Le scienze «OMICHE» e la sorveglianza

ANNALISA PANTOSTI

ISTITUTO SUPERIORE DI SANITÀ

Di cosa parleremo

1. COSA SONO LE SCIENZE OMICHE
2. LA RIVOLUZIONE GENOMICA
3. APPLICAZIONI DELLA GENOMICA MICROBIOLOGICA IN SANITÀ PUBBLICA
4. GENOMICA PER LA SORVEGLIANZA DELL' AMR

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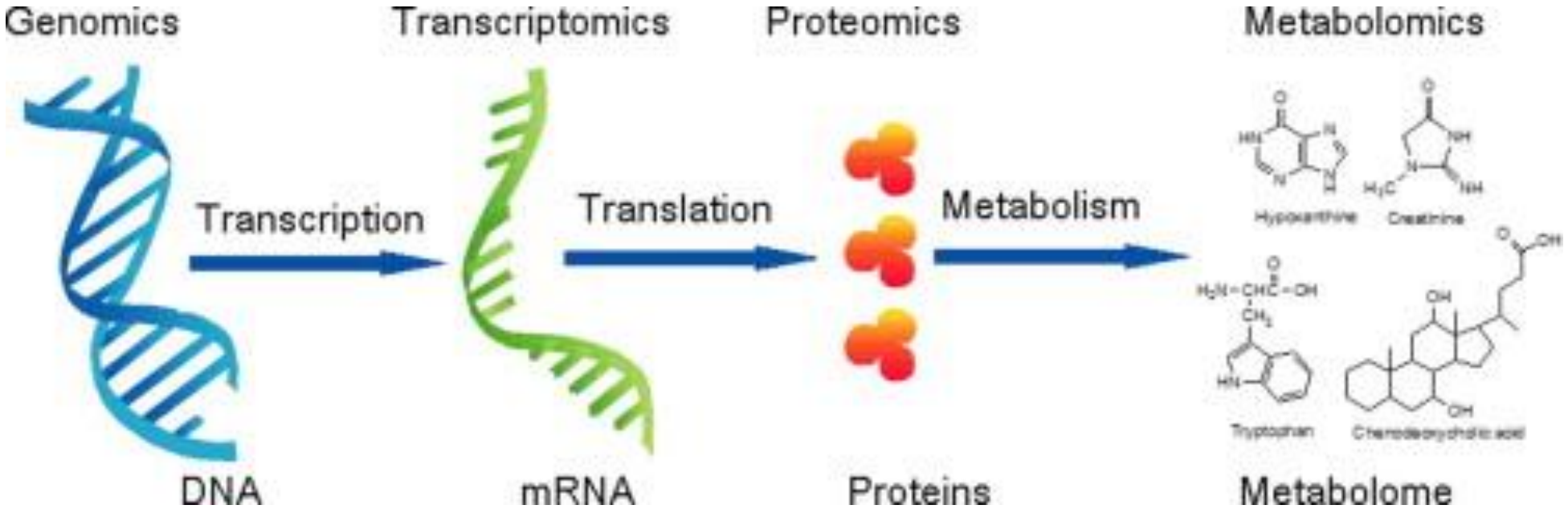
5. IL FUTURO ?

SCIENZE «OMICHE»: scienze che si occupano dell'ANALISI GLOBALE DI UN INSIEME DI MOLECOLE IN UN SISTEMA BIOLOGICO



Da: Ying-YongZhao, & Rui-ChaoLin

Numerose declinazioni di «Genomics»:

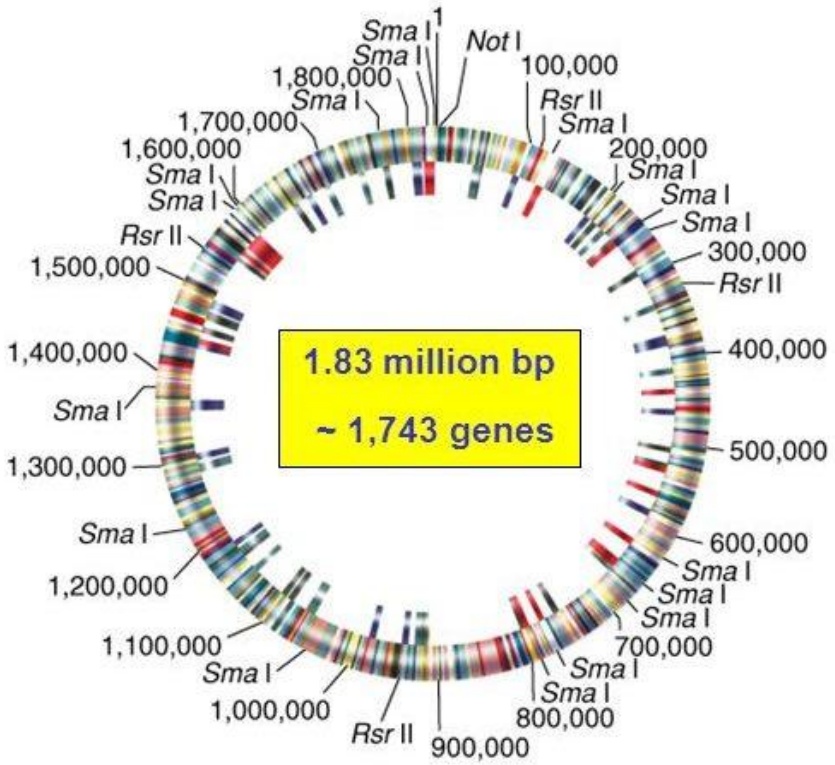
- Epigenomics
- Pharmacogenomics
- Nutritional Genomics
- Psycogenomics

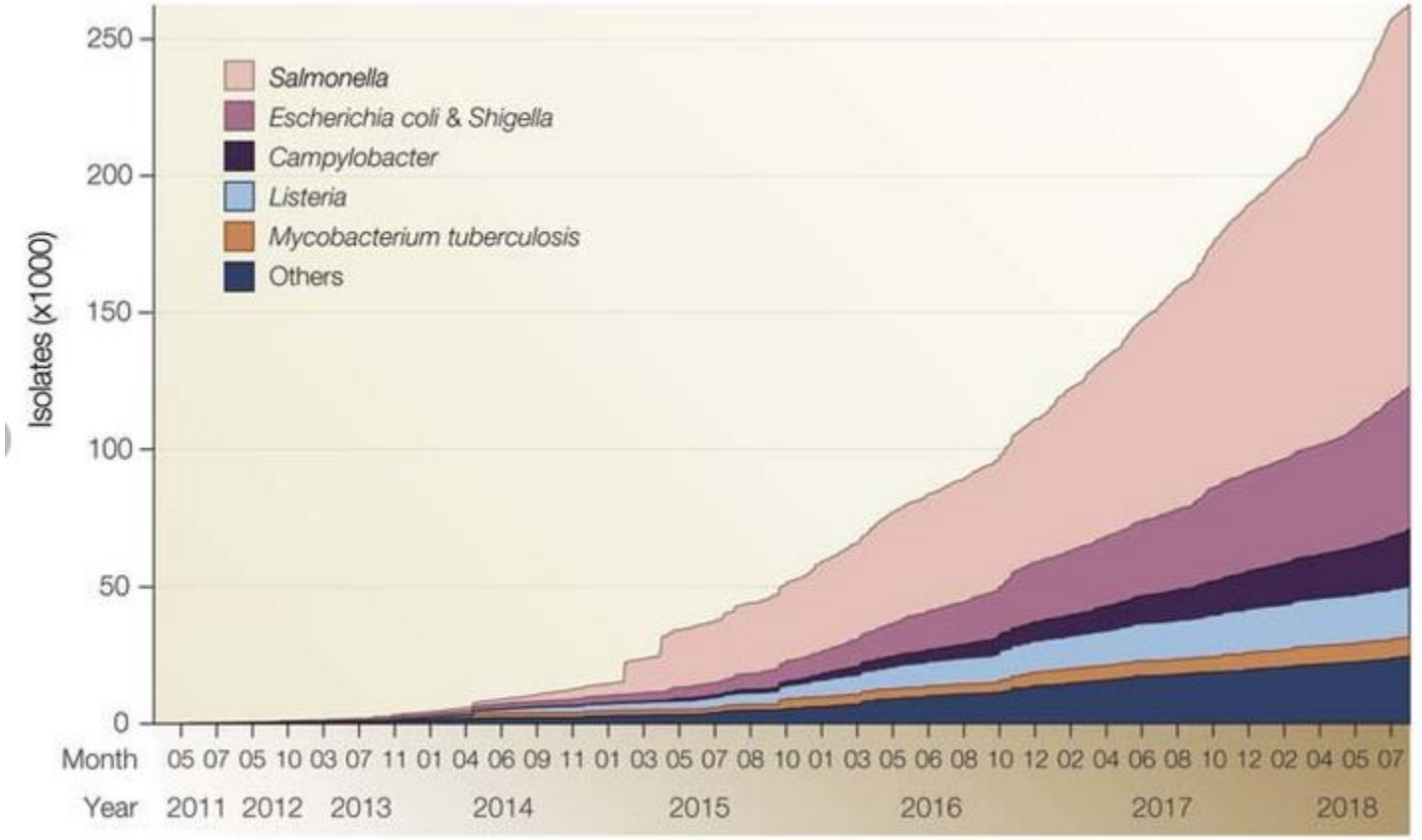
Ma anche numerosi altri «OMICS»:

- Lipidomics
- Glycomics
- Connectomics
- Microbiomics

Whole Genome Sequencing (WGS)

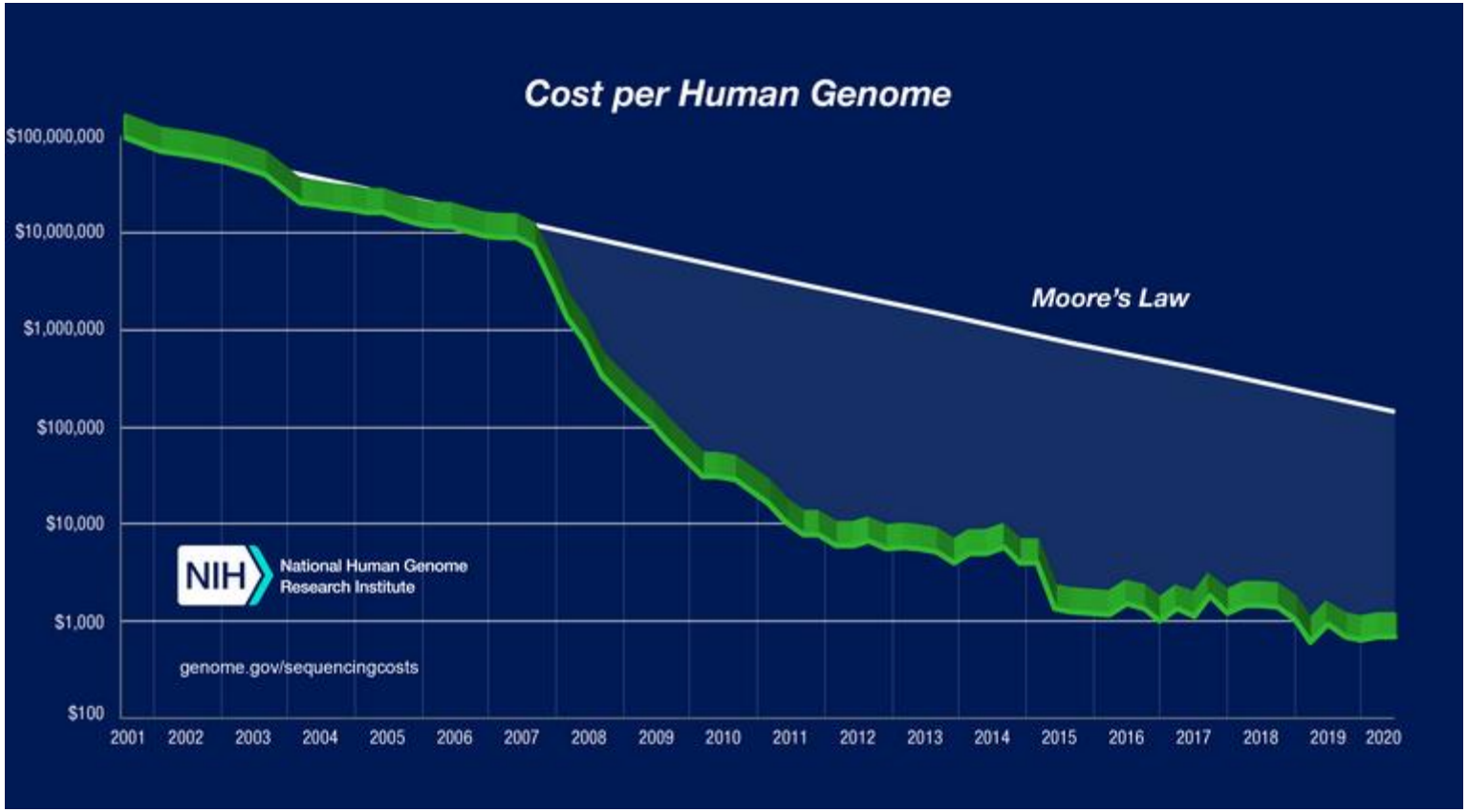
WGS DI PATOGENI BATTERICI (Database NCBI)





Genoma di *Haemophilus influenzae* (1995)

ResearchGate


Cost per Human Genome
$100,000,000
$10,000,000
$1,000,000
$100,000
$10,000
$1,000
$100
Moore's Law
NIH
National Human Genome
Research Institute
genome.gov/sequencingcosts
2001
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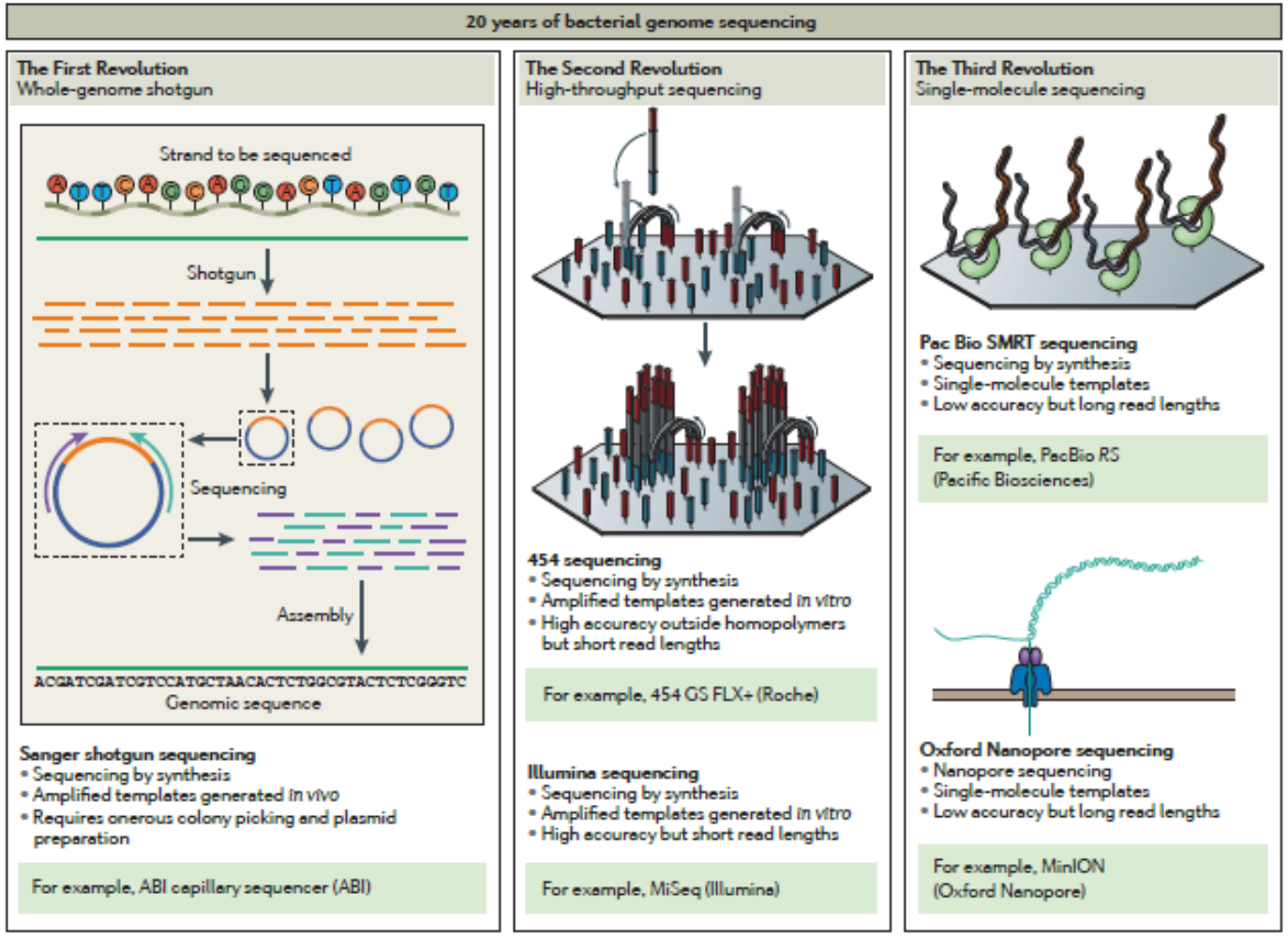
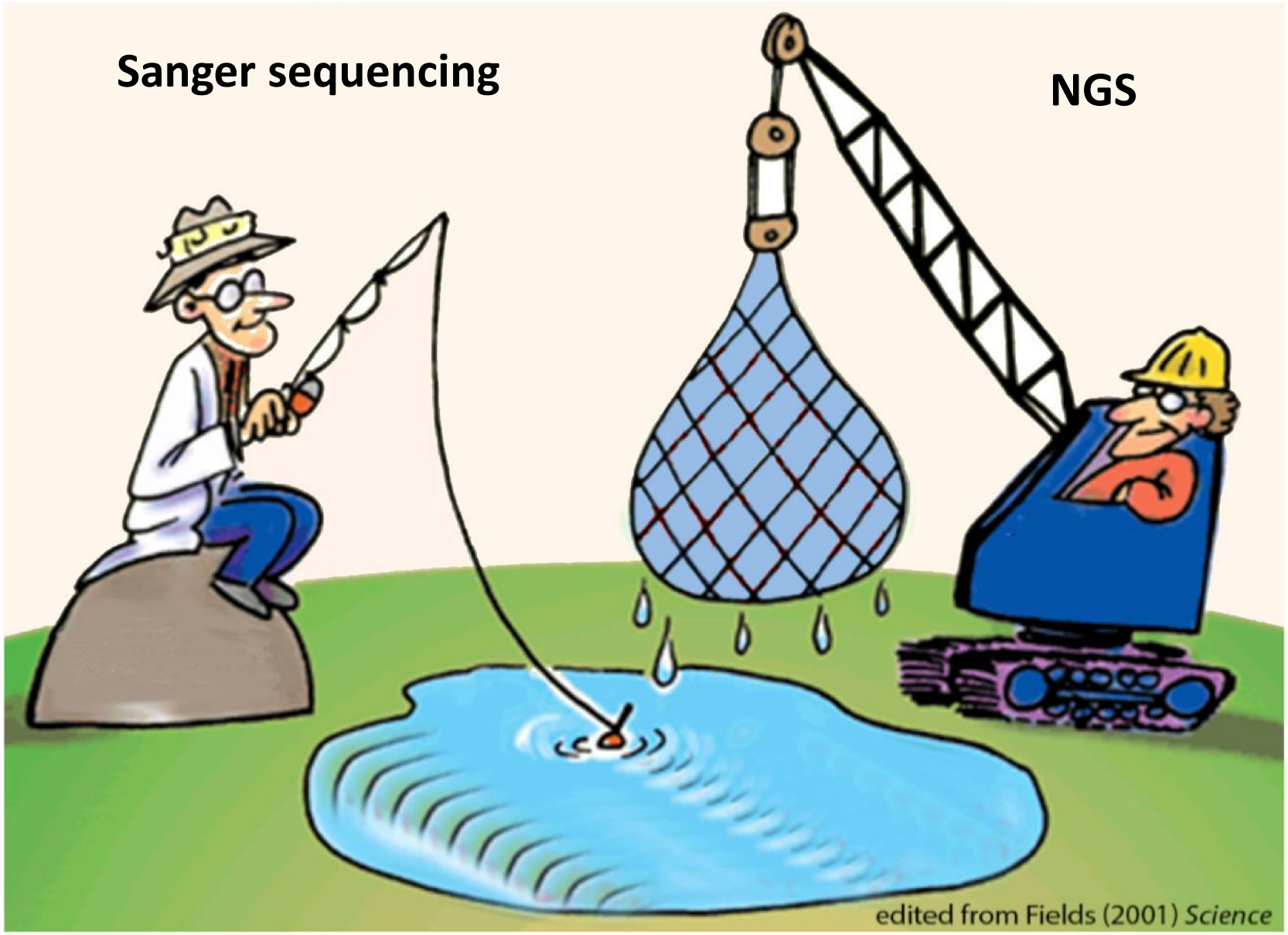
2020

Nature Microbiol, 2015



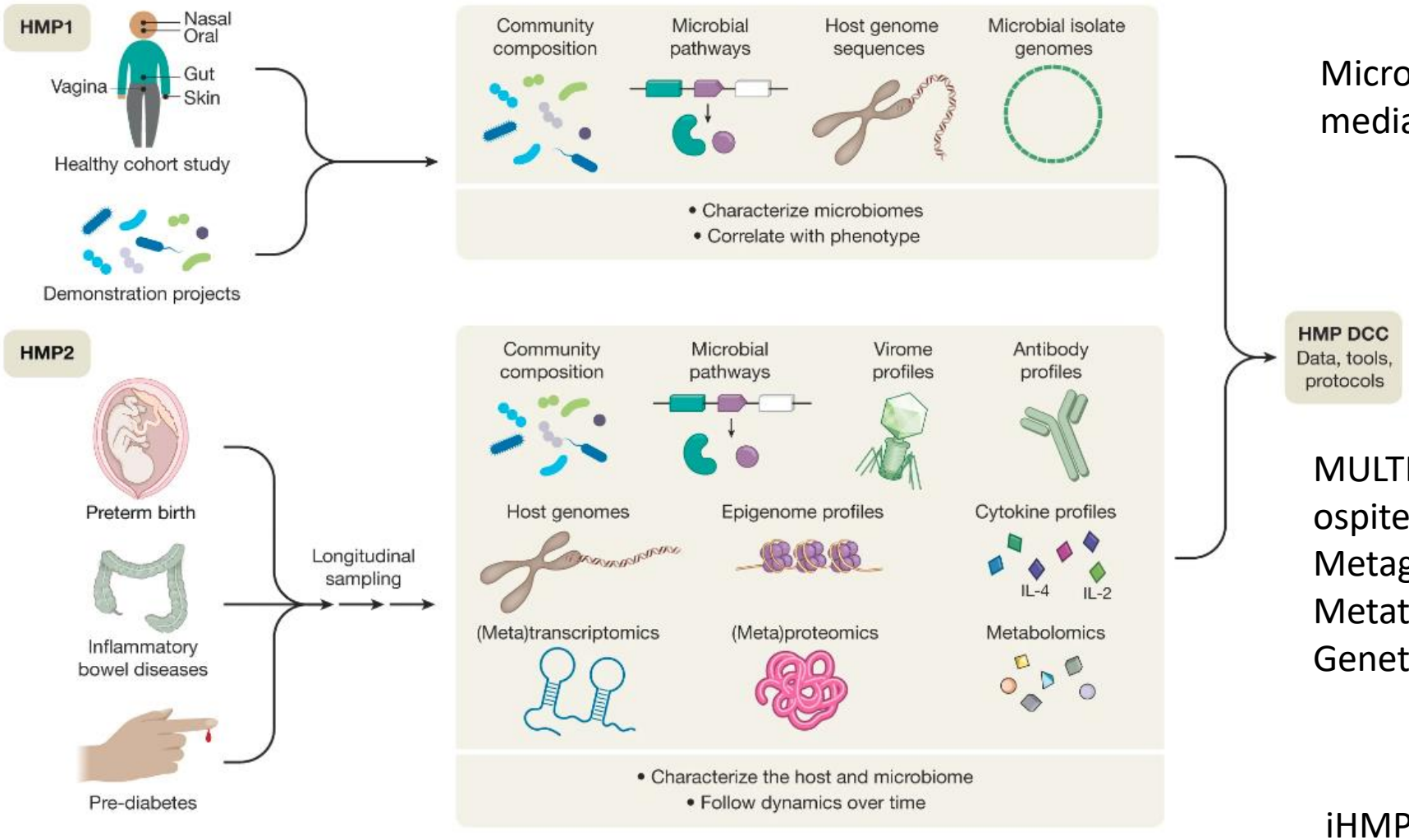
Genomica batterica: 3 rivoluzioni tecnologiche in 20 anni


Sanger sequencing
NGS
edited from Fields (2001) *Science*

Metagenomica

1. STUDIO DEL MATERIALE GENETICO (GENOMI) OTTENUTO COLLETTIVAMENTE DA UNA COMUNITA' DI MICRORGANISMI DIVERSI
2. IN GENERE SI RIFERISCE A COMUNITA' MICROBICHE IN UN DETERMINATO ECOSISTEMA (ES. INTESTINO UMANO, ACQUA, SUOLO)
3. I MICRORGANISMI NON POSSONO ESSERE SEPARATI TRA LORO O CRESCIUTI SEPARATAMENTE QUINDI SI STUDIA DIRETTAMENTE IL MATERIALE GENETICO TOTALE
4. LA TECNOLOGIA E LE ANALISI BIOINFORMATICHE PERMETTONO DI RICONOSCERE I MICRORGANISMI PRESENTI

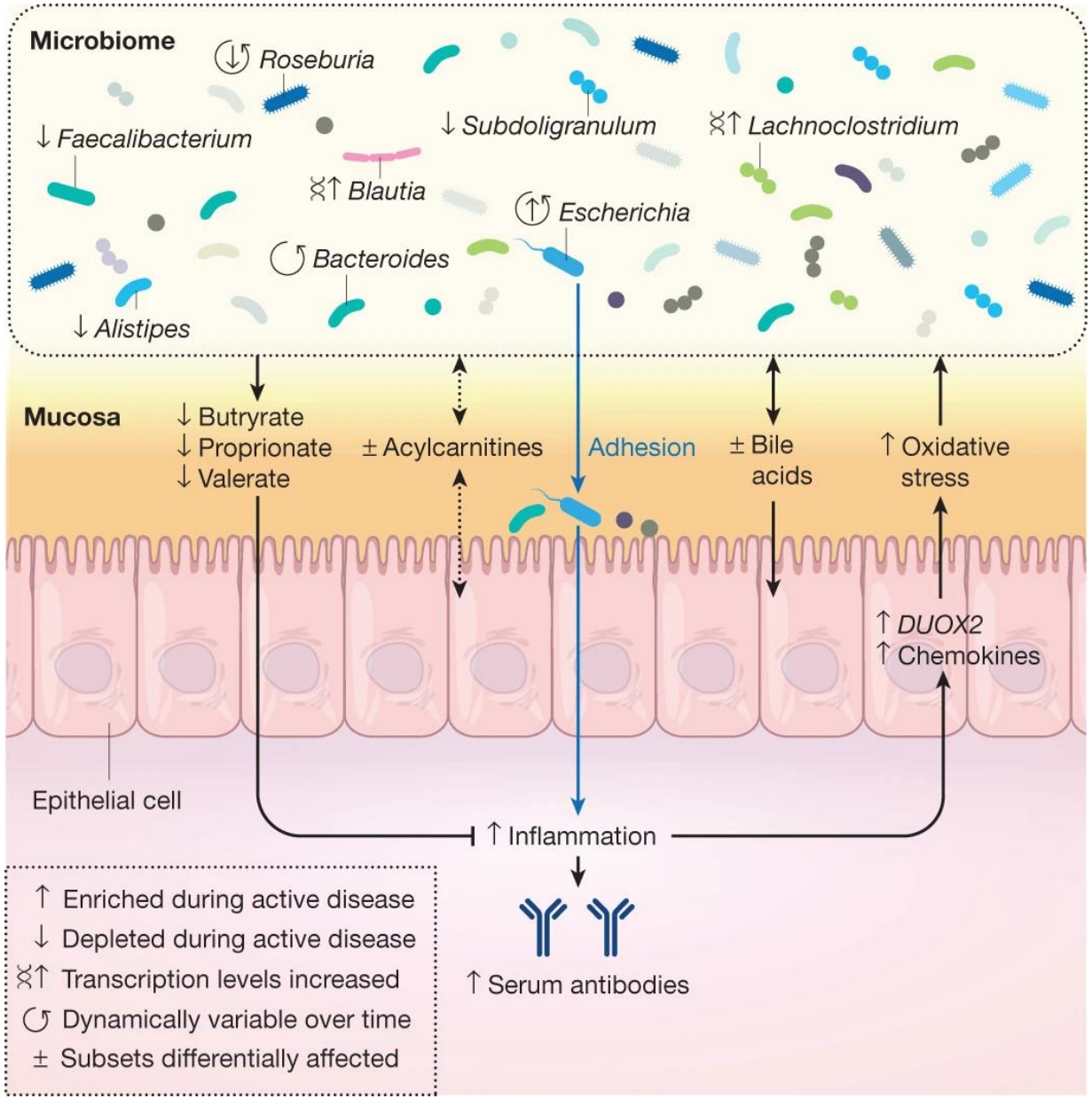
NIH Human Microbiome Project



Microbioma in 5 siti corporei mediante 16S e metagenomica

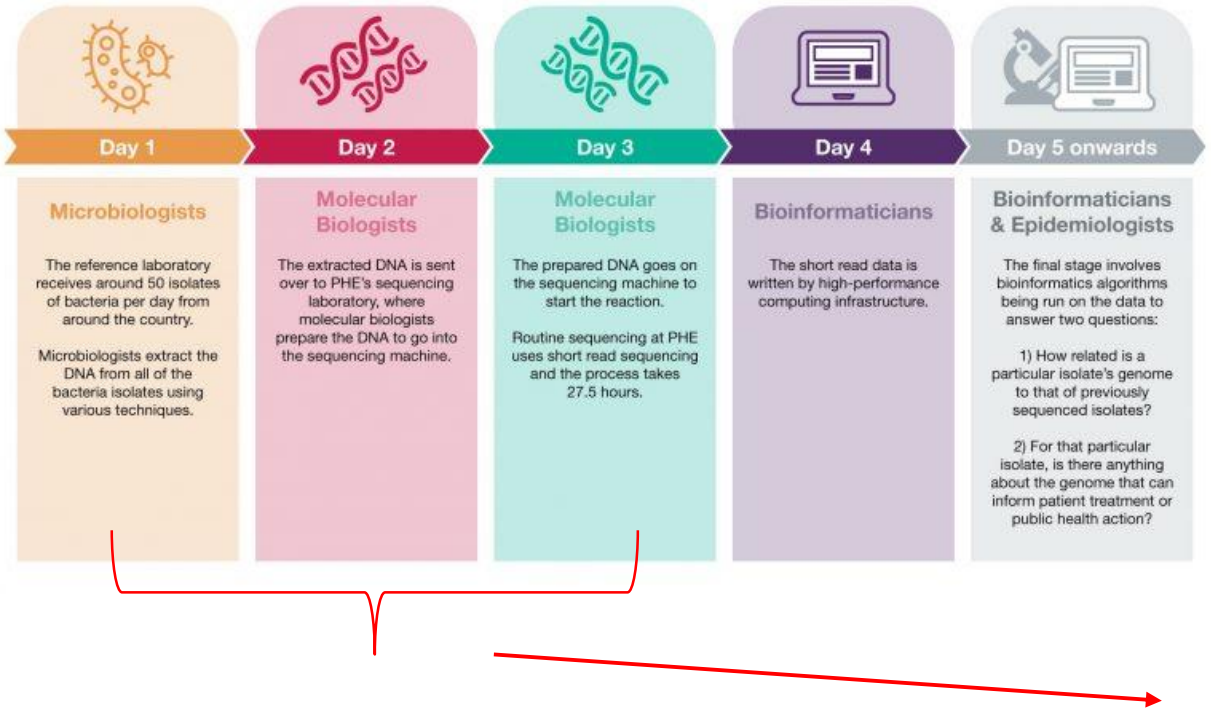
MULTIOMA (microbioma e ospite).
Metagenomica
Metatrascrittomica
Genetica umana ecc.

iHMP Consortium, Nature 2019

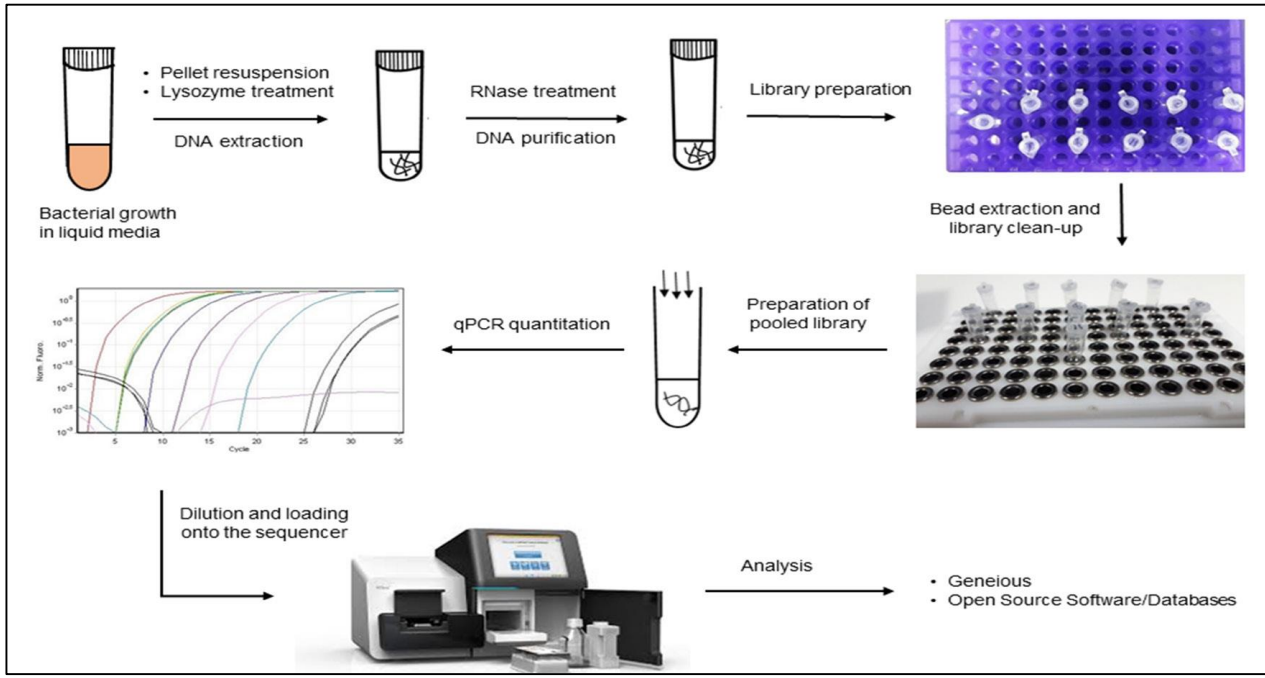


Rilevazione di «nuove» specie batteriche nel microbiota intestinale

WGS E' UN PROCESSO MULTIDISCIPLINARE



Gautam et al. J Mol Methods 2019



Graphical summary of the process of obtaining whole genome sequence data from a bacterial culture (3 working days)

«short read sequencing» (Illumina)

Public Health England (PHE)

Trasformazione del laboratorio microbiologico nazionale di riferimento e della sorveglianza di Salmonella per utilizzare WGS

October 2012 to February 2013
Reconfiguration of laboratory space

March 2013 to April 2014
First validation phase

April 2014
WGS service launched

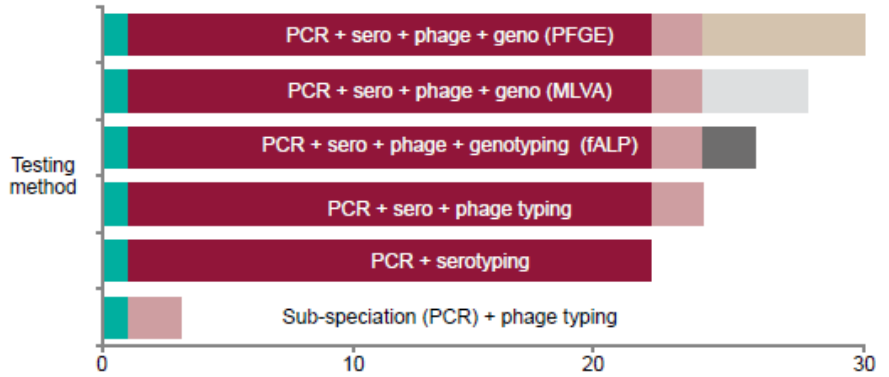
April 2014 to March 2015
Second validation phase

April 2015
Salmonella identification and typing transferred to WGS

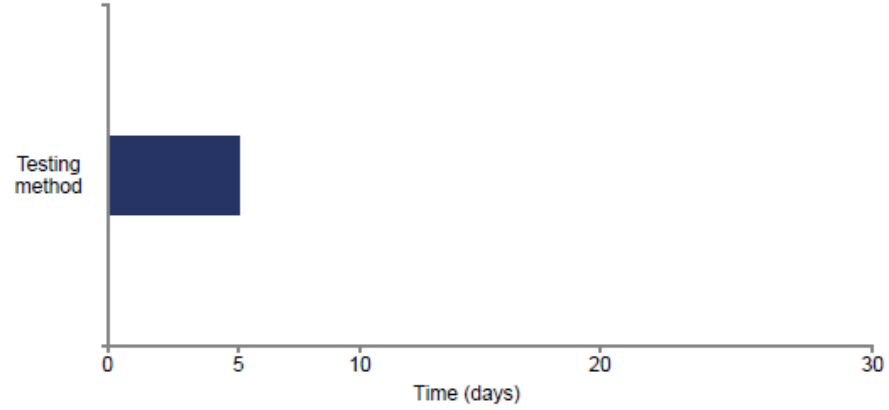
April 2015
Salmonella serotyping phased out

September 2015
WGS analysis of Salmonella outbreaks becomes available

September 2015 to December 2015
Genotyping, PCR assays and phage typing of Salmonella phased out



Tipizzazione tradizionale



WGS

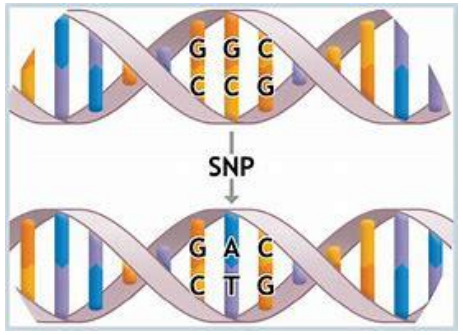
Applicazione di WGS ai microrganismi

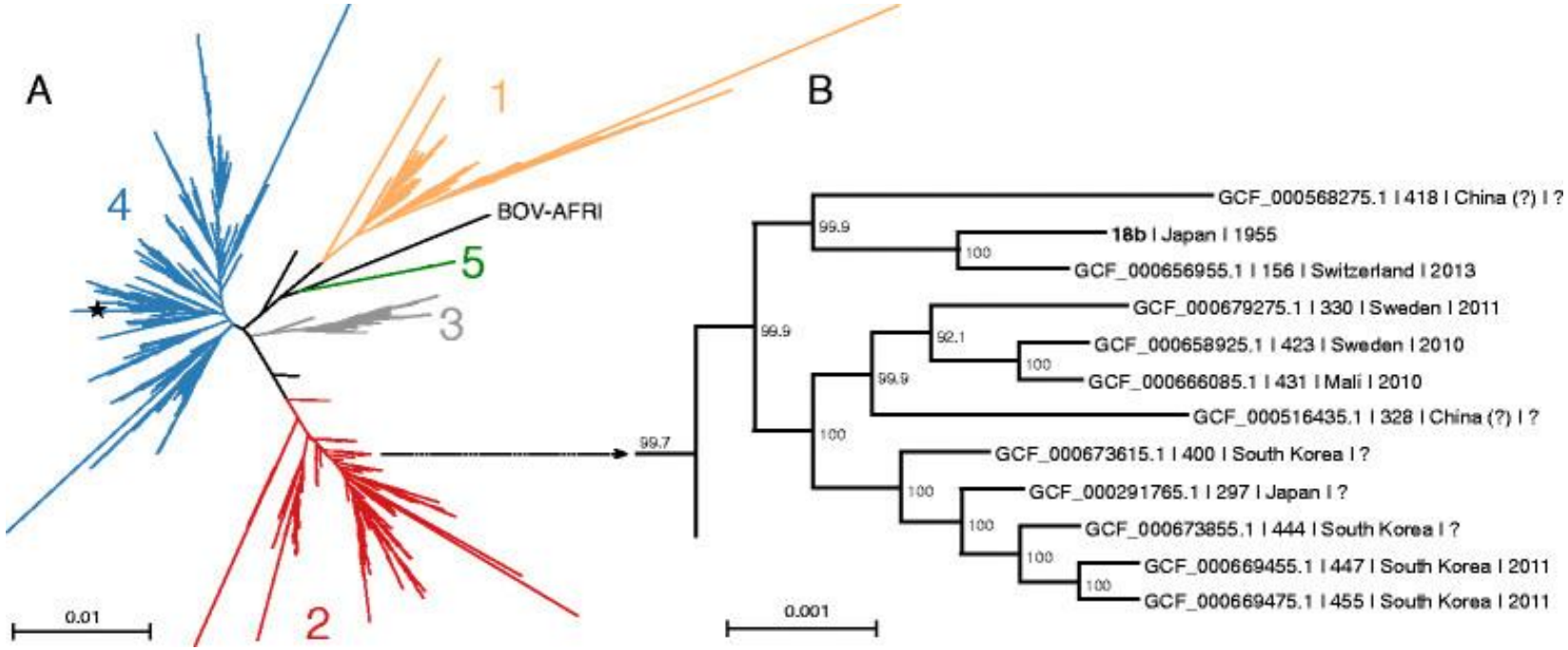
- **Metodo robusto**
- **Applicabile a tutti i microrganismi**
- **I dati possono essere conservati, riesaminati e comparati a livello internazionale**
- **In microbiologia umana**:
  - può sostituire i metodi di tipizzazione fin qui utilizzati e dare informazioni su resistenza agli antimicrobici
- **In sanità pubblica**:
  - tracciare rapidamente outbreak
  - individuare catene di trasmissione (es. patogeni zoonosici o provenienti da matrici alimentari ecc.)
  - Individuare rapidamente ceppi patogeni emergenti
  - Individuare rapidamente nuove resistenze

Come utilizzare i dati di WGS di batteri?

- **TIPIZZAZIONE MOLECOLARE**
  - **MLST (7 geni housekeeping)**
  - **cgMLST (1500-4000 geni del core genoma a seconda della specie batterica)**
  - **Sierotipo (capsulare, O-sierotipo ecc)**
- **VIRULOMA (geni di virulenza)**
- **RESISTOMA (mutazioni o geni di resistenza acquisiti)**
- **MOBILOMA**
- **ecc.**
  - **FILOGENESI (basata su Single Nucleotide Polymorphism o SNPs): rapporti tra microrganismi della stessa specie o gruppo per verificare reciproca derivazione ed evoluzione nel tempo**

ALBERO FILOGENETICO BASATO SU SNPs





Albero filogenetico di *Mycobacterium tuberculosis*

Center for Genomic Epidemiology

Home | Services | Publications | Contact

Overview of Services

Phenotyping

ResFinder
Identifcation of acquired antibiotic resistance genes.

ResFinderFG
Identifcation of functional metagenomic antibiotic resistance determinants.

LRE-finder
Identifcation of genes and mutations leading to linezolid resistance.

KmerResistance
Identifcation of acquired antibiotic resistance genes using Kmers.

Phylogeny

MINTyper
Identification of SNPs with automatic filtering, masking and site validation together with inferred phylogeny based on both long and short sequencing data.

CSIPhylogeny
CSI Phylogeny calls SNPs, filters the SNPs, does site validation and infers a phylogeny based on the concatenated alignment of the high quality* SNPs.

NDtree
NDtree constructs phylogenetic trees from Single-End or Pair-End

Typing

MLST
Multi Locus Sequence Typing (MLST) from an assembled genome or from a set of reads.

PlasmidFinder
PlasmidFinder identifies plasmids in total or partial sequenced isolates of bacteria.

pMLST
Multi Locus Sequence Typing (MLST) from an assembled plasmid or from a set of reads.

cgMLSTFinder
Core genome Multi Locus Sequence Typing (cgMLST) from a set of reads.

KmerFinder
Prediction of bacterial species using a fast K-mer algorithm.

MGE
Identification of mobile genetic elements and their relation to antimicrobial resistance genes and virulence factors.

SpeciesFinder
Prediction of bacterial species using the S16 ribosomal DNA sequence.

SeroTypeFinder
Prediction of serotypes in total or partial sequenced isolates of E. coli.

SeqSero
SeqSero predicts the Salmonella serotype of either the pre-assembled or raw read sequence data provided to the service.

spaTyper
spaTyper predicts the S. aureus spa type.

FimTyper
FimTyper predicts the E. coli Fim type.

CHTyper
CHTyper predicts the E. coli FimH type and FumC type.

PAst
PAst predicts the P. aeruginosa serotypes.

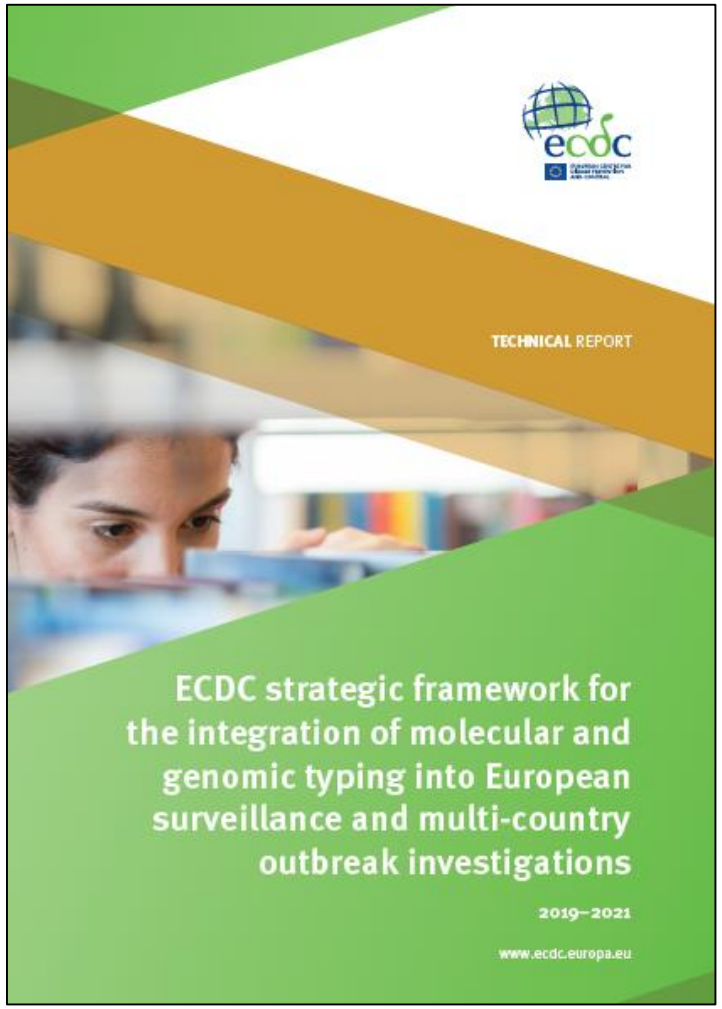
SCCmecFinder
SCCmecFinder identifies SCCmec elements in sequenced S. aureus isolate.

- Vantaggi e limitazioni di WGS nella sorveglianza dell'AMR
- Esempi dell'uso di WGS nella sorveglianza dell'AMR
  - Studio di outbreak (locali o nazionali)
  - Integrazione nella sorveglianza
- Requisiti per l'introduzione di WGS in un sistema di sorveglianza dell'AMR
  - Laboratori
  - Piattaforme
  - Bioinformatica
  - Storage dei dati, Finanziamenti ecc.
- WGS nello sviluppo di diagnostici, nuovi farmaci e vaccini

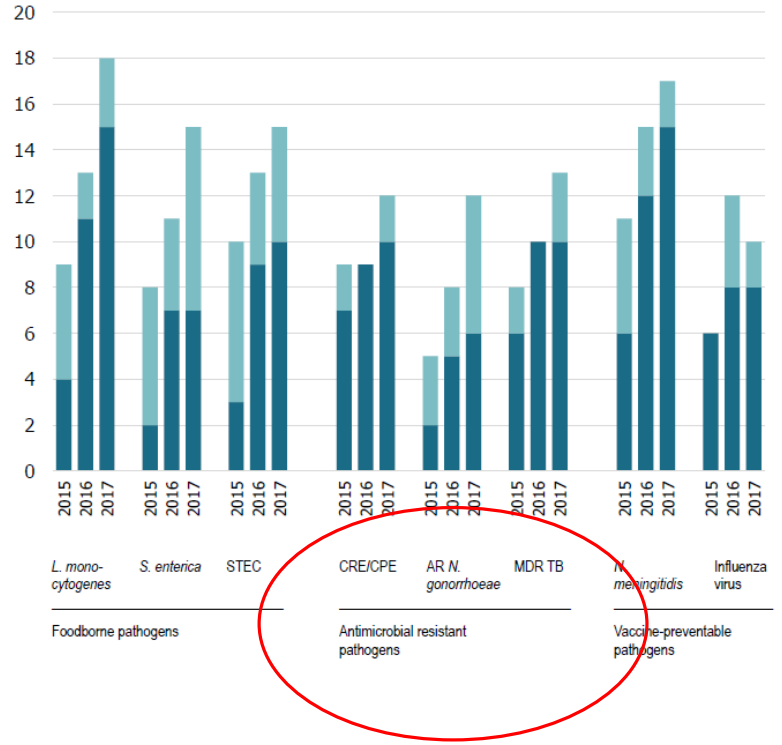
Consultazione delle autorità dei paesi:

- **Necessità di chiarire meglio i vantaggi**
- **Necessità di armonizzare approcci, tecnologie e analisi**

WHO, 2020



Numero di paesi UE che utilizzano WGS per sorveglianza o solo per studio di outbreak per gruppo di patogeni



- 20 paesi EU usano WGS in almeno una sorveglianza routinaria nel 2018
- In 3 anni sono stati sequenziati >2000 genomi per identificare outbreak transnazionali

efsa European Food Safety Authority

ecdc

JOINT ECDC-EFSA RAPID OUTBREAK ASSESSMENT

Multi-country outbreak of *Salmonella* Enteritidis infections linked to eggs

Third update

6 February 2020

Abstract

A multi-country outbreak of *Salmonella* Enteritidis, delineated by whole genome sequencing (WGS), linked to eggs, has been ongoing in the EU/EEA for several years. From 1 February 2017 to 14 January 2020, 15 EU/EEA countries reported 656 confirmed cases and 202 probable cases. Before February 2017, 385 historical-confirmed cases and 413 historical-probable cases were identified, resulting in 18 affected countries. Due to differences in capacity for case confirmation, more countries are likely to be affected.

This prolonged outbreak peaked during the summer months of 2016–2018. A notable decrease in the frequency of the cases reported to ECDC has been observed in 2019, which is a deviation from the three previous years.

Epidemiological, microbiological and food tracing investigations have linked cases before 2018 to consumption of eggs originating from laying hen farms of a Polish consortium. A national investigation in 2018 in the UK identified epidemiological links between some cases and consumption of table eggs or egg products, with traceability possibly pointing to the Polish consortium.

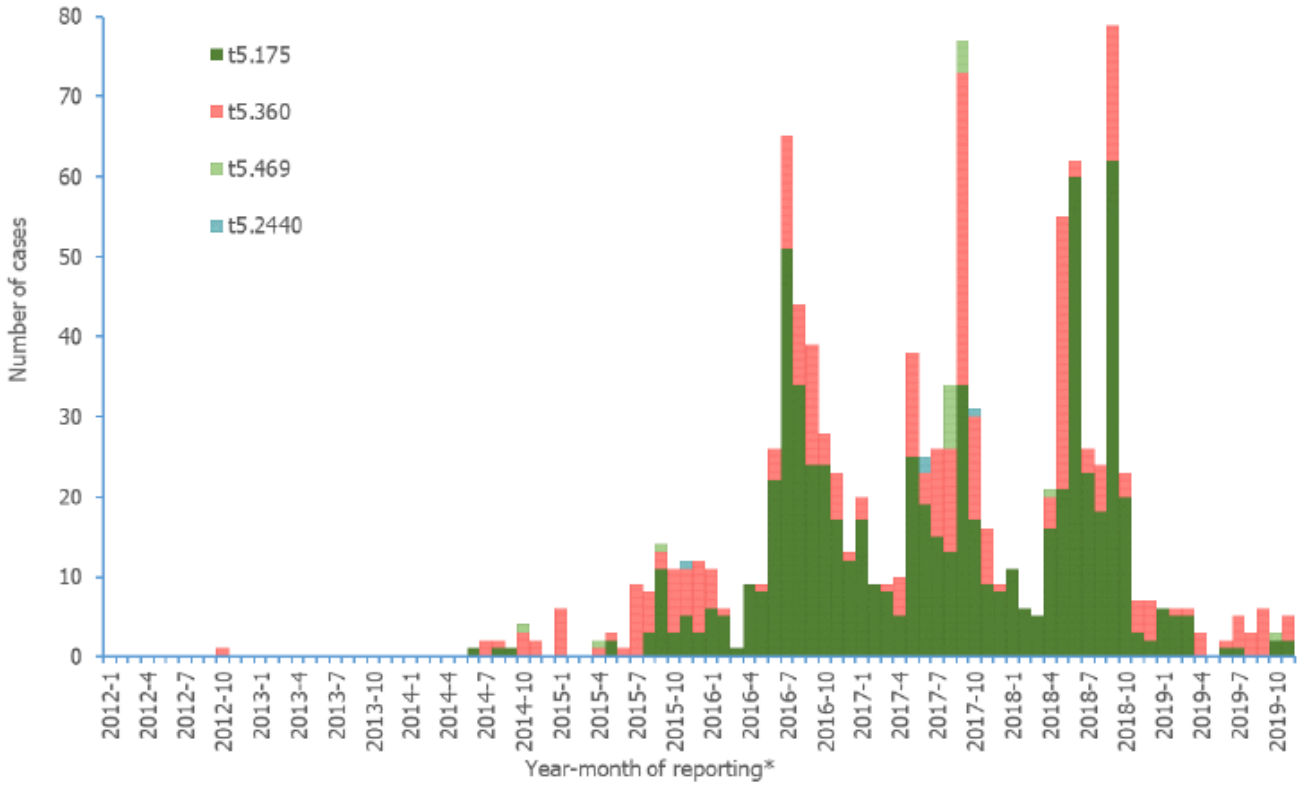
Despite the control measures implemented in 2016–2017, the farms of the Polish consortium were positive in 2018–2019 with outbreak strains, suggesting persistent contamination. Investigations focusing on the laying hen production and feed supply chains did not reveal any significant insights on the possible origin of the contamination.

One of the outbreak strains was found in the period 2017-2019 in primary production in Germany.

In conclusion, the outbreak is still ongoing and since no evidence was provided that the source of contamination has been eliminated, it is expected that further infections will occur and that new cases will be reported in the coming months. Additional investigations are necessary to identify the source of contamination.

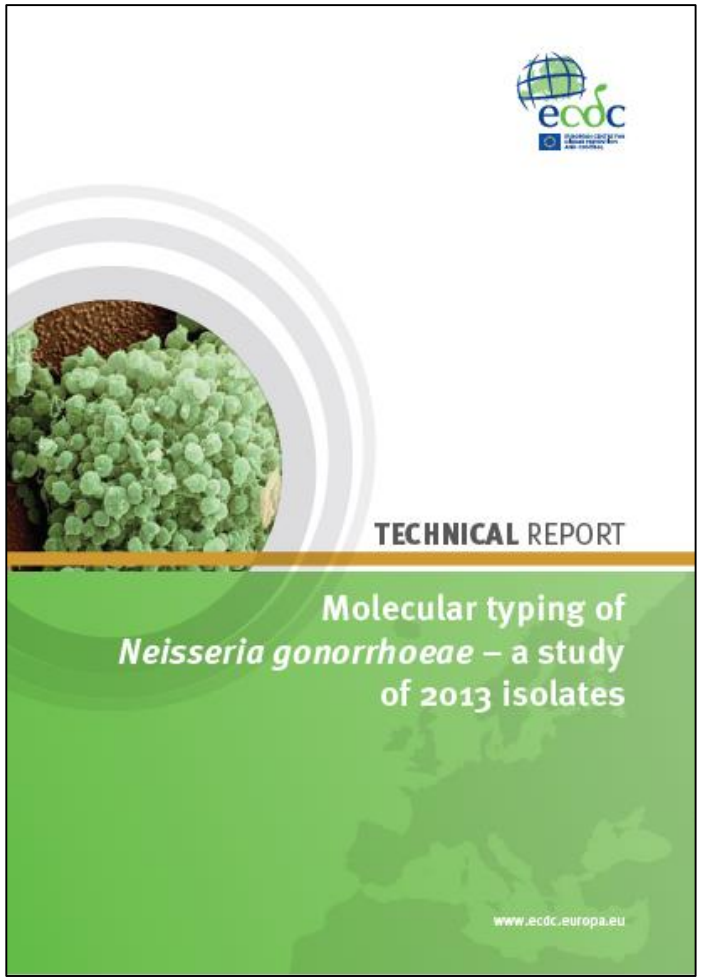
Suggested citation: European Centre for Disease Prevention and Control, European Food Safety Authority, 2020. Multi-country outbreak of *Salmonella* Enteritidis infections linked to eggs, third update – 6 February 2020.

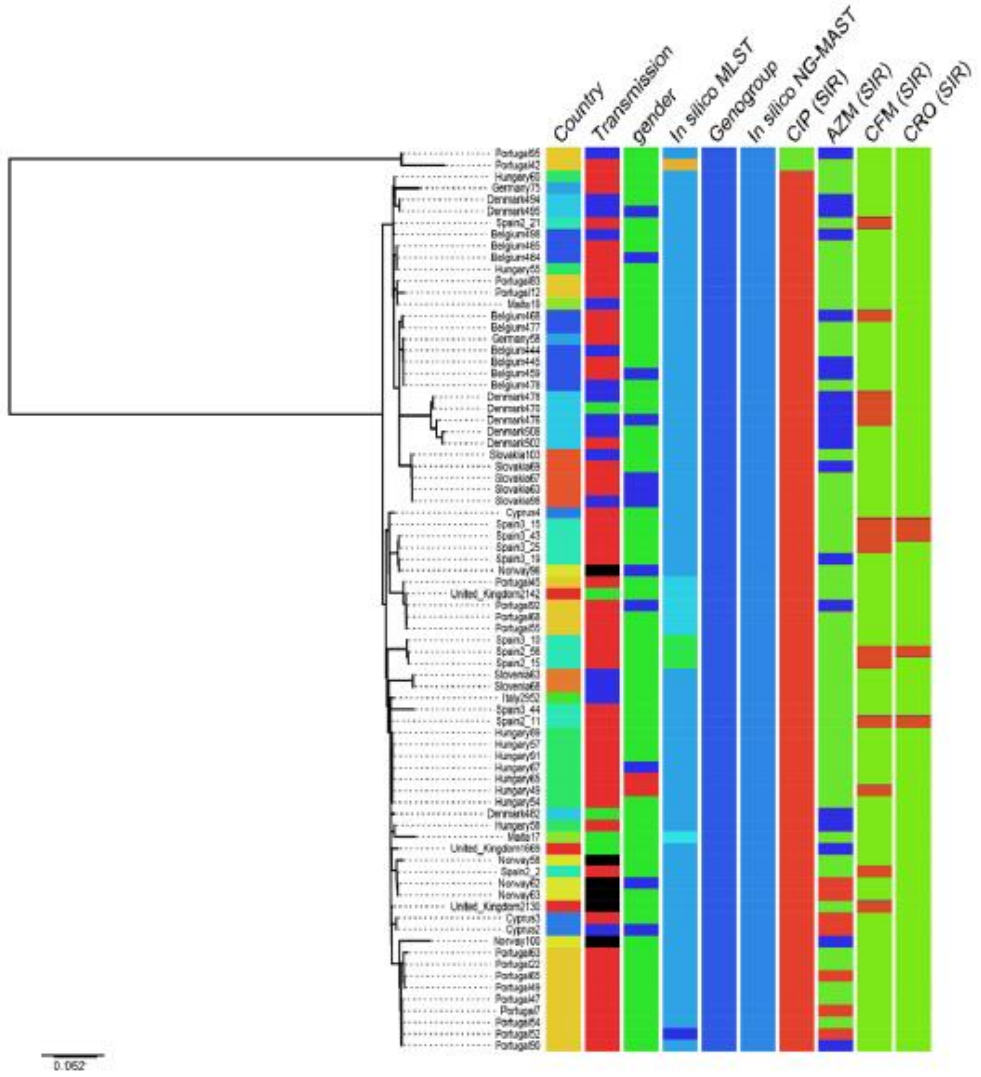
Definizione di caso confermato basato su t-5 SNP type (PHE SNP pipeline)



Distribuzione dei casi per cluster genetico e mese di isolamento

GONO





Filogenomica di 78 ceppi di *Neisseria gonorroheae* NG-MAST ST1407 isolati in EU nel 2013.
Sono evidenziate cladi minori che rappresentano evoluzioni all'interno di ogni paese, spesso associate con determinanti di antibiotico-resistenza

Use of a whole genome sequencing-based approach for *Mycobacterium tuberculosis* surveillance in Europe in 2017–2019: an ECDC pilot study

Mtb

Tagliani E, ERJ 2021

Country	Isolates submitted by year of isolation n			Total n
	2017	2018	2019	
Austria	0	19	6	25
Belgium	5	8	6	19
Bulgaria	25	24	16	65
Croatia	0	2	1	3
Cyprus	0	0	0	0
Czech Republic	5	9	11	25
Denmark	0	4	4	8
Estonia	28	25	13	66
Finland	4	4	2	10
France	8	66	25	99
Germany	77	124	45	246
Hungary	5	13	4	22
Ireland	6	7	10	23
Italy	63	44	20	127
Latvia	18	33	34	85
Lithuania	77	60	42	179
Luxembourg	0	0	0	0
Malta	0	0	0	0
Netherlands	12	6	6	24
Norway	2	6	2	10
Poland	31	57	10	98
Portugal	12	19	6	37
Romania	335	336	195	866
Slovakia	2	4	2	8
Slovenia	0	1	0	1
Spain	17	37	12	66
Sweden	9	11	5	25
UK	27	30	24	81
Total per year	**768**	**949**	**501**	**2218**

a)

Lineage	Strains n (%)
1	32 (1.5)
2.2.1	636 (29.6)
2.1	2 (0.1)
3	63 (2.9)
4.1	390 (18.1)
4.2	199 (9.3)
4.3	183 (8.5)
4.4; 4.5; 4.6	77 (3.6)
4.7; 4.8	548 (25.5)
4.9	7 (0.3)
5	1 (0)
Unknown	13 (0.6)

b)

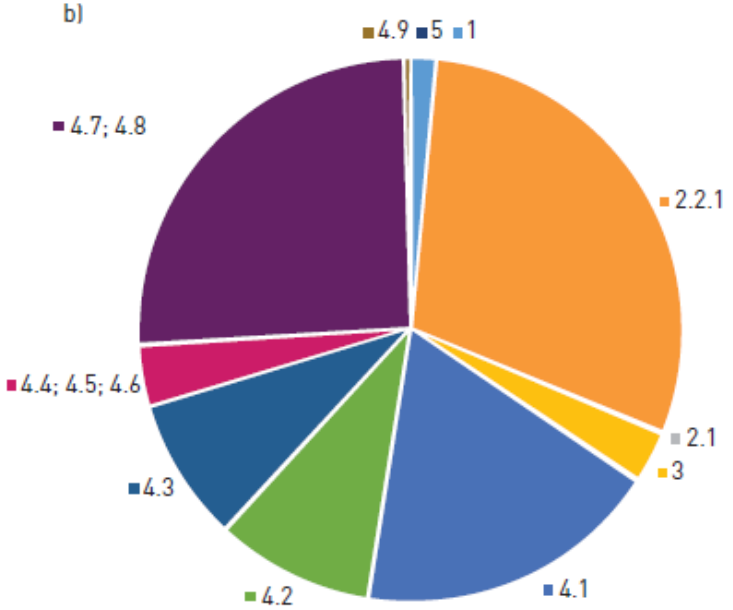


FIGURE 2 a, b) Lineage distribution of the 2151 rifampicin-resistant (RR)/multidrug-resistant (MDR) *Mycobacterium tuberculosis* complex (MTBC) isolates included in the EUSeqMyTB study. Lineages: 1: East-African Indian (EAI) (includes EAI and EAI Manila); 2: East-Asian (includes 2.2.1 Beijing and 2.1 East-Asian non-Beijing); 3: Delhi-CAS; 4.1: Euro-American (includes 4.1 and 4.1.2: Euro-American; 4.1.1: X-type; and 4.1.2.1: Haarlem); 4.2: Euro-American (includes 4.2 and 4.2.2: Euro-American; 4.2.1: Ural; and 4.2.2.1: TUR); 4.3: LAM; 4.4 (includes 4.4.1.1: S-type); 4.5: Euro-American; 4.6: Euro-American; 4.7: mainly T; 4.8: mainly T; 4.9: H37Rv-like; 5: West-Africa 1.

Mtb

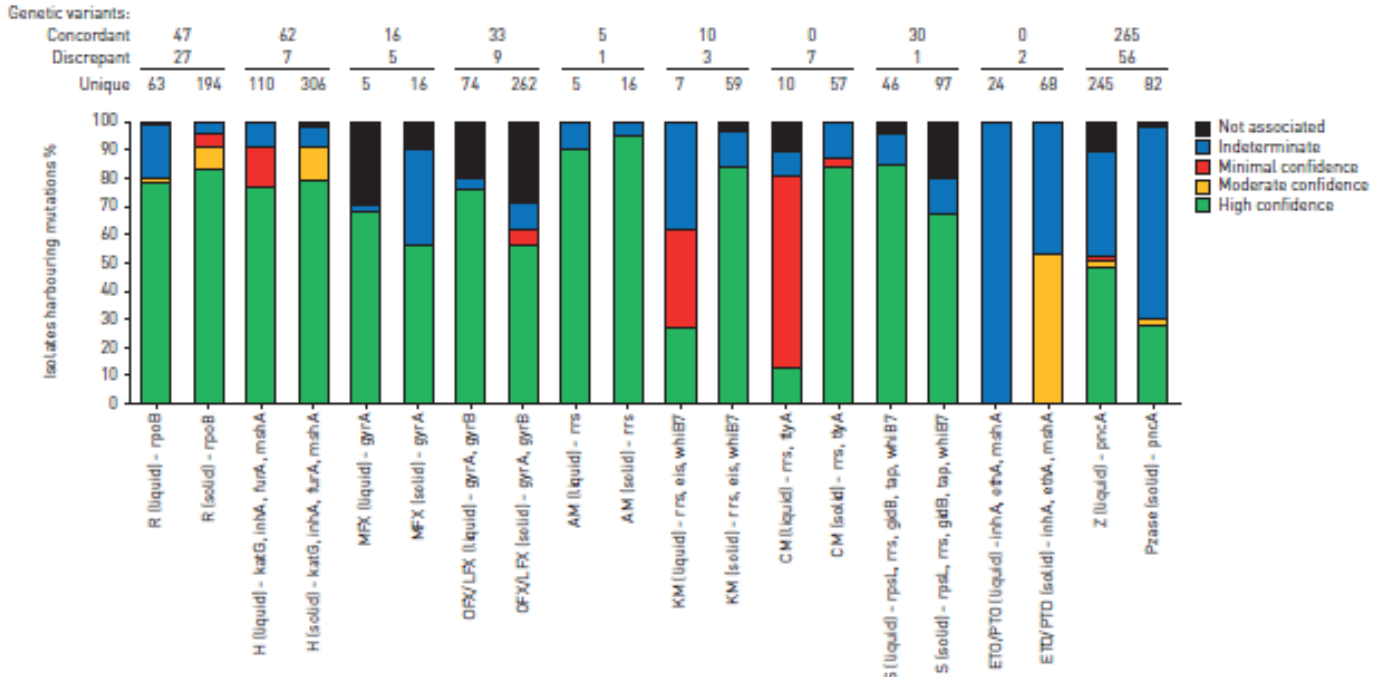
A standardised method for interpreting the association between mutations and phenotypic drug resistance in *Mycobacterium tuberculosis*

Miotto P et al. ERJ 2017

		Collected data		
	Loci of interest	Total isolates	Isolation time frame years	Countries represented
Rifampicin (R)	*rpoB*	13424	1999–2014	37
Isoniazid (H)	*katG*	11847	1992–2014	42
	inhA-mabA	9407		
	furA	361		
	mshA	288		
Ethionamide and prothionamide (ETO/PTO)	*inhA-mabA*	346		
	ethA	181		
	mshA	117		
Ofloxacin (OFX)	*gyrA*	5911	1991–2013	36
	gyrB	3078		
Moxifloxacin (MFX)	*gyrA*	1019		
	gyrB	735		
Levofloxacin (LFX)	*gyrA*	449		
	gyrB	218		
Pyrazinamide (Z)	*pncA*	4949	1990–2014	36
Streptomycin (S)	*rpsL*	3263	1985–2013	43
	tap	0		
	rrs	2598		
	whiB7	0		
	gidB	812		
Amikacin (AM)	*rrs*	2105		
Capreomycin (CM)	*rrs*	2533		
	tlyA	1854		
Kanamycin (KM)	*rrs*	1727		
	eis	2029		
	whiB7	56		

20 geni di resistenza/loci
286 mutazioni associate con la resistenza

VALORI MEDI DI CONFIDENZA TRA SENSIBILITA FENOTIPICA E GENI DI RESISTENZA/LOCI CON MUTAZIONI



Anche sulla base di questi risultati un report tecnico del WHO (2021) ha abbassato l'ECOFF per la rifampicina a 0,5mg/L e stabilito che un isolato di Mt con mutazioni nel «hotspot» del gene rpoB deve essere considerato resistente alla rifampicina, anche se è sensibile al test fenotipico

CRE

European Survey of carbapenemase-producing Enterobacteriaceae (EuSCAPE) 2013-2014

ECDC EVIDENCE BRIEF

November 2015

Update on the spread of carbapenemase-producing *Enterobacteriaceae* in Europe

RAPID COMMUNICATIONS

Colistin resistance superimposed to endemic carbapenem-resistant *Klebsiella pneumoniae*: a rapidly evolving problem in Italy, November 2013 to April 2014

M. Monaco[1,2], T Giani[2,3], M Raffone[1,4], F Arena[3], A Garcia-Fernandez[1], S Pollini[3], Network EuSCAPE-Italy[5], H Grundmann[6], A Pantosti (annalisa.pantosti@iss.it)[1], G M Rossolini[3,7,8]

Eurosurveillance, 2014

Occurrence of carbapenemase-producing *Klebsiella pneumoniae* and *Escherichia coli* in the European survey of carbapenemase-producing Enterobacteriaceae (EuSCAPE): a prospective, multinational study

Hajo Grundmann, Corinna Glasner*, Barbara Albiger, David M Aanensen, Chris T Tomlinson, Arjana Tambić Andrasević, Rafael Cantón, Yehuda Carmeli, Alexander W Friedrich, Christian G Giske, Youri Glupczynski, Marek Gniadkowski, David M Livermore, Patrice Nordmann, Laurent Poirel, Gian M Rossolini, Harald Seifert, Alkiviadis Vatopoulos, Timothy Walsh, Neil Woodford, Dominique L Monnet, and the European Survey of Carbapenemase-Producing Enterobacteriaceae (EuSCAPE) Working Group†*

Lancet Infect Dis., 2017

nature microbiology

ARTICLES

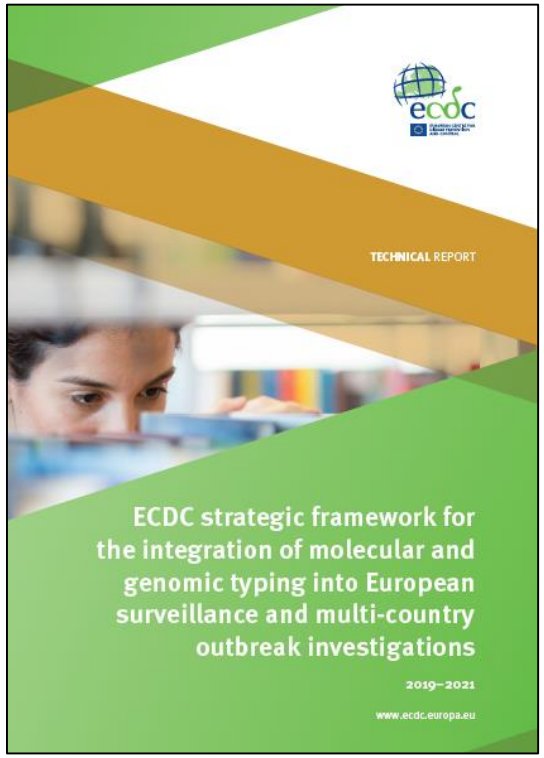
https://doi.org/10.1038/s41564-019-0492-8

Epidemic of carbapenem-resistant *Klebsiella pneumoniae* in Europe is driven by nosocomial spread

Sophia David[1], Sandra Reuter[2], Simon R. Harris[3], Corinna Glasner[4], Theresa Feltwell[3], Silvia Argimon[1], Khalil Abudahab[1], Richard Goater[1], Tommaso Giani[5], Giulia Errico[6], Marianne Aspbury[7], Sara Sjunnebo[8], the EuSCAPE Working Group[9], the ESGEM Study Group[10], Edward J. Feil[11], Gian Maria Rossolini[5,12], David M. Aanensen[1,13,14]* and Hajo Grundmann[2,4,14]*

Nature Microbiol, 2019

ECDC Road Map 2.1. Implementation of activities



Antimicrobial Resistance and Healthcare-Associated Infections Programme

- *Clostridium difficile*
- *Enterobacterales* carbapenem e/o colistina resistenti
- (C/CRE)

NEW
- *Acinetobacter baumannii* resistente ai carbapenemi (CRAB)
- *Staphylococcus aureus* resistente alla meticillina (MRSA)

NEW
- Outbreak di patogeni/plasmidi/cloni emergenti multiresistenti

CCRE

European Centre for Disease Prevention and Control
An agency of the European Union

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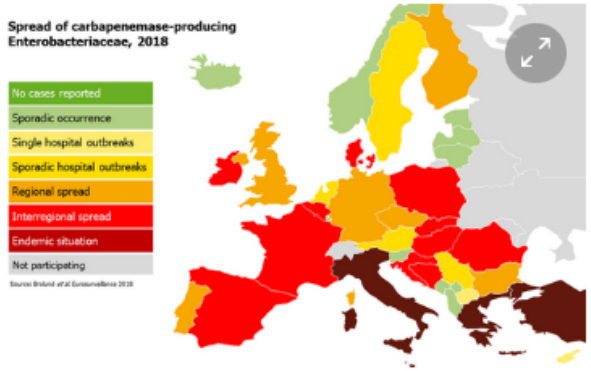
> European Antimicrobial Resistance Genes Surveillance Network (EURGen-Net)

European Antimicrobial Resistance Genes Surveillance Network (EURGen-Net)

The European Antimicrobial Resistance Genes Surveillance Network (EURGen-Net) is a network for genomic-based surveillance of multidrug-resistant bacteria of public health importance, coordinated by the European Centre for Disease Prevention and Control (ECDC). National reference laboratories or equivalent laboratories of 37 European countries currently participate in EURGen-Net.



The public health objectives of this European whole genome sequencing (WGS)-based surveillance are to determine the geographic distribution and population dynamics of multidrug-resistant clones and transmissible resistance elements to inform risk assessment, prevention and control polices and to support countries in developing technical capability and proficiency for genomic-based surveillance of multidrug-resistant bacteria with epidemic potential.

In 2019, the network starts its activity with a Europe-wide survey of carbapenem- and/or colistin-resistant Enterobacteriaceae (CCRE survey). A similar survey of carbapenem-resistant Acinetobacter baumannii is planned for 2020/21.

SORVEGLIANZA BASATA SU WGS
Obiettivi:
Determinare la distribuzione geografica e la dinamica di popolazione di

- Cloni multi-resistenti
- Elementi trasmissibili di resistenza

CCRE survey: carbapenem-and/or colistin-resistant *Enterobacteriaceae*

CCRE

Study protocol

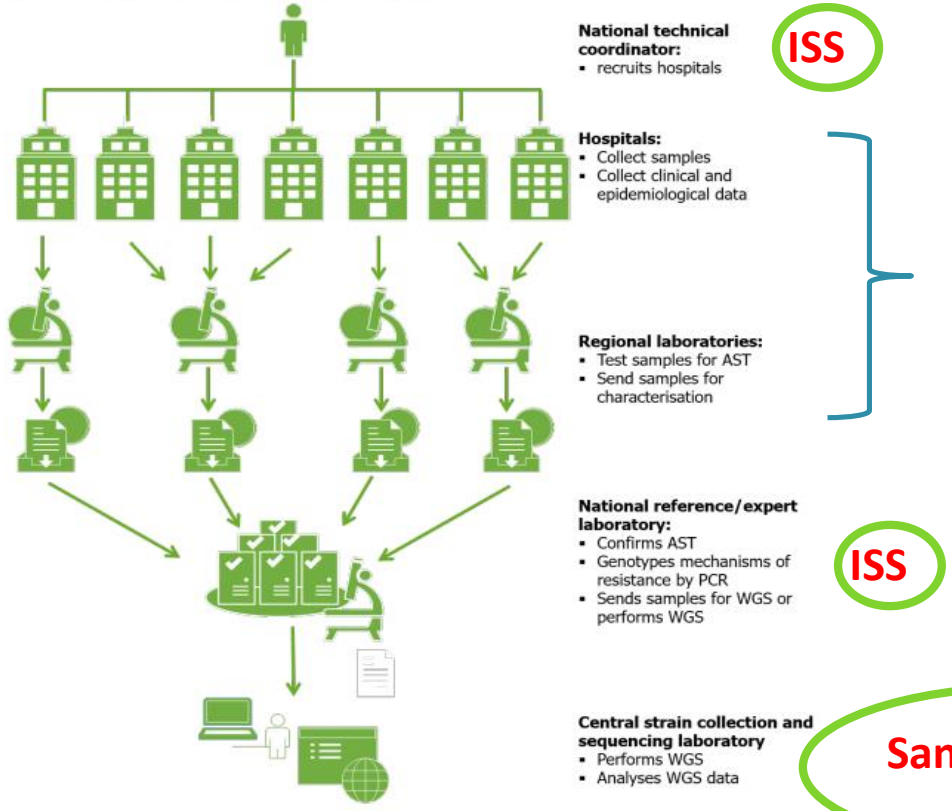
Study and surveillance design

The study design follows the EuSCAPE project model [7] and structured survey protocol. A stepwise workflow is performed in each country (Figure 1).

The proposed surveillance design is a structured and periodically repeated pan-European multicentre molecular epidemiological survey of the prevalence and distribution at the regional level of CRE and/or ColRE by genotype among patients seeking hospital care.

These surveys are expected to take place every three years, or more frequently as indicated by the epidemiological situation, and subject to resource availability at ECDC and national and regional levels.

Figure 1. National workflow for participation in EU-level genomic-based surveillance of carbapenem-resistant and/or colistin-resistant Enterobacteriaceae



AST: antimicrobial susceptibility testing; PCR: polymerase chain reaction; WGS: whole genome sequencing

Laboratori AR-ISS

Molecular survey of carbapenem-and/or colistin-resistant Enterobacterales (CCRE survey)

CCRE survey: current status

Country	Number of registered hospitals	Number of registered / received isolates	Country	Number of registered hospitals	Number of registered / received isolates
Albania	1	23	Latvia	1	8
Austria	9	50	Lithuania	4	20
Belgium	20	140	Luxembourg	4	15
Bosnia and Herzegovina	1	20	Malta	1	29
Bulgaria	11	184	Montenegro	1	19
Croatia	16	148	Netherlands	38	112
Cyprus	1	21	North Macedonia	3	28
Czechia	10	96	Norway	19	24
Denmark	5	11	Poland	27	123
Estonia	1	12	Portugal	7	104
Finland	20	26	Romania	11	138
France	18	120	Serbia	14	142
Germany	35	126	Slovakia	3	60
Greece	18	324	Slovenia	14	61
Hungary	10	76	Spain	26	440
Iceland	1	6	Sweden	10	84
Ireland	8	45	Turkey	28	408
Italy	46	605	United Kingdom	84	234
Kosovo	1	2	**Total**	**527**	**4084**

ECDC, preliminary data

Sorveglianza dell'antibioticoresistenza AR-ISS

Coordinamento ISS

Partecipazione di tutte le Regioni/Province autonome

Isolati invasivi (sangue e liquor) di 8 specie batteriche

Dati routinari prodotti dai laboratori

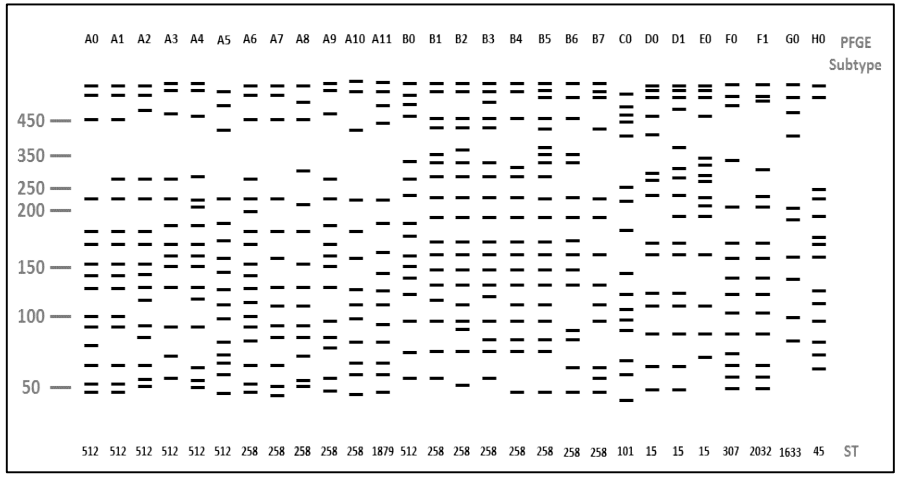
150 laboratori hanno trasmesso dati del 2019

Dati trasferiti alla rete europea Ears-Net

Molecular epidemiology of KPC-producing *Klebsiella pneumoniae* from invasive infections in Italy: increasing diversity with predominance of the ST512 clade II sublineage

Viola Conte[1], Monica Monaco[2], Tommaso Giani[1], Fortunato D'Ancona[3], Maria Luisa Moro[4], Fabio Arena[1], Marco Maria D'Andrea[1], Gian Maria Rossolini[1,5–7]* and Annalisa Pantosti[2] on behalf of the AR-ISS Study Group on Carbapenemase-Producing *K. pneumoniae*†

JAC 2016

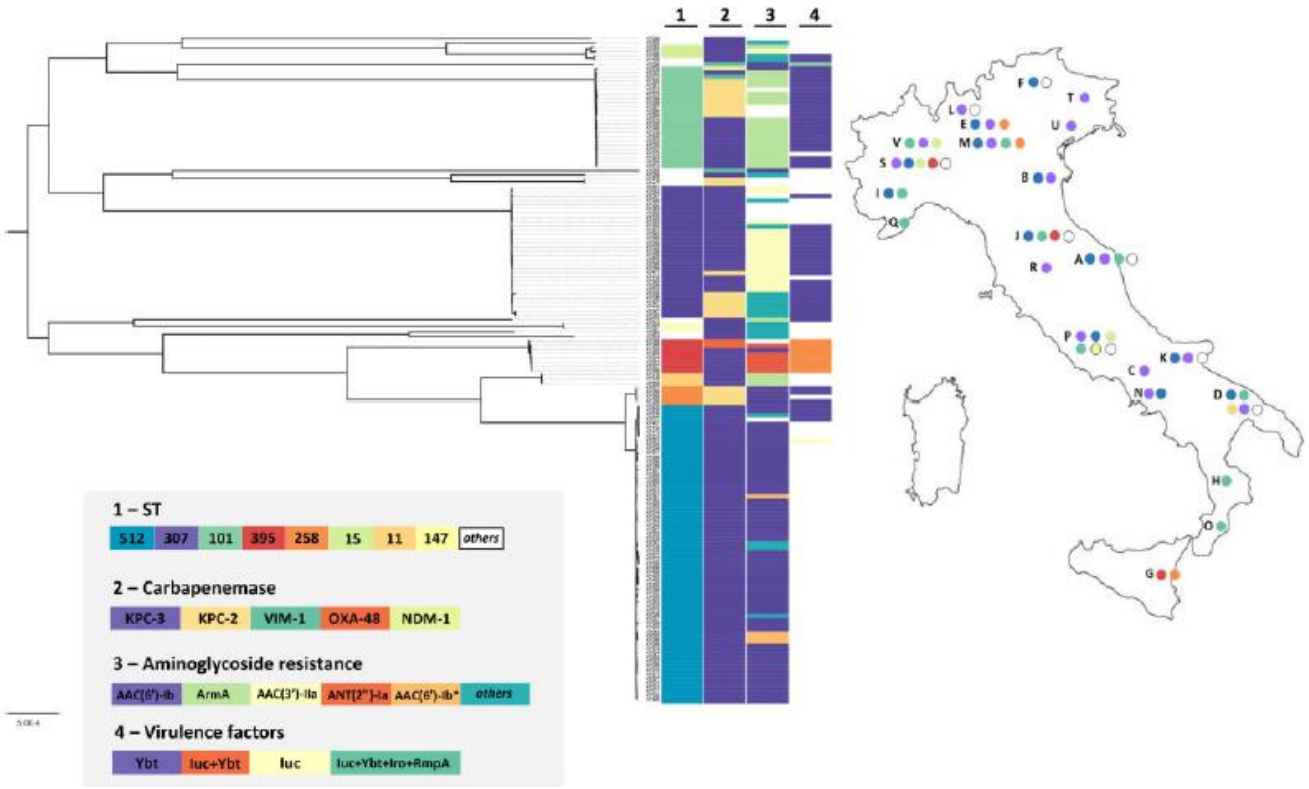


Profili PFGE profiles di 162 KPC-KP in combinazione con tipi MLST (ceppi 2011-2013)

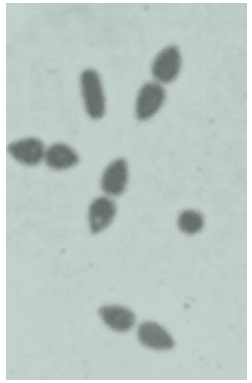
The changing epidemiology of carbapenemase-producing *Klebsiella pneumoniae* in Italy: toward polyclonal evolution with emergence of high-risk lineages

Vincenzo Di Pilato [1]†‡, Giulia Errico[2,3]†, Monica Monaco[2], Tommaso Giani[1,4], Maria Del Grosso[2], Alberto Antonelli [1], Sophia David[5], Erika Lindh[2,3], Romina Camilli[2], David M. Aanensen[5,6], Gian Maria Rossolini[1,4] and Annalisa Pantosti[2]* on behalf of the AR-ISS Laboratory Study Group on carbapenemase-producing *Klebsiella pneumoniae*§

JAC 2020



Diversità genetica dei ceppi di K. pneumonia produttori di carbapenemasi e distribuzione nei laboratori partecipanti allo studio (ceppi 2016)



RESISTOMA di 27 ceppi di *Streptococcus pneumoniae* sierotipo 24F resistenti a penicillina e/o eritromicina mediante WGS

N° isolates	ST	CC	Acquired AMR genes	PBP profiles (n° isolates)	Capsular variant	Resistance Phenotype
17	230	230	erm(B) tet(M)	17:15:22 (13) IT1a:15:22 17:15:77 17:53:22 17:15:IT1b	24F	PEN ERI CLI TET
2	230	230	erm(B)	17:15:22	24F	PEN ERI CLI
1	230	230	erm(B) tet(M) aac(6')-aph("2)	17:15:22	24F	PEN ERI CLI GEN/AMK
1	6227	230	erm(B) tet(M)	17:15:22		PEN ERI CLI TET
5	162	156	erm(B) tet(M)	2:0:363	24F (+ 15 nt)	ERI CLI TET
1	New	72	mef(A) msr(D)	2:0:0		ERI

(manuscript in preparation)

MICROBIAL GENOMICS

OUTBREAK REPORT

Arena *et al.*, *Microbial Genomics* 2020;6

DOI 10.1099/mgen.0.000308

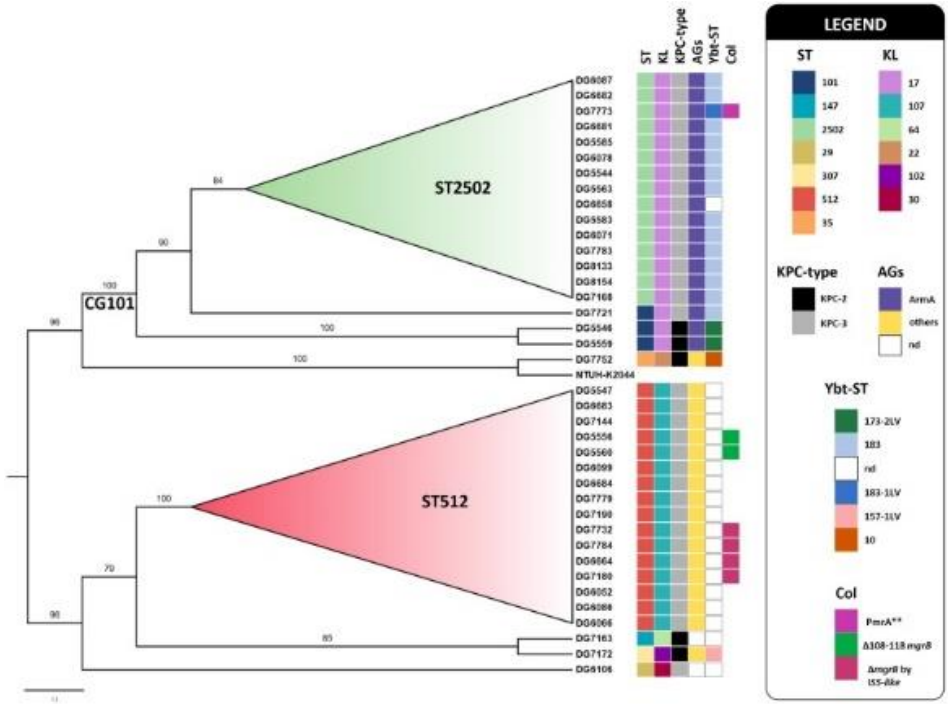
MICROBIOLOGY SOCIETY

OPEN DATA OPEN MICROBIOLOGY

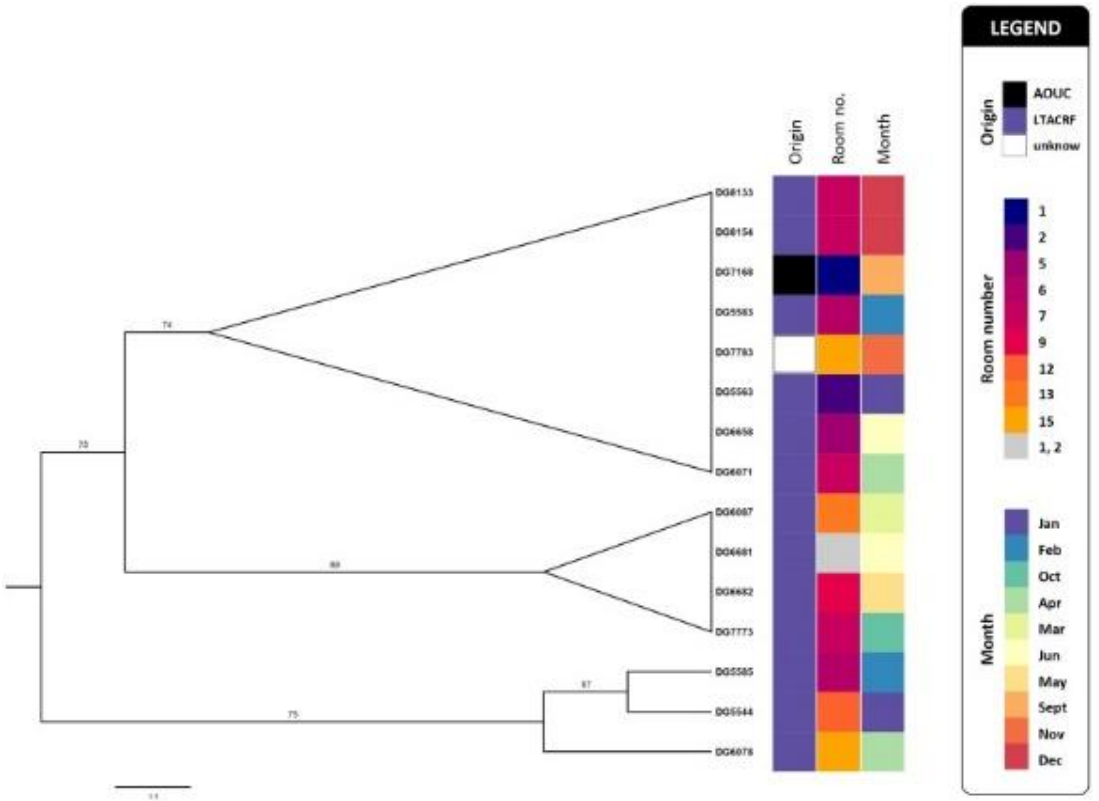
Population structure of KPC carbapenemase-producing *Klebsiella pneumoniae* in a long-term acute-care rehabilitation facility: identification of a new lineage of clonal group 101, associated with local hyperendemicity

Fabio Arena[1†,‡,§], Vincenzo Di Pilato[2†,#], Federica Vannetti[3], Laura Fabbri[3], Alberto Antonelli[2], Marco Coppi[2], Roberto Pupillo[3], Claudio Macchi[3] and Gian Maria Rossolini[2,4,*]

Ceppi di *K. pneumoniae* KPC isolati nel 2016 in una grande RSA



Origine dei ceppi ST2502



Center for Genomic Epidemiology

Home Services Publications

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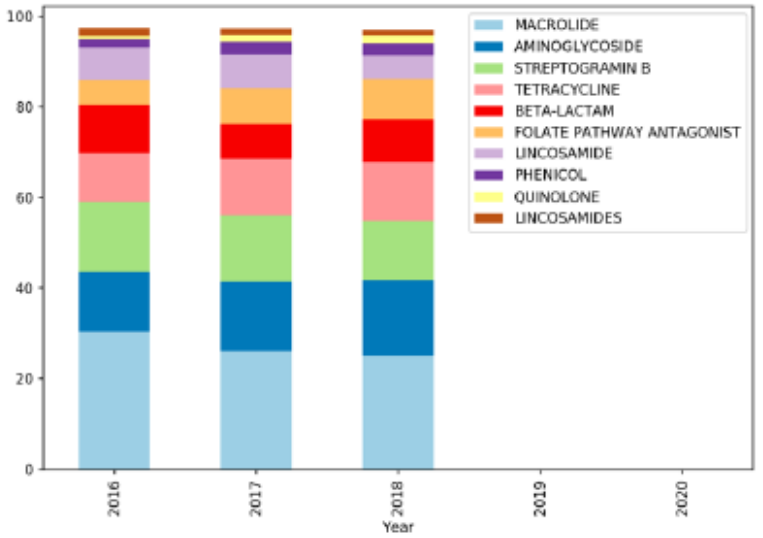
Global Surveillance of Antimicrobial Resistance

The multidisciplinary Center will work from the hypothesis that metagenomic sequencing of human sewage can be used to detect, and in combination with epidemiological / ecological modeling, explain and predict emergence and trends of AMR.

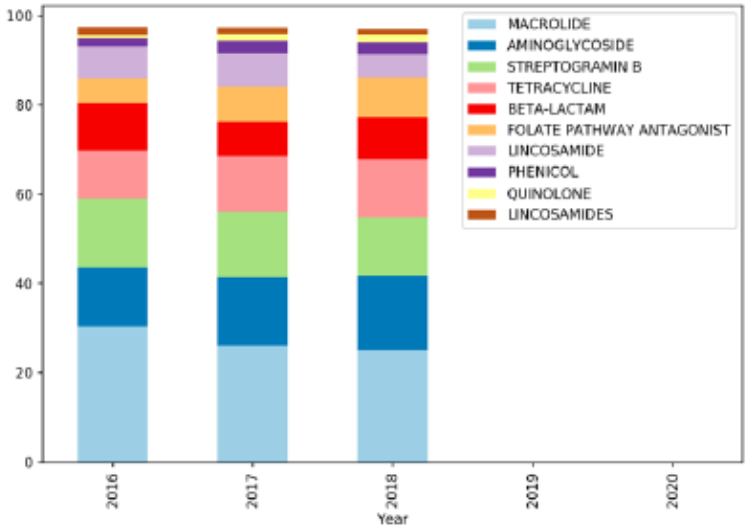
Global-Surveillance-of-Antimicrobial-Resistance

SORVEGLIANZA MEDIANTE METAGENOMICA DELLE ACQUE REFLUE DI ORIGINE UMANA IN COMBINAZIONE CON MODELLISTICA EPIDEMIOLOGICA ED ECOLOGICA PER RICONOSCERE ED ANTICIPARE EMERGENZE E TREND DI AMR

RESISTOMA GLOBALE PER ANNO DI CAMPIONAMENTO



RESISTOMA GLOBALE PER AREA GEOGRAFICA



Conclusioni

1. LA RIVOLUZIONE «OMICA» STA PORTANDO ENORMI CAMBIAMENTI NELLA CONOSCENZA DEI FENOMENI BIOLOGICI E SOPRTTUTTO DEL MONDO DEI MICRORGANISMI
2. LA GENOMICA STA DIVENTANDO LO STANDARD PER STUDI DI OUTBREAK E APPROFONDIMENTI DI SORVEGLIANZE
3. CI SONO RICHIESTE DI IMPLEMENTAZIONE DA PARTE DI WHO e ECDC
4. LE ATTIVITA' E GLI APPROCCI DEL MICROBIOLOGO DOVRANNO RAPIDAMENTE CAMBIARE
   - COMPETENZE MULTIDISCIPLINARI
   - E' NECESSARIO MANTENERE LE COMPETENZE DI MICROBIOLOGIA CLASSICA E DI EPIDEMIOLOGIA
5. LA STRUTTURA DEI LABORATORI DEVE ESSERE ADATTA ALLE NUOVE ESIGENZE
   - **STORAGE DEI DATI E DATABASE INTEGRATI PER LE SORVEGLIANZE**
6. SONO NECESSARI INVESTIMENTI ADEGUATI PER STRUTTURE, APPARECCHIATURE E FORMAZIONE PERSONALE

Uno sguardo al futuro prossimo

1. IL COSTO DI WGS STA DIVENTANDO SEMPRE PIU' BASSO
2. E' SEMPRE PIU' CONVENIENTE UTILIZZARLO PER TIPIZZAZIONE ANZICHE' ALLESTIRE DIVERSI TEST E NUMEROSI SAGGI DI PCR
3. RAPPRESENTA IL GOLD STANDARD PER LO STUDIO DI OUTBREAK COMUNITARI E OSPEDALIERI PER LA SUA SENSIBILITA' RAPIDITA' E COMPARABILITA
4. PER LE SORVEGLIANZE, SOPRATTUTTO DI PATOGENI MDR, SI PASSERA' DA «STUDI AD HOC» ALLA SORVEGLIANZA ROUTINARIA
5. STUDI DI METAGENOMICA AMBIENTALE PER INTERCETTARE RESISTENZE EMERGENTI PRIMA CHE DIVENTINO CLINICAMENTE RILEVANTI

Il futuro

1. LE SCIENZE «OMICHE» SARANNO PIU' ABBORDABILI TECNICAMENTE
2. LA DIAGNOSTICA SI BASERA' SULLA METAGENOMICA DEL SITO INFETTO
3. LA SORVEGLIANZA INTEGRERA' GENOMICA BATTERICA CON GENOMICA/PROTEOMICA UMANA DEL SOGGETTO INFETTO (PER LA IDENTIFICAZIONE DEI FATTORI DI RISCHIO, PREVENZIONE, TERAPIA, VACCINI ECC.)

LA TRANSIZIONE OMICA E' GIA' INIZIATA