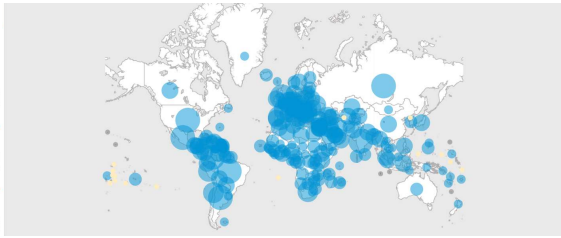


I laboratori di sanità pubblica veterinaria e la ricerca nella genomica di SARS Cov2: Esperienze a confronto

Sfide, opportunità e limiti dello studio delle sequenze genomiche di SARS-COV2. Esperienza in Puglia e Basilicata



Dr. Antonio Parisi

1

I laboratori di sanità pubblica veterinaria e la ricerca nella genomica di SARS Cov2: Esperienze a confronto





ARTICLE IN PRESS

IDCases

Case report
SARS-CoV-2 isolation from a 10-day-old newborn in Italy: A case report
Giuseppe Iacono¹, Daniela Calace², Antonella Cori³, Virginia Mancini⁴, Angela Maria Marimón⁵, Anna Chiancone⁶, Giuseppina Labate⁷, Simona Latavina⁸, Annalisa Bucci⁹, Lorenza Pardi¹⁰, Valeria Bonadonna¹¹, Antonio Parisi¹², Dora Capolera¹³, Leonardo Marini¹⁴, Silvana Padalino¹⁵, Luigina Serenelli¹⁶, Angela Acci¹⁷, Michela Marone¹⁸, Francesca Tiberi¹⁹, Antonia Pizzarello²⁰

2

I laboratori di sanità pubblica veterinaria e la ricerca nella genomica di SARS Cov2: Esperienze a confronto

OXFORD UNIVERSITY PRIMA | Briefings in Bioinformatics

NEXT GENERATION SEQUENCING FOR THE COVID-19 PANDEMIC: CHALLENGES, APPLICATIONS AND OPPORTUNITIES

Matteo Chiara^{1,2}, Anna Maria D'Erchia^{3,4}, Carmela Gissi^{5,6}, Caterina Manzari⁷, Antonio Parisi⁸, Nicoletta Resta⁹, Federico Zambelli¹⁰, Ernesto Picardi¹¹, Giulio Pavani¹², David S. Hanger¹³ and Graziano Pesole¹⁴

Library preparation	Sequencing technology	Reads	Notes
Ampliflex	Illumina	14,714	12735 from COG-UK (ARIC)
Hybrid Capture	Illumina	376	9000 from COG-UK (ARIC)
Metatranscriptomics	Illumina	1,349	

Reads	Sequencing technology	Amplification method	Read length	Read depth	Read NGS throughput
10 ⁶ -10 ⁷	150 bp paired-end	SARS-CoV-2 primer	150 bp	~100x	~100x
10 ⁶ -10 ⁷	150 bp paired-end	SARS-CoV-2 primer	150 bp	~100x	~100x
10 ⁶ -10 ⁷	150 bp paired-end	SARS-CoV-2 primer	150 bp	~100x	~100x
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3

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NEXT GENERATION SEQUENCING FOR THE COVID-19 PANDEMIC: CHALLENGES, APPLICATIONS AND OPPORTUNITIES

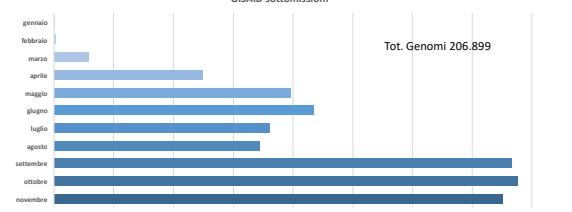
Approach	Platform or commercial site	Web site / reference ID	Short description	Notes	NGS technology
Metatranscriptomics sequencing	DNB	bioRxiv preprint doi: https://doi.org/10.1101/2020.11.19.371111 ; this version posted November 19, 2020. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.	Sequencing metatranscriptomes for SARS-CoV-2 detection in the nasal secretions of patients for research (2020) and for clinical diagnosis.	Feasible in practice for low amount of starting RNA	DNB Illumina
	DNB	bioRxiv preprint doi: https://doi.org/10.1101/2020.11.19.371111 ; this version posted November 19, 2020. 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 aCC-BY 4.0 International license.	Sequencing metatranscriptomes for SARS-CoV-2 detection in the nasal secretions of patients for research (2020) and for clinical diagnosis.	Feasible in practice for low amount of starting RNA	DNB Illumina
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	DNB	bioRxiv preprint doi: https://doi.org/10.1101/2020.11.19.371111 ; this version posted November 19, 2020. 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 aCC-BY 4.0 International license.	Sequencing metatranscriptomes for SARS-CoV-2 detection in the nasal secretions of patients for research (2020) and for clinical diagnosis.	Feasible in practice for low amount of starting RNA	DNB Illumina

4

I laboratori di sanità pubblica veterinaria e la ricerca nella genomica di SARS Cov2: Esperienze a confronto

GISAID SARS-Cov-2 Genomes Dataset

GISAID sottomissioni



Tot. Genomi 206,899

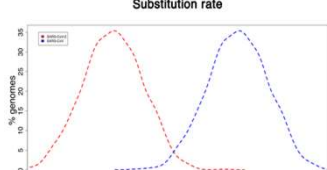
5

I laboratori di sanità pubblica veterinaria e la ricerca nella genomica di SARS Cov2: Esperienze a confronto

SARS-Cov-2 (n= 42.976) > SARS-Cov (n= 66)

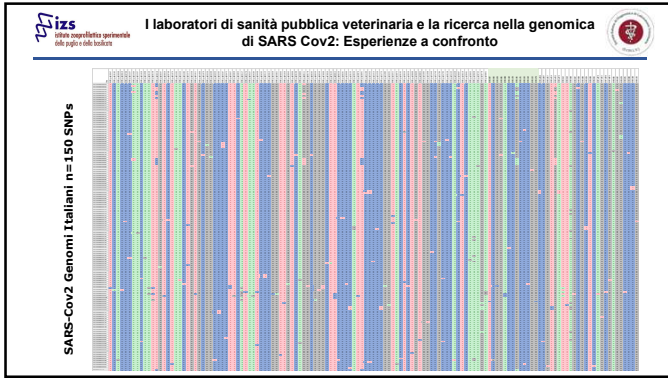
SARS-Cov-2 has a mutation rate of **1.96 x 10⁻³ substitutions per site per year** slightly lower than **2.38 x 10⁻³ substitutions per site per year** observed in SARS-Cov. Both estimates are in line with those of other known (+)ssRNA viruses.

Substitution rate



How fast does SARS-CoV-2 evolve?

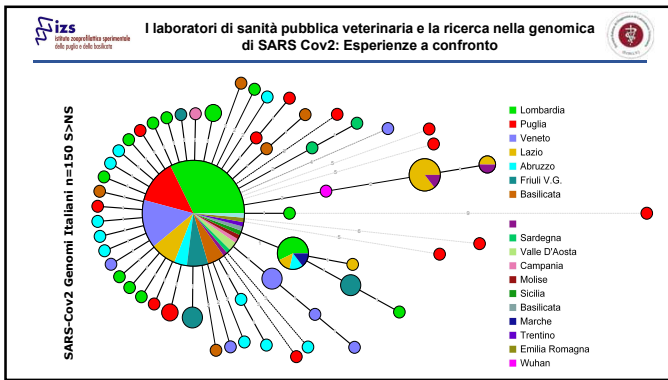
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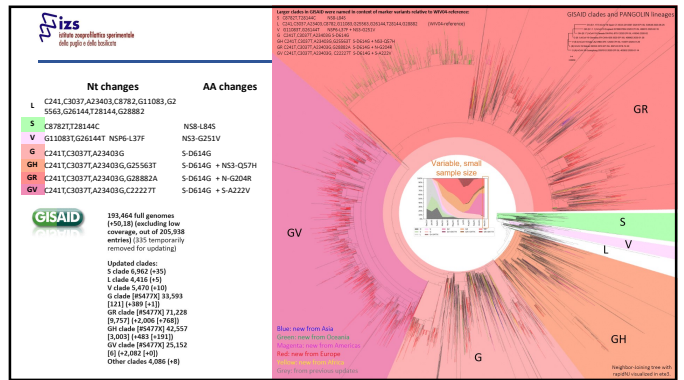
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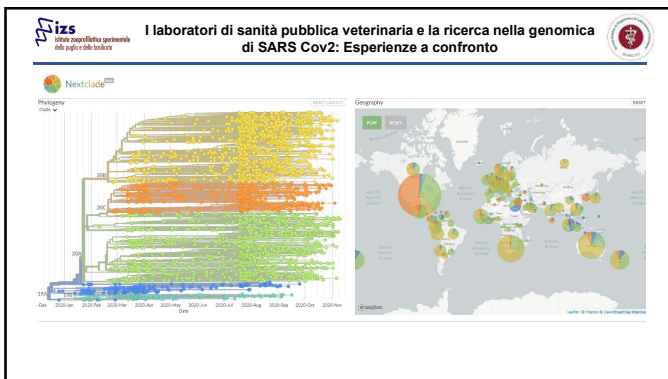
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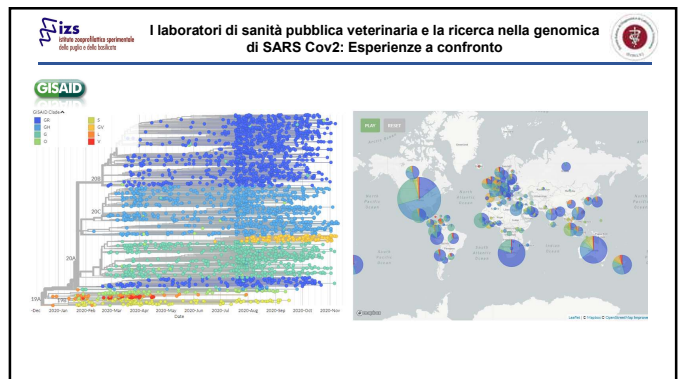
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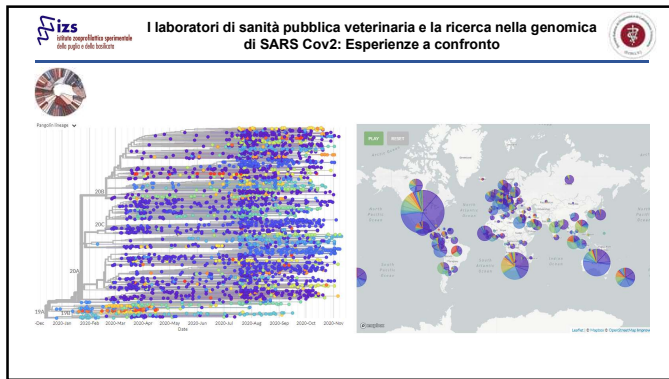
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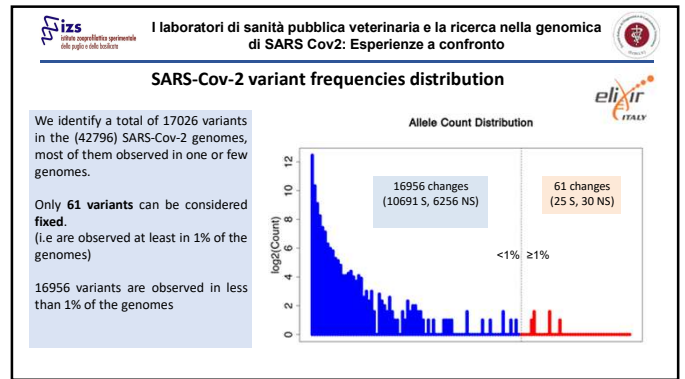
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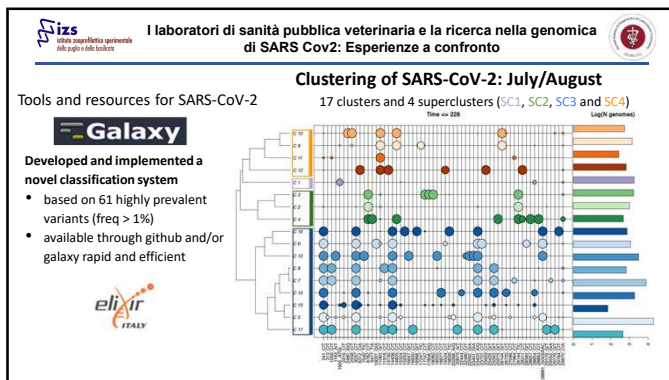
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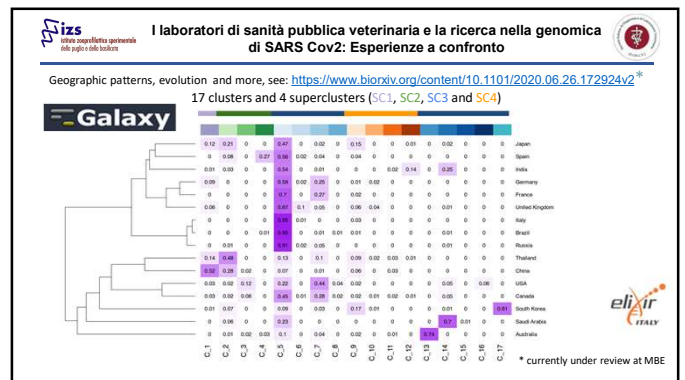
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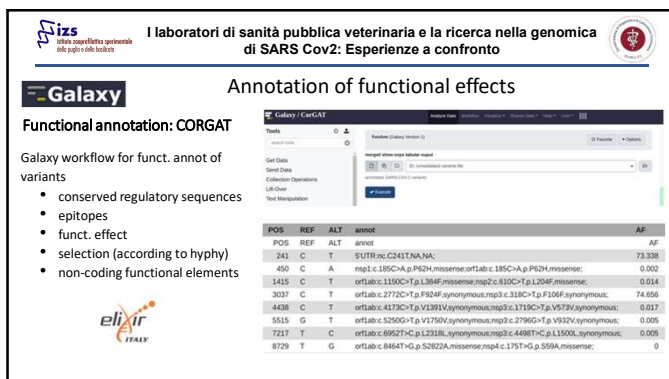
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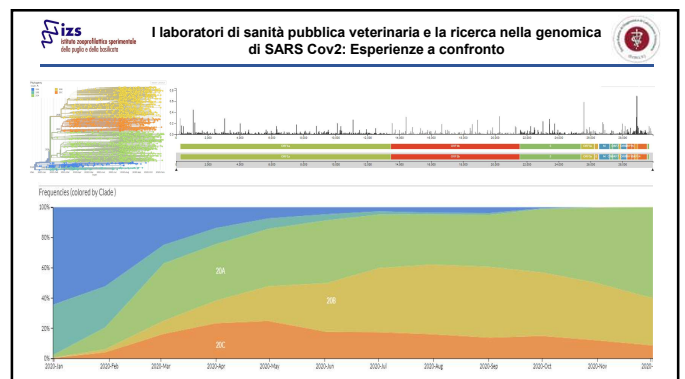
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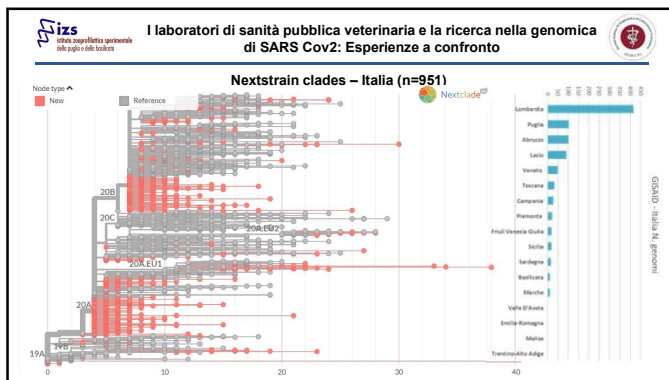
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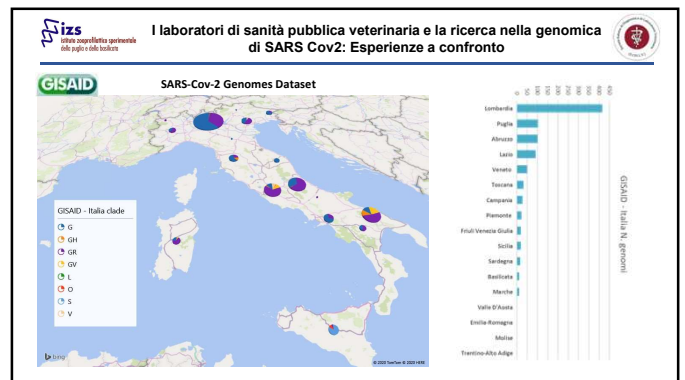
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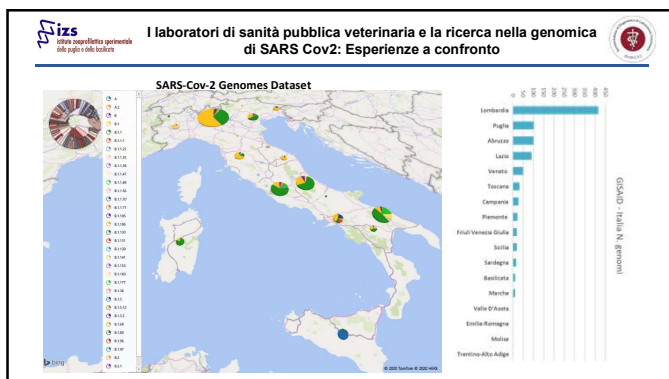
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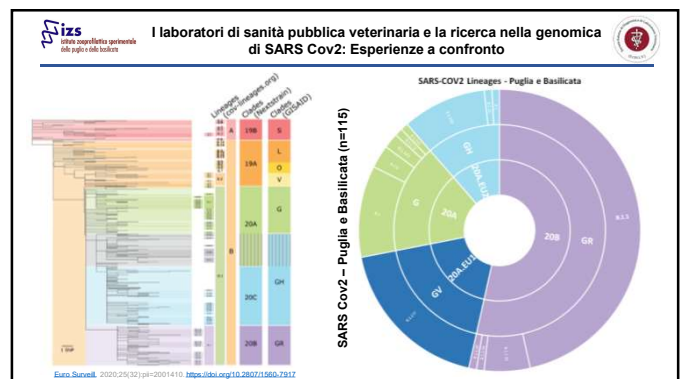
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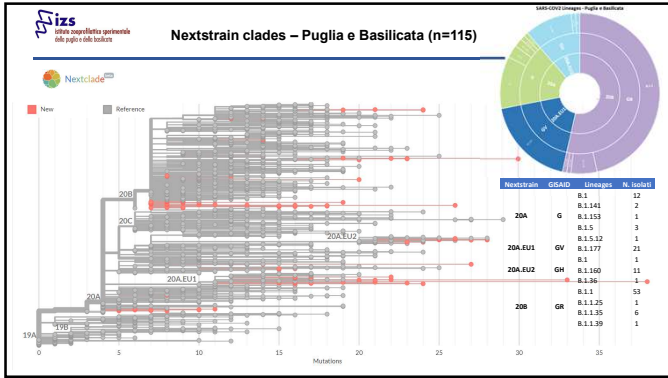
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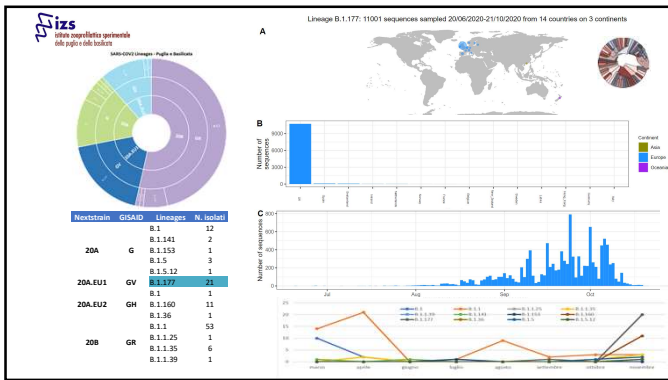
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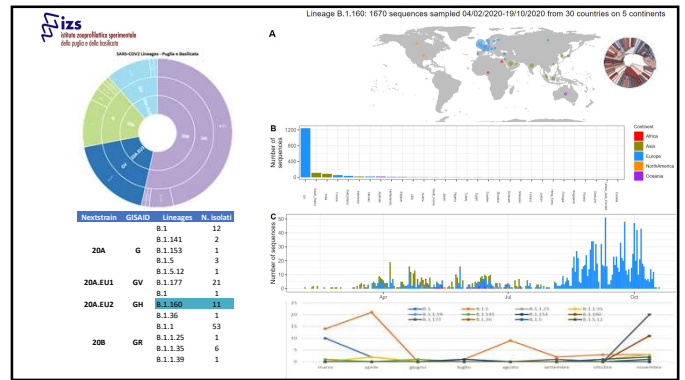
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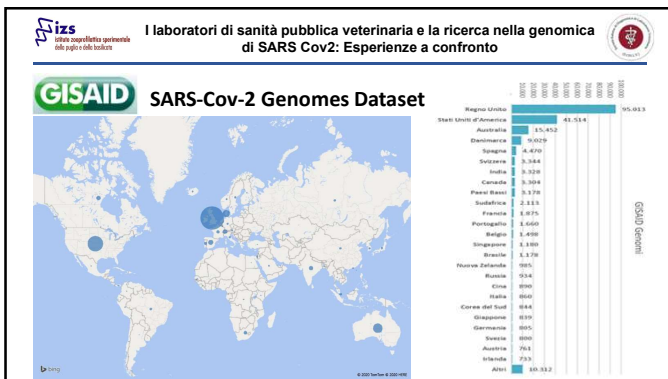
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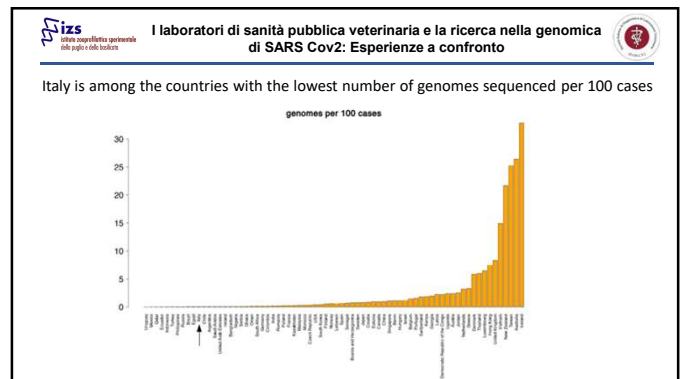
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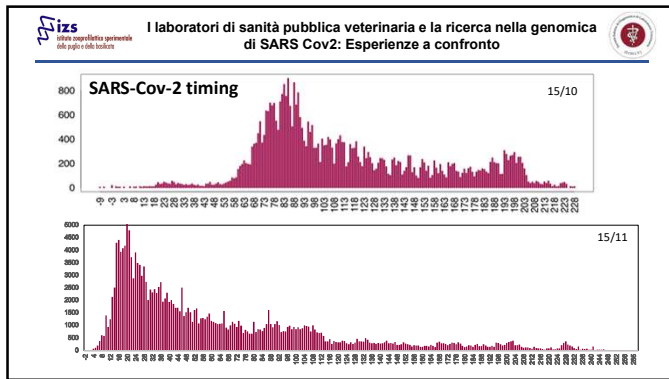
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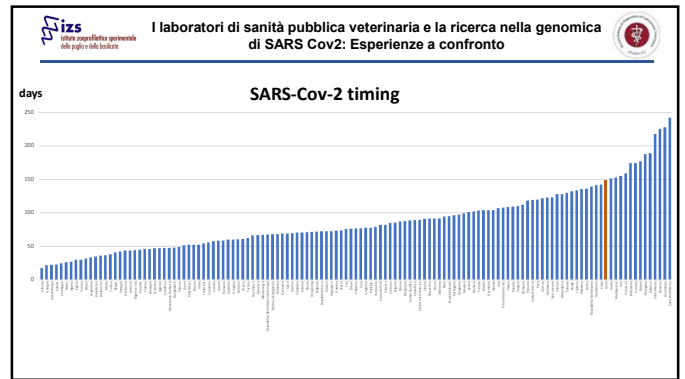
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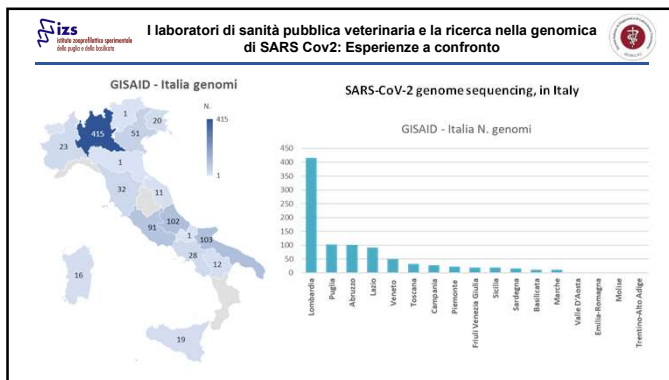
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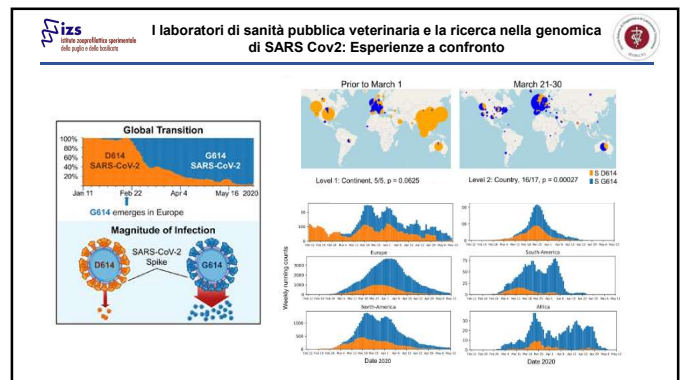
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ISARIC

COVID-19

Clinical research resources

Clinical Data Collection - The COVID-19 Case Report Forms (CRFs)


CORE CRF

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Global Transition

Magnitude of Infection

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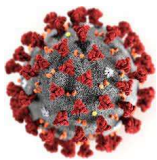
 **IZS**
Istituto zooprofilattico sperimentale
della Puglia e della Basilicata

**I laboratori di sanità pubblica veterinaria e la ricerca nella genomica
di SARS Cov2: Esperienze a confronto**



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Lorenzo Pace

Graziano Pesole
Matteo Chiara
Caterina Manzari



**Grazie per la
cortese attenzione**