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人类活动导致的生态屏障破坏对人类健康造成致命威胁

张大奕^a, 杨云锋^a, 李淼^a, 陆韻^a, 刘毅^{a,*}, 蒋靖坤^a, 刘锐平^a, 刘建国^a, 黄霞^a, 李广贺^a, 曲久辉^{a,b,*}

^a School of Environment, Tsinghua University, Beijing 100084, China

^b Key Laboratory of Drinking Water Science and Technology, Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, Beijing 100085, China

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摘要

近期暴发的新型冠状病毒肺炎(COVID-19)疫情与21世纪以来多次暴发的新兴传染病疫情吸引了全球关注。这些新兴传染病对全球公共健康构成威胁,促生了大量针对病毒从动物到人类社会传播机制的研究。尽管已有许多研究论述了新兴传染病如何突破物种屏障和地理屏障传播的现象,但对于物种屏障和地理屏障在野生动物栖息地中存在的协同作用仍不清晰。尚未有针对病毒在生态系统中扩散、迁移和传播机制的系统性研究。为此,本文提出了生态屏障的新概念,综合了物种屏障和地理屏障概念中自然和中间宿主对病毒传播的影响,系统讨论了影响病毒突破生态屏障,实现传染病从野生动物到人群传播的多个关键影响因素,包括传播途径、接触概率、接触频率和病毒特征等。针对人类活动和全球化进程对生态屏障强度的显著影响,本文也分析了人类活动削弱生态屏障的机制,包括全球气候变化可以诱发和扩大新兴传染病的范围,人类活动可以增加病毒与人类社会的接触频率和进入人群的传播概率,全球化还会在城市中形成新的高风险区域等。本文阐明了生态屏障阻碍病毒感染人群的传播机制,相关结论为保护生态屏障、降低新兴传染病传播风险和保障公共安全提供了理论支撑。

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1. 引言

1970年以来,人类已发现和分离出超过1500种致病微生物,其中70%来自动物。世界卫生组织(WHO)将15种致病微生物列为可能具有国际威胁的传染病[1–4]。近50年来,埃博拉、狂犬病、禽流感、登革热、寨卡和艾滋病等病毒所引发的流行性传染病已经造成超过10亿人感染和超过8000万人死亡,且影响范围和感染人群逐年增加(表1)[5–54]。其中,几次重大新兴传染病事件包括:西尼罗河病(West Nile River disease)造成4161人

感染,277人死亡[23,55];2003年暴发的严重急性呼吸综合征(非典型肺炎,SARS)导致8422人感染,919人死亡[43,56];2012年暴发的中东呼吸综合征(MERS)已累计造成701人感染,249人死亡[51]。2019年年底暴发的新型冠状病毒肺炎(COVID-19)由新型冠状病毒(SARS-CoV-2)引发,截至2020年10月25日,已经导致全球4300万人感染,超过110万人死亡[57],引起社会各界的高度关注。

新兴传染病的频繁出现引发一个重大科学问题,即病毒如何从在野生动物栖息地生活的自然宿主向人群传播。

* Corresponding authors.

E-mail addresses: Yi.liu@tsinghua.edu.cn (Y. Liu), jhqu@tsinghua.edu.cn (J. Qu).

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表1 病毒性新兴传染病或大流行最初暴发地点和相关数据

Virus	Type	First record	Epidemic area	Infected cases	Death	Mortality	References
Dengue virus	Flavivirus, enveloped, single-stranded RNA	16th century	Global	~390 million/year	Unknown	1%–5%	[5–8]
Hanta virus	Bunyaviridae, enveloped, single-stranded RNA	1913, Soviet Union	Global	> 1 000 000	Unknown	1%–60%	[9–11]
Spanish flu, H1N1 pandemic	Orthomyxovirus, enveloped, single-stranded RNA	1918, United States	Global	~ 500 to 1000 million	~25 to 50 million	0.1%–5%	[12–14]
West Nile virus	Flavivirus, enveloped, single-stranded RNA	1937, Uganda	Global	> 57 354	> 2447	3%–15%	[15–20]
Zika virus	Flavivirus, enveloped, single-stranded RNA	1947, Uganda	Global	> 200 000	Unknown	Unknown	[21–22]
Chikungunya virus	Alphaviruses, single-stranded RNA	1952, Tanzania	Global	> 1.5 million	Unknown	< 1%	[23–26]
Kyasanur forest disease virus	Flavivirus, enveloped, single-stranded RNA	1957, India	India	3 263	Unknown	2%–10%	[27–29]
Marburg virus	Filovirus, enveloped, single-stranded RNA	1967, Germany	Africa	587	475	24%–88%	[30–31]
Ebola virus	Filovirus, enveloped, single-stranded RNA	1976, South Sudan	Africa	31 161	12 999	20%–90%	[32–34]
Hendra virus	Paramyxoviruses, enveloped, single-stranded RNA	1994, Australia	Australia	7	3	30%–60%	[35–37]
H5N1	Orthomyxovirus, enveloped, single-stranded RNA	1997, Hong Kong (China)	Hong Kong (China), Thailand	650	386	53%	[38–40]
Nipah virus	Paramyxoviruses, enveloped, single-stranded RNA	1998, Malaysia	South-East Asia	477	248	52%	[35,41–42]
SARS-CoV	Coronavirus, enveloped, single-stranded RNA	2002, China	32 countries	8 439	812	9.6%	[43–45]
H1N1 pdm	Orthomyxovirus, enveloped, single-stranded RNA	2009, Mexico	Global	0.7–1.4 billion	18449 (confirmed);201 200 (estimated)	0.01%	[46–50]
MERS-CoV	Coronavirus, enveloped, single-stranded RNA	2012, Saudi Arabia	27 countries	815	313	38.4%	[51]
H7N9	Orthomyxovirus, enveloped, single-stranded RNA	2013, China	China	1 568	616	39%	[40,52]
SARS-CoV-2	Coronavirus, enveloped, single-stranded RNA	2019, China	Global	> 30 million	> 1 million	~3%	[53–54]

SARS-CoV: severe acute respiratory syndrome coronavirus.

基于病毒传播需突破物种屏障和地理屏障的假设[58], 新兴传染病疫情暴发主要取决于自然环境和人类社会之间的关系。人类活动在全球范围内产生了许多环境问题, 包括严重污染[59]、全球变暖[60]、自然灾害[61]、野生动物栖息地破坏[62]、生物多样性丧失[63]等。这些问题显著改变了全球生态系统, 影响了野生动植物(其中也包括病原微生物[64–65])的行为和栖息地, 进而造成传染性疾病暴发频率和范围的变化。新兴传染病出现的频率剧增, 已有传染病影响范围逐渐扩大, 导致疫情的暴发严重威胁人

类健康[66]。逐渐增多的病毒种类、多样化的感染和传播途径、升高的暴发频率和扩大的影响范围都给预防与控制新兴传染性病毒带来了严峻挑战[67–68]。

现阶段, 疫苗是保护易感人群最经济有效的策略。然而, 目前针对大多数RNA病毒和新兴人畜共患病病毒缺乏有效的疫苗[69]。对于新兴传染病来说, 提前预防比事后控制更加经济有效[70]。因此, 识别病毒从自然宿主向人群传播的途径和机制, 有助于形成长期有效的传染病防控策略, 具有重大的现实意义[71]。

已有研究表明,病毒突破生态屏障进行传播是新兴传染病出现的根源[58,72]。生态屏障具有生态系统限制新兴传染病大范围传播的作用,包含物种屏障与地理屏障两个核心内容,从微观和宏观两个层面共同决定新兴病毒性病毒在人群中的传播。物种屏障限制了病毒在新宿主中的有效传播[58]。物种屏障的有效突破被称为宿主溢出,主要由病毒突变或进化概率决定,决定了病毒适应新宿主并最终在新宿主种群中传播的可能性[58,73]。另一方面,地理屏障的突破取决于病毒区域传播的概率与频率,与病毒宿主和潜在宿主或人群之间的接触情况密切相关[72]。尽管已有大量研究报道了物种屏障与地理屏障在新兴传染病暴发初期的作用,但以往工作主要聚焦在流行病学和免疫学领域,仍缺乏深入的和系统性病毒迁移与传播的宏观尺度研究。

病毒的遗传稳定性较弱,其进化和变异过程与生态环境密切相关[74]。与此同时,病毒、环境介质和宿主之间的相互作用决定了病毒的传播,而且相关影响因素存在较大的地理差异[75]。人类活动对生态系统具有显著影响,例如,对病毒自然宿主野生栖息地的入侵[72]和对气候变化的影响改变了病毒自然宿主或中间宿主的地理分布格局[76]。因此,日益增强的人类活动通过改变人类与自然之间的关系而削弱生态屏障,进而加速病毒在人类社会的传播。以流感、艾滋病、严重急性呼吸综合征、中东呼吸综合征和 COVID-19 为代表的新兴传染病的加速暴发,暗示了人类活动和生态屏障退化之间的关系,将对人类社会的公共安全和可持续发展产生重要影响。但由于缺乏人类活动和生态屏障退化之间关系的清晰阐述,因此亟需系统性总结病毒在自然生态系统中的传播规律,揭示病毒跨生态屏障的传播机制,识别人类活动削弱生态屏障、加速病毒传播的原理。相关理论研究有助于新兴传染病的预防与控制。

2. 生态屏障——影响病毒从自然宿主向人群传播的关键因素

病毒的传播和感染一般局限于少数物种。因此,以野生动物为自然宿主的病毒对人类的感染必须突破生态屏障。具体而言,生态屏障影响着病毒从自然宿主向人类社会的传播,主要体现在四个分子或地理层面的关键因素:传播途径、传播概率、接触频率和病毒特征(图1)。生态屏障综合了上述病毒从自然宿主向人群传播的关键因素,是新兴传染病出现和传播的制约因素。

2.1. 传播途径

病毒突破生态屏障传播首先取决于不同物种(包括自然宿主、人工饲养禽畜宿主和野生传播载体)之间病毒溢出与传播的机制。自然宿主可以通过分泌物排泄、粪便和尿液排泄、尸体腐烂等多个途径向周边环境释放病毒[77]。病毒在某些土壤、水体和固体表面可以存活较长时间[78],通过直接接触或摄食,造成包括人类在内的其他物种感染。通过接触被病毒污染的环境介质,禽畜人工饲养、运输和销售过程中产生大量粪便和废弃物,使得病毒更易于突破生态屏障进入人类社会[35]。蚊蝇等病毒野生传播载体还可以通过叮咬等方式直接导致禽畜和人类感染,是一种具有较大威胁的病毒跨物种传播媒介[79]。

近几十年来,人类活动的增加导致了区域乃至全球的气候变化,极大地改变了野生动物的栖息地和活动轨迹[80-81]。气候变化可以扩大部分病毒自然宿主和中间宿主的生存区域,使病毒能够传播更远的距离;全球变暖还可能从永久冻土中释放古老的病毒[82-83]。此外,快速的城市化进程增加了对土地资源的需求,导致土地利用类型的频繁变化和野生动物栖息地的大规模破坏[84]。森林和草原等生态系统逐渐遭到侵蚀,野生动物的生存空间被

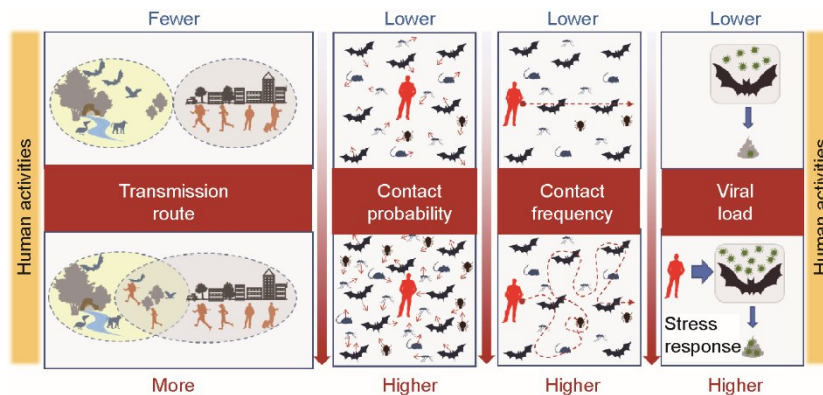


图1. 生态屏障影响病毒从自然或中间宿主向人群传播,有四个关键因素,包括传播途径、传播概率、接触频率和病毒特征。人类活动可以削弱生态屏障,增加新兴传染病的出现和传播概率。

显著压缩。人类生活水平的提高和农牧业的发展增加了家畜的种类和数量[85]，为人畜共患病病毒跨越生态屏障传播提供了新途径。这些人为因素共同作用，增加了新兴传染病病毒从自然环境进入人类社会的传播概率。

2.2. 传播概率

病毒从野生动物向人类社会的传播除了受传播途径影响外，还取决于特定区域内病毒宿主与人类接触的概率。人类活动的范围和强度是决定传播概率的关键因素，其中在人类和野生动物活动的重叠区域尤为关键。同时，由全球和区域气候变化驱动的野生动物栖息地的变化也可能导致野生动物入侵人类居住区，增加人类与病毒自然宿主直接接触的可能性[76]。与封闭的野生动物栖息地相比，病毒自然宿主在野生动物和人类共同生活的碎片化地区的动态数量和地理分布与病毒传播概率关系更为密切[72]。此外，随着城市化进程的加快，人类聚居区中的禽畜繁殖和活动密度加强，提高了病毒通过禽畜饲养、运输、屠宰和销售过程传播的可能性[86]。城市地区的贫民区、城中村和棚户区作为主要的禽畜繁殖地，为新兴传染病提供了集中传播场所[87]。

2.3. 接触频率

接触频率是指人类在一定时间范围内接触病毒宿主的强度，是决定病毒跨越生态屏障的重要影响因素。在一定的传播途径和传播概率下，接触频率与野生动物栖息地的人口密度和人类活动强度直接相关[72]。对于大多数人畜共患病病毒而言，人类和人工饲养禽畜的接触频率还取决于生活方式和城镇化水平[35]。

2.4. 病毒特征

病毒存活时间、载量和感染性等特征是影响病毒突破生态屏障传播的关键内在因素。许多学者已经针对多种病毒在固体表面、市政污水、空气和土壤等复杂环境介质中的存活时间和失活规律开展了大量研究。温度是影响病毒活性的重要环境因子，通常与病毒存活时间呈负相关[88–93]。在水体中，非典型肺炎冠状病毒10 d后的活性降低99.9%，而在4 °C条件下可以存活100 d [94]。空气传播的病毒主要存在于气溶胶颗粒表面，而气溶胶可以通过气流传播数百米，远超过飞沫的传播范围，是流感和其他呼吸道传染病的重要传播途径[95]。土壤也是重要的病毒环境载体，世界各地的沙漠、农田、森林、湿地和牧场土壤中均检测出较高水平的球形无尾病毒和噬菌体 ($2.2 \times 10^3 \sim 5.8 \times 10^9 \text{ g}^{-1}$) [96–103]。引起呼吸道传染病的流感病毒 (H1N1、H9N9、H5N1) 和冠状病毒 (MERS-CoV、

SARS-CoV 和其他人类冠状病毒) 在土壤中的存活时间相对较短。流感病毒在固体表面可以存活数小时到3 d，在口罩、手套和羽毛表面可以存活6 d [104–113]。冠状病毒在固体表面可以存活2~6 d [114–120]。已有数据表明，土壤含水率与病毒活性存在正相关性 [121–122]，不同土壤干湿条件下的病毒失活机制存在差异。在干燥土壤中，RNA病毒衣壳蛋白容易脱水和失活，失去保护RNA的能力，导致病毒无法复制和感染，但病毒仍然没有彻底失活；在含水率较高的土壤中，微生物活性较强，蛋白酶和RNA酶活性也较高，具有更高的病毒衣壳和RNA降解率[123]。

自然宿主中的病毒载量与人类入侵野生动物栖息地显著相关[124]。野生动物栖息地的破坏会给野生动物带来额外的环境压力，诱发应激响应，提高病毒在尿液和唾液中的载量[125]。此外，病毒在其他宿主中的传染性和致病性是新兴传染病频繁发生的关键因素。对于存活时间较长或传播途径较多的病毒，从自然宿主向其他宿主传播的可能性较大，而病毒容易因环境变化而发生大幅度变异和迅速复制，因此它们更易突破生态屏障，具有更高的适应新宿主的机[126]。

3. 人类活动对自然屏障的削弱作用

新兴传染性病毒之所以能够突破生态屏障，与许多生态过程有关，且受到人类活动的显著影响，包括全球气候变化、野生动物栖息地破坏、农业活动和快速城镇化等 [124,127–128]。因此，生态屏障阻断病毒从自然宿主向人群的传播主要与自然宿主传播途径、人工饲养禽畜传播途径和环境介质传播途径有关 (图2)。

3.1. 全球气候变化增加新兴传染病出现频率

全球气候变化导致了一系列全球性问题，包括海平面上升、极端气候、洪水、干旱、大气与空气质量恶化等 [129]。全球气候变化还可以影响病毒宿主的生态行为，通过多种途径诱发新兴传染病的暴发[130]。例如，全球气候变化可以改变病毒宿主和中间宿主的栖息地范围和分布，或者融化永久冻土以释放古老病毒，造成新兴传染病暴发风险增加。

3.1.1. 野生动物栖息地

工业化导致的全球气候变化显著改变了野生动物的栖息地范围和行动轨迹[80–81]。全球气候变化扩大了部分病毒自然宿主或载体的种群数量和分布范围，增加了其与人类

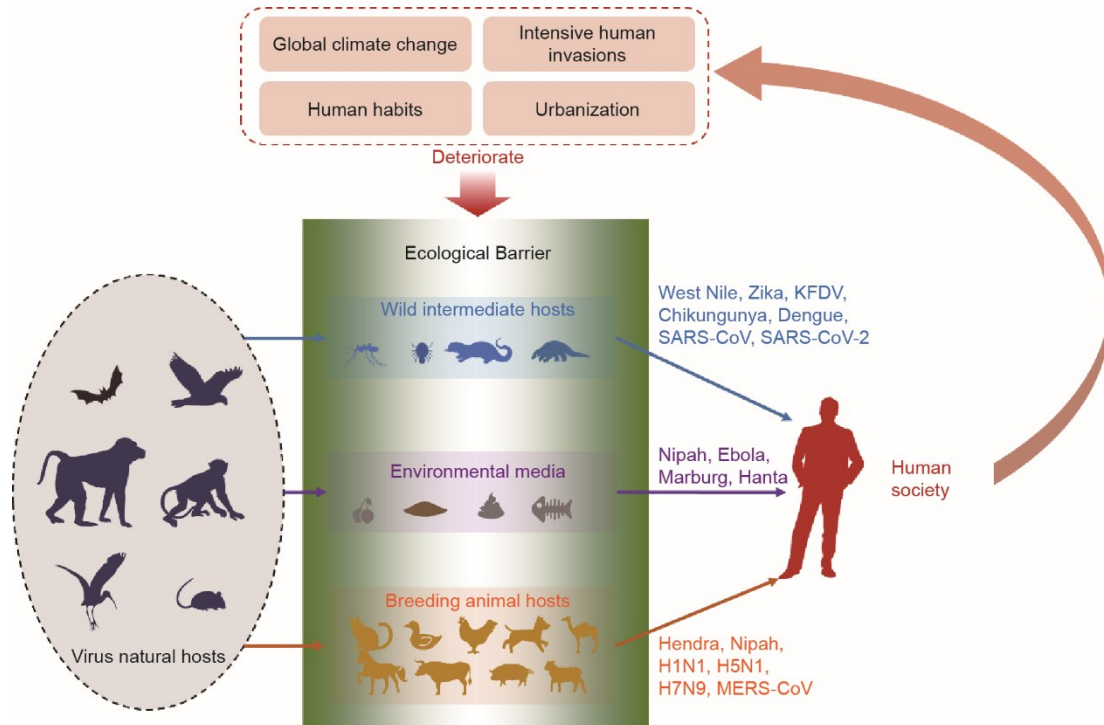


图2. 人类活动对生态屏障的破坏作用。生态屏障阻断三个主要病毒传播途径，包括野生中间宿主传播途径、人工饲养禽畜传播途径和环境介质传播途径。削弱生态屏障的典型人类活动包括全球气候变化、野生动物栖息地入侵、日益增加的人类活动范围和城镇化。

社会接触的可能性和频率，导致某些病毒跨越生态屏障传播新兴传染病[76]。西尼罗河、基孔肯雅（chikungunya）、寨卡和登革热病毒均为虫媒病毒，尽管自然宿主不同，但都通过“蚊-自然宿主-蚊”循环进行传播。人类很容易被携带病毒的蚊子感染[79]，其中埃及伊蚊（*Aedes aegypti*）和白纹伊蚊（*Aedes albopictus*）是两种典型的气候敏感媒介。温度、降雨量和湿度是埃及伊蚊和白纹伊蚊繁殖、扩张和活动的关键因素[131–132]。西尼罗河病的暴发主要与高温有关，温度从26 °C降至18 °C可使尖音库蚊（*Culex pipiens*）的感染率从97%降至18% [133]。由于全球变暖会促使蚊虫在更高纬度地区活动[134]，《柳叶刀2030倒计时：人群健康与气候变化》（*Lancet Countdown to 2030: Public Health and Climate Change*）指出，气候变化正在使埃及伊蚊传播登革热的能力增强；从1950年到2015年，登革热感染率已经增加了9.4% [135]。

3.1.1.2. 古老病毒释放

全球气候变化还可以造成永久冻土带的融化，导致远古病毒的释放和新兴传染病的传播。在30 000年前的永久冻土中发现的巨型二十面体DNA病毒[136]和西伯利亚软体动物病毒（*Mollivirus sibericum*）[82]在复苏后对宿主仍有感染能力。最近的一项研究在青藏高原冰川约15 000年前的冰层中发现了33个病毒种群，包括4个已知属和

28个潜在新病毒属[83]。在最不利的情况下，所有的古老病毒可随全球气候变暖从融化的永久冻土或冰川中释放出来。

3.2. 人类活动增加接触概率和传播机率

人类活动强度决定了人类入侵野生动物栖息地的程度、自然宿主的病毒载量，以及家畜（包括家畜、家禽和宠物）的种类、数量和密度。这些活动增加了人类与病毒自然宿主之间的接触频率和有效接触时间，显著增加了病毒跨生态屏障传播的风险[137]。尽管野生动物栖息地的碎片化可以隔离低移动性种群，但为高移动性动物提供了更多进入人类活动区域的机会，从而改变了未受干扰地区的物种多样性[125]。这种影响改变了病毒媒介动物栖息环境和新兴传染病的传播途径[138]。

3.2.1. 碎片化区域免疫应激响应

人类活动引起的环境胁迫可能导致野生动物产生免疫反应，从而改变自然宿主或中间宿主体内的病毒载量。据报道，应激反应会改变免疫功能，改变野生动物、家畜和人类之间的传播和感染模式[139]。虽然仍缺乏令人信服的实验数据来证实应激反应和宿主病毒载量之间的关系，但已有研究提出了解释这一现象的两个假说。“意外溢出”（accidental spillover）假说认为，病毒宿主免疫应答抑制了病毒持续感染，只有当免疫应答被内部或外部压力削弱

而失去病毒与宿主之间的平衡时,病毒才会复制和周期性释放[140–141]。这一假说解释了亨德拉病毒的驱动机制之一,即人类应激诱导的果蝠免疫反应可以增加病毒载量和跨物种传播概率[125,142]。“暂时流行”(transient epidemic)假说则认为,病毒灭绝和再定植之间存在动态平衡,脉冲式的跨物种传播现象仅在传染宿主暴发一波感染时才会发生。影响非致命性病毒短暂流行的关键因素是宿主感染后的恢复和免疫情况[125],而随着时间的推移,整个种群免疫力逐渐下降,病毒载量随之增加。一项关于土地利用变化与埃博拉出血热暴发之间关系的研究称,在11例埃博拉出血热首发传染病例中,8例发生在森林破坏程度较高的地区[72]。这些地区是携带埃博拉病毒的蝙蝠的栖息地,而蝙蝠体内的埃博拉病毒载量只有在疫情暴发期间才能检出。蜱类在受破坏森林中的迁移和分布与科萨努尔森林病(Kyasanur forest disease)[143]、莱姆病(Lyme disease)[144]和克里米亚-刚果出血热(Crimean-Congo hemorrhagic fever)[145]的病例数及地理特征密切相关。

3.2.2. 直接接触环境介质

除了直接接触野生动物外,接触野生动物栖息地中含有病毒的环境介质也可造成感染。病毒自然宿主可以通过残留在水果上的唾液和饲料中的体液、进入水或土壤的粪便或尿液、动物尸体等多种方式将病毒释放到环境介质中。典型的例子包括尼帕病毒[146–147]、埃博拉病毒[30, 33, 148–149]、马尔堡病毒和汉坦病毒[9]。尼帕病毒于1998年在马来西亚被首次发现,其自然宿主印度狐蝠的主要栖息地靠近枣树。印度狐蝠粪便和尿液中含有的尼帕病毒会污染枣汁和采汁罐,导致人类感染[146–147]。埃博拉病毒的自然宿主是果蝠,而从果蝠到人类最常见的传播途径包括食用带有活病毒的蝙蝠肉、食用被蝙蝠排泄物污染的食物,以及在洞穴中与果蝠直接接触[30, 33, 148–149]。汉坦病毒可追溯到1913年,其自然宿主是啮齿动物,包括黑线姬鼠、褐家鼠和大丽花姬鼠等。汉坦病毒的主要传播途径是通过唾液、尿液和粪便等动物源性接触,将病毒释放到周围环境。接触携带汉坦病毒的粉尘、摄入受病毒污染的食物和水、直接接触自然宿主或其排泄物,以及通过受损皮肤可直接感染汉坦病毒[9]。

值得警惕的是,某些病毒可在部分环境介质中存活很长时间,从而长时间隐蔽地感染动物和人类,引起新兴传染病的暴发。在合适的条件下,病毒可在环境介质中存活数百甚至数千天。例如,猪细小病毒可以在土壤中存活超过43周[150],人诺如病毒在地下水中1266 d后仍保持

10%的活性[151]。新型冠状病毒RNA在COVID-19患者病房的地板[152]和门诊部周围的土壤中被大量检出[153]。因此,自然宿主携带的病毒可能在野生动物栖息地的环境介质中长期存活,特别在土壤、淤泥、洞穴或森林内部落叶等阴冷、黑暗和潮湿的环境中具有更长的存活时间。这些残留病毒可能通过降雨污染地表水,通过下渗污染地下水。人类在野游、采矿、伐木或狩猎活动中,可以直接接触这些环境介质,食用受污染的水果或饮用受污染的水源,为病毒突破生态屏障提供了机会。由于新型冠状病毒在塑料表面至少能存活3 d[154],受病毒污染的衣物有可能在人群聚居区广泛传播病毒,最终导致新兴传染病在人群中暴发。

科萨努尔森林病的暴发证实了新兴传染病可以通过直接接触含病毒的环境介质进行跨生态屏障传播。科萨努尔森林病是由科萨努尔森林黄病毒引起,自然宿主包括猴子和啮齿动物(猕猴和大鼠),蜱虫(主要是血蜱,尤其是刺血蜱)是科萨努尔森林黄病毒的野生虫媒中间宿主[155]。科萨努尔森林病的流行具有明显的季节性,与当地携带病毒的蜱虫的生活习性一致。患者或易感人群主要包括年轻的农民、牧民和林业工人,他们在日常工作中经常进入野生动物栖息地,与蜱虫等病毒中间宿主的接触概率较高,比其他人拥有更高的感染概率[27–29, 156]。

3.2.3. 国际贸易

国际贸易为病毒或病原体的远距离传播提供了新的机会。频繁的跨国贸易增加了野生或家养动物的长距离迁移,从而增加了新兴传染病全球暴发的可能性[157]。例如,2003年美国暴发的猴痘源于跨国宠物贸易[158];亚洲地区禽流感病毒通过国际家禽贸易给其他国家带去了禽流感传播风险[159]。此外,一些病原体可以通过农作物国际贸易进行传播,并感染其他国家的人群和动物[160],这一现象解释了许多食源性传染病的来源。一个重要的例子是美国1998–2003年的沙门氏菌感染事件,其源头是被沙门氏菌污染的巴西进口芒果[161]。

3.3. 人类行为增加传播途径

病毒自然宿主可通过食物链(被中间宿主咬伤或摄入)或虫媒(蜱虫或跳蚤)将病毒传播给其他野生动物(中间宿主)。经过适应和进化,病毒可以感染中间宿主并进一步传播,形成更大范围的天然病毒库。病毒在这一过程中有效地突破了生态屏障,产生更多的中间宿主,增加新兴传染病暴发概率。食用野生动物、人工禽畜养殖、农业活动和个人卫生等方面的居民生活习惯也会影响病毒的

传播途径和传染概率。

3.3.1. 食用野生动物

亚洲东部和非洲的一些当地居民认为野生动物是有益健康的营养食品。因此，食用野生动物在一些国家是常见的行为[162]。这种习惯促使野生动物偷猎、饲养和屠宰产业链的形成，增加了病毒从自然宿主或中间宿主传播到人类社会的风险。在所有病毒自然宿主中，蝙蝠是冠状病毒（包括非典型肺炎和新型冠状病毒）的重要宿主[163]。传播给人类的可能的途径是通过野生中间宿主（如果子狸和鼯鼠）。野生动物食品市场的厨师和雇员由于频繁接触非典型肺炎冠状病毒或新型冠状病毒的中间宿主，因此感染概率增加[44,56,164]；食用野生动物促进了整个野生动物供应链的发展，增加了野生动物与猎人、饲养者、商贩或消费者直接或间接接触的可能性，进而增加病毒跨种传播和感染人类的概率。

3.3.2. 人工禽畜饲养

除野生中间宿主外，马、骆驼、鸡、鸭等家畜家禽也可成为中间宿主。人工饲养的禽畜动物可以通过分享食物、啮咬和捕食病毒自然宿主等途径与野生动物直接接触，增加病毒在人工饲养的禽畜和野生动物之间的传播频率[85]。家畜混养还加速了病毒突变和种间传播概率，导致人工饲养的禽畜动物成为许多人畜共患病的关键中间宿主[86]。这些病毒可以在家养动物种群中感染和传播，并通过饲养、销售和食用等途径传播到人类社会。因此，涉及人工禽畜行业的养殖者、运输者、农民和海鲜市场销售者更容易感染亨德拉病毒、中东呼吸综合征冠状病毒和流感病毒（H1N1、H5N1）等新兴传染病。

亨德拉病毒最早于1994年在亨德拉（澳大利亚昆士兰州布里斯班）发现，导致22匹马和3人死亡。果蝠是亨德拉病毒的自然宿主[165]，栖息地范围接近当地马匹饲养场。这些饲养场为果蝠提供了额外的栖息地，日益增加的马匹数量使马有更多机会接触果蝠的尿液或分泌物[35]，造成亨德拉病毒在马之间传播，最终导致与马密切接触的农场工作人员感染[166–169]。

中东呼吸综合征冠状病毒于2012年在沙特阿拉伯首次从重症肺炎死亡病例的肺组织中分离，自然宿主可能是蝙蝠。该病的暴发与单峰骆驼密切相关。每年有数千头单峰骆驼从非洲国家被运送到沙特阿拉伯，中东呼吸综合征的暴发与骆驼交易量显著相关[170]。有充分证据表明，单峰骆驼是中东呼吸综合征冠状病毒的重要中间宿主，中东呼吸综合征冠状病毒是由骆驼传染给人类的，与骆驼密

切接触的养殖人员的感染率远远高于其他人。血清学研究也表明，养殖场和屠宰场工作人员的中东呼吸综合征冠状病毒抗体阳性率分别是普通人群的15倍和23倍[43,51,171–172]。

流感病毒具有易突变的特性，拥有感染家禽和人类的巨大潜力。禽流感H5N1是一种人畜共患病，于1997年在香港首次暴发并传播到其他国家[173]。野生鸟类和家禽是H5N1病毒的自然宿主和中间宿主[174]，野生鸟类季节性迁移促进了H5N1病毒在西伯利亚、中国青海、印度和东南亚等地区间的远距离传播，H5N1病毒在家禽种群间的传播与进化进一步加快了其跨越生态屏障最终感染人类的速度[39–40]。2009年，H1N1病毒在墨西哥暴发，影响了214个国家和地区，感染了数百万人，造成至少18449人死亡；家猪被认为是H1N1病毒感染人类的中间宿主[46,175]。H7N9病毒来自野生鸟类，通过与人工饲养家禽中其他流感病毒基因重组获得了感染人类的能力[127]。在逐渐适应家禽的过程中，H7N9从低致病性禽流感演变为高致病性禽流感；2017年在中国暴发了严重疫情，造成1564例感染，600多人死亡[38,176–177]。综上所述，人工饲养禽畜是流感病毒的主要中间宿主，是流感暴发的关键因素之一。

3.3.3. 农业活动

一些传统农业活动会增加病毒向人类社会传播的风险。在世界各地的许多农村地区，未经处理的污水和污泥通常用于灌溉或施肥。新鲜的污水或粪便中含有大量病原体，如病毒（诺如病毒、肠道病毒、戊型肝炎病毒等）[178–179]、细菌（沙门氏菌、大肠杆菌、霍乱弧菌等）[180]和寄生虫卵（蛔虫卵、鞭虫卵等）[181–182]。戊型肝炎病毒存在于养殖场的猪粪或废水中[183]，粪口传播是其传播途径。在美国爱荷华州的22个养猪场中，从15个养猪场的猪粪中可以检出传染性戊型肝炎病毒[184]，因此施用猪粪肥料和养殖场废水可能污染农产品和周围水源[185–186]。例如，在印度普纳的一个污水处理厂中，未经处理和浓缩的污水样本中戊型肝炎病毒阳性率高达10.97%，证实污水处理厂工人面临更高的戊型肝炎感染风险[187]。因此，污水灌溉可以直接增加病毒从污水到人类社会的传播风险，也可以间接污染土壤、水和食品，引起食源性传播。禽畜养殖和产品储藏也能吸引野生动物主动接近，从而增加一些病毒的传播途径和接触频率，促使病毒跨越生态屏障向人群传播[72]。例如，埃博拉病毒可以通过受果蝠粪便污染的水果传播给人类，而村庄里的水果储藏可将果蝠从洞穴吸引到人类活动区域，加

速了传播进程[162]。

3.3.4. 个人卫生

个人卫生是阻断病毒传播和感染的关键方法[188]。不当的文化习俗和个人卫生习惯会增加病毒的接触和感染概率[189]。手足口病由肠道病毒（主要是柯萨奇病毒A16和肠道病毒71）引起，易感人群主要为免疫力弱的儿童[190]。研究表明，有吮吸手指习惯的儿童比其他儿童面临更高的感染风险，而饭前洗手的儿童患手足口病的风险只有其他人的一半[191]。在西非一些农村地区，停尸数天后触摸尸体是传统丧葬习俗的一部分，这会增加新兴传染病的传播风险[192]。

3.4. 城镇化过程产生的新型高风险地区

城市化水平的不断提高显著改变了全球传染病的分布格局[193]。尽管城市化可以改善基础设施和卫生条件，在一定程度上保护公众健康[84]，但也改变了城市地区野生动物的数量、多样性和群落结构[194]，形成新兴传染病暴发的新热点。一些市政基础设施成为病毒在人类社会传播的新节点或新网络。例如，寨卡病毒主要由已经适应人口稠密城市环境的埃及伊蚊传播[195]。在全球气候变化和城市化进程的双重推动下，这些虫媒有着更广泛的分布，是寨卡病毒病在全球暴发的重要因素[196]。许多国家在废水中检测出新型冠状病毒，这使得污水流行病学成为新兴传染病预防和控制的诊断工具，也反映了病毒可以通过城市管网隐蔽传播[197]。

3.4.1. 填埋场

垃圾填埋场是城市地区病毒传播的重要来源。垃圾填埋场中倾倒的废物非常复杂，是一个巨大的病毒库，包括可能死于传染性疾病的动物尸体或携带多种传染性病毒的医疗废弃物。在美国，通常在垃圾填埋场对患有传染病的家禽和牲畜进行处理；在传染病暴发期间，一些携带病毒的医疗废物也被掩埋。这些活动增加了病毒二次传播的机会，使得垃圾填埋场成为城市地区病毒传播的新热点。研究表明，在适当的温度和pH条件下，城市垃圾填埋场中的家禽尸体含有的禽流感H6N2病毒可存活2年甚至30年以上，而其他病毒可在垃圾渗滤液中存活至少30 d [198]。较长的存活时间可造成病原细菌（如大肠杆菌和沙门氏菌）和病毒的广泛传播，导致禽流感、手足口病、鸡新城疫和猪流行性腹泻[199–200]。研究还表明，垃圾填埋场的垃圾处理设施还可以以生物气溶胶形式释放各种病毒，从而将新兴传染性病毒传播给野生动物甚至垃圾填埋场的工作人员[201]。

此外，垃圾填埋场内或周围有大量啮齿动物和鸟类生存。鸟类白天成群觅食，晚上返回居住地，可能感染病毒并排出含病毒粪便；啮齿动物可以摄入、携带和传播病毒。例如，生活在伊斯特拉半岛垃圾填埋场的啮齿动物比野生啮齿动物更容易感染淋巴细胞性脉络丛脑膜炎病毒和蜱传脑炎病毒等人畜共患病[202]。鸟类及其粪便中含有60多种病原体，包括禽流感[203]和其他人类流行性病毒（H1N1、H2N1和H3N2）[204–205]。变异的流感病毒可以在候鸟体内积聚和进化，直至突破生态屏障感染人类[73,206]。英国的研究表明，垃圾填埋场为海鸥和乌鸦等鸟类提供了广泛的觅食场所，这些鸟类携带大量已知的人类传染性病原体，如沙门氏菌、大肠杆菌、弯曲杆菌和甲型流感病毒等[207]。它们日常穿梭于垃圾填埋场和水库之间，容易造成水源地的病原微生物污染，严重威胁饮用水安全。在垃圾填埋场筑巢的白鹳比自然筑巢的白鹳携带更多的病原体[208]。根据美国高致病性禽流感野生候鸟监测计划（wild migratory bird surveillance program for highly pathogenic avian influenza），生活在垃圾填埋场的野鸭是最有可能感染流感病毒的鸟类[209]。据报道，生活在巴塔哥尼亚垃圾填埋场（阿根廷）的美国黑秃鹫以有机废物为食物来源，经常感染并传播沙门氏菌等人畜共患病病原体[210]。综上所述，垃圾填埋场周围的鸟类是病原体的潜在宿主，可通过粪便、受污染水体等多种途径向人类传播病毒；垃圾填埋场是传染性病原体库，是鸟类和啮齿动物跨生态屏障传播新兴传染病的高危场所。

3.4.2. 供水与排水管网系统

农业生产活动，如修建水坝、池塘和灌溉用储水设施，可以为虫媒传染病的中间宿主提供栖息地。埃及阿斯旺水坝、塞内加尔河贾马大坝（Jama Dam）和马里/几内亚马南塔利大坝（Manantari Dam）的修建加剧了曼氏血吸虫病的暴发频率[211]。此外，大约60种按蚊（*Anopheles*）是蚊媒疟疾的传播媒介，可以在靠近农田的开放池塘中繁殖，是许多国家疟疾流行的重要原因[212]。

落后的市政基础设施（如供水和排水管网、污水处理厂、临时储水设施等）可以为病毒中间宿主提供新的栖息环境，诱发新兴传染病疫情。例如，伊蚊和库蚊在城市排水系统中的大量繁殖会导致裂谷热和其他疾病的暴发[138,212]。

新型冠状病毒已经在中国武汉[213]、法国巴黎[197]和澳大利亚[214]等地的污水中被大量检出，浓度从每毫升几拷贝到数千拷贝。这些数据表明，城市和农村水环境可能会扩散和传播新冠病毒，导致COVID-19疫情蔓延，

威胁公共安全[215]。

3.4.3. 城市卫生条件

城市卫生条件与城区病毒传播密切相关，改善卫生条件可以保护公众健康，使公众免受新兴传染病的侵害。在快速城市化的早期阶段，大量人口从农村地区转移到城市，产生因基础设施不发达所造成的贫困问题[87]。1963—2010年，中国湖南省报告了11万例以上由汉坦病毒引起的肾综合征出血热，其发病率与城市流动人口数量呈正相关[84]。城市公共卫生问题也是某些传染病出现的关键因素[216]。许多城市的贫民窟或棚户区卫生条件差，易导致传染病在这些人口密集、相对封闭的地区肆虐。亚洲和非洲的一些发展中国家卫生条件差，基础医疗能力有限，疫苗覆盖率不足，无法充分应对新兴传染病，因此疫情大规模暴发的可能性更大[185]。1955—1956年，新德里大规模暴发的急性病毒性肝炎（AVH）主要发生在卫生条件差、社会经济水平低的贫民窟[217]。

4. 结论与展望

综上所述，生态屏障对于病毒从野生或中间宿主传播至人类具有至关重要的作用。生态屏障的强度决定了新兴传染性病毒引发传染性疾病的可能性。未来的研究重点应为病毒跨生态屏障的动态过程，该过程是预防和控制新兴传染病的关键步骤。影响生态屏障的主要因素包括传播途径、传播概率、接触频率和病毒特征，而环境介质是生态屏障的重要组成部分。日益加剧的人类活动破坏了生态屏障，造成新兴传染病愈演愈烈的全球性传播趋势。工业化和全球化进程推动了全球气候变化，引发并加剧了新兴传染病的出现；野生动物栖息地的持续流失大大增加了人类与病毒自然宿主的接触概率和新兴传染性病毒突破生态屏障的概率。随着社会经济的快速发展，国际航空和海陆运输日趋密集，进一步推动了病毒的长距离跨境传播，造成新兴传染病的全球大暴发，给公共卫生和生物安全管理带来了巨大挑战。不同国家间存在的文化和生活差异为病毒的出现和传播提供了机会，贫困地区和城市卫生条件差的地区成为传染病传播的新热点，致使新兴传染病在人类社会的广泛传播。

未来研究应进一步探索人类活动对生态屏障强度的影响程度，深入了解新兴传染病跨越生态屏障传播的机制。由于许多病毒是环境介质中的“暗物质”，因此还应加强野生动物栖息地环境病毒数据库建设，全面解析病毒、宿主和环境介质之间的相互作用，从而更好地认识生态屏障

破坏对新兴传染病传播产生的影响。

为有效预防和控制新兴传染病，应开展保护生态屏障的战略措施，阻断病毒从自然宿主向人类社会的传播途径。首先，应开展针对野生动物栖息地的大型环境病毒调查，追溯引发新兴传染病的病毒来源和地理分布格局，识别高风险或生态屏障脆弱地区。其次，应在人畜共患病病毒的自然宿主（如蝙蝠、穿山甲、候鸟等）或中间宿主（如骆驼、蚊蝇、蜚虫等）的活跃地区开展动态监测，聚焦野生动物栖息地碎片化造成的病毒溢出风险。再次，应建立生物安全预警体系（生物安全天网），作为控制突发性新兴传染病快速传播的战略手段。该生物安全预警体系应包含环境介质（气溶胶、污水等）中病毒载量的在线检测终端和用于预警与应急响应决策的实时大数据分析系统。应定期开展生物安全管理，适时启动应急预警，有效运用生态屏障控制潜在的新兴传染病。最后也是最重要的一点，人类社会在可持续发展过程中亟需重新思考与全球生态的关系，加倍重视对生态屏障的保护。

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Compliance with ethics guidelines

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