Epidemiology

1- Epidemiology of Hepatocellular Carcinoma

By:

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 (provided by Clarivate)

Abstract

Liver cancer is a major contributor to the worldwide cancer burden. Incidence rates of this disease have increased in many countries in recent decades. As the principal histologic type of liver cancer, hepatocellular carcinoma (HCC) accounts for the great majority of liver cancer diagnoses and deaths. Hepatitis B virus (HBV) and hepatitis C virus (HCV) remain, at present, the most important global risk factors for HCC, but their importance will likely decline in the coming years. The effect of HBV vaccination of newborns, already seen in young adults in some countries, will be more notable as vaccinated cohorts age. In addition, effective treatments for chronic infections with both HBV and HCV should contribute to declines in the rates of viral-associated HCC. Unfortunately, the prevalence of metabolic risk factors for HCC, including metabolic syndrome, obesity, type II diabetes and non-alcoholic fatty liver disease (NAFLD) are increasing and may jointly become the major cause of HCC globally. Excessive alcohol consumption also remains an intractable risk factor, as does aflatoxin contamination of food crops in some parts of the world. While significant efforts in early diagnosis and better treatment are certainly needed for HCC, primary prevention efforts aimed at decreasing the prevalence of obesity and diabetes and controlling mycotoxin growth, are just as urgently required.

Epidemiology

2- Epidemiology and determinants of obesity in China

By:

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 (provided by Clarivate)

Abstract

Obesity has become a major public health issue in China. Overweight and obesity have increased rapidly in the past four decades, and the latest national prevalence estimates for 2015-19, based on Chinese criteria, were 6.8% for overweight and 3.6% for obesity in children younger than 6 years, 11.1% for overweight and 7.9% for obesity in children and adolescents aged 6-17 years, and 34.3% for overweight and 16.4% for obesity in adults (>= 18 years). Prevalence differed by sex, age group, and geographical location, but was substantial in all subpopulations. Strong evidence from prospective cohort studies has linked overweight and obesity to increased risks of major non communicable diseases and premature mortality in Chinese populations. The growing burden of overweight and obesity could be driven by economic developments, sociocultural norms, and policies that have shaped individual level risk factors for obesity through urbanisation, urban planning and built environments, and food systems and environments. Substantial changes in dietary patterns have occurred in China, with increased consumption of animal-source foods, refined grains, and highly processed, high-sugar, and high-fat foods, while physical activity levels in all major domains have decreased with increasing sedentary behaviours. The effects of dietary factors and physical inactivity intersect with other individual-level risk factors such as genetic susceptibility, psychosocial factors, obesogens, and in-utero and early-life exposures. In view of the scarcity of research around the individual and collective roles of these upstream and downstream factors, multidisciplinary and transdisciplinary studies are urgently needed to identify systemic approaches that target both the population-level determinants and individual level risk factors for obesity in China.

Keywords

Epidemiology

3- Epidemiology and Diagnosis of Mucormycosis: An Update
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Abstract

Mucormycosis is an angioinvasive fungal infection, due to fungi of the order Mucorales. Its incidence cannot be measured exactly, since there are few population-based studies, but multiple studies have shown that it is increasing. The prevalence of mucormycosis in India is about 80 times the prevalence in developed countries, being approximately 0.14 cases per 1000 population. Diabetes mellitus is the main underlying disease globally, especially in low and middle-income countries. In developed countries the most common underlying diseases are hematological malignancies and transplantation. tau he epidemiology of mucormycosis is evolving as new immunomodulating agents are used in the treatment of cancer and autoimmune diseases, and as the modern diagnostic tools lead to the identification of previously uncommon genera/species such as Apophysomyces or Saksenaea complex. In addition, new risk factors are reported from Asia, including post-pulmonary tuberculosis and chronic kidney disease. New emerging species include Rhizopus homothallicus, Thamnostylum lucknowense, Mucor irregularis and Saksenaea erythrospora. Diagnosis of mucormycosis remains challenging. Clinical approach to diagnosis has a low sensitivity and specificity, it helps however in raising suspicion and prompting the initiation of laboratory testing. Histopathology, direct examination and culture remain essential tools, although the molecular methods are improving. The internal transcribed spacer (ITS) region is the most widely sequenced DNA region for fungi and it is recommended as a first-line method for species identification of Mucorales. New molecular platforms are being investigated and new fungal genetic targets are being explored. Molecular-based methods have gained acceptance for confirmation of the infection when applied on tissues. Methods on the detection of Mucorales DNA in blood have shown

promising results for earlier and rapid diagnosis and could be used as screening tests in high-risk patients, but have to be validated in clinical studies. More, much needed, rapid methods that do not require invasive procedures, such as serology-based point-of-care, or metabolomics-based breath tests, are being developed and hopefully will be evaluated in the near future.

4- Contemporary Epidemiology of Chronic Liver Disease and Cirrhosis

By:
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 (provided by Clarivate)

Abstract

BACKGROUND & AIMS: Accurate estimates for the contemporary burden of chronic liver disease (CLD) are vital for setting clinical, research, and policy priorities. We aimed to review the incidence, prevalence, and mortality of CLD and its resulting complications, including cirrhosis and hepatocellular carcinoma (HCC).

METHODS: We reviewed the published literature on the incidence, prevalence, trends of various etiologies of CLD and its resulting complications. In addition, we provided updated data from the Centers for Disease Control and Global Burden of Disease Study on the morbidity and mortality of CLD, cirrhosis, and hepatocellular carcinoma (HCC). Lastly, we assessed the strengths and weaknesses of available sources of data in hopes of providing important context to these national estimates of cirrhosis burden.

RESULTS: An estimated 1.5 billion persons have CLD worldwide and the age-standardized incidence of CLD and cirrhosis is 20.7/100,000, a 13% increase since 2000. Similarly, cirrhosis prevalence and mortality has increased in recent years in the United States. The epidemiology of CLD is shifting, reflecting implementation of large-scale hepatitis B vaccination and hepatitis C treatment programs, the increasing prevalence of the metabolic syndrome, and increasing alcohol misuse.

CONCLUSIONS: The global burden of CLD and cirrhosis is substantial. Although vaccination, screening, and antiviral treatment campaigns for hepatitis B and C have reduced the CLD burden in some parts of the world, concomitant increases in injection drug use, alcohol misuse, and metabolic syndrome threaten

Epidemiology

these trends. Ongoing efforts to address CLD-related morbidity and mortality require accurate contemporary estimates of epidemiology and outcomes.

5- Global epidemiology of NAFLD-related HCC: trends, predictions, risk factors and prevention

By:

Huang, DIQ (Huang, Daniel Q.) [1] , [2] ; El-Serag, HB (El-Serag, Hashem B.) [3] , [4] , [5] , [6] ; Loomba, R (Loomba, Rohit) [7] , [8]

 (provided by Clarivate)

Abstract

The prevalence of nonalcoholic fatty liver disease (NAFLD)-related hepatocellular carcinoma (HCC) is projected to continue to increase worldwide. In this Review, Huang, El-Serag and Loomba discuss the global epidemiology and risk factors for NAFLD-related HCC, and propose strategies to tackle this problem. One quarter of the global population is estimated to have nonalcoholic fatty liver disease (NAFLD). The incidence of nonalcoholic steatohepatitis (NASH) is projected to increase by up to 56% in the next 10 years. NAFLD is already the fastest growing cause of hepatocellular carcinoma (HCC) in the USA, France and the UK. Globally, the prevalence of NAFLD-related HCC is likely to increase concomitantly with the growing obesity epidemic. The estimated annual incidence of HCC ranges from 0.5% to 2.6% among patients with NASH cirrhosis. The incidence of HCC among patients with non-cirrhotic NAFLD is lower, approximately 0.1 to 1.3 per 1,000 patient-years. Although the incidence of NAFLD-related HCC is lower than that of HCC of other aetiologies such as hepatitis C, more people have NAFLD than other liver diseases. Urgent measures that increase global awareness and tackle the metabolic risk factors are necessary to reduce the impending burden of NAFLD-related HCC. Emerging evidence indicates that reduced immune surveillance, increased gut inflammation and gut dysbiosis are potential key steps in tumorigenesis. In this Review, we discuss the global epidemiology, projections and risk factors for NAFLD-related HCC, and propose preventive strategies to tackle this growing problem.

Epidemiology

Epidemiology

6- A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology

By:
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 (provided by Clarivate)

Abstract

The ongoing pandemic spread of a new human coronavirus, SARS-CoV-2, which is associated with severe pneumonia/disease (COVID-19), has resulted in the generation of tens of thousands of virus genome sequences. The rate of genome generation is unprecedented, yet there is currently no coherent nor accepted scheme for naming the expanding phylogenetic diversity of SARS-CoV-2. Here, we present a rational and dynamic virus nomenclature that uses a phylogenetic framework to identify those lineages that contribute most to active spread. Our system is made tractable by constraining the number and depth of hierarchical lineage labels and by flagging and delabelling virus lineages that become unobserved and hence are probably inactive. By focusing on active virus lineages and those spreading to new locations, this nomenclature will assist in tracking and understanding the patterns and determinants of the global spread of SARS-CoV-2.

7- Genomic characterization and epidemiology of an emerging SARS-CoV-2 variant in Delhi, India

By:

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Group Author:

Indian SARS-CoV-2 Genomics Consort (Indian SARS-CoV-2 Genomics Consort)
 (provided by Clarivate)

Abstract

Delhi, the national capital of India, experienced multiple severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) outbreaks in 2020 and reached population seropositivity of >50% by 2021. During April 2021, the city became overwhelmed by COVID-19 cases and fatalities, as a new variant, B.1.617.2 (Delta), replaced B.1.1.7 (Alpha). A Bayesian model explains the growth advantage of Delta through a combination of increased transmissibility and reduced sensitivity to immune responses generated against earlier variants (median estimates: 1.5-fold greater transmissibility and 20% reduction in sensitivity). Seropositivity of an employee and family cohort increased from 42% to 87.5% between March and July 2021, with 27% reinfections, as judged by increased antibody concentration after a previous decline. The likely high transmissibility and partial evasion of immunity by the Delta variant contributed to an overwhelming surge in Delhi.

Epidemiology

8- Omicron (B.1.1.529) - variant of concern - molecular profile and epidemiology: a mini review

By:
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 (provided by Clarivate)

Abstract

Recently a new variant of SARS-as a variant of concern - Omicron (B.1.1.529) on 26th November 2021. This variant exhibited more than thirty amino acid mutations in the spike protein. This mutation rate is exceeding the other variants by approximately 5-11 times in the receptor-binding motif of the spike protein. Omicron (B.1.1.529) variant might have enhanced transmissibility and immune evasion. This new variant can reinfect individuals previously infected with other SARS-CoV-2 variants. Scientists expressed their concern about the efficacy of already existing COVID-19 vaccines against Omicron (B.1.1.529) infections. Some of the crucial mutations that are detected in the receptor-binding domain of the Omicron variant have been shared by previously evolved SARS-CoV-2 variants. Based on the Omicron mutation profile in the receptor-binding domain and motif, it might have collectively enhanced or intermediary infectivity relative to its previous variants. Due to extensive mutations in the spike protein, the Omicron variant might evade the immunity in the vaccinated individuals.

10- Individuals with obesity and COVID-19: A global perspective on the epidemiology and biological relationships

By:

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 (provided by Clarivate)

Abstract

The linkage of individuals with obesity and COVID-19 is controversial and lacks systematic reviews. After a systematic search of the Chinese and English language literature on COVID-19, 75 studies were used to conduct a series of meta-analyses on the relationship of individuals with obesity-COVID-19 over the full spectrum from risk to mortality. A systematic review of the mechanistic pathways for COVID-19 and individuals with obesity is presented. Pooled analysis show individuals with obesity were more at risk for COVID-19 positive, >46.0% higher (OR = 1.46; 95% CI, 1.30-1.65;p< 0.0001); for hospitalization, 113% higher (OR = 2.13; 95% CI, 1.74-2.60;p< 0.0001); for ICU admission, 74% higher (OR = 1.74; 95% CI, 1.46-2.08); and for mortality, 48% increase in deaths (OR = 1.48; 95% CI, 1.22-1.80;p< 0.001). Mechanistic pathways for individuals with obesity are presented in depth for factors linked with COVID-19 risk, severity and their potential for diminished therapeutic and prophylactic treatments among these individuals. Individuals with obesity are linked with large significant increases in morbidity and mortality from COVID-19. There are many mechanisms that jointly explain this impact. A major concern is that vaccines will be less effective for the individuals with obesity.

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Epidemiology

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