1	The SARS-CoV-2 reproduction number R_0 in cats
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20 ABSTRACT

21	Domestic cats are susceptible to SARS-CoV-2 virus infection and given that they are in close
22	contact with people, assessing the potential risk cats represent for the transmission and
23	maintenance of SARS-CoV-2 is important. Assessing this risk implies quantifying transmission
24	from humans-to-cats, from cats-to-cats and from cats-to-humans. Here we quantified the risk of
25	cat-to-cat transmission by reviewing published literature describing transmission either
26	experimentally or under natural conditions in infected households. Data from these studies were
27	collated to quantify the SARS-CoV-2 reproduction number R_0 among cats. The estimated R_0 was
28	significantly higher than 1, hence cats could play a role in the transmission and maintenance of
29	SARS-CoV-2. Questions that remain to be addressed are the risk of transmission from humans-
30	to-cats and cats-to-humans. Further data on household transmission and data on virus levels in
31	both the environment around infected cats and their exhaled air could be a step towards assessing
32	these risks.
33	
34	KEYWORDS SARS-CoV-2, cats, transmission, reproduction number

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37 A relevant concern in the control of the ongoing Covid-19 pandemic is the risk domestic 38 animals could play in the maintenance and transmission of SARS-CoV-2. Assessing this risk implies quantifying transmission from humans-to-animals, from animals-to-animals and from 39 40 animals-to-humans. Large epidemics in farmed minks have confirmed this risk for that specific 41 species (1). The role of cats is of particular interest, because they are in close contact with 42 humans and frequently in contact with other cats. Available field (2-9) and experimental data 43 (10-14) indicate that cats are susceptible to infection, occasionally show mild clinical signs and may be able to transmit the infection between cats. Indeed, transmission experiments confirmed 44 45 this possibility (10-14), however, the lack of a proper statistical assessment of transmission in the reported experiments limits confident extrapolation of the results from the experiment to the 46 47 population. An important question when assessing the risk of transmission is whether cat-to-cat 48 transmission can be sustained. A key measure to answer this question is the basic reproduction 49 number R_0 , which is the average number of individuals to whom a typical infectious individual 50 will transmit the infection to in a naive population. R_0 is a key parameter in infectious disease 51 epidemiology, it provides an indication of the transmissibility of a pathogen and the risk of 52 epidemic transmission. When $R_0 > 1$, one can expect sustained transmission with high risk of a major outbreak and endemicity to occur, whereas when $R_0 < 1$ the infection is likely to peter out. 53 54 Other parameters which contribute to quantitatively describe transmission are: 1) the latent period L, which is the time from becoming infected to becoming contagious, 2) the infectious 55 period T, which is the average period of time an individual is contagious and 3) the transmission 56 57 rate parameter β which is the number of contact infections caused by one typical infectious individual per unit of time. Here, published experiments and observational studies describing 58 59 infection and transmission of SARS-CoV-2 between cats were reviewed. Data from these studies

were collated and analysed to statistically confirm whether cat-to-cat transmission can besustained and to provide estimates of relevant transmission parameters.

A systematic literature search was conducted which identified 115 publications. Upon
 screening and selection of relevant studies for data collection and analysis, five experimental
 studies and 8 observational studies were included for analysis. A detailed description of the

65 systematic review process is provided as supplemental material (Text S1).

66 In Tables 1 and 2 the experimental and household studies included for analyses are

67 summarised. Of the experimental studies, four (10-12) assessed direct-contact transmission and

one (13) indirect (droplet) transmission. These studies used different study designs with respect

69 to age and the number of inoculated (donor) and contact cats included within an experimental

70 group. All experiments used inoculation doses $\ge 10^5$ PFU (Gaudreault et al (12) used 10^6

71 TCID₅₀) and the predominant inoculation route was intra-nasal inoculation. Following

72 inoculation, infection and transmission were monitored by longitudinally detecting and

73 measuring virus shedding in nasal, faecal or oropharyngeal samples collected from inoculated

and contact- or droplet-infected cats. The laboratory methods used to monitor infection were

either virus isolation (VI) (10, 11) or RT-PCR (12, 13). From the observational studies, data

76 from 12 households housing infected people and at least one infected cat were included for

analysis. Eight of these households (4-9) had either two or three cats and four households (15,

16) had only one cat (Tables 2, S3, S4). The infection process of owners and cats was

79 longitudinally followed in most of these households.

For the statistical analysis of the transmission experiments, temporal data on infection of
inoculated and contact-or droplet-infected cats was collected. Within each experimental group,
an inoculated cat was classed as infectious when it was reported as shedding virus, regardless of

83 the viral load and of the detection method (virus isolation or RT-PCR). Contact cats were 84 considered susceptible for the period of days before the first day they were shown to shed virus (one day latent period (Table 3)). The prepared datasets (Tables S1, S2) were used to estimate L 85 (days), T (days), β (day⁻¹) and R₀. The first two parameters were estimated using parametric 86 87 survival regression models, β was estimated by using a SEIR model fitted by using a generalised linear regression model and R_0 was estimated either as the product of $T * \beta$ or by using the final 88 89 size method (FSM). The latter only requires information of the total number of infections in a group/household at the end of the infection process, when there is either no more infectious or no 90 91 more susceptible hosts present (17, 18). For analysis of the household data (Table 2), 92 transmission was analysed using the FSM, and the length of shedding was estimated using 93 parametric survival models. To simplify the analysis of transmission, it was assumed that the 94 source of infection of secondary infected cats was the first infected cat (infected by the owner) in 95 the household and the contribution of infected owners to the infection of secondary infected cats 96 was not included in the analysis. A detailed explanation of the statistical analysis is provided as 97 Supplemental material (Text S2). 98 For all experiments, L was estimated to be about one day, with no significant differences 99 observed between inoculated and contact infected cats (Table 3). The type of test has a clear 100 influence in the estimation of T, with estimates done using RT-PCR data leading to an

101 overestimation of T and consequently R_0 when compared with the FSM estimates. Using VI data

102 from contact-infected cats (assumed to closely reflect a "natural" infection) to estimate T and the

103 corresponding R_0 led to similar estimates to those done using the FSM (Table 2). The

104 experimental design had a large influence in the estimation of β ; with the design used in two of

the studies (11, 12) leading to an overestimation of this parameter and large standard errors.

106 Although a small sample size was used, the pair-transmission design used by Shi et al (13), 107 Halfmann et al (10) and Bao et al. (14) allowed the estimation of β and R_0 with good certainty 108 The former experiment assessed droplet-transmission whilst the latter two experiments assessed 109 direct transmission and allowed confirmation that R_0 is significantly higher than 1 (p < 0.05). 110 When combining these two experiments, the estimated $R_0 (T * \beta)$ for cats was 3.9 (95%) 111 confidence intervals: 2.2 - 6.8) or 3.3 (FSM) (1.1 - 11.8). These estimates were similar to the 112 estimates done at household level, with the estimated R_0 (FSM) being 3.8 (1.2 – 42.2) (Table 3). 113 Similarly, the estimates of T and virus shedding levels from household data were similar to those 114 estimates from the experiments (Table 3). Noting the assumptions made for the analysis of 115 household data, the results indicate that pair-transmission experiments appear to provide a 116 reliable approximation of the expected transmission dynamics of SARS-CoV-2 between cats at 117 household level. Compared to direct transmission, droplet transmission was slower $\beta = 0.14$ $(0.02 - 0.44) day^{-1}$ and may happen to a lower extend $R_0 = 1.0 (0.2 - 4.7)$ than direct 118 119 transmission (Table 3). 120 This study shows the importance of quantitatively assessing transmission when performing 121 transmission experiments and the relevance of a proper experimental design to obtain reliable 122 estimates of different parameters that describe the transmission process. Pair-transmission 123 experiments are a suitable design to assess transmission. By using both data from the studies that

used this type of experimental design (10, 14) and data from studies which followed infected households, we statistically confirmed that sustained transmission of SARS-CoV-2 among cats can be expected ($R_0 > 1$). To put this into perspective, scenarios in which contacts between stray and household cats take place (3) could lead to persistence of the virus in the cat population.

128 By combining field and experimental observations we could partly validate the suitability of 129 pair-transmission experiments to study transmission and the validity of the estimated parameters. 130 Whilst field observations would be ideal, it is practically impossible to obtain detailed temporal 131 data to have a thorough understanding of the transmission dynamics. Given this limitation, in 132 order to analyse the household data we had to make assumptions which influence our estimates. 133 The main assumption being that secondary infected cats were infected by the first infected cat in 134 the household, ignoring the possibility of these cats becoming infected by contact with the 135 infected owner. As a result the R_0 estimates could be overestimated. As for T and shedding 136 levels, observations were left censored, since first diagnosis of the cats was around five to seven 137 days after clinical onset of the infected owner (Table S4) and not all cats were followed daily, 138 which may affect the accuracy of these estimates. Nevertheless, they were similar to the 139 experimental estimates. The combination of experimental and field data in this study improved 140 the characterization of transmission between cats and increased the certainty in the estimated 141 parameters.

142 Interestingly, levels of virus shedding in household infected cats, were as high as those observed experimentally (Table 3), with reported shedding levels as high as 10^{8.5} RNA 143 144 copies/swab sample or RT-PCR CT values as low as 21 (Table S4). Considering both that 145 infected cats shed high levels of virus, and that droplet transmission is possible, the risk for cat-146 to-human transmission of SARS-CoV-2 may not be low. There is a need to further investigate 147 this risk. Experimental assessment of, for example, the probability of transmission via a 148 contaminated environment around an infected cat and measurements of virus concentrations in 149 infected cats' exhaled air would provide further information to quantify the risk for cat-to-human 150 transmission. This data combined with more detailed transmission and environmental

151	conta	mination data (5, 16) from infected household cats could aid to further quantify the
152	comb	ined risks of human-to-cat and cat-to-human transmission. Thorough understanding of
153	transr	nission of SARS-CoV-2 at the human-animal interplay is important to obtain a better
154	insigh	nt into the population dynamics of this virus.
155		
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162		
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243 Supplemental material

- **Text S1.** Literature search and selection of manuscripts
- **Text S2.** Data analysis methods for the estimation of transmission parameters
- **Table S1.** Collated data for the quantification of the transmission rate β (day⁻¹). Data for each
- 247 pair of cats (inoculated + contact) was collated daily from day one post inoculation to the day the
- 248 contact cat was assumed infected (one day before shedding virus).
- **Table S2.** Collated data for the estimation of the infectious and latent periods.
- **Table S3.** Collated data from infected households with more than one cat. These data were used
- 251 for the estimation of the reproductive number R_0 using the final size method.
- **Table S4.** Collated data from observational studies describing the longitudinal follow up of
- 253 infection in infected cats from infected households. These data were used to estimate the
- 254 duration of observed shedding in naturally infected cats.
- **Table S5.** Estimated Weibull parameters (Shape and Scale) describing the length of the
- 256 infectious period *T*.

- 257 Table 1. Summary of the experimental procedures showing the study design, the age of the cats, the inoculation route and dose, the
- type of samples taken and the diagnostic method used to quantify virus levels in time.

Study	Type of	Design	Cat's age	Inoculation	Dose	Units ^b	Sample	Diagnostic
	transmission	I x S ^a	(months)	Route	(\log_{10})		(route) ^c	test
Halfmann et al.(10)	Direct contact	1 x 1	3.5 to 4.2	Nasal, Tracheal,	5.7	PFU	Respiratory	\mathbf{VI}^{d}
				Oral,Ocular				
Bosco-Lauth et al.(11)	Direct contact	2 x 2	60 - 96	Nasal	5.4	PFU	Respiratory/rectal	VI
Gaudreault et al. (12)	Direct contact	3 x 1	4.5 - 5	Nasal, Oral	6	TCID ₅₀	Respiratory	RT-PCR
Bao et al.(14)	Direct contact	1 x 1	8 - 18	Nasal	6	TCID ₅₀	Respiratory/rectal	RT-PCR
Shi et al. juveniles.(13)	Indirect-droplet	1 x 1	2.3 to 3.3	Nasal	5	PFU	Respiratory	RT-PCR
Shi et al. subadults.(13)) Indirect-droplet	1 x 1	6 to 9	Nasal	5	PFU	Rectal	RT-PCR

 a I = number of inoculated cats and S = number of susceptible contacts per group at the start of the experiment.

- 260 ^b PFU = Plaque-forming units, $TCID_{50}$ = Fifty-percent tissue culture infective dose
- ^c Type of samples considered as respiratory were: nasal swabs, oropharyngeal swabs, nasal washes. Rectal samples were: rectal swabs

or faeces.

263 ^d VI = Virus Isolation

265 Table 2. Summary description of the households studies included for estimation of the shedding (infectious) period and the

266 Reproductive Number R_0 .

Studies	No. of households	Total No. of cats per household	Number of households with > 1 cat infected ^a	Sample (Route) ^b	Diagnostic test	Data used for estimation of	
Chaintoutis et al. (4), Hamer et al.(7), Neira et al.(6)	3	3	1	Respiratory/rectal	PCR, Serology	<i>R</i> ₀ , Shedding	
Hamer et al.(7), Klaus et al.(5), Segales et al.(9), Neira et al.(6) Goryoka et al.(8)	5	2	3	Respiratory/rectal	PCR, Serology	R_{0} , Shedding	
Barrs et al.(15), Bessiere et al.(16)	4	1		Respiratory/rectal	PCR, Serology	Shedding	
^a For a cat to be considered	l infected it ha	d to be seropo	sitive the last time	the cats in the house	hold were san	npled.	
or faeces.	ed as respirat	ory were. hasa	n swabs, oropharyn	igeal swabs of oral sy	wabs. Rectai s	amples were. rectar swabs	

Table 3. Quantified parameters for direct contact and droplet transmission of SARS-CoV-2 between cats using data from transmission 274

Study	No. groups	Peak shedding $(\log_{10} x/ml)^{b}$	Latent period $L (days)^{c}$	Infectious period $T(days)^{c}$	Transmission rate $B(day^{-1})$	R_0 mean (95% CI)		
	(No. without transmission)	$mean \pm SD$	mean (95% CI)	mean (95% CI)	mean (95% CI)	$T \ge \beta$	Final Size	
Direct transmission								
Halfmann et al.(10)	3 (0)	$4.0 \pm 0.5 \text{ PFU}^{d}$ $3.5 \pm 0.6 \text{ PFU}^{e}$		$4.6 (3.0 - 5.7)^{d}$ 5.4 (3.6 - 6.8) ^e	0.64 (0.16 - 1.66)	2.9 (1.0 - 7.6)	> 1.2	
Bosco-Lauth et al.(11)	1 (0)	$4.0 \pm 0.6 \text{ PFU}^{\text{d}}$ $4.1 \pm 1.4 \text{ PFU}^{\text{e}}$		$6.8 (4.5 - 8.4)^{d}$ 4.7 (3.0 - 5.8) ^e	2.77 (0.45 - 8.93)	15.2 (4.4 - 50.9)		
Gaudreault et al.(12)	2 (0)	9.0 RNA ^d		$6.6(3.8-8.7)^d$	1.46 (0.23 - 5.04)	9.6 (2.7 - 33.1)		
Bao et al. (14)	8 (4)	$3.4 \pm 0.5 \text{ RNA}^{d}$ $4.9 \pm 0.6 \text{ RNA}^{e}$		$10.0 (6.5 - 12.4)^{d}$ 11.6 (7.5 - 14.4) ^e	0.69 (0.21 - 1.65)	6.8 (2.8 - 16.3)	2.0 (0.5 - 7.7)	
Combined ^f			$\frac{1.1 \ (0.5 - 2.2)^d}{0.8 \ (0.3 - 1.9)^e}$	4.6 (3.0 - 5.7) ^d	0.88 (0.45 - 1.52)	3.9 (2.2 - 6.8) ^f	3.3 (1.1 - 11.8) ^g	
Droplet transmission								
Shi et al.juveniles(13)	3 (2)	$7.0 \pm 0.3 \text{ RNA}^{\text{e}}$		8.1 (4.6 - 10.6) ^e	0.10 (0.01 - 0.46)	0.8 (0.2 - 4.4)	1.0 (0.1 - 7.6)	
Shi et al.subadults(13)	3 (2)	$4.9 \pm 0.4 \text{ RNA}^{\text{e}}$		5.7 (3.3 - 7.5) ^e	0.22 (0.01 - 0.99)	1.2 (0.2 - 6.7)	1.0 (0.1 - 7.6)	
Combined			$0.8 (0.3 - 1.9)^{e}$		0.14 (0.02 - 0.44)	$1.1 (0.3 - 3.6)^{h}$	1.0 (0.2 - 4.7)	
Household transmission	n							
Households (4-6, 8, 9)	8 (2)	6.1 ±1.6 RNA 28.0 ±4.9 CT		6.6 (1.8 - 13.6)			3.8 (1.2 - 42.2)	

275	experiments	or obser	vational	studies	describing	infection	and tran	smission a	at household	l level. ^a
210	experiments	01 00501	varionai	bluarob	acoulonic	moonom	und trun		at mousemore	1 10 101.

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^b x values are plaque-forming units (PFU), RNA copy numbers. CT = Real time PCR (RT-PCR) cycle threshold. SD = standard 277

deviation 278

- c L was estimated fitting an exponential distribution. T was estimated fitting a Weibull distribution using either virus isolation data or
- 280 PCR data (see column peak shedding) (Text S2). CI = Confidence Intervals.
- ^d These are estimates for the contact-infected cats.
- ^e These are estimates for the inoculated-infected cats.
- 283 ^f Estimates done combining data from the different studies or groups when a combined analysis was possible. For estimation of R_0 the
- estimated *T* from the contact infected cats from Halfmann et al.(10) was used. This was because contact infected cats were assumed to
- resemble "natural" infection better than inoculated cats and that virus isolation is a better indicator of infectiousness than RT-PCR.
- ^g This estimate was done combining the data from Halfmann et al.(10) and Bao et al.(14).
- h Estimated using the estimated *T* from the juvenile group. This estimate was based on nasal shedding.