

· 述评 ·

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## 亚洲地区不同人群丁型肝炎病毒感染的流行情况

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**摘要:** 丁型肝炎病毒(HDV)感染是病毒性肝炎中最严重的类型,但因筛查策略不一致及监测有限,在亚洲地区长期被忽视。本文系统综述了1970—2025年亚洲地区的社区/普通人群、肝病门诊/医院队列及高危人群3个亚组分层的HDV流行率,其中,巴基斯坦、哈萨克斯坦及吉尔吉斯斯坦的社区/普通人群HDV流行率高;蒙古国、乌兹别克斯坦的肝病门诊/医院队列呈高地方性流行;中国香港、中国台湾及越南、阿曼苏丹国的高危人群中存在传播集中现象。此外,许多国家尚缺乏可查的亚组数据。HDV流行分布不均且因人群特征而异的疾病负担凸显。HDV感染是进展期肝病的重要驱动因素,加强常规HDV筛查及RNA检测,对于明确疾病负担和推进实现世界卫生组织提出的“2030年消除病毒性肝炎公共卫生危害”这一目标至关重要。

**关键词:** δ肝炎病毒; 流行病学; 亚洲

### Subgroup stratified burden of hepatitis D virus in Asia

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**Abstract:** Hepatitis D virus (HDV) infection, the most severe form of viral hepatitis, remains underrecognized in the Asia due to inconsistent screening and limited surveillance. This systematic review (1970—2025) stratified HDV prevalence by population subgroups: community, hospital-based, and high-risk. Community studies showed high prevalence in Pakistan, Kazakhstan, and Kyrgyzstan; hospital cohorts revealed hyperendemicity in Mongolia and Uzbekistan; high-risk populations showed concentrated transmission in [Hong Kong, China], [Taiwan, China], Vietnam, and Sultanate of Oman. Many countries and regions lacked subgroup-specific data. The uneven, population-dependent burden underscores HDV as a major driver of advanced liver disease in Central and South Asia. Routine HDV screening and RNA-based diagnostics are essential to define burden and advance WHO 2030 elimination targets.

**Key words:** Hepatitis Delta Virus; Epidemiology; Asia

[本文原始版本为英文,以中英对照形式发表]

丁型肝炎病毒(hepatitis D virus, HDV)是一种有缺陷的单链RNA病毒,其复制和传播依赖于乙型肝炎病毒表面抗原(HBV surface antigen, HBsAg)。HDV感染仅发生于乙型肝炎病毒(hepatitis B virus, HBV)感染者中,感染形式包括共感染和重叠感染。与单纯HBV感染相比,合并HDV感染可加速肝纤维化进程,并显著增加肝硬化、肝细胞癌和肝病相关死亡的风险<sup>[1]</sup>。尽管HDV感染的临床结果严重,但由于筛查实践的不统一以及HDV检测尚未常规纳入HBV管理流程,该病在全球范围内仍面临诊断不足的困境。

Hepatitis D virus (HDV) is a defective, single-stranded RNA virus that requires hepatitis B surface antigen (HBsAg) for replication and transmission. Infection occurs only in individuals with hepatitis B virus (HBV) infection, either as co-infection or super-infection. HDV accelerates hepatic fibrosis and markedly increases the risks of cirrhosis, hepatocellular carcinoma, and liver-related mortality compared with HBV mono-infection<sup>[1]</sup>. Despite its severe clinical consequences, HDV remains underdiagnosed worldwide because of inconsistent screening practices and limited incorporation of HDV testing into routine HBV management.

由于不同监测体系、诊断能力与管理政策的差异,全球关于HDV感染情况的估测值存在较大差异,这一问题在HBV高流行地区尤为突出<sup>[2-3]</sup>。亚洲地区作为全球慢性HBV感染人数最多的区域,是评估全球HDV疾病负担的核心区域。现有证据表明,亚洲地区HDV流行病学数据存在显著的地域性差异:高地方性流行区与流行病学数据匮乏、陈旧甚至完全缺失的地区并存。东亚、南亚、中亚和中东多个国家及地区已报告较高的HDV流行率,尤以进展期肝病患者为甚<sup>[4-9]</sup>。然而,其他HBV高流行地区却缺乏可靠的HDV流行病学数据。这种分布不均的现象,叠加HDV特异性治疗药物的涌现以及世界卫生组织提出的“2030年消除病毒性肝炎公共卫生危害”目标,凸显了开展覆盖全区域、数据更新的流行病学调查的迫切必要性。本文旨在通过亚组分层分析框架,系统整合亚洲地区HDV流行率相关数据,识别高、中疾病负担国家和地区,并厘清关键数据缺口,从而为监测重点的确定和公共卫生政策的制订提供参考依据。

Global estimates of HDV infection range widely, reflecting heterogeneity in surveillance systems, diagnostic capacity, and testing policies, particularly in regions with high HBV endemicity<sup>[2-3]</sup>. The Asia region, which harbors

the largest global reservoir of chronic HBV infection, is therefore central to understanding the global HDV burden. Available evidence indicates profound geographic variability, with hyperendemic hotspots coexisting alongside countries and regions where epidemiologic data are sparse, outdated, or entirely absent. High prevalence has been reported in several countries and regions across East, South, and Central Asia and the Middle East, especially among patients with advanced liver disease<sup>[4-9]</sup>, whereas other high-HBV settings lack dependable HDV estimates. This uneven distribution, together with the emergence of HDV-specific therapies and the WHO 2030 viral hepatitis elimination targets, underscores the need for updated and region-wide epidemiologic mapping. The present review aims to synthesize available data on HDV prevalence across the Asia region using a subgroup-stratified framework, identifying high and moderate burden countries and regions, and delineating critical data gaps to inform surveillance priorities and public health policy.

笔者对1970—2025年发表的文献开展系统综述,以绘制涵盖亚洲地区所有国家和地区的HDV流行率分布图,包括巴林<sup>[4]</sup>、文莱<sup>[4]</sup>、不丹<sup>[4]</sup>、柬埔寨<sup>[4]</sup>、塞浦路斯<sup>[4]</sup>、马尔代夫<sup>[4]</sup>、缅甸<sup>[4]</sup>、蒙古国<sup>[5-6]</sup>、新加坡<sup>[4]</sup>、斯里兰卡<sup>[4]</sup>、叙利亚<sup>[4]</sup>、阿拉伯联合酋长国<sup>[4]</sup>、朝鲜<sup>[4]</sup>、巴勒斯坦国<sup>[4]</sup>、东帝汶<sup>[4]</sup>、土库曼斯坦<sup>[4]</sup>、中国澳门<sup>[4]</sup>、乌兹别克斯坦<sup>[7]</sup>、中国内地<sup>[10-12]</sup>、印度尼西亚<sup>[13]</sup>、巴基斯坦<sup>[9, 14-21]</sup>、印度<sup>[21-26]</sup>、孟加拉国<sup>[27]</sup>、日本<sup>[28-30]</sup>、菲律宾<sup>[31]</sup>、越南<sup>[32-35]</sup>、伊朗<sup>[36-41]</sup>、土耳其<sup>[8, 42]</sup>、泰国<sup>[43-44]</sup>、韩国<sup>[45-47]</sup>、伊拉克<sup>[48-49]</sup>、阿富汗<sup>[50-51]</sup>、也门<sup>[52]</sup>、马来西亚<sup>[53-54]</sup>、沙特阿拉伯王国<sup>[55-57]</sup>、尼泊尔<sup>[58]</sup>、哈萨克斯坦<sup>[59-60]</sup>、约旦<sup>[61]</sup>、塔吉克斯坦<sup>[62-63]</sup>、阿塞拜疆<sup>[64]</sup>、以色列<sup>[65-67]</sup>、老挝<sup>[68]</sup>、吉尔吉斯斯坦<sup>[69]</sup>、黎巴嫩<sup>[70]</sup>、阿曼苏丹国<sup>[71]</sup>、科威特<sup>[72]</sup>、格鲁吉亚<sup>[73]</sup>、卡塔尔<sup>[74]</sup>、亚美尼亚<sup>[75]</sup>、中国台湾<sup>[76-77]</sup>、中国香港<sup>[78-79]</sup>以及俄罗斯的亚洲部分<sup>[80]</sup>。

We conducted a comprehensive literature review of studies published between 1970 and 2025 to map HDV prevalence across the Asia region, encompassing all countries and regions, including Bahrain<sup>[4]</sup>, Brunei<sup>[4]</sup>, Bhutan<sup>[4]</sup>, Cambodia<sup>[4]</sup>, Cyprus<sup>[4]</sup>, Maldives<sup>[4]</sup>, Myanmar<sup>[4]</sup>, Mongolia<sup>[5-6]</sup>, Singapore<sup>[4]</sup>, Sri Lanka<sup>[4]</sup>, Syria<sup>[4]</sup>, The United Arab Emirates<sup>[4]</sup>, The Democratic People's Republic of Korea<sup>[4]</sup>, The State of Palestine<sup>[4]</sup>, Timor Leste<sup>[4]</sup>, Turkmenistan<sup>[4]</sup>, [Macao, China]<sup>[4]</sup>, Uzbekistan<sup>[7]</sup>, Chinese mainland<sup>[10-12]</sup>, Indonesia<sup>[13]</sup>,

Pakistan<sup>[9,14-21]</sup>, India<sup>[21-26]</sup>, Bangladesh<sup>[27]</sup>, Japan<sup>[28-30]</sup>, Philippines<sup>[31]</sup>, Vietnam<sup>[32-35]</sup>, Iran<sup>[36-41]</sup>, Turkey<sup>[8,42]</sup>, Thailand<sup>[43-44]</sup>, The Republic of Korea<sup>[45-47]</sup>, Iraq<sup>[48-49]</sup>, Afghanistan<sup>[50-51]</sup>, Yemen<sup>[52]</sup>, Malaysia<sup>[53-54]</sup>, The Kingdom of Saudi Arabia<sup>[55-57]</sup>, Nepal<sup>[58]</sup>, Kazakhstan<sup>[59-60]</sup>, Jordan<sup>[61]</sup>, Tajikistan<sup>[62-63]</sup>, Azerbaijan<sup>[64]</sup>, Israel<sup>[65-67]</sup>, Laos<sup>[68]</sup>, Kyrgyzstan<sup>[69]</sup>, Lebanon<sup>[70]</sup>, Sultante of Oman<sup>[71]</sup>, Kuwait<sup>[72]</sup>, Georgia<sup>[73]</sup>, Qatar<sup>[74]</sup>, Armenia<sup>[75]</sup>, [Taiwan, China]<sup>[76-77]</sup>, [Hong Kong, China]<sup>[78-79]</sup>, and the Asian part of Russia<sup>[80]</sup>.

符合标准的文献需报告经确证的HBsAg阳性人群中的HDV抗体血清阳性率和/或HDV RNA检出率,研究对象涵盖全国/地区性或亚全国/地区性队列,包括社区调查、医院或肝病门诊队列、献血者及高危人群。将HDV抗体作为既往感染的标志物,逆转录聚合酶链反应检出HDV RNA提示活动性感染。流行率分层标准参照既往流行病学阈值:高流行定义为HDV抗体≥10.0%或HDV RNA≥30.0%;中等流行为HDV抗体2.0%~9.9%或HDV RNA5.0%~29.9%;低流行为HDV抗体<2.0%或HDV RNA<5.0%。本文数据基于现有亚组研究估算,不具有全国/地区代表性,且跨国比较需谨慎解读。

Eligible studies reported anti-HDV seropositivity and/or HDV RNA detection among confirmed HBsAg-positive individuals in national or subnational cohorts, including community-based surveys, hospital or liver clinic cohorts, blood donors, and high-risk populations. Anti-HDV antibodies were used as markers of exposure, while HDV RNA detection by quantitative RT-PCR indicated active infection. High prevalence was defined as anti-HDV ≥ 10.0% or HDV RNA ≥30.0%; moderate prevalence as anti-

HDV 2.0%—9.9% or HDV RNA 5.0%—29.9%; and low prevalence as anti-HDV <2.0% or HDV RNA <5.0%, consistent with previously applied epidemiologic thresholds. Notably, estimates in this review are based on available subgroup studies and are not nationally representative, and cross-country comparisons should be interpreted cautiously.

1 社区/普通人群的HDV流行情况

1 Prevalence of HDV in the community/general population

基于社区的研究显示,亚洲地区HBsAg阳性人群的HDV流行率存在显著的地域性差异(图1),高流行地区主要集中于中亚和南亚部分地区,提示在上述地区的社区层面存在持续的传播,而非仅限于转诊或医院人群<sup>[9, 59, 69]</sup>。部分国家和地区呈中等水平流行,提示HDV在一般人群中仍有传播,但强度较低<sup>[28, 66, 72, 74]</sup>。此外,东亚和东南亚多个国家及地区报告了较低或可忽略的流行率<sup>[40, 45, 50, 62, 68, 73, 75, 78]</sup>。

Community-based studies demonstrated marked geographic heterogeneity in HDV prevalence among HBsAg-positive individuals across the Asia region (Figure 1), high-prevalence settings were primarily concentrated in parts of Central and South Asia, indicating sustained community-level transmission beyond referral or hospital-based populations<sup>[9, 59, 69]</sup>. Several countries and regions showed moderate endemicity, suggesting ongoing but less intense circulation within the general population<sup>[28, 66, 72, 74]</sup>. In contrast, multiple East and Southeast Asian countries and regions reported low or negligible prevalence<sup>[40, 45, 50, 62, 68, 73, 75, 78]</sup>.

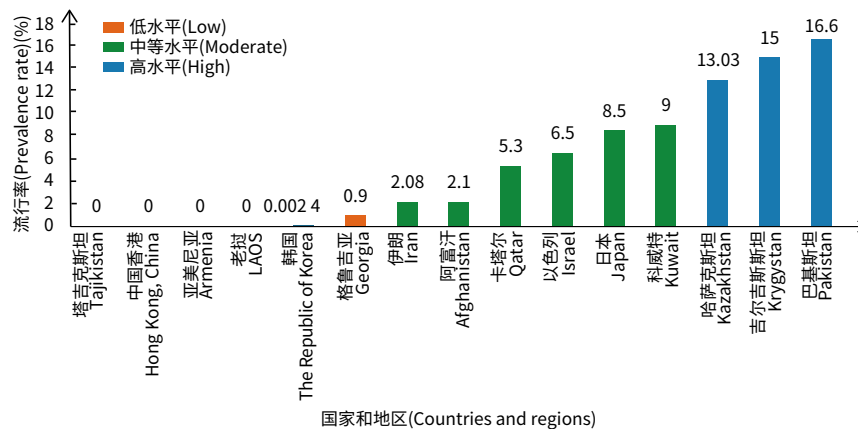


图1 基于社区/普通人群研究的亚洲地区丁型肝炎病毒感染风险分布图

Figure 1 Bar charts representing risk distribution of hepatitis D virus infection in Asia regions based on community/ general population based studies

值得注意的是,相当数量的国家和地区缺乏具有全国代表性的社区层面HDV流行数据。这些监测空白限制了对真实人群负担的准确评估,凸显了在现行HBV防治框架内整合开展标准化HDV血清流行病学调查的必要性。

Notably, a substantial number of countries and regions lacked nationally representative community-level data. These surveillance gaps limit accurate assessment of true population burden and highlight the need for standardized sero-epidemiologic studies integrated within HBV care frameworks.

## 2 肝病门诊/医院的HDV流行情况

### 2 Prevalence of HDV in the liver clinic/hospital

在肝病门诊及医院队列中,HDV的流行率高于社区人群,与进展期肝病患者的聚集和转诊偏倚有关(图2)。中亚部分地区,特别是蒙古国和乌兹别克斯坦,呈现超高度地方性流行;南亚及西亚多个国家和地区亦报告持续高流行<sup>[5,7]</sup>。上述结果提示,HDV是导致HBV相关重症肝病的重要因素<sup>[15, 27, 42, 48, 60-61, 63-64, 80]</sup>。

HDV prevalence in liver clinic and hospital-based cohorts was higher than in community-based populations, reflecting concentration of patients with advanced liver disease and referral bias (Figure 2). Hyperendemic levels were observed in parts of Central Asia, particularly in Mongolia and Uzbekistan, while persistently high prevalence was also documented in several countries and regions across South and West Asia<sup>[5,7]</sup>. These findings highlight the significant contribution of HDV to severe HBV-related liver disease in these regions<sup>[15, 27, 42, 48, 60-61, 63-64, 80]</sup>.

东南亚和中东的多个国家及地区报告了中度流行率,提示即使在非超高度流行区,HDV仍造成不可忽视的临床疾病负担<sup>[13, 21, 32, 39, 50, 53, 56, 65]</sup>。相比之下,东亚和东南亚部分国家及地区则呈现HDV低流行率<sup>[12, 29, 31, 43, 46, 53, 58, 70, 76]</sup>。

Moderate prevalence was reported in multiple countries and regions spanning Southeast Asia and the Middle East, indicating clinically meaningful HDV burden even outside hyperendemic zones<sup>[13, 21, 32, 39, 50, 53, 56, 65]</sup>. In contrast, several East and Southeast Asian countries and regions demonstrated low prevalence within hospital-based settings<sup>[12, 29, 31, 43, 46, 53, 58, 70, 76]</sup>.

尽管多个亚洲地区HDV流行数据已有发布,但针对住院患者的监测仍有不足,且部分地区尚无基于医院的HDV流行率公开数据。因此,在三级医疗机构和转诊中心对HBsAg阳性患者开展标准化HDV筛查,对于准确界定疾病负担及指导临床管理策略至关重要。

Despite available data from numerous countries and regions, gaps in inpatient surveillance remain, and several Asia settings lack published hospital-based HDV estimates. Standardized screening of HBsAg-positive patients in tertiary and referral centers is therefore essential to better define disease burden and inform clinical management strategies.

## 3 高风险人群的HDV流行情况

### 3 Prevalence of HDV in the high risk population

在已明确的高风险人群(包括具有行为、临床或病毒学风险因素的个体)中,HDV的流行率通常高于社区环境(图3)。在东亚、东南亚及中东的部分地区呈现高

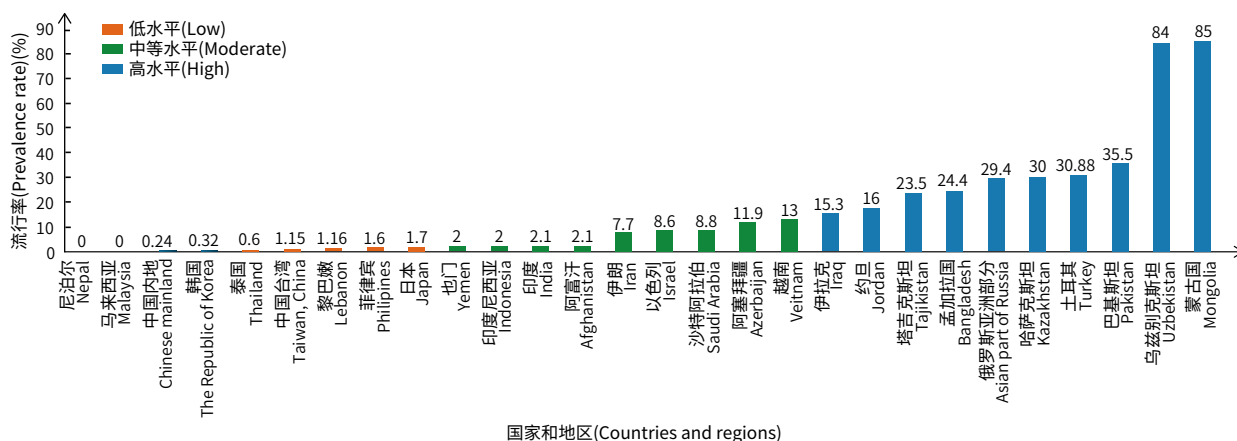


图2 基于肝病门诊/医院研究的亚洲地区丁型肝炎病毒感染风险分布图

Figure 2 Bar charts representing risk distribution of hepatitis D virus infection in Asia regions based on liver clinic/ hospital based studies

流行率,提示在该亚组中存在集中的传播,并凸显了开展针对性筛查和采取预防策略的重要性<sup>[34, 71, 77, 79]</sup>。

HDV prevalence among defined high-risk populations, including individuals with behavioural, clinical, or virologic risk factors, was generally higher than in community-based settings (Figure 3). High prevalence was identified in selected East and Southeast Asian and Middle Eastern settings, indicating concentrated transmission within vulnerable subgroups and underscoring the importance of targeted screening and prevention strategies<sup>[34, 71, 77, 79]</sup>.

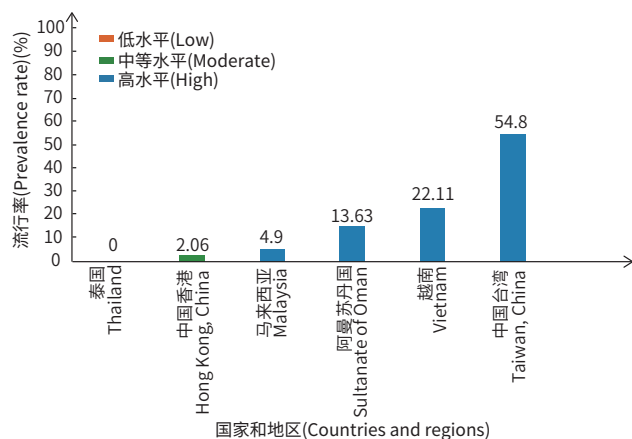


图3 基于高风险人群的亚洲地区丁型肝炎病毒感染风险分布图

Figure 3 Bar charts representing risk distribution of hepatitis D virus infection in Asia regions based on high-risk population

部分国家报告了中等流行率,反映出HDV在已确定的高风险人群中仍持续传播,但流行程度相对较低<sup>[53]</sup>。相比之下,部分地区的HDV流行率较低<sup>[44]</sup>,提示在所研究人群中传播有限,或数据可及性受限。

Moderate prevalence was reported in certain countries and regions, reflecting ongoing but comparatively lower HDV circulation within identified high-risk cohorts<sup>[53]</sup>. In contrast, low prevalence<sup>[44]</sup> was documented in some regions, suggesting either limited transmission within studied groups or constrained data availability.

值得注意的是,亚洲地区部分国家和地区缺乏高风险人群中HDV流行率的已发表数据。考虑到高风险人群常可作为新发或未被充分认识的传播动态的早期预警人群,因此,针对该人群的监测是目前一个关键的流行病学缺口。

Notably, many countries and regions across the Asia region lack published estimates for HDV prevalence in high-risk populations. This absence of subgroup-focused

surveillance constitutes a critical epidemiologic gap, particularly given that high-risk groups often function as sentinel populations for emerging or underrecognized transmission dynamics.

57项研究报告了HBV阳性患者中HDV抗体血清学阳性情况。在HBV阳性患者中,HDV抗体血清阳性率为18.88%(11 530/61 048),比值为0.15(95%CI: 0.13 ~ 0.17,  $P < 0.001$ ,  $I^2 = 99.88%$ )(图4)。

57 studies reported anti-HDV seropositivity in HBV-positive patients. Anti-HDV seropositivity was observed in 18.88% (11 530/61 048) of the HBV-positive patients with an odds ratio of 0.15 (95%CI: 0.13—0.17;  $P < 0.001$ ,  $I^2 = 99.88%$ ) (Figure 4).

15项研究报告了HBV阳性患者中HDV流行率/活动性感染情况。在HBV阳性患者中,HDV检出率为18.39%(1 957/10 641),比值为0.17(95%CI: 0.11 ~ 0.23,  $P < 0.001$ ,  $I^2 = 99.50%$ )(图5)。

15 studies reported HDV prevalence/active infection in HBV-positive patients. HDV was found in 18.39% (1 957/10 641) of the HBV-positive patients with an OR of 0.17 (95%CI: 0.11—0.23;  $P < 0.001$ ;  $I^2 = 99.50%$ ) (Figure 5).

#### 4 数据缺失国家和地区

#### 4 Data gap countries and regions

尽管已建立HBV监测体系,16个国家和地区仍无可查的HDV流行率研究数据。其中,多数国家和地区与中高流行率地区接壤,相关地区未知的HDV流行情况令人担忧。数据缺失反映了检测能力有限、HBV诊疗中缺乏常规HDV筛查以及文献发表不足,而非已证实无感染存在<sup>[1-2,4]</sup>,涉及国家和地区包括缅甸、柬埔寨、新加坡、东帝汶、文莱、朝鲜、中国澳门、斯里兰卡、不丹、马尔代夫、叙利亚、阿拉伯联合酋长国、巴勒斯坦、巴林、塞浦路斯及土库曼斯坦。

Sixteen countries and regions had no identifiable published data on HDV prevalence despite inclusion in regional HBV surveillance efforts. Many of these countries and regions border moderate-to-high prevalence regions, raising concern for undetected transmission. The absence of data reflects limited testing, lack of routine HDV screening in HBV care, and insufficient publication rather than confirmed absence of infection<sup>[1-2,4]</sup>, Myanmar, Cambodia, Singapore, Timor-Leste, Brunei, The Democratic People's Republic of Korea, [Macao, China], Sri Lanka, Bhutan, Maldives, Syria, United Arab Emirates, Palestine, Bahrain, Cyprus and Turkmenistan.

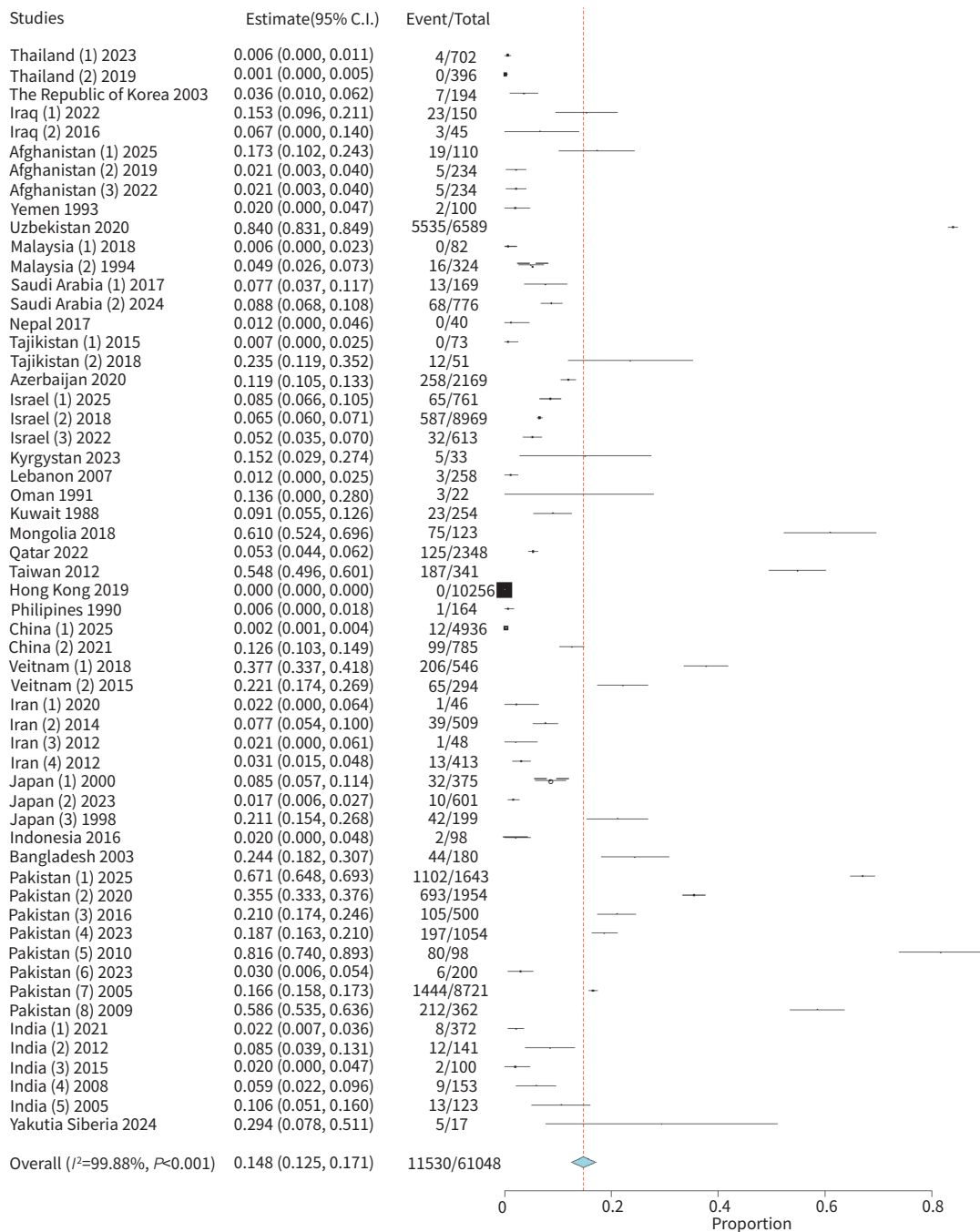


图4 乙型肝炎病毒阳性患者中丁型肝炎病毒阳性率的森林图

Figure 4 Forest plot demonstrating hepatitis D virus seropositivity in hepatitis B virus-positive patients

## 5 小结与展望

### 5 Conclusions and future directions

HDV在亚太、中东及中亚地区的流行病学分布呈现出显著差异,其流行程度从高地方性流行到无公开数据不等。据估算,全球有1 200万~7 200万人感染HDV,亚洲地区承担着不成比例的疾病负担。本研究通过亚组分层分析,将纳入的研究划分为社区/一般人群、肝病

门诊/医院队列以及高危人群,从而为HDV流行差异提供了更为细致的解析,并凸显了当前疾病监测体系中存在的缺口。

The epidemiology of HDV across the Asia Pacific, Middle East, and Central Asia demonstrates striking heterogeneity, ranging from hyperendemic hotspots to countries and regions with no published data. Globally, an

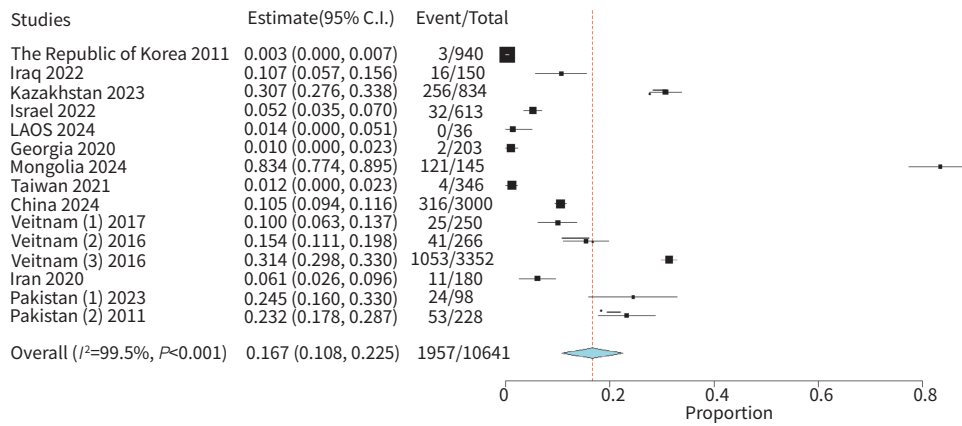


图5 乙型肝炎病毒阳性患者中丁型肝炎病毒RNA检出率的森林图

Figure 5 Forest plot demonstrating hepatitis D virus RNA prevalence in hepatitis B virus-positive patients

estimated 12—72 million people are infected, with Asia bearing a disproportionate burden. Our subgroup stratified analysis dividing studies into community/general population, liver clinic/hospital cohorts, and high-risk populations provides a nuanced view of this variability and highlights critical gaps in surveillance.

基于社区的研究显示,在巴基斯坦(16.6%)、哈萨克斯坦(13.03%)和吉尔吉斯斯坦(15%)存在较为明显的HDV流行,而中国香港(0)、塔吉克斯坦(0)、亚美尼亚(0)、老挝(0)和韩国(0.002 4%)等地区报告的患病率可忽略不计。基于医院的队列研究揭示了更严重的疾病负担,其中,蒙古(85%)和乌兹别克斯坦(84%)处于HDV超高水平流行,巴基斯坦(35.5%)、土耳其(30.88%)、哈萨克斯坦(30%)、孟加拉国(24.4%)和塔吉克斯坦(23.5%)的患病率较高。在非热点地区的越南(13%)、伊朗(7.7%)、沙特阿拉伯(8.8%)和以色列(8.6%)的中等患病率也凸显了亟需关注的HDV流行。在高风险人群,包括婴幼儿、儿童及HBV相关肝病患者中,中国香港(93%)、中国台湾(54.8%)、越南(22.1%)和阿曼苏丹国(13.6%)呈现HDV高水平流行,而马来西亚(4.9%)和泰国(0)的较低流行水平既反映了真实的流行病学差异,也反映了数据获取的局限性。缅甸、朝鲜、斯里兰卡、柬埔寨、阿联酋、土库曼斯坦、新加坡、文莱、不丹、马尔代夫、东帝汶、中国澳门和塞浦路斯缺乏各亚组相关公开数据,构成了极大的监测盲区。

Community based studies show substantial background transmission in Pakistan (16.6%), Kazakhstan (13.03%), and Kyrgyzstan (15%), while countries and regions such as [Hong Kong, China] (0), Tajikistan (0), Armenia (0), Laos (0), and The Republic of Korea (0.002 4%) report negligible prevalence. Hospital-

based cohorts reveal more severe burdens, with hyperendemic levels in Mongolia (85%) and Uzbekistan (84%), and high prevalence in Pakistan (35.5%), Turkey (30.88%), Kazakhstan (30%), Bangladesh (24.4%), and Tajikistan (23.5%). Moderate prevalence in Vietnam (13%), Iran (7.7%), Saudi Arabia (8.8%), and Israel (8.6%) underscores clinically relevant transmission even in non-hotspot regions. High-risk populations, including infants, children, and patients with HBV-related liver disease, show concentrated transmission in Hong Kong, China (93%), [Taiwan, China] (54.8%), Vietnam (22.1%), and Oman (13.6%), while lower rates in Malaysia (4.9%), and Thailand (0) reflect both true epidemiologic differences and limited data availability. Across all subgroups, many countries and regions including Myanmar, The Democratic People’s Republic of Korea, Sri Lanka, Cambodia, UAE, Turkmenistan, Singapore, Brunei, Bhutan, Maldives, Timor-Leste, [Macao, China], and Cyprus lack published data, creating substantial blind spots.

上述结果提示,当前存在一个地域相连的HDV流行带,该流行带从中亚延伸至蒙古国和中国西部地区,并向南穿过阿富汗、巴基斯坦及中东部分地区。中亚地区类似于HDV的“长期储存库”,该区域的HDV流行负担可能因人口迁移、贸易及劳动力流动而加剧。蒙古国、乌兹别克斯坦及巴基斯坦部分地区极高的HDV流行率,凸显了HDV在HBV高流行人群中的持续存在。包括难民及劳工流动在内的区域性跨境活动进一步延续了HDV传播,这强调了HDV流行的跨国性特征,而非孤立的局部流行。

These findings suggest a geographically connected belt of HDV endemicity extending from Central Asia into

Mongolia and western China, and southward through Afghanistan, Pakistan, and parts of the Middle East. Central Asian republics appear to act as long-standing reservoirs, with dissemination likely facilitated by migration, trade, and labor mobility. The exceptionally high prevalence in Mongolia, Uzbekistan, and parts of Pakistan highlights sustained viral persistence in highly HBV endemic populations. Regional cross-border movements, including refugee and labour flows further perpetuate the transmission, emphasizing the transnational nature of HDV rather than isolated epidemics.

临床上,HDV感染可加速肝脏疾病的进展,显著增加肝硬化、肝细胞癌风险。世界卫生组织建议,针对所有处于高流行区或高危环境中的HBsAg阳性人群中,应常规HDV检测。本研究结果进一步证实,在越南、土耳其、伊拉克、乌兹别克斯坦、哈萨克斯坦、伊朗、巴基斯坦及印度部分地区等HDV中高流行率国家和地区,有必要在HBV诊疗路径中实行“附加式”(reflex)HDV检测。对于高疾病负担人群,例如肝硬化患者,迫切需要将HDV诊断整合进常规诊疗,并提升患者对HDV感染新兴疗法的可及性。

Clinically, HDV accelerates liver disease progression, significantly increasing the risk of cirrhosis and hepatocellular carcinoma. WHO recommends routine HDV testing for all HBsAg-positive individuals in high-prevalence or at-risk settings. Our findings reinforce the need for reflex HDV testing within HBV care pathways in countries and regions with moderate-to-high prevalence, including Vietnam, Turkey, Iraq, Uzbekistan, Kazakhstan, Iran, Pakistan, and parts of India. High-burden cohorts, such as cirrhosis patients in Uzbekistan where HDV positivity exceeds 80%, require urgent diagnostic integration and access to emerging therapies.

不同国家和地区结果存在的异质性,既反映了流行病学差异,也反映了方法学差异,包括研究人群和诊断方法的不同,以及HDV RNA检测实践的不一致。基因I型HDV感染在亚洲多数地区占主导地位。在孤立的原住民社区(例如西伯利亚的雅库特人群)和高风险人群(包括注射吸毒者)中,HDV感染流行率较高。与高流行区接壤的国家和地区尚缺乏HDV感染亚组人群数据,未来亟需通过标准化的监测体系、分子诊断技术和具有代表性的血清流行病学研究,以准确掌握HDV感染疾病负担情况,并予以针对性干预。

Observed heterogeneity reflects both epidemiologic factors and methodological variation, including differences

in study populations, diagnostic methods, and inconsistent use of HDV RNA testing. Genotype I predominate in much of the region, isolated indigenous communities (e. g., Yakutia populations in Siberia) and high-risk groups, including people who inject drugs consistently show elevated prevalence. Many countries and regions bordering high-prevalence regions remain unstudied, highlighting the critical need for standardized surveillance, molecular diagnostics, and representative sero-epidemiological studies to accurately map HDV burden and guide targeted interventions.

笔者团队建议优先采取以下措施:(1)对所有HBsAg阳性人群开展常规HDV检测;(2)将HDV血清学、RNA诊断纳入全国性基础检测项目;(3)加强HDV感染从诊断到治疗的临床管理路径;(4)保障HDV感染特异性疗法的临床应用。此外,在数据缺乏的国家和地区开展有针对性的试点调查,对于揭示潜在的HDV隐匿性传播至关重要。加强分子监测、建立纵向队列以及进行基因型谱分析,对于准确评估区域疾病负担、指导干预措施并最终实现世界卫生组织提出的“2030年消除病毒性肝炎公共卫生危害”的目标具有决定性意义。

Priority actions include routine HDV testing for all HBsAg-positive individuals, integration of both serology and RNA diagnostics into national essential testing, strengthening linkage-to-care pathways, and ensuring access to HDV-specific therapies. Targeted pilot surveys in data-deficient countries and regions are essential to uncover hidden transmission. Strengthening molecular surveillance, longitudinal cohorts, and genotype mapping will be crucial to define regional burden accurately, guide interventions, and achieve WHO 2030 viral hepatitis elimination targets.

本文回顾了亚洲地区50年跨度的HDV流行病学情况,通过整合不同人群和临床数据,识别出高负担地区和监测空白。研究局限性在于既往文献潜在的发表偏倚和研究方法的异质性,可能影响结果的可比性。此外,国家流行率估算常基于非代表性样本(如单中心或高风险人群队列),不应视为具有全国代表性。样本和患者来源的差异性进一步限制了跨国比较,需谨慎解读区域间的表面差异。尽管存在这些限制,研究结果为确定公共卫生优先事项和规划未来研究提供了可行的指导。

This review synthesizes five decades of HDV epidemiology data across a broad region, identifying high-burden areas and surveillance gaps by integrating diverse population and clinical data. Key limitations include

potential publication bias and heterogeneity in study methods, which affect comparability. Additionally, national prevalence estimates are often based on non-representative samples (e. g., single-center or high-risk cohorts) and should not be viewed as nationally representative. Variability in sampling and patient sources further limits cross-country comparisons, cautioning against overinterpreting regional differences. Despite these constraints, the findings offer actionable guidance for public health prioritization and future research.

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