Criteri di scelta dei metodi diagnostici da utilizzare in sanità animale per la concessione e il mantenimento dello status di indenne da malattia
Ricerca del virus dell'epatite A negli alimenti
Ricerca del virus dell'epatite E negli organi e tessuti animali
Diagnosi sierologica della brucellosi nei ruminanti
Metodi di prova per la determinazione della sensibilità dei batteri agli antimicrobici
Meccanismi di sviluppo dell'antibioticoresistenza nei batteri

Ricerca di anticorpi e antigeni mediante test ELISA
Diagnosi diretta di agenti virali
Tecniche di metagenomica per l'analisi del microbiota
Numerazione di microrganismi patogeni negli alimenti
Test di sieroneutralizzazione per la ricerca di anticorpi
Test di fissazione del complemento: principi e controlli

Metodi di analisi per la ricerca di organismi geneticamente modificati
Vantaggi e svantaggi nell'impiego dei diversi metodi di biologia molecolare (MLVA, PFGE, MLST) per la tipizzazione batterica
Principi e applicazione dei microarray in microbiologia
Tecniche di tipizzazione molecolare dei batteri
Applicazione dei dati del sequenziamento genomico per il controllo delle malattie trasmesse dagli alimenti
Applicazione dei dati del sequenziamento genomico per il controllo delle malattie trasmissibili degli animali

Diagnostica degli aborti nei ruminanti
Fasi delle analisi bioinformatiche a partire da dati di Next Generation Sequencing (NGS)
Le principali attività di laboratorio per la ricerca di Clostridium botulinum negli alimenti
Principali geni di virulenza degli Escherichia coli verocitotossici
Ricerca di anticorpi mediante western blotting

Responsabilità e compiti dei laboratori nazionali di riferimento
Responsabilità e compiti dei laboratori di riferimento dell'Unione Europea
Responsabilità e compiti degli Istituti Zooprofilattici Sperimentali
Scopo e campo di applicazione del manuale della qualità
Obiettivi e principi dell'accreditamento dei laboratori
Principali elementi che caratterizzano la gestione delle apparecchiature di laboratorio

Principali voci che compongono il budget di una struttura organizzativa
Atteggiamenti professionali e comportamentali da tenere nella gestione del personale assegnato
Gestione dei materiali di consumo di un laboratorio all'interno di un ciclo di programmazione
Controllo qualità dei terreni di coltura
Principali fonti di finanziamento destinati alla ricerca negli Istituti Zooprofilattici Sperimentali
Composizione e funzioni del consiglio di amministrazione dell'Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise

Principali caratteristiche di un sistema informativo per la gestione dei dati di laboratorio
Criteri per il trasporto e conservazione dei campioni biologici
Principali informazioni da riportare in un MTA (Material Transfer Agreement)
Come redigere una relazione tecnica di un progetto di ricerca
Come redigere un progetto di ricerca
Gestione del rischio biologico nei laboratori

Norme di comportamento da seguire in un laboratorio microbiologico con livello 3 di biosicurezza
Impiego dei materiali di riferimento nei laboratori di prova

1. Whole-genome sequencing (WGS) provides a vast amount of information and the highest possible resolution for pathogen subtyping. The application of WGS for global surveillance can provide information on the early emergence and spread of AMR and further inform timely policy development on AMR control. Sequencing data emanating from AMR surveillance may provide key information to guide the development of rapid diagnostic tools for better and more rapid characterization of AMR, and thus complement phenotypic methods.

2. Data on antimicrobial-resistant pathogens are essential to inform public health policy and to monitor the effectiveness of interventions. Currently, AMR surveillance relies mainly on microbiological characterization of isolates and phenotypic antimicrobial susceptibility testing (AST). Addition of molecular methods can in some cases provide better understanding of the mechanisms of resistance and the relatedness of strains for investigating the emergence and spread of AMR. (64)

3. Molecular diagnostic tests for AMR are becoming available for use in surveillance, as outlined in a previous WHO document. WGS can be used to identify and characterize pathogens rapidly and precisely. When combined with epidemiological information, it can facilitate linkages during the early detection phase of outbreaks, accurate tracing of transmission chains, precise delineation of the geographical spread of an outbreak and identification of sources of infection. (68)

4. Whole-genome sequencing (WGS) offers a vast amount of information and the highest resolution for molecular subtyping of pathogens. When used to answer specific questions, it could further strengthen AMR surveillance. During the past decade, WGS has transformed biomedical research and could transform epidemiological surveillance of pathogens and aid clinical decision-making on infectious diseases and the treatment of individual patients (“precision medicine”). (62)

5. New microbial genomes are sequenced daily and added to large databases of genome and gene sequences. Improvements in sequencing technologies and analysis have rapidly increased the output and speed of analysis and reduced the overall cost of WGS (9), although price reduction has slowed down, and proprietary tools may still be costly. Epidemiological data on antimicrobial-resistant pathogens are essential to inform policy and to monitor the effectiveness of interventions. (70)

6. The first step in deciding which tests should be available for AMR surveillance is to define the objectives, which should advance strategies to tackle AMR. Objectives such as analysis of trends in AMR rates, assessment of the frequency of AMR infections and their impact on human health, data to inform the national list of essential antimicrobial medicines and data to inform treatment guidelines can be fully met by using phenotypic methods. (72)

7. WGS can be used to identify and characterize pathogens rapidly and precisely. When combined with epidemiological information, it can facilitate linkages during the early detection phase of outbreaks, accurate tracing of transmission chains, precise delineation of the geographical spread of an outbreak and identification of sources of infection. Timely outbreak detection and removal of sources of infection can lead to substantial cost savings in public health. (67)

8. WGS data are digital, and tests are done on computer systems. Consequently, use of WGS enables better standardization and reproducibility, providing greater interlaboratory comparability than phenotypic testing. The fact that sequence data are digital and different algorithms can be used to analyse the same set of data also means that old data can be re-analysed, ensuring backward compatibility between new and old analyses. (64)

9. Predictions of AMR based on sequence data can be triangulated by comparison with archived sequences with AST results. If an isolate has the same or a similar sequence as that of a previously seen isolate and AST data indicate that the previous isolate was resistant, this provides additional confidence in the predicted AMR and builds a virtuous cycle of evidence that can ultimately be of direct clinical relevance. (69)

10. WGS is useful for analysing individual isolates with complex antimicrobial susceptibility profiles or multiple isolates with considerable genetic heterogeneity in the same AMR phenotype to determine the mechanism of AMR. In outbreaks, in which isolates with the same AMR phenotype have highly similar underlying genotypes and resistant isolates of the same strain, WGS can be used to infer the relatedness among isolates and hence transmission chains. (67)

11. A major limitation of WGS as compared with other molecular methods is the high initial and recurrent investment and the complex technological and infrastructure requirements. For example, targeted sequencing or screening PCR, rather than WGS, can be effective for rapid sequencing of pathogen genes directly from clinical samples and when the presence of specific genes must be confirmed or excluded rapidly.

12. The sensitivity and specificity of WGS-based AMR prediction will fluctuate over time, as more AMR mechanisms are discovered. Ongoing research and the expansion of surveillance databases with WGS and AST data will eventually increase the sensitivity of genotypic AMR predictions to the degree required for clinical and public health decision-making. Phenotypic data will still be required, however, to detect emerging mechanisms of AMR. (64)

13. The economic advantages of WGS for AMR surveillance have not yet been proven unequivocally. The cost of establishing one or more WGS laboratories depends on existing laboratory facilities and the country. Not every country requires WGS facilities in order to participate in AMR surveillance that includes WGS. The cost of setting up a new WGS laboratory depends on the intended sequencing capacity, whether culture facilities are required, space requirements and available public infrastructure. (74)

14. WGS is used in many different applications in medicine and biomedical research and is not restricted to AMR surveillance or pathogen genomics, unlike phenotypic AST, which is performed only in AMR surveillance and clinical microbiology. Consequently, the market forces that are driving down the cost of WGS technology should be much stronger than for phenotypic methods, and the prices are expected to decrease faster. (65)

15. A limited number of isolates can be studied by WGS in laboratories established for local pathogen typing and surveillance. Laboratories should have experience in microbiological methods and the capacity to isolate bacteria from clinical specimens and isolate DNA. Personnel must be trained in WGS and bioinformatics. Contamination must be avoided to obtain meaningful results and should be assessed and verified when analysing the WGS data with software such as Kraken. (70)

16. Individual isolates from a single site (such as a hospital, a health care centre or a city) can be analysed by WGS to identify AMR genes and determine whether there is transmission. The genome sequences of several isolates from the same clinical centre can be compared to confirm whether a local outbreak has occurred, allowing the design of strategies to manage it. (62)

17. RRLs and NRLs should maintain not only global reference databases for typing pathogens and identifying AMR genes but also their own databases of the epidemiology of AMR organisms in their area that link WGS data to relevant phenotypic AST data and epidemiological and clinical metadata. Data from WGS of isolates from different geographical sites can be used to infer mechanisms of AMR acquisition, clustering of different strains and transmission routes. (70)

18. International use of WGS requires high-throughput sequencing instruments, advanced laboratory infrastructure and teams of highly trained personnel who can efficiently handle and process samples of various pathogens from various sites, which may require different methods of handling, sequencing and analysis. It also requires sufficient storage capacity and plans for data-sharing according to international protocols. Experience in conducting large-scale, structured epidemiological surveys will be necessary but can be supplied by external groups. (72)