

Virus e batteri: esperienze e vantaggi della metagenomica

Simone Peletto, DVM PhD
S.S. Genetica e Immunobiochimica

simone.peletto@izsto.it



Analisi di microbiota e miRNoma di ectoparassiti ematofagi da uccelli migratori mediante Next Generation Sequencing

Cerutti F., Modesto P., Mandola M.L., Rizzo F., Goria M.,
Cattonaro F., Costa S., Giammarino M., Radovic S., Acutis P.L.,

Peletto S.

Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle D'Aosta, Torino

Istituto di Genomica Applicata (IGA), Udine

Laboratorio Chimico Camera di Commercio, Torino

ASL CN1, Savigliano



Progetto di ricerca corrente IZS PLV 16/12 RC realizzato con il
finanziamento del **Ministero della Salute**



Introduzione

Gli uccelli migratori possono diffondere patogeni in 3 modi (Hubálek, 2004):

- Carrier biologici (il patogeno si replica nell'ospite)
- Carrier meccanici (il patogeno viene trasportato meccanicamente)
- Carrier di ectoparassiti ematofagi infetti
 - Trasmissione a un altro ospite
 - Co-feeding





Approccio allo studio

- Isolamento: poche linee cellulari permissive
- [RT-]PCR: applicabile per pochi patogeni per volta
- Microarray: bassa sensibilità nonostante sonde con mismatch
- Representational difference analysis e random amplification:
identificazione di virus sconosciuti, ma poco sensibili e
laboriose





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- Representational difference analysis e random amplification: identificazione di virus sconosciuti, ma poco sensibili e laboriose

- **Next Generation Sequencing:**
 - Nessuna conoscenza a priori sul target
 - Identificazione sia di virus che di batteri





Obiettivi

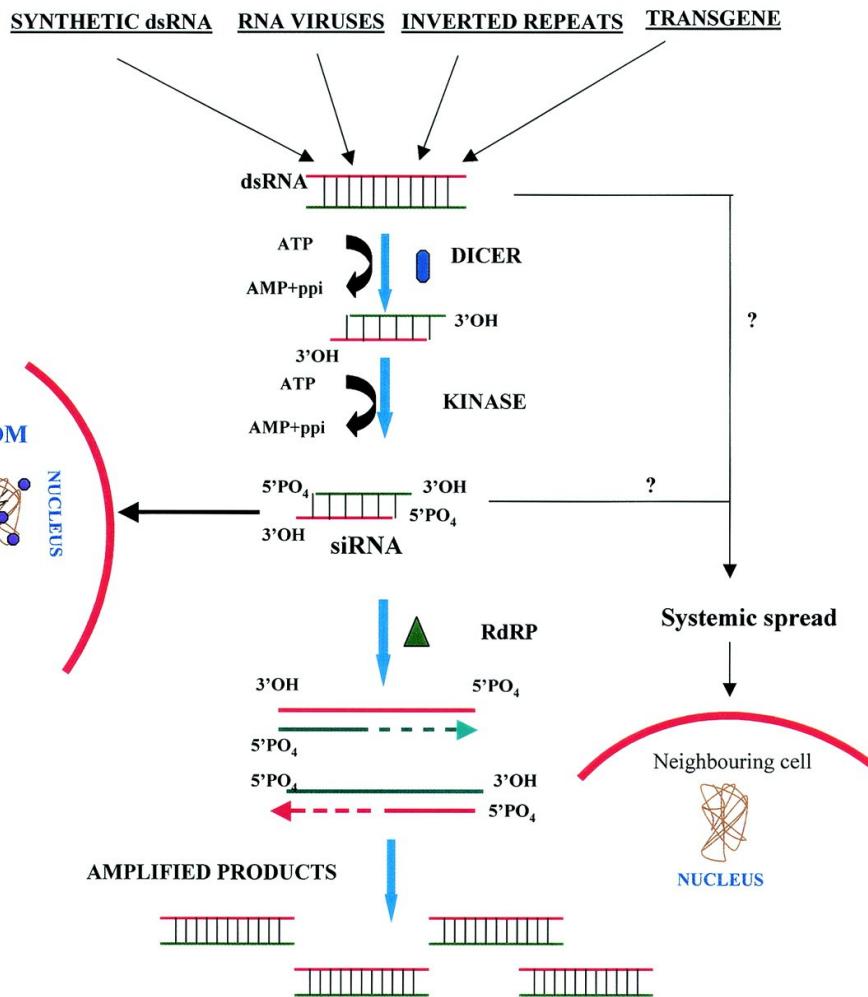
Approccio innovativo per lo studio della biodiversità microbica degli ectoparassiti degli uccelli migratori tramite tecnologia NGS:

- **Metabarcoding 16S** e sequenziamento di **small RNA** per l'identificazione di sequenze microrganismi negli ectoparassiti degli uccelli migratori
- Mettere a punto delle pipeline bioinformatiche per l'identificazione di organismi patogeni da dati di **miRNoma**
- Caratterizzare il **microbioma** degli ectoparassiti rilevati su uccelli migratori
- Indagare la presenza sul territorio regionale di agenti infettivi esotici o nuovi importati attraverso gli ectoparassiti degli uccelli migratori



Small RNA per identificazione di nuovi virus

STEP I



- Small interfering RNA (siRNA) si legano a mRNA, e ne inducono la degradazione
- I virus sono sia attivatori che target dell'RNA interference
- RNAi è il principale meccanismo di immunità innata nelle zanzare per il controllo di infusione e trasmissione di arbovirus

Virus discovery by deep sequencing and assembly of virus-derived small silencing RNAs

Qingfa Wu^a, Yingjun Luo^a, Rui Lu^a, Nelson Lau^b, Eric C. Lai^c, Wan-Xiang Li^a, and Shou-Wei Ding^{a,1}

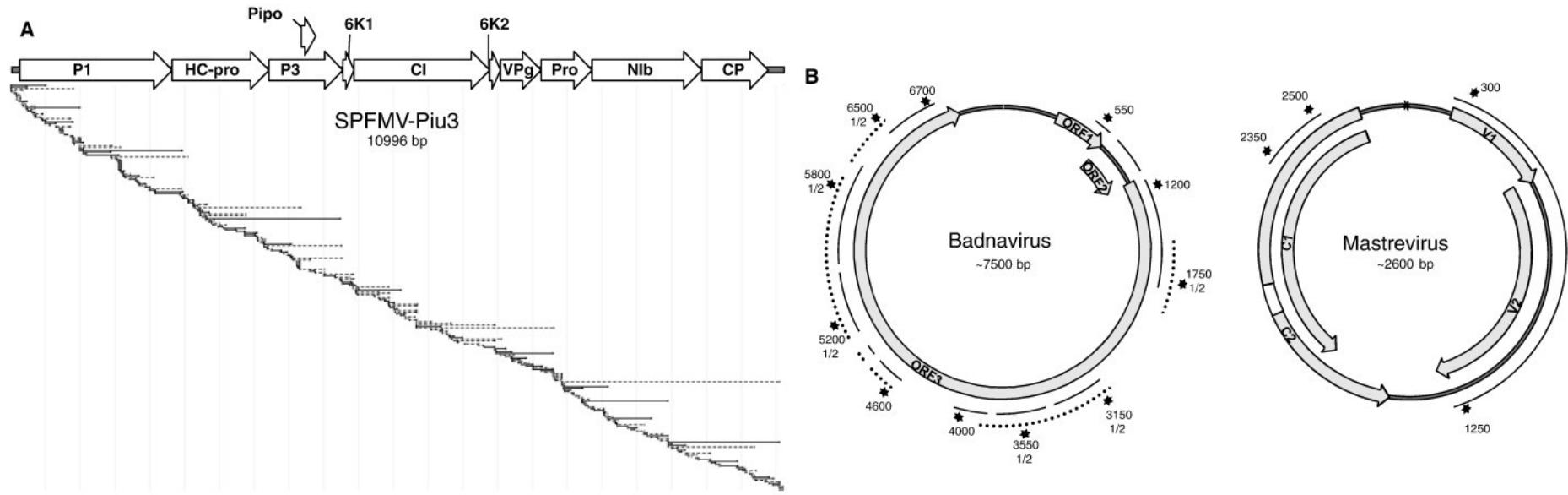
^aDepartment of Plant Pathology and Microbiology, Institute for Integrative Genome Biology, University of California, Riverside, CA 92521; ^bDepartment of Biology, Brandeis University, Waltham, MA 02454; and ^cDepartment of Developmental Biology, Sloan-Kettering Institute, New York, NY 10065

Edited by Peter Palese, Mount Sinai School of Medicine, New York, NY, and approved December 3, 2009 (received for review October 1, 2009)

In response to infection, invertebrates process replicating viral RNA genomes into siRNAs of discrete sizes to guide virus clearance by intermediates (vRI-dsRNAs) are the substrate of DCR2 and the precursor of viral siRNAs (11, 12). Drosophila susceptibility to



Small RNA per identificazione di nuovi virus



Ricostruzione di genomi virali da siRNA

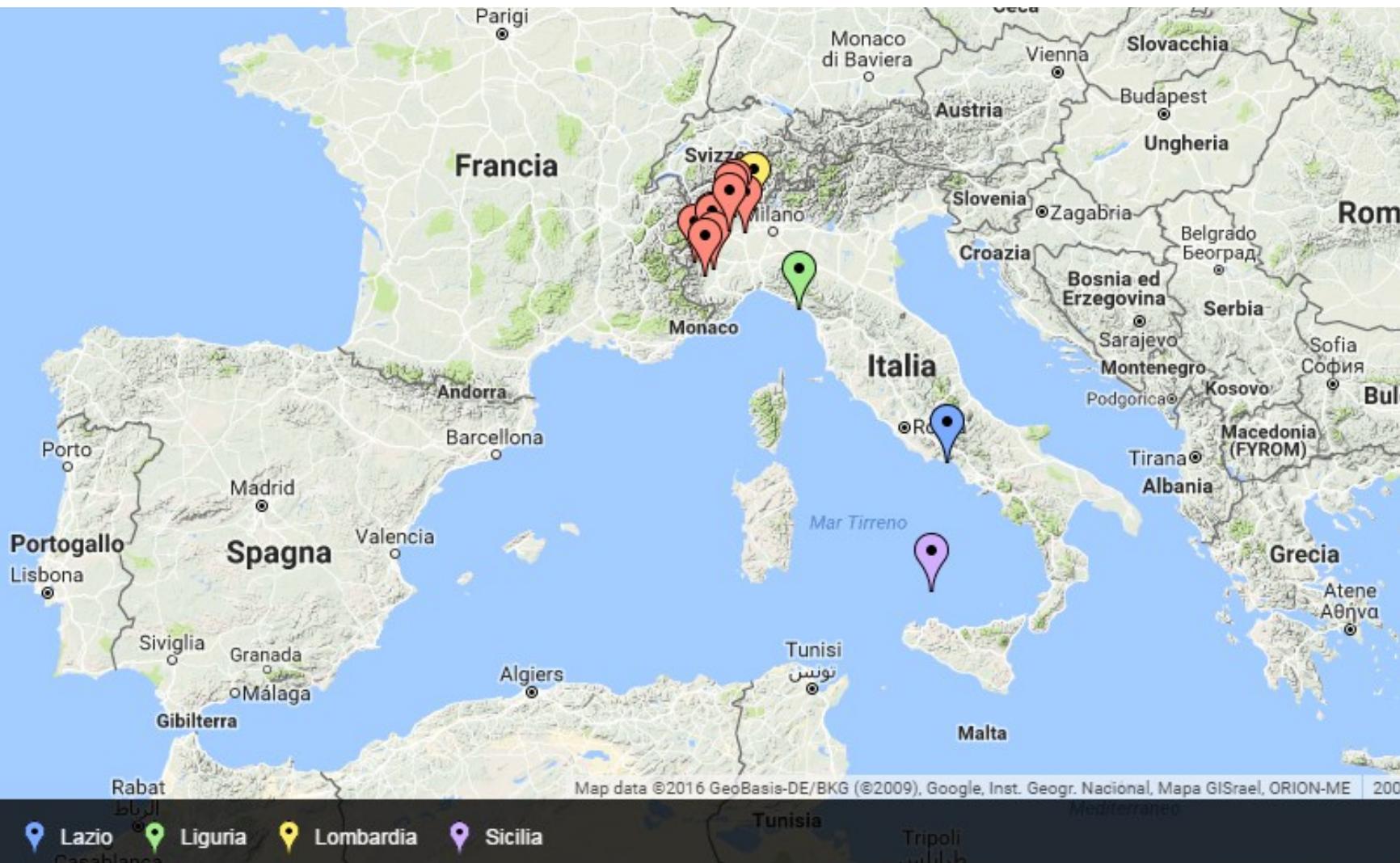
Rapid Communication

Complete viral genome sequence and discovery of novel viruses by deep sequencing of small RNAs: A generic method for diagnosis, discovery and sequencing of viruses

Jan F. Kreuze ^{a,d,*}, Ana Perez ^c, Milton Untiveros ^a, Dora Quispe ^a, Segundo Fuentes ^c, Ian Barker ^c, Reinhard Simon ^b



Siti di campionamento

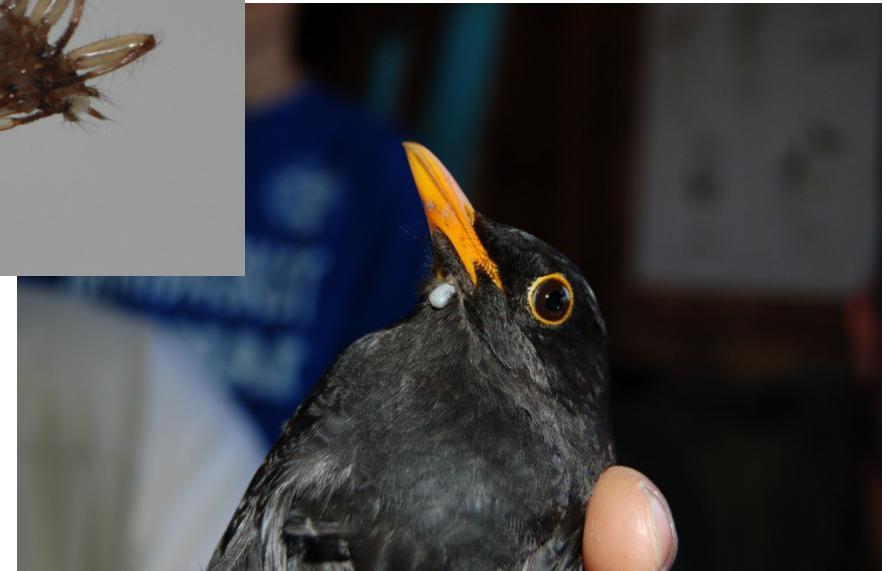
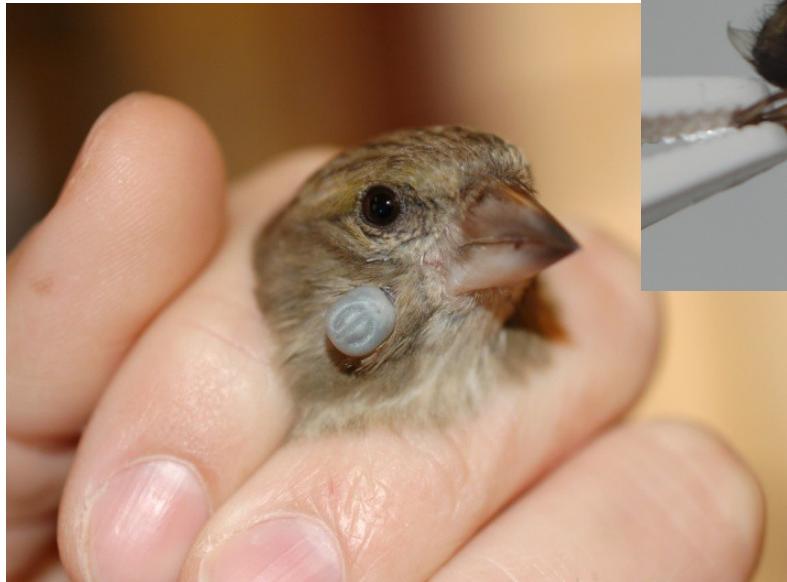




Materiali

Raccolta di **194 ectoparassiti** in **RNAlater®** (ditteri ippoboscidi, zecche, mallofagi, pidocchi e altri ectoparassiti) da **115 uccelli**.

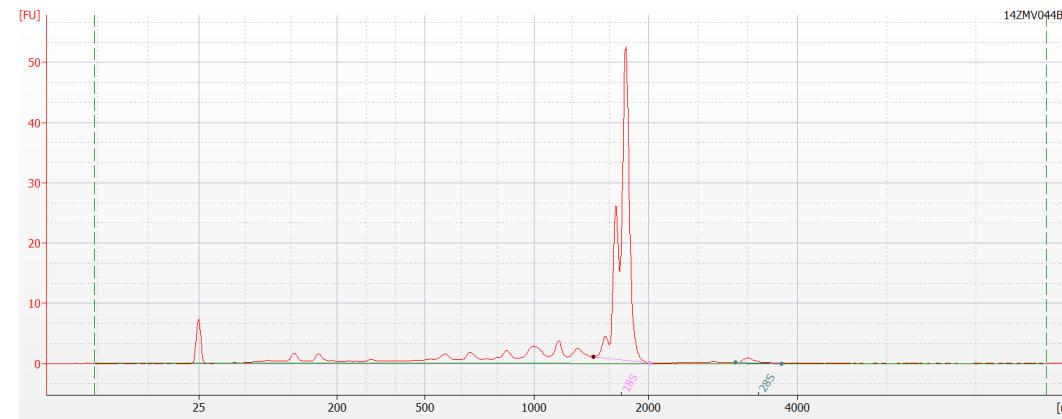
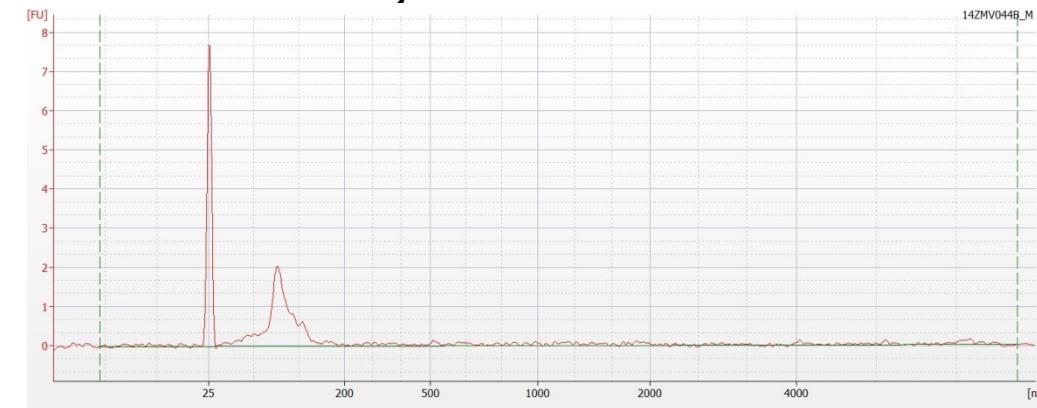
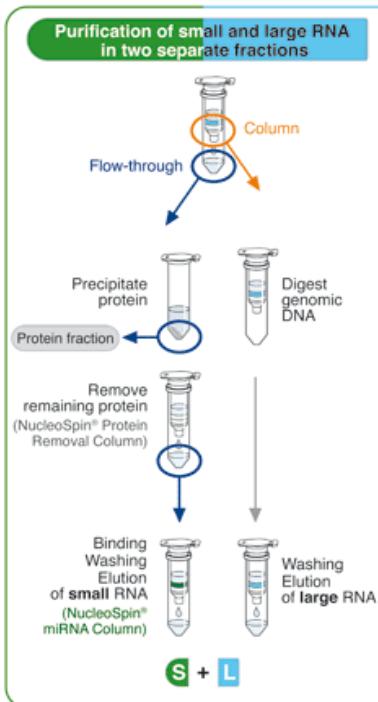
28 specie di uccelli campionati (migratori a lungo raggio, a breve raggio, stanziali) durante sessioni di inanellamento.





Metodi

Estrazione di RNA totale e small RNA in frazioni separate, sequenziamento del gene mitocondriale COI per identificazione molecolare del vettore, valutazione degli RNA con Bioanalyzer 2100.





Metodi

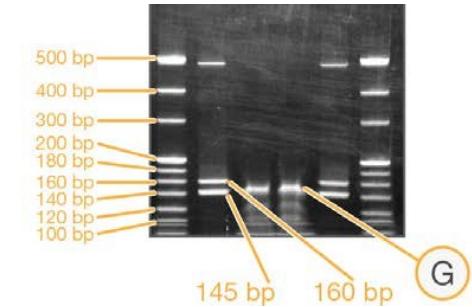
Metabarcoding 16S dell'rRNA secondo protocollo Illumina (regioni V3-V4 del 16S)



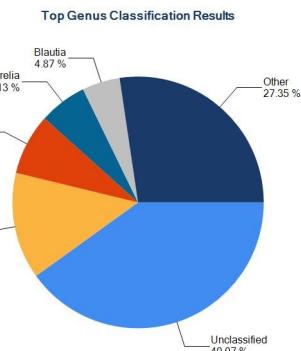
**Allestimento di 10 pool di small RNA,
preparazione library (TrueSeq Small
RNA) e sequenziamento su HiSeq2000**

©2012 Illumina Inc. All rights reserved.

**Analisi dati metabarcoding con MiSeq
Reporter Metagenomics Workflow,
Blastn, Silva e Megan**



**Analisi dati small RNA secondo pipeline
home-made**



**Conferma delle infezioni rilevate
mediante PCR**



Risultati - 16S

I generi potenzialmente zoonosici riscontrati: *Rickettsia*, *Anaplasma*, *Borrelia*, *Coxiella*, *Francisella* e *Ehrlichia*

Genere	Hit	Prevalenza	Conferme PCR
Francisella	4	3,3%	2
Bartonella	4	3,3%	0
Borrelia	17	14,2%	10
Rickettsia	110	91,7%	47
Coxiella	6	5,0%	0
Anaplasma	3	2,5%	3
Ehrlichia	98	81,7%	-



SCIENTIFIC REPORTS

OPEN

A *Francisella*-like endosymbiont in the Gulf Coast tick evolved from a mammalian pathogen

Received: 27 June 2016

Accepted: 30 August 2016

Published: 20 September 2016

bioRxiv preprint doi: <https://doi.org/10.1101/062223>; this version posted September 20, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under a [aCC-BY-ND 4.0 International license](https://creativecommons.org/licenses/by-nd/4.0/).

Jonathan G. Gerhart, Abraham S. Moses & Rahul Raghavan

Ticks (order Ixodida) vector pathogenic bacteria that cause diseases in humans and other mammals. They also contain bacteria that are closely related to pathogens but function as endosymbionts that provide nutrients that are missing from mammalian blood—their sole food source. For instance, mammalian pathogens such as *Coxiella burnetii* and *Francisella tularensis*, as well as *Coxiella*-like and

Folia Microbiol (2013) 58:419–428

DOI 10.1007/s12223-013-0222-1

Hard ticks and their bacterial endosymbionts (or would be pathogens)

Arunee Ahantariig · Wachareeporn Trinachartvanit ·



CrossMark

January 2013 / Published online: 22 January 2013
of Sciences of the Czech Republic, v.v.i. 2013

Coxiella symbionts are widespread into hard ticks

Erik Machado-Ferreira¹ · Vinicius F. Vizzoni¹ · Emilia Balsemão-Pires¹ ·Leonardo Moerbeck² · Gilberto S. Gazeta² · Joseph Piesman³ · Carolina M. Vargas¹ ·Carlos A. G. Soares¹

Journals.ASM.org

Coinfection of *Dermacentor silvarum* Olenev (Acari: Ixodidae) by *Coxiella*-Like, *Arsenophonus*-Like, and *Rickettsia*-Like Symbionts

Ji Meng Liu,² Ling Xia Li,² Jian Nan Liu,² Yong Hong Hu,² Zhao Liu,² Lida Guo,² Jing Ze Liu²ey Laboratory of Animal Physiology, Biochemistry and Molecular Biology of Hebei Province, College of Life Sciences, Hebei Normal University, Shijiazhuang, Hebei, eople's Republic of China^a; Department of Environment and Chemical Engineering, Hebei College of Industry and Technology, Hebei, People's Republic of China^b

We report that multiple symbionts coexist in *Dermacentor silvarum*. Based on 16S rRNA gene sequence analyses, we prove that *Coxiella*-like and *Arsenophonus*-like symbionts, with 95.6% and 96.7% sequence similarity to symbionts in the closest taxon, respectively, are novel. Moreover, we also provide evidence that the *Coxiella*-like symbiont appears to be the primary symbiont.

RESEARCH ARTICLE

The Recent Evolution of a Maternally-Inherited Endosymbiont of Ticks Led to the Emergence of the Q Fever Pathogen, *Coxiella burnetii*

Olivier Duron^{1*}, Valérie Noël¹, Karen D. McCoy¹, Matteo Bonazzi², Karim Sidi-Boumedine³, Olivier Morel⁴, Fabrice Vavre⁴, Lionel Zenner⁴, Elsa Jourdain⁵, Patrick Durand¹, Céline Arnathau¹, François Renaud¹, Jean-François Trape¹, Abel S. Biguezton^{1,6}, Julie Cremaschi¹, Muriel Dietrich¹, Elsa Léger¹, Anais Appelgren¹, Marlène Dupraz¹, Elena Gómez-Díaz^{1,7}, Georges Diatta⁸, Guiguigbaza-Kossigan Dayo⁶, Hassane Adakal^{6,9}, Sébastien Zoungrana⁶, Laurence Vial¹⁰, Christine Chevillon¹





Risultati - 16S

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Anaplasma	3	2,5%	3
Ehrlichia	98	81,7%	-

Simbionti *Francisella-like*

Simbionti *Rickettsia-like*

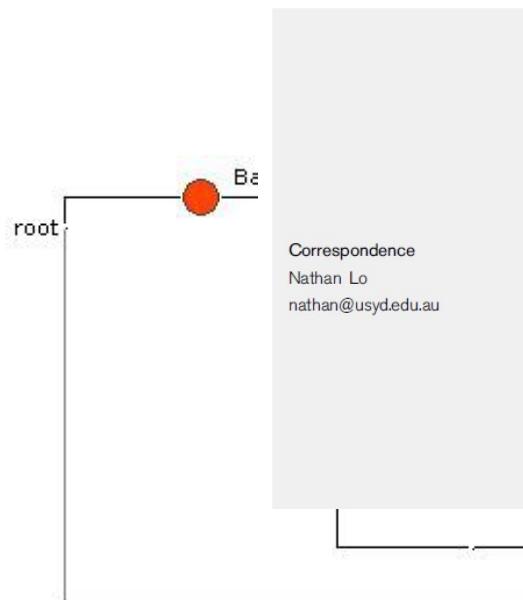
Simbionti *Coxiella-like*

Errore di identificazione?



Risultati - 16S

International Journal of Systematic and Evolutionary Microbiology (2006), 56, 2535–2540 DOI 10.1099/ijs.0.64386-0 Streptosporangineae



'*Candidatus Midichloria mitochondrii*', an endosymbiont of the tick *Ixodes ricinus* with a unique intramitochondrial lifestyle

Davide Sassera,¹ Tiziana Beninati,² Claudio Bandi,¹ Edwin A. P. Bouman,³ Luciano Sacchi,⁴ Massimo Fabbri⁵ and Nathan Lo²

¹Dipartimento di Patologia Animale, Igiene e Sanità Pubblica Veterinaria, Università degli studi di Milano, 20133 Milan, Italy

²School of Biological Sciences, The University of Sydney, New South Wales 2006, Australia

³Biology Centre, Institute of Parasitology, Academy of Sciences of the Czech Republic, Branišovská 31, 370 05 České Budějovice, Czech Republic

^{4,5}Dipartimento di Biologia Animale, Università di Pavia, Piazza Botta 9⁴ and Sezione Diagnostica di Pavia, Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna "Bruno Ubertini"⁵, 27100 Pavia, Italy

Risultati di Blast-Megan di un campione con *E. ovina*



Risultati - 16S

Specie confermate mediante PCR e sequenziamento Sanger:

- *Rickettsia aeschlimanii, asiatica, bellii, canadensis, helvetica, monacensis*
- *Anaplasma phagocytophilum*
- *Borrelia valaisiana*

Coinfezioni confermate:

- *Borrelia-Rickettsia (n=9)*
- *Anaplasma-Rickettsia (n=2)*



ORIGINAL RESEARCH ARTICLE

Molecular methods routinely used to detect *Coxiella burnetii* in ticks cross-react with *Coxiella*-like bacteria

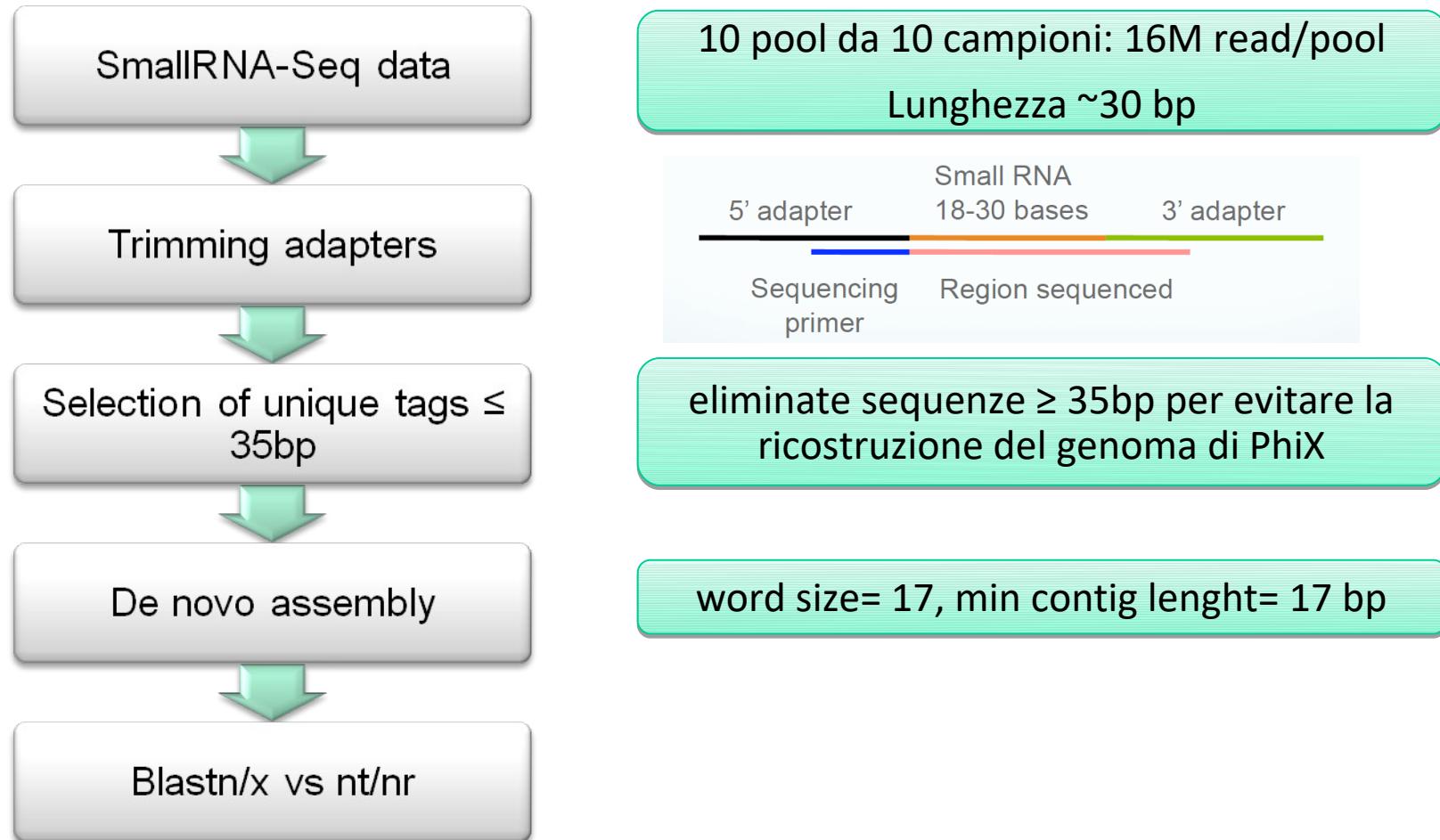
Joudain Elsa, PhD, DVM^{1*}, Olivier Duron, PhD², Barry Séverine¹, Daniel González-Acuña, PhD, DVM³ and Karim Sidi-Boumedine, PhD, DVM⁴

¹INRA, UR0346 Animal Epidemiology Unit, Saint Genès Champanelle, France; ²Laboratoire MIVEGEC (Maladies Infectieuses et Vecteurs: Ecologie, Génétique, Evolution et Contrôle), Centre National de la Recherche Scientifique (CNRS) Unité Mixte de Recherche UMR 5290, Université Montpellier 1 – Université Montpellier 2 – Institut pour la Recherche et le Développement, Unité de Recherche UR 224, Montpellier, France; ³Veterinary School, University of Concepción, Chillán, Chile; ⁴Anses, Sophia-Antipolis Laboratory, Animal Q fever Unit, Sophia-Antipolis, France



I generi simbionti riscontrati: *Wolbachia, Arsenophonus, Candidatus Midichloria mitochondrii, Francisella-like, Rickettsia-like, Coxiella-like*

Risultati – small RNA

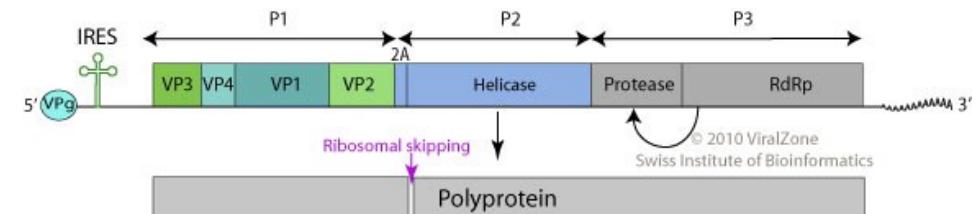
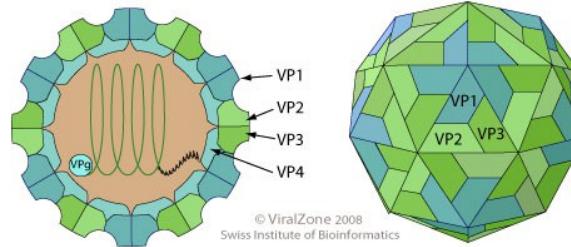




Risultati - small RNA

Risultati dall'output di BlastX:

- Due pool con sequenze correlate (similarità 49–92%) a Sacbrood virus (SBV) – Iflavirus





Microbiota delle alte e basse vie respiratorie in vitelli di razza Piemontese

Cerutti F., Nicola I., Grego E., Bertone I., Cagnasso A.,
D'Angelo A., Acutis P.L., Bellino C., **Peletto S.**

*Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle D'Aosta, Torino
Dipartimento di Scienze Veterinarie, Università degli Studi di Torino*



Introduzione

Microbioma nasofaringe

Microbioma polmone

...



?

Microbioma polmone

Microbioma nasofaringe

Viroma polmone



?



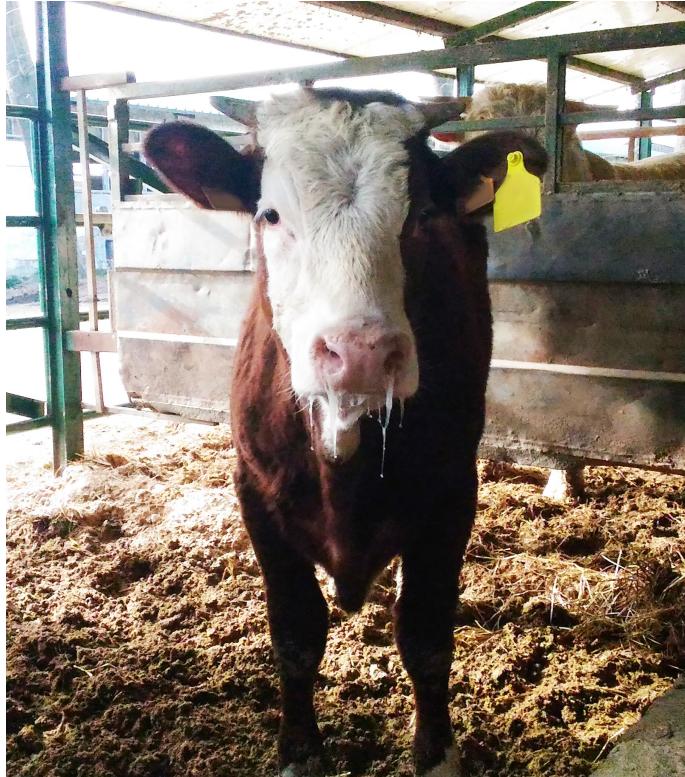
Scopo del lavoro



**Caratterizzare le alte e basse vie respiratorie
in vitelli di razza Piemontese affetti e non da
BRD mediante metabarcoding del 16S rRNA**



BRD= Bovine Respiratory Disease





BRD= Bovine Respiratory Disease

Sindrome di difficile controllo

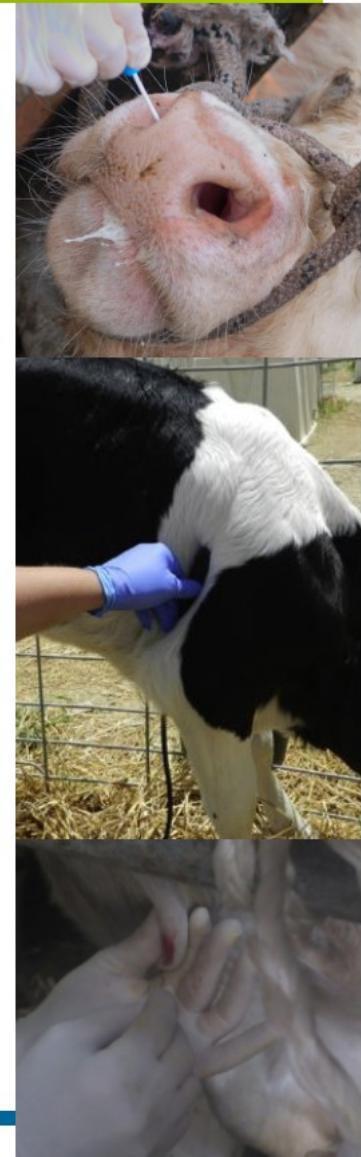
Fatale per i vitelli

Grave danno economico



Materiali & Metodi

- ◆ 22 vitelli svezzati di razza Piemontese
- ◆ Follow-up ogni 7 gg





Materiali & Metodi

Esecuzione dei BAL:

- ◆ Sedazione animale
- ◆ Tracheotomia
- ◆ Inserimento catetere sterile
- ◆ Iniezione 60ml di fisiologica 0.9% NaCl
- ◆ Immediata aspirazione

- ◆ 9 casi BRD
- ◆ 13 controlli

Ulteriori analisi:

- ◆ Batteriologico
- ◆ Virologico
- ◆ Analisi biochimiche



Materiali & Metodi

Metabarcoding 16S

DNA totale

PCR su
V3-V4
16S
rRNA

MiSeq

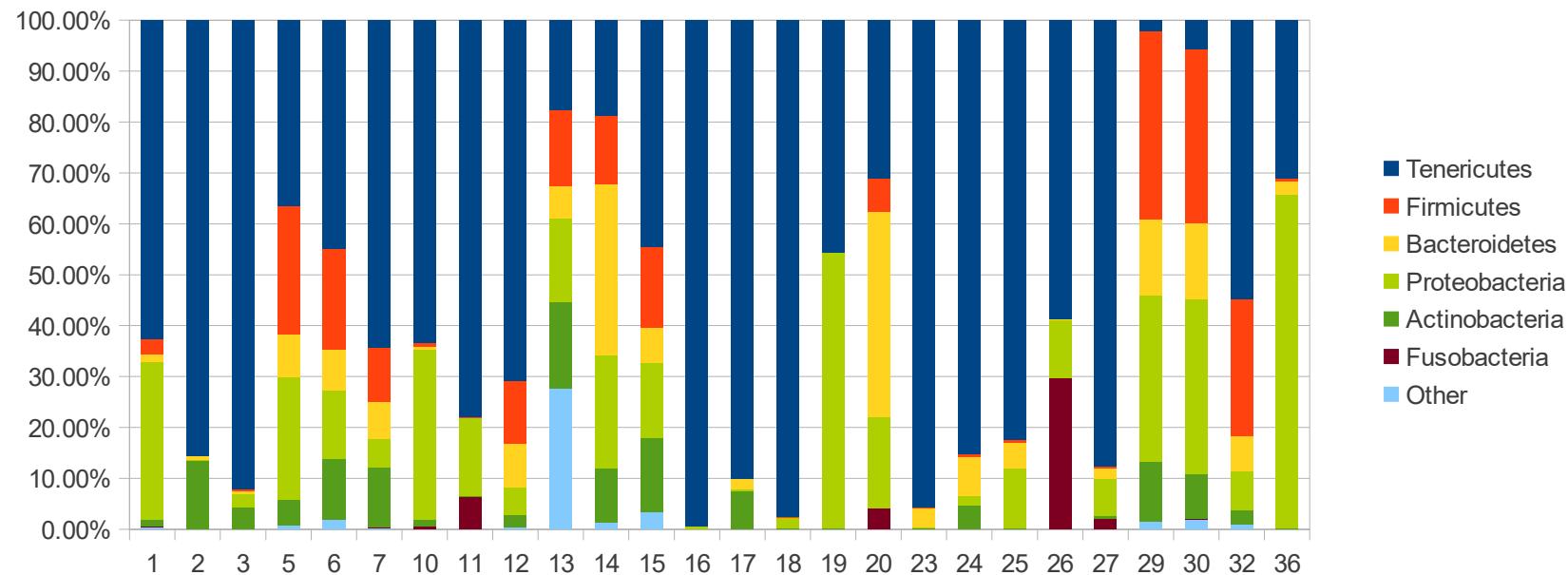
QIIME

n. read totali: 3.482.819
Lunghezza media: 407 ± 80
810 read uniche chimeriche



Risultati

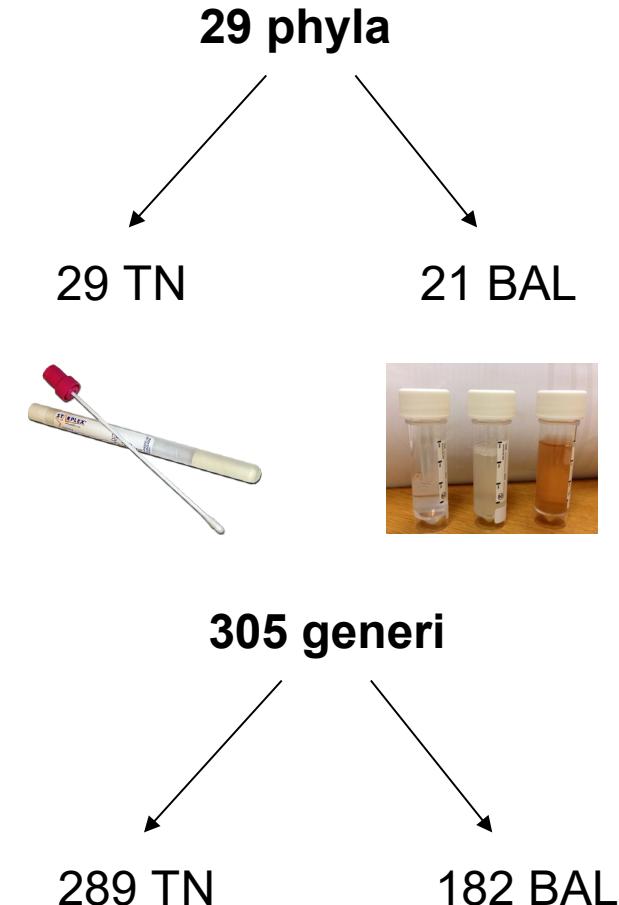
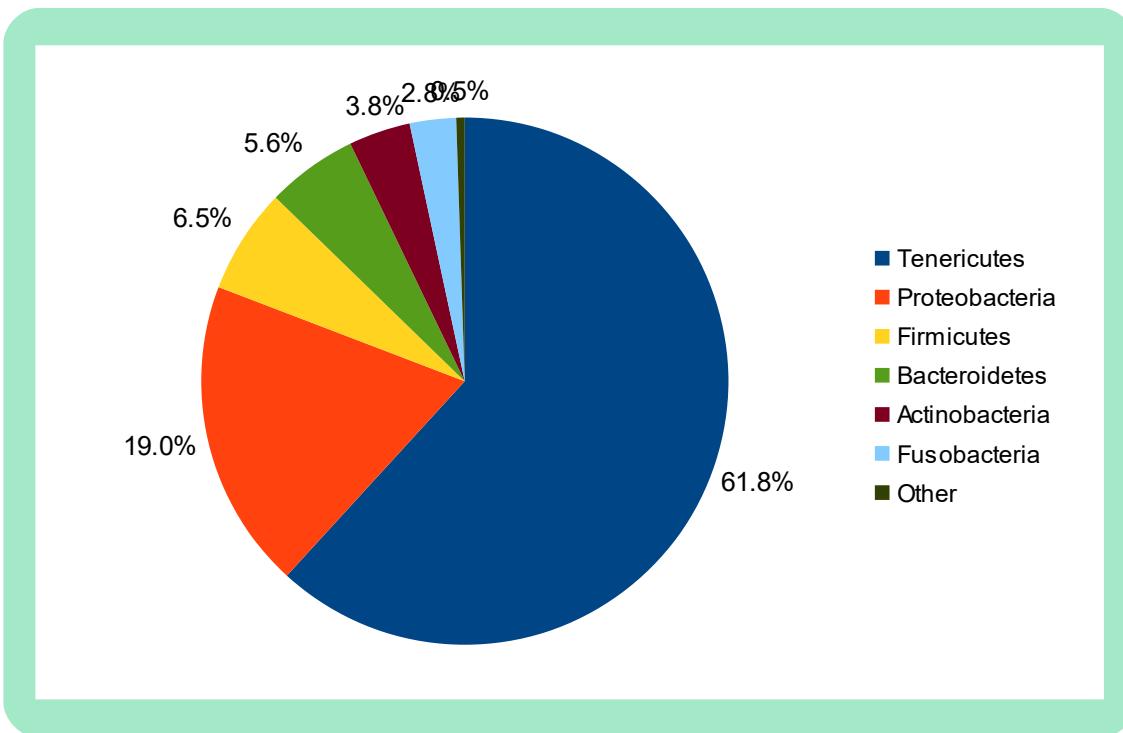
Microbiota per singolo campione





Risultati

Microbioma totale





Risultati

Core biome

Tutti i campioni
Mycoplasma

BAL
Mycoplasma

Tamponi
Succinivibrio
Mycoplasma
Sphingomonas
Corynebacterium



Risultati

Gruppi testati

- ◆ Tipologia campione
- ◆ Lesioni ecografiche
- ◆ Score ecografia >3
- ◆ Segni clinici
- ◆ Batteriologico BAL
- ◆ Batteriologico tamponi
- ◆ Tipologia campione e lesioni ecografiche
- ◆ Sesso
- ◆ Allevamento
- ◆ Animale



Risultati

Gruppi testati

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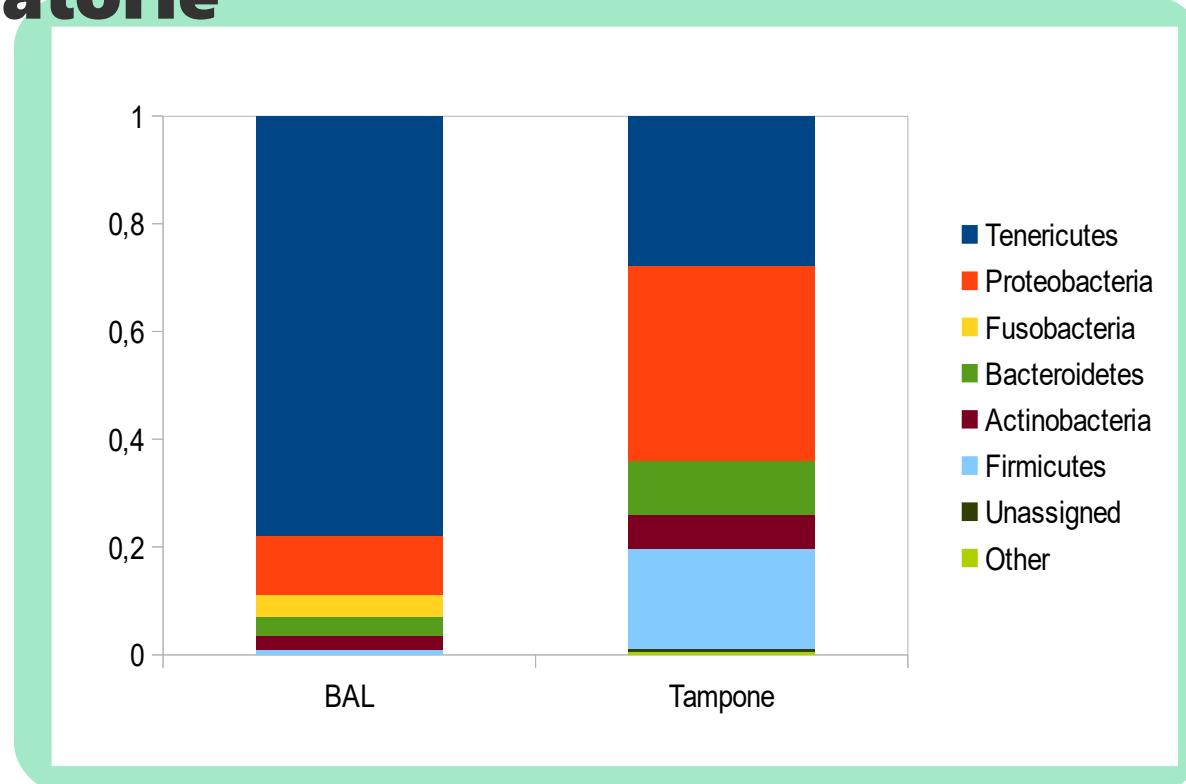
Gruppi significativi

- ◆ Tipologia campione ←
- ◆ Lesioni ecografiche
- ◆ Score ecografia >3
- ◆ Segni clinici
- ◆ Batteriologico BAL
- ◆ Batteriologico tamponi
- ◆ Tipologia campione e lesioni ecografiche ←
- ◆ Sesso
- ◆ Allevamento
- ◆ Animale



Risultati

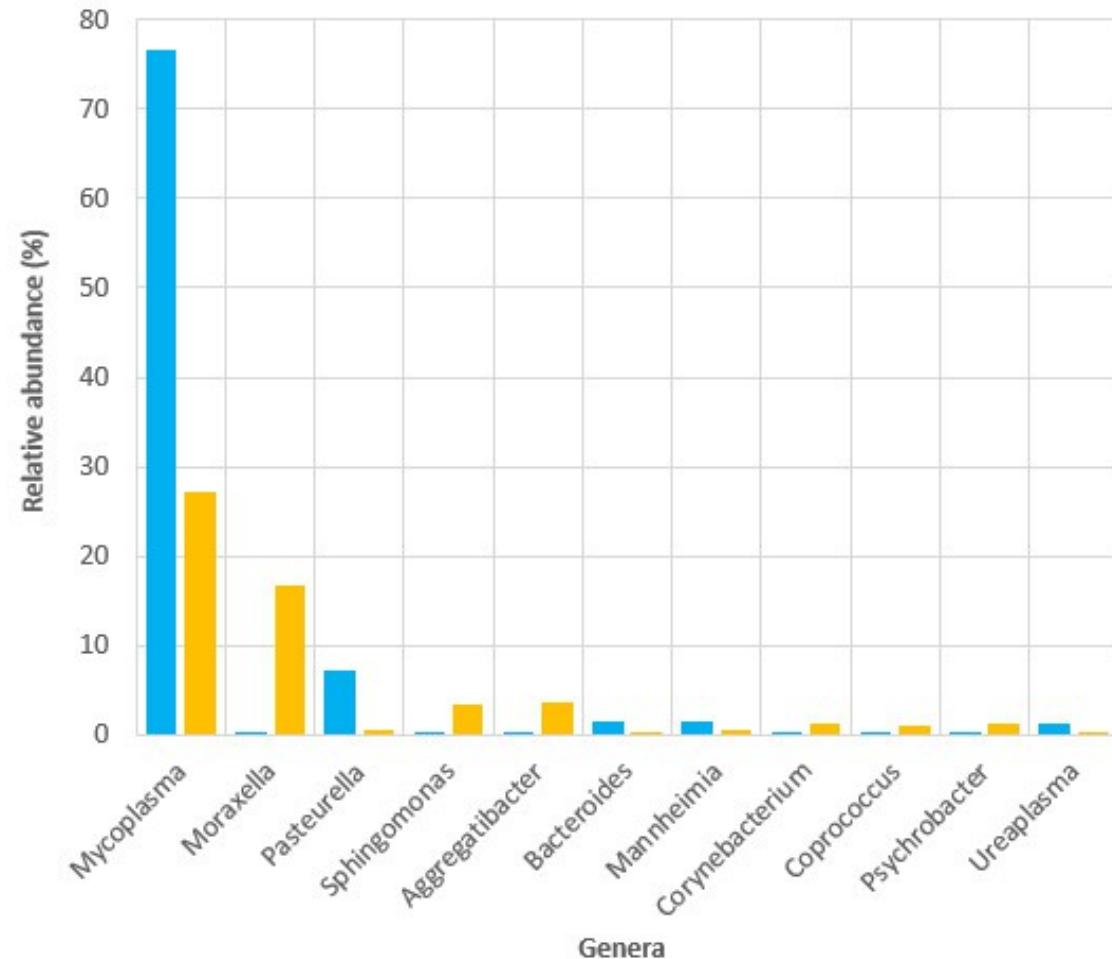
Confronto microbiota alte e basse vie respiratorie



Differenza statisticamente significativa (ADONIS)



Abbondanza relativa dei generi identificati in TN e BAL



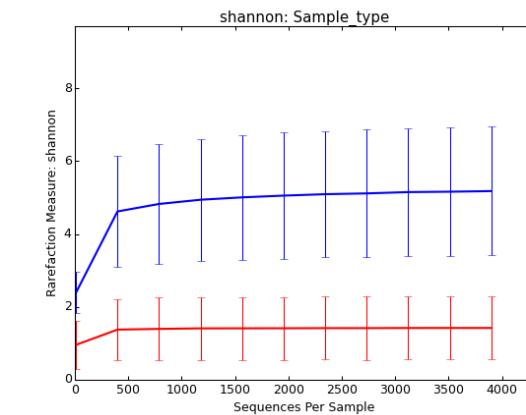
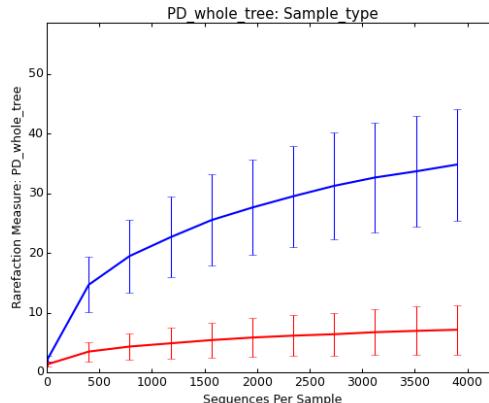
BAL
TN



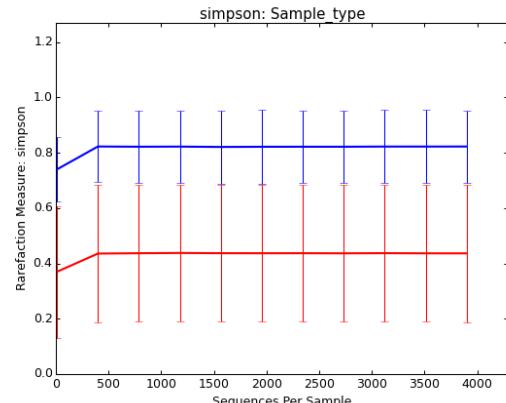
Risultati

Diversità alpha del microbiota

	BAL	Tamponi	<i>p</i> -value
Species richness	1708.91 ± 59.2	4057.29 ± 7.74	0.001
Shannon index	4.82 ± 0.018	100.04 ± 0.67	0.001
Simpson index	2.2 ± 0.01	15.18 ± 0.09	0.001



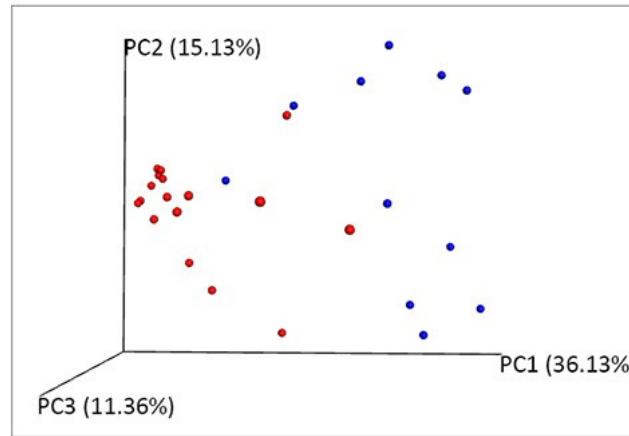
- BAL - Tamponi



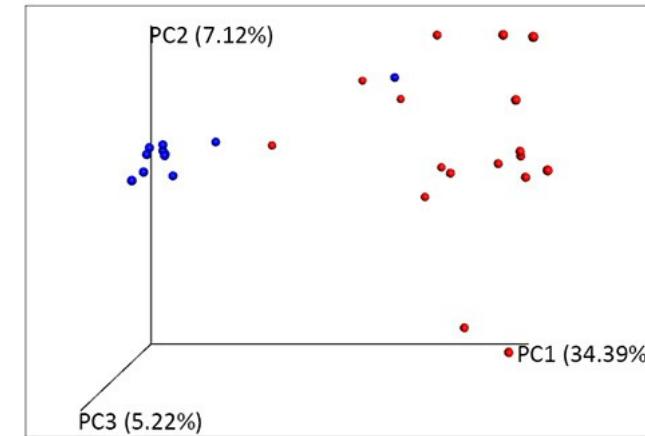


Confronto microbiota alte e basse vie respiratorie (Diversità beta – PCA)

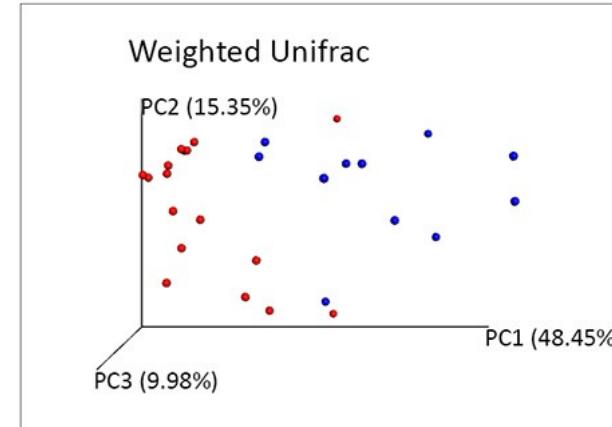
Bray-Curtis



Unweighted Unifrac



Weighted Unifrac

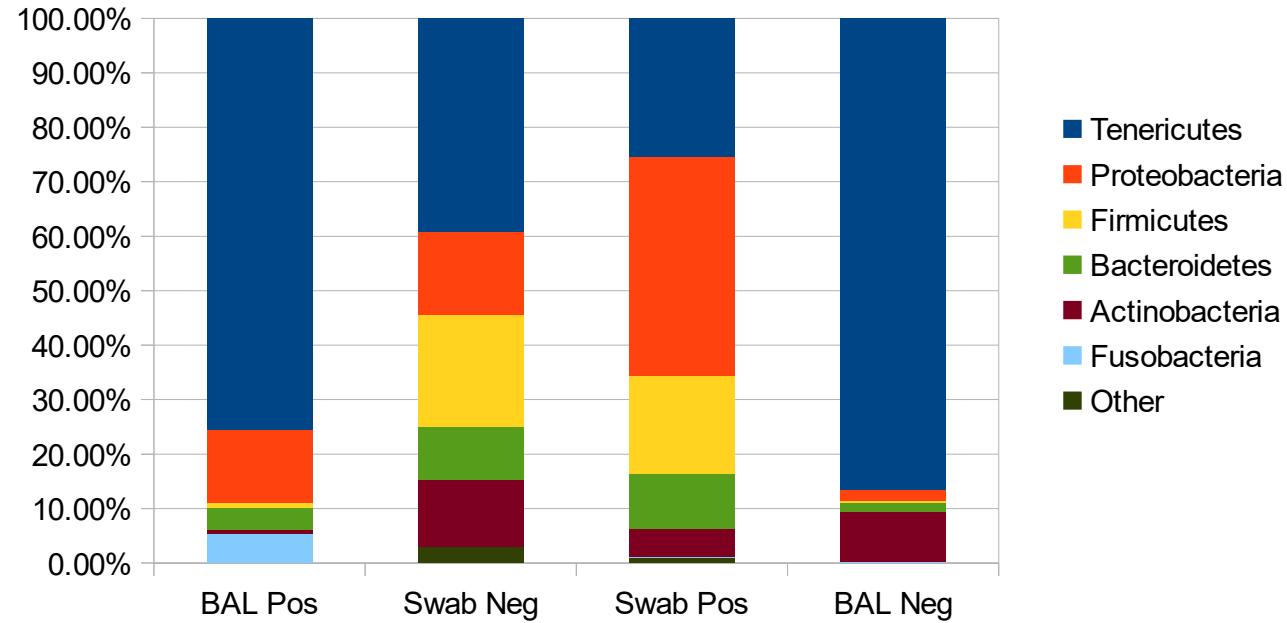


-BAL - TN



Confronto microbiota – Lesioni ecografiche

Tipo campione e positività ecografica



Differenza statisticamente significativa (ADONIS)





Conclusioni





Efficient isolation on Vero.DogSLAMtag cell line and whole genome characterization by next generation sequencing of Dolphin Morbillivirus

Peletto S., Caruso C., Cerutti F., Modesto P., Biolatti C.,
Pautasso A., Grattarola C., Giorda F., Mazzariol S., Mignone W.,
Masoero L., Casalone C., Acutis P.L.

Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle D'Aosta, Torino

C.Re.Di.Ma

Università di Padova, Padova





+ Order: Caudovirales	(3 Families)	
+ Order: Herpesvirales	(3 Families)	
+ Order: Ligamenvirales	(2 Families)	
■ Order: Mononegavirales	(5 Families)	
+ Family: Bornaviridae	(1 Genus)	
+ Family: Filoviridae	(3 Genera)	
+ Family: Nyamiviridae	(1 Genus)	
■ Family: Paramyxoviridae	(2 Subfamilies)	
■ Subfamily: Paramyxovirinae	(7 Genera)	
+ Genus: Aquaparamyxovirus	(1 Species)	
+ Genus: Avulavirus	(9 Species)	
+ Genus: Ferlavivirus	(1 Species)	
+ Genus: Henipavirus	(2 Species)	
■ Genus: Morbillivirus	(6 Species)	
Species: Canine distemper virus		
Species: Cetacean morbillivirus		
★ Species: Measles virus		
Species: Peste-des-petits-ruminants virus		
Species: Phocine distemper virus		
Species: Rinderpest virus		



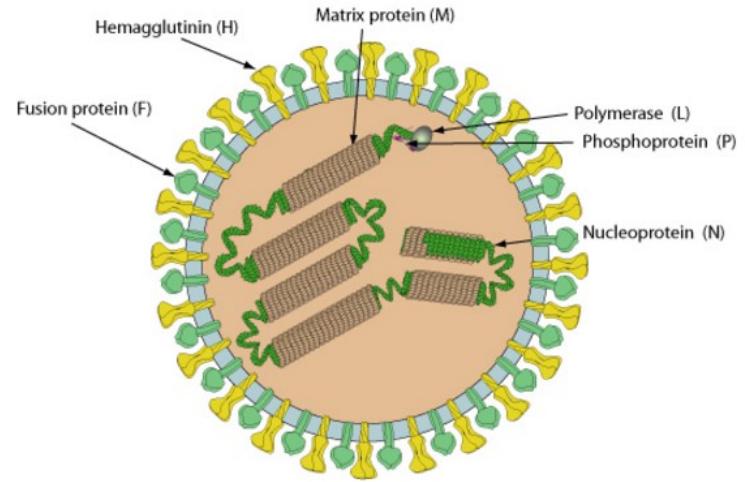
Species: *Cetacean morbillivirus*

STRAINS

- Porpoise morbillivirus (PMV);
- Dolphin morbillivirus (DMV);
- Pilot whale morbillivirus (PWMV).

3 nuovi ceppi identificati

- Longman's beaked whale morbillivirus (LBWMV);
- Guiana dolphin morbillivirus;
- Indo-Pacific Bottlenose dolphin morbillivirus





CeMV nel Mar Mediterraneo



Van Bressem et al. 2014; Viruses

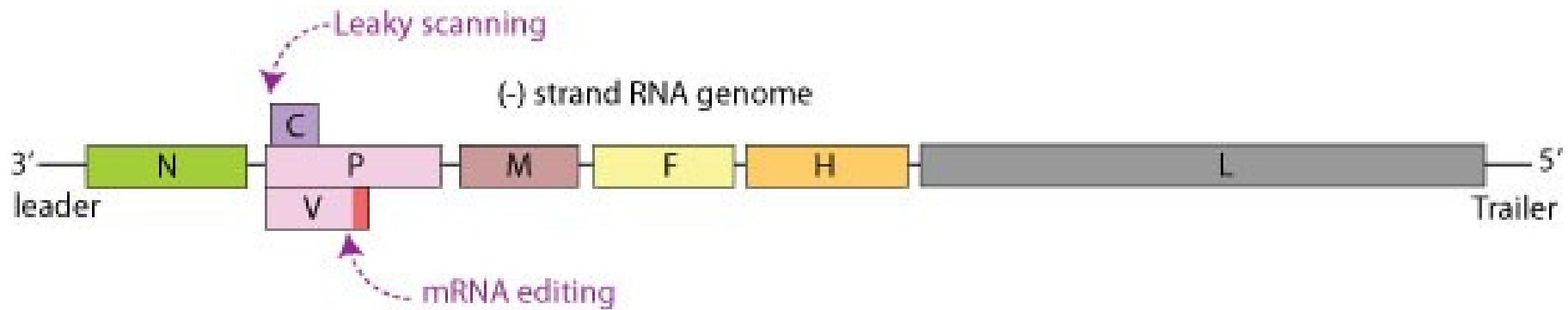
Mediterranean Sea

<i>S. coeruleoalba</i>	1990–1992	Spain, France, Italy, Greece	epidemic	VI, IHC, S, RT-PCR	DMV
<i>S. coeruleoalba</i>	2006–2008	Spain, France, Italy	epidemic	IHC, RT-PCR	DMV
<i>T. truncatus</i>	1994; 2007–2008, 2011	Israel, Spain, France, Italy	periodic mortalities	IHC, RT-PCR, S	DMV
<i>D. delphis</i>	1990	Italy	unknown	S	CeMV
<i>Globicephala melas</i>	2006–2007	Spain, France	epidemic	IHQ, RT-PCR	DMV
<i>Grampus griseus</i>	1997, 1999	Valencia, Spain	unknown	S	CeMV
<i>Balaenoptera acutorostrata</i>	1993	Tuscany, Italy	unknown	S	unknown
<i>B. physalus</i>	2011	Tuscany, Italy	periodic mortalities	RT-PCR	DMV



Species: *Cetacean morbillivirus*

Il genoma del DMV responsabile dell'epidemia del 1990-1992 è il solo genoma di CeMV completamente sequenziato (Rima et al., 2005).



Completion of the Sequence of a Cetacean Morbillivirus and Comparative Analysis of the Complete Genome Sequences of Four Morbilliviruses

B.K. RIMA,* A.M.J. COLLIN & J.A.P. EARLE

School of Biology and Biochemistry, The Queen's University of Belfast, Belfast BT9 7BL, N.Ireland

Received August 18, 2003; Accepted August 2, 2004



IL RECETTORE SLAM

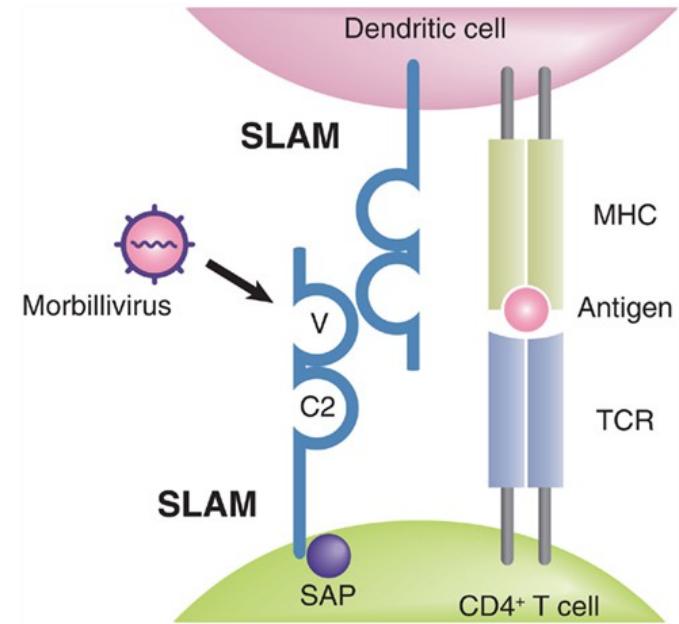
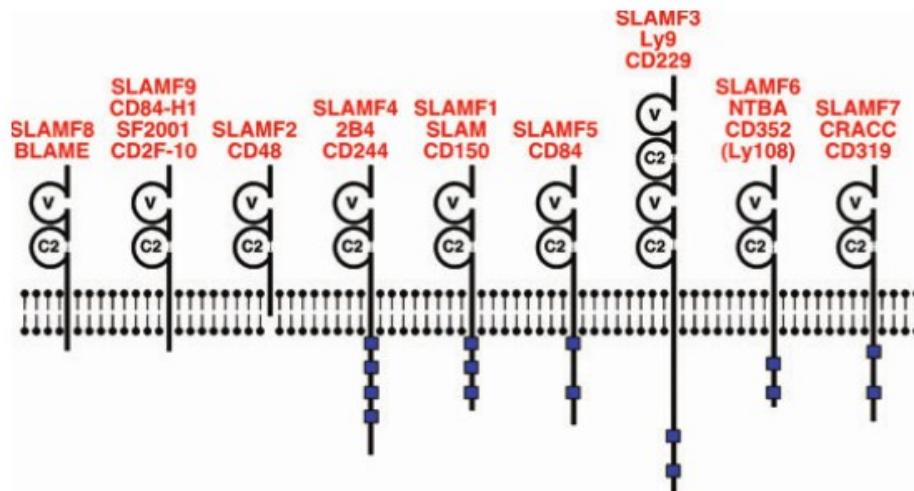
nature

Nature. 2000 Aug 24;406(6798):893-7.

SLAM (CDw150) is a cellular receptor for measles virus.

Tatsuo H¹, Ono N, Tanaka K, Yanagi Y.

Signaling lymphocyte activation molecule (SLAM o CD150)



**Journal of
Virology**

J Virol. 2003 Sep;77(18):9943-50.

Efficient isolation of wild strains of canine distemper virus in Vero cells expressing canine SLAM (CD150) and their adaptability to marmoset B95a cells.

Seki F¹, Ono N, Yamaguchi R, Yanagi Y.



dogSLAM vs DMV

J Wildl Dis. 2008 Jul;44(3):600-11.

Use of a SLAM transfected Vero cell line to isolate and characterize marine mammal morbilliviruses using an experimental ferret model.

Nielsen O¹, Smith G, Weingartl H, Lair S, Measures L.

Vero dog SLAM

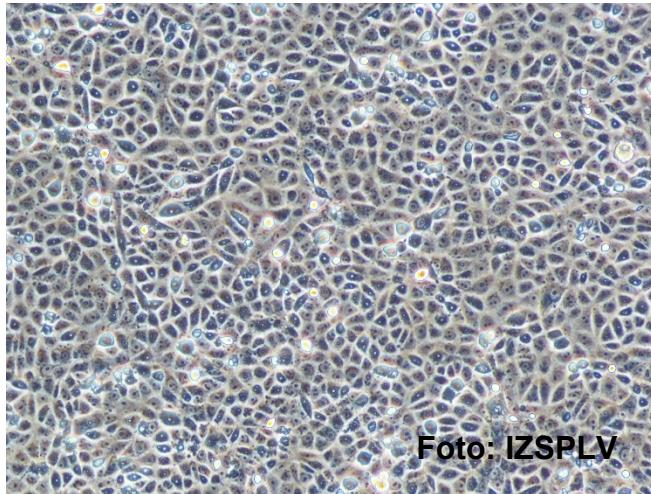
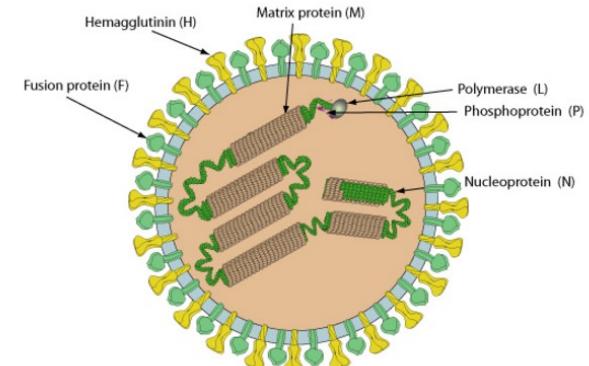


Foto: IZSPLV



DMV



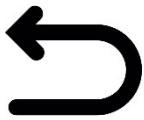


Foto: IZSPLV

CARCASSA *Stenella coeruleoalba*

- stato di nutrizione scadente
- edemi sottocutanei gelatinosi

SNC

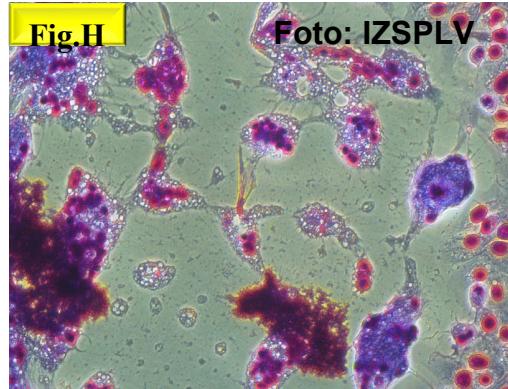
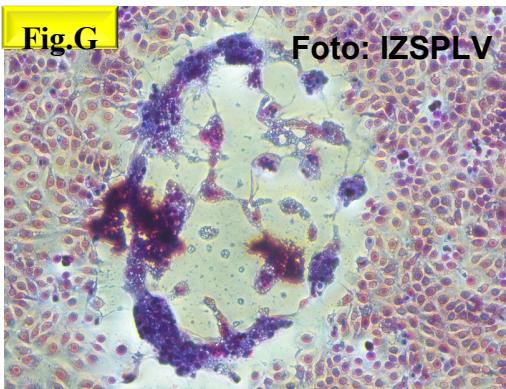
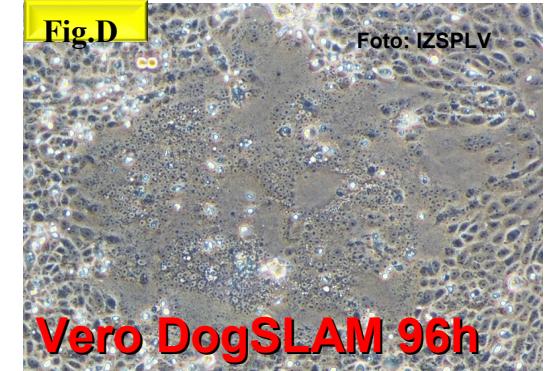
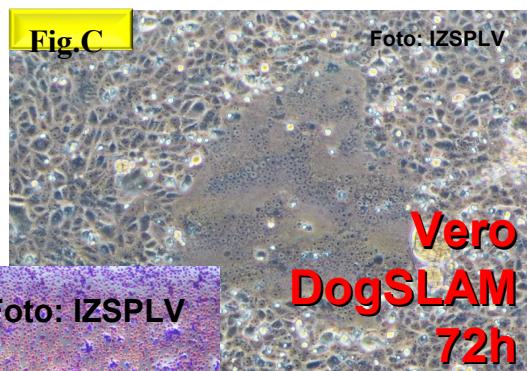
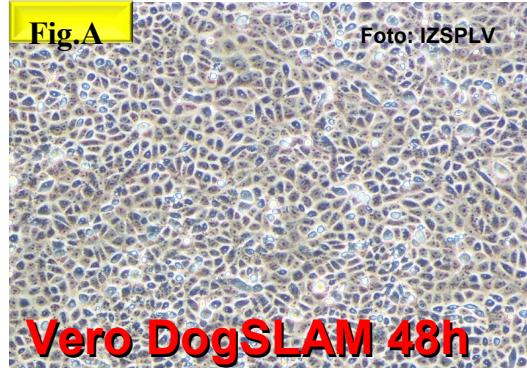
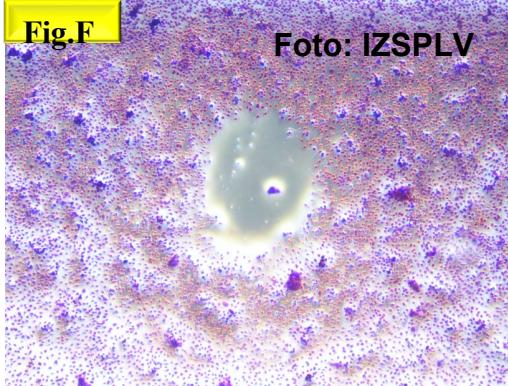
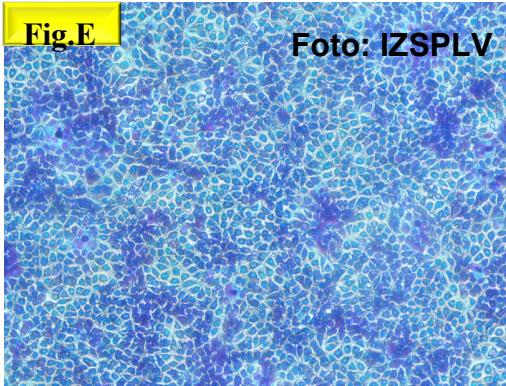
- congestione;
- meningite linfocitaria;
- manicotti perivascolari e vasculite linfocitaria

SNC - INDAGINI

- Positività IHC CDV, RPV cervelletto
 - Positività RT-PCR DMV
- Isolamento ?

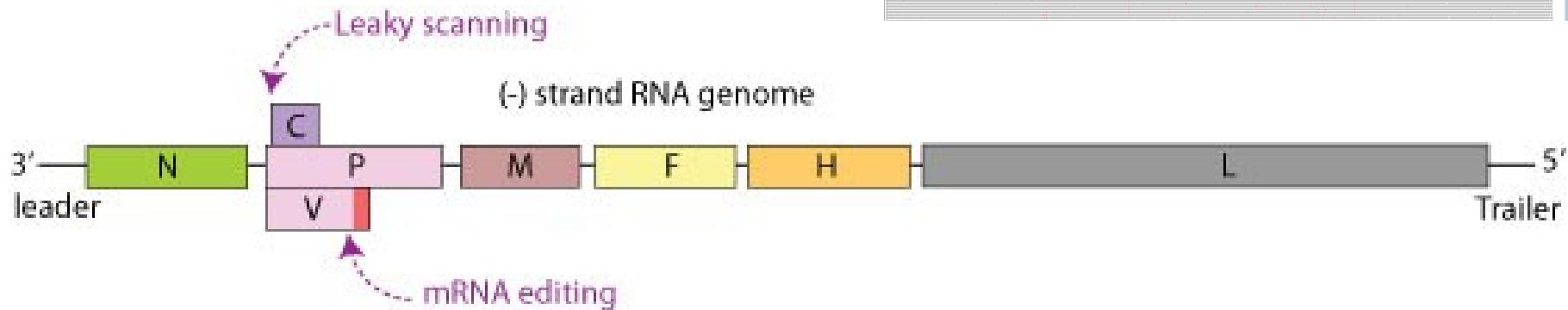
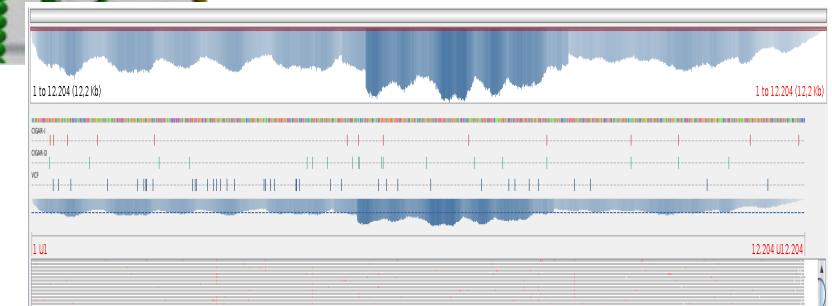
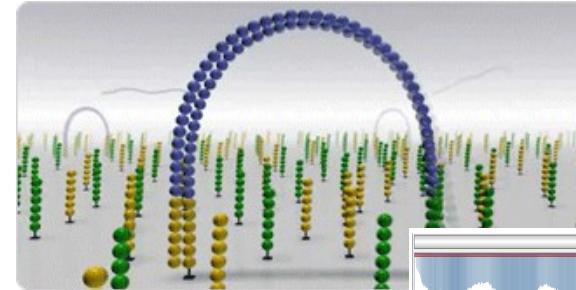


Isolamento DMV su Vero.DogSLAMtag

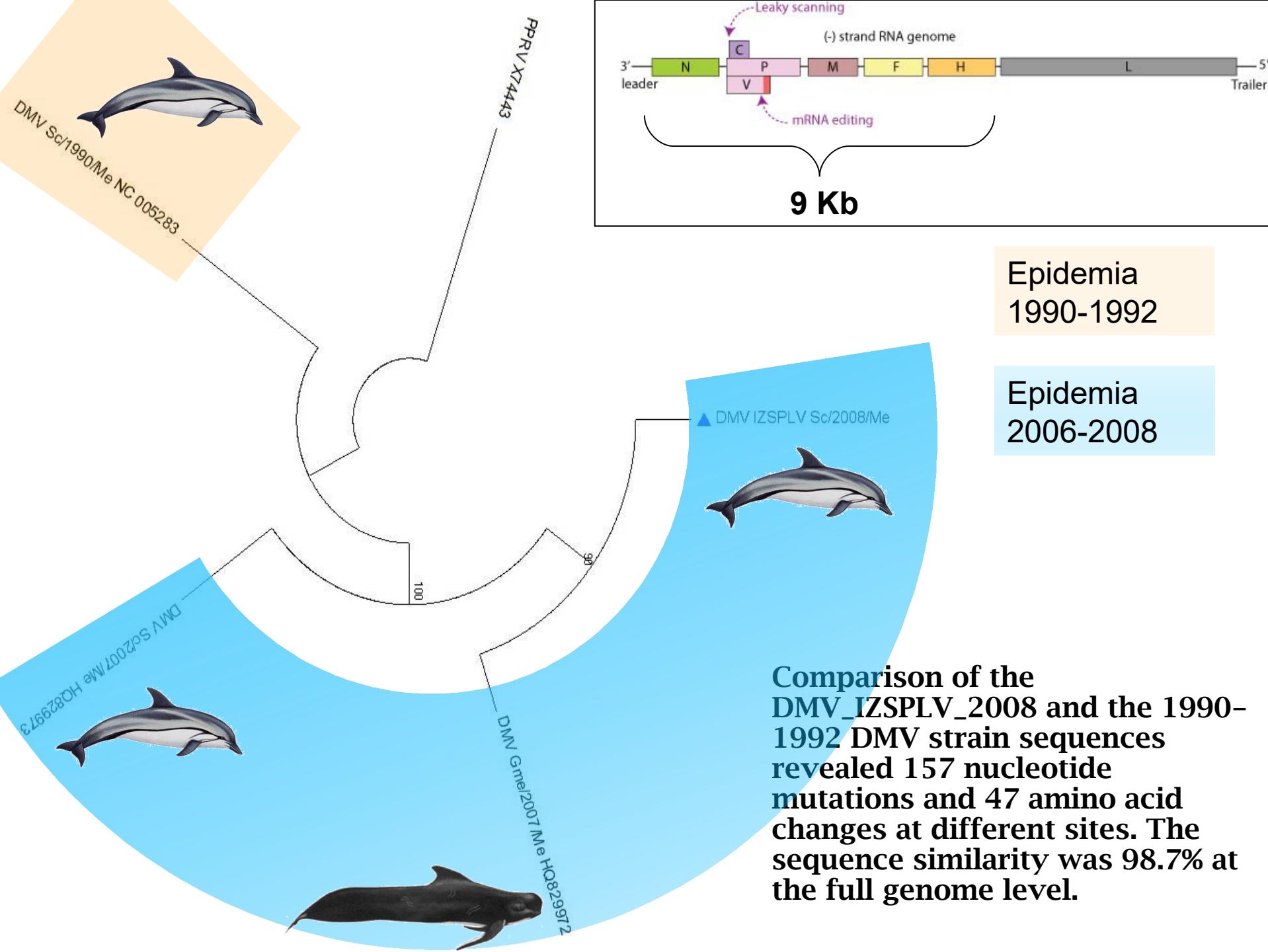


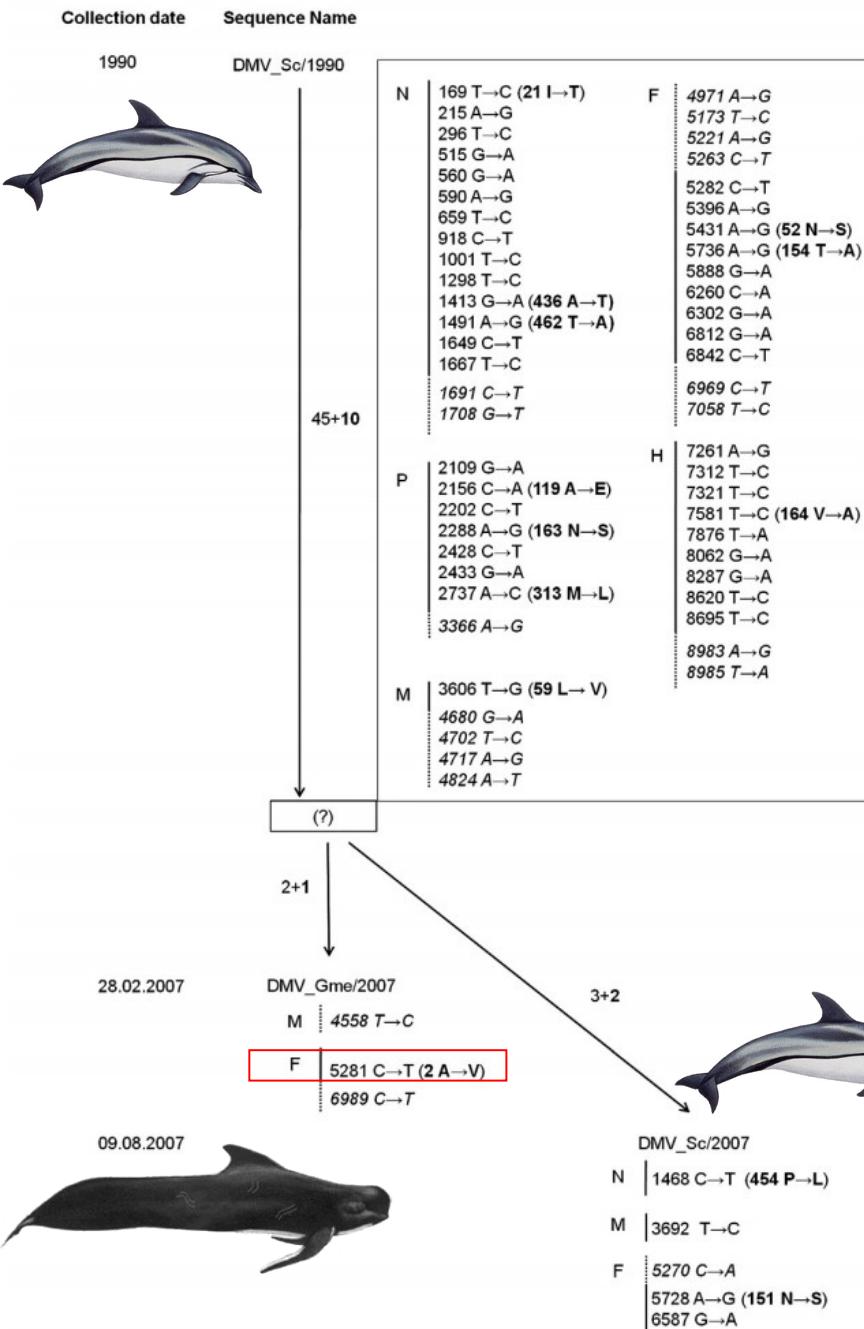


SEQUENZIAMENTO NGS



The final length obtained from the read assembly was 15,667 nucleotides (nt) covering 99.8% of the DMV reference genome





Genetic comparison among dolphin morbillivirus in the 1990–1992 and 2006–2008 Mediterranean outbreaks

Edwige Nina Bellière ^{a,*}, Fernando Esperón ^a, José Manuel Sánchez-Vizcaíno ^b

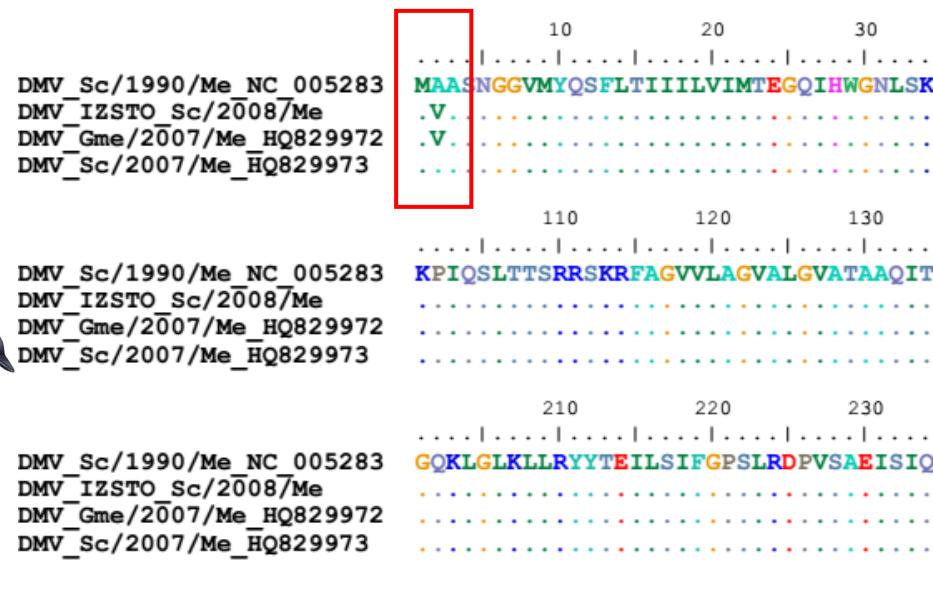
^a National Institute for Agricultural and Food Research and Technology (INIA), Research Center for Animal Health (CISA), Ctra Algete a El Casar, s/n, 28130 Valdeolmos, Spain

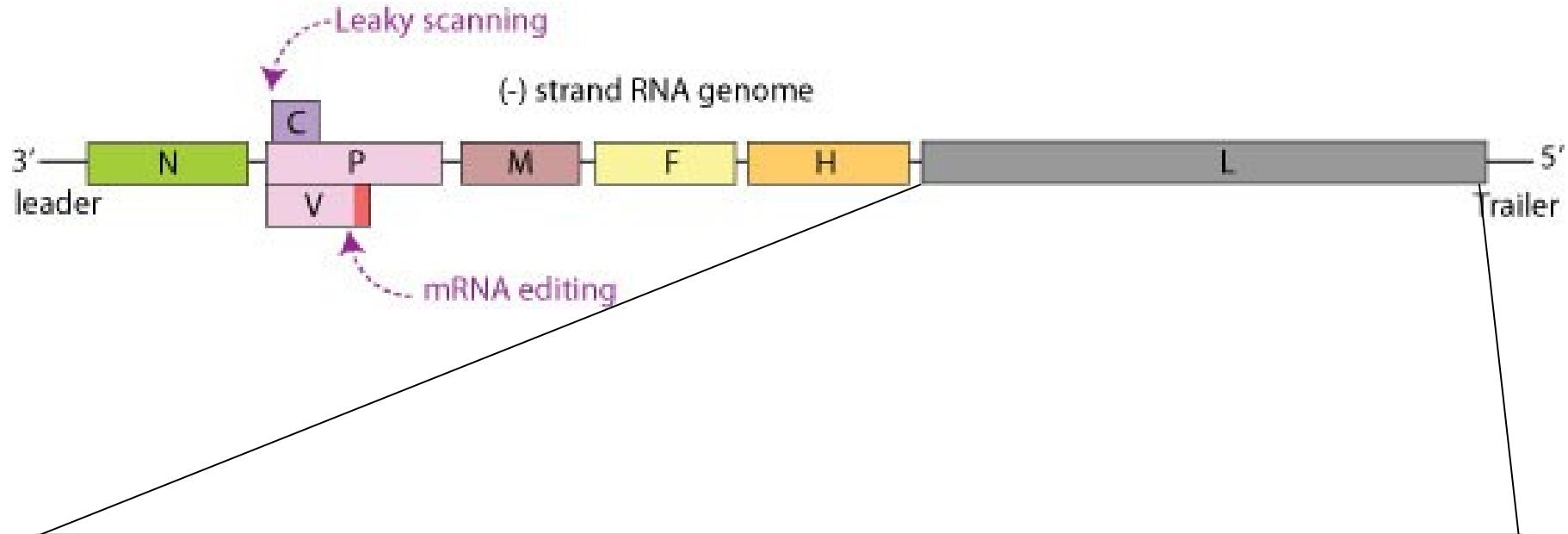
^b Complutense University of Madrid (UCM), Faculty of Veterinary, Avda Puerta de Hierro, s/n, 28040 Madrid, Spain

Four expressed mutations were found in the F gene: (2 A→V), (52 N→S), (151 N→S) and 154 (T→A). The (2 A→V) mutation in the DMV_Gme/2007 sequence (nt 5281, Fig. 2) is located in the signal peptide sequence (Bolt et al., 1994). No other published morbillivirus F sequence contains a valine at this position. This is a species-specific region among morbilliviruses, probably because its functions are linked to those of the host cell (Bolt et al., 1994; Meyer and Diallo, 1995); thus, this species-specific region reflects the fact that a given morbillivirus is specific for a given host. Since this mutation is missing in the DMV_Sc/2007 sequence, it may be associated with host adaptation to long-finned pilot whales.

E.N. Bellière et al./Infection, Genetics and Evolution 11 (2011) 1913–1920

F protein





Interestingly, genome comparison revealed that the neglected L gene, although encompassing ~40% of the DMV genome, indeed includes 74% (35 out of 47) of the diversity (amino acid changes) that differentiate the strains of the two epidemics

Sequenze del gene L di CeMV in GenBank

Nucleotide Nucleotide ▼ [cetacean morbillivirus L gene](#) [X](#) [Search](#)

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genomic DNA/RNA (5)
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Release date
Custom range...

Revision date
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See [L large subunit of RNA dependent RNA polymerase \(RdRp\); RNA synthesis, capping, and polyadenylation](#) in the Gene database
[1 reference sequences](#) [Protein \(1\)](#)

Items: 5

- [Cetacean morbillivirus isolate DMV_Sc/2007 nucleoprotein \(N\), phosphoprotein \(P\), matrix protein \(M\), fusion protein \(F\), and hemagglutinin \(H\) genes, complete cds; and large protein \(L\) gene, partial cds](#)
9,050 bp linear cRNA
Accession: HQ829973.1 GI: 346969708
[GenBank](#) [FASTA](#) [Graphics](#)
- [Cetacean morbillivirus isolate DMV_Gme/2007 nucleoprotein \(N\), phosphoprotein \(P\), matrix protein \(M\), fusion protein \(F\), and hemagglutinin \(H\) genes, complete cds; and large protein \(L\) gene, partial cds](#)
9,050 bp linear cRNA
Accession: HQ829972.1 GI: 346969701
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- [Dolphin morbillivirus, complete genome](#)
3. 15,702 bp linear RNA
Accession: NC_005283.1 GI: 38707562
[GenBank](#) [FASTA](#) [Graphics](#)
- [Dolphin morbillivirus compete genome, genomic RNA](#)
4. 15,702 bp linear RNA
Accession: AJ608288.1 GI: 38490143
[GenBank](#) [FASTA](#) [Graphics](#)
- [Porpoise morbillivirus L protein gene, partial cds](#)
5. 430 bp linear RNA
Accession: AY949834.1 GI: 61608380

Results by taxon
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Cetacean morbillivirus (5)

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[cetacean morbillivirus L gene \(5\)](#)
Nucleotide

[peleto \(44\)](#)
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Sequenze del gene L di CeMV in GenBank

Nucleotide Nucleotide ▼ cetacean morbillivirus L gene Search Help

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genomic DNA/RNA (5)
Customize ...

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INSDC (GenBank) (4)
RefSeq (1)
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Sequence length
Custom range...

Release date
Custom range...

Revision date
Custom range...

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See [L large subunit of RNA dependent RNA polymerase \(RdRp\); RNA synthesis, capping, and polyadenylation](#) in the Gene database
1 reference sequences [Protein \(1\)](#)

Items: 5

 [Cetacean morbillivirus isolate DMV Sc/2000 nucleoprotein \(N\), phosphoprotein \(P\), matrix protein \(M\), fusion protein \(F\), and hemagglutinin \(H\) genes, complete cds; and large protein \(L\) gene, partial cds](#)
1. 9,050 bp linear cRNA
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[GenBank](#) [FASTA](#) [Graphics](#)

 [Cetacean morbillivirus isolate DMV Gme/2000 nucleoprotein \(N\), phosphoprotein \(P\), matrix protein \(M\), fusion protein \(F\), and hemagglutinin \(H\) genes, complete cds; and large protein \(L\) gene, partial cds](#)
2. 9,050 bp linear cRNA
Accession: HQ829972.1 GI: 346969701
[GenBank](#) [FASTA](#) [Graphics](#)

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5. 430 bp linear RNA
Accession: AY949834.1 GI: 61608380

Results by taxon
Top Organisms [Tree]
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Analyze these sequences
Run BLAST

Find related data
Database: [Select](#)

Find items

Search details
("Cetacean morbillivirus"[Organism] OR cetacean morbillivirus[All Fields]) AND L[All Fields] AND gene[All Fields]

Search See more...

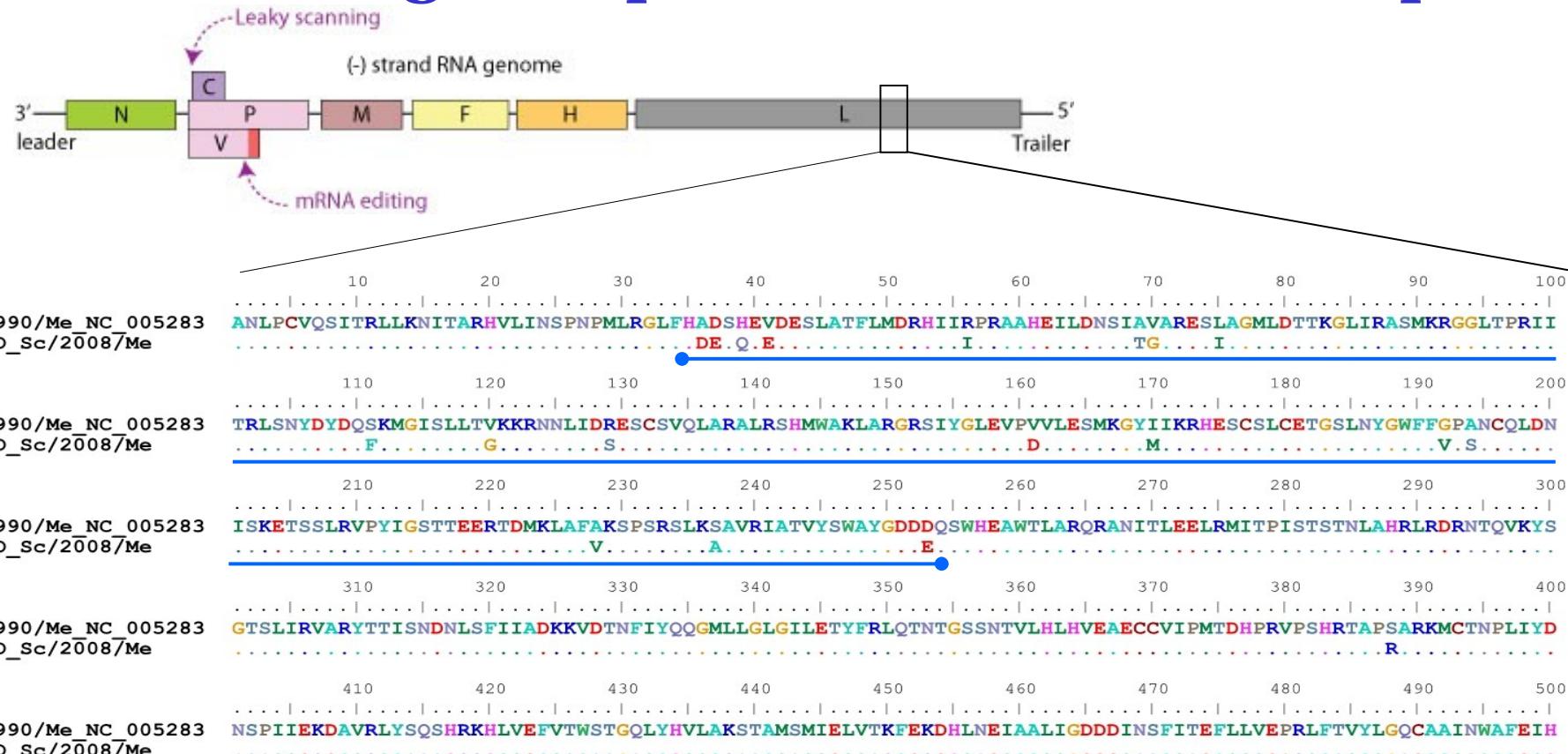
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 cetacean morbillivirus L gene (5)
Nucleotide

 peleto (44)
PubMed



Gene L – “regione ipervariabile” di ~600 bp



Nuovo target per filogenesi e epidemiologia molecolare di CeMV?

Grazie per l'attenzione!

