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CLINICAL OUTCOMES OF VIRAL RESPIRATORY INFECTIONS AMONG IMMUNOSUPPRESSED INDIVIDUALS

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ABSTRACT

Viral respiration infections (VRIs) pose an enormous danger to immunocompromised sufferers, which includes cancer sufferers and recipients of hematopoietic stem cellular transplants, leading to high morbidity and mortality globally. These infections, because of pathogens consisting of influenza viruses, coronaviruses, respiration syncytial virus (RSV), and rhinoviruses, variety from slight top respiration tract infections to excessive lower breathing tract headaches. Immunocompromised people, along with the aged and younger children, are mainly at risk of severe results. The financial and clinical burden of VRIs is sizeable, exacerbated through demanding situations in diagnosis and management. Traditional diagnostic methods, including viral culture and serology, offer specificity but are restricted by means of gradual turnaround times and decrease sensitivity. Advances in molecular technique, including next-generation sequencing (NGS), polymerase chain reaction (PCR), and real time PCR, have revolutionized the detection of respiration viruses by providing fast, accurate and high- through put consequences. These technology enable early prognosis, essential for timely intervention and outbreak manipulate. However, demanding situations including price, technical complexity, and the need for nonstop updates to stumble on viral mutations persist. This review highlights the importance of integrating speedy screening checks with confirmatory molecular assays to stability pace and accuracy, mainly in aid - constrained settings. Emerging point of care technologies and the ability of synthetic intelligence in diagnostics ate also discussed. Strengthening global surveillance networks and improving public health guidelines are vital to mitigating the effects of VRIs. Future efforts ought to consciousness on growing low cost diagnostics, vast- spectrum antivirals, and powerful vaccines to guard vulnerable populations and decrease the world wide burden of respiratory viral infections.

Key words: Viral, Respiratory, Infection, Immunocompromised, Molecular Diagnostics, Mass Spectrometry.

1. INTRODUCTION

Among the most common mischievous issues in cancer cases and/ or donors of hematopoietic stem mobile transplants, infections constitute a principal trouble to the lives of vulnerable compromised

people (Vliora, Papadakis et al. 2019). Immune- compromised humans, the aged, and youthful youths are especially prone to breathing infections, which could variety from minor or asymptomatic ails to violent and reality-hanging issues. The maturity of deaths and ails encyclopedically is caused by respiratory infections, which also area a considerable profitable and clinical burden on health systems. (Zhang, Akmar et al. 2020). Viral respiratory infections disproportionately affect children (Pavia 2011). According to studies, the primary cause of death and morbidity in children under five is viral Tics (Lafond, Nair et al. 2016). They generally beget benign, tone-limiting upper respiratory tract infections (URTIs) in healthy children (Tregoning and Schwarze 2010, Meissner 2016). Still, people with weakened vulnerable systems, especially those entering transplants, are more susceptible to serious infections (Campbell, Guthrie et al. 2015). While rare or unusual pathogens or accidental contact may trigger infections of the airways, community respiratory viruses typically results in hospitalizations for these individuals (Fisher, Danziger-Isakov et al. 2018).

The respiration system is made from some of the organs which are divided into drop airlines (bronchi, bronchioles, and lungs) and upper breathing tracts (nasal concave space, pharynx, larynx, and trachea). An important thing of ingrain impunity, the epithelial cells that cover the inside of these organs offer an energetic physical hedge against infections. The maturity of mortal contagions enter the frame via the respiration contrivance, along with via aerosols released through other lit hosts once they cough or sneeze (Shors 2009, Flint, Racaniello et al. 2020). Mortal respiratory contagions include a wide variety of contagions that infect breathing tract cells, beget respiratory signs and symptoms, and are more frequently than not unfold by using the respiratory concealment of lit people. In clinical setting, it is frequently impossible to differentiate between respiratory contagious diseases. Respiratory infections are members of a group that is distinguished by its infections and genetic armature, susceptible communities, complaint inflexibility and paths of administration different families of contagion. When combined, they significantly increase morbidity,,(James, Lucchesi et al. 2020), morality and attendant profitable losses annually worldwide. Among the many crucial key factors in containing a new epidemic is the complaint's transmissibility, or how easily it will spread from a carrier to a susceptible one. A susceptible contact person's airways may get infected when a contagion is released from a contaminated individual's respiratory system and travels through environment. People may acquire respiratory infections in this way. Viral, host, and environmental factors can alter the liability of transmission through a variety of distinct pathways (or modes) (Leung 2021). Respiratory contagions can spread through respiratory concealment in a number of ways, both singly and coincidentally. It is known that respiratory infections may propagate in two ways: through close contact between an infected person (also referred to injector) along with a vulnerable person (also referred to infected), laterally via exposure to objects or shells that have been defiled, or instantly by airborne germs to one person's lungs to the next via massive respiratory driblets or fine respiratory aerosols.(Brankston, Gitterman et al. 2007, Killingley and Nguyen-Van-Tam 2013)

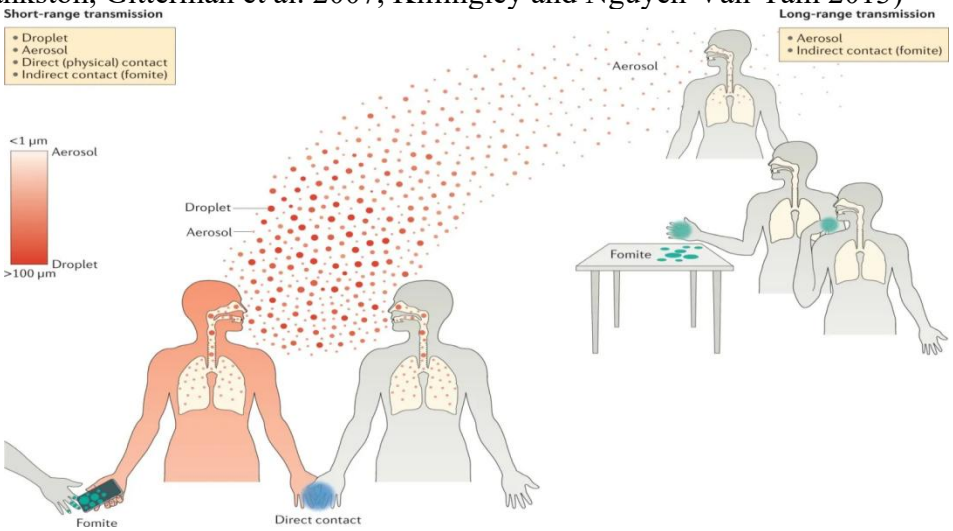

Figure 1: Significant respiratory viral transmission pathways, including short- and long-range,

an infected person (infector) can spread viruses by inhaled droplets and aerosols, contamination objects and surfaces during and acute respiratory viral infection. The virus can spread to susceptible people either locally through direct touch or inhalation of droplets, or over large distances through aerosols and contaminated surfaces. The classification of transmission modes, particularly regarding the size threshold between droplets and aerosols, is currently being debated.(Leung 2021).

2. RESPIRATORY AFFECTING VIRAL INFECTION

One of the most vital international fitness problem that affect individuals of all ages worldwide is virus-caused respiration infections, which lead to both mortality and morbidity. Viral infections can set off acute respiration sickness that simply have an effect on the top airlines or that also affect the lower respiratory tract. Viral infections can result in chronic respiratory conditions that generate significant financial burdens. (Kurai, Saraya et al. 2013, van Doorn and Yu 2020).

2.1 Influenza virus (A)

The Orthomyxoviridae family, which comprises influenza contagions, is divided in to four rubrics: influenza A, B, C, and D. To organize particular rubrics, antigenic interpretations between matrix 1 (M1) protein and nucleoprotein (NP) are utilized (Hause, Collin et al. 2014). IAV can spread to people. However, the main cause of reoccurring epidemic complaints and worldwide aliments each year is type A. (Peteranderl, Herold et al. 2016, Paules, Marston et al. 2017). Even while IAV may generate a one hundred nm spherical or filament structure with a 20 micro cadence length, the filaments form is significantly diminished. Influenza causes both lower and upper RTIs with colorful clinical instantiations similar as pneumonia, tracheobronchitis, sinusitis, and otitis media.

2.2 Coronaviruses

The corona virus are broad family of single stranded, enclosed, positive sense, spherical or pleomorphic RNA viruses with unique virion shape. in addition these infections may occasionally results in severe bronchiolitis and pneumonia in immune compromised people, the elderly, young children and new born (Liu, Liang et al. 2021). SARCoV2, another transmissible virus of the coronavirdae genus that can affect the lungs, was discovered globally in 2019 and caused an additional worldwide pandemic and high-mortality disease known as COVID-19. Similar to SARS-CoV, MERS-CoV infection is linked to great mortality, greater- pulmonary involvement, and extreme LRIs (Chan, Lau et al. 2015).

2.3 Respiratory syncytial virus (RSV)

RSV is a single-stranded virus that is a member of the paramyxoviriade family. Pulmonary syncytial infection is the most common cause of pediatric pneumonia in children. Morbidity and demise are more in early infants, infants with heart problems, and victims with inordinate vulnerable compromised conditions (Hall, Simões et al. 2013). Of all respiratory illness caused by viruses, RSV was the second most common cause, accounting for 31% cases (Hakim et al., 2016). RSV LRTI is linked to fatalities and long-term hospitalizations. A number of risk factors for RSV LRTI have been identified (Chemaly, Shah et al. 2014, Kim, Guthrie et al. 2014). RSV begins to replicate in the nasopharynx and spreads to the bronchiolar epithelium, most likely by aspiration of secretions or cell-to-cell transmission. The contagion spares the rudimentary cells and latterly extends to the alveolar pneumocytes.

2.4 Rhinovirus

The RhVs are members of the family Picornaviridae and fall under the category Enterovirus. They are divides in to three distinctive genetic groups, A, B, C. They are positive-sense, single-stranded RNA viruses. One peptide encoded by the genome is attaches to seven non-structural amino acids and four protiens with structure (VPI-4). With more than 100 variants identified to date, RhVs differ antigenically (Greenberg 2011, Jacobs, Lamson et al. 2013). The rhinovirus has been identified as the most prevalent respiratory infections found in susceptible children undergoing HCT (Loria, Domm

et al. 2015, Fisher, Danziger-Isakov et al. 2018), with an circumstance as inordinate as 22, Three % by way of day a hundred (Milano, Campbell et al. 2010). Rhinoviruses are the maximum common place etiologic marketers of common place cold. They are responsible for between one-third and half of all adult upper respiratory tract infections reported each year. In healthy individualities, rhinoviruses infections are generally restrained to the top breathing tract with rhinorrhea and nasal inhibition being the maximum distinguished signs and symptoms (Kennedy, Turner et al. 2012).

3. METHODOLOGY

Respiratory contagions(RVs), account for about eighty of acute breathing affections, are a many of the maximum essential mortal microorganism that are causing the tremendous death and morbidity global (Larios, Coleman et al. 2011). Nowadays, From nasal tissues, epithelial cells with cilia or cell-free pathogens have been extracted, (Ngaosuwankul, Noisumdaeng et al. 2010, Irving, Vandermause et al. 2012, Frazee, de la Guardia et al. 2018) throat, (Jin, Wu et al. 2014, Ali, Han et al. 2015) mid-turbinate, (Faden 2010, Bell and Selvarangan 2014) nose-throat,(Ortiz de la Tabla, Masiá et al. 2010), oropharyngeal (Holter, Müller et al. 2015) and nasopharyngeal swabs (Goyal, Prasert et al. 2017). The NPS gathered by a medical professional is the gold standard for RV testing, as a significant and practical method of integrating circular and direct attestation.
(Giacoppo, Gargiulo et al. 2015).

3.1 Conventional laboratory techniques for diagnosing viral infections

For many years, clinical labs have considered a variety of methods for identifying viral infections. For a long time, advanced nations have regarded electron microscope (EMs) as a useful instrument for directly detecting infectious diseases by visualizing and counting viral dribbles in body fluids, excrement, or histopathological samples. Embroyonated ova and lab animals were employed to insulate contagious in the 1900s. In order to obtain cells appropriate for insulating contagious, cell cultures are typically created from tissue samples and them broken down using mechanical, chemical, and enzymatic methods. Cells can be insulated from tissues for ex vivo culture in several ways. Every cell type has a wide range of culture circumstances, and changes to the circumstances for a given cell type can result in a variety of morphologies. (Hematian, Sadeghifard et al. 2016). There are three types of cell cultures Primary Cells,Semi-Continous Cells and Continous Cells.

3.2 Current techniques for diagnosing viral infections

As previously said, this review will outline the primary benefits and drawbacks of the diagnostics technology advancements that have ushered in the modern era of clinical virology will be summarized in Table 1.

3.2.2 Amplification-based assays

The diagnostics virology lab employs a variety of NAAT techniques, such as PCR, RT-PCR, real-time RT-PCR, pyrosequencing, conventional Sanger sequencing, PCR in conjunction qith mass spectrometry, and microarrays, to analyze the viral causes of respiratory infections.

1. Polymerase chain reaction

Although there are noteworthy exceptions, the majority of commercial rRT –PCR technologies show similar efficacy in identifying respiratory viruses (Pillet, Lardeux et al. 2013). Human rhinovirus and human enterovirus cannot be consistently distinguish from one another using conventional techniques aimed at the 5'UTR of HRV. Additionally, certain HRV and human adenovirus variants may be difficult for commercial rRT –PCR techniques to identify with high efficiency (Anderson, Werno et al. 2013). Nested PCR is typically more sensitive, but at the expences of an increased risk of infection. It involves two PCR operations carried out consecutively with one target located 3' according to of the initial primed set. (Quan, Briese et al. 2008, Mahony 2010). Multiplex PCR allows for the concurrently identification of numerous respiratory viruses in comparison to single-plex or duplex test. Along with influenza agents will also be catagorised (Szewczuk, Thapa et al. 2010).

2. High resolution melting analysis

The primary basis for HRM evaluation is the dissociation behavior of DNA, which changes from double-stranded structure when a DNA interfering agent is present. HRM assessment is able to identify pathogens by identifying variations in PCR amplicons according to their cycle duration, base arrangement, and strand base pairing, Detection of pathogens, species, and sequencing can all be done with HRM assessment (Varillas, Bermejo-Martin et al. 2011, Kalthoff, Beer et al. 2013). By identifying the His275Tyr alteration, SNP detection can be utilized to determine antiviral resistance in a further influenza type (Tong, Dakh et al. 2011).

3. Loop-mediated isothermal amplification

Detection of pathogens, species, and sequencing can all be done with HRM assessment. LAMP is anticipated on the vehicle, which uses opposing transcriptase to cycle strand shifting and produce DNA or RNA. Many viral respiratory infections have been diagnosis by rapid amplification, including the Middle East respiration syndrome coronavirus, mammalian and bird flu viruses, RSV, hMPV, and individuals COVID-19-NL63. (Pyrc, Milewska et al. 2011, Bell, Bonner et al. 2014, Liu, Nian et al. 2014, Shirato, Yano et al. 2014, Song, Zhu et al. 2014). Unlike rRT-PCR, LAMP assays are not as effective at detecting numerous respiratory viruses at once as rRT –PCR is. However, multiple enzymes and templates can be used to identify influenza viruses A and B (Nie, Roth et al. 2014). Extremely precise LAMP assays can be carried out with tiny, bench-top detectors that use Alere I influenza A&B without aid of thermal cycling with specialized equipment. Despite being far less sensitive than rRT –PCR, this assay can be used as a "factor-of-care" because of its quick reaction period of fifteen minutes (Bell and Selvarangan 2014, Hazelton, Gray et al. 2015).

Table 1: Standard assay types for the detection of respiratory viruses

Technologies	Types of assay	Identified pathogens	Turn-around duration	Random access	Samples/ run	Effectiveness
Melting curve analysis coupled with PCR	AusDiagnostics	The influenza viruses A/H1, B, RSV, HRV/HEV, PIV 1-4, HAdV, HMPV, and CoV	4 h	No	6	Good agreement for influenza A, RSV, PIV, Picornaviridae, HAdV, hMPV, CoV, and HBoV40; 92.1% with xTAG RVP & FTD
rRT-PCR	Simplexa Direct Flu A/B and RSV	Influenza A, influenza B, RSV	1h	yes	96	High sensitivity in obtaining RNA for the detection of influenza A & B
RT-PCR with automated nested multiplex and complete nucleic acid extraction	FilmArray RVP	Influenza A/H1N1, A/H3N2, A(HINI) pdm09, influenza B, RSV, PIV 1-4, hMPV, HAdV, HRV/HEV, CoV	1h	yes	1	The assay demonstrated 85% sensitivity and 100% specificity for target respiratory agent
Nanoparticle probes	Verigene RVþ	RSV, influenza B, influenza A/H1, influenza A/H3, influenza A(H1N1) pdm09	<2.5 h	yes	1	Sensitivity for influenza A was 96.6%, while that of influenza B and RSV was 100% in contrast to Simplexa Flu A/B & RSV.

3.2.3 Next-generation sequencing

One of the modern technology's greatest innovations is next generation sequencing. Beyond sequencing the genome of a living thing, it made it possible to identify new viruses that cause unidentified human diseases and to monitor outbreaks and pandemics, such as influenza, to understand their development and pattern of propagation (Leung, Bull et al. 2014, Isakov, Bordería et al. 2015). Sanger and Barrel's research from the 1970s set the stage for Maxam and Gilbret, who employed radiolabeled probes to first introduce the idea of decoding oligonucleotides via enzymatic polymerization process.

Technically NGS is which include 3 essential steps: pattern practices, sequencing and statistics evaluation. System available with in the market place range on the whole of their sequencing or studying strategies. Diagnostic analysis of viral infections that is precise and efficient. The goal of using NGS is to give lengthier, more accurate evaluations in a brief period of time and at a lesser cost. Despite the fact that alumina is thought to be the most widely used pirosequencing technology, Roche subsidiary FLX was the first high throughput analyzer to arrive on the market and was used to determine the varieties of HPV virus (Barzon, Militello et al. 2011), Species and subcategories found in cervical specimens. A different version might include hydrogen electrons that are released by the incorporation of nucleic acids reactions (Rothberg, Hinz et al. 2011).

3.2.4 Mass spectrometry

Recently, mass spectrometry has become a standard for both statistical and qualitative laboratory studies, particularly in the field of bacterial science (Sauer and Kliem 2010) . Due to their ability to handle analyte characteristics of huge magnitude, matrix-assisted laser desorption ionization (MALD) and electrospray (ES) are the most commonly utilized ionization techniques in medical research (Emonet, Shah et al. 2010). These strategies have been thoroughly tested in experiments and have produced excellent results when used alone or in conjunction with various molecular techniques, such as PCR, that enhance sensitivity. The combination (RT-PCR/ESI-MS) produced quick and specific results in a brief period of time and was able to identify viral infections that were previously unidentified with the use of standard testing methods (Lévêque, Legoff et al. 2014).

Identification of influenza polymorphisms, or genetic modifications. One important method for managing pandemics involves the use of MALD-TOF (Chen, Rothman et al. 2011). The effectiveness of MALD-TOF-MS in conjunction with antibody magnetic nanoparticle for influenza virus detection was demonstrated by the use of MS in the structural examination of biomolecule (Chou, Hsu et al. 2011, Yea, McCorrister et al. 2011), Via outcomes that are consistent with the highest-standard PCR-based technique. Whenever assays are multiplexed, this combination of two potent instruments (PCR-MS) can diagnose multiple infections, identify resistance strains to therapy with antivirals, and identify the possibility of numerous viruses in an identical samples.

Table 2: An overview of the primary viral diagnostic techniques

Method of diagnosis	Principle	Advantages	Disadvantages	Variety	References
Immunoassay	Formation of antigen-antibody through recognition and binding.	High sensitivity, high specificity through put quick TAT (20 minute or less) different type of tags, labels, Automated method	Must rely on QC assurance high risk of interference high cost	RIA EIA (FPIA, MEIA, CLIA)	(Gupta, Pandey et al. 2015)
NAAT	Amplification and detection of sequences from the viral genome, DNA or RNA	Amplification and detection of sequences from the viral genome (DNA or RNA)	Longer run-time requires specific primers for the target	RT-PCR qPCR NASBA TMA	(Mercier-Delarue, Vray et al. 2014, García-Arroyo, Prim et al. 2016)
NGS	Polymerization of DNA template by incorporation of labeled DNTPs and terminate the extension	High sensitivity high specificity, Identification of novel genomeic sequences, Genotyping accurate detection of mutation and drug resistant mutation	High cost needs bioinformatics skills for data analysis delay in use for routine clinical diagnostics	Pyrosequencing Fluorescently labelled dNTP Detection of released hydrogen ion (H+)	(Rothberg, Hinz et al. 2011, Lowe, Merrick et al. 2016)
MS	Ionization of the sample then separation and detection of the particles according to their mass to charge ratio (m/z).	High sensitivity, versatility, cost effectiveness ,high workload	Expensive equipments limited database library	MALDI-TOF MS ESI MS Often combined with other methods: PCRMS	(He, Zhu et al. 2014)

Discussion:

Viral breathing infections (VRIs) are a major cause of high rates of morbidity around the world and provide a serious risk to people with weakened immune systems. Over the years, diagnostics method have developed from conventional techniques like viral lifestyle and serology, which can be particular

however time-eating and less touchy, to superior molecular techniques together with polymerase chain reaction (PCR) and subsequently-era sequencing (NGS) (Barzon, Lavezzo et al. 2011). This discussion explores the strength and obstacles of both conventional and contemporary diagnostics strategies, emphasizing the significance of a balanced method that integrates speedy screening with confirmatory testing (Hayden, Carroll et al. 2020).

Table 3:

Virus type	Genus and Family	Methods of diagnostic	References
Influenza virus	Influenza virus A, Influenza B, Influenza virus C, Influenza virus D, Isa virus, Quaranjavirus & Togavirus genus	Viral culture; IFA; ELISA-based test; PCR-based; DNA- microarray-based; sequencing-based tests	(Nakauchi, Takayama et al. 2014)
Human RSV	Pneumovirus genus	IFA; ELISA-based test; DFA; LFIA; real-time PCR based; RT-RAA assay; RT-SIBA	(Zhao, Wang et al. 2019)
Coronavirus	Alphacoronavirus Deltacoronavirus and gammacoronavirus genus	RT-PCR; rRT-PCR; RT-LAMP; Real-time RT-LAMP	(Shirato, Semba et al. 2018)
Adenovirus	Adenoviridae family & Atadenovirus, Aviadenovirus, Mastadenovirus and Siadenovirus genus	Viral culture; indirect ELISA; IFA; LAT; EIA; Real-time PCR based	(Zhang, Jing et al. 2017)
Rhinovirus	Enterovirus genus	CFT; HI; IFA; ELISA; Semi-nested RT-PCR assay; WGS-based assays	(Schibler, Yerly et al. 2012)

The set off and correct identification of pathogens is critical for efficiently treating ARIs. (Peeling, Heymann et al. 2022). Current diagnostic strategies for breathing infections often depend on symptomatic identification, point of-care assessment, and laboratory-based totally assays. However, those strategies often lack sensitivity, pace, or ease of use, leading to delays in diagnostic and treatment (He, Zhang et al. 2025). Immunoassay are now essential tools identifying viral respiratory infections, offering prompt outcomes of usage in healthcare environments (Avarre 2017). Chemiluminescent immunoassays (CLIAs), enzyme-associated immunosorbent assays (ELISA), immunofluorescence assays (IFAs), and fast antigen testing are the most widely used codecs with superb advantages and programs (Chan, Tse et al. 2009). From nasopharyngeal swabs, they detect viral nucleoproteins. The advantages of immunoassays consist of speedy turnaround instances, value-effectiveness for huge scale screening, and minimal instrumentation necessities for a few codecs. (McCarty, Cumagun et al. 2023)**.** However, barriers persist, specially false-bad outcomes all through early contamination levels and capacity pass-reactivity with related viruses (Tang, Schmitz et al. 2020).

Molecular amplification techniques have grown to be the cornerstone of viral respiratory contamination diagnostics due to their advanced sensitivity and specificity in comparison to standard strategies (Mori, Kanda et al. 2013). These nucleic acid amplification tests (NAATs) can hit upon minute quantities of viral genetic fabric, enabling early prognosis even earlier that symptoms onset or antibody manufacturing (Briese, Kapoor et al. 2015). Real-time PCR structures have turn out to be the diagnostic gold popular, imparting quantitative consequences with sensitivity exceeding 95%r for most respiratory viruses (Babady, England et al. 2018). Multiplex PCR systems can concurrently locate 20 breathing pathogens in a single reaction, substantially enhancing diagnostic efficiency for complex respiration infections. Digital PCR offers absolute quantification of viral load without fashionable curves, proving specifically precious for tracking treatment response in immune compromised patients.specifically precious for tracking treatment response in immune compromised patients (Shi, Hu et al. 2024).

Conclusion

Viral respiratory infections keep to pose a massive worldwide health burden, mainly for immune compromised patients who face heightened dangers of extreme complications and mortality. This evaluates highlights the critical evolutions in diagnostics strategies, from conventional techniques like viral subculture and serology – valued for his specificity but restricted by slow turnaround instances and mild sensitivity to advanced molecular techniques which includes PCR and subsequently generation sequencing that offer rapid, precise detection vital for weel-timed scientific intervention. While these technological advancements have revolutionized respiratory virus analysis, persistent challenges inclusive of high expenses, technical complexity, and the need for continuous updates to viral mutation underscore the significance of developing extra accessible solutions. A highest quality diagnostics strategy need to combine speedy screening exams in useful resources restrained settings. Looking in advance, the development of less expensive factor-of-care technology, coupled with ongoing studies in to vast-spectrum antivirals and progressed vaccines, might be vital to deal with emerging viral threats. Furthermore, strengthening worldwide surveillance networks, improving healthcare employee education, and enforcing study public fitness regulations are vital components of a complete techniques to reduce the enormous morbidity, mortality and financial impact associated with VRIs, especially amongst inclined population global. To acquire those goals, global collaboration may be vital in standardization diagnostic protocols and sharing genomics surveillance statics to viral evolution in actual-time. Health care structure should prioritize the integration of synthetic intelligence and systems gaining knowledge of diagnostic accuracy prevention measures inclusive of vaccination and infection manage practices, in particular for excessive-danger groups. By fostering innovation in diagnostics and prevention while addressing healthcare disparities, we are able to build greater resilient systems able to mitigate the effects of present day and destiny respiratory viral threats. This multi-pronged approach lessen the lengthy-terms socioeconomics burden of these infections on global groups.

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