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Dall'ION Torrent al MinION: i progressi dell'IZSAM nella Next Generation Sequencing

Maurilia Marcacci

Teramo, 14 giugno 2018
Sala Convegni “V. Prencipe”, CIFIV

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IZS AM 01/14 RC

Approccio metagenomico per una diagnosi rapida ed accurata di alcune infezioni batteriche e virali

Area tematica: Sanità animale

Responsabile scientifico: Giovanni Savini

FAST D

Responsabile U.O.1: Giovanni Savini IZSAM
Responsabile U.O.2: Elisabetta Di Giannatale IZSAM
Responsabile U.O.3: Patrizia Colangeli IZSAM

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Journal of Virological Methods

journal homepage: www.elsevier.com/locate/jviromet

Short communication

Whole genome sequence analysis of the arctic-lineage strain responsible for distemper in Italian wolves and dogs through a fast and robust next generation sequencing protocol

Maurilia Marcacci, Massimo Ancora, Iolanda Mangone, Liana Teodori, Daria Di Sabatino, Fabrizio De Massis, Cesare Camma', Giovanni Savini, Alessio Lorusso*

National Reference Centre for Urban Hygiene and Non-Epidemic Emergencies, Istituto Zooprofilattico Sperimentale dell'Abruzzo e Molise "G. Caporale", 64100 Teramo, Italy

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Complete Genome Sequence of a *Brucella ceti* ST26 Strain Isolated from a Striped Dolphin (*Stenella coeruleoalba*) on the Coast of Italy

Massimo Ancora,[a] Maurilia Marcacci,[a] Massimiliano Orsini,[b] Katiuscia Zilli,[a] Elisabetta Di Giannatale,[a] Giuliano Garofolo,[a] Cesare Cammà[a]

OIE Reference Laboratory for Brucellosis, Istituto Zooprofilattico Sperimentale dell'Abruzzo e Molise G. Caporale, Campo Boario, Teramo, Italy[a]; CRS4, Bioinformatics, POLARIS Scientific Park, Pula, Italy[b]

***Brucella* spp. are important pathogens affecting a wide range of terrestrial and aquatic animals. We report the complete and annotated genome sequence of *Brucella ceti* ST26 strain TE10759-12, isolated from a striped dolphin (*Stenella coeruleoalba*) stranded along the Italian shoreline in March of 2012.**

Received 22 January 2014 **Accepted** 6 February 2014 **Published** 6 March 2014

Citation Ancora M, Marcacci M, Orsini M, Zilli K, Di Giannatale E, Garofolo G, Cammà C. 2014. Complete genome sequence of a *Brucella ceti* ST26 strain isolated from a striped dolphin (*Stenella coeruleoalba*) on the coast of Italy. Genome Announc. 2(2):e00068-14. doi:10.1128/genomeA.00068-14.

Address correspondence to Massimo Ancora, m.ancora@izs.it.

Molecular epidemiology of bluetongue virus serotype 1 circulating in Italy and its connection with northern Africa

Short communication

A new member of the *Pteropine Orthoreovirus* species isolated from fruit bats imported to Italy

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Sviluppo di protocolli per il sequenziamento di DNA e RNA

Protocollo sequenziamento RNA

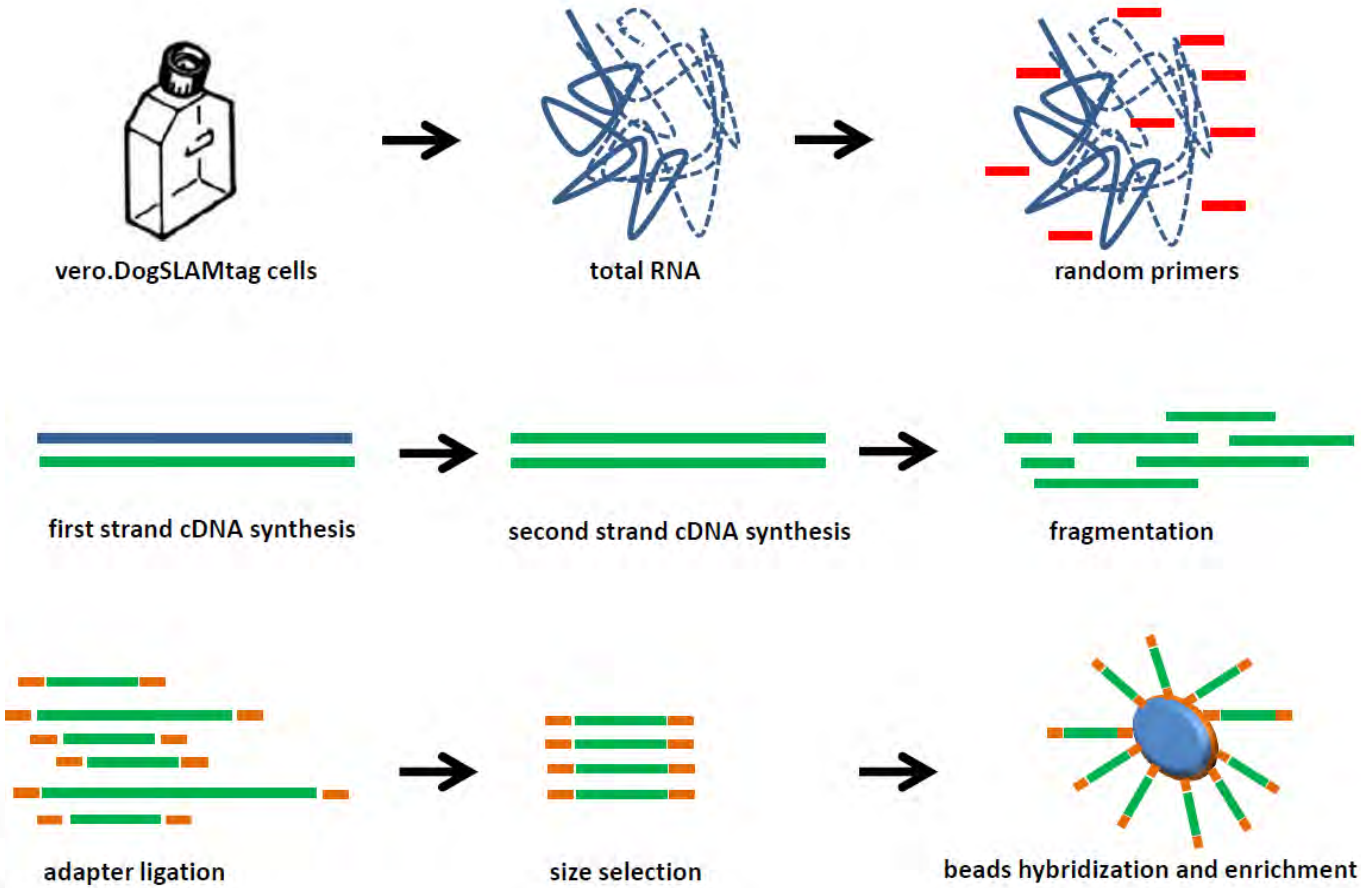

Fig 1

Morbillivirus

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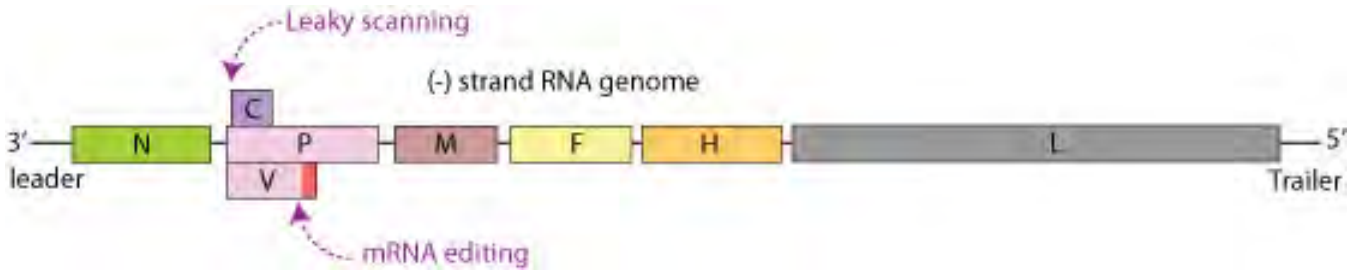
PLOS | ONE

Arctic Lineage-Canine Distemper Virus as a Cause of Death in Apennine Wolves (*Canis lupus*) in Italy

Daria Di Sabatino[1], Alessio Lorusso[1]*, Cristina E. Di Francesco[2], Leonardo Gentile[3], Vincenza Di Pirro[3], Anna Lucia Bellacicco[1], Armando Giovannini[1], Gabriella Di Francesco[1], Giuseppe Marruchella[1], Fulvio Marsilio[2], Giovanni Savini[1]

1 Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise "G. Caporale", Teramo, Italy, **2** Unit of Infectious Diseases, Faculty of Veterinary Medicine of Teramo, Teramo, Italy, **3** Veterinary Services, National Park of Abruzzi, Lazio and Molise, Pescasseroli (AQ), Italy



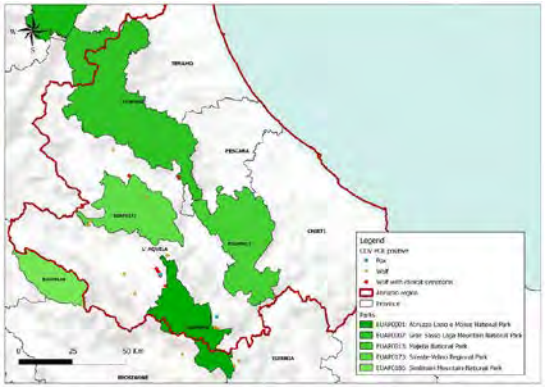


Figure 1. Map illustrating the distribution of CDV positive animals in Abruzzi region. Map was generated using Quantum GIS (QGIS) software, version 1.8.0.
doi:10.1371/journal.pone.0092356.g001

Cluster lineage


Philippines
Malaysia
Indonesia
Jakarta
Singapore
Papua New Guinea
Timor Leste
Australia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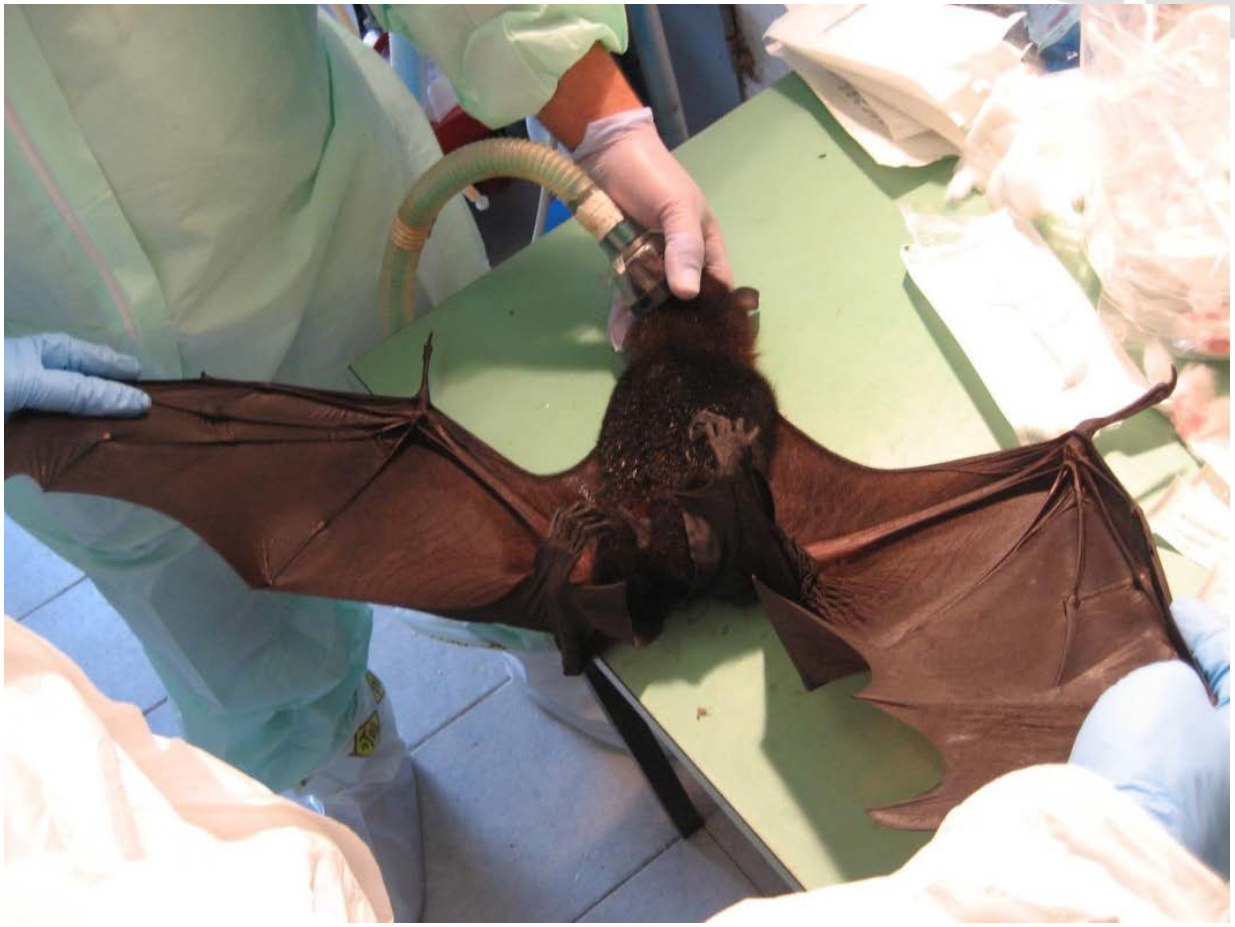

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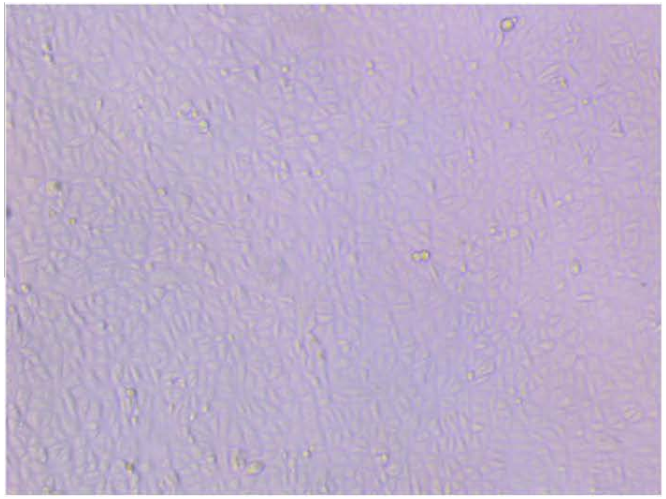

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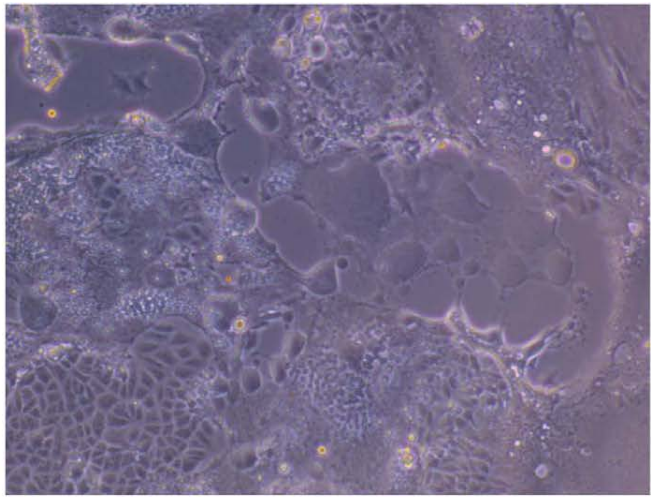

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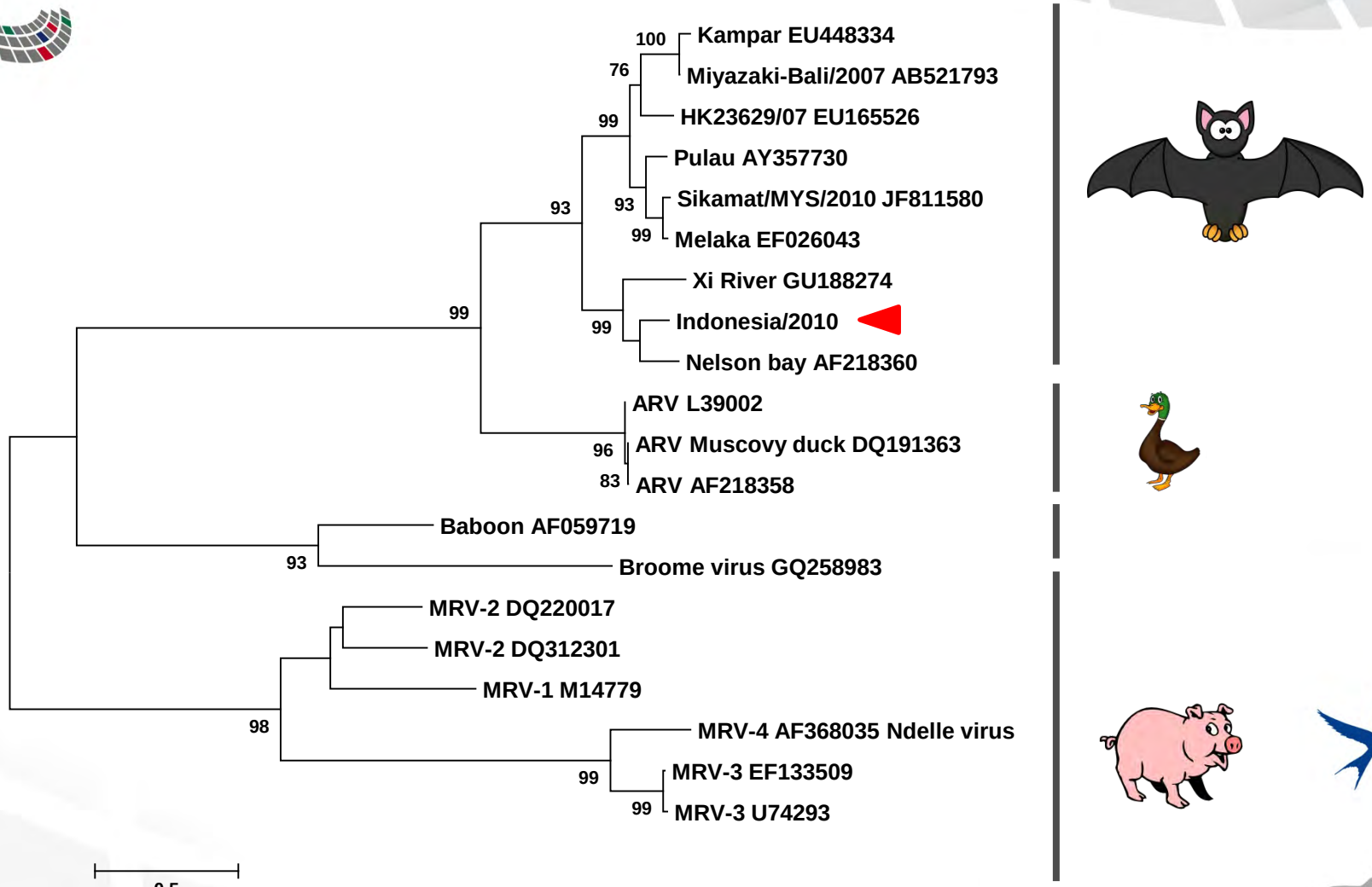

S1

Indonesia/2010 PRV9IND 2010 Bat Italy!

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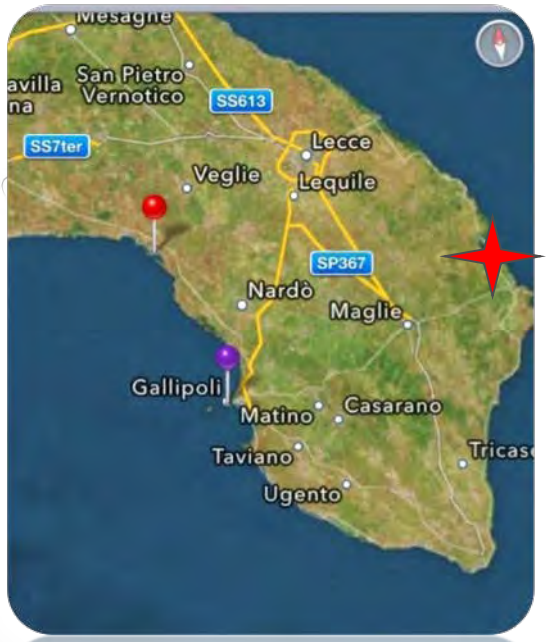
Caso studio



Otranto

Journal of Medical Microbiology (2014), **63**, 325–329 DOI 10.1099/jmm.0.065672-0

Case Report

Brucella ceti from two striped dolphins stranded on the Apulia coastline, Italy

Giuliano Garofolo,[1] Katiuscia Zilli,[1] Pasquale Troiano,[2] Antonio Petrella,[2] Francesca Marotta,[1] Gabriella Di Serafino,[1] Massimo Ancora[1] and Elisabetta Di Giannatale[1]

[1]Istituto Zooprofilattico Sperimentale dell'Abruzzo e Molise 'G. Caporale', National and OIE Reference Laboratory for Brucellosis, Via Campo Boario 64100, Teramo, Italy

[2]Istituto Zooprofilattico Sperimentale della Puglia e della Basilicata, Diagnostic Unit, Via Manfredonia 20, 71100, Foggia, Italy

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Complete Genome Sequence of a *Brucella ceti* ST26 Strain Isolated from a Striped Dolphin (*Stenella coeruleoalba*) on the Coast of Italy

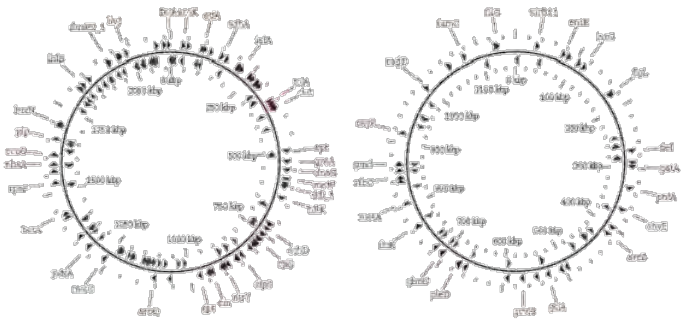
Massimo Ancora,[a] Maurilia Marcacci,[a] Massimiliano Orsini,[b] Katiuscia Zilli,[a] Elisabetta Di Giannatale,[a] Giuliano Garofolo,[a] Cesare Cammà[a]

OIE Reference Laboratory for Brucellosis, Istituto Zooprofilattico Sperimentale dell'Abruzzo e Molise G. Caporale, Campo Boario, Teramo, Italy[a]; CRS4, Bioinformatics, POLARIS Scientific Park, Pula, Italy[b]

Brucella spp. are important pathogens affecting a wide range of terrestrial and aquatic animals. We report the complete and annotated genome sequence of *Brucella ceti* ST26 strain TE10759-12, isolated from a striped dolphin (*Stenella coeruleoalba*) stranded along the Italian shoreline in March of 2012.

	Size	rRNA	Gene	CDS	tRNA
TE28753-12_chrI	2124631	8	2219	2167	44
TE28753-12_chrII	1161499	4	1181	1163	14
TE10759-12_chrI	2117314	8	2252	2202	44
TE10759-12_chrII	1160044	4	1186	1168	14

Identità reciproca fra i cromosomi pari al 99% delle regioni allineate



NCBI Taxonomy Browser

Entrez | PubMed | Nucleotide | Protein | Genome

Search for [ ] as complete name ☑ lock Go Clear

Display 3 levels using filter: none

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☐ Domains ☐ GEO Datasets ☐ UniGene ☐ UniSTS ☐ PubMed Central ☐ Gene ☐ HomoloGene ☐ SRA Experiments
☐ MapView ☐ LinkOut ☐ BLAST ☐ TRACE ☐ Probe ☐ Assembly ☐ Bio Project ☐ Bio Sample
☐ Bio Systems ☐ dbVar ☐ Epigenomics ☐ GEO Profiles ☐ PubChem BioAssay ☐ Protein Clusters ☐ Host

Lineage (full): root; cellular organisms; Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Brucellaceae; Brucella

- **Brucella ceti** *Click on organism name to get more information.*
  - **Brucella ceti B1/94**
  - **Brucella ceti M13/05/1**
  - **Brucella ceti M490/95/1**
  - **Brucella ceti M644/93/1**
  - **Brucella ceti str. Cudo**
  - **Brucella ceti TE28753-12**

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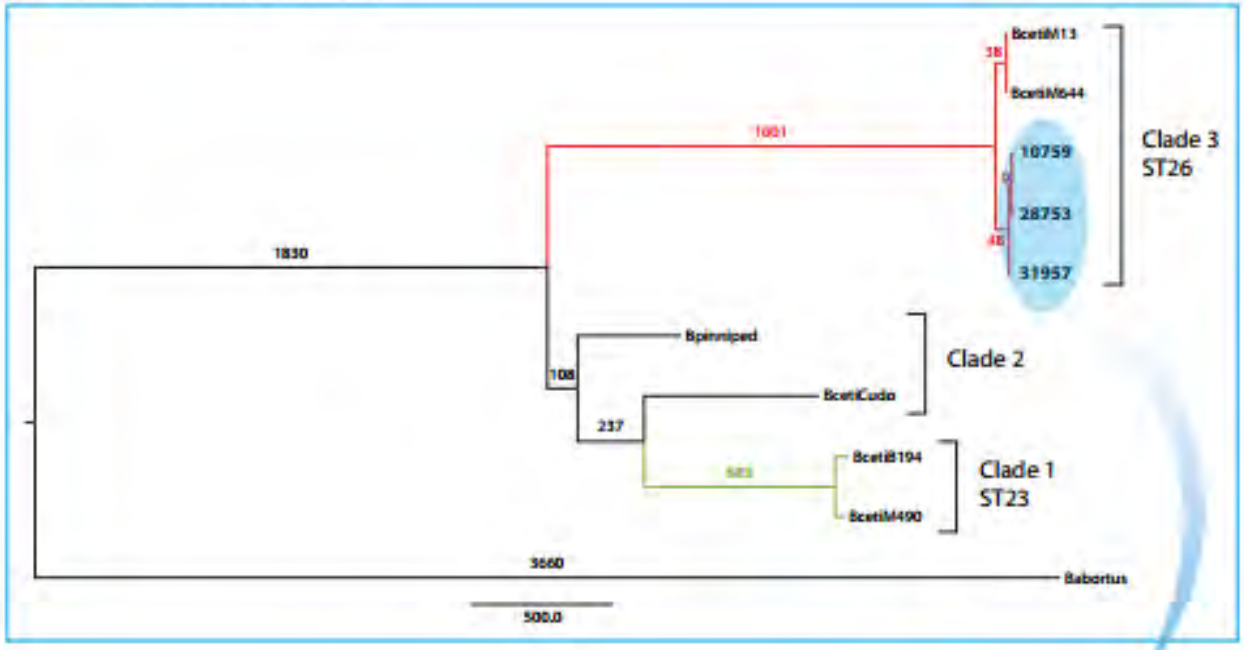
Figure 1. Maximum parsimony tree of B. ceti isolates.



Mediterranean clade

Figure 2. Minimum spanning tree for B. ceti MLVA-16.

Focolaio Salmonella 2013-2014

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SURVEILLANCE AND OUTBREAK REPORT

Outbreak of unusual *Salmonella enterica* serovar Typhimurium monophasic variant 1,4 [5],12:i:-, Italy, June 2013 to September 2014

F Cito [1], F Baldinelli [1], P Calistri [1], E Di Giannatale [1], G Scavia [2], M Orsini [1], S Iannetti [1], L Sacchini [1], I Mangone [1], L Candeloro [1], A Conte [1], C Ippoliti [1], D Morelli [1], G Migliorati [1], NB Barile [1], C Marfoglia [1], S Salucci [1], C Cammà [1], M Marcacci [1], M Ancora [1], AM Dionisi [2], S Owczartek [2], I Luzzi [2], on behalf of the outbreak investigation group [9]

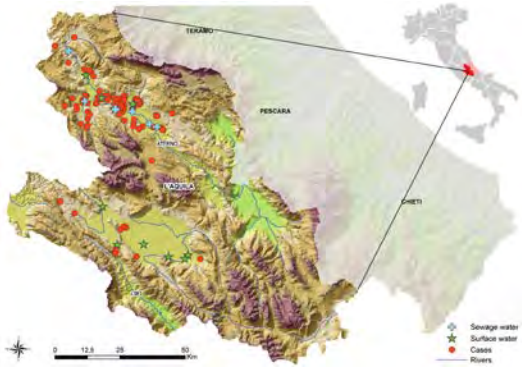
1. Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise, Teramo, Italy
2. Istituto Superiore di Sanità, Rome, Italy
3. Pediatric Unit, San Salvatore Hospital of L'Aquila, Italy
4. Analytical Laboratory, San Salvatore Hospital of L'Aquila, Italy
5. Veterinary and Food Hygiene Service, Abruzzo Region, L'Aquila, Italy
6. Food Hygiene and Nutrition Service, Abruzzo Region, L'Aquila, Italy
7. Public Health Service, Abruzzo Region, L'Aquila, Italy
8. Regional Environmental Protection Agency, Abruzzo Region, L'Aquila, Italy
9. The members of the group are listed at the end of the article

Correspondence: Francesca Cito (f.cito@izs.it)

Citation style for this article:
Cito F, Baldinelli F, Calistri P, Di Giannatale E, Scavia G, Orsini M, Iannetti S, Sacchini L, Mangone I, Candeloro L, Conte A, Ippoliti C, Morelli D, Migliorati G, Barile NB, Marfoglia C, Salucci S, Cammà C, Marcacci M, Ancora M, Dionisi AM, Owczartek S, Luzzi I, on behalf of the outbreak investigation group. Outbreak of unusual Salmonella enterica serovar Typhimurium monophasic variant 1,4 [5],12:i:-, Italy, June 2013 to September 2014. Euro Surveill. 2016;21(15):pii=30194. DOI: http://dx.doi.org/10.2807/1560-7917.ES.2016.21.15.30194

Article submitted on 15 April 2015 / accepted on 14 April 2016 / published on 14 April 2016

FIGURE 2
Geographical distribution of outbreak cases (n = 115)[a] and of surface and sewage water samples (n = 21) with a monophasic *Salmonella* Typhimurium outbreak strain isolate, L'Aquila province, Italy, April–October 2014



[a] Although there were a total of 179 outbreak cases in the Abruzzo region, only 115 are depicted in this figure because for 64 cases the residential address was missing information.

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Draft Genome Sequences of 19 *Salmonella enterica* Serovar Typhimurium [4,5:i:−] Strains Resistant to Nalidixic Acid from Long-Term Outbreak in Italy

Massimiliano Orsini, Iolanda Mangone, Adriano DiPasquale, Samuel Perticara, Lorena Sacchini, Francesca Cito, Simona Maurilia Marcacci, Massimo Ancora, Paolo Calistri, Elisabetta Di Giannatale, Cesare Cammà

Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise G. Caporale, Teramo, Italy

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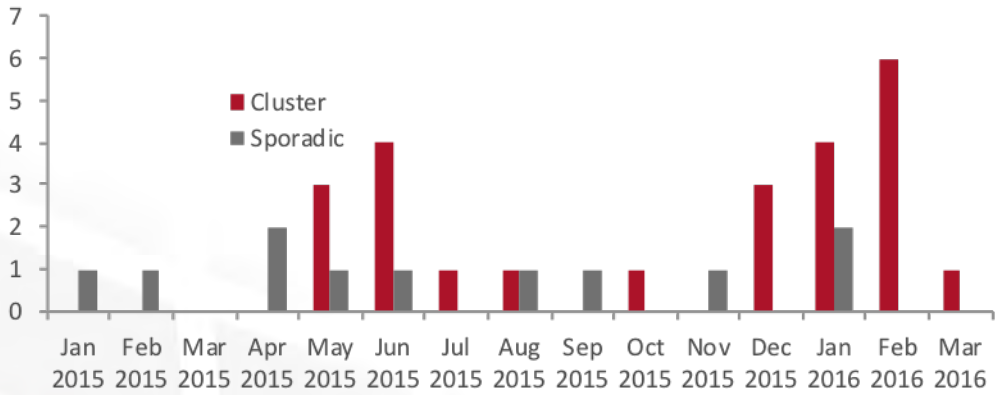
NextSeq 500 Illumina

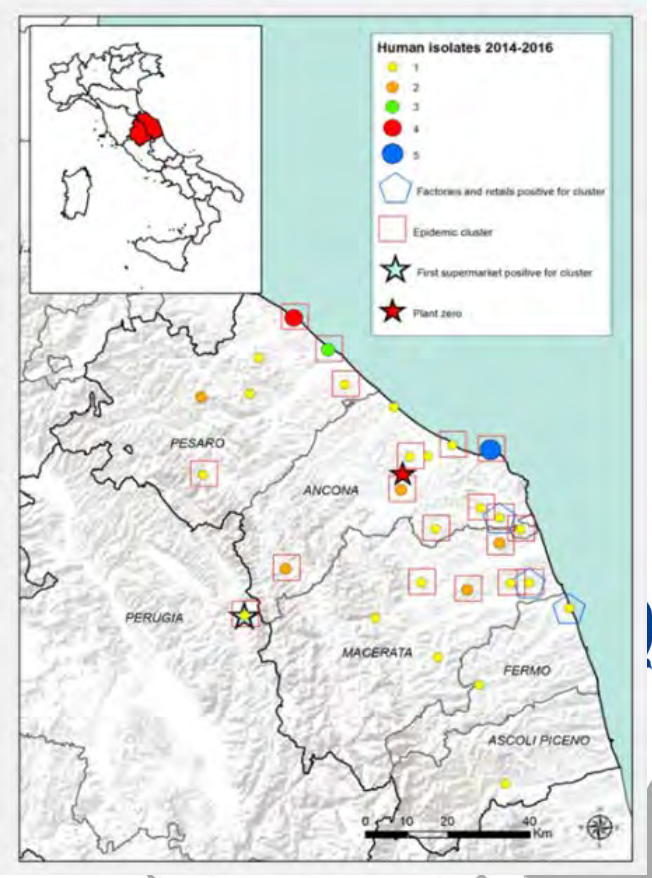
NextSeq 500 MidOutput Cartridge
300 cycles

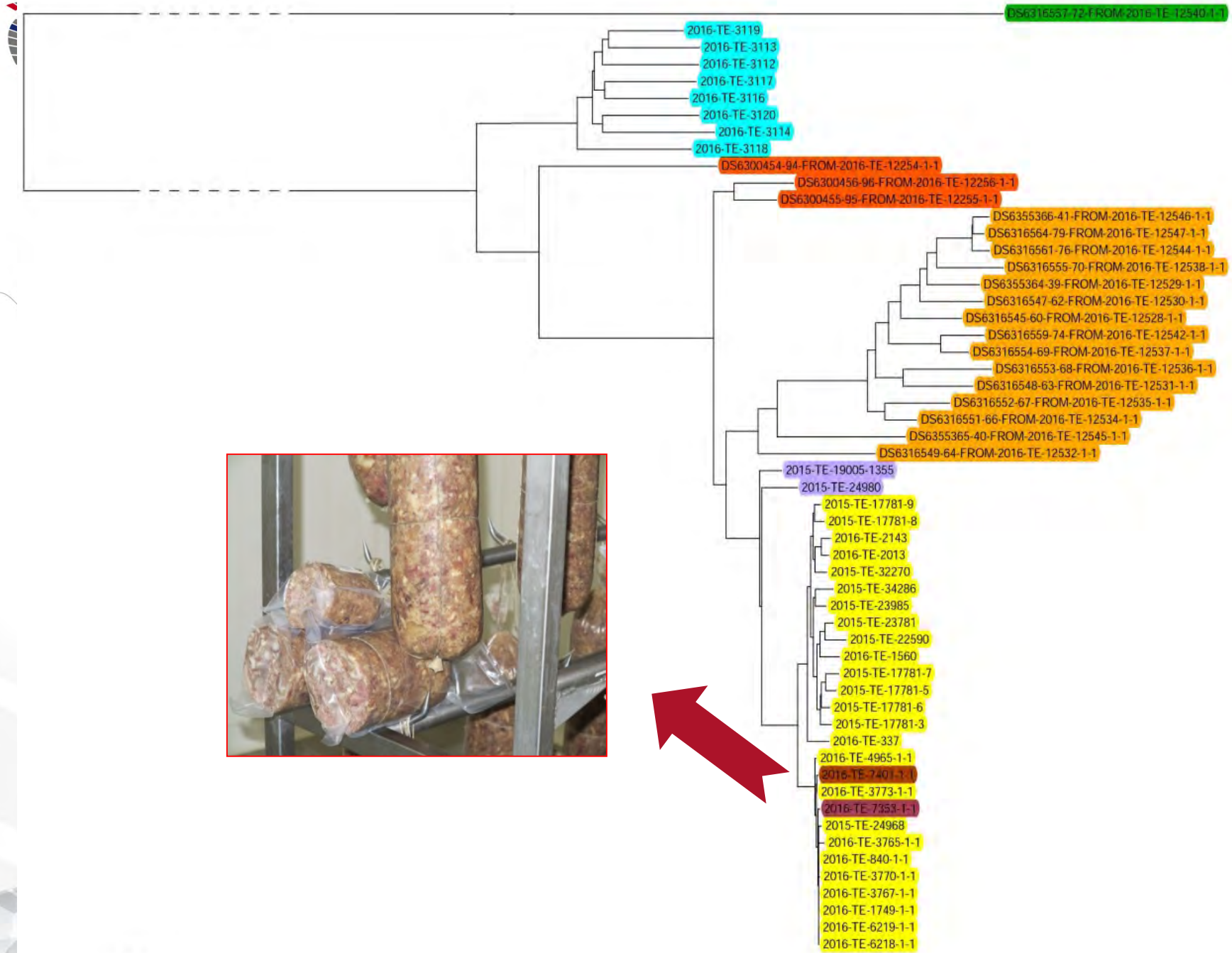
Focolaio Listeria Marche 2015-2016

ST7 e Nuovo pulsotipo in Italia:
24 casi umani fino a marzo 2016



Curva epidemica

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2016-TE-6218-1-1
20

Tempi/Costi=Vantaggi!!!

- **Costo/genoma**
  80 €
- **Tempo prep libreria + Run**
  48/72 ore

NGS

Campylobacter Brucella Listeria

Banca ceppi

Campylobacter* MLST + *flaA

***Brucella* Matrice SNPs/Core genome (MLST plus)**

***Listeria* Matrice SNPs/MLST/Core genome (MLST plus)**