**3rd Worldwide Conference on**

# Infectious Diseases

## April 29-30, 2024 | Tokyo, Japan

### Venue: ANA Crowne Plaza, Narita

*infectiousdiseases@averconferences.com*
*https://infectious-diseases.averconferences.com/*

# AVER CONFERENCES

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## April 29, 2024 (Monday)

| | |
|---|---|
| **09:30 - 04:00** | Registrations |
| **09:45 - 10:00** | Opening Ceremony |

### Keynote Forum

**10:00 - 10:30**

**Title: Clinical Characteristics and Outcome of Covid-19 Patients and Predictors of In-hospital Mortality in Saudi Arabia**
Prof. Mostafa A. Abolfotouh, King Abdullah International Medical Research Center, Saudi Arabia

**10:30 - 11:00**

**Title: Caring, treating and preventing infectious diseases in developing countries - best we can do with artificial intelligence in medicine**
Dr. Tummalapalli Venkateswara Rao, TMC Kollam, Kerala, India

### Group Photo

Networking & Refreshment Break 11:00 -11:15

### Plenary Sessions

**11:15 - 11:35**

**Title: Immunization effects of COVID-19 inactivated vaccines in inoculation population: An observation study**
Ms. Zhang Li, Fudan University, Shanghai, China

**11:35 - 11:55**

**Title: History of vaccine-induced immunity**
Mrs. Panagiota Kalatzi, University of Peloponnese, Greece

**11:55 - 12:15**

**Title: Decoding Dengue: A Comprehensive Analysis of Cases at Holy Family Hospital (2019–2023) and Anticipating Pakistan's Future Dengue Dynamics under Climate Change**
Dr. Saira Karimi, Rawalpindi Medical University, Pakistan

**12:15 - 12:35**

**Title: Epidemiological characteristics of leprosy during the period 2005-2020: A retrospective study based on the Chinese surveillance systems**
Dr. Xiang Li, Southeast University, China

**12:35 - 12:55**

**Title: Role of Artificial Intelligence in Reducing Antibiotic Resistance (AMR) in Developing Countries**
Dr. Tummalapalli Venkateswara Rao, TMC Kollam, Kerala, India

Lunch Break @13:00 - 14:00

### Plenary Sessions

**14:00 - 14:20**

**Title: Effectiveness of COVID-19 vaccines with heterologous and homologous prime-boost regimens in healthcare workers: a systematic review and network meta-analysis**
Dr. Lairun Jin, Southeast University, China

**14:20 - 14:50**

**Title: Diagnostic Stewardship and Its Impact**
Dr. Afreenish Amir, National Institute of Health, Pakistan

**14:50 - 15:15**

**Title: Comparison of the yield of two tuberculosis screening approaches among household contacts in a community setting of Silti Zone, Central Ethiopia: A prospective cohort study**
Mr. Habtamu Milkias Wolde, Ministry of Health, Ethiopia

**15:15 - 15:40**

**Title: Antimicrobial Resistance Profile of Helicobacter pylori, Obtained from endoscopic patients in Bahir Dar, Northwest Ethiopia**
Mr. Mulat Erkihun, Debre Tabor University, Ethiopia

Networking & Refreshment Break 15:40 - 16:00

**16:00 - 16:20**

**Title: The Phylogenetic Trajectory of a Human H10N5 Avian Influenza Virus**
Dr. Chenglong Xiong, Fudan University, China

**16:20 - 16:50**

**Title: Application of logistic regression methods in predicting severity of Covid-19 infection**
Dr. Hokuma Mammadova, Azerbaijan Medical University, Azerbaijan

**16:50 - 17:15**

**Title: Dosimetric Comparison between Intensity-modulated Radiotherapy versus Volumetric Modulated Arc Therapy Treatment Plans for Breast Cancer**
Mr. Mahfuzur Rahman, Bangladesh Medical Physics Society, Bangladesh

**17:15 - 17:30**

**Title: "Antimicrobial Resistance Profile of Helicobacter pylori, Obtained from endoscopic**
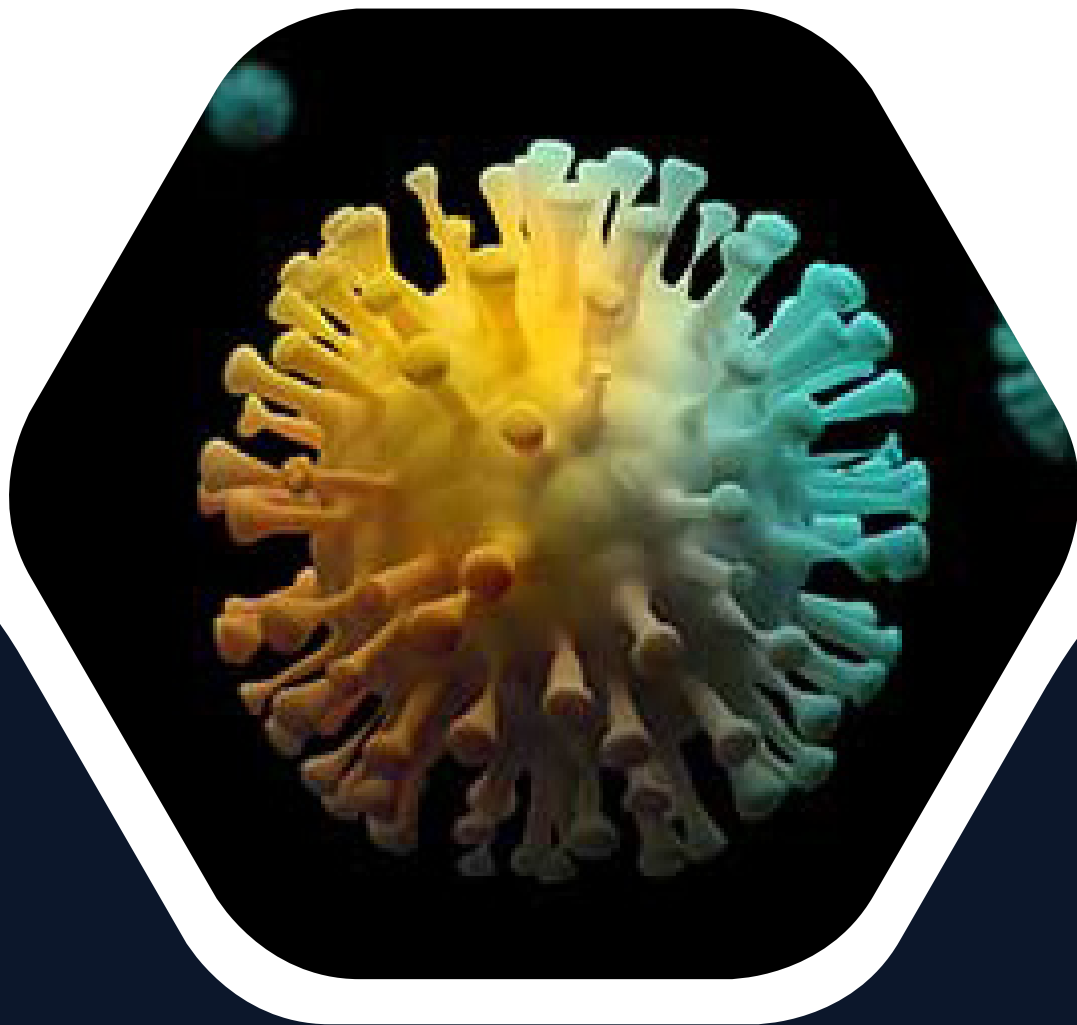Dr. Rogelio Navarrete Castro, Centro de Atencion y Capacitacion en Enfermedades Infecciosas, Mexico

### End of Day-1

### Meeting Adjourns

# 3rd Worldwide Conference on

# Infectious Diseases

## April 29-30, 2024 | Tokyo, Japan



# Keynote Forum

# 3rd Worldwide Conference on
# Infectious Diseases

## Prof. Mostafa A. Abolfotouh

*King Abdullah International Medical Research Center*
*Saudi Arabia*

**Co-authors:** [1] **Abrar Musattat,** [1] **Maha Alanazi,** [1,2] **Suliman Alghnam,** [1,2,3] **Mohammad Bosaeed**
[1] King Abdullah International Medical Research Center, [2] King Saud bin-Abdulaziz University for Health Sciences, and [3] King Abdulaziz Medical City, Ministry of National Guard-Health Affairs, Riyadh, Saudi Arabia

### Clinical Characteristics and Outcome of Covid-19 Patients and Predictors of In-hospital Mortality in Saudi Arabia

**Background:** Patients' race and ethnicity may play a role in mortality from Covid-19. Studies in China, the US, and Europe have been conducted on the predictors of COVID-19 mortality, yet in the EMR countries, such studies are scarce. Therefore, we aimed to describe the hospitalization rate, ICU admission, and in-hospital mortality of COVID-19 and predictors of in-hospital mortality in Saudi Arabia.

**Methods:** E-medical records were examined for all COVID-19 patients diagnosed in five tertiary hospitals affiliated with the Saudi National Guard Health Affairs between March 21, 2020, and September 12, 2021, based on a positive SARS-CoV-2 RT-PCR test, (n=35284). Data were collected on patients' characteristics, comorbidities, laboratory findings, hospitalization, ICU admission, and in-hospital and overall mortality. Logistic regressions were used to identify the independent predictors of in-hospital mortality. The best laboratory parameters cut-off values to predict in-hospital mortality were identified using the area under the receiver operating characteristic curve (AUC). Significance was considered at $p < 0.05$.

**Results:** Of all 35,284 Covid-19 patients, 81.8% were adults and 21.7% were hospitalized. Compared to non-hospitalized patients, hospitalized patients were more of female gender (52.1% versus 47.3%, $p<0.001$) and had higher mean age ($p<0.001$), higher mean BMI ($p<0.001$), and higher rates of diabetes ($p<0.001$), hypertension ($p<0.001$), ischemic heart disease ($p<0.001$), cancer ($p<0.001$), COPD ($p<0.001$) and asthma ($p=0.011$). The study showed 3.1% overall case fatality, 20.3% ICU admission rate, and 9.7% in-hospital mortality. Predictors of in-hospital mortality among adult patients were; patients age ≥70 years (OR=6.93, 95% CI: 1.94-24.79), ischemic heart disease (OR=1.80, 95% CI: 1.05-3.09), ICU admission (OR=24.38, 95% CI: 15.64-38.01), abnormal C-reactive protein "CRP" (OR=1.85, 95% CI: 1.08-3.16), abnormal D-dimer (OR=1.96, 95% CI:1.15-3.36), lymphopenia (OR=2.76, 95% CI:2.03-3.3.76), high neutrophil count (OR=2.10, 95% CI: 1.54-2.87), and abnormal procalcitonin (OR=3.33, 95% CI:1.88-5.90). The best laboratory parameters cut-off values to predict in-hospital mortality were CRP>72.25mg/L (AUC=0.64), D-dimer >1125 ug/L (AUC=0.75), neutrophils count >5,745x10^9/L (AUC=0.70), lymphocytic count <1.10 x10^9/L (AUC=0.72), and procalcitonin >0.18 ng/mL (AUC=0.76).

**Conclusions:** Rates of hospitalization, ICU admission, in-hospital mortality, and overall case fatality were nearly comparable to the rates in western countries. Early interventions are necessary for high-risk COVID-19 patients, especially elderly patients and those with cardiac diseases.

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## Dr. Tummalapalli Venkateswara Rao
*TMC Kollam, Kerala, India*

### Caring, treating and preventing infectious diseases in developing countries - best we can do with artificial intelligence in medicine

The management of infectious diseases is a complex task that involves considering a multitude of dynamic variables. Artificial Intelligence (AI) has found valuable applications in this field, aiding clinicians and researchers in various ways, Artificial intelligence is an emerging tool, influencing every branch of science and humanities and now in addition to diagnosing treat and preventing infectious diseases, we can develop and use Artificial intelligence tools to control the Infectious diseases and in turn, reducing mortality and morbidity, In real time Artificial intelligence track the infection outbreaks faster, Aimed to assist public health officials identify and treat individuals with undiagnosed infectious diseases The algorithm was created with the hope how quickly disease spread can the reduced to infect many in many regions in the world Additionally, the algorithm takes other factors like resources into account for optimum impact in communities, modeling is an improvement over standard documentation, artificial intelligence (AI) technology is evolving at a very rapid rate. The ability of AI technology to augment decision-making processes is attributed to the speed of pattern recognition and the robust amount of data that are digested and analyzed for optimal health outcomes. Currently, we can retrieve data derived from electronic health records, health exchanges, and other digital sources, which provide real-time, detailed information on various infectious disease processes and outbreaks, Let's explore how AI contributes to reducing infections: in developing countries

1. Clinical Decision Support Systems (CDSS): These AI-based systems enhance clinical decision-making. For instance, tools like Sepsis, Pandemics, and Watch can be adopted at institutional levels in resource-poor countries to improve patient management and reduce the impact of infectious diseases

2. Disease Surveillance and Outbreak Response: AI can track and predict the spread of infections. It aids in identifying high-risk areas and monitoring disease progression. by analyzing data, In Addition, AI helps public health authorities respond effectively to outbreaks.

3. Diagnosis and Prognosis: AI algorithms can assist in diagnosing infections and predicting patient outcomes. Early detection and accurate prognoses lead to timely interventions and better patient care. Based on the review findings, ML and AI have revolutionized infectious diseases in patients and research by analyzing large datasets and providing valuable insights.

**Conclusion:** However with many, challenges in developing countries with poor diagnostic facilities low data quality, and few qualified personal we should find the solutions to make the better use of Artificial intelligence to deal with matters related to Artificial Intelligence
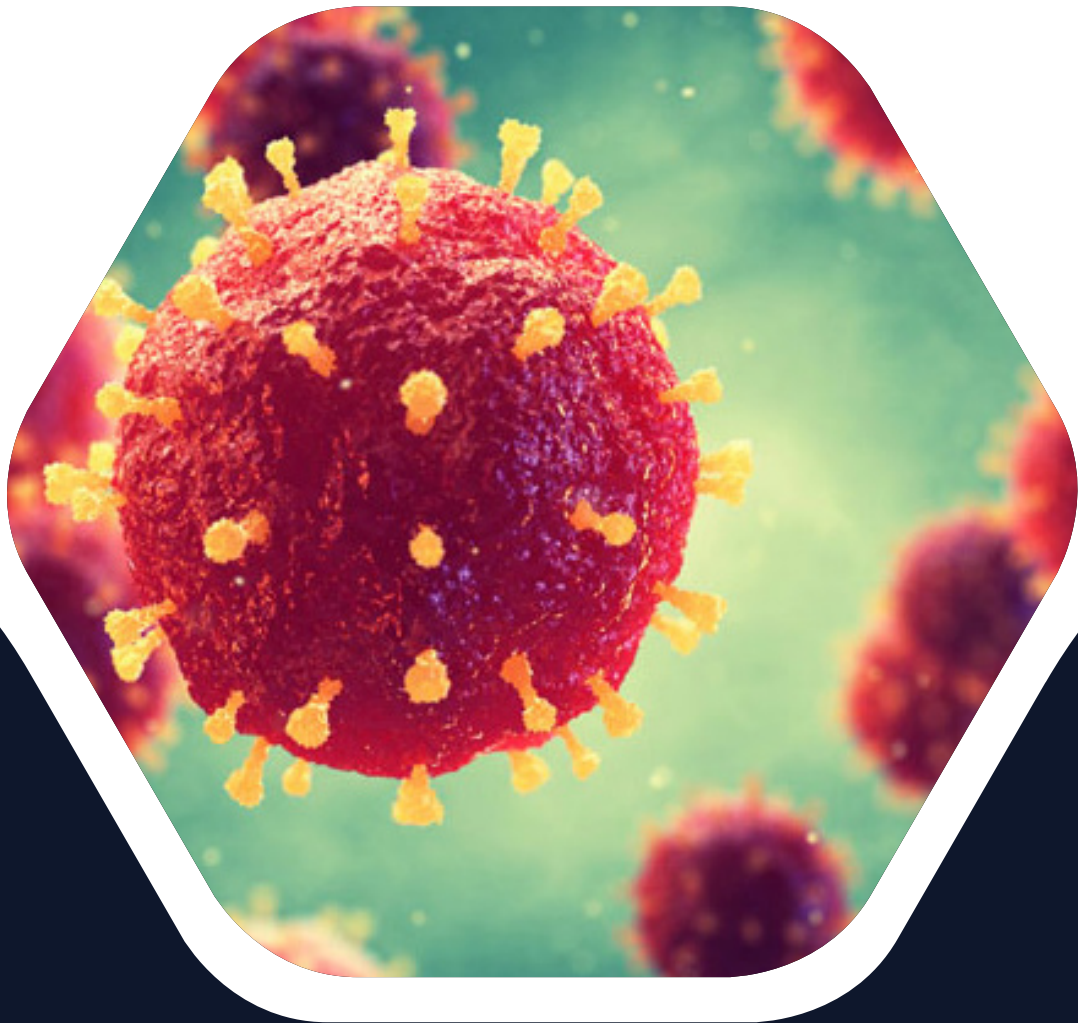
## Plenary Sessions

**Title: Immunization effects of COVID-19 inactivated vaccines in inoculation population: An observation study**
Ms. Zhang Li, Fudan University, Shanghai, China

**Title: History of vaccine-induced immunity**
Mrs. Panagiota Kalatzi, University of Peloponnese, Greece

**Title: Decoding Dengue: A Comprehensive Analysis of Cases at Holy Family Hospital (2019–2023) and Anticipating Pakistan's Future Dengue Dynamics under Climate Change**
Dr. Saira Karimi, Rawalpindi Medical University, Pakistan

**Title: Epidemiological characteristics of leprosy during the period 2005-2020: A retrospective study based on the Chinese surveillance systems**
Dr. Xiang Li, Southeast University, China

**Title: Topic- Role of Artificial Intelligence in Reducing Antibiotic Resistance (AMR) in Developing Countries**
Dr. Tummalapalli Venkateswara Rao, TMC Kollam, Kerala, India

**Title: Effectiveness of COVID-19 vaccines with heterologous and homologous prime-boost regimens in healthcare workers: a systematic review and network meta-analysis**
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**Title: Diagnostic Stewardship and Its Impact**
Dr. Afreenish Amir, National Institute of Health, Pakistan

**Title: Comparison of the yield of two tuberculosis screening approaches among household contacts in a community setting of Silti Zone, Central Ethiopia: A prospective cohort study**
Mr. Habtamu Milkias Wolde, Ministry of Health, Ethiopia

**Title: Multi resistance to new antiviral molecules in the treatment of C viruses**
Dr. Rogelio Navarrete Castro, Centro de Atencion y Capacitacion en Enfermedades Infecciosas, Mexico

**Title: The Phylogenetic Trajectory of a Human H10N5 Avian Influenza Virus**
Dr. Chenglong Xiong, Fudan University, China

**Title: Application of logistic regression methods in predicting severity of Covid-19 infection**
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**Title: Dosimetric Comparison between Intensity-modulated Radiotherapy versus Volumetric Modulated Arc Therapy Treatment Plans for Breast Cancer**
Mr. Mahfuzur Rahman, Bangladesh Medical Physics Society, Bangladesh

## Immunization effects of COVID-19 inactivated vaccines in inoculation population: An observation study

**Ms. Zhang Li**
*Fudan University, Shanghai, China*

**Co-authors: Dong Xiaolian, Mao Chuanwu, Chen Yingfeng, Jiang Lufang, Chen Yue, Jiang Qingwu**

**Objectives:** This study aimed to evaluate the antibody response to the SARS-CoV-2 inactivated vaccine in a population and identify influential factors, contributing valuable insights to the global fight against the ongoing COVID-19 pandemic.

**Method:** A cross-sectional study was conducted in Zhejiang Province, China, from January 21, 2021, to October 21, 2022. A total of 2,884 residents (adults and adolescents) were enrolled using cluster random sampling from communities and schools. Basic information and serum samples were collected for evaluation. Focusing on BBIBP-CorV and CoronaVac, both inactivated COVID-19 vaccines, immune responses were assessed using the if lash 3000 Chemiluminescence Immunoassay to measure Immunoglobulin-G (IgG) levels specific to the SARS-CoV-2 anti-spiking protein (S) and anti-nucleoprotein (N). Differences in antibody level distribution among different populations were analyzed.

**Result:** Categorized into three vaccination groups (N1, N2, N3), demographic analysis revealed no significant gender or vaccine-type differences. Notable age distribution variations were observed due to China's vaccination strategies. IgG antibody levels indicated that Group N3 (booster dose) exhibited significantly elevated levels compared to N2 (two doses) and N1 (one dose), emphasizing the impact of booster doses. Females displayed higher IgG levels in N2 and N3. While Groups N1 and N2 showed age-related differences, Group N3 consistently demonstrated high IgG levels across age groups. Vaccine-type analysis indicated higher IgG levels in N3, suggesting a balancing effect. Antibody decay assessment revealed that Group N3 maintained consistently high levels, while N1 and N2 demonstrated a decline over time, emphasizing the sustained effectiveness of booster doses.

**Conclusion:** Several factors significantly influenced the production of specific antibodies post-immunization, including the number of doses, gender, age, and vaccine type. Individuals receiving one or two doses experienced a decline in IgG levels, while those with three doses maintained high levels. Timely booster shots are crucial for sustaining specific antibody levels post inactivated COVID-19 vaccination. Antibody levels difference between gender groups within groups N1, N2, and N3(A、B、C). Antibody levels difference between age groups within groups N1, N2, and N3(D、E、F). Antibody levels difference between vaccine type groups within groups N1, N2, and N3(G、H、I). Red solid lines represent the median IgG index. Red dashed lines represent the interquartile range of the IgG index. Black dashed lines represent the positive threshold of the IgG index. The numbers below each violin plot represent the median and upper and lower quartiles of the IgG index of each group. $*p<0.05$ $**p<0.01$ $***p<0.001$

**Biography:**
Li Zhang is a current master's in public health student at Fudan University, China, holding a Bachelor's in Preventive Medicine from Suzhou University, China. With a strong foundation from her undergraduate research on arsenic-induced cell transformation published in the "Journal of Environment and Health," Li actively researches the immune effectiveness of COVID-19 vaccination. In her master's program, she has authored three academic papers, showcasing innovation and a profound understanding of scientific principles. Li aspires to contribute to public health development, aiming for innovative breakthroughs benefiting societal health.

### History of vaccine-induced immunity

**Mrs. Panagiota Kalatzi**
*University of Peloponnese, Greece*

**Co-authors: Travlos K. Antonios**
*Prof., Department of Sports Organization and Management, University of Peloponnese, Sparti, Greece*

**Mihopoulos Alexandros**
*Asst. Prof., Department of Nursing, University of Peloponnese, Tripoli, Greece*

**Sakellari Evanthia**
*Assoc. Prof., Department of Public and Community Health, University of West Attica, Athens, Greece*

**Tziaferi Styliani**
*Assoc. Prof., Department of Nursing, University of Peloponnese, Tripoli, Greece*

**Objectives:** To describe the evolution of vaccine-induced immunization.

**Method:** Literature review in online databases PubMed, CINAHL and Google Scholar was conducted in December 2023 with the following keywords: history, vaccines, vaccination, and active immunization. English-written reports that addressed the development of vaccines over time were included. Results were not restricted by publication date.

**Result:** Centuries have passed between the first recorded description of microbes (mumps and diphtheria) by Hippocrates (400 B.C.) and the inoculation of biologic material to prevent smallpox infections, in 1100 A.D. by Edward Jenner. During the nineteenth century Louis Pasteur introduced the "Germ Theory of disease", Robert Koch discovered the germ tubercle bacillus and George Miller Sternberg isolated pneumococcus. The first live-attenuated viral vaccine against rabies was introduced, followed by typhoid and plague vaccines. Vaccines for the protection against pertussis (1914), diphtheria (1926), and tetanus (1938) were generated early in the 20th century. Vaccines against measles, mumps, and rubella were developed in the 1960s. The vaccine for Hepatitis B was licensed in 1981, while that of Hemophilus influenza type b, in 1994. More vaccines added to the list, including Varicella (chickenpox-1996), Rotavirus (1998), Hepatitis A (2000), Pneumococcal (2001), HPV (2006), Herpes Zoster (2008), and Meningococcal serogroup B vaccine (2014). Finally, the recent coronavirus disease 2019 (COVID-19) pandemic urged the need for the scientific community to develop a safe and effective vaccine. Today, more than 50 COVID-19 vaccines have been approved by at least one country and are roughly divided into the following categories: whole virus, viral vector, protein-based, and nucleic acid vaccines.

**Conclusion:** Vaccine-induced immunity has been of great importance for human longevity and global security. Progress in the development of vaccines continues, as vaccines against emerging viruses (e.g. Zika virus) as well as immunoregulating pathogens (e.g. HIV, HCV, Malaria), are under investigation.

**Biography:**
Panagiota Kalatzi is a registered nurse with fourteen years of working experience in the clinical field. She holds a Ph.D. degree in public health from the University of Peloponnese in Greece. Her research interests are focused on public health and infection prevention. She works as an infection preventionist at the general hospital of Sparta, Greece.

## Decoding Dengue: A Comprehensive Analysis of Cases at Holy Family Hospital (2019– 2023) and Anticipating Pakistan's Future Dengue Dynamics under Climate Change

**Dr. Saira Karimi[1]**
*Rawalpindi Medical University, Pakistan*

**Co-Authors: Prof. Dr. Naeem Akhtar[2] Dr. Olodo Katiana[3], Dr. Burhan Ahmed[4], Prof. Dr. Mujeeb Khan[5] Dr. Muhammad Umer***

This retrospective study considers the comprehensive analysis of dengue fever (DF) cases reported at Holy Family Hospital from 2019 to 2023. Patient data, including demographic features, age, gender, relatedness to DF, Dengue Shock Syndrome (DSS), and Dengue Hemorrhagic Fever (DHF), were collected and analyzed to understand the prevalence and patterns of dengue in this healthcare setting. Notably, comorbid diseases were explored, and a significant linkage was observed between patients with comorbidities and an increased likelihood of contracting dengue. The study revealed that NS1 positivity was more frequent among individuals above 50 years of age, emphasizing the age-dependent nature of dengue susceptibility. Furthermore, our findings highlighted a gender-based vulnerability, indicating that males were more prone to DF in all cases studied. These retrospective insights set the stage for a forward-looking approach, prompting us to propose an analysis of the future scenario of dengue in Pakistan. Leveraging the climate change and infectious diseases being a point of concern in the recent climate change scenario in Pakistan, which assessed Pakistan, we aim to predict the impact of climate change on dengue transmission suitable days (DTSD) and how the observed patterns in Holy Family Hospital may evolve in the changing climate. The proposed predictive model incorporates the baseline (2019-2023) and future (2025–2035, 2041–2070, and 2071–2099) periods under Representative Concentration Pathway (RCP4.5 and RCP8.5) scenarios. CMIP5 models, downscaled and bias-corrected with the quantile delta mapping technique, will be employed to project the potential spatiotemporal shifts and future hotspots of DTSD due to climate change. Drawing from the insights gained in the retrospective study, our predictive analysis aims to contribute to proactive public health measures by anticipating and preparing for the evolving dynamics of dengue in the context of a changing climate.

**Objectives:** 1. Investigate demographic patterns and associations with Dengue Fever (DF), Dengue Shock Syndrome (DSS), and Dengue Hemorrhagic Fever (DHF) in dengue cases at Holy Family Hospital (2019–2023).
2. Analyze comorbidity linkages to understand their impact on the severity and susceptibility to dengue. Examine NS1 positivity patterns, focusing on individuals aged 50 and above, to identify age-related susceptibility to dengue infection. Assess gender-based vulnerability by quantifying the prevalence of dengue cases among males and females.
3. Propose a predictive climate model utilizing climate data to anticipate future Dengue Transmission Suitable Days (DTSD) in Pakistan. Identify potential spatiotemporal shifts and future hotspots of DTSD due to climate change.

**Methodology:** Conduct a retrospective analysis of dengue cases at Holy Family Hospital (2019–2023) and integrate findings with a climate model, utilizing downscaled and bias-corrected data from CMIP5 models with the quantile delta mapping technique.

**Results:** Demographic analysis from the hospital data reveals patterns of dengue cases, comorbidity associations, NS1 positivity trends, and gender-based vulnerabilities. The climate model predicts spatiotemporal shifts and future hotspots of Dengue Transmission Suitable Days (DTSD) in Pakistan.

**Conclusion:** The study provides insights into current dengue dynamics, highlighting vulnerabilities and associations. The predictive climate model aids in anticipating future trends, emphasizing the importance of proactive public health measures in the face of evolving dengue scenarios.

**Biography:**
Dr. Saira Karimi, an Assistant Professor at the Department of Pathology, Rawalpindi Medical University, holds a Ph.D. in Biosciences from COMSATS University Islamabad, with part of her research conducted at the Center of Functional Ecology, CNRS IRD Montpellier, France. With expertise in Microbiology, Molecular Genetics, Public Health, and Epidemiology, Dr. Karimi has served as a team lead for manipulative experimentation at the Snow Leopard Foundation, where she induced climate change impacts on Medicinal plants and associated microbiota at Khunjerab National Park for over five years.

## Epidemiological characteristics of leprosy during the period 2005-2020: A retrospective study based on the Chinese surveillance systems

**Dr. Xiang Li**
*Southeast University, China*

**Objectives:** Although leprosy has been eliminated, there are still 300-500 new cases reported annually in China. Since 1949, more than 55,000 cases have been registered in Jiangsu Province. As a result, the province has been considered a priority area for public health interventions in China. Therefore, it is crucial to analyze the epidemiological characteristics of leprosy in Jiangsu, aiming to identify high-risk areas and facilitate the eradication of leprosy.

**Method:** This paper mainly described the population, time, and spatial distribution of the newly detected leprosy cases in Jiangsu between 2005 and 2020. All the epidemiology data were entered into SPSS for the descriptive analysis. ArcGIS was applied to create statistical maps, and Geoda was used to conduct spatial autocorrelation analysis with local Moran's I statistics.

**Results:** 363 new cases were reported. 232 were men and 131 were women (1.77:1). The mean age at diagnosis was 60.56, and no adolescent cases were identified. 327 (90.08%) were diagnosed with MB and 36 (9.92%) with PB. 31.68% of the patients presented with G2D. Farmers accounted for 74.9%, and most cases were identified in skin clinics (68.32%). We observed a decreasing trend in the detection rate, with a higher concentration of new cases diagnosed between July and October. Spatial analysis showed that the new cases were primarily distributed in the northwest of Jiangsu, and Suqian county has the highest incidence rate. Special attention should be paid to Wuzhong, a county with a potential risk of inter-provincial transmission. Furthermore, 55 new cases came from other Chinese provinces but lived in Jiangsu.

**Conclusion:** The NCDR of leprosy decreased, but the new cases showed disabilities, a sign of a delayed diagnosis. Some regions were still suffering from the burden of leprosy. We recommend that the government should adopt effective strategies to promote leprosy control in these areas.

**Biography:**
Xiang Li is a doctoral candidate in Public Health and Preventive Medicine at the School of Public Health, Southeast University, China. His current research encompasses statistics, epidemiology, and genetics in leprosy-related studies. He has published five SCI-indexed papers as the first author. In his study, he focused on investigating the epidemiological distributional characteristics of leprosy, to promote early detection, reduce morbidity, mitigate the risk of leprosy-associated complications, and offer reference for policy development towards disease eradication.

## Role of Artificial Intelligence in Reducing Antibiotic Resistance (AMR) in Developing Countries

**Dr. Tummalapalli Venkateswara Rao**
*TMC Kollam, Kerala, India*

The widespread use and misuse of antibiotics in clinical practice has resulted in drug resistance, in addition to increasing the threat of super-resistant bacterial emergence. Antimicrobial resistance (AMR) has become one of the biggest threats in the global public health field. Need of the Time we have to fundamentally change our approach and adopt newer modalities to control Antibiotic resistance, However Artificial intelligence (AI) represents a new paradigm to combat AMR. As it happens Development of Antimicrobial resistance (AMR) AMR occurs when microorganisms (such as bacteria, viruses, fungi, and parasites) become resistant to drugs that were once effective in treating infections. Many developing countries are using AI in antibiotic therapy optimization, saving drug costs and reducing morbidity and mortality. How Artificial Intelligence comes to our rescue AI, especially deep learning and machine learning, offers a new direction for Challenges and Opportunities: Challenges include selecting relevant input features, ensuring robustness, and achieving high accuracy in AI models. Antimicrobial Stewardship Although AI can help address the large amount of data gathered nowadays and performing repetitive tasks, there are some risks and ethical concerns that must be considered, for example, the possibility of the algorithm making associations between features and outcomes that are not relevant or are without physiological/ clinical rationale, the blind obedience/overdependence on AI, liability, or accountability in case of mistakes Developing countries to be partners to develop protocols in Use of Article Intelligence to control the Antimicrobial resistance reduction. The Developing countries too must develop their resources to Implement Artificial Intelligence. The research on AI applications in ASP is mostly from high-income countries, which can introduce bias on the algorithms and inequalities in healthcare because it does not represent the entire population This may happen because low- and middle-income countries may face more challenges to implementing systems allowing for the collection of large amounts of structured health data, access to health is scarcer, and the financial support for implementing AI algorithms needs to be improved., Conclusion- Application of AI in efforts to control high AMR rates with their advantages and disadvantages. Additionally, artificial intelligence applications are commonly used in the development of new antibiotics and the exploration of synergistic medication combinations.

## April 29-30, 2024 | Tokyo, Japan

### Effectiveness of COVID-19 vaccines with heterologous and homologous prime-boost regimens in healthcare workers: a systematic review and network meta-analysis

**Dr. Lairun Jin**
*Southeast University, China*

**Objectives:** To evaluate the effectiveness of COVID-19 vaccines with heterologous and homologous prime-boost regimens in healthcare workers in preventing COVID-19 infection.

**Method:** PubMed, Embase, Cochrane Library, Medline, and Web of Science databases for studies published between 1 January 2020 and 1 March 2024. Studies were eligible when they reported the vaccine effectiveness (VE) of documented or symptomatic COVID-19 infections among healthcare workers who were vaccinated and unvaccinated. The primary outcome was the ranking of vaccine effectiveness against documented COVID-19 infection using surface under the cumulative ranking curve scores. The study was registered with PROSPERO, CRD42022368734.

**Results:** 24 studies were included in the network meta-analysis and 12 vaccine regimens were identified. Of these regimens, a homologous three-dose mRNA regimen was observed to be the most effective against documented COVID-19 infections (VE 98%, 95% CI 95% to 99%), followed by heterologous boosting using two-dose inactivated whole virus vaccine with one-dose mRNA vaccine (VE 96%, 95% CI 81% to 99%) and a homologous two-dose mRNA regimen (VE 92%, 95% CI 87% to 95%). In the subgroup analyses, a homologous two-dose mRNA regimen had a VE of 90% (95 CI 84% to 94%) during periods of alpha variant dominance. Homologous three-dose and two-dose mRNA regimens had satisfactory VE (98%, 95% CI 79% to 100%, and 90%, 95 %CI 51% to 98%) during periods of delta variant dominance. Moreover, two-dose mRNA was found to be the most effective against symptomatic COVID-19 infections (VE 94%, 95% CI 87% to 97%) among single-dose and two-dose vaccine regimens.

**Conclusion:** Homologous or heterologous boosting using a third dose of mRNA vaccine is recommended to prevent COVID-19 infection in healthcare workers.

**Biography:**
Lairun Jin is a doctoral candidate at the School of Public Health, Southeast University, China, specializing in Public Health and Preventive Medicine. His research focuses on vaccine effectiveness assessment. He has published a total of nine SCI-indexed papers as the first author, one of which has been recognized as an ESI highly cited and hot paper. His work underlines his commitment to advancing the understanding of vaccination strategies and their practical applications, aiming to improve infectious disease outcomes globally through rigorous vaccine clinical assessment and evidence-based approaches.

## Diagnostic Stewardship and Its Impact

**Dr. Afreenish Amir**
*National Institute of Health, Pakistan*

**Concept:** Diagnostic stewardship is coordinated guidance and interventions to improve the appropriate use of diagnostics to guide therapeutic decisions. Diagnostic stewardship is an integral part of patient safety, and antibiotic stewardship programs and essential for infection prevention and control activities in health-care facilities. Timely and accurate laboratory results help clinicians select the most appropriate antibiotics or antibiotic combinations for their patients, as well as implement the necessary precautions to reduce the risk of transmission and prevent outbreaks due to bacterial pathogens in healthcare facilities.

**Key areas of stewardship:** Diagnostic stewardship includes all three stages of the diagnostic process in laboratory management. The pre-analytical approach begins with the practice and procedures that guide specimen selection, collection, and the completion of clinical, demographic, and epidemiological data that must accompany each specimen. Further, it includes the correct storage and transportation of specimens to the laboratory. Analytical stages cover how laboratories receive, register, and process specimens, including how appropriate tests are selected and performed. Post analytical approach deals with reporting and interpretation of the results and guides patient management. The success of each stage in this process is dependent upon the quality and effective use of available resources.

**Core Principles of Diagnostic Stewardship:** Diagnostic stewardship is based on certain core principles including ordering the right tests for the right patient, at the right time, understanding test performance and quality, considering the pre-test probability of the suspected disease or result, using diagnostic tools wisely based on clinical signs, and symptoms, and combining with the concept with antimicrobial stewardship and patient safety.

**Impact of Diagnostic Stewardship:** Diagnostic stewardship is important because it improves the overall process of diagnosing diseases. It also helps to limit the overuse of unnecessary tests and promote the appropriate use of diagnostic tools for every patient. It supports the early discontinuation of antimicrobial therapy, which can limit the risk of AMR and improve clinical outcomes. It has an impact on reduced antibiotic use and cost-effective health care.

## Comparison of the yield of two tuberculosis screening approaches among household contacts in a community setting of Silti Zone, Central Ethiopia: a prospective cohort study

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**Background:** Household contacts of tuberculosis (TB) patients are at a higher risk of infection and developing TB disease. Despite recommendations to actively screen such high-risk groups for TB, it is poorly implemented in Ethiopia. We employed community-based household contact screening to compare the yield of two different screening approaches and to identify factors associated with TB occurrence.

**Methods:** Smear-positive pulmonary TB index cases from six health facilities in six districts of Silti Zone were identified and enrolled prospectively between September 2020 and December 2022. Trained healthcare workers conducted house visits to screen household contacts for TB. WHO recommended symptom-based screening algorithm was used. The yield of screening was compared between a two-time screening at Study Site I and a single baseline screening at Study Site II, which is the current programmatic approach. We used generalized estimating equations to identify factors associated with TB occurrence.

**Results:** A total of 387 index TB cases (193 at site I and 194 at site II) with 1,276 eligible contacts were included for analysis. The TB yield of the repeat screening approach did not show a significant difference compared to a single screening (2.3% at site I vs 1.1% at site II, p<0.072). The screening algorithm for patients with comorbidities of asthma and heart failure had a 100% sensitivity, 19.1% specificity, and a positive predictive value of 5.6%. Cough [AOR: 10.9, 95%CI: 2.55,46.37], fatigue [AOR: 6.1, 95%CI: 1.76,21.29], daily duration of contact [AOR: 4.6, 95%CI; 1.57,13.43] and age of index cases [AOR: 0.9, 95% CI; 0.91- 0.99] were associated with the occurrence of TB among household contacts.

**Conclusion:** Our study showed that the yield of TB was not significantly different between one-time screening and repeat screening. Repeat screening has made an addition to case notification, but it should be practiced only if resources permit. Cough, fatigue, duration of contact, and age of index cases were factors associated with TB. Further studies are needed to establish the association between older age and the risk of transmitting TB.

### The Phylogenetic Trajectory of a Human H10N5 Avian Influenza Virus

**Dr. Chenglong Xiong**
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**Objectives:** to analyze the phylogenetic trajectory and characteristics of the first reported human H10N5 avian influenza virus (AIV), and to discuss its future epidemic trend among humans.

**Method:** BLAST and fetch 100 sequences exhibiting the highest similarity to each genomic segment of the human H10N5 AIV from NCBI and GISAID databases, a total of 800 sequences. After extracting the strain names and eliminating duplicates, the complete genomes of the retained strain were retrieved. The sequences were aligned using MAFFT, and the segments belonging to each strain were concatenated according to their subtypes: PB2-PB1-PA-HA-NP-MP-NS (H10Ny), PB2-PB1-PA-NP-NA-MP-NS (HxN5), and PB2-PB1-PA-NP-MP-NS (HxNy, including H10Ny and HxN5). Reassortment events were detected through the RDP4 software and further confirmed using Ray Soft.

**Result:** Among the 298 source strains (including 62 H10Ny and 45 HxN5 strains), 39 reassortment events associated with the human H10N5 strain were identified. A/bean goose/Korea/KNU-10/2022 (H10N7) and A/mallard/Novosibirsk region/962k/2018 (H12N5) were determined to be its potential parents. A/bean goose/Korea/KNU-10/2022 (H10N7) provided five segments (PB2, PB1, HA, MP, NS), while A/mallard/Novosibirsk region/962k/2018 (H12N5) contributed three gene segments (PA, NP, NA). The H10N5 virus likely emerged by 2022 and has been isolated multiple times in Bangladesh. Reassortments between the parental viruses frequently occur during the migration of waterfowl from Siberia to Southeast Asia, resulting in multiple AIVs subtypes, for example, H10N4 and H6N5. The HA protein of the virus exhibited the Q/E-X-R cleavage site characteristic of low-pathogenic AIVs at sites 334-PEVVQGRGLF-343. Conserved residues associated with Oseltamivir or amantadine resistance were not observed in NA and M2 proteins. Multiple host-tropism sites in PB2 protein were highly conserved. The virus demonstrated features of low pathogenicity, non-resistance, and avian tropism.

**Conclusion:** The emergence of the H10N5 subtype of avian influenza virus in humans appears to be incidental, and the likelihood of a widespread epidemic caused by this subtype in the future is extremely low. The region along the migratory route of waterfowl in Northeast Asia is gradually becoming a distinct center for influenza virus evolution, variation, and recombination, separate from Europe, the Americas, and the Yangtze River Delta and Pearl River Delta regions of China. Close surveillance of this region is warranted.

**Biography:**
Xiong, Chenglong, Ph. D, is an associate professor of the Department of Epidemiology, School of Public Health, Fudan University. His research interests are primarily focused on Bioinformatics of viral infectious diseases, Pathology, and Epidemiology of Hospital hospital-acquired infections. He published more than 80 papers. As PI, Co-PI, or Partner, he led or took part in more than 18 projects funded by the National Natural Science Foundation of China (NSFC), the National Key Research and

## Application of logistic regression methods in predicting the severity of Covid-19 infection

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The coronavirus infection caused by the SARS-CoV-2 virus is considered to be the most urgent problem facing the world health system, as it causes global socio-economic tension. Usually, in studies conducted to study the infection of COVID-19, to determine the severity of the disease, preference is given to the study of respiratory symptoms, which play an important role in several clinical and laboratory indicators and prognosis.Thus, changes in blood parameters were detected in the patients we observed during the acute period of the COVID-19 disease. Pro-inflammatory parameters, which have a role in the pathogenesis of inflammatory diseases and influence their progression, play a role in the proliferation, differentiation, and activation of immune system cells (9,10). Indeed, early identification of COVID-19 patients at risk in the first stage of the disease using routine biomarkers can lead to acute respiratory failure and may be crucial to prevent the development of multiple organ damage. The results of the studies clearly show that for patients already in the emergency department, the simultaneous increase in the level of some biomarkers was significantly associated with the severity of the disease.

**Material and methods:** The contingent of the study was made up of examination results of 212 patients who were diagnosed with COVID-19 in 2021 and received inpatient treatment at the Clinical Medical Center. Among the patients included in the study, 117 (55.2%) were female and 95 (44.8%) were male. Patients were divided into 2 groups according to the degree of severity: 110 (51.9%) patients with no complications and 102 patients with severe complications (48.1%) were included in group I. No multiple organ failure or death was recorded in the patients included in this study. Methods of examination of patients include anamnestic data collected from the history of the disease. At the same time, clinical, instrumental and laboratory examinations (general and biochemical blood analysis, coagulation markers - prothrombin time, INR, D dimer and inflammatory indicators - ferritin, CRP, ECS, and procalcitonin were included. Examinations were carried out during the acute period of the disease. Typical COVID-19 diagnosis was determined by polymerase chain reaction (PCR) of the nasopharyngeal swab according to the protocol. The SARS CoV-2 virus RNA test was positive in the pathological material taken from the nasopharynx area of all the studied patients, and unilateral or bilateral pneumonia was determined in the X-ray examination of their lungs. Statistical data processing was carried out using variation (U-Mann-Whitney), discriminant (Pearson Chi-square), correlation (Rho-Spearman), and variance (ANOVA test, F-Fisher, and F-S-Fisher-Snedekor tests). tests, as well as multiple logistic regression analysis (Backward Wald) using ROC analysis. All statistical calculations were performed in MS EXCEL-2019 and IBM Statistics SPSS-26 programs. The null hypothesis was rejected at $p < 0.050$.

**Discussion:** In the course of the study, the evaluation of the severity of complications based on the category of age, gender, and comorbid background in patients with a diagnosis of Covid-19 was investigated. According to gender, 47 (46.1%) of the total 95 male patients and 55 (53.9%) of the female patients had a severe course. Paying attention to the age group, 35 (31.8%) of the patients with a diagnosis of COVID-19 who were over 65 did not have a severe course, and 39 (38.2%) had a severe course. Both age and gender indicators were not significantly different, so the groups are representative of the degree of complication $p=0.327$, $p=0.721$. When performing a comparative analysis on comorbidities, if 50 (49.0%) people without comorbidities had a severe course, this indicator was 52 (51.0%) people with comorbidities, and the difference between the groups was statistically significant $p=0.022$. Thus, we divided the patients included in our study, which started on 31 indicators, into two groups according to the degree of complications. At the initial stage, we began to study these parameters using dispersion and Pearson Chi methods on patients with severe course. Then the obtained results were checked by the Mann-Whitney method and it was clarified that 11 indicators were statistically significant in the evaluation

of the complication rate. Then, ROC analysis curves were constructed to determine the specificity and sensitivity of the 11 indicators, and we selected specific points for each indicator with a cut-off value. The practical importance of the specificity and sensitivity of each indicator in the obtained cut-off value was studied. The obtained results showed that the impact of these indicators on the severity of the COVID-19 infection in a complex manner was considered to be of practical importance, not separately. Therefore, we included these 11 indicators in the logistic regression model and applied different methods: backward, forward, and input (enter 1,2,3). Regression models were built on 53 patients by entering 3 methods for all non-correlated indicators, and the results were analyzed on 212 patients. The sensitivity level of the indicators obtained with the Enter 3 module is 100.0±0.0%, specificity is 3.6±1.8%, RR is 50.0±3.4%, positive predictive value (pPV) is 49.0±3, 5 organized. This result was considered unfavorable ("useless") from the point of view of complication assessment. The negative predictive value (nPV) was 100.0±0.0 and the practical value was also considered

**Conclusion:** Thus, changes in blood parameters were detected in the patients we observed during the acute period of the COVID-19 disease. Pro-inflammatory parameters, which have a role in the pathogenesis of inflammatory diseases and influence their progression, play a role in the proliferation, differentiation, and activation of immune system cells (9,10). Indeed, early identification of COVID-19 patients at risk in the first stage of the disease using routine biomarkers can lead to acute respiratory failure and may be crucial to prevent the development of multiple organ damage. The results of the studies clearly show that for patients already in the emergency department, the simultaneous increase in the level of some biomarkers was significantly associated with the severity of the disease.

## Dosimetric Comparison between Intensity-modulated Radiotherapy versus Volumetric Modulated Arc Therapy Treatment Plans for Breast Cancer

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**Purpose:** This study compared the dosimetric characteristics of volumetric modulated arc therapy and Intensity-modulated radiotherapy techniques regarding target volume coverage and dose to heart, spinal cord, and lung for patients with breast cancer. We analyzed the dosimetric differences of plans in the treatment planning system between VMAT and IMRT in treating breast cancer.

**Method and Materials:** Treatment plans were analyzed for 10 patients. Patients were treated with a technique that concurrently combines IMRT beams and the VMAT technique. IMRT treatments are generated using 4 tangential fields IMRT and VMAT plans were made with one arcs field for the same patients. IMRT and VMAT treatment plans were planned for 50 Gy in 25 fractions. All treatment plans were planned due to protocols & the patient's condition. Comparative endpoints were dose homogeneity within PTV, target dose coverage, doses to the critical structures and number of monitor units, and treatment delivery time. Both plans were optimized to Dose-volume histogram values.

**Result:** The IMRT & VMAT average mean heart dose was (cGy), V30 (%) and V33 (%) for the heart were 453.7±75.5, 0.85%±0.06% and 0.19%±0.017% by VMAT, and 421.7±48.6 0.25%±0.11% and 0.016%±0.011% by IMRT, respectively. The left lung means dose (cGy), V10 (%), V20 (%) were significantly reduced from 1459.5±36.99, 36.5%±0.96% and 19.1%±0.51% with VMAT to 1356.2±48.77, 35.7%0.49% and 18.27%±0.64 with IMRT, respectively. The mean dose (Gy), 0.03 cc for the spinal cord was by 1 872.6 ± 25.64 cGy VMAT, and 872.6 ± 25.64 cGy by IMRT, respectively.

**Conclusion:** IMRT plans showed significantly higher mean dose coverage to the PTV and conformity, homogeneity Index better than the VMAT plans. The IMRT plans typically had more favorable dose characteristics to the lung, heart, spinal cord, and body dose when compared with VMAT. The main advantage of VMAT is MU & treatment delivery time is better than IMRT. Committee and other government organizations.

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