



НАУКОВО-ПРАКТИЧНА КОНФЕРЕНЦІЯ
З МІЖНАРОДНОЮ УЧАСТЮ,
присвячена 100-річчю
з дня народження
К. БАРНАРДА



СУЧАСНІ ТЕОРЕТИЧНІ ТА ПРАКТИЧНІ АСПЕКТИ КЛІНІЧНОЇ МЕДИЦИНИ

(для студентів та молодих вчених)

2–3 червня 2022 року

Тези доповідей



ОДЕСЬКИЙ
МЕДУНІВЕРСИТЕТ



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ous scientific schools. D. H. Bartenev points out that international health care law is at the stage of forming a new complex branch of international law that regulates cooperation between states and other subjects of international law in the field of medicine and health care. L. Hostin expands the subject of regulation of international health care law, including related aspects (environmental protection, bioethics, social welfare, etc.)

International health care law, as A. Taylor points out, covers increasingly diverse and complex problem areas of international legal regulation, including various aspects of biomedicine, human reproduction and cloning, control of infectious and non-infectious diseases, control over the safety of health services, products and pharmaceuticals. Jean-Marie Crouzat, who substantiates the affiliation of international health care law to international public law in the field of industry. The scholar points out that international health care law covers areas related to the human right to health: international medical law; international pharmaceutical law; international humanitarian law on health activities in times of international and domestic conflicts; provisions of international human rights law concerning the right to life and health.

Thus, international health care law can be considered as the emerging branch of international law, which is a system of international legal principles and norms that regulate the relations between the subjects of international law on cooperation in the protection of collective and individual health.

OMICRON STRAINS MUTATIONS SARS-COV-2 AMONG INDIAN POPULATION

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Introduction. COVID-19 was declared a public health emergency of international concern. Genomic sequencing of SARS-CoV-2 structure of the virus allows to detect transmission chains, track contacts and identify new strain variants, namely variants of concern (VOC), which is responsible for increasing the transmission of the virus, the formation of immune evasion and reducing the susceptibility of vaccinated individuals to infection with new strains. However, the analysis of the spread of mutations in the SARS-CoV-2 genome in India remains completely unexplored.

The goal of investigation: assess the prevalence of mutations SARS-CoV-2 genome among the population of Ukraine

Methods. Data on COVID-19 epidemiology trends of cases of infection and death in Ukraine were obtained on the open platform Google Public Data. Analysis of meta-data of all SARS-CoV-2 genomes from Ukrainian population (n=617) submitted to the GISAID database was performed from 2020 to 2021. The analysis includes data about the type and subtype of the genome identified in the GISAID database. Genome evolution analysis was performed on the Nextstrain web platform. Statistical analysis. Results: Analysis of trends showed that 20 January 2022 have been high level in daily new cases (n=34562) and mortalities (n=491) of COVID-19 in India, it revealed high levels with 3 peak growth rates. Vaccination trends in

India showed that the total number of vaccinated with 1 dose is 52%, and 2 doses — 20% of the population. Average age of population was 35.7 ± 16.1 (from 11 months to 84 years old). Among population with Omicron mutation of SARS-CoV-2 was 337 males (54.6%) and 280 females (45.6%). In the samples, the proportion of strain GRA was 99.5% and strain GR — 0.5% strain according to GISAID classification. We found strong negative association between sex and Omicron mutation ($\tau = -0.06$; $p < 0.05$).

Conclusions. It was shown high prevalence of Omicron strains of SARS-CoV-2 virus mutations during 2020-2021 among Indian population. Currently, the Omicron strain poses a new potential threat. The emergence of new strains in the country coincided with a new peak of COVID-19.

SIGNIFICANCE OF CLINICAL PEPTIDOMIC ANALYSIS IN MATERNAL HYPERTENSIVE DISORDERS IN PREGNANCY

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Hypertensive pregnancy disorders remain one of the leading causes of disability in women and maternal mortality, as well as infant perinatal morbidity and mortality. There are 4 variants of hypertensive disorders in pregnant women — chronic hypertension, gestational hypertension, preeclampsia-eclampsia and chronic hypertension with preeclampsia.

Adequate diagnosis of these diseases still remains a topical issue in modern obstetrics.

We analyzed the literature from the scientometric databases Scopus, Web of Science, Google Scholar and British Medical Journal (BMJ) in the amount of 96 papers on the keywords: “Hypertensive disorders”, “Preeclampsia-eclampsia”, “peptidomic analysis”, “chromatography”. It has been found that many authors use liquid chromatography and mass spectrometry to elucidate the molecular mechanisms involved in the development of hypertensive pregnancy disorders.

But this method was uncomfortable to determine biomarkers in a clinical blood sample, because it requires large amounts of biological materials. Therefore, according to other scientists, a more appropriate technique is BLTCHIP, as one that does not require protein depletion in the sample. Further reflection requires new research and an increase in the number of results.

VARIANTS OF GENOME MUTATIONS IN WOMEN WITH DYSREGULATION OF THE REPRODUCTIVE SYSTEM

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Most human tumors, including cancers of the female reproductive system, arise from changes caused by pathogenic mutations in so-called “cancer genes.” Based on this concept, the identification of somatic mutations in tumor genomes is the starting point in the detection of “cancer genes”. According to the au-