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Strain typing of Mycoplasma cynos isolates from dogs with
respiratory disease
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Abstract
The association of Mycoplasma cynos with canine infectious respiratory disease is
increasingly being recognised. This study describes the strain typing of 14 M. cynos
isolates cultured from trachea and bronchoalveolar lavage samples of six dogs with
respiratory disease, from two separate kennels in the United Kingdom. The genetic
similarity of the isolates was investigated using pulsed-field gel electrophoresis
(PFGE) and random amplified polymorphic DNA (RAPD). Most of the isolates from
four dogs housed at a re-homing kennel were genetically similar and some isolates

25	from different dogs were indistinguishable by both PFGE and RAPD. These isolates
26	were cultured from dogs with non-overlapping stays in the kennel, which may
27	indicate maintenance of some strains within kennels. A small number of isolates
28	showed much greater genetic heterogeneity and were genetically distinct from the
29	main group of <i>M. cynos</i> strains. There was also a high degree of similarity of the <i>M</i> .
30	cynos type strain (isolated from a dog with respiratory disease in Denmark in 1971) to
31	at least one of the United Kingdom isolates using PFGE analysis, which may suggest
32	possible conservation of pathogenic strains of <i>M. cynos</i> .
33	
34	
35	Keywords
36	Mycoplasma cynos; canine infectious respiratory disease (CIRD); kennel cough;
37	PFGE; RAPD
38	
39	
40	1. Introduction
41	Canine infectious respiratory disease (CIRD or kennel cough) is a multifactorial
42	disease complex and the agents traditionally associated with this disease are
43	Bordetella bronchiseptica, canine parainfluenza virus (CPIV), canine adenovirus
44	(CAV), and canine herpesvirus (Chvala et al.). Recently, a novel canine respiratory

- 45 coronavirus (CRCoV; (Erles et al., 2003) and *Streptococcus equi* subsp.
- 46 *zooepidemicus* (Chalker et al., 2003a) have also been found to be associated with the

47 disease.

49 Within this microbial complex, *Mycoplasma* spp. are found to be ubiquitous in the 50 upper respiratory tract of dogs and are thought to be normal flora (Rosendal, 1982; 51 Randolph et al., 1993). However, mycoplasmas have also been the sole bacterial 52 isolate in a number of clinical cases of canine respiratory disease, but unfortunately 53 these isolates were not speciated and viral causes of CIRD were not investigated 54 (Kirchner et al., 1990; Jameson et al., 1995; Chandler and Lappin, 2002). The involvement of M. cynos in CIRD has been noted for some time (Rosendal, 1972, 55 56 1978, 1982). Evidence for this has been mounting recently, as Chalker et al. (2004) 57 found that *M. cynos* was the only mycoplasma significantly associated with canine 58 respiratory disease. In addition, dogs entering a re-homing kennel that developed an 59 antibody response to *M. cynos* were more likely to suffer respiratory disease (Rycroft 60 et al., 2007). M. cynos has been isolated from dogs with pneumonia (Rosendal, 1972, 61 1978; Chvala et al., 2007) and was particularly abundant in the most necrotic areas of 62 the lung (Chvala et al., 2007). Furthermore, M. cynos was the only detected agent in a 63 case of severe bronchopneumonia in a litter of young puppies which resulted in the 64 deaths of some puppies, but which was resolved in the surviving littermates after the 65 administration of appropriate antibiotics (Zeugswetter et al., 2007).

66

Recently molecular epidemiological studies of isolates of the *Mycoplasma* species *M*. *bovis* (Kusiluka et al., 2000; McAuliffe et al., 2004), *M. ovipneumoniae* (Parham et
al., 2006) *M. gallisepticum* and *M. synoviae* (Feberwee et al., 2005) have been
conducted using the genetic typing techniques amplified fragment length
polymorphism (AFLP), random amplified polymorphic DNA (RAPD) and pulsedfield gel electrophoresis (PFGE). This is the first genetic typing study performed on *M. cynos*.

74	
75	
76	2. Materials and Methods
77	2.1. Mycoplasma cynos isolates
78	Mycoplasma cynos isolates cultured from respiratory samples from dogs with
79	moderate to severe respiratory disease were identified from an earlier large study.
80	Isolation and identification of these isolates has been previously described (Chalker et
81	al., 2004). Briefly, bronchoalveolar lavage (BAL) and trachea samples were obtained
82	from euthanized dogs from a re-homing centre with a history of endemic CIRD
83	(population A). Alternately, BAL samples were taken from dogs with persistent
84	coughs at a training centre (population B). Dogs were graded for respiratory signs
85	prior to sampling or euthanasia. Mycoplasma cynos was cultured on Mycoplasma
86	media (Mycoplasma Experience) and identified by PCR specific for the 16S/23S
87	rRNA intergenic spacer region. Cultures of the single-cloned M. cynos isolates were
88	stored frozen at -70°C.
89	
90	The type strain <i>M. cynos</i> H381 NCTC10142 was obtained from the National
91	Collection of Type Cultures (NCTC), Collindale, London.
92	
93	2.2. Bacterial and viral screening
94	Bacteriological screening of the samples has been previously described (Chalker et
95	al., 2003a; Chalker et al., 2003b). Briefly, BAL and trachea samples were inoculated
96	onto MacConkey agar and two blood agar plates (incubated aerobically and
97	anaerobically) and incubated at 37°C. Gram positive, catalase negative, beta-

98 haemolytic colonies were identified as streptococci and sero-grouped into Lancefield

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99	Groups, the	en identified t	to the species	s level with	API 20STREP	(Biomerieux).	Oxidase

- 100 positive colonies with typical *B. bronchiseptica* growth characteristics were identified
- 101 as such with API 20NE.
- 102
- 103 Virus screening of the samples has been previously described (Erles et al., 2004).
- 104 Briefly, RNA and DNA were extracted from the respiratory tissue samples and PCR
- 105 and reverse transcription-PCR were used to detect canine parainfluenza virus (CPIV),

106 canine herpesvirus (Chvala et al.), canine adenovirus (CAV), canine distemper virus

107 (CDV), and canine respiratory coronavirus (CRCoV). In addition, RT-PCR for canine

108 influenza virus (CIV) was carried out using primers AMP227F and AMP622R

109 directed to the M gene (Ellis and Zambon, 2001). Equine influenza virus (H3N8)

110 served as a positive control.

- 111
- 112 2.3. Pulsed-field gel electrophoresis

113 Aliquots (20 ml) of stationary phase *M. cynos* culture (maximum absorbance A₆₀₀ of

approximately 0.3) were used for PFGE analysis. Cells were harvested by

115 centrifugation (3,500 x g for 20 min at 4 $^{\circ}$ C), washed three times with PBS buffer

116 with 10% (w/v) glucose and resuspended in 300 ml cold PBS/glucose buffer. Agarose

117 plugs were made from a 1:1 mixture of 2% low-melting-point agarose (Biorad) and

118 the cell suspension. Plugs were incubated in lysis buffer (10 mM Tris- HCl, 1 mM

119 EDTA, 1% lauroyl sarcosine, 1 mg / ml proteinase K) for 48 h at 56 °C. Plugs were

120 washed four times with Tris-EDTA buffer for 30 min at 4 °C. Slices (2 mm) were cut

- aseptically from plugs and equilibrated in restriction buffer (Promega) for 1 h.
- 122 Subsequently, restriction digestion was performed by using 30 U of *Sma*I (Promega)
- 123 for 16 h according to the manufacturer's instructions. The fragments were resolved on

124	1 % pulsed field certified agarose (Biorad) gels using a CHEF-DRIII system (Biorad)
125	at 6 V/cm, with a running time of 20 h at 14 °C; included angle of 120°; initial pulse
126	time of 4 sec; final pulse time of 40 sec. Gels were stained with ethidium bromide (0.5
127	mg/ml) for 15 min, destained in distilled water for 1h and photographed under UV
128	light. A lambda ladder PFGE marker (Sigma) was used for fragment size
129	determination. The Bionumerics package (Applied Maths) was used for gel analysis
130	and dendrograms were produced using the Jaccard Coefficient and unweighted pair
131	group method using arithmetic averages (UPGMA) cluster analysis.
132	
133	2.4. RAPD
134	The single primer Hum4 5'- ACGGTACACT – 3' (Hotzel et al., 1998) was used for
135	the generation of RAPD profiles. Amplification was performed in a 50 μ l total
136	reaction volume containing 100 ng of DNA sample, 10 mM Tris-HCl (pH 9.0), 1.5
137	mM MgCl ₂ , 50 mM KCl, 0.1% Triton X-100, 0.2 mM each deoxynucleoside
138	triphosphate, and 0.5 U of TaqGold (Perkin-Elmer). Cycling conditions included an
139	initial denaturation step at 94 °C for 5 min, followed by 40 cycles of 94 °C for 15 sec,
140	37 °C for 60 sec and 72 °C for 90 sec. The last cycle included a final elongation at 72
141	°C for 7 min. PCR products were resolved by electrophoresis on 10 cm 2% agarose
142	gels at 60 mA for 1.5 h, stained with ethidium bromide and visualized under UV
143	illumination. The Bionumerics package (Applied Maths) was used for gel analysis
144	and dendrograms were produced using the Jaccard Coefficient and unweighted pair
145	group method using arithmetic averages (UPGMA) cluster analysis
146	
147	

148 **3. Results**

149	3.1.	Dogs
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150	Six dogs with moderate to severe respiratory disease from which M. cynos was
151	isolated were identified from an earlier large study (Chalker et al., 2004). Four dogs
152	were housed at a re-homing centre with a history of endemic CIRD (population A)
153	and two dogs at a training centre (population B). All six dogs had respiratory disease
154	with symptoms of either bronchopneumonia (respiratory score 5) or cough and nasal
155	discharge (score 3). Trachea and/or BAL samples were taken from the dogs within 4
156	weeks of the first symptoms of CIRD. The dogs were 1-3 years old and of various
157	breeds. The group consisted of entire and neutered males and females (Table 1).
158	
159	3.2. Bacteriology and virology screening
160	Mycoplasma cynos was cultured from the BAL of each dog and also the trachea
161	where that sample was available (Tables 1 and 2).
161 162	where that sample was available (Tables 1 and 2).
	where that sample was available (Tables 1 and 2). Testing of BAL samples from the two dogs from the training centre (B-1 and B-2)
162	
162 163	Testing of BAL samples from the two dogs from the training centre (B-1 and B-2)
162 163 164	Testing of BAL samples from the two dogs from the training centre (B-1 and B-2) was negative for the viruses CRCoV, CHV, CPIV, CAV, CDV and CIV. In addition,
162 163 164 165	Testing of BAL samples from the two dogs from the training centre (B-1 and B-2) was negative for the viruses CRCoV, CHV, CPIV, CAV, CDV and CIV. In addition, these samples yielded no bacterial growth except that of <i>M. cynos</i> . In comparison, the
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- 172 profiles consisted of 3-5 DNA bands, which ranged in size between approximately 6
- and 425 kb. The PFGE profiles of the isolates can be divided by similarity into three

174	groups. Group 1 contains ten isolates and it is a genetically homogeneous group with
175	at least 78% similarity; isolates 185, 190, 191, 210, 253, 312, 387, 417, 428, and 429
176	all form this group. These are all of the isolates from the population A dogs except
177	isolate 214 from dog A-1.
178	
179	Group 2 contains 491 and 492 and these isolates are indistinguishable from each other
180	but quite distinct to all the other isolates with only 28% similarity by cluster analysis.
181	These isolates are from two different dogs from the training centre population (dogs
182	B-1 and B-2).
183	
184	The third group contains the type strain and isolates 510 and 214. The type strain and
185	510 are indistinguishable from each other, but 214 is distinctly different with only
186	about 46% similarity to the other two. Isolate 510 was from dog B-2 while isolate 214
187	was from dog A-1.
188	
189	3.4. RAPD analysis of M. cynos isolates
190	When the same <i>M. cynos</i> isolates were subjected to analysis with RAPD with the
191	primer Hum4, 12 different profiles were obtained (Figure 2). The profiles consisted of
192	3-13 bands which ranged in size between approximately 240 and 2,200 bp. Two broad
193	groups of similar isolates were formed. The type strain and the 11 isolates 185, 190,
194	191, 210, 253, 312, 387, 417, 428, 429 and 510 had similar profiles and are
195	considered to be a homogeneous group with more than 68 % similarity (group 1). This
196	group comprises all of the isolates from the population A dogs, except for isolate 214,
197	but also includes 510 from dog B-2 and the type strain.
198	

199	Isolates 214, 491 and 492	formed a heterogeneous	group about 60 % s	similar to each

- 200 other, but only about 26% similar to the group 1 isolates. These isolates are from dogs
- 201 B-1, B-2 and isolate 214 from dog A-1.
- 202

203 The PFGE and RAPD grouping of isolates is summarised in Table 2.

204

205 **4. Discussion**

206 This is the first genetic typing study of *M. cynos*. The isolates from each kennel were found to be genetically similar. Indeed, isolates from dogs that had been housed in the 207 208 same kennel 4 and 8 months apart were found to be indistinguishable using both 209 genetic analysis methods (isolates 417 and 191 from dogs A-2 and A-3, and isolates 429 and 387 from dogs A-1 and A-4, respectively). The dogs had stayed at the 210 211 kennels for between 8 and 16 days. This may suggest that there is maintenance of M. 212 cynos strains within a kennel situation. M. cynos can be isolated from the upper 213 respiratory tract of healthy dogs (Chalker et al., 2004) and it is probable that some 214 strains are passed between subsequent dogs, resulting in the survival of these strains. In addition, environmental survival may aid the continued existence of some strains. 215 216 Although the environmental survival of *M. cynos* is not known, the environmental 217 survival of other mycoplasma species varies from a week to several months 218 (Nagatomo et al., 2001) and *M. cynos* can be isolated from the air (Chalker et al., 219 2004). Recently it has been shown that biofilm formation is important for persistence 220 of mycoplasmas and may aid environmental survival (McAuliffe et al., 2006), it 221 seems feasible that *M. cynos* may be able to persist in the kennel environment as an 222 adherent biofilm layer.

224 The *M. cynos* type strain was isolated from the lung of a dog with CIRD in Denmark 225 in 1971 (Rosendal, 1973). This *M. cynos* type strain was indistinguishable by PFGE to 226 isolate 510 from dog B-2 and was more than 68 % similar by RAPD analysis to 11 of 227 the *M. cynos* isolates from both kennels. The high degree of similarity of the type 228 strain to these United Kingdom isolates from 1999 and 2000 suggests a low level of 229 diversity of this organism in CIRD. However, this study also shows that some isolates 230 have a relatively low level of similarity with each other (for example isolates 214, 491 231 and 492 appear to be dissimilar to the group 1 isolates). Indeed, this study suggests the 232 potential for mixed *M. cynos* infections, as the same bronchoalveolar lavage sample from dog B-2 yielded M. cynos isolates 492 and 510, which are dissimilar strains. 233 234 Similarly, the BAL sample from dog A-1 resulted in the culture of the 214 isolate 235 which was dissimilar to the other isolates from this sample. A larger strain typing 236 study of more isolates is required to consolidate these observations.

237

Mycoplasma cynos was the only CIRD agent detected in two out of the six dogs (dogs 238 239 B-1 and B-2). Similarly, recently Zeugswetter et al. (2007) described lethal 240 bronchopneumonia in puppies where *M. cynos* was the only CIRD agent detected 241 from the puppies. Mycoplasmas have been the sole bacterial isolate in a number of 242 other cases of CIRD, but unfortunately these isolates were not speciated (Kirchner et 243 al., 1990; Jameson et al., 1995; Chandler and Lappin, 2002). However, in the current 244 study, both dogs were on a course of antibiotics preceding the sampling date (dog B-1 245 cephalosporin; B-2 erythromycin), which may have precluded the isolation of other 246 bacterial agents. Likewise, in the case of Zeugswetter et al. (2007), the puppies had 247 been treated with amoxicillin prior to isolation of *M. cynos* from the lung tissue.

249 Mycoplasma cynos has also been previously implicated in canine respiratory disease 250 along with other bacterial or viral pathogens (Rosendal, 1978; Chalker et al., 2004; 251 Chvala et al., 2007). This was also found in the current study as other respiratory 252 pathogens apart from *M. cynos* were detected in the four dogs from the re-homing kennel, for example B. bronchiseptica, S. equi subsp. zooepidemicus, CHV and 253 254 CRCoV. Multi-pathogen respiratory disease is commonly reported and it has been 255 suggested that the pathogens may interact synergistically to produce disease 256 (Randolph et al., 1993).

257

Escherichia coli, which was detected in one dog in the present study, has been
previously isolated from BAL from a puppy with CIRD and was thought to be a
contaminant (Williams et al., 2006). This is likely to be the case in this study as *Enterococcus* spp. was co-isolated from the same sample. In addition, *M. spumans*was isolated from two dogs, one of which also had *M. canis* and *Ureaplasma* spp.,
however these species were not found to be significantly associated with respiratory
disease in dogs (Chalker et al., 2004).

265

In summary, the PFGE and RAPD genetic typing methods were in basic agreement and showed that many of the isolates were highly similar. Strain maintenance is suggested by strains which are indistinguishable by genetic typing, being isolated from dogs housed months apart within the same kennel. There was also a high degree of similarity of the *M. cynos* type strain (isolated from a dog with respiratory disease in Denmark in 1971) to at least one of these United Kingdom isolates, which suggests possible conservation of pathogenic strains of *M. cynos*.

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279	
280	
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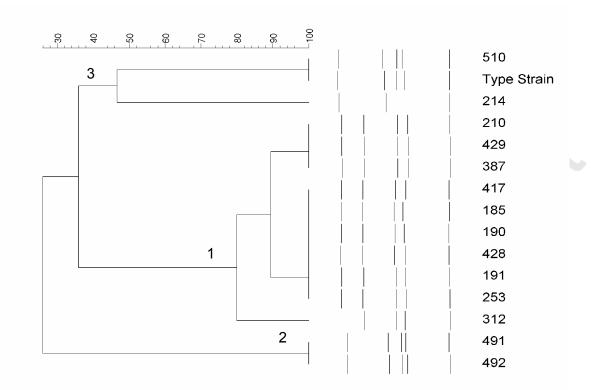
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365	

Figure Captions

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3	6/	

- 368 **Figure 1.** Similarity analysis of the *Sma*I PFGE profiles of the 14 *M. cynos* canine
- 369 respiratory isolates from six dogs. Numbers 1-3 denote the groupings of similar
- 370 profiles.
- 371
- 372
- 373 Figure 2. Similarity analysis of the profiles produced by RAPD with the primer
- Hum4. Numbers 1 and 2 denote the groupings of similar profiles.



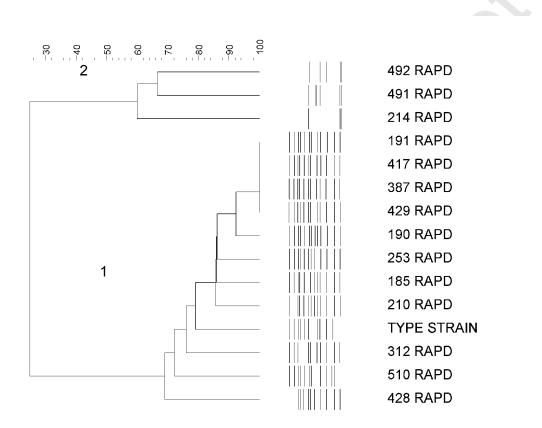




Table 1. Details of dogs with respiratory disease from which *M. cynos* isolates were cultured, and bacteriology and virology screening results of

trachea (T) and bronchoalveolar lavage (BAL) samples.

Dog ¹	Age (years)	Sex ²	Breed	Respiratory score ³	Date sampled	Bacteriology	Virology
A-1	1	MN	German shepherd	3	03Jun99	<i>B. bronchiseptica & M. spumans</i> in BAL; <i>M. cynos</i> in BAL & T	negative
A-2	2	М	Staffordshire bull terrier	3	03Jun99	<i>B. bronchiseptica</i> & <i>Pasteurella</i> spp. in BAL; <i>M. cynos</i> in BAL & T	CRCoV in T
A-3	2	М	Dalmatian	5	11Oct99	<i>S. equi</i> subsp. <i>zooepidemicus</i> in BAL; <i>M. cynos & M. spumans</i> in BAL & T	negative
A-4	3	FN	Mongrel	5	24Feb00	S. equi subsp. zooepidemicus, Enterococcus spp., Ureaplasma spp. & Escherichia coli in BAL; M. canis & M. cynos in BAL & T	CHV in BAL
B-1	1	MN	Labrador	5	08Nov00	<i>M. cynos</i> in BAL ⁴ negative	
B-2	1	F	Labrador	3	23Nov00	<i>M. cynos</i> in BAL ⁴	negative4

¹A, re-homing centre; B, training centre.

²N, neutered.

³3, cough and nasal discharge; 5, bronchopneumonia.

⁴No trachea sample available.

Dog	<i>M. cynos</i> isolate #	Source	PFGE group	RAPD group
	185	BAL	1	1
	210	BAL	1	1
A-1	214	BAL	3	2
A-1	253	BAL	1	1
	428	Т	1	1
	429	Т	1	1
A-2	190	BAL	1	1
A-2	417	Т	1	1
A-3	191	BAL	1	1
A 4	312	BAL	1	1
A-4	387	Т	1	1
B-1	491	BAL	2	2
B-2	492	BAL	2	2
D-2	510	BAL	3	1

Table 2. Mycoplasma cynos isolate source and genetic typing groups.