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The genomic structure of *Brucella* strains isolated from marine mammals gives clues to evolutionary history within the genus.

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Abstract

The genomic structure and the restriction maps were studied in 24 Brucella strains isolated from marine mammals. From SpeI restriction profiles, the strains could be ascribed to three clonal groups, each corresponding to a specific host. Cross contamination between exclusively terrestrial and exclusively marine hosts is unlikely suggesting the divergence of the different species of the genus Brucella may have taken place 60 million years ago, concomitant with the radiation of their mammalian hosts (Artiodactyla) from other mammalian orders.

Key words: Brucella; genomic organisation; physical map; evolution; marine mammal; PFGE

1. Introduction

Brucella is a small Gram negative bacterium usually isolated from ruminants, pigs and rodents. Classically the genus is divided into six species which are further subdivided into several biovars, each infecting a preferential but not exclusive host (Boschiroli et al., 2001). From the mid 1990s Brucella-like bacteria were isolated from carcasses of marine mammals, such as seals, dolphins, porpoises and whales. These bacteria have been found in a wide range of tissues and have been shown to cause both abortion and meningoencephalitis (Foster et al., 2002; Ohishi et al., 2003; Miller et al., 1999; Gonzalez et al., 2002) however very few human infections have been reported (Sohn et al., 2003; Brew et al., 1999; McDonald et al., 2006). These strains isolated form marine mammals could not be ascribed to the known six species based on classical typing methods but could, however, be subdivided into three groups based on CO₂ dependence, galactose oxidation, dominant antigen and animal host (Jahans et al., 1997).
Over the past few years, molecular analysis using DNA/DNA hybridization and ribotyping (Verger et al., 2000), genomic fingerprinting of XbaI profiles using PFGE (Jensen et al., 1999), analysis of insertion sequence profiles (Cloeckaert et al., 2000) and DNA polymorphism in outer membrane protein genes (Cloeckaert et al., 2001a; Vizcaino et al., 2004), has confirmed that the marine strains are genetically distinct from the terrestrial strains and, therefore, two new species, *Brucella pinnipediae* (group I strains) and *Brucella cetaceae* (group II and III strains) have been proposed (Cloeckaert et al., 2001b). However, these names have not yet been validly published and there remains some debate about the genetic relationships within this group. Here we present the physical maps of the genomes of three representative strains of marine *Brucella* which suggest that the group II and III strains represent two distinct species.

**2 Materials and Methods**

**2.1 Bacterial Strains**

The *Brucella* strains used in this study and their hosts are listed in Table 1. Isolates were from seals, dolphins, porpoises, an otter and a minke whale (Jahans et al., 1997; Clavareau et al., 1998).

**2.2 Pulsed Field Gel Electrophoresis**

PFGE was performed as previously described (Jumas-Bilak et al., 1995; Michaux-Charachon et al., 1997). Briefly, intact genomic DNA was prepared from bacterial embedded in agarose plugs and subjected to PFGE (BioRad CHEF DRII), either undigested or after digestion with *PacI* or *SpeI*. Pulse conditions are described in figure legends.
2.3 Phylogenetic Analysis

Similarity between strains was calculated as the Dice coefficient as described by Grothues and Tummler (Grothues and Tummler, 1991) and clustered using the Phylip programme.

3. Results and Discussion

3.1 Restriction fragment length polymorphism (RFLP) within marine Brucella strains.

The genomes of Brucella marine strains contain two chromosomes with sizes of about 2.1 Mb and 1.15 Mb, similar to that of the reference strain of the genus, B. melitensis 16M (data not shown). The macrorestriction profiles obtained for genomic DNA digested by SpeI are shown in Fig. 1. The restriction patterns fell into three groups that were identical to the groups defined by Jahans et al. (Jahans et al., 1997) based on classical typing methods. The group I pattern was found in strains isolated from common, grey and hooded seals, and an otter, group II pattern in strains isolated from common and striped dolphins and group III pattern in strains isolated from porpoises, a white-sided dolphin and a mink whale. One 182 kb fragment was missing from two group I strains (39-94 and 44-94; isolated from common seals). Strain 56-94 (isolated from a hooded seal) shows the most divergence from the group as it lacks the 182 kb fragment, a 62 kb and has other minor differences in the 20-30 kb region. The 62 kb fragment missing from strain 56-94 is specific to group I strains, since it failed to hybridize with genomic DNA from any of the classical Brucella species or other marine mammal strains (not shown). Comparison of the published Brucella genome sequences (Paulsen et al., 2002; Halling et al., 2005; DelVecchio et al., 2002) suggests that such species specific regions are rare in the genus, however, we have previously reported a 34kb SpeI fragment specific to B. ovis (Michaux-Charachon et al., 1997). Digestion of the genomic DNA of the same strains by XbaI gives a similar strain grouping (Jensen et al.,
1999). In group II strains, an inversion in the large chromosome (see below) has increased
the size of the 330kb fragment to 390 kb in strain 5-94.

3.2 Restriction mapping of the *Brucella marine isolates*. The *Pac* I and *Spe* I restriction
maps and localization of *rrn* loci and insertion sequences were determined as described
previously (Michaux-Charachon *et al.*, 1997; Jumas-Bilak *et al.*, 1998). The maps are shown
in Fig. 2, together with the previously published map of *B. melitensis* 16M (Michaux-
Charachon *et al.*, 1997). The location of the restriction sites on the large chromosome of the
marine strain shows few modifications when compared to that of *B. melitensis*. In a dolphin
isolate, strain 5-94, there is a large inversion of at least 550 kb in the large chromosome.
This rearrangement was first suggested by our observation that the 305 kb and 420 kb *Spe* I
fragments from *B. melitensis* both hybridized with the 390 kb and 260 kb *Spe* I fragments of
strain 5-94. The two fragments flanking the inversion contain copies of IS650/IS711,
suggesting a possible role for the insertion sequence in the rearrangement. On the contrary,
the maps of the small chromosome differed greatly from one strain to another, with numerous
indels (including the 62 kb *Spe* I fragment unique to the seal isolates) and/or with creation or
loss of restriction sites. The reason for this observation is unknown. All the strains contained
three *rrn* loci, two in the large chromosome and one in the small.

3.3 Phylogenetic analysis of the marine *Brucella isolates*. A phylogenetic tree (Fig. 3) was
obtained from the restriction data to complete the tree proposed previously (Michaux-
Charachon *et al.*, 1997). The tree is unrooted, since the macrorestriction patterns are very
specific for *Brucella* and definition of a related extra group to place the root is artificial. The
marine isolates form a new group, which originates very near the *B. ovis* branch. Within this
group, the three clones are separated from each other by branches that are deeper than those
between members of the *melitensis-abortus* group or the *suis* group. This suggest a probable ancient divergence of the three restriction groups described within the marine isolates.

3.4 Evolutionary history of the *Brucella* genus

The genus *Brucella* was proposed to be monospecific based on the high levels of homology revealed by DNA-DNA hybridization (Verger et al., 1985). This, however, does not reflect the 'classical' classification based on phenotypic characteristics and host specificity and recently the 'classical' system has been readopted. Since *Brucella* grow poorly in the environment and since each species infects a preferential host, we and others proposed that each species is an evolutionary line adapted to a particular mammalian host (Michaux-Charachon et al., 1997; Moreno et al., 2002; Michaux-Charachon et al., 2002). It has been proposed that *B. suis* is the closest to the common ancestor of the genus (Moreno et al., 2002; Jumas-Bilak et al., 1998). Recent investigation of the distribution of a 18.3 kb genomic island inserted downstream of *guaA* supports this theory, being present in the genomes of *B. suis*, *B. neotomae* and the marine strains, but not *B. ovis*, *B. abortus* and *B. melitensis* (Lavigne et al., 2005). Interestingly, three point mutations in the 23S *rrn* gene group the marine strains with *B. melitensis*, *B. ovis* and *B. neotomae* (Halling and Jensen, 2006), giving rise to the question of whether the loss of the *incP* island occurred once or at different times during the evolution of the genus. The divergence could be concomitant either with the radiation of mammalian species, since each natural host harbors a particular clone, or with the emergence of domestication, allowing cross-contamination by close contact of different animal species. The phylogeny of the marine strains supports arguments for a divergence of the *Brucella* strains concomitant with the radiation of mammals, since each of the different hosts is infected by a specific clone and cross contamination between exclusively terrestrial and exclusively marine hosts is unlikely. Moreno et al (Moreno et al., 2002) have suggested that *B. abortus* and *B. melitensis* became
isolated about 20 million years ago with the radiation of the artiodactyls. This isolation could be more ancient, since seals and otters belong to the order of Carnivora, which diverged from the Artiodactyla more than 60 million years ago, and since wild rodents, another anciently isolated order, are natural hosts for *B. suis*. However, a cross-contamination cannot be excluded in this last case, rodents and wild pigs having similar territories. Finally, our results further highlight how the results of the classical typing methods reflect the groups defined by genome organization. From the tree in Fig 3 (where the length of a branch is represents evolutionary distance), we divergence between the three marine groups is far greater than that between, for example, *B. melitensis* and *B. abortus*, suggesting that the three groups could each be classified as a separate species. Further, recent data from both VNTR and MLST typing also suggest that the strains can be divided into three groups (A Whatmore, personal communication). These data are compatible with the proposition in the latest Bergey's Manual of three new species; *B. phocae* (seals), *B. phoecoenae* (porpoises) and *B. delphini* (dolphins) (Corbel and Banai, 2005). Determination of the complete genome sequences of these, and more *Brucella* strains is the next step in deciphering their evolutionary history.

4. Acknowledgments

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Ref Type: Generic


Ref Type: Generic

Table 1. *Brucella* strains included in this study.

<table>
<thead>
<tr>
<th><em>Brucella</em> strain</th>
<th>Host</th>
<th>Vernacular name</th>
<th>Scientific name</th>
</tr>
</thead>
<tbody>
<tr>
<td>Group I*</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2-94</td>
<td>Common seal</td>
<td>Phoca vitulina</td>
<td></td>
</tr>
<tr>
<td>40-94</td>
<td>Common seal</td>
<td>Phoca vitulina</td>
<td></td>
</tr>
<tr>
<td>41-94</td>
<td>Common seal</td>
<td>Phoca vitulina</td>
<td></td>
</tr>
<tr>
<td>48-94</td>
<td>Common seal</td>
<td>Phoca vitulina</td>
<td></td>
</tr>
<tr>
<td>46-94</td>
<td>Common seal</td>
<td>Phoca vitulina</td>
<td></td>
</tr>
<tr>
<td>54-94</td>
<td>Common seal</td>
<td>Phoca vitulina</td>
<td></td>
</tr>
<tr>
<td>61-94</td>
<td>Grey seal</td>
<td>Halichoerus grypus</td>
<td></td>
</tr>
<tr>
<td>55-94</td>
<td>Otter</td>
<td>Lutra lutra</td>
<td></td>
</tr>
<tr>
<td>39-94</td>
<td>Common seal</td>
<td>Phoca vitulina</td>
<td></td>
</tr>
<tr>
<td>44-94</td>
<td>Common seal</td>
<td>Phoca vitulina</td>
<td></td>
</tr>
<tr>
<td>56-94</td>
<td>Hooded seal**</td>
<td>Cystophora cristata</td>
<td></td>
</tr>
<tr>
<td>Group II</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>47-94</td>
<td>Common dolphin</td>
<td>Delphinus delphis</td>
<td></td>
</tr>
<tr>
<td>14-94</td>
<td>Common dolphin</td>
<td>Delphinus delphis</td>
<td></td>
</tr>
<tr>
<td>59-94</td>
<td>Striped dolphin</td>
<td>Stenella coeruleoalba</td>
<td></td>
</tr>
<tr>
<td>5-94</td>
<td>Striped dolphin</td>
<td>Stenella coeruleoalba</td>
<td></td>
</tr>
<tr>
<td>Group III</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>202-R</td>
<td>Mink whale</td>
<td>Balaenoptera acutorostrata</td>
<td></td>
</tr>
<tr>
<td>49-94</td>
<td>White-sided dolphin</td>
<td>Lagenorhynchus actus</td>
<td></td>
</tr>
<tr>
<td>1-94</td>
<td>Harbour porpoise</td>
<td>Phocoena phocoena</td>
<td></td>
</tr>
<tr>
<td>34-94</td>
<td>Harbour porpoise</td>
<td>Phocoena phocoena</td>
<td></td>
</tr>
<tr>
<td>35-94</td>
<td>Harbour porpoise</td>
<td>Phocoena phocoena</td>
<td></td>
</tr>
<tr>
<td>36-94</td>
<td>Harbour porpoise</td>
<td>Phocoena phocoena</td>
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<td>45-94</td>
<td>Harbour porpoise</td>
<td>Phocoena phocoena</td>
<td></td>
</tr>
<tr>
<td>52-94</td>
<td>Harbour porpoise</td>
<td>Phocoena phocoena</td>
<td></td>
</tr>
<tr>
<td>57-94</td>
<td>Harbour porpoise</td>
<td>Phocoena phocoena</td>
<td></td>
</tr>
</tbody>
</table>

* Groups I, II and III contain strains with a similar *SpeI*-restriction pattern.
** The *SpeI* profile of this isolate differs from the other strains included in this group by the absence of a 62 kb fragment.
Figure Legends

Figure 1. Pulsed field gel electrophoresis of SpeI-digested DNA from Brucella marine isolates. SpeI fragments were separated in a contour clamped electric field apparatus (CHEF-DRII Biorad) with pulse ramps of 35 s - 4 s for 40 h at 180 V. The strains are organized as described in Table 1. λ concatamer size markers are on the left of the figure. Patterns of SpeI-digests of B. melitensis 16M, B. abortus 544 and B. suis 1330 DNA are shown at the right. Arrowheads indicate bands migrating differently or absent.

Figure 2. SpeI-PacI restriction maps of the chromosomes of B. melitensis 16M, strains 59-94 and 5-94 (isolated from dolphins), 34-94 (isolated from a porpoise) and 2-94 (isolated from a seal). The two circular chromosomes are represented in linear form, each one starting from a conserved SpeI fragment. A: large chromosomes; B: small chromosomes. For each chromosome map, SpeI sites are located above, and PacI sites below. Sizes are given in kilobases for all the restriction fragments of the B. melitensis chromosomes, and only for those different from B. melitensis for the other species. Fragments carrying rrm loci are represented by open squares, and fragments carrying IS6501/IS711 copies by stars. The inversion in the large chromosome of strain 5-94 is shown by two broken lines.

Figure 3. Phylogenetic tree of the marine isolates and the different species and biovars of the genus Brucella (modified from Boschiroli et al., 2001). The terrestrial strains are represented by the reference strains for each species and/or biovar using data from (Michaux-Charachon et al., 1997). B. abortus contains two major groups, represented by Bv 1 and 5, due to the 600kb inversion in the small chromosome in certain strains.