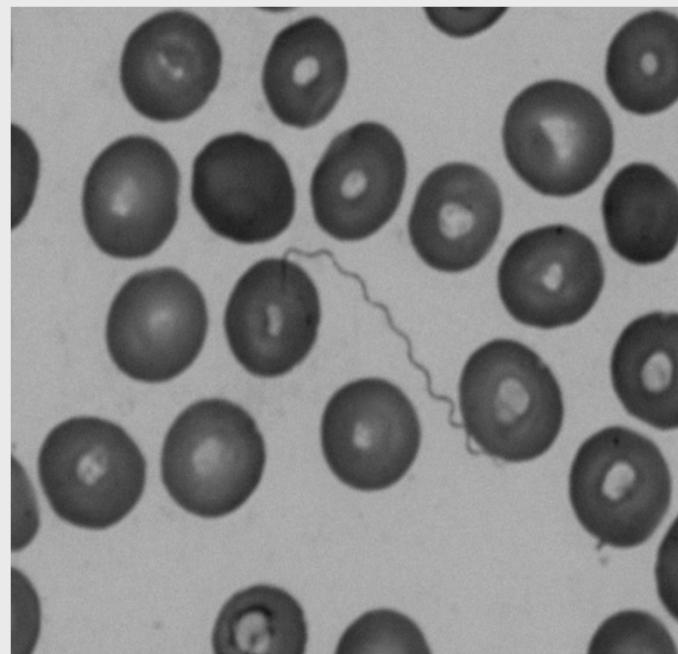
A 24-year-old man was hospitalised in February 2008 for fever, rigors and myalgia. The patient had visited his relatives in Marena's area, Mali for 2 months in December and January 2008. The patient recalled rat bite. He had no antimalarial prophylaxis.

At the end of January, he consulted in a local hospital in Mali for fever, headaches and rigors and was given intravenous quinine. The patient has been vaccinated against hepatitis A virus, yellow fever virus and diphtheria but did not benefit from anti malaria prophylaxis. Clinical examination found a high grade fever of 39°6 C, heart rate of 91/mn and bilateral inguinal lymph nodes. The electrocardiogram was normal.

Pertinent laboratory parameters included leukocytes of 6.34 Giga/liter with polymorphonuclear leucocytes of 4.61 Giga/liter, haemoglobin of 13.8 Giga/liter and platelet of 121 Giga/liter. Fibrine level was 6.88 Giga/liter and C-reactive protein of 290 mg/L. ALAT was 88 IU and ASAT of 92 IU. Three blood cultures remained sterile and serology for hepatitis B virus, hepatitis C virus, *Coxiella burnetii*, syphilis and human immunodeficiency virus were negative.

Thin blood smear did not find *Plasmodium* parasites.

Here's the patient's blood film
after giemsa staining



What's your diagnosis ?

Further microbiological investigations

16S rDNA sequencing : 100% sequence similarity with 10 homologous sequences for *B. crocidurae* and 7 homologous sequences for *B. recurrentis*

Fla sequencing : 100% sequence similarity with homologous sequence for *B. crocidurae*, *B. duttonii* and *B. recurrentis*.

16S-23S rDNA intergenic spacer (IGS) sequencing : 567/570 (99%) base position identical to *B. crocidurae* (GenBank accession number DQ000287) and 542/575 (94%) base positions identical to *B. duttonii* (GenBank accession number DQ000282).

And the diagnosis was...

Borrelia crocidurae infection

NOM : Prénom : Sexe :
Date de naissance:

Hôpital/Service: APHP Pompidou Med int
Médecin/Tel : Dr Planturu (interne) 01 56 09
27 86

Borrelia

SYMPTOMATOLOGIE

- Date de début des symptômes :
- Durée d'incubation:
- Fièvre
- X Escarre unique / localisation : interieur du bras G infra centimétrique (pas de BCU, escarre tombé pdt le we du 7/03)**
- Escarres multiples / localisation :
- X radiculite objectivée à l'EMG**
- X placard érythémateux sur la face interne du bras gauche**
- Rash : Maculo-papuleux Purpurique Vésiculeux
- Confusion Syndrôme méningé Forme maligne

EPIDEMIOLOGIE

- X Lieu / date : Ethiopie en janvier 2010, piqûre sur les hauts plateaux d'éthiopie**
- X Piqûre de tique : intérieur du bras G partiellement retirée avec une pince à épiler le 20/01/10**
- Piqûre de puce/ Identification :
- Piqûre de pou :
- Piqûre d'autre insecte / Identification :
- Piqûre unique / localisation :
- Piqûres multiples/ localisation :
- X Contact avec des animaux : singe**
- Contact avec les chats

TRAITEMENT : Antibiotique / molécule: doxy 15 j, amélioration cutanée mais pas d'amélioration neuro, rocéphine 3 semaines

PHOTO: OUI NON

NB: séro rick neg chez eux, lyme IgG pos

| Date | smarlab | Bartonella | | C. burnetii | | Rickettsies | | F. tularensis | | Borrelia | | 16S |
|------------|------------|------------|-----|-------------|-----|-------------|-----|---------------|-----|-----------|-------|-----|
| | | Sérologie | PCR | Sérologie | PCR | Sérologie | PCR | Sérologie | PCR | Sérologie | PCR | |
| 19/03/2010 | 25/02/2183 | | | | | | neg | | | | 33,49 | |
| | | | | | | | | | | | | |

WB pos, séro IgG lyme pos



2010, CMIP, Dr PHC

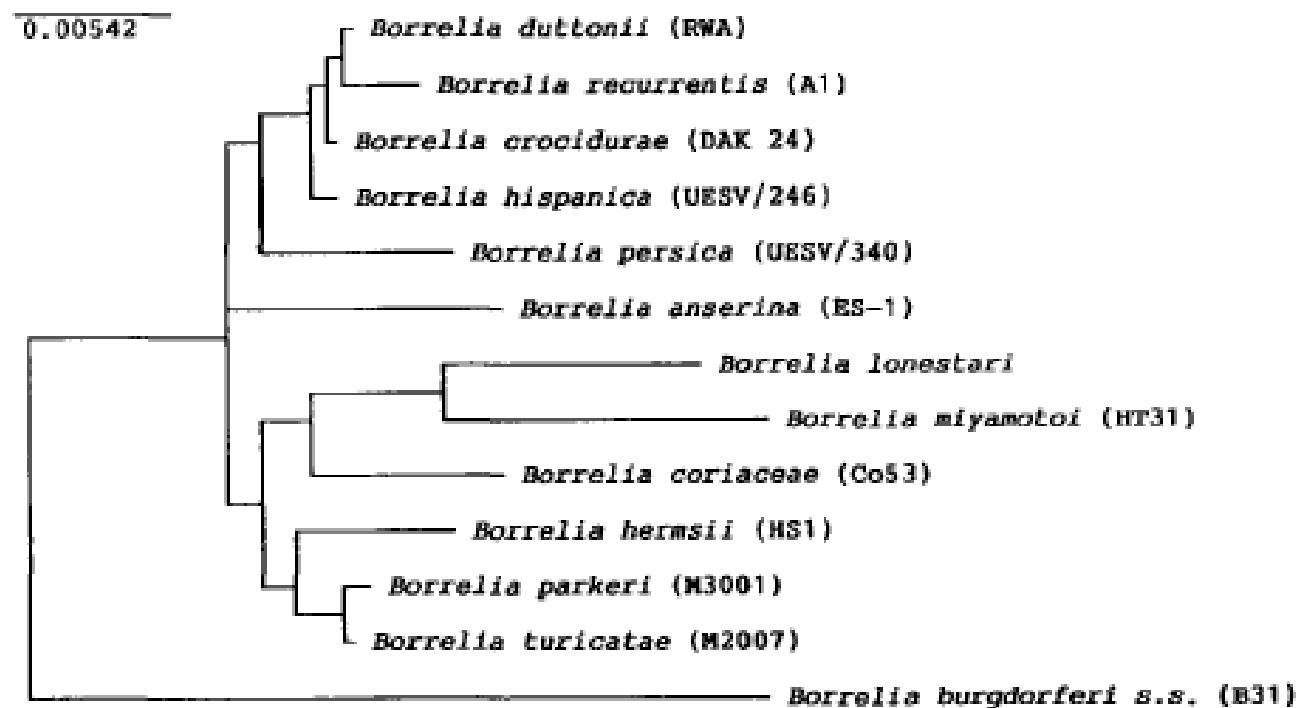


FIG. 1. Phylogenetic tree based on a comparison of the 16S rRNA sequences of RF *Borrelia* species. The branching pattern was generated by the neighbor-joining method.

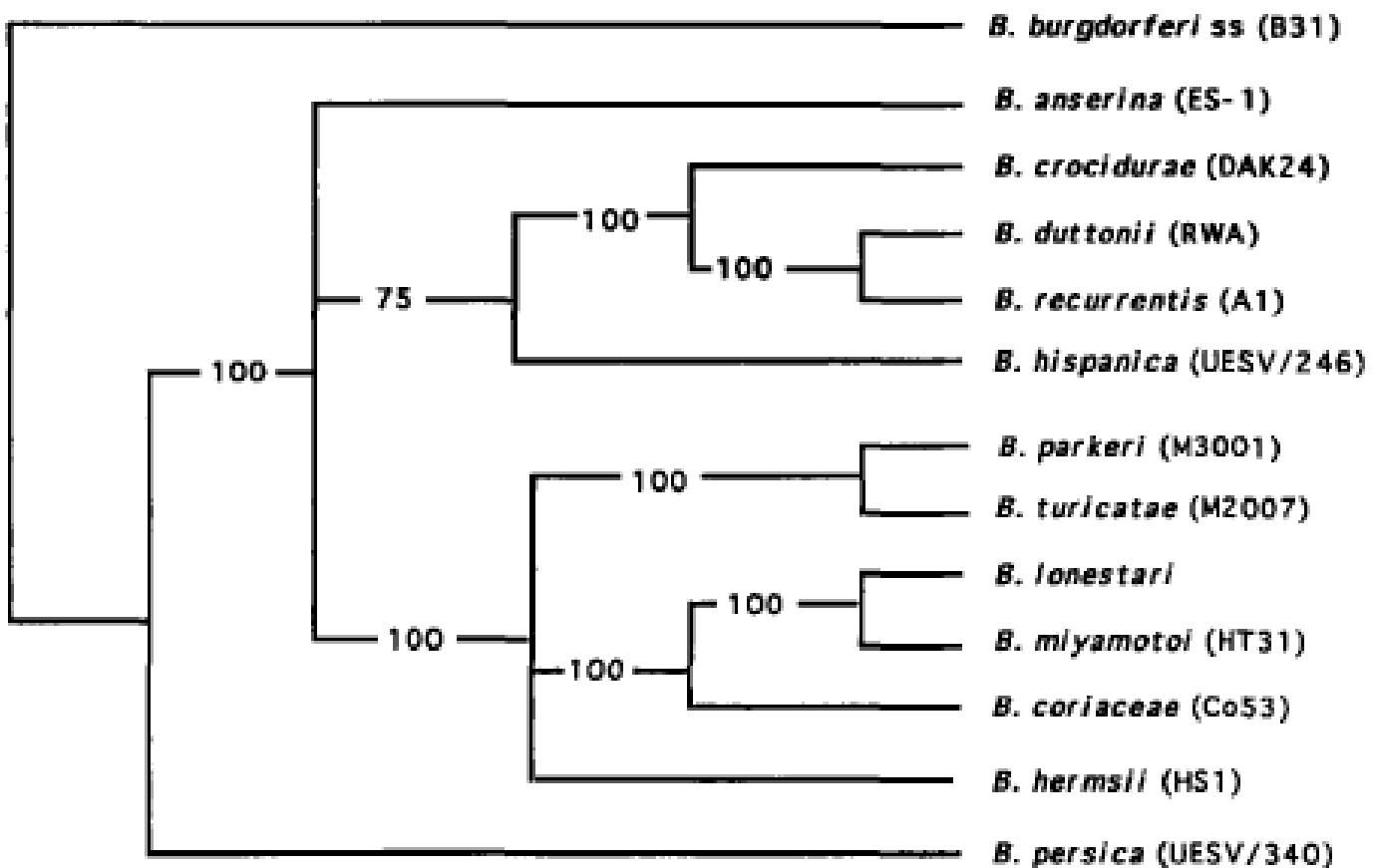


FIG. 2. Phylogenetic tree based on a comparison of the 16S rRNA sequences of RF *Borrelia* species. This 50% majority rule consensus tree based on 12 trees was obtained by using a maximum-parsimony method.

ORNITHODOROS SOFT TICKS COLLECTED INSIDE HUMAN DWELLINGS FROM DIELMO AND NDIOP VILLAGES, SINE-SALOUM, SENEGAL



Burrow examined in a pantry from Ndiop village



Burrow examined in a bedroom from Dielmo village



Ticks Vector: *Ornithodoros sonrai* group; Taille: 3-4 mm

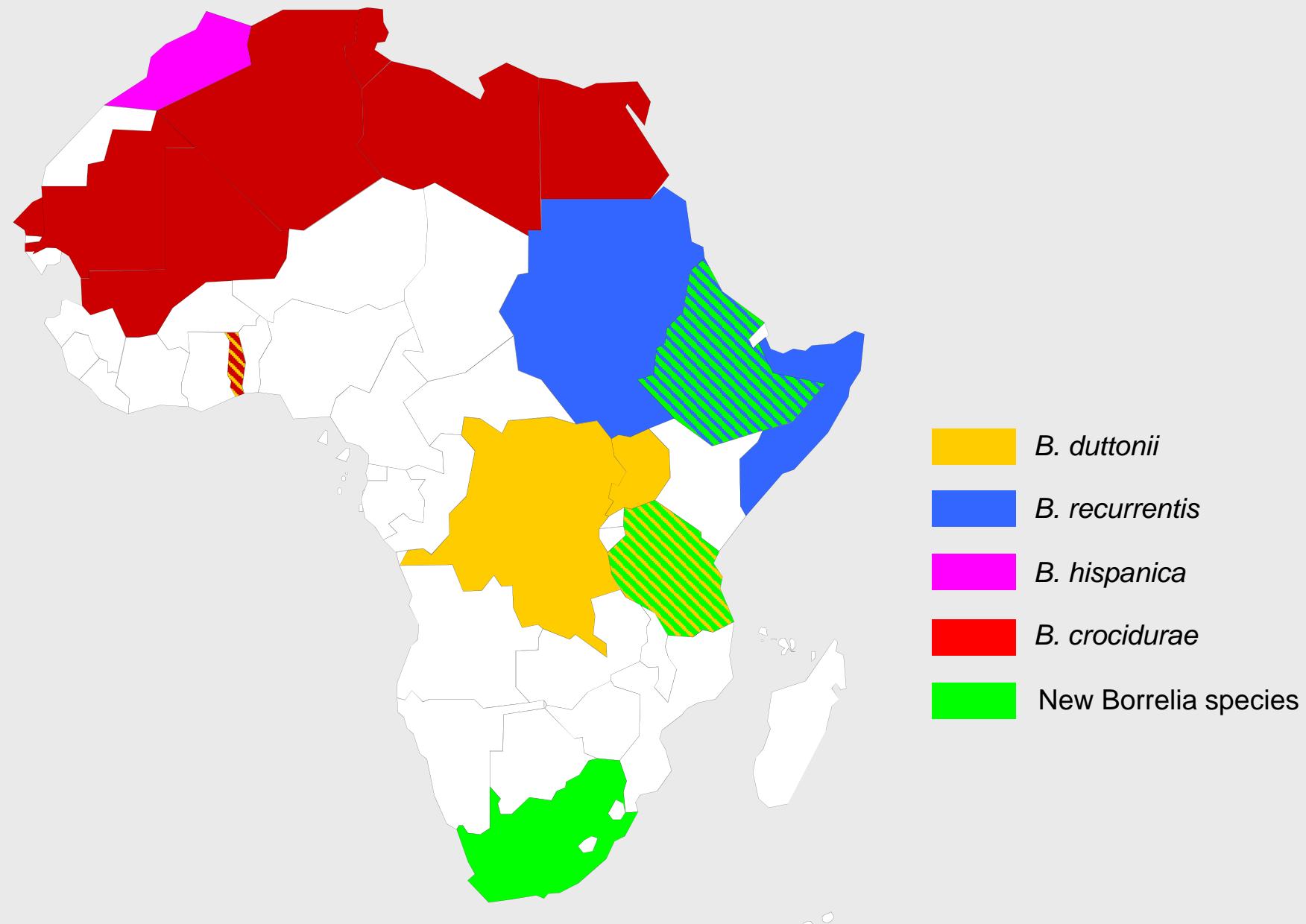


Burrow examined in a bedroom from Ndiop village

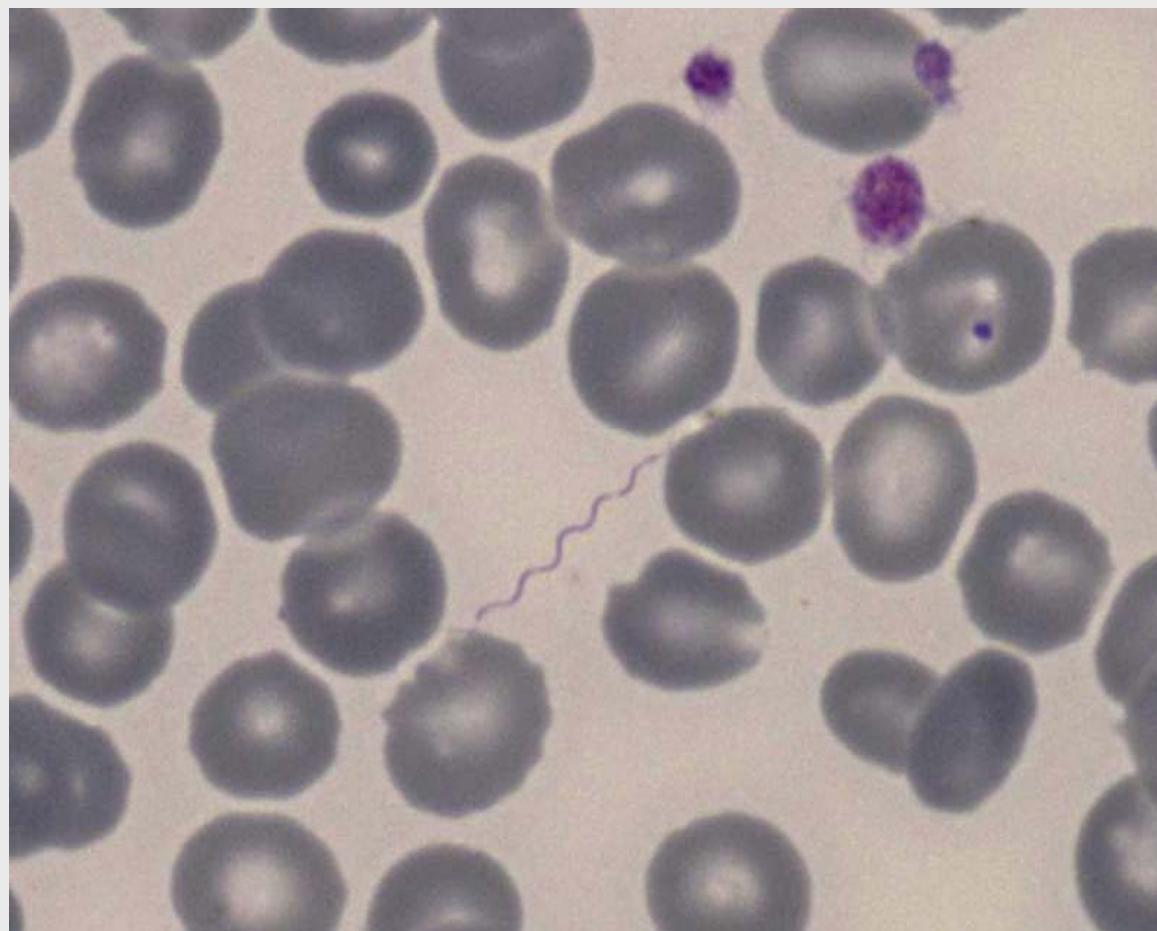


Burrows examined in a bedroom from Dielmo village

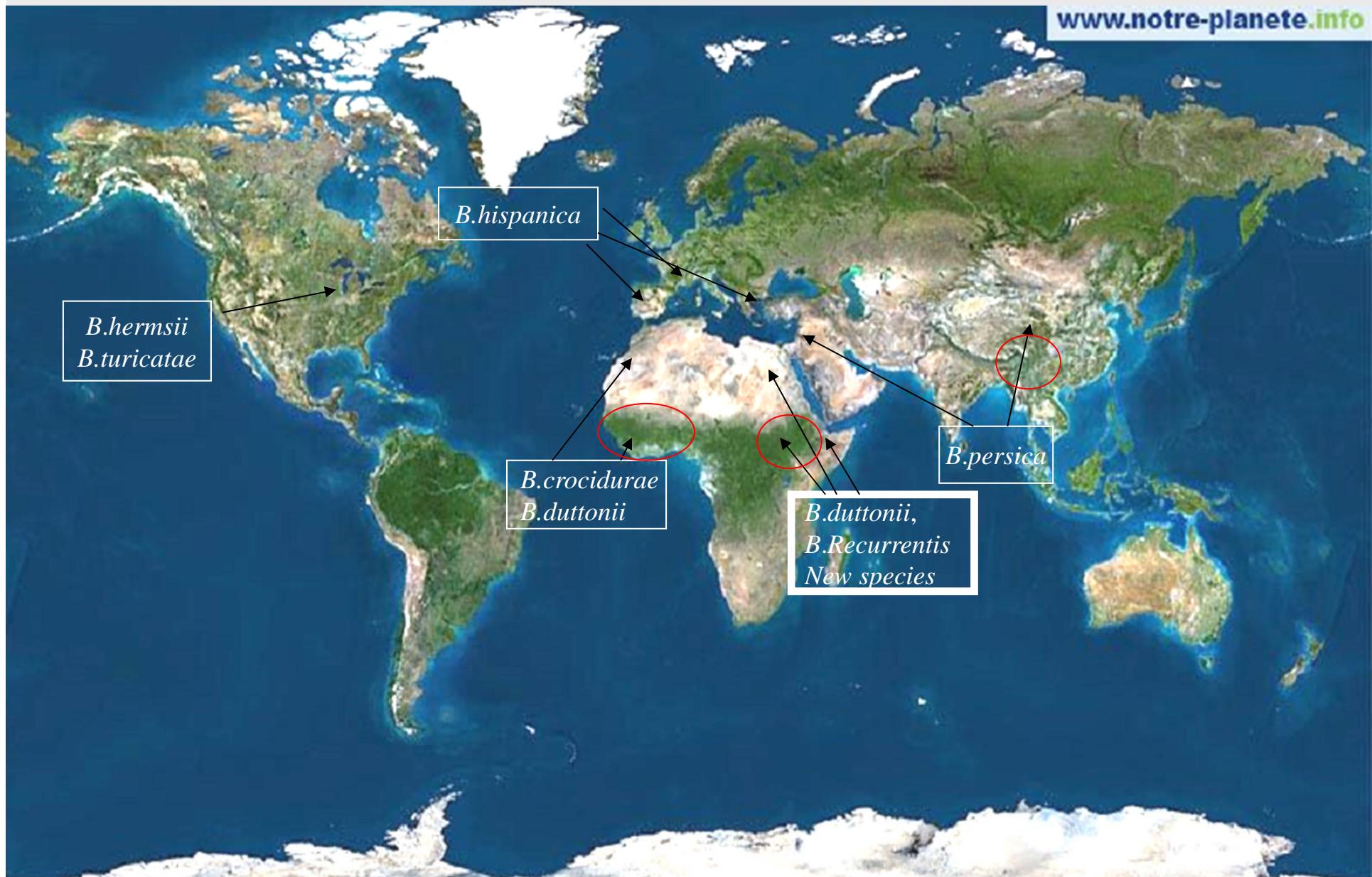
Relapsing fever borreliae in Africa



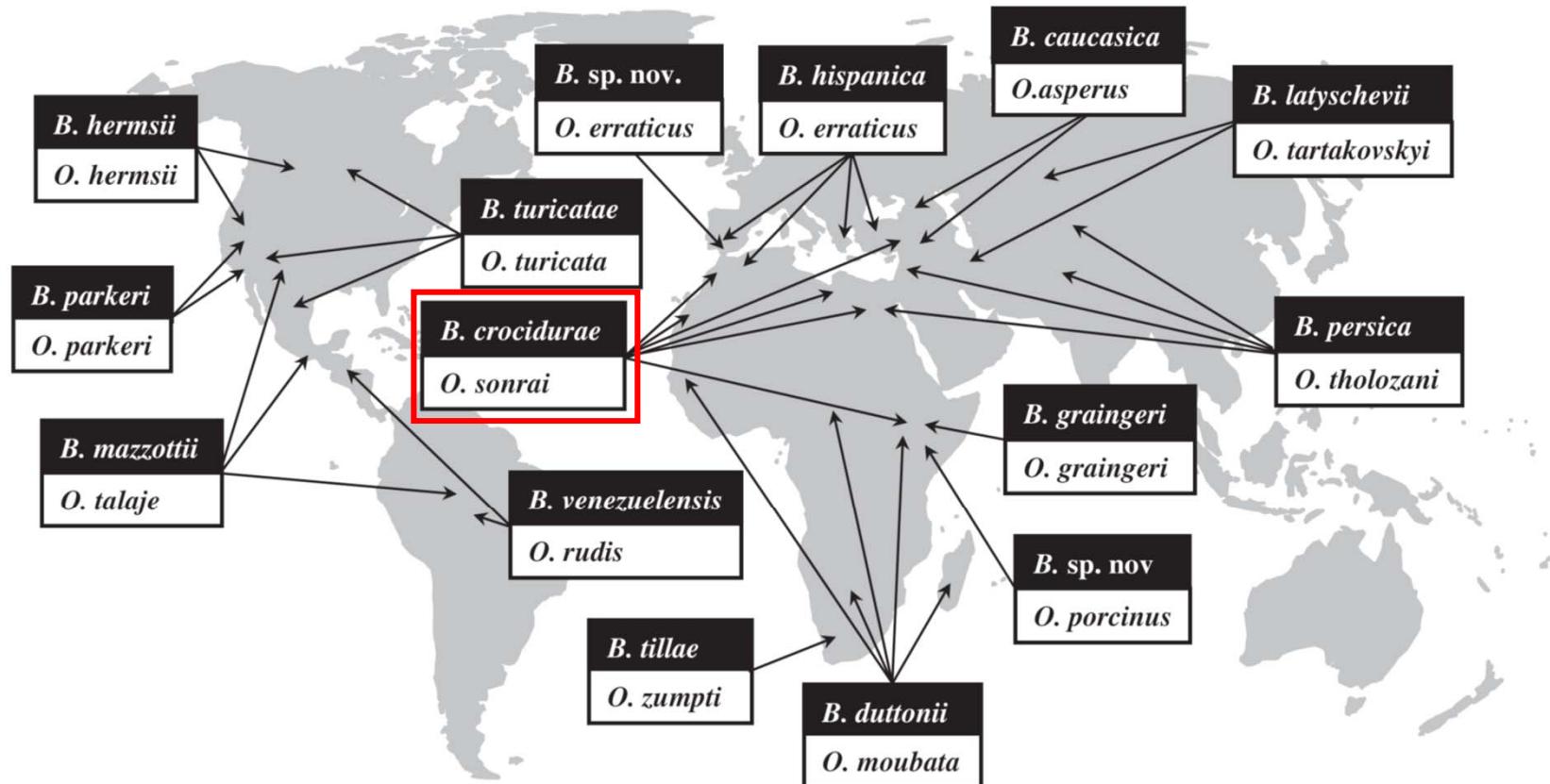
Diagnostic direct: examen microscopique



Worldwide distribution of RFG Borrelia spp.



Distribution of tick-borne relapsing fever borreliosis agents and their specific vectors of the genus *Ornithodoros*



Rebaudet S, Parola P. Epidemiology of relapsing fever borreliosis in Europe. FEMS Immunol Med Microbiol. 2006;48:11-15.

Body Lice and their Infecting Bacteria Around the World

