ENTERITES VIRAIS

Prof. Dr. Paulo Eduardo Brandão
Departamento de Medicina Veterinária Preventiva e Saúde Animal
Faculdade de Medicina Veterinária e Zootecnia
Universidade de São Paulo

ENTERITES VIRAIS

1. DEFINIÇÃO
2. IMPACTO EM SAÚDE PÚBLICA E PRODUÇÃO
3. DISTRIBUIÇÃO E FORMAS DE OCORRÊNCIA
4. CORONAVÍRUS
5. ROTAVÍRUS
6. OUTROS VÍRUS
7. FISIOPATOLOGIA
8. CORONAVÍRUS E ROTAVÍRUS EM DIVERSAS ESPÉCIES
9. CADEIA EPIDEMIOLÓGICA
10. DIAGNÓSTICO
11. PREVENÇÃO E CONTROLE
12. TRATAMENTO
13. REFERÊNCIAS

√ Presentes diariamente na vida do MV

√ Não apenas em neonatos/jovens

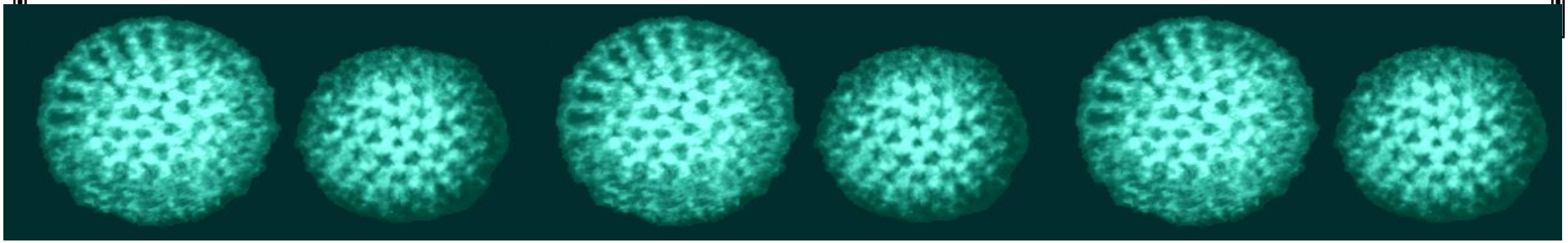
√ Interação entre diferentes vírus

√ Zoonoses

ENTERITES VIRAIS

1. DEFINIÇÃO

ENTIDADES MÓRBIDAS INFECTO-CONTAGIOSAS DO SISTEMA DIGESTÓRIO QUE ACOMETEM PRINCIPALMENTE ANIMAIS NEONATOS, MANIFESTANDO-SE SOB A FORMA DE VARIADOS GRAUS DE ENTERITE, CAUSADA POR VÍRUS DOS GÊNEROS *CORONAVIRUS*, *ROTAVIRUS*, *ADENOVIRUS*, *BREDAVIRUS* E *PARVOVIRUS*.



ENTERITES VIRAIS

2. IMPACTO EM SAÚDE PÚBLICA E PRODUÇÃO

√ A CADA 24 h: 200 MILHÕES DE PESSOAS COM GASTROENTERITES

√ UBIQUITÁRIA EM CRIANÇAS < 5 ANOS

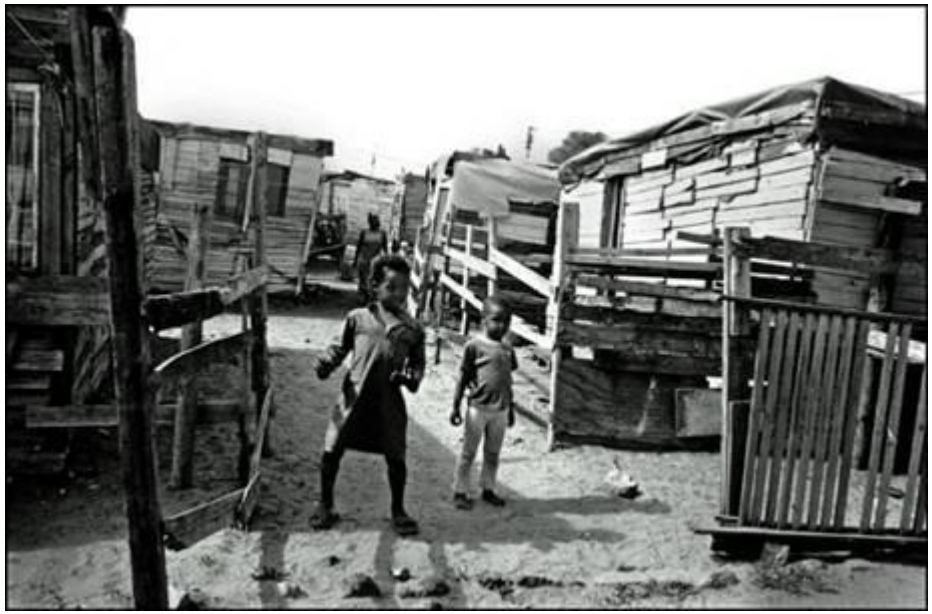
√ A CADA ANO: 500.000 MORTES INFANTIS POR ROTAVÍRUS

ENTERITES VIRAIS

2. IMPACTO EM SAÚDE PÚBLICA E PRODUÇÃO

ZOONOSES CLÁSSICAS (ROTAVÍRUS)

ZOONOSES POTENCIAIS (CORONAVÍRUS)



ENTERITES VIRAIS

2. IMPACTO EM SAÚDE PÚBLICA E EXPLORAÇÃO ANIMAL

NEONATOS

RETARDO NO CRESCIMENTO
MORTALIDADE

ADULTOS

↓PRODUÇÃO DE LEITE
↓GANHO DE PESO
PERDA DE CONDIÇÃO CORPORAL

ADULTOS/ NEONTATOS

INFECÇÕES SECUNDÁRIAS
CUSTO COM TRATAMENTOS

ENTERITES VIRAIS

3. DISTRIBUIÇÃO E FORMAS DE OCORRÊNCIA

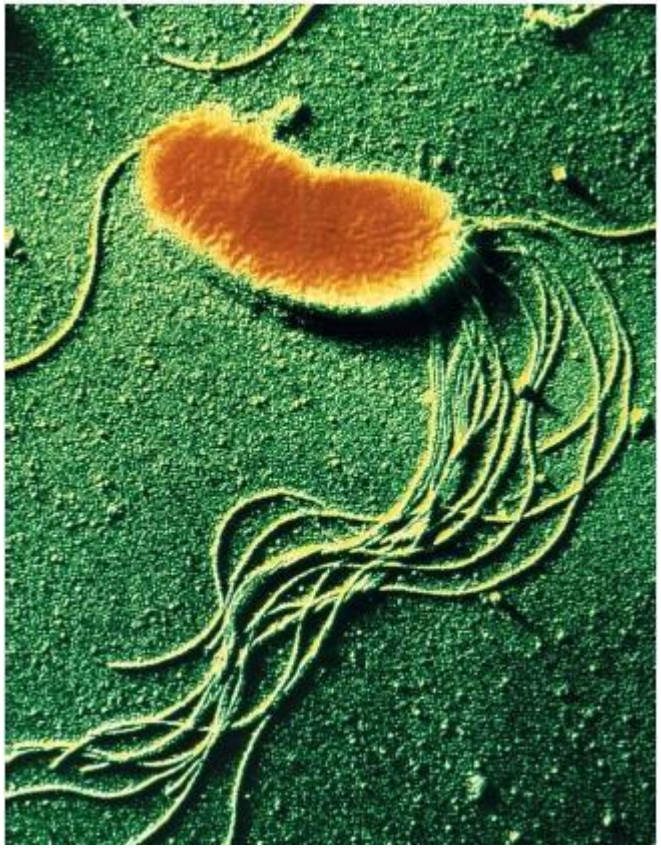
DISTRIBUIÇÃO: MUNDIAL

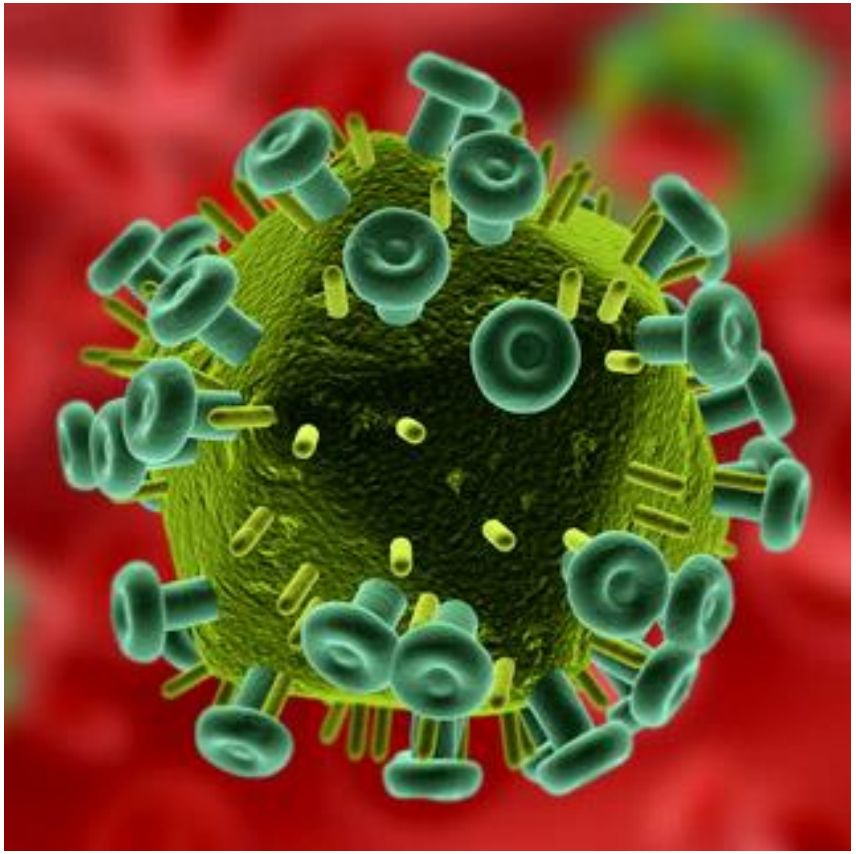
MAIS COMUM: ENDÊMICA

ADULTOS: EPIDÊMICA

ENTERITES VIRAIS

3. DISTRIBUIÇÃO E FORMAS DE OCORRÊNCIA





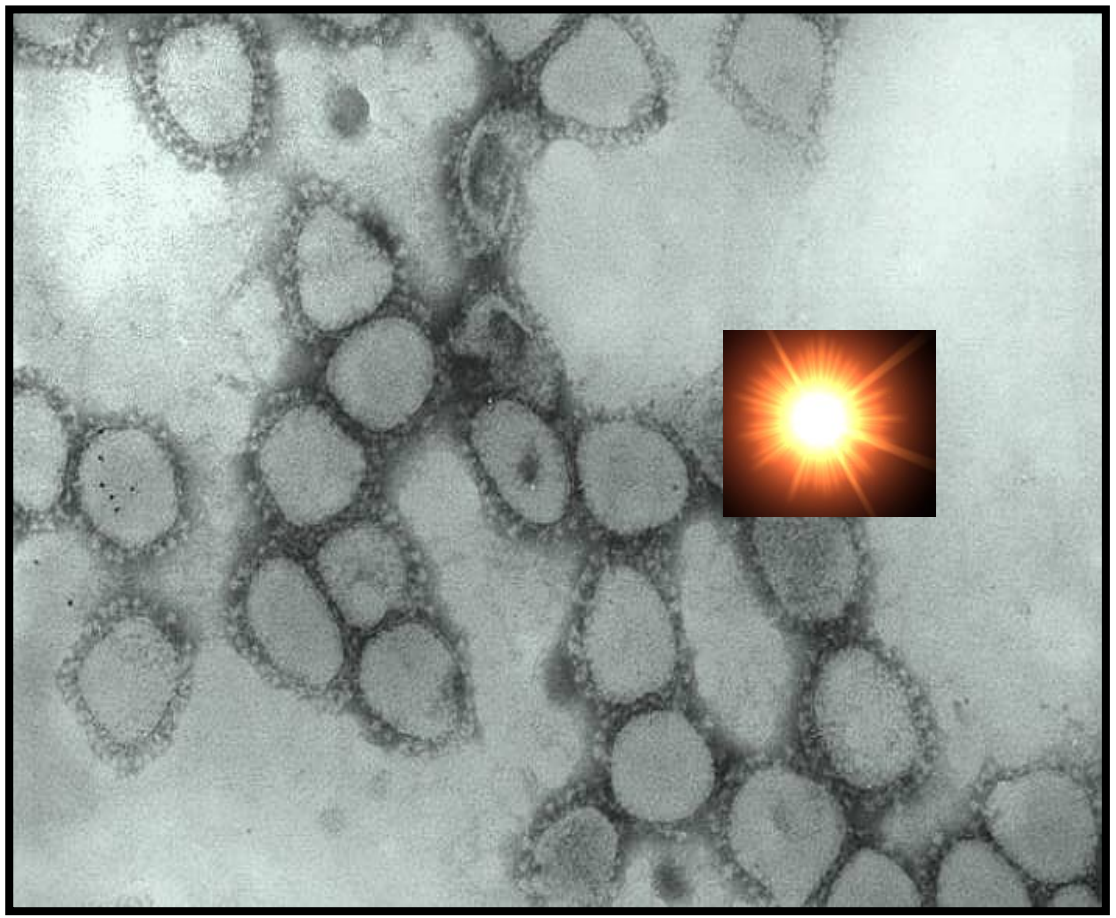
TENDÊNCIA SAZONAL DE DIARRÉIAS VIRAIS: ↓ TEMPERATURAS***

→

↓UV
↓UMIDADE
ESTRESSE TÉRMICO
↑ DENSIDADE POPULACIONAL

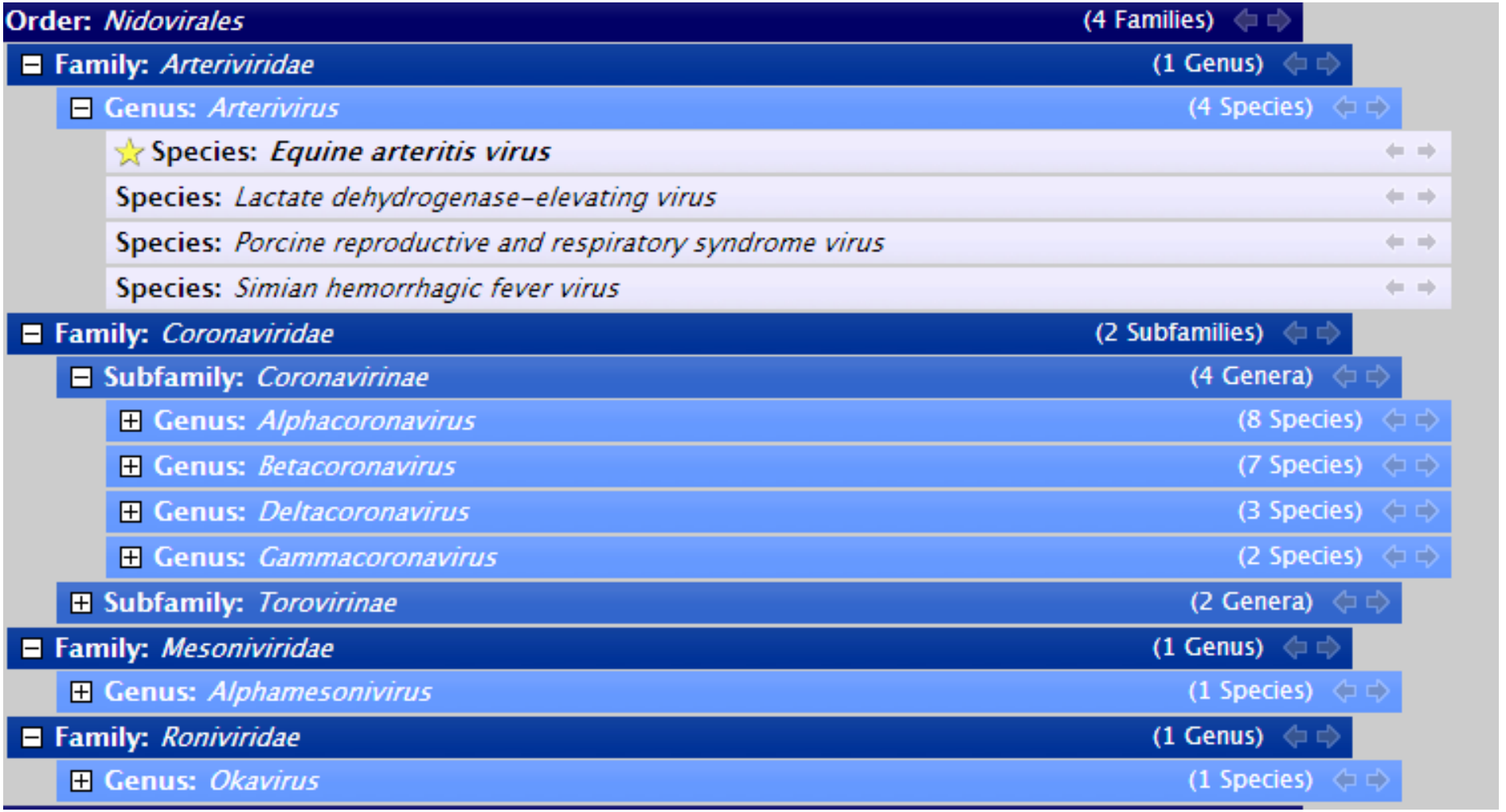
ENTERITES VIRAIS

4. CORONAVÍRUS



ENTERITES VIRAIS

4. CORONAVÍRUS



http://ictvonline.org/virusTaxonomy.asp

ENTERITES VIRAIS

4. CORONAVÍRUS

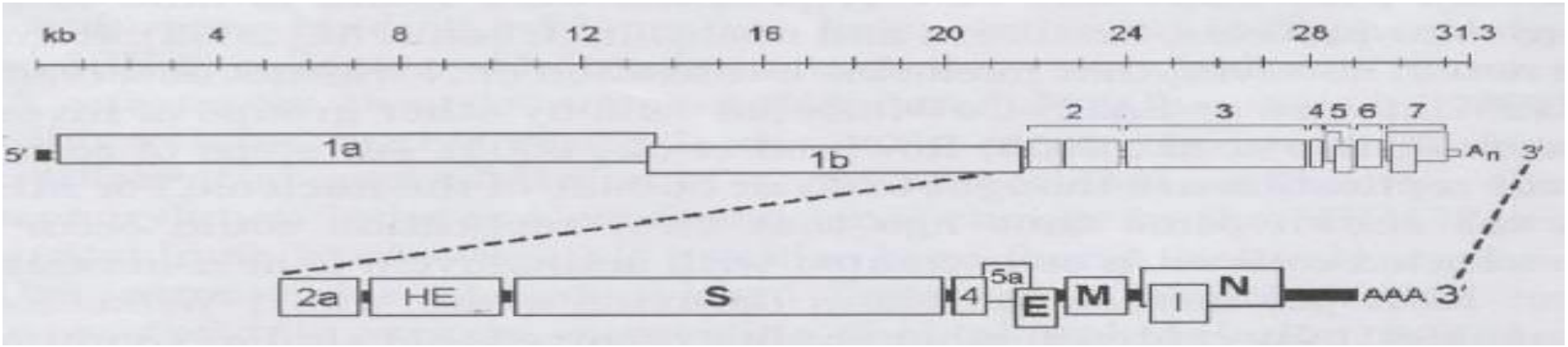
de Groot RJ et al. Middle East respiratory syndrome coronavirus (MERS-CoV): announcement of theCoronavirus Study Group. J Virol. 2013 Jul;87(14):7790-2.

ENTERITES VIRAIS

4. CORONAVÍRUS

GENOMA

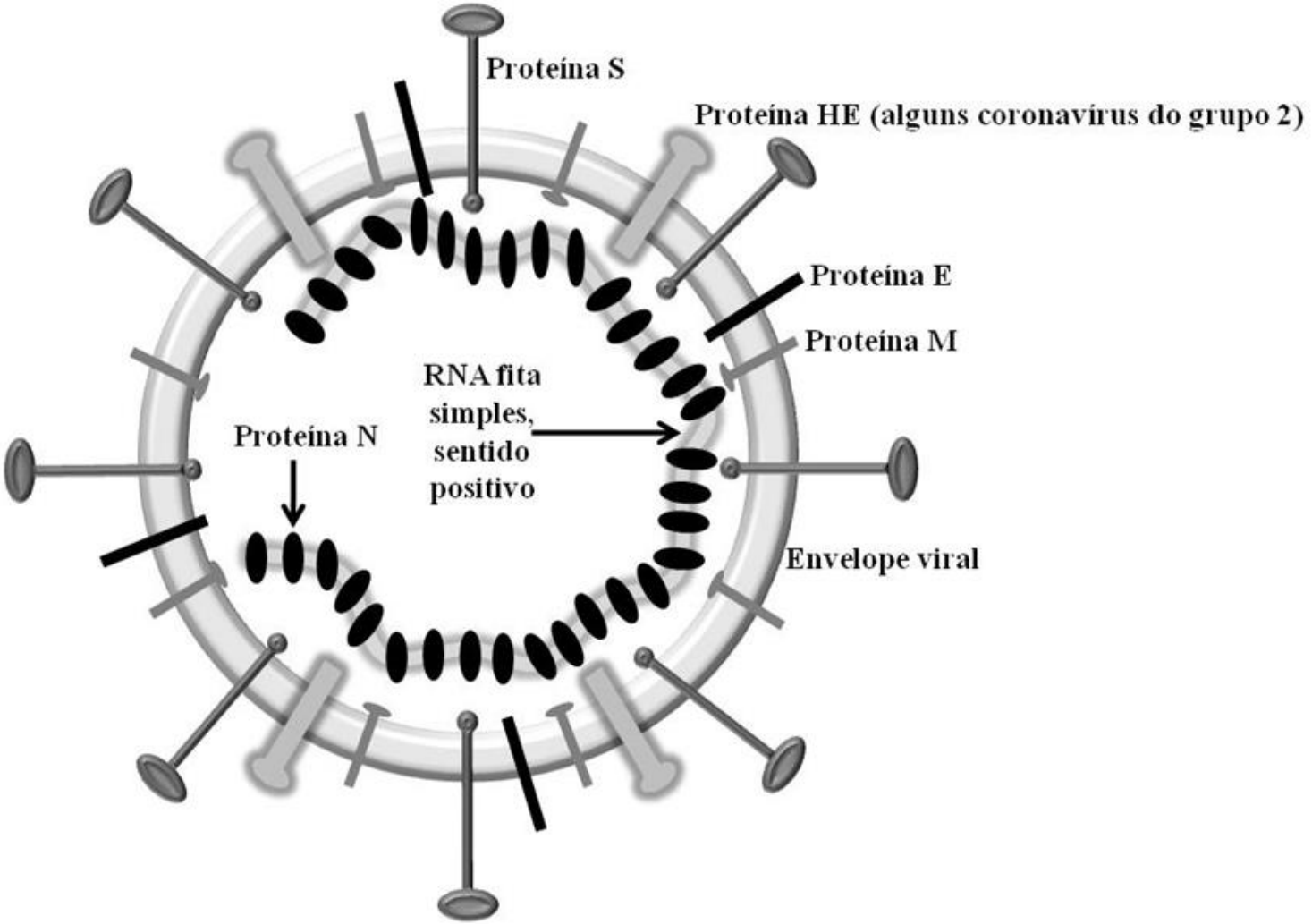
ssRNA
SENTIDO POSITIVO
NÃO-SEGMENTADO
27-32kb



Masters, P. S. The molecular biology of coronaviruses. **Advances in Virus Research, v. 66,**p. 193-292, 2006.

ENTERITES VIRAIS

4. CORONAVÍRUS



Brandão et al., 2012

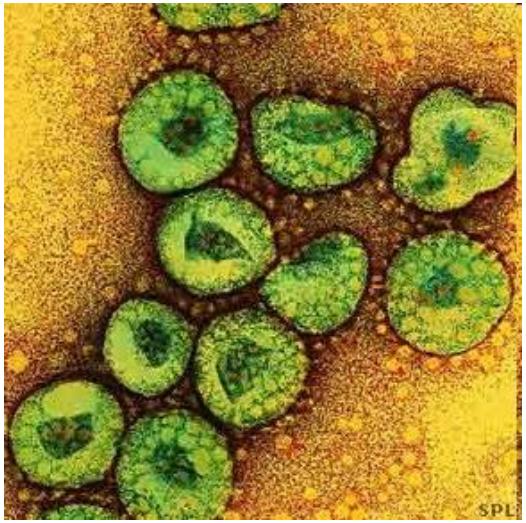
ENTERITES VIRAIS

4. CORONAVÍRUS

ESTABILIDADE

pH 5 a 7.4 (37° C)

pH 3 a 10 (4° C)



ENTERITES VIRAIS

4. CORONAVÍRUS

CÉLULAS-ALVO

- ENTERÓCITOS DAS VILOSIDADES (INTESTINO DELGADO)
- ENTERÓCITOS DAS CRIPTAS (INTESTINO GROSSO)
- EPITÉLIO RESPIRATÓRIO !

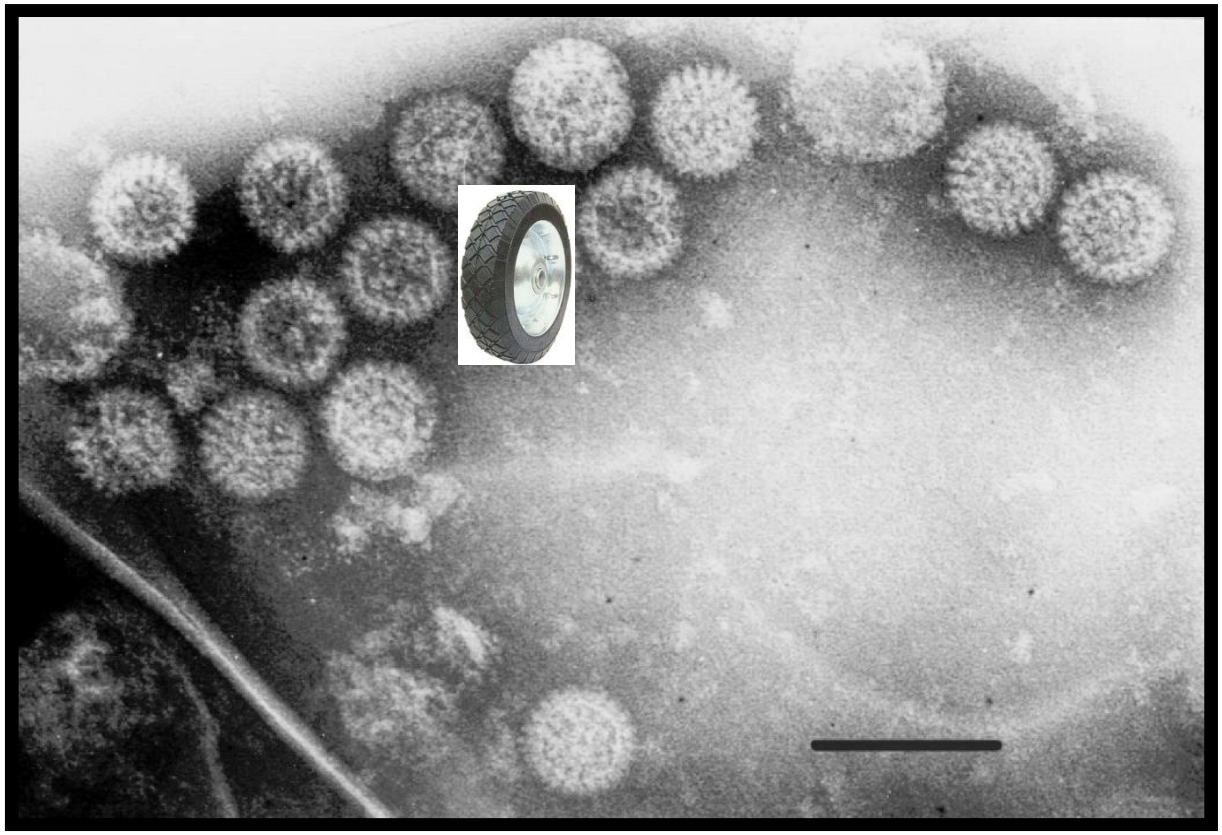
} CoV entéricos

- SNC, MACRÓFAGOS, TRATO REPRODUTIVO*, RINS, FÍGADO

} Outros CoV

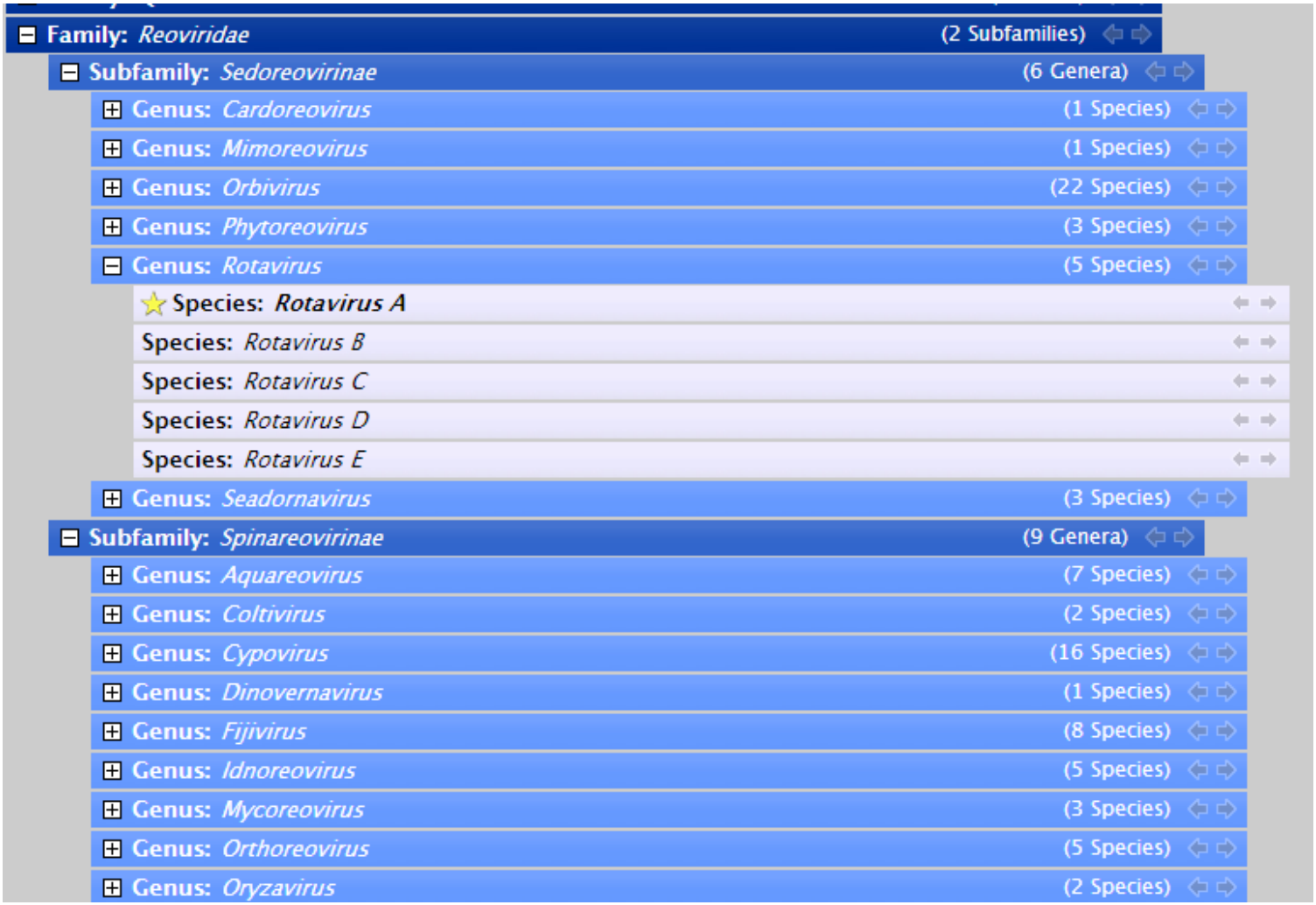
ENTERITES VIRAIS

5. ROTAVÍRUS



ENTERITES VIRAIS

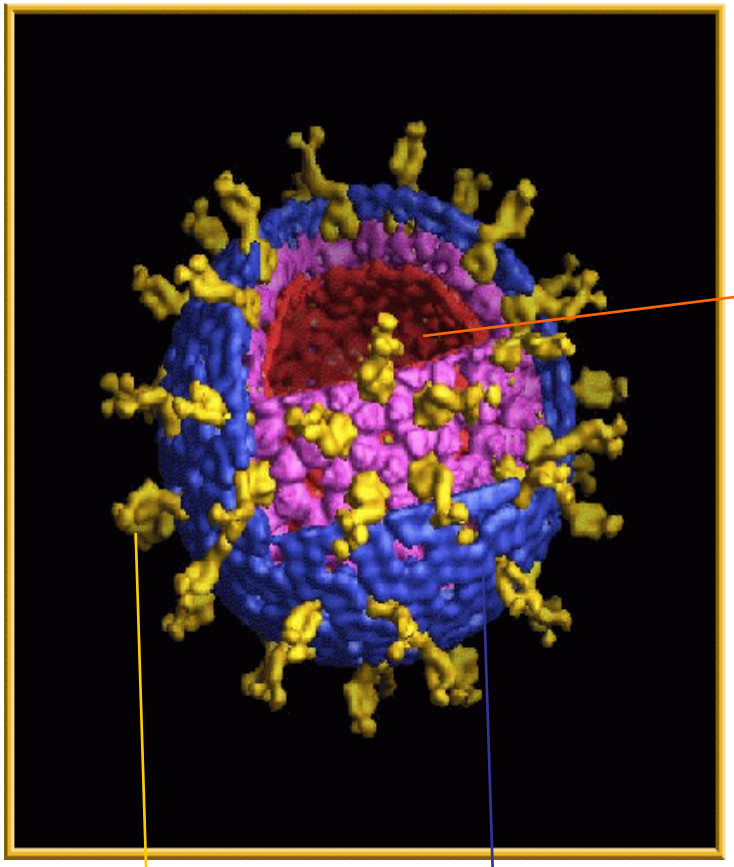
5. ROTAVÍRUS



http://ictvonline.org/virusTaxonomy.asp

ENTERITES VIRAIS

5. ROTAVÍRUS



dsRNA SEGMENTADO
SENTIDO NEGATIVO

Ñ ENVELOPADO

60-70 NM

CAPSÍDEO DUPLO

PROTEÍNA P

PROTEÍNA G

ENTERITES VIRAIS

5. ROTAVÍRUS

SOROGRUPO A

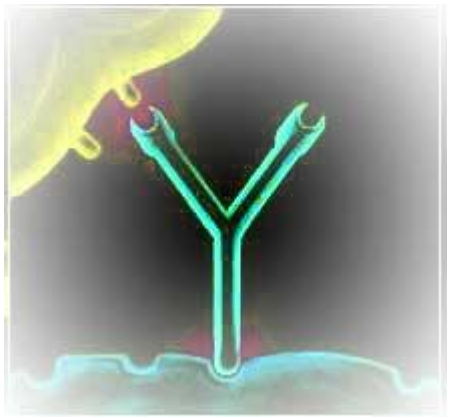
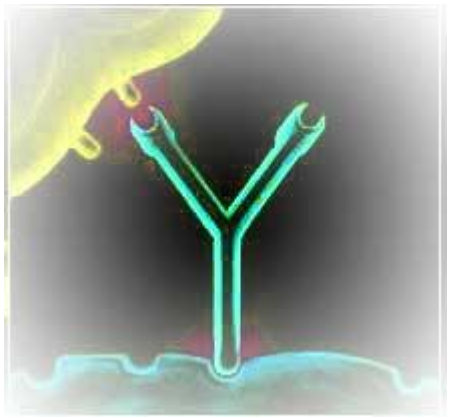
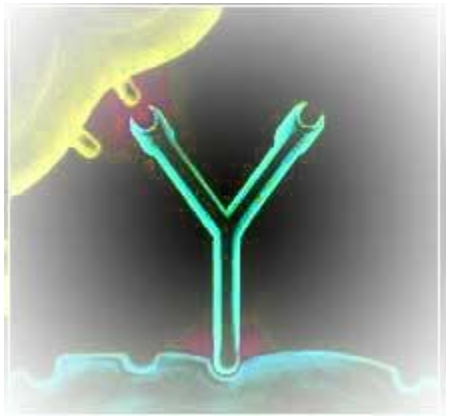
12 TIPOS DE PROTÉINA G

14 TIPOS DE PROTEÍNA P

sorotipos

CONSEQÜÊNCIAS ?

IMUNIDADE SOROTIPO-ESPECÍFICA

ENTERITES VIRAIS

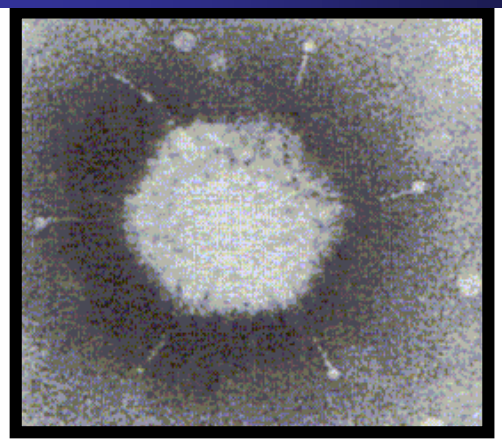
5. ROTAVÍRUS

REASSORTMENT GENÉTICO: ↑↑↑ DIVERSIDADE GENÉTICA

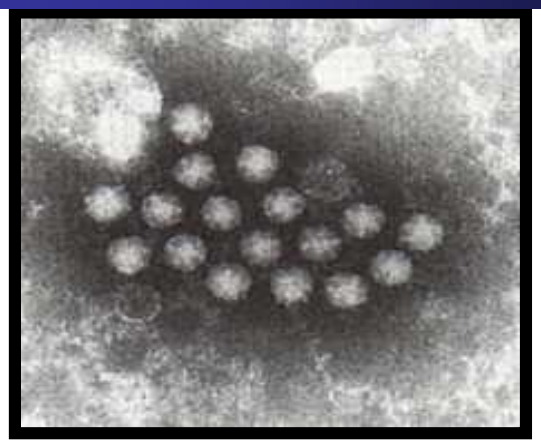
ENTERITES VIRAIS

6. OUTROS VÍRUS

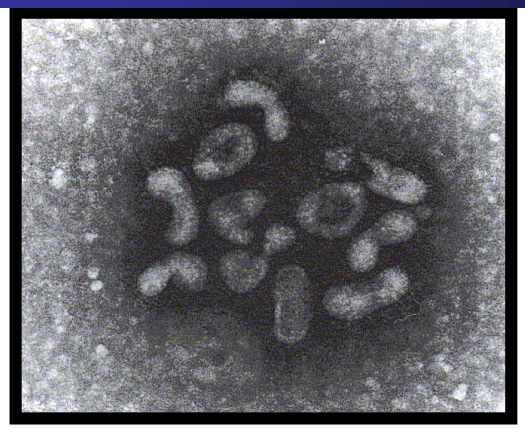
ADENOVÍRUS



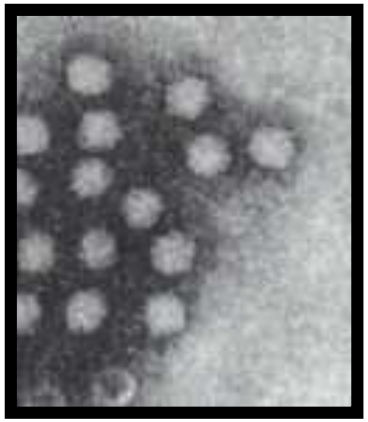
ASTROVÍRUS



TOROVÍRUS

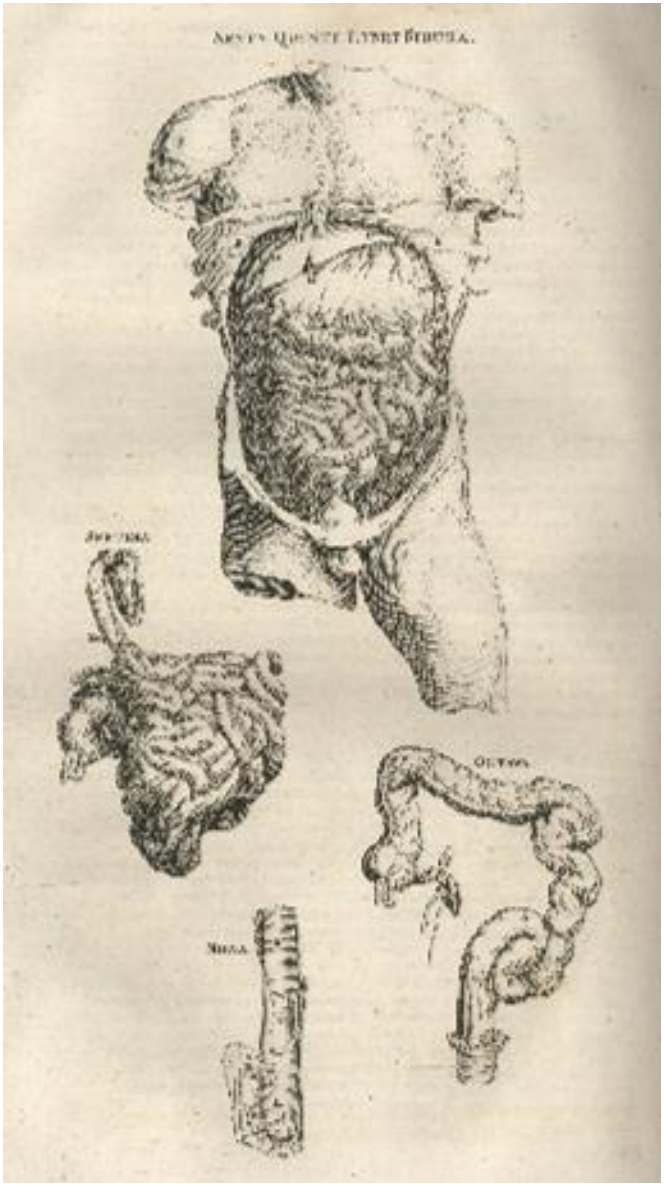


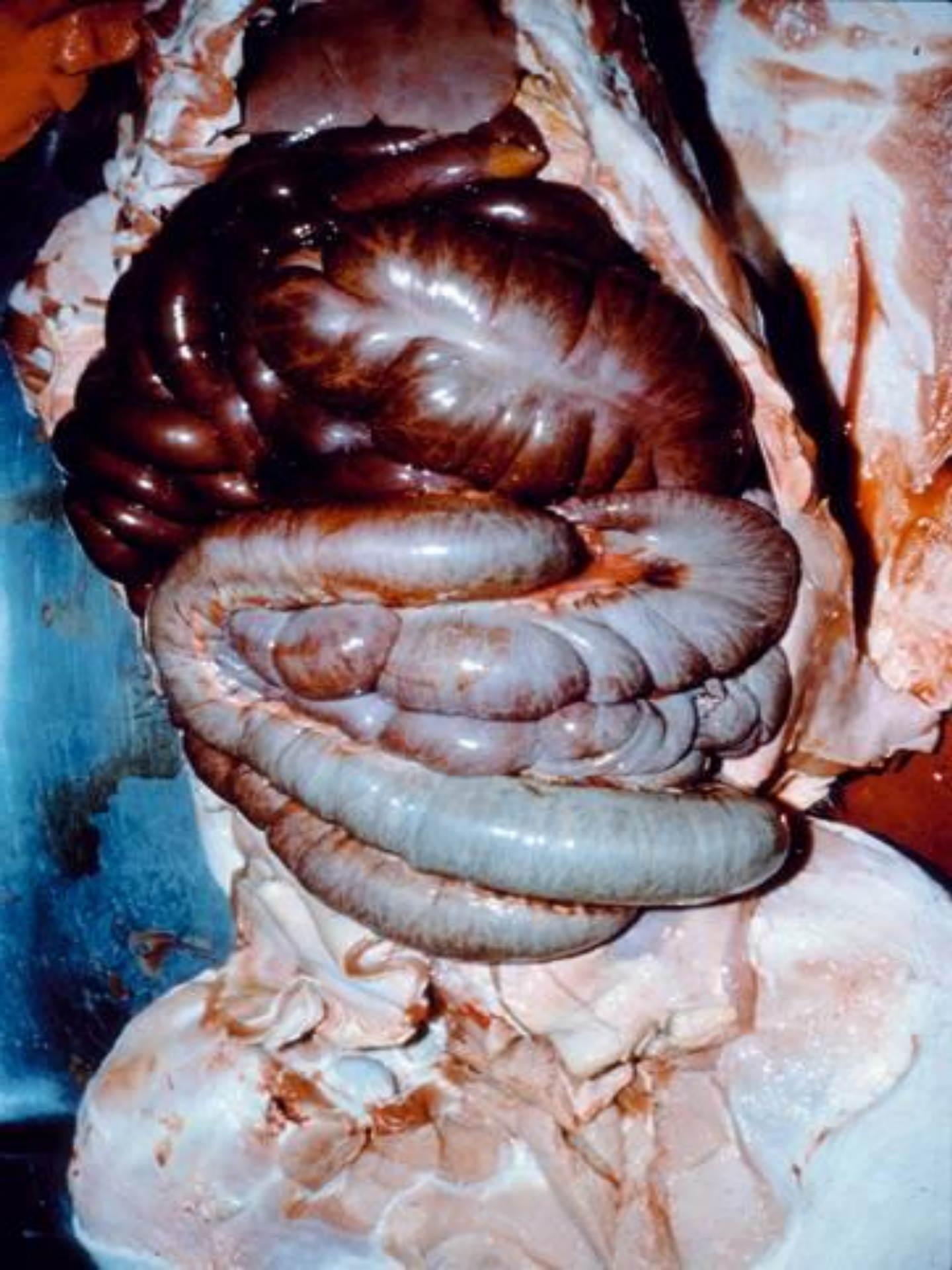
PARVOVÍRUS**



ENTERITES VIRAIS

7. FISIOPATOLOGIA



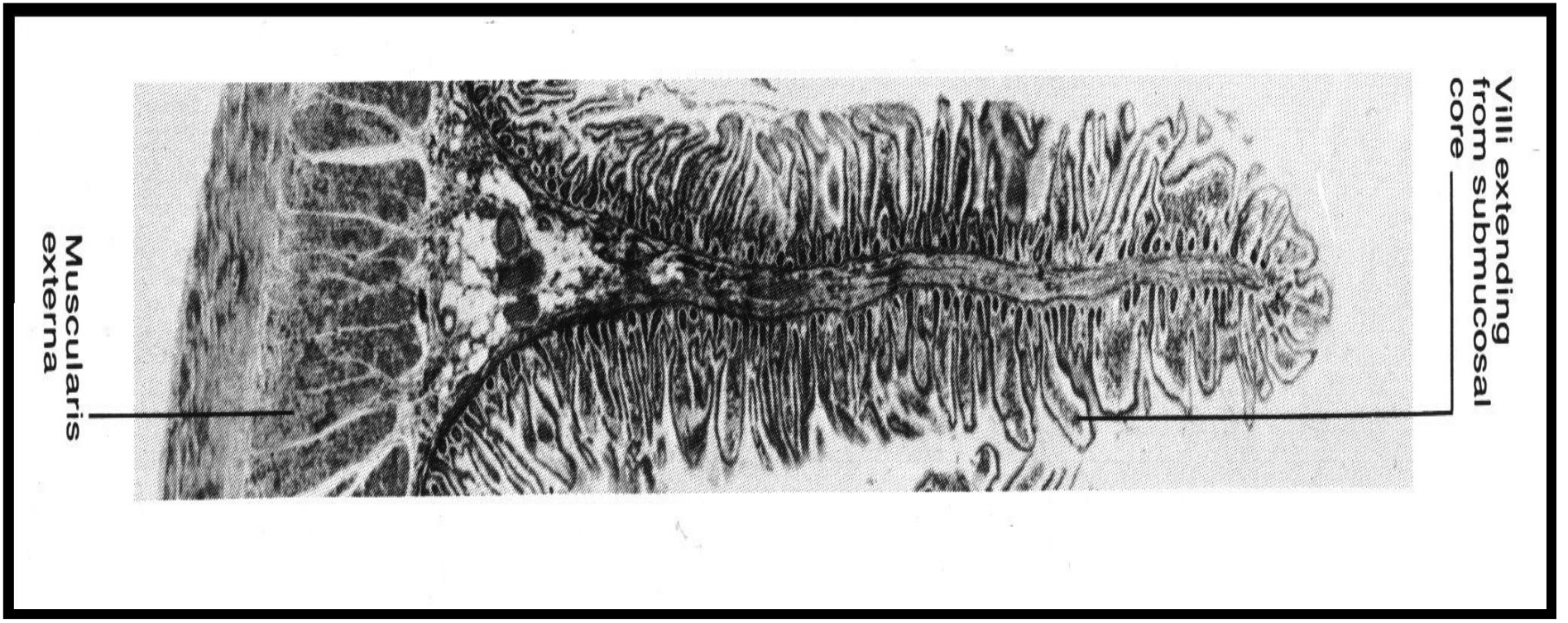


ENTERITES VIRAIS

7. FISIOPATOLOGIA

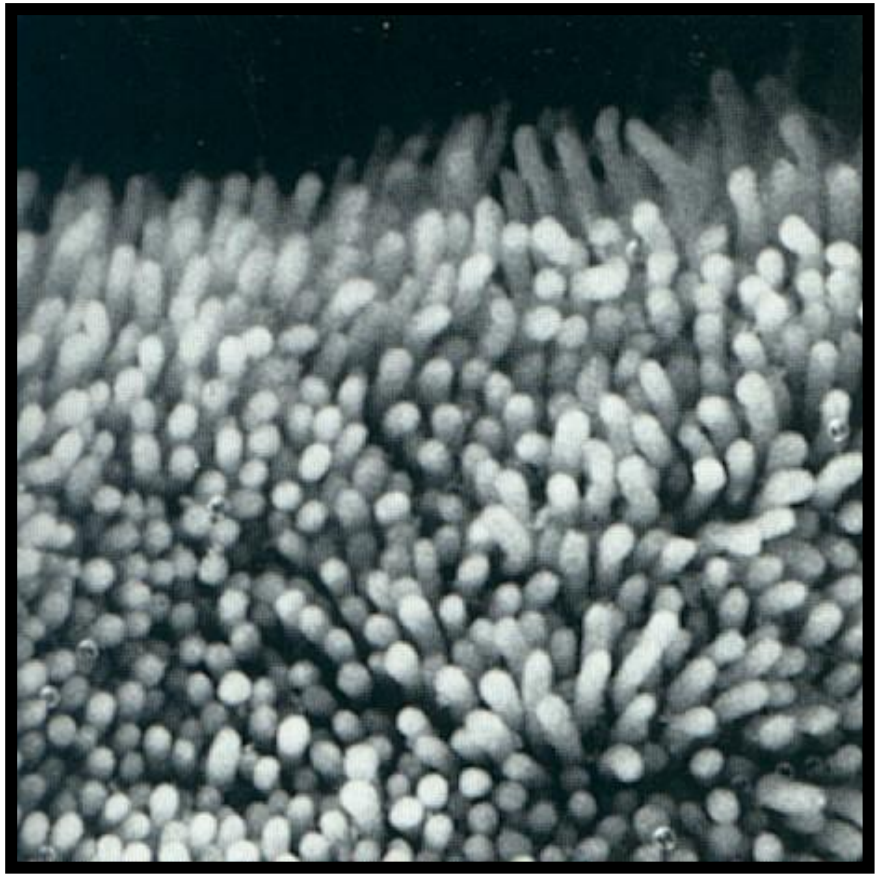
Dobras, vilosidades e microvilosidades intestinais

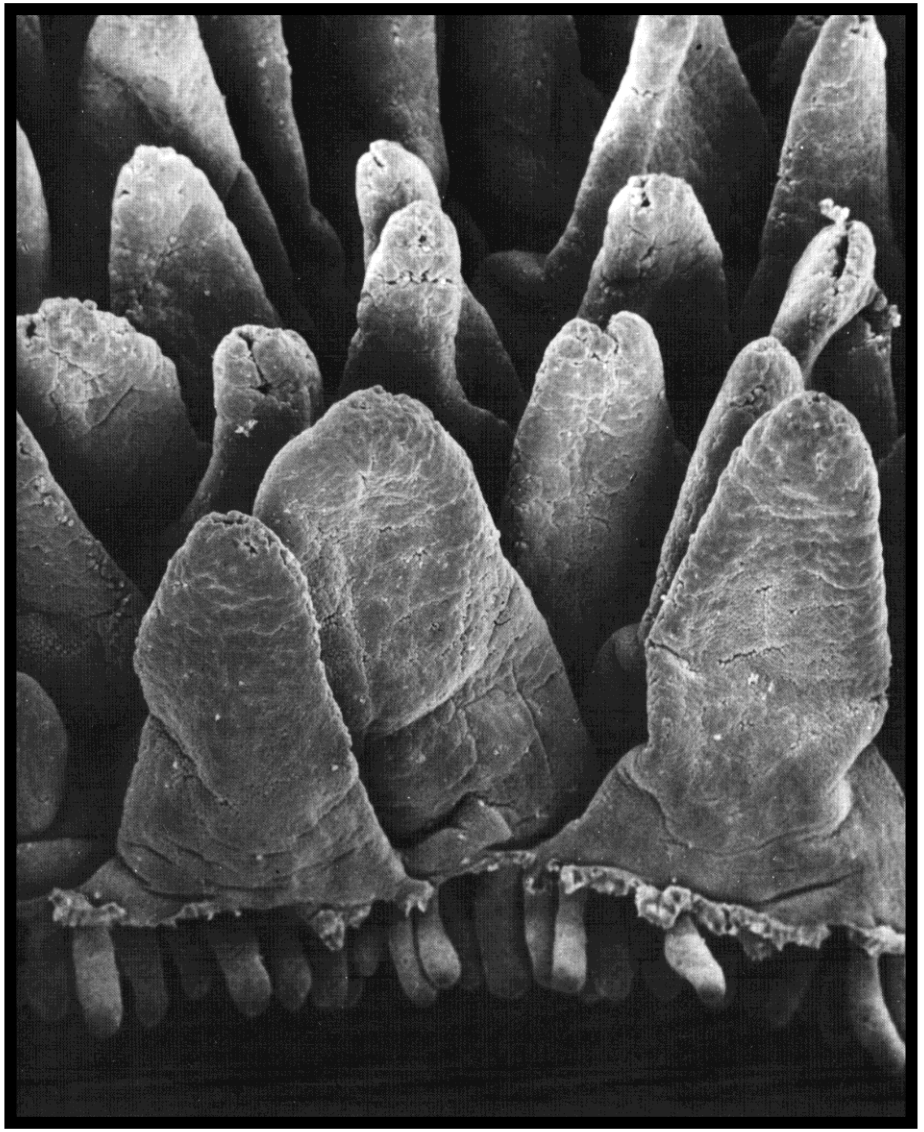
Dobras



ENTERITES VIRAIS

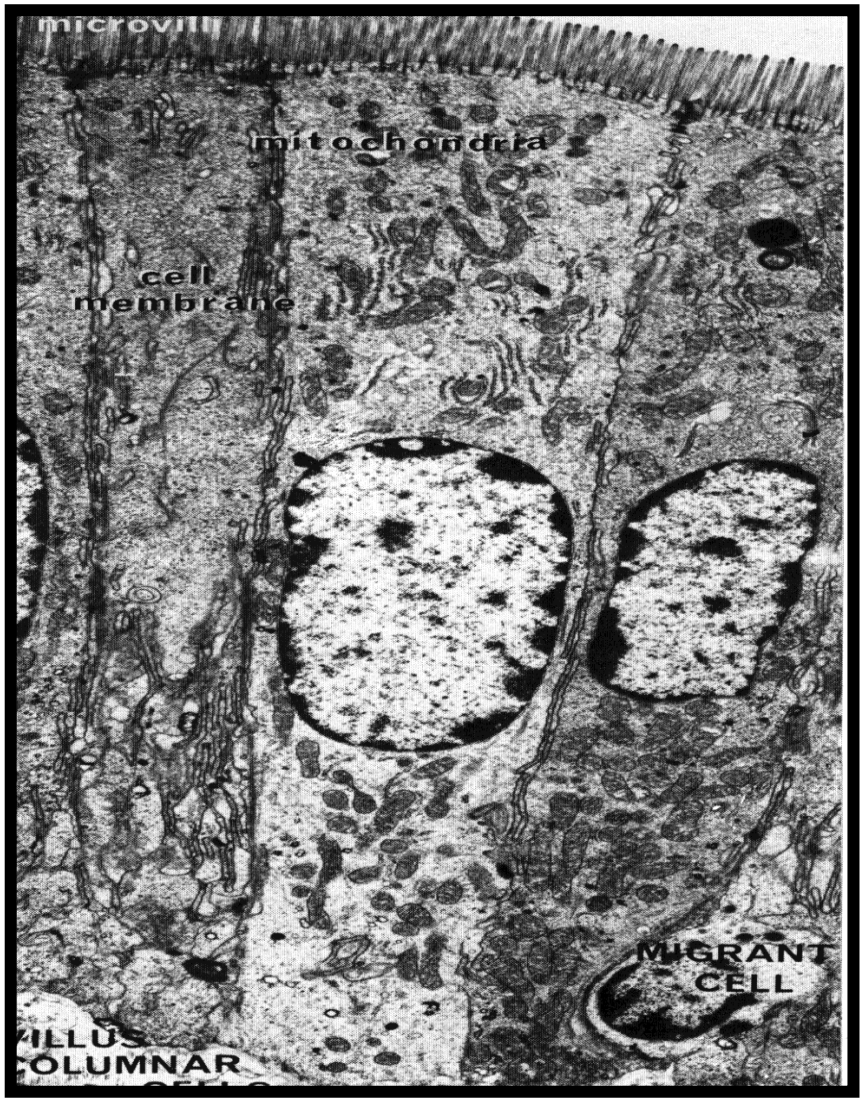
Vilosidades



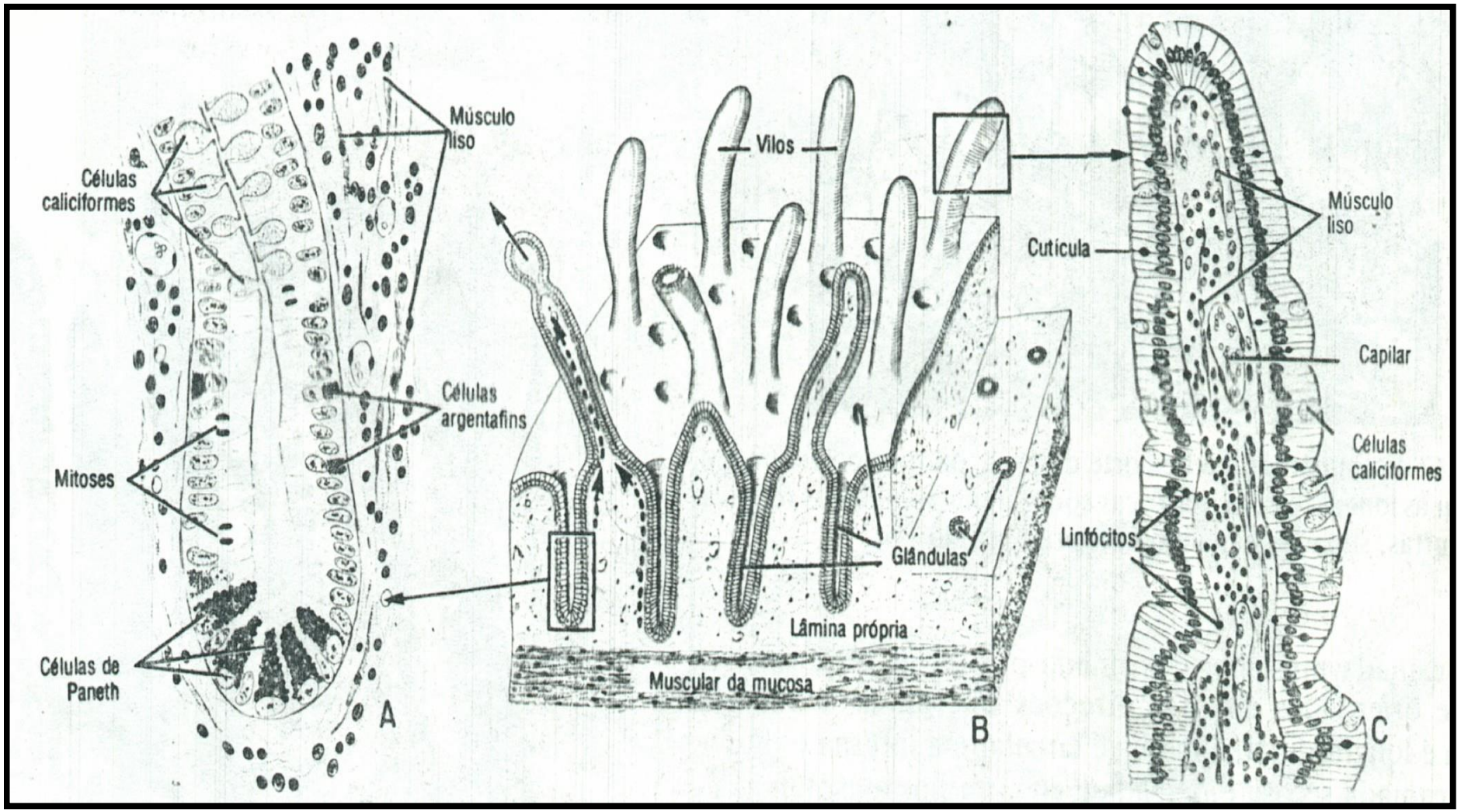


ENTERITES VIRAIS

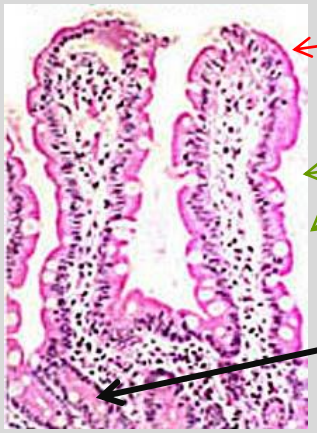
Microvilosidades



ENTERITES VIRAIS



REPLICAÇÃO EM ENTERÓCITOS

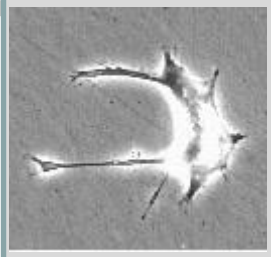


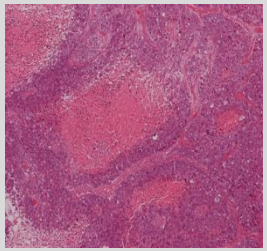
rotavírus

Coronavírus bovino

Parvovírus***

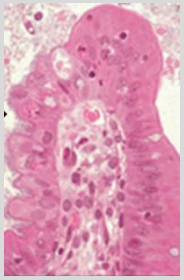
APOPTOSE/ NECROSE





- √ EXFOLIAÇÃO
- √ ATROFIA DE VILOSIDADES
- √ PERDA DE CÉLULAS DAS CRIPTAS

REPOSIÇÃO POR ENTERÓCITOS IMATUROS

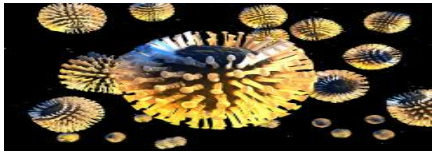


↓B-GALACTOSIDASE
↑FUNÇÃO SECRETÓRIA

↑ PRESSÃO OSMÓTICA INTRA-LUMINAL

ACÚMULO DE ÁGUA INTRA-LUMINAL ***

↓ DIGESTÃO E ABSORÇÃO DE GLICOSE
↑ SECREÇÃO Na, Cl e bicarbonato



Rotavírus: proteína não-estrutural 4:enterotoxina

ENTERITES VIRAIS

8. CORONAVÍRUS E ROTAVÍRUS EM DIVERSAS ESPÉCIES

CORONAVÍRUS BOVINO (*BCoV*)

1. **DIARRÉIA NEONATAL: BEZERROS**
2. **PROCESSOS RESPIRATÓRIOS: BEZERROS**
4. **DISENTERIA DE INVERNO: BOVINOS ADULTOS**
4. **RUMINANTES SILVESTRES**

Molecular analysis of Brazilian strains of bovine coronavirus (BCoV) reveals a deletion within the hypervariable region of the S1 subunit of the spike glycoprotein also found in human coronavirus OC43

P. E. Brandão[1,3], F. Gregori[2,3], L. J. Richtzenhain[1], C. A. R. Rosales[1,3], L. Y. B. Villarreal[1,3], and J. A. Jerez[1,3]

[1]Faculdade de Medicina Veterinária e Zootecnia, Universidade de São Paulo, São Paulo, Brazil
[2]Instituto Biológico de São Paulo, São Paulo, Brazil
[3]Coronavirus Research Group, São Paulo, Brazil

Received April 18, 2005; accepted February 27, 2006
Published online April 3, 2006

Summary. Bovine coronavirus (BCoV) causes enteric and respiratory disorders in calves and dysentery in cows. In this study, 51 stool samples of calves from 10 Brazilian dairy farms were analysed by an RT-PCR that amplifies a 488-bp fragment of the hypervariable region of the spike glycoprotein gene. Maximum parsimony genealogy with a heuristic algorithm using sequences from 15 field strains studied here and 10 sequences from GenBank and bredavirus as an outgroup virus showed the existence of two major clusters (1 and 2) in this viral species, the Brazilian strains segregating in both of them. The mean nucleotide identity between the 15 Brazilian strains was 98.34%, with a mean amino acid similarity of 98%. Strains from cluster 2 showed a deletion of 6 amino acids inside domain II of the spike protein that was also found in human coronavirus strain OC43, supporting the recent proposal of a zoonotic spillover of BCoV. These results contribute to the molecular characterization of BCoV, to the prediction of the efficiency of immunogens, and to the definition of molecular markers useful for epidemiologic surveys on coronavirus-caused diseases.

Brandão et al. Molecular analysis of Brazilian strains of bovine coronavirus (BCoV) reveals a deletion within the hypervariable region of the S1 subunit of the spike glycoprotein also found in human coronavirusOC43. Arch Virol. 2006 Sep;151(9):1735-48.

ENTERITES VIRAIS

8. CORONAVÍRUS E ROTAVÍRUS EM DIVERSAS ESPÉCIES

ROTAVÍRUS BOVINO

Molecular characterization of G and P-types bovine rotavirus strains from Goiás, Brazil: high frequency of mixed P-type infections

Thabata Alessandra Ramos Caruzo[1]/+, Willia Marta Elsner Diederichsen de Brito[2], Veridiana Munford[3], Maria Lúcia Rácz[3]

[1]Departamento de Genética, Evolução e Bioagentes, Instituto de Biologia, Universidade Estadual de Campinas, Campinas, SP, Brasil
[2]Instituto de Patologia Tropical e Saúde Pública, Laboratório de Virologia Animal, Universidade Federal de Goiás, Goiânia, GO, Brasil
[3]Departamento de Microbiologia, Instituto de Ciências Biomédicas, Universidade de São Paulo, São Paulo, SP, Brasil

In this study, 331 samples from calves less than one month old from a dairy herd in the district of Piracanjuba, state of Goiás, Brazil were tested for rotavirus. Thirty-three samples (9.9%) tested positive for rotavirus. Out of those, 31 were submitted to G and P characterization by reverse transcription followed by semi-nested polymerase chain reaction. Two samples were characterized as G6P[1], three as G10P[11] and five as G6P[11]. The majority of the samples (51.6%) displayed multiple P genotypes (P-genotype mixtures), including typical human genotypes P[4] and P[6M], suggesting the occurrence of co-infections and genetic reassortment. Also, the detection of human genotypes in bovine samples may be considered evidence of the zoonotic potential of rotaviruses. To our knowledge, this is the first report of such a high frequency of P genotype mixtures in bovine rotavirus samples. It also increases data on G and P rotavirus genotypes circulating in dairy herds in Brazil and can help in the development of more efficient immunization approaches, thereby controlling infection and reducing economical losses.

Caruzo et al. Molecular characterization of G and P-types bovine rotavirus strains from Goiás, Brazil: high frequency of mixed P-type infections. Mem Inst Oswaldo Cruz. 2010 Dec;105(8):1040-3.

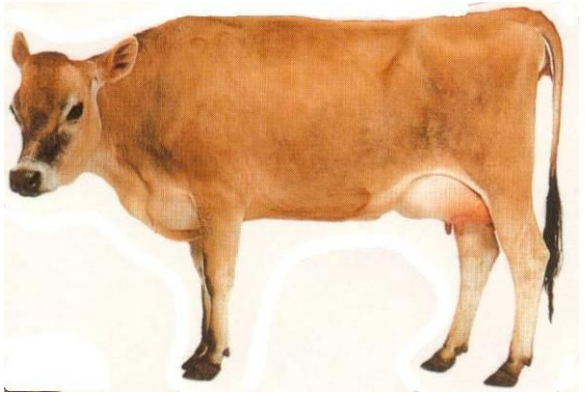
ENTERITES VIRAIS

8. CORONAVÍRUS E ROTAVÍRUS EM DIVERSAS ESPÉCIES

CORONAVÍRUS BOVINO (*BCoV*) EM ADULTOS

DISENTERIA DE INVERNO
WINTER DYSENTERY
DIARRÉIA EPIZOÓTICA DE BOVINOS ADULTOS

DIARRÉIA SANGUINOLENTA
BOVINOS ADULTOS
SURTOS ANUAIS ≅ 10 DIAS
TENDÊNCIA SAZONAL→INVERNO
TAXA DE ATAQUE: 100%
↓ 90% PRODUÇÃO DE LEITE



On the etiology of an outbreak of winter dysentery in dairy cows in Brazil[1]

Paulo E. Brandão[2,5*], Laura Y.B. Villarreal[2,5], F. Gregori[3,5], Silvio L.P. de Souza[2], Marco A.E. Lopes[2], Cleise R. Gomes[2], Angelo J. Sforsin[4], Alexandre A. Sanches[2,5], Cesar A.R. Rosales[2,5], Leonardo J. Richtzenhain[2,5], Antonio J.P. Ferreira[2] and José A. Jerez[2,5]

ABSTRACT.- Brandão P.E., Laura Y. B. Villarreal L.Y.B., F.Gregori F., Souza S.L.P., Lopes M.A.E., Gomes C.R., Sforsin A.J., Sanches A.A., Rosales C.A.R., Richtzenhain L.J., Ferreira A.J.P. & Jerez J.A. 2007. **On the etiology of an outbreak of winter dysentery in dairy cows in Brazil.** *Pesquisa Veterinária Brasileira 27(10):398-402*. Faculdade de Medicina Veterinária e Zootecnia, Universidade de São Paulo, Av. Prof. Dr. Orlando Marques de Paiva 87, São Paulo, SP 05508-270, Brazil. E-mail: paulo7926@yahoo.com

Winter dysentery (WD) is a seasonal infectious disease described worldwide that causes a marked decrease in milk production in dairy cows. In the Northern hemisphere, where the disease is classically recognized, bovine coronavirus (BCoV) has been assigned as a major etiologic agent of the disease. Nonetheless, in the Southern hemisphere, an in-deep etiological survey on WD cases had not been carried out. This study aimed to survey for BCoV by nested-RT-PCR, rotavirus by polyacrylamide gel electrophoresis (PAGE) and ELISA, bacteria by classical bacteriological methods and PCR for virulence factors and parasites by sugar flotation test on fecal samples of 21 cows from a farm during an outbreak of WD in São Paulo state, Southeastern Brazil. BCoV was detected in all 21 samples, while rotavirus was detected in two symptomatic cows. *Escherichia coli*, *Yersinia intermedia*, *Providencia rustigianii* *Proteus penneri*, *Klebsiella terrigena* and *Enterobacter aglomerans* were detected in samples from both asymptomatic and healthy cows in different associations. The study of *E. coli* virulence factors revealed that the strains isolated were all apathogenic. Cysts of *Eimeria* sp. and eggs of *Strongyloidea* were detected at low numbers in four of the symptomatic cows, with one co-infestation. These results suggest BCoV as the main etiologic agent of the cases of WD in Brazil, a conclusion that, with the clinical and epidemiological patterns of the disease studied herein, match those already described elsewhere. These findings give basis to the development of preventive measures and contribute to the understanding of the etiology of WD.

ENTERITES VIRAIS

8. CORONAVÍRUS E ROTAVÍRUS EM DIVERSAS ESPÉCIES

A Multigene Approach for Comparing Genealogy of *Betacoronavirus* from Cattle and Horses

Iracema N. Barros,[1,2] Sheila O. S. Silva,[1,2] Francisco S. Nogueira Neto,[3] Karen M. Asano,[1,2] Sibele P. Souza,[1,2] Leonardo J. Richtzenhain,[1,2] and Paulo E. Brandao[1,2]

[1] *Department of Preventive Veterinary Medicine and Animal Health, College of Veterinary Medicine, University of São Paulo, Avenue Professor Dr. Orlando Marques de Paiva 87, Cidade Universitária, 05508-270 São Paulo, SP, Brazil*
[2] *Coronavirus Research Group, College of Veterinary Medicine, University of São Paulo, Avenue Professor Dr. Orlando Marques de Paiva 87, Cidade Universitária, 05508-270 São Paulo, SP, Brazil*
[3] *Jockey Club of São Paulo, Bento Frias Street 248, Group 555, 05423-050 São Paulo, SP, Brazil*

Correspondence should be addressed to Iracema N. Barros; cemavet@gmail.com

Received 6 September 2013; Accepted 3 October 2013

Academic Editors: E. F. Guèye and H. Suzuki

Gastroenteritis is one of the leading causes of morbidity and mortality among young and newborn animals and is often caused by multiple intestinal infections, with rotavirus and bovine coronavirus (BCoV) being the main viral causes in cattle. Given that BCoV is better studied than equine coronaviruses and given the possibility of interspecies transmission of these viruses, this research was designed to compare the partial sequences of the spike glycoprotein (S), hemagglutinin-esterase protein (HE), and nucleoprotein (N) genes from coronaviruses from adult cattle with winter dysentery, calves with neonatal diarrhea, and horses. To achieve this, eleven fecal samples from dairy cows with winter dysentery, three from calves, and two from horses, all from Brazil, were analysed. It could be concluded that the enteric BCoV genealogy from newborn and adult cattle is directly associated with geographic distribution patterns, when S and HE genes are taken into account. A less-resolved genealogy exists for the HE and N genes in cattle, with a trend for an age-related segregation pattern. The coronavirus strains from horses revealed *Betacoronavirus* sequences indistinguishable from those found in cattle, a fact previously unknown.

Barros et al. A multigene approach for comparing genealogy of Betacoronavirus from cattle and horses. ScientificWorldJournal. 2013 Nov 17;2013:349702.

ENTERITES VIRAIS

8. CORONAVÍRUS E ROTAVÍRUS EM DIVERSAS ESPÉCIES

CORONAVÍRUS CANINO (CCoV)

GASTROENTERITE (VÍRUS CCoV)

INFECÇÃO RESPIRATÓRIA (CORONAVÍRUS RESPIRATÓRIO CANINO)

SOROTIPOS 1 E 2

Canine Coronavirus Highly Pathogenic for Dogs

Canio Buonavoglia,* Nicola Decaro,* Vito Martella,* Gabriella Elia,* Marco Campolo,* Costantina Desario,* Massimo Castagnaro,† and Maria Tempesta*

Canine coronavirus (CCoV) is usually responsible for mild, self-limiting infections restricted to the enteric tract. We report an outbreak of fatal disease in puppies caused by a pathogenic variant of CCoV that was isolated from organs with severe lesions.

Coronaviruses are large, enveloped, positive-stranded RNA viruses (*1*). Three different coronaviruses have been identified in dogs (*2,3*). Canine coronavirus (CCoV) type I and type II are included in group 1 coronaviruses, and their evolution is related to that of feline coronavirus (FCoV) type I and type II. FCoV type II originated by heterologous recombination between CCoV type II and FCoV type I, while CCoV type I is genetically more similar to FCoV type I than to CCoV type II (*3*). In addition, 2 FCoV biotypes that differ in pathogenicity have been observed in cats.

The onset of acute fatal disease (feline infectious peritonitis) is caused by pantropic variants (able to disseminate throughout the organism) of enteric FCoVs with deletions or recombinations in the 3c and 7b genes at the 3′ end of the FCoV genome (*4*). Similarly, changes in tissue tropisms in porcine and murine coronaviruses (*5,6*) and adaptation of the recently recognized severe acute respiratory syndrome–associated coronavirus (*7*) to humans have been related to mutations or deletions. A third canine coronavirus, CRCoV, detected in the respiratory tract, has ≤96.0% amino acid (aa) conservation in the spike (S) protein with bovine coronavirus within group 2 coronaviruses, which provides strong evidence for a recent host-species shift (*2*).

Coronavirus infection in dogs is usually restricted to the enteric tract. The infection is self-limiting and in general produces only mild or asymptomatic forms of enteritis (*8*). We report the identification of a pantropic, highly pathogenic variant of CCoV type II.

The Study

In May 2005, a severe outbreak of fatal systemic disease occurred in a pet shop in Bari, Italy. Clinical symptoms were initially observed in 3 miniature pinschers (45 days of age) and 1 cocker spaniel (53 days of age) and consisted of fever (39.5°C–40°C), lethargy, inappetence, vomiting, hemorrhagic diarrhea, and neurologic signs (ataxia, seizures) with death after 2 days. The same symptoms were observed 3–4 days later in 2 other miniature pinschers (45 days of age) and 1 Pekinese (56 days of age). Necropsy of the dogs showed hemorrhagic enteritis, abundant serosanguineous fluid in the abdominal cavity, and severe lesions in the parenchymatous organs. The lungs had multiple, patchy, red areas of consolidation. Livers were yellow-brown and congested, with hemorrhages on their surfaces, and spleens were enlarged with subcapsular hemorrhages. Variable gross changes in other organs included multifocal hemorrhagic renal cortical infarcts and petechial hemorrhages on lymph node surfaces.

Virologic and bacteriologic investigations on the parenchymatous organs did not detect common canine pathogens, notably canine parvovirus type 2, canine distemper virus, canine adenovirus type 1 and type 2. CCoV type I and type II were identified in the intestinal contents of all puppies by genotype-specific real-time reverse transcription–polymerase chain reaction (RT-PCR) assays (*9*). CCoV type II RNA was also detected in lungs (median 1.08×10^6 RNA copies/μL of template), spleen (median 4.46×10^6 RNA copies/μL of template), liver (median 9.02×10^4 RNA copies/μL of template), kidney (median 7.54×10^4 RNA copies/μL of template), and brain (median 5.23×10^3 RNA copies/μL of template). Virus-induced cytopathic effect was observed in A-72 cells, and CCoV type II strain (CB/05) was isolated from all tissues examined except brain tissue. Immunohistochemical analysis with a CCoV-specific monoclonal antibody detected CCoV antigen in the organs with gross lesions that were examined (lungs, kidneys, liver, spleen, gut, and lymph nodes) (Figure 1).

The sequence of the 3′ end of the genome (8.8 kb) of the pantropic CCoV strain was determined by RT-PCR amplification and sequencing of overlapping fragments. The S, envelope, and membrane proteins and nucleoprotein showed a high degree of amino acid identity with the cognate open reading frame (ORF) of CCoV type II. The S protein of strain CB/05 had the highest identity to FCoV type II strain 79-1683 (Figure 2). Comparison with strain CB/05 was possible only with CCoV type II strains Insavc-1 (*10*) and BGF (*11*) and CCoV type I strains Elmo/02 and 23/03 (*3,12*) because of a lack of data on the 3′ end of the CCoV genome in the genes encoding for nonstructural proteins (NSPs) 3a, 3b, 3c, 7a, and 7b. NSPs 3a, 7a, and 7b were not altered. NSP 3b (22 aa) was 49 aa shorter than expected because of a 38-nucleotide deletion and a frame shift mutation in the downstream sequence that introduced

*University of Bari, Bari, Italy; and †University of Padua, Padova, Italy

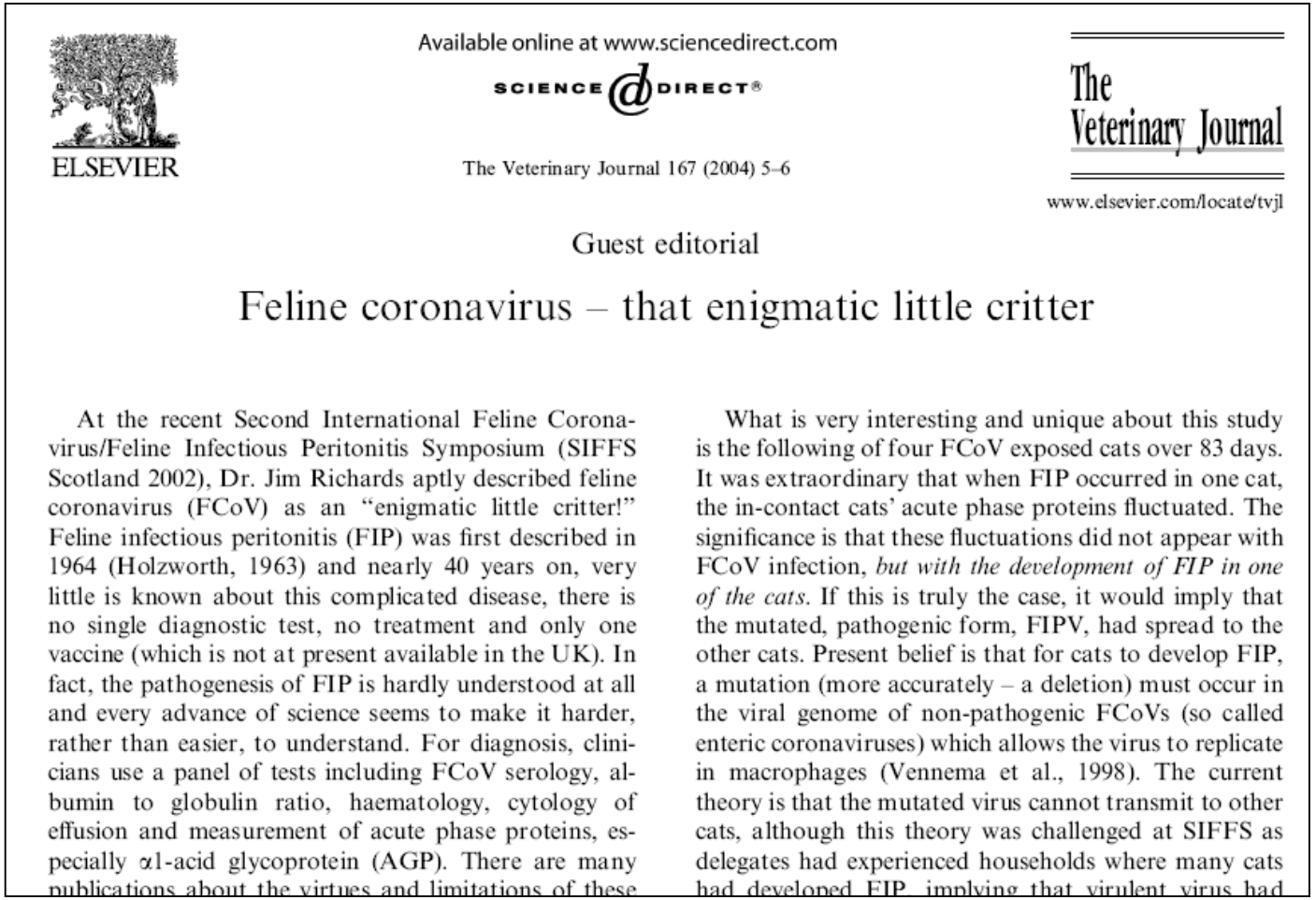
Coronavirus infection in dogs is usually restricted to the enteric tract. The infection is self-limiting and in general produces only mild or asymptomatic forms of enteritis (*8*). We report the identification of a pantropic, highly pathogenic variant of CCoV type II.

Buonavoglia et al. Canine coronavirus highly pathogenic for dogs. Emerg Infect Dis. 2006 Mar;12(3):492-4.

ENTERITES VIRAIS

8. CORONAVÍRUS E ROTAVÍRUS EM DIVERSAS ESPÉCIES

CORONAVÍRUS FELINO (FCoV)



ELSEVIER

Available online at www.sciencedirect.com

SCIENCE DIRECT®

The Veterinary Journal 167 (2004) 5–6

The Veterinary Journal

www.elsevier.com/locate/tvjl

Guest editorial

Feline coronavirus – that enigmatic little critter

At the recent Second International Feline Coronavirus/Feline Infectious Peritonitis Symposium (SIFFS Scotland 2002), Dr. Jim Richards aptly described feline coronavirus (FCoV) as an "enigmatic little critter!" Feline infectious peritonitis (FIP) was first described in 1964 (Holzworth, 1963) and nearly 40 years on, very little is known about this complicated disease, there is no single diagnostic test, no treatment and only one vaccine (which is not at present available in the UK). In fact, the pathogenesis of FIP is hardly understood at all and every advance of science seems to make it harder, rather than easier, to understand. For diagnosis, clinicians use a panel of tests including FCoV serology, albumin to globulin ratio, haematology, cytology of effusion and measurement of acute phase proteins, especially α1-acid glycoprotein (AGP). There are many publications about the virtues and limitations of these

What is very interesting and unique about this study is the following of four FCoV exposed cats over 83 days. It was extraordinary that when FIP occurred in one cat, the in-contact cats' acute phase proteins fluctuated. The significance is that these fluctuations did not appear with FCoV infection, *but with the development of FIP in one of the cats*. If this is truly the case, it would imply that the mutated, pathogenic form, FIPV, had spread to the other cats. Present belief is that for cats to develop FIP, a mutation (more accurately – a deletion) must occur in the viral genome of non-pathogenic FCoVs (so called enteric coronaviruses) which allows the virus to replicate in macrophages (Vennema et al., 1998). The current theory is that the mutated virus cannot transmit to other cats, although this theory was challenged at SIFFS as delegates had experienced households where many cats had developed FIP, implying that virulent virus had

Addie Feline coronavirus--that enigmatic little critter. Vet J. 2004 Jan;167(1):5-6.

ENTERITES VIRAIS

8. CORONAVÍRUS E ROTAVÍRUS EM DIVERSAS ESPÉCIES

CORONAVÍRUS AVIÁRIO (IBV)

Research Note—

Molecular Characterization of Infectious Bronchitis Virus Strains Isolated from the Enteric Contents of Brazilian Laying Hens and Broilers

L. Y. B. Villarreal,[A] P. E. Brandão,[B] J. L. Chacón,[A] A. B. S. Saidenberg,[A] M. S. Assayag,[A] R. C. Jones,[C] and A. J. P. Ferreira[AD]

[A]Department of Pathology
[B]Department of Preventive Veterinary Medicine and Animal Health, College of Veterinary Medicine–University of São Paulo, São Paulo, SP, Brazil
[C]Department of Veterinary Pathology, University of Liverpool, Liverpool, United Kingdom

Received 16 April 2007; Accepted and published ahead of print 1 July 2007

SUMMARY. Infectious bronchitis virus (IBV) is the causative agent of avian infectious bronchitis, which is characterized by respiratory, reproductive, and renal signs. However, the role of IBV as an enteric pathogen in still controversial. In Brazil, antigenic groups of IBV divergent from the Massachusetts serotype used for vaccination schedules in that country have already been demonstrated. The present study aimed to assess the different genotypes of IBV in Brazilian commercial poultry flocks by partial sequencing of the S1 amino-terminus coding region using enteric contents as samples and examine their relationship with the vaccine serotype currently in use. Samples of enteric contents were taken as pools of five birds from each of 18 poultry farms (17 broiler and one laying farm) from five Brazilian states between 2002 and 2006. Birds were presenting watery diarrhea and poor general condition but were without respiratory, renal, or reproductive signs. Conventional antibacterial and anticoccidial therapies were unsuccessful and, furthermore, all samples proved negative for rotavirus, reovirus, and astrovirus. Eleven IBV samples were isolated in embryonated eggs and resulted in S1 sequences. Phylogenetic analysis showed that these segregated into an exclusive cluster, close to serotype D274, but distant from Massachusetts. Mean amino acid identity amongst these Brazilian strains was 94.07%; amongst these and serotypes D274, 4/91, and Massachusetts, mean amino acid identity was 77.17%, 69.94%, and 68.93%, respectively. In conclusion, the presence of genotype variant strains of IBV in Brazilian poultry flocks has been demonstrated and might be the reason for the unsuccessful control of IBV in Brazil. Furthermore, these results also strengthen the implications of IBV in enteric diseases of poultry.

Villarreal et al. Orchitis in roosters with reduced fertility associated with avian infectious bronchitis virus and avian metapneumovirus infections. Avian Dis. 2007 Dec;51(4):900-4.

ENTERITES VIRAIS

8. CORONAVÍRUS E ROTAVÍRUS EM DIVERSAS ESPÉCIES

ROTAVÍRUS AVIÁRIO

Research Note—

Occurrence and Characterization of Rotavirus A in Broilers, Layers, and Broiler Breeders from Brazilian Poultry Farms

L. A. R. Beserra,[A] B. R. P. Barbosa, N. T. C. G. Bernardes, P. E. Brandão, and F. Gregori

Department of Preventive Veterinary Medicine and Animal Health, College of Veterinary Medicine, University of São Paulo, Av. Professor Dr. Orlando Marques de Paiva, 87, 05508-270 São Paulo, Brazil

Received 5 August 2013; Accepted 30 September 2013; Published ahead of print 1 October 2013

SUMMARY. Rotaviruses are a major cause of diarrhea in humans and animals, including several mammalian and avian species. Using different PCR protocols, we report the occurrence of rotavirus A in 21 (53.84%; 21/39) from 39 fecal pool samples of broilers, layers, and broiler breeders from Brazilian avian farms. We typed the G5, G8, G11, G19, and P[31] genotypes.

RESUMEN. *Nota de Investigación*—Presentación y caracterización de rotavirus A en pollos de engorde, gallinas de postura y en reproductores pesados.

Los rotavirus son una causa importante de diarrea en los seres humanos y animales, incluyendo varias especies de mamíferos y aves. Mediante el uso de diferentes protocolos de PCR, se reporta la presentación de rotavirus A en 21 (53.84%, 21/39) de 39 muestras fecales agrupadas de pollos de engorde, ponedoras, reproductoras pesados de granjas avícolas brasileñas. Se detectaron los genotipos G5, G8, G11, G19 y P [31].

Key words: rotavirus, avian, group A, genotypes, PCR

Abbreviations: bp = base pair; NSP = nonstructural protein; RT = reverse transcriptase; VP = viral protein

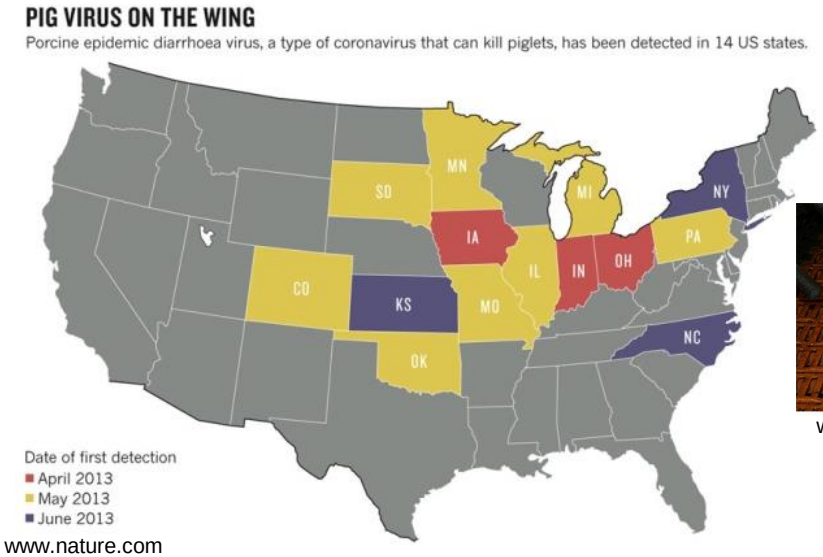
Beserra et al. Occurrence and characterization of rotavirus A in broilers, layers, and broiler breeders from Brazilian poultry farms. Avian Dis. 2014 Mar;58(1):153-7.

ENTERITES VIRAIS

8. CORONAVÍRUS E ROTAVÍRUS EM DIVERSAS ESPÉCIES

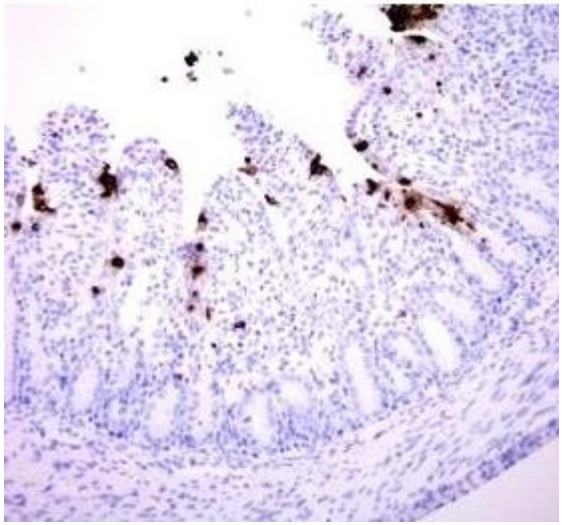
CORONAVÍRUS SUÍNO PEDV (PORCINE EPIDEMIC DIARRHEA VIRUS)

Morbidade e mortalidade: 80-100%



www.nature.com

www.pig333.com



http://www.nationalhogfarmer.com

ENTERITES VIRAIS

8. CORONAVÍRUS E ROTAVÍRUS EM DIVERSAS ESPÉCIES

ROTAVÍRUS SUÍNO

Phylogenetic Analyses of the VP4 and VP7 Genes of Porcine Group A Rotaviruses in São Paulo State, Brazil: First Identification of G5P[23] in Piglets

Paloma O. Tonietti,[a] Aline S. Hora,[a] Fernanda D. F. Silva,[a] Vera L. A. Ruiz,[b] Fabio Gregori[a]

Department of Preventive Veterinary Medicine and Animal Health, College of Veterinary Medicine, University of São Paulo, Sao Paulo, SP, Brazil[a]; Animal Science Department, Faculty of Animal Science and Food Engineering, University of São Paulo, Pirassununga, SP, Brazil[b]

This study determined the group A rotavirus occurrence in pig farms from 7 different cities in São Paulo State, Brazil. Out of 143 samples, 70 tested positive. Sequence analyses of 37 strains indicated that the strains had the G3, G5, G9, and P[6], P[13]/P[22]-like, and P[23] genotypes.

Rotaviruses are one of the most frequently detected viral agents associated with diarrhea in various animal species worldwide, including swine. Rotaviruses have a genome of 11 segments of double-stranded RNA with genes that encode six structural viral proteins (VP) and six nonstructural (NS) proteins (1, 2). Rotaviruses are classified as the *Reoviridae* family and the *Rotavirus* genus, which includes at least seven serogroups (groups A to G). Recently, a new serogroup, group H, was created, and a virus designated "new adult diarrhea rotavirus," which was isolated from pigs (3), was assigned to this group.

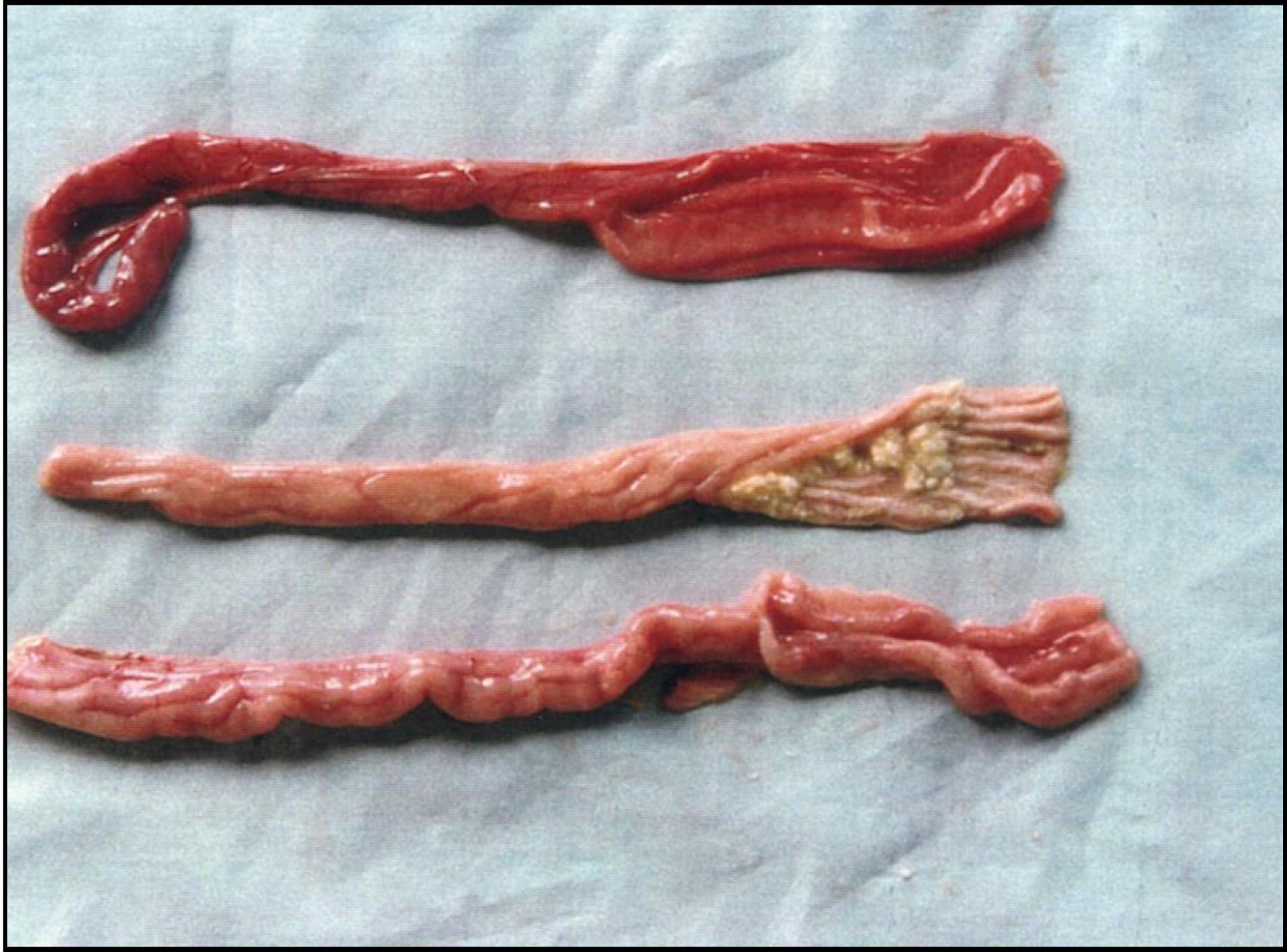
Rotavirus antigenic classification has been replaced by a classification system of rotaviruses into VP4 or VP7 genotypes, which is accomplished via sequence analysis and based on the sequence identities of cognate rotavirus gene segments (4). Thus far, 27 G and 35 P genotypes have been identified (5).

The aims of this study were to determine the frequency of group A porcine rotavirus circulating on pig farms and to perform phylogenetic analyses of the VP4 and VP7 genes of rotavirus

supernatants of the samples was conducted with TRIzol reagent (Invitrogen, Carlsbad, CA, USA), and cDNA was synthesized using random primers (Invitrogen, Carlsbad, CA, USA) and Moloney murine leukemia virus (M-MLV) reverse transcriptase (Invitrogen, Carlsbad, CA, USA) following the manufacturer's recommended protocol. Rotavirus screening was conducted using nested reverse transcription-PCR (RT-PCR) (6) with Platinum *Taq* DNA polymerase (Invitrogen, Carlsbad, CA, USA) according to the manufacturer's instructions.

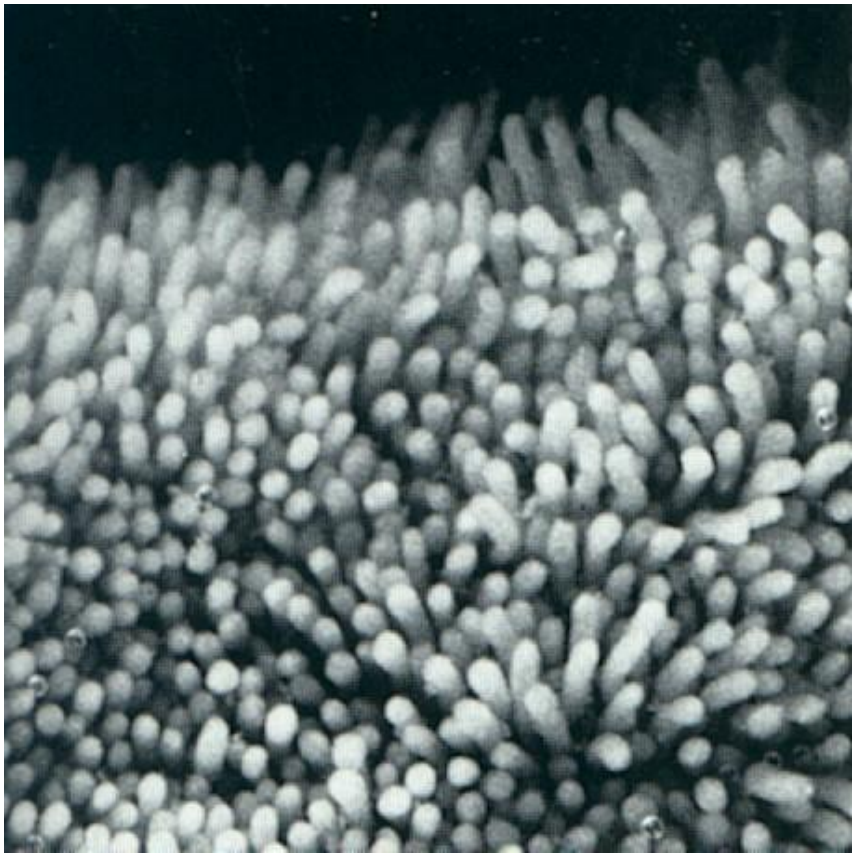
Three consensus primers were designed in this study (VP4FW, VP4RV, and VP7RV [Table 1]). These primers were used with the following protocol: (i) 3 min at 94°C; (ii) 40 amplification cycles, with 1 cycle consisting of 1 min at 94°C, 1.5 min at 50°C, and 1 min at 72°C; and (iii) a final extension step of 10 min at 72°C. The VP7 gene was amplified with the primers sBeg9 and End9CRW8 (1,062 bp) (7) or VP7RV (933 bp). For the VP4 gene, the primers VP4FW and Con2 (873 bp) (8) or VP4RV (815 bp) were used (Table 1).

Tonietti et al. Phylogenetic analyses of the VP4 and VP7 genes of porcine group A rotaviruses in Sao Paulo State, Brazil: first identification of G5P[23] in piglets. J Clin Microbiol. 2013 Aug;51(8):2750-3.



NECROSE, ATROFIA E FUSÃO DE VILOSIDADES

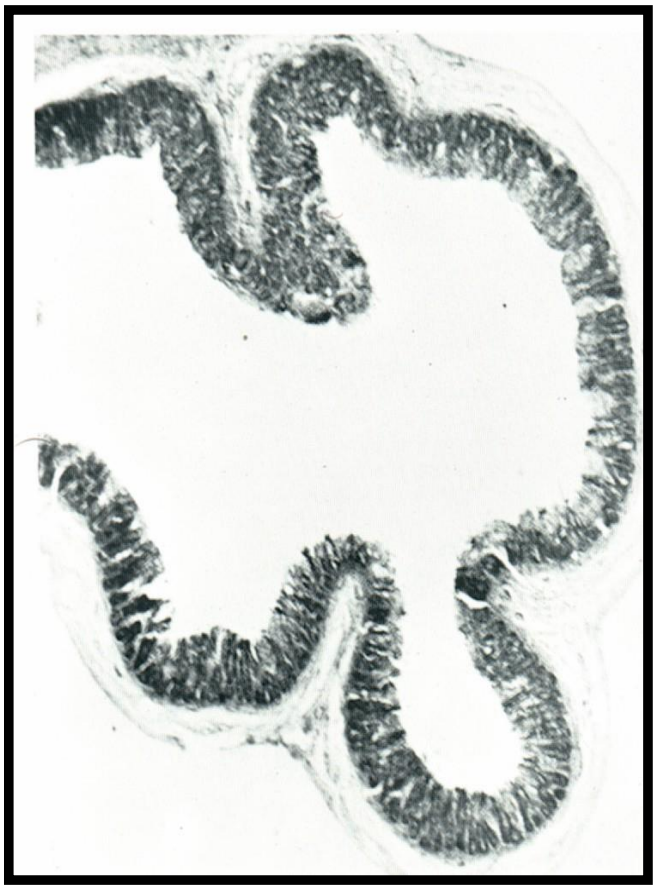
HIPERPLASIA DE CRIPTAS



NORMAL

APÓS ENTERITE

NORMAL



APÓS ENTERITE

ENTERITES VIRAIS

9. CADEIA EPIDEMIOLÓGICA

FONTES DE INFECÇÃO
-NEONATOS, ADULTOS DOENTES***
-ADULTOS PORTADORES
-RESERVATÓRIOS
(SILVESTRES, DOMÉSTICOS)

→

VIAS DE ELIMINAÇÃO
-FEZES
-SECREÇÕES RESPIRATÓRIAS

VIAS DE TRANSMISSÃO
-AEROSSÓIS
-FÔMITES
-VETORES MECÂNICOS

→

PORTAS DE ENTRADA
-MUCOSA ORAL
-MUCOSA RESPIRATÓRIA

↓

SUSCEPTÍVEIS
-NEONATOS < 1 MÊS
-VACAS EM LACTAÇÃO
-IMUNOSSUPRIMIDOS

ENTERITES VIRAIS

10. DIAGNÓSTICO

10.1 FATORES DE RISCO

FÊMEAS PRIMÍPARAS

FALHA COLOSTRAL

ANIMAIS DE IDADES DIFERENTES EM MESMO ESPAÇO

LOCALIZAÇÃO DO BEZERREIRO, CANIL *ETC*

COLEÇÕES DE ÁGUA

VETORES

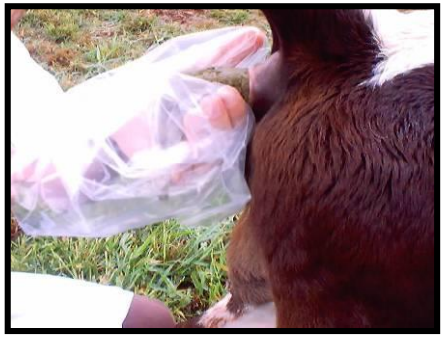
OUTRAS CRIAÇÕES

ENTERITES VIRAIS

10. DIAGNÓSTICO

10.2 DIAGNÓSTICO DIRETO

COLHEITA DE AMOSTRAS



4ºC

1º DIA DE SINTOMAS ⟹ **10^8 – 10^9 partículas virais/mL de fezes**

RETO

ENTERITES VIRAIS

10. DIAGNÓSTICO

10.2 DIAGNÓSTICO DIRETO

MÉTODOS

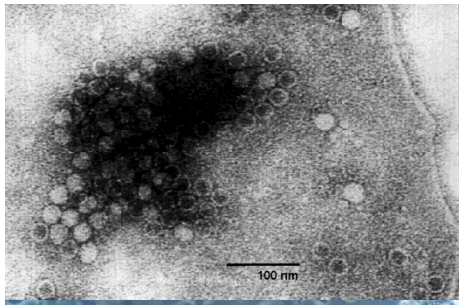
MICROSCOPIA ELETRÔNICA

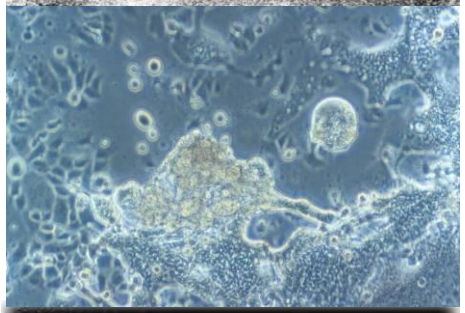
ISOLAMENTO VIRAL

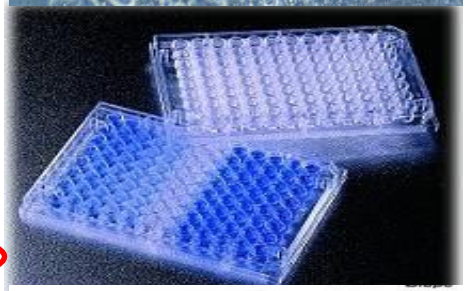
ELISA

PCR

ELETROFORESE EM GEL DE POLIACRILAMIDA (ROTAVÍRUS)

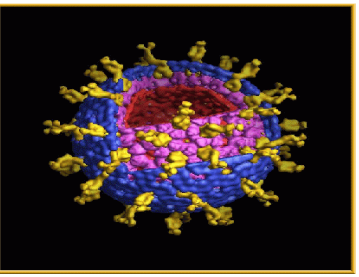




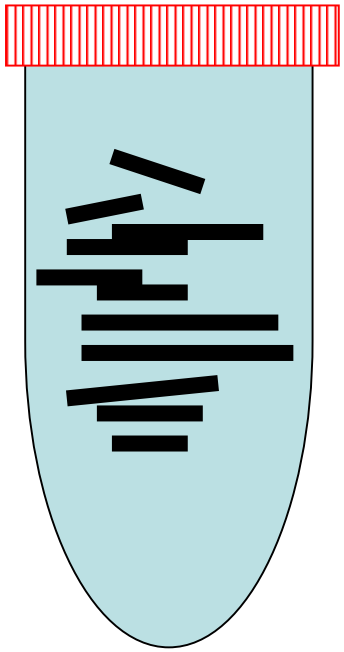


ELETROFORESE EM GEL DE POLIACRILAMIDA (PAGE): DIAGNÓSTICO DE ROTAVÍRUS

ELETROFORESE EM GEL DE POLIACRILAMIDA (PAGE): DIAGNÓSTICO DE ROTAVÍRUS

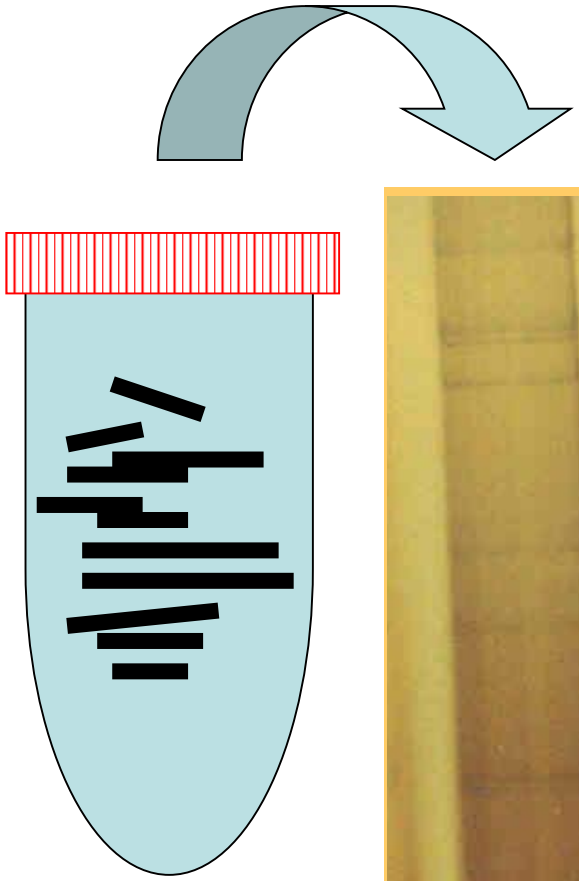


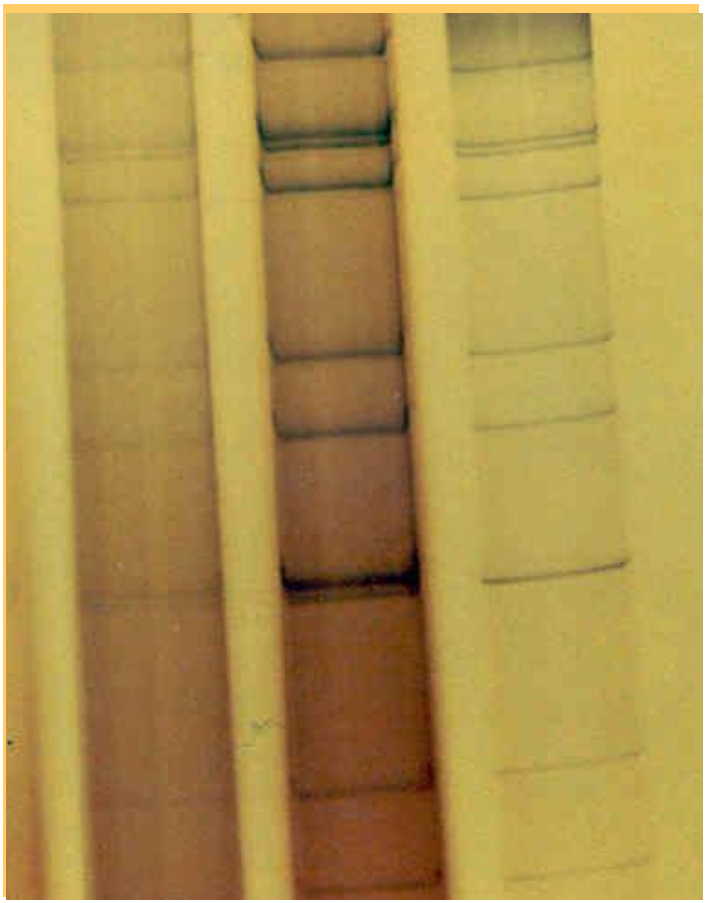
EXTRAÇÃO DE RNA



RNA SEGMENTADO

ELETROFORESE EM GEL DE POLIACRILAMIDA (PAGE): DIAGNÓSTICO DE ROTAVÍRUS





ENTERITES VIRAIS

10. DIAGNÓSTICO

10.2 DIAGNÓSTICO DIRETO

☞ **LABORATÓRIO DE BIOLOGIA MOLECULAR APLICADA E SOROLOGIA VPS/FMVZ/USP: ROTAVÍRUS, CORONAVÍRUS, PARVOVÍRUS**

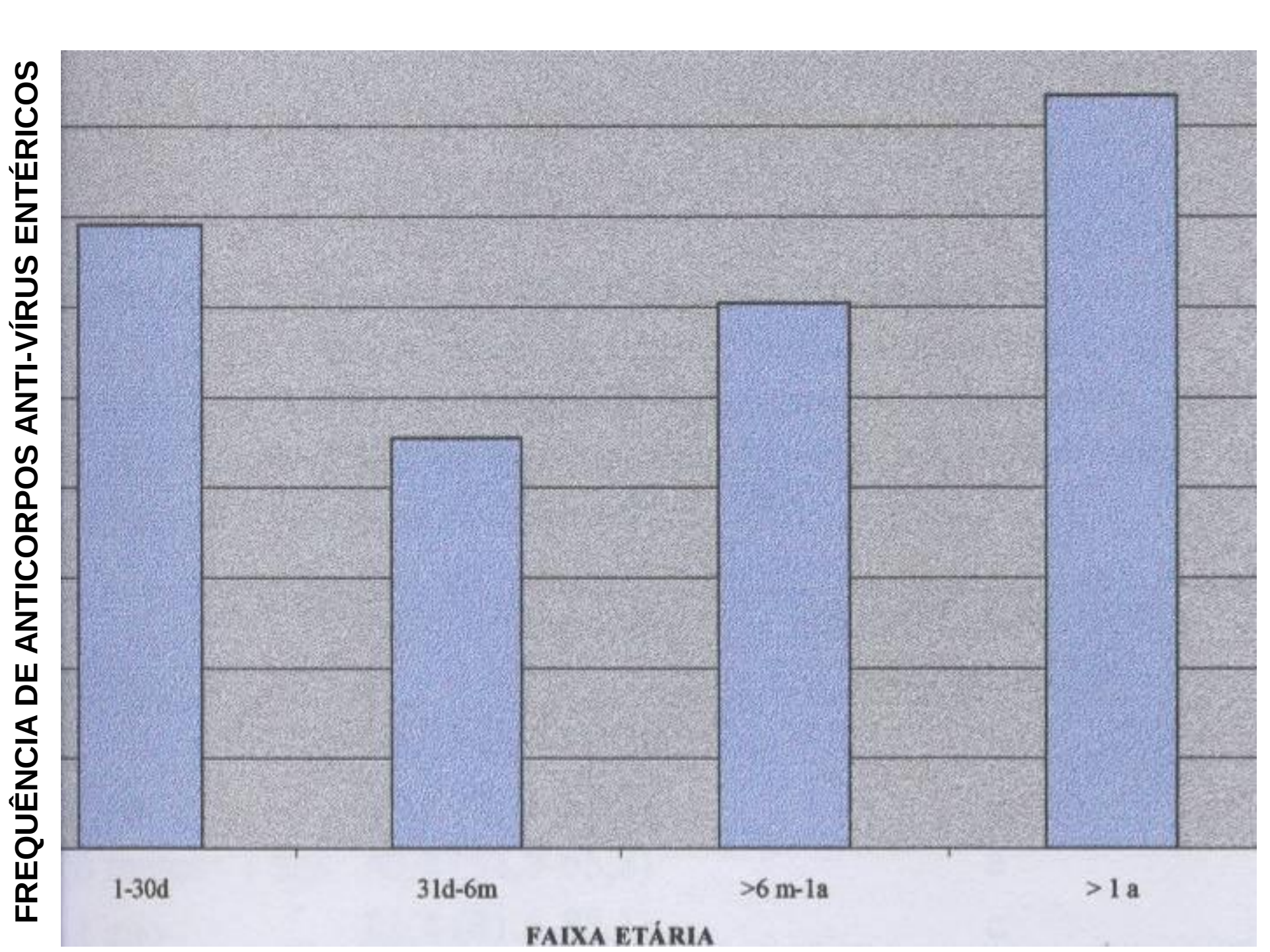
ENTERITES VIRAIS

10. DIAGNÓSTICO

10.3 DIAGNÓSTICO INDIRETO

AMOSTRA: SORO

1 AMOSTRA ÚNICA **SEM SIGNIFICADO DIAGNÓSTICO**


FREQUÊNCIA DE ANTICORPOS ANTI-VÍRUS ENTÉRICOS
1-30d
31d-6m
>6 m-1a
> 1 a
FAIXA ETÁRIA

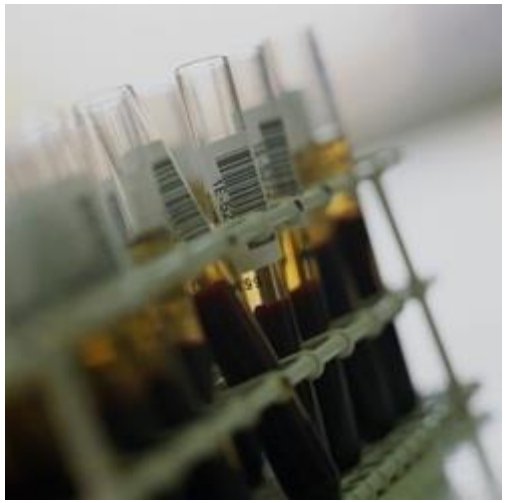
ENTERITES VIRAIS

10. DIAGNÓSTICO

10.3 DIAGNÓSTICO INDIRETO

2 AMOSTRAS PAREADAS DE SORO

INDICA INFECÇÃO RECENTE SE HOUVER SOROCONVERSÃO



ENTERITES VIRAIS

10. DIAGNÓSTICO

10.4 DIAGNÓSTICO DIFERENCIAL

Escherichi coli

***Salmonella* sp**

Clostridium perfringens

***Campylobacter* sp**

Cryptosporidium parvum

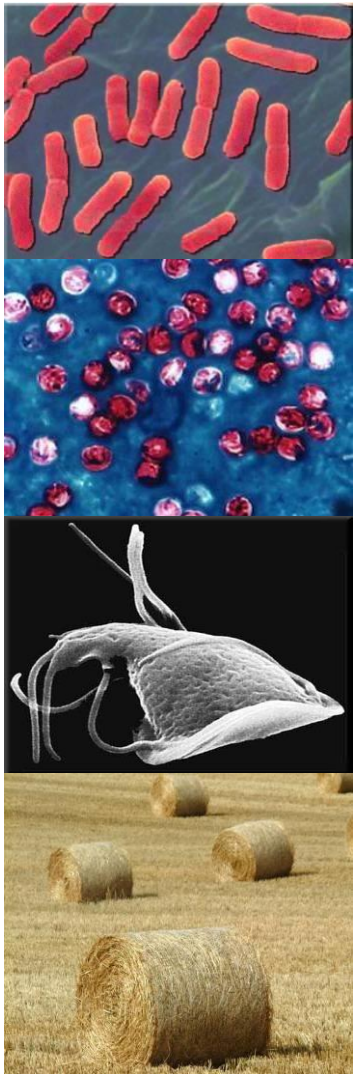
***Eimeria* sp**

***Giardia* sp**

ALTERAÇÕES EM DIETA

STRESS

DIARRÉIAS NÃO-VIRAIS



ENTERITES VIRAIS

11. PREVENÇÃO E CONTROLE

11.1 MEDIDAS APLICÁVIES ÀS FONTES DE INFECÇÃO

DIAGNÓSTICO PERIÓDICO

AMBIENTAÇÃO

SEPARAÇÃO ENTRE IDADES

SEPARAÇÃO DE ANIMAIS COM SINTOMAS

ENTERITES VIRAIS

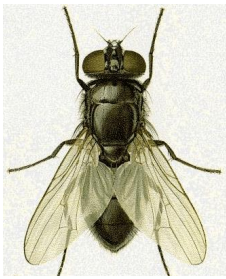
11. PREVENÇÃO E CONTROLE

11.2 MEDIDAS APLICÁVIES ÀS VIAS DE TRANSMISSÃO

DESTINO DE EXCRETAS

HIGIENIZAÇÃO

CONTROLE DE VETORES



DESINFECÇÃO

Rotavírus	**Fenol** **Formol** **Cloro** **β-propiolactona** **Etanol 95%**
Coronavírus	**Formol** **Cloro** **Iodo** **Amônio quaternário**

ENTERITES VIRAIS

11. PREVENÇÃO E CONTROLE

11.3 MEDIDAS APLICÁVIES AOS SUSCEPTÍVEIS

BIOSSEGURIDADE

COLOSTRO
(IgA)
1AS HORAS PÓS-NASCIMENTO

BANCO DE COLOSTRO
-20 ºC

ENTERITES VIRAIS

11. PREVENÇÃO E CONTROLE

11.3 MEDIDAS APLICÁVIES AOS SUSCEPTÍVEIS

⇒VACINAÇÃO (RUMINANTES)
VACAS PRENHES*, 7º E 9º MESES DE GESTAÇÃO, IM**

↑↑↑ **IgA COLOSTRAL**

⇒ VACINAÇÃO EM CARNÍVOROS

⇒ VACINAS

ENTERITES VIRAIS

12. TRATAMENTO

ENTERITES VIRAIS

13. REFERÊNCIAS

http://ictvonline.org/virusTaxonomy.asp

de Groot RJ et al. Middle East respiratory syndrome coronavirus (MERS-CoV): announcement of theCoronavirus Study Group. J Virol. 2013 Jul;87(14):7790-2.
Masters, P. S. The molecular biology of coronaviruses. Advances in Virus Research, v. 66,p. 193-292, 2006.

Brandão et al. Coronaviridae. In : Flores, E. F. (ed) Virologia Veterinária 2ed., Editora UFMSM, Santa Maria. 2012

Alfieri et al., 2012. Reoviridae. In : Flores, E. F. (ed) Virologia Veterinária 2ed., Editora UFMSM, Santa Maria. 2012

Matthijnssens et al. Uniformity of rotavirus strain nomenclature proposed by the Rotavirus Classification Working Group (RCWG). Arch Virol. 2011 Aug;156(8):1397-413.

Brandão et al. Molecular analysis of Brazilian strains of bovine coronavirus (BCoV) reveals a deletion within the hypervariable region of the S1 subunit of the spike glycoprotein also found in human coronavirusOC43. Arch Virol. 2006 Sep;151(9):1735-48.

Caruzo et al. Molecular characterization of G and P-types bovine rotavirus strains from Goiás, Brazil: high frequency of mixed P-type infections. Mem Inst Oswaldo Cruz. 2010 Dec;105(8):1040-3.

Brandão et al. On the etiology of an outbreak of winter dysenter On the etiology of an outbreak of winter dysentery in dair y in dairyy cows in Brazil Pesq. Vet. Bras. 27(10):398-402, outubro 2007

Buonavoglia et al. Canine coronavirus highly pathogenic for dogs. Emerg Infect Dis. 2006 Mar;12(3):492-4.

Addie Feline coronavirus--that enigmatic little critter. Vet J. 2004 Jan;167(1):5-6.

Villarreal et al. Orchitis in roosters with reduced fertility associated with avian infectious bronchitis virus and avian metapneumovirus infections. Avian Dis. 2007 Dec;51(4):900-4.

Beserra et al. Occurrence and characterization of rotavirus A in broilers, layers, and broiler breeders from Brazilian poultry farms. Avian Dis. 2014 Mar;58(1):153-7.

Huang et al. Origin, evolution, and genotyping of emergent porcine epidemic diarrhea virus strains in the United States. MBio. 2013 Oct 15;4(5):e00737-13
.
Tonietti et al. Phylogenetic analyses of the VP4 and VP7 genes of porcine group A rotaviruses in Sao Paulo State, Brazil: first identification of G5P[23] in piglets. J Clin Microbiol. 2013 Aug;51(8):2750-3.