

1 **Title: Insight into motility-dependent pathogenicity of the zoonotic spirochete**

2 *Leptospira*

3 **Short title:** Motility-dependent spirochetal pathogenicity

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16

17 **Abstract**

18 Bacterial motility is crucial for many pathogenic species in the process of invasion and/or
19 dissemination. The spirochete bacteria *Leptospira* spp. cause symptoms, such as hemorrhage,
20 jaundice, and nephritis, in diverse mammals including humans. Although loss-of-motility attenuate
21 the spirochete, the mechanism of the motility-dependent pathogenicity is unknown. Here, focusing
22 on that *Leptospira* spp. swim in liquid and crawl on solid surfaces, we investigated the spirochetal
23 dynamics on the host tissues by infecting cultured kidney cells from various species with pathogenic
24 and nonpathogenic leptospires. We found that, in the case of the pathogenic leptospires, a larger
25 fraction of bacteria attached to the host cells and persistently traveled long distances using the
26 crawling mechanism. Our results associate the kinetics and kinematic features of the spirochetal
27 pathogens with their virulence.

28 **One Sentence Summary:** Adhesivity and crawling motility over host tissue surfaces are closely
29 related to the pathogenicity of a zoonotic spirochete.

31 **Introduction**

32 Many bacteria utilize motility to explore environments for survival and prosperity. For
33 pathogenic species, the motility is a virulence factor, harming the host animal or plant health(6). For
34 example, *Helicobacter pylori* requires motility to migrate towards the epithelial tissue in the
35 stomach(7), and motility and chemotaxis are key factors that guide host invasion in different
36 *Salmonella* serovars (8, 9). Movement and adhesion of the Lyme disease spirochete *Borrelia*
37 *burgdorferi* in blood vessels are thought to be important during the process of host cell invasion(10).
38 In the enteric pathogens, such as the enteropathogenic *Escherichia coli* (EPEC), the motility

39 machinery flagella are also important for adhesion to the host intestinal epithelium(11).

40 In this study, we address the association of bacterial motility with pathogenicity in the
41 worldwide zoonosis leptospirosis. The causative agent of leptospirosis *Leptospira* spp. are
42 Gram-negative bacteria belonging to the phylum Spirochaetes. The genus *Leptospira* is comprised of
43 pathogenic, intermediate, and nonpathogenic species, which are classified into over 300 serovars
44 defined based on the structural diversity of lipopolysaccharide (LPS)(2, 12). The pathogenic species
45 affect various mammalian hosts such as livestock (cattle, pigs, horses, and others),
46 companion animals (dogs and others), and humans, causing severe symptoms, such as hemorrhage,
47 jaundice, and nephritis in some host-serovar pairs(2–4). The leptospire can be maintained in the
48 renal tubules of recovered animals or reservoir hosts, and the urinary shedding of leptospire to the
49 environment leads to infection in humans and other animals through contact with contaminated soil
50 or water. Although the pathogenic mechanism of leptospirosis is not well elucidated, in addition to
51 the pathogen-specific proteins such as Loa22(13), their motility using two periplasmic flagella
52 (PFs) beneath the outer cell membrane (Fig. 1A) is known to be somehow involved in the infection
53 and pathogenicity based on studies in animal models that have shown attenuation of the spirochetes
54 by loss-of-motility(14, 15).

55 The rotation of the PFs in *Leptospira* gyrates both ends of the cell body and rotates the coiled
56 cell body, allowing the spirochete not only to swim in fluids but also to crawl over solid surfaces(16,
57 17). Adherence and entry of pathogenic leptospire in the conjunctival epithelium(4) and in the
58 paracellular routes of hepatocytes(18) were previously observed using scanning electron microscopy,
59 suggesting adhesion to the host tissue surfaces and subsequent crawling of pathogenic leptospire. To
60 verify this hypothesis, assuming the transition of leptospire between swimming and adhesion states

61 and between adhesion and crawling states in the equilibrium (Fig. 1B), we investigated the adhesion
62 and crawling motility of *Leptospira* on the cultured kidney cells of various mammalian species.

63

64 **Results**

65 **Steady-state analysis of *Leptospira* on the kidney cells.** We infected cultured kidney cells from six
66 different host species (rat, dog, monkey, mouse, cow, and human) with three *Leptospira* strains (the
67 pathogenic *L. interrogans* serovars Icterohaemorrhagiae and Manilae, and the nonpathogenic *L.*
68 *biflexa* serovar Patoc) expressing green fluorescent protein (GFP) within a chamber slide (Fig. 2A).
69 We observed the *Leptospira* cells by epi-fluorescent microscopy (Fig. 2B) and measured the
70 fractions of swimming [S], adhered [A], and crawling [C] bacteria on the kidney cells (Fig. 2C). Figs.
71 2D-E show that almost half of the pathogenic population transited from the swimming state to the
72 adhesion and crawling states, whereas >75% non-pathogenic leptospires remained in the swimming
73 state. We calculated the equilibrium constant between swimming and adhesion states (K_{S-A}) and
74 between adhesion and crawling states (K_{A-C}) from the cell fractions using $K_{S-A} = [A] / [S]$ and $K_{A-C} =$
75 $[C] / [A]$, respectively. The pathogenic leptospires had a significantly larger K_{A-C} in comparison with
76 the nonpathogenic strain ($P < 0.05$); K_{S-A} did not seem to correlate to virulence (Fig. 2F). These
77 thermodynamic parameters suggest that the biased transition from adhesion to crawling would be
78 responsible for the virulence of *Leptospira* (Fig. 2G).

79

80 **Crawling motility.** Taking the results of the steady-state analysis, we focused on the crawling
81 motility of individual *Leptospira* cells on the kidney cells. Although the crawling speed varied
82 among the measured host-bacterium pairs, *L. interrogans* serovar Icterohaemorrhagiae showed

83 significantly faster speed than the others, indicating the species/serovar dependence of the crawling
84 ability (Fig. 3A). On the other hand, there is no difference in crawling speed between *L. interrogans*
85 serovar Manilae and *L. biflexa* serovar Patoc, suggesting that the crawling speed itself is not related
86 to leptospiral virulence. Meanwhile, we observed that some leptospiral cells attached to the kidney
87 cells and moved smoothly for periods, migrating over long-distances (upper panels of Figs. 3B-C;
88 Movie S2), whereas others frequently reversed the crawling direction (lower panels of Figs. 3B-C;
89 Movie S3). Cell movements with reversals are considered to be diffusive and thus can be evaluated
90 by plotting the mean square displacement (MSD) against time, a general methodology for diffusion
91 (Brownian motion) analysis(19). The MSD of simple diffusion without directivity is proportional to
92 time, and therefore double-logarithmic MSD plots from such non-directional diffusion represent
93 slopes of ~ 1 , whereas those from directive movements show MSD slopes of ~ 2 , representing the
94 relatively long distance traveled by the cells (Fig. S1). Double-logarithmic MSD plots obtained from
95 each individual leptospire showed a wide range of MSD slopes (example data are shown in Fig. 3D)
96 and differed for each host-*Leptospira* pair (Fig. 3E left and Fig. S2). The nonpathogenic strain
97 showed the slope of ~ 1 , while the pathogenic strains had significantly larger slopes that denote
98 directive motion (Fig. 3E right). Thus, concerning the crawling motility, directivity and persistency
99 rather than speed could be crucial for virulence.

100

101 **Discussion**

102 Our results suggested the importance of adhesion to and persistent crawling on the host tissue for the
103 pathogenicity of *Leptospira*. The thermodynamic and kinematic parameters are associated in Fig 4A,
104 showing the tendency that pathogenic species are biased to the crawling state and can migrate longer

105 distance on the host tissue surfaces. The crawling motility of *Leptospira* is caused by the attachment
106 of the spirochete cell body to surfaces via adhesive cell surface components(16, 20). The successive
107 alternation in the attachment and detachment of adhesins allows for this progressive movement by
108 the spirochetes, however, an excessively strong adhesion can inhibit crawling(16). LPS, the
109 molecular basis for the identification of the different *Leptospira* serovars(2, 12), is thought to be a
110 crucial adhesin important for this crawling motion(16). Thus, it is possible that compatibility of the
111 serological characteristics of leptospires and the surface properties of the host tissue might affect the
112 crawling behavior over the tissue surfaces and the subsequent clinical consequences. The results of
113 our biophysical experiments outline a plausible framework for the adhesion and crawling-dependent
114 pathogenicity of *Leptospira* (Fig. 4B). The biased transition from the adhesion to the crawling state
115 and the long-distance, persistent crawling allows leptospires to explore the host's cell surfaces,
116 increasing the probability of encountering routes for invasion through their intracellular tight
117 junctions (Fig. 4B, left). In contrast, the swimming or weakly attached leptospires can be swept by
118 external forces, such as intermittent urination, and diffusive crawling by which leptospires cannot be
119 disseminated over host tissues will not be involved in invasion (Fig. 4B, right).

120 Some bacterial pathogens are specialized to invade a very limited array of hosts, whereas others
121 can infect multiple host species. The host range differs for each pathogen and the clinical symptoms
122 depend on each host-pathogen combination. The same applies for leptospirosis, the outcome of
123 *Leptospira* infection depends on the host-serovar association, and some animal species can become
124 an asymptomatic reservoir for particular *Leptospira* serovars. The present experiments also provided
125 data allowing us to discuss the host dependence of the leptospiral dynamics. Among the investigated
126 materials, serovar Manilae vs rats and serovar Icterohaemorrhagiae vs rats are typically

127 asymptomatic pairs, and Fig. 4A shows that the pairs with reservoirs have lower scores in
128 comparison with those causing severe symptoms, such as Manilae vs humans, Icterohaemorrhagiae
129 vs dogs, and others. This implies that the surface dynamics of the spirochete could be related to their
130 host-dependent pathogenicity. Understanding the mechanism of the host preferences by pathogens is
131 important for prevention of the infection spread, but the host-pathogen association in leptospirosis is
132 ambiguous. Also, microarray analyses have revealed that regulation of gene expression in *Leptospira*
133 is affected by its interaction with host cells(21, 22). Although host immune responses against
134 *Leptospira* infection remain mostly unknown, pathogenic leptospire interfere with the complement
135 system through the degradation of complement proteins(23) and inhibition of coagulation via binding
136 to thrombin(24). Thus, abundant factors in both bacteria and hosts should be investigated for a
137 deeper understanding of the host-dependent pathogenicity.

138

139 **Materials and Methods**

140 ***Leptospira* strains and growth conditions.** Pathogenic serovars of *L. interrogans* serovar
141 Icterohaemorrhagiae (strain WFA135), an isolate from *Rattus norvegicus* in Tokyo, Japan, serovar
142 Manilae (strain UP-MMC-NIID)(25, 26) and a saprophytic *L. biflexa* serovar Patoc (strain Patoc I)
143 were used in this study. The serovar of WFA135 was determined by multiple loci variable number of
144 tandem repeats analysis (MLVA) and DNA sequencing of the *lic12008* gene(26, 27). Bacteria were
145 cultured in enriched Ellinghausen-McCullough-Johnson-Harris (EMJH) liquid medium (BD Difco,
146 NJ, USA) containing 25 µg/mL spectinomycin at 30 °C for 2 (*L. biflexa*) or 4 (*L. interrogans*) days
147 until the stationary phase. To track *Leptospira* cells when in co-culture with mammalian kidney cells,
148 a green fluorescent protein (GFP) was constitutively expressed in each strain (Fig. 1D; Movie S1).

149

150 **Mammalian cells and media.** Mammalian kidney epithelial cell lines used included MDCK-NBL2
151 (dog), NRK-52E (rat), Vero (monkey), MDBK-NBL1 (cow), TCMK-1 (mouse), and HK-2 (human).
152 MDCK, Vero, TCMK, and MDBK cells were maintained in Eagle's minimum essential media
153 (MEM) (Sigma-Aldrich, Darmstadt, Germany) containing 10% fetal bovine serum or 10% horse
154 serum (Nacalai Tesque, Kyoto, Japan) at 37 °C and 5% CO₂. NRK cells were maintained in
155 Dulbecco's modified Eagle's media (DMEM) (Thermo Fisher Scientific, MA, USA) with 4 mM
156 L-glutamine, adjusted to contain 1.5 g/L sodium bicarbonate and 4.5 g/L glucose, and with 5%
157 bovine calf serum (Nacalai Tesque) at 37 °C and 5% CO₂. HK-2 cells were maintained in
158 keratinocyte serum-free (KSF) media with 0.05 mg/mL bovine pituitary extract and 5 ng/mL human
159 recombinant epidermal growth factor (Gibco - Thermo Fisher Scientific, MA, USA). All culture
160 conditions contained a 5% antibiotic / antimycotic mixed solution (Nacalai Tesque). Cells were
161 treated with a 0.1% trypsin - EDTA solution (Nacalai Tesque) to dislodge the cells during each
162 passage process.

163

164 **GFP expression in *L. interrogans* and *L. biflexa*.** For the construction of a replicable plasmid in *L.*
165 *interrogans*, the corresponding *rep-parB-parA* region of the plasmid pGui1 from the *L. interrogans*
166 serovar Canicola strain Gui44 plasmid pGui1(28) was amplified from a *L. interrogans* serogroup
167 Canicola isolate, and the amplified product was cloned into the PCR-generated pCjSpLe94(29) by
168 NEBuilder HiFi DNA Assembly cloning (New England BioLabs), generating pNKLiG1. The *flgC*
169 promoter region and *gfp* were amplified from pCjSpLe94 and pAcGFP1 (Clontech), respectively,
170 and the amplified products were cloned into the *SalI*-digested pNKLiG1 for *L. interrogans* or the

171 *SalI*-digested pCjSpLe94 for *L. biflexa*. The plasmids were transformed into strains WFA135,
172 UP-MMC-NIID or Patoc I by conjugation with *E. coli* β 2163 harboring the plasmid(30). Primer
173 sequences used in this study are listed in Table S1. Expression of GFP did not affect motility in the
174 *Leptospira* serovars (Fig. S3).

175

176 **Preparation of kidney cells and *Leptospira* cells in a chamber slide.** Kidney cells were harvested
177 with 0.1% trypsin and 0.02% EDTA in a balanced salt solution (Nacalai Tesque) and plated onto a
178 chamber slide (Iwaki, Tokyo, Japan) using their corresponding media without antibiotics. The slides
179 were incubated for 48 h until a monolayer was formed and washed twice with media to remove
180 non-adherent cells. The cells were incubated for a further 2 h at 37 °C and 5% CO₂. Approximately
181 500 ml of stationary phase *Leptospira* cells were harvested by centrifugation at 1,000 g for 10 min at
182 room temperature, washed twice in PBS, then resuspended in the corresponding kidney cell culture
183 media without antibiotics at 37 °C to a concentration of 10⁷ cells / ml. These suspensions (1 ml) were
184 then added into the corresponding chamber slides containing the kidney cell layer, and the chamber
185 slides were incubated at 37 °C for 1 h.

186

187 **Microscopy observation and adhesion-crawling assay.** The movement behaviors, swimming,
188 adhesion and crawling of the *Leptospira* cells on the kidney cells were observed using a dark-field
189 microscope (BX53, Splan 40 \times , NA 0.75, Olympus, Tokyo, Japan) with an epi-fluorescent system
190 (U-FBNA narrow filter, Olympus) and recorded by a CCD-camera (WAT- 910HX, Watec Co.,
191 Yamagata, Japan) at 30 frames per second. *Leptospira* cells were tracked using an ImageJ (NIH, MD,
192 USA)-based tracking system and the motion parameters such as motile fraction, velocity and MSD

193 were analyzed using Excel-based VBA (Microsoft, WA, USA). The two-dimensional MSD of
194 individual leptospiral cells during a period Δt was calculated by the following equation: $MSD(\Delta t) =$
195 $\langle (x_{i+\Delta t} - x_i)^2 + (y_{i+\Delta t} - y_i)^2 \rangle$, where (x_i, y_i) is the bacterial position at I (see also Supplementary
196 Fig. 1).

197

198 **Statistical analysis.** All experiments were performed in triplicate. Statistical differences between
199 data were evaluated using a Student's t -test. The data clustering was performed independently for
200 each experiment using the k-means method in OriginPro (OriginLab Corp., MA, USA). The
201 clustering method grouped the data population into a specified number of clusters referring to the
202 Euclidian distance of each data point from the centroid of the cluster, calculated at every clustering
203 process, and reclassifying the data point to the nearest cluster.

204

205 **Supplementary Materials**

206 Tables S1. Primer sequences used in this study

207 Fig. S1. Explanation of MSD plot.

208 Fig. S2. Histograms of the MSD slopes

209 Fig. S3. Effect of GFP expression on the *Leptospira* motility.

210 Movie S1. Epi-fluorescent images of *L. interrogans* on the rat kidney cell

211 Movie S2. Progressive, long-distance crawling of *L. interrogans* on the monkey kidney cells

212 Movie S3. Crawling of *L. interrogans* with highly frequent reversal on the dog kidney cells

213

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295

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301

302 **Author contributions** J.X., N.K. and S.N. planned the project; J.X and N.K. carried out the

303 experiments; S.N. set up the optical system and programs for data analysis; J.X. and S.N. analyzed
304 the data; J.X., N.K. and S.N. wrote the paper.

305

306 **Competing interests** The authors declare that they have no competing interests.

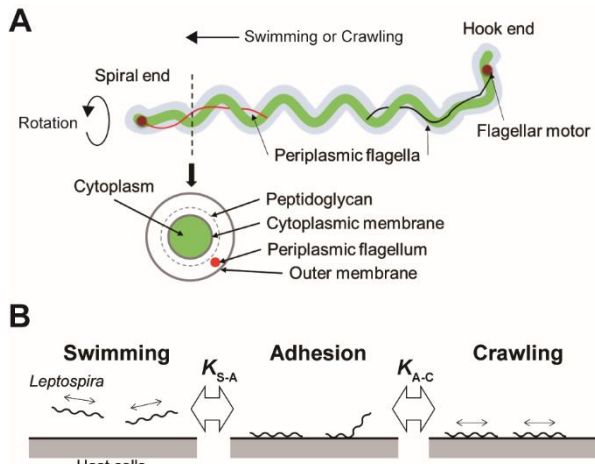
307

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311

312 **Data availability** The data supporting the findings of this study are available from the corresponding
313 author upon request.



314

315 **Fig. 1. Structure of *Leptospira* and working model.** (A) Schematic diagram of the *Leptospira* cell

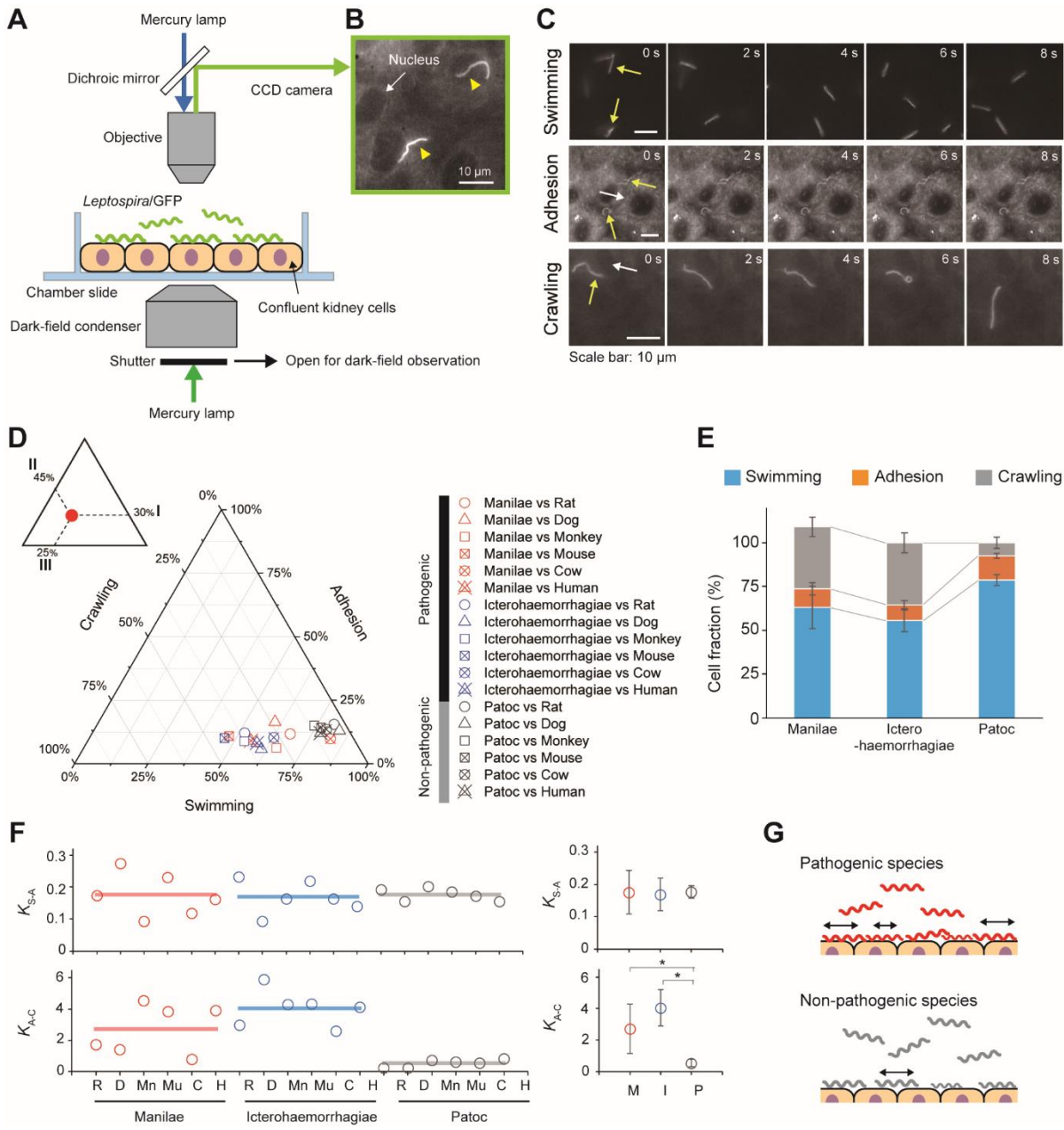
316 structure. (B) A three-state kinetic model assuming a transition between “swimming” (floating above

317 cell layers without physical contact to the cells) and “adhesion” (attachment to the cell layer without

318 migration), and between “adhesion” and “crawling” (attachment to the cell layer and movement over

319 surfaces), with K_{S-A} and K_{A-C} represent the equilibrium constants of each transition, respectively.

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322 **Fig. 2. Steady-state motility and adhesion of *Leptospira* cells on kidney cells.** (A) Schematic of

323 the motility assay on the cultured kidney cells by epi-fluorescent microscopy. Fully confluent kidney

324 cells from either animals or humans were cultured in an observation chamber, and *Leptospira* cells

325 that constitutively expressed GFP were added to the cultures. (B) Example of an epi-fluorescence

326 image of the *L. interrogans* serovar Icterohaemorrhagiae, as indicated by the yellow triangles, on the

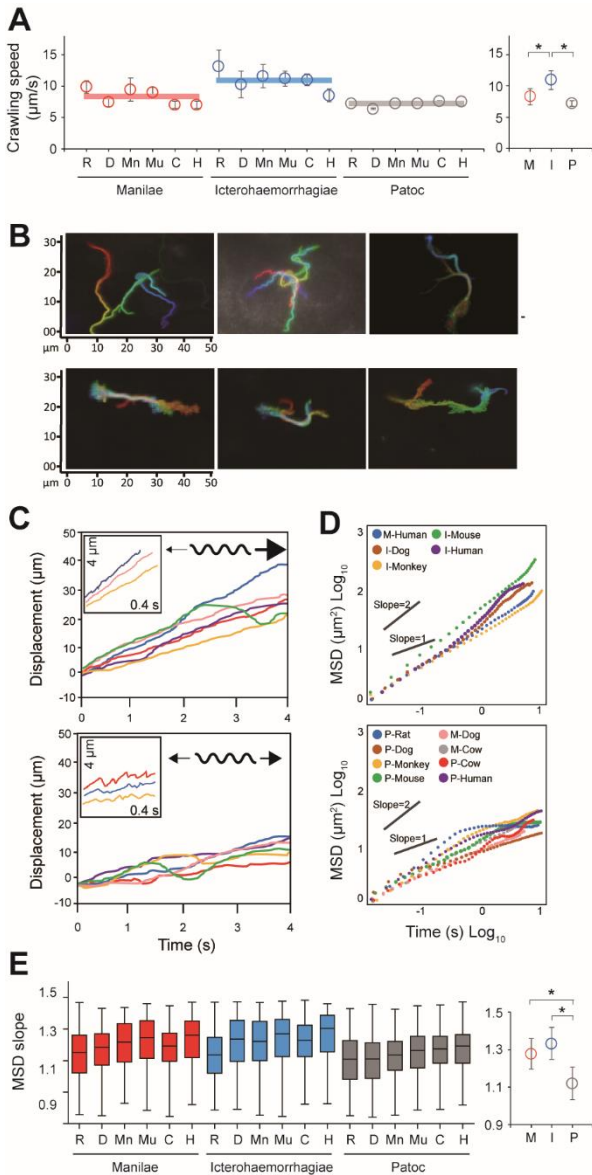
327 rat kidney cell line, NRK-52E. The nucleus of the kidney cell is shown by the white arrow (Movie

328 S1). (C) Image sequences of swimming (top), adhered (middle), and crawling (bottom) leptospiral

329 cells. Yellow and white arrows indicate *Leptospira* cells and kidney cells, respectively. No kidney
330 cells were observed due to out of focus during the measurement of *Leptospira* cells swimming in
331 liquid media. (D) Ternary plot of the cell fractions in a state of swimming, adhesion, or crawling. The
332 inset schematically explains how to read the ternary plot using an example plot with 30% for I, 45%
333 for II, and 25% for III. Legend is shown to the right of the ternary plot, and M, I and P indicate the *L.*
334 *interrogans* serovar Manilae, *L. interrogans* serovar Icterohaemorrhagiae, and *L. biflexa* serovar
335 Patoc, respectively. Each data point represents the mean of triplicate experiments and ~ 2,400
336 leptospiral cells were measured per host-serovar pair. (E) Average values of the cell fractions. Error
337 bars are the standard deviation. (F) The host-bacterium dependence of the equilibrium constants K_{S-A}
338 and K_{A-C} , calculated from the data shown in **D**; rat (R), dog (D), monkey (Mn), mouse (Mu), cow (C),
339 and human (H). The averaged values determined for each bacterial strain are shown by horizontal
340 lines and are plotted with the standard deviation in the right; *L. interrogans* Manilae (M), *L.*
341 *interrogans* Icterohaemorrhagiae (I), and *L. biflexa* Patoc I (P). The statistical analysis was
342 performed by Mann-Whitney U test (* $P < 0.05$). (G) Schematic explanation of the kinetic difference
343 between pathogenic and non-pathogenic leptospires.

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347 **Fig. 3. Analysis of the crawling movement of *Leptospira* on kidney cell layers. (A) Average**

348 crawling speeds determined for each host-bacterium pair. More than 90 bacteria were measured for

349 each pair. The averaged values calculated for each bacterial strain are shown by horizontal lines (left)

350 and are plotted with the were (B) Examples of persistent crawling (upper panels) and diffusive

351 crawling (lower panels) of *Leptospira* cells obtained by single-cell tracking in 10 s. Colors indicate

352 time courses in the order of red orange yellow green blue, and indigo. (C) Example time courses of

353 leptospires crawling on the kidney cell surfaces; inset, expanded view of cell displacements and

354 schematics of motion patterns. The upper and lower panels show the long-distance migration

355 represented by directive crawling and the limited migration due to frequent reversal, respectively.

356 (D) Examples of MSD vs time plots, evaluating the directivity of individual leptospiral cell

357 movements: Plots with slopes ~ 2 indicate persistently directive crawling (upper), whereas those with

358 ~ 1 indicate a non-directional movement (lower), i.e., motion with high frequency of reversal

359 patterns and short net migration distance (refer to the schematic explanation of motion pattern in

360 insets of C). (E) MSD slopes determined for each host-bacterium pair. The boxes show the 25th (the

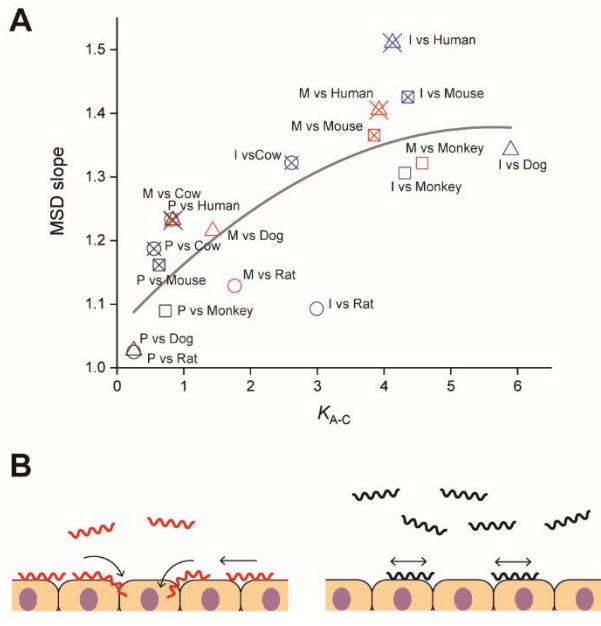
361 bottom line), 50th (middle), and 75th (top) percentiles, and the vertical bars show the minimum and

362 maximum values. The right panel show the strain-dependence of the medians. The statistical analysis

363 was performed by Mann-Whitney U test (* $P < 0.05$).

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367 **Fig. 4. Correlation of adhesion, motility and pathogenicity.** (A) Relationship between K_{A-C} and

368 MSD slope (i.e., crawling persistency). The gray line is the result of quadratic curve fitting. The

369 correlation coefficient is 0.77. See Fig. 2D for symbols. (B) A plausible model for

370 crawling-dependent pathogenicity of *Leptospira*. In the cases that lead to severe symptoms (left),

371 leptospiral cells were biased to the crawling state, and most of the crawling cells showed directional

372 translation persistently over host tissue surfaces, increasing the invasion probability. For the

373 asymptomatic or non-infectious cases, many leptospires remained in the swimming state and might

374 be removed through body fluids or urination. Some fractions of the adhered leptospires were able to

375 crawl, but their migration distances were limited due to frequent reversal.

376

377 **Supplementary Materials**

378 Title: Insight into motility-dependent pathogenicity of the zoonotic spirochete *Leptospira*

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380 Correspondence to: naka@bp.apph.tohoku.ac.jp

381

382 **This file includes:**

383 Tables S1. Primer sequences used in this study

384 Fig. S1. Explanation of MSD plot.

385 Fig. S2. Histograms of the MSD slopes

386 Fig. S3. Effect of GFP expression on the *Leptospira* motility.

387

388 **Other Supplementary Materials for this manuscript include the following:**

389 Movie S1. Epi-fluorescent images of *L. interrogans* on the rat kidney cell

390 Movie S2. Progressive, long-distance crawling of *L. interrogans* on the monkey kidney cells

391 Movie S3. Crawling of *L. interrogans* with highly frequent reversal on the dog kidney cells

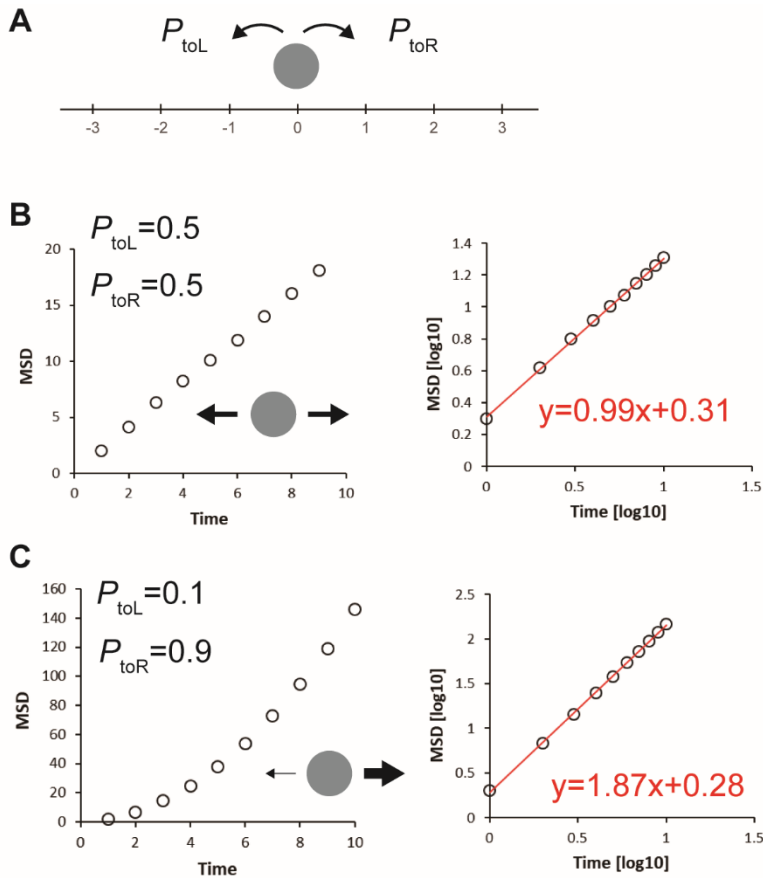
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393 **Table S1. Primer sequences used in this study**

Target	Primer sequence (5' → 3')	
	Forward	Reverse
<i>rep-parB-parA</i> (pGui1)	TCGACGCCGGCCAGCGTTACTTCATAGCATCTTGGTTC	GCTGGAGCTCCACCGGCTCGACTCTTACGGTGTGTTAG
pNKLIG1 (pCjSpLe94 derivative)	CGGTGGAGCTCCAGCTTTG	GCTGGCCGGCGTCGAAAAGTAAGCACCTGTTATTGC
<i>flgC</i> promoter	TATCGATACCGTCGACCCGAGCTTCAAGGAAGATTTCTTA	ATGGAAACCTCCCTCATTTA
AcGFP	GAGGGAGGTTTCCATATGACCATGATTACGCCAAGC	TATCGATACCGTCGATCACTTGTACAGCTCATCCATG

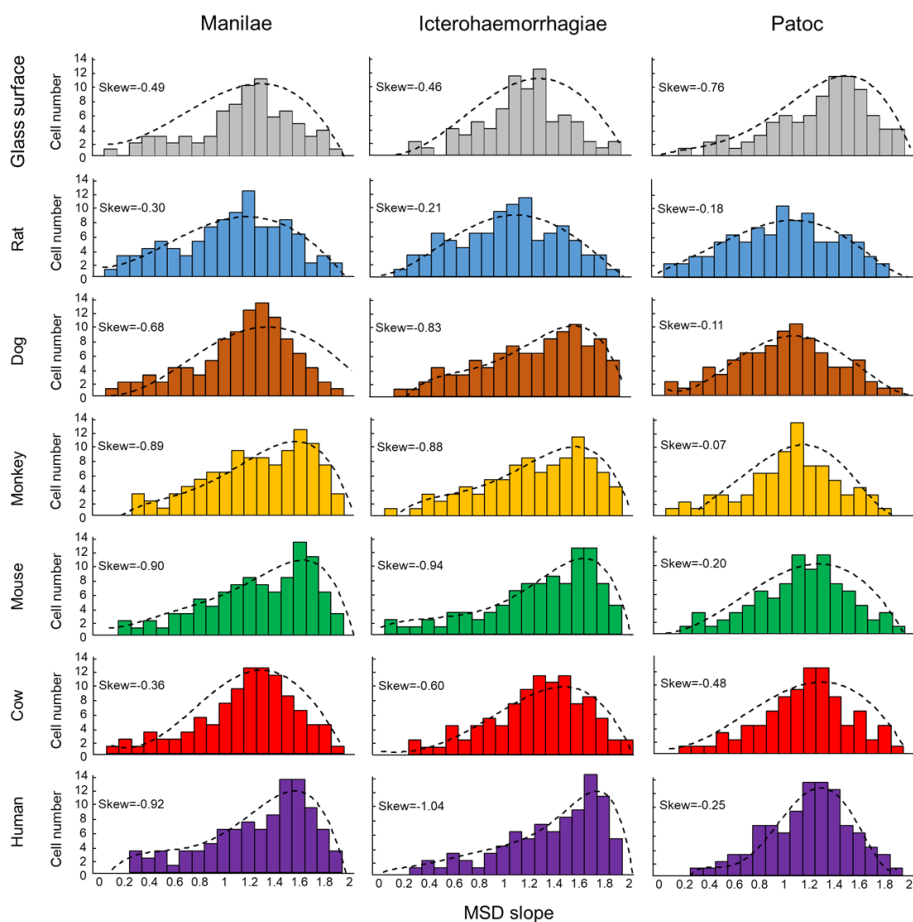
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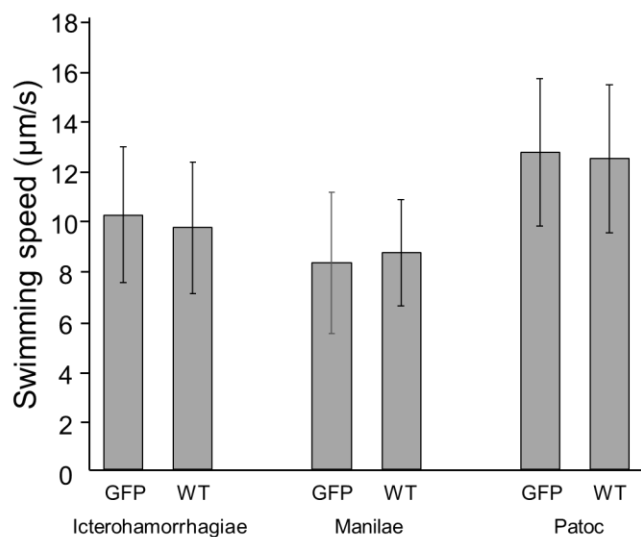
397 **Fig. S1. Explanation of MSD plot.** (A) To explain the difference in MSD vs time plot of “directed
398 movement” (Figs. 3B-C upper) from that of “diffusive movement” (Figs. 3B-C lower), we performed
399 a computer simulation by considering a particle stepping to the left (-1) or to the right ($+1$) with the
400 probability of P_{toL} and $P_{\text{toR}} (= 1 - P_{\text{toL}})$, respectively, in a time interval Δt . $P_{\text{toL}} = 0.5$ ($P_{\text{toR}} = 0.5$) and
401 $P_{\text{toL}} = 0.1$ ($P_{\text{toR}} = 0.9$) were assumed for simulating simple diffusion and movement biased to the
402 right, respectively, and the step direction was determined by a random number (rnd) from 0.0 to 1.0
403 generated in each event: If $rnd < P_{\text{toL}}$, the particle steps to the left ($+1$). The time course of the
404 particle position was analyzed as shown in Methods. MSD vs time plots obtained by the simulation
405 show that (B) simple diffusion and (C) directed movement give a linear line and a quadratic curve,
406 respectively (left panels), therefore exhibiting linear lines with slopes of ~ 1 and ~ 2 in
407 double-logarithmic plots (right panels). Red lines are regression lines fitted to data points obtained
408 by simulation.



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410 **Fig. S2. Histograms of the MSD slopes. Dashed lines are the results of curve fitting.**

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413 **Fig. S3. Effect of GFP expression on the *Leptospira* motility.** No significant difference found
414 between the swimming speeds of GFP expressing strains and wild type strains in each serovar.

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