The Journal of Veterinary Medical Science

NOTE

Virology

Feline coronavirus isolates from a part of Brazil: insights into molecular epidemiology and phylogeny inferred from the *7b gene*

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J. Vet. Med. Sci.
81(10): 1455–1460, 2019
doi: 10.1292/jvms.19-0090

Received: 13 February 2019
Accepted: 23 July 2019
Advanced Epub:
23 August 2019

ABSTRACT. The *Feline coronavirus* (FCoV) can lead to Feline infectious peritonitis (FIP), which the precise cause is still unknown. The theory of internal mutation suggests that a less virulent biotype of FCoV (FECV) would lead to another more pathogenic biotype (FIPV) capable of causing FIP. In this work, the *7b gene* was amplified from 51 domestic cat plasma samples by semi-nested PCR and tested through phylogenetic and phylogeographical approaches. The *7b gene* of Brazilian isolates displayed high conservation, a strong correlation between the geographic origin of the viral isolates and their genealogy, and its evolution was possibly shaped by a combination of high rates of nucleotide substitution and purifying selection.

KEY WORDS: *7b gene*, *Feline coronavirus*, molecular epidemiology, phylogeny

The *Feline coronavirus* (FCoV) is an important pathogen of domestic and wild felids, which can cause subclinical infection, mild enteritis or lead to feline infectious peritonitis (FIP), a fatal disease characterized by inflammatory lesions of serous membranes and systemic granulomatous lesions of parenchymatous organs [23].

Although the precise cause of FIP pathogenesis is still unknown, several hypotheses have been suggested [20]. The most accepted hypothesis, called internal mutation theory, suggests that during the replication of FCoV in the intestinal epithelium, a mutation occurs that makes the virus more pathogenic and able to infect monocytes and macrophages and cause FIP [23, 27]. This virulent mutant variant was designated *Feline infectious peritonitis virus* (FIPV), while a variant that leads to enteric infection has been termed *Feline enteric coronavirus* (FECV) [25]. The precise nature of the mutation responsible for the pathogenesis has not been identified in the FCoV genome [10]. Nevertheless, it has been deduced that the non-structural glycoprotein 7b, codified by ORF7b, plays a determinative role in FCoV virulence [31], besides having a strong phylogenetic sign for the differentiation between FECV and FIPV [3].

To better understand the molecular epidemiology of FCoV in Brazilian domestic cats, phylogenetic hypothesis and viral population dynamics were inferred from the *7b gene*. A phylogenetic hypothesis and the reconstructed population history of FCoV isolates are presented in this work, providing insights into the origins of FCoV in Brazil. Furthermore, the molecular analysis of *7b gene* dispenses considerations about the internal mutation theory, regarding to the virulence of the serotypes of FCoV.

This study included samples from 210 domestic cats (*Felis catus*) of various breeds, random selected from different local animal hospitals (Minas Gerais, Brazil) during 2003–2010. One hundred twenty-nine animals were healthy and taken to veterinary clinics for vaccinations and/or elective surgery. Eighty-one of them showed clinical symptoms of FIP such as anorexia, weight loss,

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jaundice, recurrent fever, iritis, or neurological signs and abdominal or pleural effusion [17, 23].

Blood samples were obtained by venipuncture and collected in tubes with ethylenediaminetetraacetic acid (EDTA). The plasma was obtained and frozen at −80°C. The collection procedures were performed according to the Ethical Principles in Animal Research of the School of Veterinary Medicine of the University of Viçosa (register number 34/2010). Viral sequences isolated from healthy animals or those with clinical symptoms of FIP were designated as FECV and FIPV sequences, respectively.

The complete accessory protein *7b gene* (766 nt) was amplified by semi-nested PCR with two rounds of amplification using two pairs of primers previously described by Lin and others [17]. The reaction products of the semi-nested PCR were purified and sequenced by Macrogen Inc., Seoul, Korea. Contigs of the nucleotide sequences were assembled using Phred [12] and Phrap (http://www.phrap.org). The complete *7b gene* coding sequences were submitted to GenBank (JX239089-JX239139).

The *7b gene* complete sequences of 58 FCoV isolates were downloaded from GenBank (http://www.ncbi.nlm.nih.gov/Genbank). Thus, the final dataset selected contained 109 *7b gene* sequences, including the sequences of Brazilian isolates.

Phylogenetic evidence for recombination was tested, and recombination breakpoints were predicted using different methods (P<0.01) available in RDP3 version 3.44 [19], including RDP [18], GENECONV [21], MaxChi [28], and Bootscan/Recscan [20]. Only those recombination events predicted by at least three of the methods were taken as valid; the recombinant sequences were removed from the dataset in codon selection analysis.

Selective pressure on each codon of the *7b gene* sequence was evaluated using the difference between non-synonymous (dN) and synonymous (dS) substitution rates per codon using the single-likelihood ancestor counting (SLAC), fixed-effects likelihood (FEL), and internal branches fixed-effects likelihood (IFEL) methods found in DataMonkey (http://www.datamonkey.org/).

Phylogenetic hypotheses for the *7b gene* were inferred by Bayesian inference (BI) and maximum likelihood (ML) (Fig. 1) using MrBayes v3.1.2 [16] and GARLI 2.0 [34], respectively. The *7b gene* sequence of canine coronavirus (GenBank ID: GU146061) was added to the dataset as an out-group taxon to root the phylogenetic trees.

Sequences were aligned using MUSCLE v.3.8.31 9 [11]. Sites with gaps were excluded. To expedite the construction of phylogenetic trees, a model of nucleotide substitution was estimated using the jModelTest program [5]. The TIM3ef+I+G substitution model was selected as the best DNA evolution model according to the AIC, AICc, and BIC criteria.

The BI phylogenetic trees were calculated using the Bayesian Markov Chain Monte Carlo (MCMC) method, in two runs with 50,000,000 generations and a sample frequency of 1.000. At the end of each run, the average standard deviation of the split frequencies was 0.015022. The convergence of the parameters was analyzed in TRACER v1.5.0, and the chains reached a stationary distribution after 500,000 generations. Then, a total of 1% of the trees generated was burned to produce the consensus trees.

The TIM3ef+I+G substitution model was selected in the GARLI settings (ratematrix=(0 1 2 0 3 2); statefrequencies=estimate; ratehetmodel=gamma; numratecats=4; invariantsites=estimate), and the statistical support of the ML phylogenetic trees was calculated by 1,000 bootstrap replicates. The 50% majority rule consensus trees of all bootstrap replicates were summarized using the SumTrees of DendroPy 3.8.0 [30].

The population history of the FCoV isolates was reconstructed using a Bayesian skyline plot (BSP), which estimates changes in the effective population size over time [8]. The BSP analysis was carried out in BEAST v1.7.2 [7] according to the BSP tutorial (http://beast-mcmc.googlecode.com/files/BSP.pdf).

Only FCoV sequences were selected in BSP analysis. Sequences were aligned using MUSCLE v.3.8.31 9 [11]. Alignments were manually inspected, and the sites with gaps were excluded. The TPM3uf+I+G substitution model was selected as the best DNA evolution model by jModeltest program [8], according to the AIC, AICc, and BIC criteria.

To estimate *7b gene* mutation rates, the years of collection of FCoV isolates were retrieved from GenBank. Three molecular clock model assumptions (strict-clock, Bayesian-relaxed exponential molecular clock, and Bayesian-relaxed lognormal molecular clock) were tested. In each test, a MCMC run (1,000,000,000 generations) was performed considering TPM3uf+I+G as the substitution model, the respective molecular clock model assumption, and BSP as a coalescent tree prior. The high number of generations was selected to reach a large effective sample size (ESS>200). For this purpose, analyses were processed on graphics processing units (GPUs) in a computational cluster at UFV, using BEAGLE v1.0 (http://code.google.com/p/beagle-lib/) with BEAST v1.7.2.

For each test, the convergence of the parameters (including the estimated mutation rate) was analyzed in TRACER v1.5.0, and the chains reached a stationary distribution after 10,000,000 generations. The marginal likelihoods obtained in each test were compared by Bayes factor calculations [29] with 1,000 bootstrap replicates. The test with the highest Bayes factor corresponds to the best-fit clock model and a better estimation of the mutation rate. Following this, 1% of the trees generated were burned to produce a consensus time-tree (Fig. 2) using TreeAnnotator v1.7.2 [7].

To test the influence of geographic structure and of the virulence of strains in the FCoV population, the phylogenetic trees were analyzed in BaTS v1.0 (Bayesian Tip-Significance testing) [22]. In these tests (geographic distribution and virulence), the high credibility set of trees estimated in the BSP MCMC run were selected, and the association index (AI) [33], parsimony score (PS) [27], and maximum monophyletic clade size (MC) [22] were calculated using 10,000 replicates (Table 1).

A total of 210 plasma samples from domestic cats (*F. catus*) were analyzed by semi-nested PCR from the accessory protein *7b gene*. Fifty-one samples were positive for the *7b gene* of FCoV. In the analysis of the positive samples was found a prevalence of asymptomatic cats of 68.63%, and 31.37% of the cats had symptoms of FIP.

In sequence alignments, the *7b genes* of FCoV isolates presented overall identity ranging from 41.33% (excluding sites with gaps) to 50.48% (excluding sequences with gaps).

Estimation of codon selection pressures in the 7b protein showed that 27.67% of codons were predicted to be negative selection

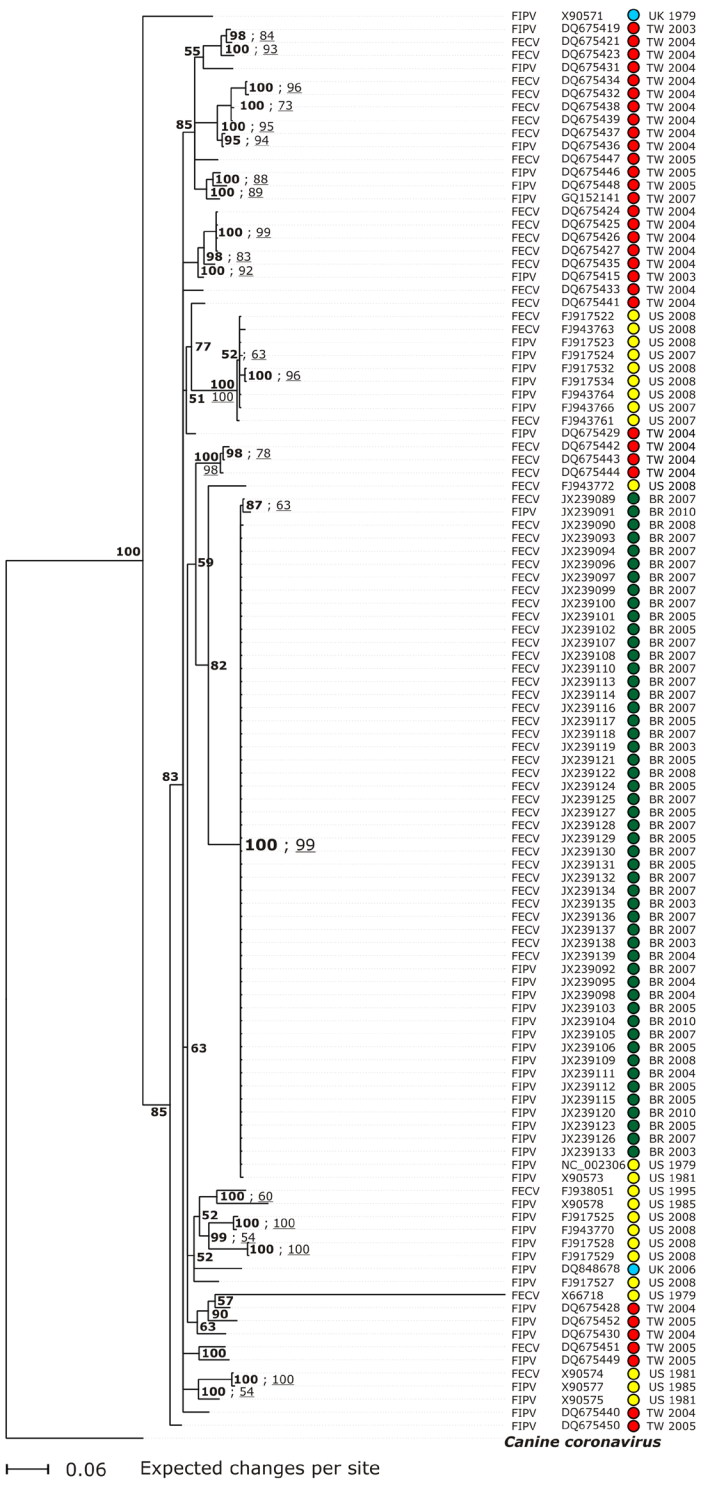

Fig. 1. Evolutionary relationships between *Feline coronavirus* (FCoV) isolates based on the *7b gene*. The majority-rule consensus tree was obtained by Bayesian MCMC coalescent analysis of 109 complete *7b gene* sequences. The posterior probability values (PP) (bold; expressed as percentages) calculated using the best trees found by MrBayes are shown beside each node. The second value corresponds to the bootstrap value (BV) (underlined; expressed as percentage) that defines the clusters in the maximum likelihood tree. The outgroup taxon is an isolate of canine coronavirus (GenBank ID: GU146061).

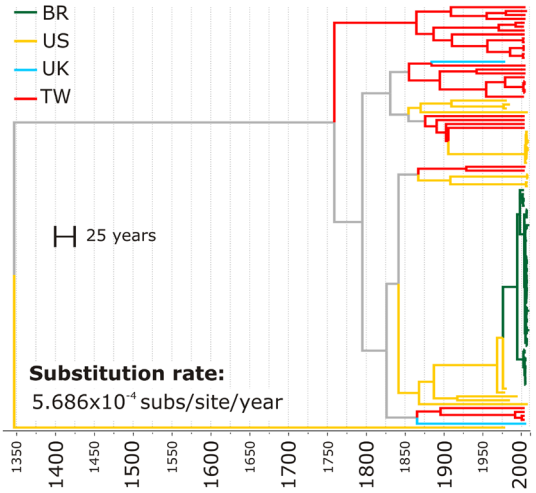

Fig. 2. Time tree of *Feline coronavirus* (FCoV) isolates reconstructed from the *7b gene*. The majority-rule consensus tree of the *7b gene* was obtained by a coalescent Bayesian skyline analysis with an exponential molecular clock model assumption using BEAST. The colors of branches indicate the geographic origin of the FCoV isolates.

sites, with a global dN/dS estimate of 0.306. Purifying selection is indicated by estimation of codon selection pressures in the 7b protein.

The Brazilian isolates presented higher conservation of *7b gene* sequence, with an overall identity of 98.87% in the sequence alignment. Only seven polymorphic sites differentiate the sequences of JX239089 (FECV), JX239090 (FECV), JX239091 (FIPV), and JX239092 (FIPV) from those of the other 47 isolates (33 FECV and 14 FIPV). These polymorphisms result in the following amino acid substitutions in the 7b protein: H160P for JX239089; H48Y for JX239090; S89F, T159N, H160P, Y167D, and C168W for JX239091; and A19S for JX239092.

To describe the correlation between geographic location, virulence of strains, and genealogy estimated by Bayesian analyses, summary statistics were calculated by BaTS [22] (Tables 1 and 2) that correlate the viral phenotypic characters with the shared ancestry (represented by the phylogenetic tree). This correlation was measured by computation of the association index (AI) [33], parsimony score (PS) [27], and maximum monophyletic clade size (MC) [22]. The AI and PS test the association between traits (geographic distribution and virulence) and tree topology. The MC index tests whether traits are associated with phylogeny. Stronger phylogeny–trait associations should produce larger monophyletic clades (MC) sharing the same trait [22].

The *7b gene* phylogenetic trees (Figs. 1 and 2) suggest a geographic pattern of the distribution of FCoV viral isolates. All Brazilian isolates (sampled between 2003 and 2010) were included in the same monophyletic clade with two other North American

Table1. Geographic effect on the population structure of *Feline coronavirus* (FCoV) isolates

Tested correlation	Statistics[a)]	Observed	Expected [b)]	*P*-value*
Geographic origin	AI	0.2413 (0.0125; 0.5361)	7.4867 (6.6256; 8.2920)	0
Geographic origin	PS	7.65 (6.0000; 9.0000)	48.5762 (45.6100; 51.2300)	0
Taiwan	MC	15.11 (14.0000; 23.0000)	2.4121 (2.0200; 3.2400)	1.00E-04
United States	MC	9.25 (9.0000; 12.0000)	1.9445 (1.4700; 2.3500)	1.00E-04
United Kingdom	MC	1 (1.0000; 1.0000)	1.005 (1.0000; 1.0200)	1
Brazil	MC	46.85 (29.0000; 51.0000)	3.5105 (2.7300; 4.5900)	1.00E-04

The numbers in parentheses correspond to the 95% lower and upper bounds of the highest-probability density intervals. a) AI: association index; PS: parsimony score; MC: maximum monophyletic clade; b) Expected value on null hypothesis (random phylogeny-trait association). *Statistical significance of tests: $P<0.01$.

FIPV isolates (NC_002306 and X90573, sampled in 1979 and 1981, respectively) (Fig. 1).

This work provides a comprehensive analysis of the molecular epidemiology of FCoV isolates circulating in Brazil through prediction of the main events of viral introduction, and it provides new insights about viral population dynamics and selection pressures that shaped the evolution of the FCoV *7b gene*.

In sequence alignments, previous studies have suggested a strong correlation between insertions/deletions (indels) in the *7b gene* and the virulence of FCoV viral strains [15, 31, 32]. However, no correlation between indels in the *7b gene* and virulence was found in sequence alignments, as also described by Battilani and others [2], Lin and others [17] and Bank-Wolf and others [1].

With higher conservation of *7b gene* sequence, the Brazilian isolates presented only seven polymorphic sites. Most of these polymorphisms were predicted to be neutral sites in the estimation of selection pressure, seeming to be random and not correlated with the virulence of strains. This high conservation of the *7b gene* among Brazilian FCoV isolates shows that the internal mutation theory [1, 23, 31] possibly could not be considered for this gene. According to this theory, virulent strains (FIPV) evolve from avirulent strains (FECV) by mutation during infection in cats.

Homologous recombination has an important role in FCoV evolution, and there is evidence of recombinant strains of FCoV that arose from recombination between FCoV and canine coronavirus (CCoV) [14]. In the recombination analysis of 7b sequences by RDP3, only one recombination event, involving three Taiwanese FCoV isolates sampled in 2004, was detected. Isolate DQ675437 (FECV) was predicted to be a recombinant of DQ675439 (FECV) and DQ675429 (FIPV) ($P=1.636 \times 10^{-3}$). This finding possibly suggests a low frequency of homologous recombination of the *7b gene* among FCoV strains.

Substitution rates also provide good insight into virus evolution, reflecting the restrictions in genetic diversity that lead to variations in adaptability and pathogenicity of the viral population [6]. Bayes factors analysis suggested that the Bayesian-relaxed exponential molecular clock was the best-fit model for the *7b gene* sequences, and the estimated mean substitution rate was 5.686×10^{-4} substitutions/site/year. This estimate agrees with what has been described for other RNA viruses, whose rates generally range from 10^{-2} to 10^{-5} substitutions/site/year [9, 13, 26].

Although most FECV and FIPV strains were included in monophyletic clades with other viral isolates that share the same geographic origin (i.e., Brazil, the United Kingdom, the United States, or Taiwan), it was not possible to define monophyletic clades that distinguish FECV and FIPV.

In geographic pattern analysis (Table 1), the topology of the *7b gene* phylogenetic tree was supported by significant values of AI and PS, and all countries, with the exception of the United Kingdom (probably due to the lower sample size), showed differentiated subpopulations supported by significant MC values. In virulence pattern analysis (Table 2), no significant correlations were found by calculation of AI, PS, or MC. Thus, 7b sequences of FCoV isolates are possibly phylogenetically structured according to their geographic origin irrespective of their pathotype as shown by others [1, 2, 4, 17]. These findings contradict the hypothesis of distinct virulent (FIPV) and avirulent (FECV) strains circulating in natural populations of FCoV, proposed by Brown and others [3]. According to this hypothesis, these two viral strains would be expected to be separated into monophyletic clusters in the phylogenetic tree inferred from the *7b gene*.

RNA viruses may present great genetic diversity variation at the population level, allowing the reconstruction of phylogeny that reflects their epidemiological history [6]. In this way, the time tree of Bayesian Skyline analysis predicted the possible events of viral introduction over time (Fig. 2). Different events of viral introduction in Taiwan, the United Kingdom, and the U.S.A. occurred between 1850 and 1950 and are highlighted in the phylogenetic time-tree (Fig. 2). These observations are consistent with the epidemiological history of FCoV. After World War II, there was a dramatic shift in the status of cats as pets. The number of pet cats greatly increased, and this is known to favor FCoV infection [24].

A possible source of FCoV introduction in Brazil is based on the inclusion of all Brazilian isolates in the same monophyletic clade with two North American FIPV isolates (NC_002306 and X90573), witch presented identical sequences to the 47 Brazilian

Table 2. Effect of virulence on the population structure of *Feline coronavirus* (FCoV) isolates

Tested correlation	Statistics[a)]	Observed	Expected[b)]	*P*-value*
Virulence	AI	4.8142 (3.7616; 5.7645)	5.6474 (4.7441; 6.5434)	0.07
Virulence	PS	32.03 (29,0000; 34.0000)	36.0344 (32,8600; 38.87004)	0.02
FECV[I)]	MC	5.81 (5.0000; 9.0000)	4.2245 (3.3500; 6.0200)	0.1
FIPV[II)]	MC	4.46 (4.0000; 6.0000)	3.3531 (2.6200; 4.3200)	0.15

The numbers in parentheses correspond to the 95% lower and upper bounds of the highest-probability density intervals. a) AI: association index; PS: parsimony score; MC: maximum monophyletic clade; b) Expected value on null hypothesis (random phylogeny-trait association). I) Less-pathogenic biotype of FCoV; II) Pathogenic biotype of FCoV. *Statistical significance of tests: $P<0.01$.

isolates (33 FECV and 14 FIPV) (Fig. 1). According to the phylogenetic time-tree (Fig. 2), the introduction of FCoV in Brazil possibly occurred since 1975.

The authors have shown that Brazilian FCoV isolates were recently introduced from the North America, and that evolution of the *7b gene* was possibly shaped by a combination of high rates of nucleotide substitution (5.686×10^{-4}) and purifying selection. Furthermore, the time tree of the present study suggests that FCoV introduction in Brazil occurred over the past of 40 years. Additionally, the findings of the present study suggest that both the internal mutation theory [23, 31] and the hypothesis of distinct virulent (FIPV) and avirulent (FECV) strains circulating [3] possibly cannot be taken as valid for the *7b gene*. The authors have reported high conservation among sequences of Brazilian isolates and a strong correlation between the geographic origin of viral isolates and the genealogy predicted from the *7b gene*. Thus, it is more plausible that FIP is clinically manifested in cats, mainly due to host and environmental factors and independent of genetic differences between FECV and FIPV. Comparative sequence analysis may eventually not be sufficient to answer the FECV/FIPV question.

CONFLICT OF INTEREST. The authors declare that they have no conflict of interest.

AUTHOR CONTRIBUTIONS. All authors contributed to this work and agreed to its publication.

ACKNOWLEDGMENTS. The authors would like to thank Mauricio Resende from the Laboratory of Comparative Virology (Institute of Biological Sciences, Federal University of Minas Gerais); José Cleydson Ferreira da Silva from BIOAGRO (Federal University of Vicosa); and the Department of Information Technology (Federal University of Vicosa; http://www.cpd.ufv.br). This research was supported by the Brazilian Government Agencies Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES), Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) and Fundação de Amparo à Pesquisa do Estado de Minas Gerais (FAPEMIG).

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