1   # The SARS-CoV-2 reproduction number R_0 in cats

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11   Running title: The R_0 of SARS-CoV-2 in cats

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14

15   Wordcount:

16   Abstract: 149

17   Main text: 1685

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19

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.

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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

39   implies quantifying transmission from humans-to-animals, from animals-to-animals and from

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

44   may be able to transmit the infection between cats. Indeed, transmission experiments confirmed

45   this possibility (10-14), however, the lack of a proper statistical assessment of transmission in the

46   reported experiments limits confident extrapolation of the results from the experiment to the

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

53   major outbreak and endemicity to occur, whereas when $R_0 < 1$ the infection is likely to peter out.

54   Other parameters which contribute to quantitatively describe transmission are: 1) the latent

55   period L, which is the time from becoming infected to becoming contagious, 2) the infectious

56   period T, which is the average period of time an individual is contagious and 3) the transmission

57   rate parameter β which is the number of contact infections caused by one typical infectious

58   individual per unit of time. Here, published experiments and observational studies describing

59   infection and transmission of SARS-CoV-2 between cats were reviewed. Data from these studies

60   were collated and analysed to statistically confirm whether cat-to-cat transmission can be

61   sustained and to provide estimates of relevant transmission parameters.

62   A systematic literature search was conducted which identified 115 publications. Upon

63   screening and selection of relevant studies for data collection and analysis, five experimental

64   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

68   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 $\geq 10^5$ PFU (Gaudreault et al (12) used 10^6

71    $TCID_{50}$) 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

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

75   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

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

78   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.

80   For the statistical analysis of the transmission experiments, temporal data on infection of

81   inoculated and contact-or droplet-infected cats was collected. Within each experimental group,

82   an inoculated cat was classed as infectious when it was reported as shedding virus, regardless of

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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

85   (one day latent period (Table 3)). The prepared datasets (Tables S1, S2) were used to estimate L

86    $(days)$, T $(days)$, β (day^{-1}) and R_0. The first two parameters were estimated using parametric

87   survival regression models, β was estimated by using a SEIR model fitted by using a generalised

88   linear regression model and R_0 was estimated either as the product of $T * \beta$ or by using the final

89   size method (FSM). The latter only requires information of the total number of infections in a

90   group/household at the end of the infection process, when there is either no more infectious or no

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

105   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 $\beta = 0.14$

118   (0.02 – 0.44) day^{-1} and may happen to a lower extend $R_0 = 1.0$ (0.2 – 4.7) than direct

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

124   used this type of experimental design (10, 14) and data from studies which followed infected

125   households, we statistically confirmed that sustained transmission of SARS-CoV-2 among cats

126   can be expected ($R_0 > 1$). To put this into perspective, scenarios in which contacts between stray

127   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

143   observed experimentally (Table 3), with reported shedding levels as high as $10^{8.5}$ RNA

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   contamination data (5, 16) from infected household cats could aid to further quantify the

152   combined risks of human-to-cat and cat-to-human transmission. Thorough understanding of

153   transmission of SARS-CoV-2 at the human-animal interplay is important to obtain a better

154   insight into the population dynamics of this virus.

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243   **Supplemental material**

244   **Text S1.** Literature search and selection of manuscripts

245   **Text S2.** Data analysis methods for the estimation of transmission parameters

246   **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).

249   **Table S2.** Collated data for the estimation of the infectious and latent periods.

250   **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.

252   **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.

255   **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

258 type of samples taken and the diagnostic method used to quantify virus levels in time.

Study	Type of transmission	Design I x S[a]	Cat's age (months)	Inoculation Route	Dose (log$_{10}$)	Units[b]	Sample (route)[c]	Diagnostic test
Halfmann et al.(10)	Direct contact	1 x 1	3.5 to 4.2	Nasal,Tracheal, Oral,Ocular	5.7	PFU	Respiratory	VI[d]
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

259 [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

261 [c] Type of samples considered as respiratory were: nasal swabs, oropharyngeal swabs, nasal washes. Rectal samples were: rectal swabs

262 or faeces.

263 [d] VI = Virus Isolation

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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	R_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

267 [a] For a cat to be considered infected it had to be seropositive the last time the cats in the household were sampled.

268 [b] Type of samples considered as respiratory were: nasal swabs, oropharyngeal swabs or oral swabs. Rectal samples were: rectal swabs

269 or faeces.

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

275   experiments or observational studies describing infection and transmission at household level.[a]

Study	No. groups /households (No. without transmission)	Peak shedding ($\log_{10}$ x/ml)[b] mean ± SD	Latent period L (days)[c] mean (95% CI)	Infectious period T (days)[c] mean (95% CI)	Transmission rate B (day^{-1}) mean (95% CI)	R_0 mean (95% CI)	
						T x β	Final Size
Direct transmission							
Halfmann et al.(10)	3 (0)	4.0 ±0.5 PFU[d] 3.5 ±0.6 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 ±0.6 PFU[d] 4.1 ±1.4 PFU[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 ±0.5 RNA[d] 4.9 ±0.6 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]			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 ±0.3 RNA[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 ±0.4 RNA[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							
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)

276   [a] Where relevant, empty cells represent analysis not done. Data was not suitable/sufficient to perform the corresponding analysis.

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

278   deviation

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279 ^{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.

281 ^{d} These are estimates for the contact-infected cats.

282 ^{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

284 estimated *T* from the contact infected cats from Halfmann et al.(10) was used. This was because contact infected cats were assumed to

285 resemble "natural" infection better than inoculated cats and that virus isolation is a better indicator of infectiousness than RT-PCR.

286 ^{g} This estimate was done combining the data from Halfmann et al.(10) and Bao et al.(14).

287 ^{h} Estimated using the estimated *T* from the juvenile group. This estimate was based on nasal shedding.