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气候变化下的流域饮用水微生物风险来源与评估

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摘　要：全球气候变暖背景下，极端天气事件如持续高温、暴雨和干旱频发，进而通过增加陆源输入或改变微生物的生存条件，直接或间接地增加饮用水系统及水源地水体中的病原微生物风险，对饮用水生物安全构成威胁。因此，饮用水生物安全问题亟待深入研究和关注。得益于病原微生物检测技术和风险评估模型的不断发展与优化，我们能够更全面地理解并评估气候变化背景下的流域饮用水微生物风险。本文旨在探讨极端气候条件下流域饮用水微生物风险的来源，并系统地归纳和分析了不同类型的微生物污染及其引发的健康风险。特别强调了高通量定量微生物风险检测方法和风险评估模型在饮用水病原微生物管控中的重要性。最后，本文提出了未来在气候变化背景下对流域饮用水病原微生物进行有效管控的研究思路和方向，为相关领域的研究提供了理论基础和实践指导。

关键词：极端气候；饮用水水源地；微生物风险；陆源输入；风险检测与评估

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Origins and assessments of microbiological risks to drinking water in watershed under climate change

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Abstract: In the context of global warming, the rising frequency of extreme weather events, including high temperatures, rainstorms, and droughts, will directly or indirectly increase the risks of pathogenic microorganisms entering drinking water systems and source waters. This is attributable to an increase in terrestrial inputs or alterations to the conditions that facilitate microbial survival and growth. It is therefore imperative to give priority to the issue of drinking water biosafety. The development of novel pathogen detection methods and risk assessment models enables a more comprehensive understanding and assessment of the microbiological risks associated with drinking water in watersheds under climate change. This review outlines the sources of microbiological risks associated with drinking water in watersheds experiencing extreme climatic conditions and summarizes various microbial contaminations and their risks to human health. Furthermore, it emphasizes the significance of high-throughput quantitative microbial risk detection methods and assessment models in the control of microbiological risks to drinking water. Finally, it provides novel insights into the effective management and control of pathogenic microorganisms in drinking water under climate change.

Keywords: extreme climate; drinking water sources; microbiological risk; terrestrial inputs; risk detection and assessment

微生物安全是确保水质安全的基本条件。经水传播的病原微生物包括细菌、病毒、原虫，以及一些其他微生物来源的污染，如抗生素抗性基因(antibiotic resistance genes, ARGs)和藻毒素等[1]，这些微生物污染可通过地表径流、城市供排水系统、农业活动等路径传播，在一定程度上威胁人体健康。气候变化加剧了极端天气事件的频发[2]，而极端天气事件造成的水温升高、降水强度增加、低流量期延长等现象，可能通过直接或间接的方式增加水源或管网中的病原微生物风险[3-4]，甚至导致许多国家和地区在极端天气事件后出现经水传播疾病的暴发[5]。例如，高温和强降水已被证实会增加隐孢子虫[6]、贾第鞭毛虫[7]、粪便大肠杆菌(*Escherichia coli*)[8]以及沙门氏菌[9]等介水病原微生物的浓度，其他极端天气如热浪、干旱等也会通过调控降水及地表径流量而影响水源中微生物污染的浓度[10]。因此，面对我国亟须提高

饮用水生物风险防控能力的科技需求，发展高通量、高灵敏度、短周期的病原微生物检测技术和科学的风险评估手段，对于有效监管饮用水中的微生物污染至关重要，是确保饮用水安全、实现病原微生物管控的重要环节。

1　极端气候背景下流域饮用水微生物风险的来源

极端天气事件对流域饮用水微生物安全的影响是多因素驱动的，如水文、温度、养分可用性等的改变[11]都会影响地下水[12]、饮用水水源[2]，甚至污水处理系统中[13]的微生物群落的多样性和结构。同时，极端天气事件对流域饮用水微生物安全的影响也是多过程耦合的，如极端降水(暴雨)导致农业和畜禽养殖场排水增加、城市污水管网超负荷溢流、地表径流增强，以及水体中病原微生物的赋存条件改变等过程均会增加流域水体中病原微生物污染风险(图 1)。

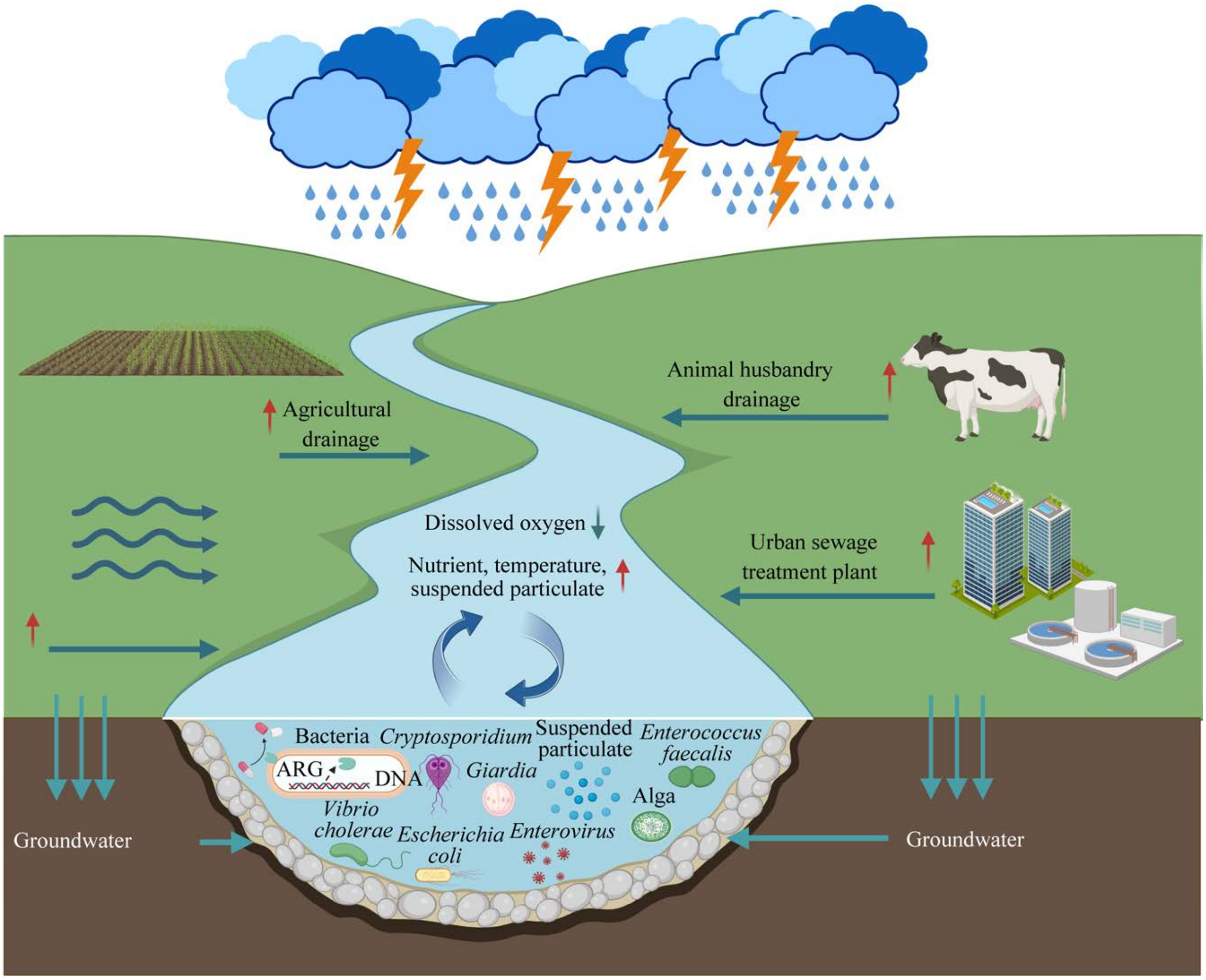

图 1　极端气候背景下流域饮用水微生物风险来源示意图　图片在 BioRender.com 中完成

Figure 1　Different sources of microbiological risks to drinking water in watersheds under climate extremes. Created with BioRender.com.

1.1 不同污染源对流域水体病原微生物污染的贡献

农业占据着全球水资源的 70%，因此农业活动更容易对环境和周边生态系统造成污染[14]。在农村地区，有相当多的农业非点源污染物，如畜牧业、水产养殖废水和化肥农药污染物，其径流往往含有高浓度的人畜共患疾病病原微生物(如大肠杆菌、微小隐孢子虫)和抗生素抗性基因(ARGs)，尤其是将粪便用作粪肥时会产生更浓密的病原微生物[15-16]。高收入国家和中低收入国家同样面临着农业污染威胁饮用水安全的风险。例如，美国国家水质清单显示，美国受污染水体中高达 50%的污染物和病原微生物来自农业和农业生产[17]；在加州萨克拉门托-圣华金三角洲地区，农业污染物威胁着 2 500 万人的饮用水源和 42.5 万 hm^2 农田的灌溉水源的水质安全[18]；同样在越南地区，由于经常在农业中使用家庭污水以及人类或者动物粪便，造成了潜在的肠道疾病健康风险，而极端降雨事件会加剧农业污染源对水资源的污染[19]。

城市污水管网超负荷溢流也是导致流域饮用水微生物健康风险增加的潜在原因之一[20]。据报道，正常情况下污水处理厂的结核病分歧杆菌感染致病主要通过气溶胶传播，通过污染地表水受感染的可能性小，但是极端气候下，污水溢流或者污水厂处理效能下降都会增加通过地表水感染的风险[21]。Larsson 等报道了瑞典发生的一次大规模水源诺如病毒感染暴发的流行病学情况，是由于极端降雨后污水处理系统超负荷运转，未经处理的污水污染水源导致的[22]。污水处理厂是病原微生物污染的一个重要点源；极端降水事件后污水处理厂中沙门氏菌属、诺如病毒、肠道病毒等病原体的浓度会升高[23]。Payment 等[24]的研究揭示，在圣劳伦斯河地区由于卫生设施差、合流下水道溢流或地表径流增加等原因，造成当地污水处理厂病原微生物数量增加，人类肠道病毒的最大值为 62 个感染单位/L，贾第鞭毛虫为 38 个卵囊/L，隐孢子虫为 15 个卵囊/L。极端降水事件会增加湍流，导致水底沉积物中的病原微生物、土壤和陈年粪便物质悬浮[25]，从而增加水体中介水病原微生物的浓度[26]。Federigi 等[23]的研究表明，降雨后污水处理厂水体浊度增加，伴随着大肠菌群、大肠杆菌、肠球菌(*Enterococcus* spp.)和肠道病毒浓度的升高。因此，农田、畜禽养殖场、城市污水处理厂都是病原物生物重要的源和汇[27]，极端气候事件的增加进一步加剧了这些污染源对水资源和公共卫生安全的威胁，因此需要加强污染控制和水质监测，以保护环境和人类健康。

1.2 地表径流对水源病原微生物污染的影响

不同污染源排放的污染物会随着地表径流迁移扩散到地表水，甚至地下水中。一方面，降雨量和暴雨强度的增加加大了污染物包括病原微生物向地表水和地下水的输送[28]，淤塞的排水管也能引发洪水并增加病媒对疾病的传播[29]。另一方面，干旱造成河流流量减小，导致水中污染物浓度上升，比如亚马孙河流域霍乱暴发表现出明显的季节性，可能与旱季时期河流的低流量导致池塘中病原微生物浓度较高有关[30]。此外，干旱后发生极端降水的可能性增加，这也会显著影响微生物群落结构。因此，降水、河川径流和饮用水生物污染之间的关系十分复杂。

分枝杆菌属和军团菌属均是土壤和水体的天然栖息者，它们主要通过地表水进入人工水系统[31]，而在极端天气的降雨事件中，地表径流量和泥沙输入的增加使得土壤侵蚀加速，土壤中的病原微生物被冲入水体中导致水源中的细菌、病毒和寄生虫等病原微生物丰度的增加[32-33]。Tryland 等[34]的研究发现，暴雨后

城市合流下水道溢流，粪便指示细菌和人类病原微生物通过地表径流进入水体，从而使水中病原微生物浓度增加了10−1 000倍。减少地表径流对水源微生物风险的影响至关重要，这可以通过改善污水处理、控制农业和工业废水排放、加强环境监测和管理等手段来实现。

1.3 气候变化引起的水体赋存条件改变增加水体病原微生物污染

随着温度升高和降雨模式的变化，水体温度、溶氧、营养物质含量、颗粒物含量，以及混合和扩散性等因素均会发生相应改变，进而影响水生微生物(包括病原微生物)的生长、繁殖和传播[35]。暴雨事件引发的水体流速增加、混合和扩散加剧会增加河流中的各种污染物的输送速率，使得微生物污染更容易传播到水源中[36]；水中的营养物浓度达到峰值[37]，颗粒物和浊度会增加，而颗粒物可作为病原微生物的庇护所会导致水体中病原微生物的富集[38]，从而改变水体中原有的微生物群落结构[39]。因此，气候变化引起的水体赋存条件改变会导致病原微生物激增，进而增加经水传播病原微生物的感染风险。

Griebler等[40]研究发现，气候变暖对全球地下水温度具有潜在的影响，而地下水温度的变化与水体化学成分和质量、生物体的新陈代谢密切相关，进而影响生物地球化学循环过程和生态系统功能。例如，极端高温引发的水温升高将减少水中溶解氧浓度[41]，进而导致食物网内相互作用的失衡，促进藻类繁殖和病原微生物的生长[42]。水温升高不仅对水源地水体有影响，对饮用水输配系统也有影响。据报道地下水变暖可能导致饮用水输配系统中的温度超过临界阈值，从而促进军团菌等病原微生物的增长[43]，对健康产生潜在影响；也可以直接或间接促进氯胺消毒管网中氨氧化细菌(ammonia oxidizing bacteria, AOB)的生长，而AOB代谢产物及细菌残体将作为基质促进包括病原微生物在内的异养细菌的生长[44]，表明在全球变暖背景下，管网中AOB的赋存可能会显著放大系统中的微生物风险。综上所述，气候变化引起的水体赋存条件变化会通过多种途径增加饮用水病原微生物风险。

2 气候变化下不同类型的水体微生物污染及其造成的健康风险

2.1 介水病毒污染及其引发的健康风险

水体病毒污染对人类健康构成直接威胁，特别是肠道病毒，包括诺如病毒和轮状病毒等[45]。经水传播的病毒能够感染人的胃肠道，并通过被感染人群的粪便排出体外，带来水污染风险；呼吸道病毒通常经飞沫传播，但有些呼吸道病毒也存在于粪便中，可能会带来潜在的水污染风险[46]。当前，我国饮用水卫生标准中尚未包含病毒指标，但已经提出了生活饮用水应经消毒处理及对消毒的具体控制要求，同时规定了浑浊度的限值，一定程度上确保饮用水生物安全[47]。

病毒引发的经水传播流行病事件多与饮水污染有关，尤其在农村地区，水源多为浅层地表水，极易受到污染。Jean等针对在我国台湾南部一个村庄暴发的肠道病毒流行病进行研究[48]，结果显示在降雨量>31 mm/h时，该村井水中检出肠道病毒，且降雨率与肠道病毒感染病例之间存在显著关联，感染原因可能是受肠道病毒污染的土壤和地表水，在强降雨的条件下迁移到地下水中进而污染了该村庄的井水。Le Guyader等[49]研究发现，洪水后贝类养殖潟湖附近出现了200多例与食用牡蛎有关的胃肠炎病例，患病个体样本中检出肠道病毒，很可能是洪水事件造成污水处理厂不堪重负，未经处理或处理不完全的含有肠道病毒的污水流入贝类养殖床，从而增加了人类感染疾病的风险。

2.2 介水细菌污染及其引发的健康风险

水中的细菌污染可能会导致多种疾病，特别是消化道疾病，包括腹泻、呕吐、恶心、发烧等症状。世界卫生组织(World Health Organization, WHO)报告，每年约有 300 万–500 万例霍乱病例和 1 万–12 万人因霍乱死亡[50]，研究人员指出霍乱感染与受污染的水之间存在关联[51]。强降水、洪水、飓风或其他自然灾害可能破坏水处理系统或直接影响水源的质量，从而增加细菌污染的风险。

弯曲杆菌、致病性大肠杆菌、志贺菌属、霍乱弧菌、军团菌等是常见的介水致病菌[52]，已有研究显示强降水或降雨量与弯曲杆菌[53]、大肠杆菌[54]、志贺氏菌[55]、沙门氏菌[56]感染发病率有显著关联。气候变化背景下，预计到 2080 年，斯堪的纳维亚地区的弯曲杆菌病的发病率将翻倍[57]，主要原因是极端气候事件增多促进了细菌繁殖，导致水源地和饮用水系统中致病菌的暴发与传播[58]。暴雨和洪水增加了人类与泥泞环境的接触，也为致病菌的传播创造了有利条件，使人们更容易接触病原微生物进而对人类健康产生巨大的威胁。据 Qadri 等[59]报道，2004 年 7 月洪水之后，孟加拉国发生了一场产肠毒素大肠杆菌和霍乱弧菌感染致腹泻的疫情，这场感染暴发期间总患病人数大于 17 000 人。Kuhn 等[60]对暴雨后丹麦城镇发生的水源性空肠弯曲杆菌感染暴发的疫情进行了血清流行病学研究，结果显示暴雨后雨水排放和污水处理系统堵塞导致饮用水污染，并且饮用水消耗量越高的人群空肠弯曲杆菌感染发病率显著增加。Lee 等[56]研究了美国乔治亚州的降水与沙门氏菌感染发病率之间的关系，研究显示极端降雨导致沙门氏菌感染患病风险增加了 5%。因此应加强对自然灾害的预防和应对，确保饮用水水源地环境的安全，最大程度地减少水体细菌污染带来的健康风险。

2.3 介水原虫污染及其引发的健康风险

污染饮用水的致病性原虫主要是肠贾第鞭毛虫、隐孢子虫和溶组织内阿米巴，它们属于寄生于人和动物内的肠道原虫，在供水中存活时间较长[61]。2017–2022 年期间报告的全球水传播寄生虫原生动物疫情中，总共有 416 起归因于寄生原生动物的经水传播，其中隐孢子虫占暴发的 77.4%[62]。我们在 Bourli 等[62]和 Ma 等[63]整理的由隐孢子虫属引起的全球水传播疾病暴发清单基础上，增加了近 2 年的病例事件，分析后发现从时间上来看，2014–2018 年间由隐孢子虫引发疾病的确诊病例数偏高(图 2A)；从病例确诊地域来看，发达国家如美国和澳大利亚，由隐孢子虫引起的全球水传播疾病确诊病例占比极高(图 2B)。这说明即使在拥有完整水源保护和先进处理技术的发达国家，微生物污染物也可能出现在从源头到水龙头的整个饮用水供应链的各个环节[64]。

极端气候事件与饮用水原虫暴发风险的关系，是一个备受关注的话题。研究显示，降雨模式和温度对原虫的传播[65]和原虫病发病率[27]有显著影响。在雨季和降雨径流期间，饮用水和地表水源中隐孢子卵囊的浓度显著增加[66]，暴发人型隐孢子虫病[67]，严重时在供水系统服务范围内约一半的人(40 多万)出现腹泻，甚至导致 69 人死亡[68]。Ikiroma 等[69]的研究结果显示，除了降雨，高温也会增加隐孢子虫感染风险，主要是因为温度升高会增加地表水相关的水上活动，从而增加隐孢子虫卵囊的意外摄入。因此气候变化背景下，需要完善饮用水微生物检测系统，加强对水源的监测和管理，以减少隐孢子虫属等水生原虫对人体健康的潜在威胁。

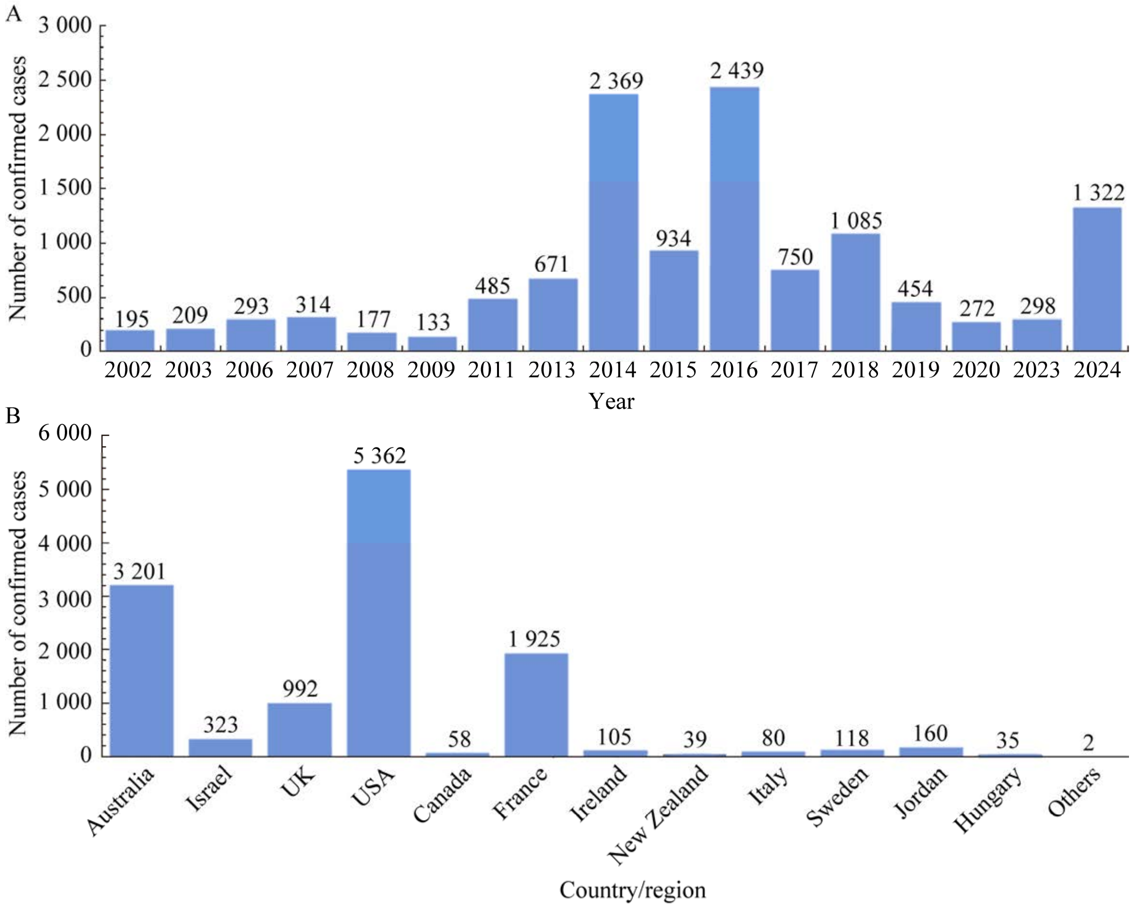

图 2　2002−2024 年由隐孢子虫引起的全球水传播疾病确诊病例

Figure 2　Global waterborne diseases caused by *Cryptosporidium* from 2002 to 2024. A: A bar chart of confirmed number of global waterborne diseases caused by *Cryptosporidium* in different years. B: A bar chart of regional differences in confirmed numbers of global waterborne diseases caused by *Cryptosporidium*.

2.4　水中藻毒素污染风险

气候变化引发河湖水库藻华频发，而藻类产生的藻毒素污染是公共健康关心的，因其摄入后有剧毒，会引起急性肝功能衰竭[70]，且具有促癌活性[71]，而常规水处理方法只能去除部分微囊藻毒素[72]。1995 年，加拿大 Manitoba 地区的调查表明，城市供水以及经处理后的池塘水微囊藻毒素的检出率仍高达 68%[73]。澳大利亚 Palm 岛水源地发生蓝藻水华，经硫酸铜处理 1 周后，在儿童为主的 140 人中出现了呕吐、肝大和肾功能异常，主要是水中蓝藻毒素引起的[74]。我国江苏海门和广西福绥的流行病学调查发现，原发性肝癌发病率与水源地水体中的微囊藻毒素有密切关系[75]。

强降雨会通过增加陆源输入，导致土壤中大量的养分、有机质以及化学物质进入水体，为藻类繁殖提供了营养条件，促进其生长[76-77]。李飞鹏等的研究发现，暴雨会导致水体营养盐浓度成倍增加，引起浮游藻类生物量的骤然升高[78]。此外，强降雨可以引起水体的混合和对流增加，导致沉积在底部的藻类或藻毒素重新悬浮到水体中，增加水体中藻毒素浓度[79]。因此，极端降水导致的陆源输入增加会加剧藻毒素对人类健康、饮用水源地和供水安全的潜在威胁。

2.5 水中耐药菌和耐药基因污染风险

中国是全球抗生素生产量和使用量最大的国家，抗生素的错误和过度使用导致其在污水处理厂[80]、土壤[81]、河流[82]等不同环境中残留，进而增加细菌耐药性[83]。环境中的 ARGs 能够加速细菌耐药性的扩散和传播[84]。地表水和地下水是居民饮用水的主要来源，其水质直接关系到人体健康[85]。然而，Shao 等[86]研究表明，地表水蕴藏着种类繁多的抗生素耐药基因。Zhang 等[87]利用宏基因组技术对中国中部地表水和地下水中 ARGs 污染进行了调查，结果表明，降雨会加强地表水和地下水中抗性基因的传输与联系，并且地表水和地下水中 ARGs 之间的相关性在雨季更强。

耐药性病原微生物在人与人之间、家畜之间，以及动物与人之间的传播可以是直接的，也可以是通过外部环境间接传播。地表水为耐药菌及其耐药基因的传播提供了便利[88]。暴雨会增强径流和冲刷效应，携带地表不同来源的耐药菌及其耐药基因进入河流和湖泊等水环境中[89]，导致耐药菌和耐药基因的污染风险显著增加[90]，甚至会随着水流发生长距离传播[91]。对于耐药菌的传播，未经处理的污水排放到水体中所带来的风险要比经处理后排放的废水大得多[92]，因此需要加强对水体耐药菌和耐药基因污染的监测和管理，以减少对生态系统和公共健康的潜在影响。

3 微生物在水体中的传播风险评估

3.1 病原微生物风险检测方法的应用

水生系统中的细菌、病毒、原虫等病原微生物对全球的公共卫生构成严重威胁[93]，因此病原微生物检测在水系统病原微生物风险监测和评估中发挥着重要作用。传统的饮用水病原微生物检测依赖于指示微生物，如粪便指示菌(fecal indicator bacteria, FIB)。常见的 FIB 包括大肠杆菌和肠球菌属。然而，依赖培养的方法具有局限性，包括检测病原微生物类型有限[94]、检测周期长[95]、病原微生物培养困难[96]等。分子生物学技术的应用使得饮用水微生物风险检测经历了巨大的转变[97]，PCR、qPCR 和微阵列检测已成功用于识别和定量饮用水和废水中的病原微生物[98]。例如，Lee 等[99]使用寡核苷酸微阵列和 qPCR 成功检测出城市废水中的多种细菌病原微生物，其中包括产气荚膜梭菌、粪肠球菌、大肠杆菌、肺炎克雷伯菌和铜绿假单胞菌等。邓闵等[100]对目前水体中不同致病菌分子生物学检测方法及其检测限，以及各检测方法的优势与不足进行了综述。高通量技术能够检测到低丰度或难培养的微生物，弥补传统检测的不足[101]。因此，现行指标与高通量技术结合能够增强监测的全面性和准确性[102]。

新一代测序和定量技术的发展开启了病原微生物广谱检测和快速定量的新时代。常规高通量测序技术能够测定物种相对丰度和群落结构，而绝对定量技术可以反映物种的真实数量变化。例如，为了能够快速、全面地同时检测多种水传播的人类致病细菌(human pathogenic bacteria, HPBs)，有研究者开发了基于高通量实时荧光定量 PCR 技术(high-throughput quantitative polymerase chain reactions, HT-qPCR)的芯片工具，称为 HPB-Chip[103]，该芯片能够在 33 nL 的反应体积中同时完成 10 752 个扩增反应，对多达 192 个样本中的 27 种 HPBs 进行检测和定量分析。此外，三代纳米孔测序技术的应用显著提高了水体环境流行病学监测的效率[95]。香港大学张彤教授团队利用三代纳米孔高通量测序结合细胞内标法，开发了一种快速(1 h 测序)的绝对定量方法[104]，用于定量和评

估污水处理厂中病原微生物和 ARGs 的去除情况；该方法允许在近实时条件下进行病原微生物和 ARGs 的监测，为基于污水的流行病学监测和定量风险评估提供了新的工具。细胞内融合基因技术(emulsion, paired isolation and concatenation PCR, epicPCR)是近年来新发展的可用于 ARGs 及其宿主检测的有效技术。有研究者比较了长读长宏基因组测序、短读长宏基因组测序以及 epicPCR 在检测污水中的 ARGs 及其细菌宿主方面的灵敏度和一致性[105]，发现检测到的宿主范围多样性依次是 epicPCR>长度长测序>短读长测序。本课题组利用 epicPCR 技术探究了典型抗性基因 *sul*1 及其宿主在污水处理厂中的时空分布特征和传播机制，发现相对于空间地理位置，季节转换更容易影响 *sul*1 基因的传播过程和宿主细菌的分布，并揭示了垂直遗传和水平转移途径在抗性基因 *sul*1 的传播过程中均发挥着重要作用[106]；根据相对贡献比例，水平转移(53.75%)主导了 *sul*1 基因在污水处理厂活性污泥中的传播过程[106]。

宏基因组学结合高通量测序和先进的生物信息学技术可用于检测环境样本中的病原微生物[107]，并识别潜在的微生物风险。本课题组构建了包含 247 个人类致病菌的清单及每一个物种的基因组特异性标记(genome specific marker, GSM)[108]，通过分析从不同环境获得的 474 个宏基因组样本序列中这些人类致病菌的类型、丰度和多样性，发现空气中致病菌检出率、多样性和丰度均高于其他生境，该方法对环境中低丰度致病菌也能进行有效检测。Fang 等采用宏基因组测序技术确定城市娱乐用水中致病菌的多样性，研究结果显示水中悬浮颗粒可能会影响致病菌的分布[39]。此外，一些研究表明，宏基因组方法成功应用于识别和评估病毒的多样性[109]。例如，Rosario 等基于宏基因组学分析发现，再生水中的病毒样颗粒比饮用水多 1 000 倍，每毫升约有 10^8 个病毒样颗粒(virus like particle, VLP)，且再生水和饮用水中的大多数病毒都是新型病毒[110]。

病原风险检测方法可以动态监测环境中病原微生物的变化，为定量微生物风险评价模型(quantitative microbial risk assessment, QMRA)提供最新的数据，及时更新风险评估[100]。在饮用水安全、食品安全、医疗环境等领域，病原风险检测方法和 QMRA 常常联合应用为风险管理和决策提供科学依据。

3.2 定量微生物风险评估模型的应用

QMRA 是以微生物污染为风险源，人体健康为风险受体，根据危害的毒理学特性或感染和毒性特征以及其他资料，确定病原微生物的摄入量及其对人体产生不良作用的概率，并用数学模型描述二者之间的关系[111]。Haas 等于 1983 年首次尝试将化学剂量反应模型用于描述病原微生物引发的感染风险，建立了剂量-反应数学模型，并最早对饮用水微生物的危险度进行了定量研究[112]。美国环保署也于 1989 年开始运用数学模型定量分析饮用水中的微生物风险[113]。Rose 等使用指数模型描述了贾第鞭毛虫感染的风险[114]。1999 年，Haas 等出版专著《定量微生物风险评价》，系统描述 QMRA 的全过程[115]。这些数学模型的建立，奠定了 QMRA 的基础。QMRA 的实施包含 4 个步骤，分别是危害识别、暴露评估、剂量-反应分析和风险表征[116]。

QMRA 已成为一种被广泛认可的模型，成功应用于从源头到龙头的各供水环节[117]。通常以典型介水病原微生物，如大肠杆菌、粪大肠菌群、弯曲杆菌、诺如病毒、隐孢子虫和贾第鞭毛虫作为参考病原微生物，进行微生物在水中传播的风险评估。根据 Hofstra 等开发的

模型，全球每年大约排放 3×10^{17} 个隐孢子虫卵囊至地表水，其中我国是排放量最大的国家之一[118]。Cao 等进行的居民饮用水风险评估调查显示，我国多个省市隐孢子虫年感染概率在 3.79×10^{-4}−1.10×10^{-2} 之间，超出了美国环保署提出的阈值 1×10^{-4} [119]。饮用水和娱乐用水引起的隐孢子虫疾病负担为 0−1.01×10^{-5} 每人每年伤残调整寿命年(disability-adjusted life-years pppy, DALYs pppy)，高于 WHO 提出的水传播疾病负担耐受阈值(1×10^{-6} DALYs pppy)。此外，Huang 等对中国重庆三峡水库流域城乡地表水和地下水隐孢子虫和贾第鞭毛虫感染进行风险评估[120]，结果显示隐孢子虫病和贾第鞭毛虫病在城市地区的累积疾病负担分别为 5.77×10^{-5} DALYs pppy 和 4.63×10^{-6} DALYs pppy；在农村地区分别为 6.35×10^{-4} DALYs pppy 和 8.84×10^{-5} DALYs pppy。Yan 等的最新研究结果显示，暴露浓度和饮用水体积对于健康风险的贡献与饮水中的病原微生物类型(大肠杆菌 *vs.* 粪大肠菌)和水源类型(钻孔水 *vs.*井水)密切相关[121]。定量评估再生水中病原微生物引发的健康风险对于保障水资源安全循环利用有重要意义[122]。史亮亮等对于中国某地区的再生水样品进行 QMRA 评估发现，致病性大肠埃希氏菌和沙门氏菌的基准浓度和水环境浓度较为接近，而隐孢子虫和贾第鞭毛虫的水环境浓度值比基准浓度值高 4−6 个数量级[123]。此外，在水质模型中纳入时空变化的灭活过程对于评估病毒感染风险至关重要。最近的一项研究首次将病毒浓度测量、病毒迁移和时空变化灭活模拟以及 QMRA 相结合，成功用于娱乐用水场所的水传播病毒风险评估[45]。生物在水体中的传播风险评估不仅有助于识别和理解微生物对公众健康的潜在影响，还为制定有效的饮用水生物风险管理和控制策略提供科学依据。

4 总结与展望

气候变化对饮用水的生物安全构成了显著的影响，它通过改变水体中微生物的数量和生理特性增加了微生物污染的风险。与理化指标相比，微生物指标具有隐蔽性和潜在的快速变化性，这使得它们在评估饮用水质量方面扮演着关键角色。极端气候事件，如强降水、高温和干旱，对流域的饮用水生物安全及人类健康产生了多方位和多过程的交互影响。鉴于此，未来的研究应加强从水源地到供水系统的全链条的病原微生物检测与监测技术的发展。

(1) 建立完善的病原微生物监测和预警系统。构建一个全面的病原微生物监测和预警系统对于保障饮用水安全至关重要。应定期对水源地的水体进行微生物污染物浓度的监测，以跟踪其变化趋势。水厂也应建立在线生物风险监测预警系统，以实时监控水质状况。除了细菌和病毒，水传播的原生动物和寄生虫如贾第鞭毛虫和隐孢子虫，也应受到重视。我国对这些微生物的检测已逐渐加强。自 2023 年 4 月 1 日起，根据最新修订的《生活饮用水卫生标准》(GB 5749—2022)[124]，贾第鞭毛虫和隐孢子虫被列为水质的扩展指标。进一步地，自 2023 年 10 月 1 日起实施的《生活饮用水标准检验方法》(GB/T 5750—2023)中[125]，不仅对“两虫”进行了常规定义，还对其外形特征进行了详细的描述，并新增了相应的检测方法。为了有效防治不同类型的介水病原微生物，必须深入研究不同地区和水体环境下这些微生物的本底浓度、分布特征及其影响因素。这些研究结果对于制定具有针对性的防治策略至关重要，有助于维护公共健康和提高饮用水的生物安全性。

(2) 发展和优化病原微生物高通量检测方法。当前，病原微生物的高通量检测方法在复

杂环境样本中对致病菌的定量和多样性分析方面仍面临重大技术挑战。特别是，由于致病菌株与其亲缘关系较近的非致病菌在基因序列上的高度同源性，不当选择特征目标片段可能导致环境样本中出现假阳性结果。此外，由于致病菌在环境样本中的相对丰度较低，假阴性的风险同样存在。针对这些挑战，未来的研究应致力于开发具有高通量和高特异性的病原微生物检测技术。同时，便携、快速且高效的致病菌浓缩富集技术的开发也是提升检测灵敏度的关键，这将有助于更准确地识别和评估微生物风险，从而为饮用水安全提供更为可靠的科学依据。

(3) 强化对水源保护区的水质保护。水质的优良是保障饮用水安全的根本。在流域内实施有效的水土保持措施，例如增强植被覆盖、防治土壤侵蚀和冲刷，能够显著降低土壤中微生物污染物直接进入水体的风险。此外，通过设立水源地保护区，加强对动物源、生活源等人类活动排放病原微生物的源头管控，可以有效减轻微生物污染物对饮用水源的潜在影响，保护水源地，从而降低经水传播的疾病风险。

(4) 加强跨地区、跨学科的交叉合作，提升流域饮用水生物安全保障能力。气候变化背景下增加的极端天气事件会加剧环境干扰，增强病原微生物的跨地域和跨物种传播的可能性，因此未来针对流域水体病原微生物的监测需要加强地区之间的协作与信息共享，统筹上下游、左右岸、地表地下的水资源管理。通过融合前沿的人工智能算法、高效的实时监测系统、先进的大数据模型构建技术，以及综合多组学的深度分析方法，实现对水体微生物动态变化的精准追踪和细致洞察。这些跨学科技术手段的集成应用，不仅提升了我们对水环境微生物生态系统认知的深度和广度，而且极大地增强了我们对饮用水生物安全保障的能力。

参考文献

[1] HU YR, JIN L, ZHAO Y, JIANG L, YAO SJ, ZHOU W, LIN KF, CUI CZ. Annual trends and health risks of antibiotics and antibiotic resistance genes in a drinking water source in East China[J]. Science of the Total Environment, 2021, 791: 148152.

[2] XIAO XY, FU JJ, YU X. Impacts of extreme weather on microbiological risks of drinking water in coastal cities: a review[J]. Current Pollution Reports, 2023, 9(2): 259-271.

[3] HALES S. Climate change, extreme rainfall events, drinking water and enteric disease[J]. Reviews on Environmental Health, 2019, 34(1): 1-3.

[4] EL-FADEL M, GHANIMEH S, MAROUN R, ALAMEDDINE I. Climate change and temperature rise: Implications on food- and water-borne diseases[J]. Science of the Total Environment, 2012, 437: 15-21.

[5] MAJEDUL ISLAM MM, IQBAL MS, D'SOUZA N, ISLAM MA. A review on present and future microbial surface water quality worldwide[J]. Environmental Nanotechnology, Monitoring & Management, 2021, 16: 100523.

[6] STERK A, SCHIJVEN J, DE RODA HUSMAN AM, DE NIJS T. Effect of climate change on runoff of *Campylobacter* and *Cryptosporidium* from land to surface water[J]. Water Research, 2016, 95: 90-102.

[7] WANG XH, WANG X, CAO JP. Environmental factors associated with *Cryptosporidium* and *Giardia*[J]. Pathogens, 2023, 12(3): 420.

[8] HONG HC, QIU JW, LIANG Y. Environmental factors influencing the distribution of total and fecal coliform bacteria in six water storage reservoirs in the Pearl River Delta Region, China[J]. Journal of Environmental Sciences, 2010, 22(5): 663-668.

[9] HALEY BJ, COLE DJ, LIPP EK. Distribution, diversity, and seasonality of waterborne salmonellae in a rural watershed[J]. Applied and Environmental Microbiology, 2009, 75(5): 1248-1255.

[10] WOLFF E, VAN VLIET MTH. Impact of the 2018 drought on pharmaceutical concentrations and general water quality of the Rhine and Meuse rivers[J]. Science of the Total Environment, 2021, 778: 146182.

[11] MISHRA A, ALNAHIT A, CAMPBELL B. Impact of land uses, drought, flood, wildfire, and cascading events on water quality and microbial communities: a review and analysis[J]. Journal of Hydrology, 2021, 596: 125707.

[12] WU M, WANG HM, WANG WQ, SONG YY, MA LY, LU XL, WANG N, LIU CY. The impact of heavy rain event on groundwater microbial communities in Xikuangshan, Hunan Province, P.R. China[J]. Journal of Hydrology, 2021, 595: 125674.

[13] TANG W, LIU YS, LI QY, CHEN L, LI Q, LI P, XIA SJ. The impact of extreme weather events on bacterial communities and opportunistic pathogens in a drinking water treatment plant[J]. Water, 2021, 14(1): 54.

[14] ZHU KH, REN HW, LU Y. Potential Biorisks of *Cryptosporidium* spp. and *Giardia* spp. from Reclaimed Water and Countermeasures[J]. Current Pollution Reports, 2022, 8(4): 456-476.

[15] STOCKER MD, PACHEPSKY YA, HILL RL, MARTINEZ G. *Escherichia coli* export from manured fields depends on the time between the start of rainfall and runoff initiation[J]. Journal of Environmental Quality, 2018, 47(5): 1293-1297.

[16] MEYERS MA, DURSO LM, GILLEY JE, WALDRIP HM, CASTLEBERRY L, MILLMIER-SCHMIDT A. Antibiotic resistance gene profile changes in cropland soil after manure application and rainfall[J]. Journal of Environmental Quality, 2020, 49(3): 754-761.

[17] PACHEPSKY Y, Shelton DR, MCLAIN JET, PATEL J, MANDRELL R. Irrigation waters as a source of pathogenic microorganisms in produce: a review[J]. Advances in agronomy, 2011, 113: 75-141.

[18] DÍAZ FJ, O′GEEN AT, DAHLGREN RA. Agricultural pollutant removal by constructed wetlands: implications for water management and design[J]. Agricultural Water Management, 2012, 104: 171-183.

[19] PHAM DUC P, NGUYEN-VIET H, HATTENDORF J, ZINSSTAG J, DAC CAM P, ODERMATT P. Risk factors for *Entamoeba histolytica* infection in an agricultural community in Hanam Province, Vietnam[J]. Parasites & Vectors, 2011, 4: 102.

[20] OLDS HT, CORSI SR, DILA DK, HALMO KM, BOOTSMA MJ, MCLELLAN SL. High levels of sewage contamination released from urban areas after storm events: a quantitative survey with sewage specific bacterial indicators[J]. PLoS Medicine, 2018, 15(7): e1002614.

[21] MTETWA HN, AMOAH ID, KUMARI S, BUX F, REDDY P. The source and fate of *Mycobacterium tuberculosis* complex in wastewater and possible routes of transmission[J]. BMC Public Health, 2022, 22(1): 145.

[22] LARSSON C, ANDERSSON Y, ALLESTAM G, LINDQVIST A, NENONEN N, BERGSTEDT O. Epidemiology and estimated costs of a large waterborne outbreak of norovirus infection in Sweden[J]. Epidemiology and Infection, 2014, 142(3): 592-600.

[23] FEDERIGI I, SALVADORI R, LAURETANI G, LEONE A, LIPPI S, MARVULLI F, PAGANI A, VERANI M, CARDUCCI A. Wastewater treatment plants performance for reuse: evaluation of bacterial and viral risks[J]. Water, 2024, 16(10): 1399.

[24] PAYMENT P, BERTE A, PRÉVOST M, MÉNARD B, BARBEAU B. Occurrence of pathogenic microorganisms in the Saint Lawrence River (Canada) and comparison of health risks for populations using it as their source of drinking water[J]. Canadian Journal of Microbiology, 2000, 46(6): 565-576.

[25] SHIH YJ, CHEN JS, CHEN YJ, YANG PY, KUO YJ, CHEN TH, HSU BM. Impact of heavy precipitation events on pathogen occurrence in estuarine areas of the Puzi River in Taiwan[J]. PLoS One, 2021, 16(8): e0256266.

[26] SENHORST HAJ, ZWOLSMAN JJG. Climate change and effects on water quality: a first impression[J]. Water Science and Technology, 2005, 51(5): 53-59.

[27] GOLOMAZOU E, MAMEDOVA S, ESLAHI AV, KARANIS P. *Cryptosporidium* and agriculture: a review[J]. Science of the Total Environment, 2024, 916: 170057.

[28] DELPLA I, JUNG AV, BAURES E, CLEMENT M, THOMAS O. Impacts of climate change on surface water quality in relation to drinking water production[J]. Environment international, 2009, 35(8): 1225-1233.

[29] PARKINSON AJ, BUTLER JC. Potential impacts of climate change on infectious diseases in the Arctic[J]. International Journal of Circumpolar Health, 2005, 64(5): 478-486.

[30] PASCUAL M, BOUMA MJ, DOBSON AP. Cholera and climate: revisiting the quantitative evidence[J]. Microbes and Infection, 2002, 4(2): 237-245.

[31] HONDA JR, VIRDI R, CHAN ED. Global environmental nontuberculous mycobacteria and their contemporaneous man-made and natural niches[J]. Frontiers in Microbiology, 2018, 9: 2029.

[32] ZHANG WW, WANG JY, FAN JF, GAO DL, JU HY. Effects of rainfall on microbial water quality on Qingdao No. 1 Bathing Beach, China[J]. Marine Pollution Bulletin, 2013, 66(1/2): 185-190.

[33] ZWART JA, SEBESTYEN SD, SOLOMON CT, JONES SE. The Influence of hydrologic residence time on lake carbon cycling dynamics following extreme

precipitation events[J]. Ecosystems, 2017, 20(5): 1000-1014.

[34] TRYLAND I, MYRMEL M, ØSTENSVIK Ø, WENNBERG AC, ROBERTSON LJ. Impact of rainfall on the hygienic quality of blue mussels and water in urban areas in the Inner Oslofjord, Norway[J]. Marine Pollution Bulletin, 2014, 85(1): 42-49.

[35] CAVICCHIOLI R, RIPPLE WJ, TIMMIS KN, AZAM F, BAKKEN LR, BAYLIS M, BEHRENFELD MJ, BOETIUS A, BOYD PW, CLASSEN AT, CROWTHER TW, DANOVARO R, FOREMAN CM, HUISMAN J, HUTCHINS DA, JANSSON JK, KARL DM, KOSKELLA B, MARK WELCH DB, MARTINY JBH, et al. Scientists' warning to humanity: microorganisms and climate change[J]. Nature Reviews Microbiology, 2019, 17(9): 569-586.

[36] LAWLER DM, PETTS GE, FOSTER IDL, HARPER S. Turbidity dynamics during spring storm events in an urban headwater river system: the Upper Tame, West Midlands, UK[J]. Science of the Total Environment, 2006, 360(1/2/3): 109-126.

[37] JEZNACH LC, HAGEMANN M, PARK MH, TOBIASON JE. Proactive modeling of water quality impacts of extreme precipitation events in a drinking water reservoir[J]. Journal of Environmental Management, 2017, 201: 241-251.

[38] BEATTIE RE, HRISTOVA KR. Manure derived nutrients alter microbial community composition and increase the presence of potential pathogens in freshwater sediment[J]. Journal of Applied Microbiology, 2022, 132(1): 747-757.

[39] FANG TT, CUI QJ, HUANG Y, DONG PY, WANG H, LIU WT, YE QH. Distribution comparison and risk assessment of free-floating and particle-attached bacterial pathogens in urban recreational water: implications for water quality management[J]. Science of the Total Environment, 2018, 613: 428-438.

[40] GRIEBLER C, BRIELMANN H, HABERER CM, KASCHUBA S, KELLERMANN C, STUMPP C, HEGLER F, KUNTZ D, WALKER-HERTKORN S, LUEDERS T. Potential impacts of geothermal energy use and storage of heat on groundwater quality, biodiversity, and ecosystem processes[J]. Environmental Earth Sciences, 2016, 75(20): 1391.

[41] RETTER A, KARWAUTZ C, GRIEBLER C. Groundwater microbial communities in times of climate change[J]. Current Issues in Molecular Biology, 2021, 41: 509-538.

[42] CHAPRA SC, BOEHLERT B, FANT C, BIERMAN VJ Jr, HENDERSON J, MILLS D, MAS DML, RENNELS L, JANTARASAMI L, MARTINICH J, STRZEPEK KM, PAERL HW. Climate change impacts on harmful algal blooms in U.S. freshwaters: a screening-level assessment[J]. Environmental Science & Technology, 2017, 51(16): 8933-8943.

[43] AGUDELO-VERA C, AVVEDIMENTO S, BOXALL J, CREACO E, de KATER H, Di NARDO A, DJUKIC A, DOUTERELO I, FISH KE, IGLESIAS REY PL, JACIMOVIC N, JACOBS HE, KAPELAN Z, MARTINEZ SOLANO J, MONTOYA PACHONGO C, PILLER O, QUINTILIANI C, RUČKA J, TUHOVČÁK L, BLOKKER M. Drinking water temperature around the globe: understanding, policies, challenges and opportunities[J]. Water, 2020, 12(4): 1049.

[44] ZHENG SK, LI JG, YE CS, XIAN XX, FENG MB, YU X. Microbiological risks increased by ammonia-oxidizing bacteria under global warming: the neglected issue in chloraminated drinking water distribution system[J]. Science of the Total Environment, 2023, 874: 162353.

[45] LI CJ, SYLVESTRE É, FERNANDEZ-CASSI X, JULIAN TR, KOHN T. Waterborne virus transport and the associated risks in a large lake[J]. Water Research, 2023, 229: 119437.

[46] BOUSSETTINE R, HASSOU N, BESSI H, ENNAJI MM. Emerging and reemerging viral pathogens[M]. Amsterdam: Academic Press, 2020: 907-932 (in Netherlands).

[47] SHI X. The safety of drinking water in China: current status and future prospects[J]. China CDC weekly, 2020, 2(13): 210-215.

[48] JEAN JS, GUO HR, CHEN SH, LIU CC, CHANG WT, YANG YJ, HUANG MC. The association between rainfall rate and occurrence of an enterovirus epidemic due to a contaminated well[J]. Journal of Applied Microbiology, 2006, 101(6): 1224-1231.

[49] le GUYADER FS, le SAUX JC, AMBERT-BALAY K, KROL J, SERAIS O, PARNAUDEAU S, GIRAUDON H, DELMAS G, POMMEPUY M, POTHIER P, ATMAR RL. Aichi virus, norovirus, astrovirus, enterovirus, and rotavirus involved in clinical cases from a French oyster-related gastroenteritis outbreak[J]. Journal of Clinical Microbiology, 2008, 46(12): 4011-4017.

[50] NELSON EJ, HARRIS JB, MORRIS JG Jr, CALDERWOOD SB, CAMILLI A. Cholera transmission: the host, pathogen and bacteriophage

dynamic[J]. Nature Reviews Microbiology, 2009, 7(10): 693-702.

[51] PANDEY PK, KASS PH, SOUPIR ML, BISWAS S, SINGH VP. Contamination of water resources by pathogenic bacteria[J]. AMB Express, 2014, 4: 51.

[52] RIDDLE MS, GUTIERREZ RL, VERDU EF, PORTER CK. The chronic gastrointestinal consequences associated with *Campylobacter*[J]. Current Gastroenterology Reports, 2012, 14(5): 395-405.

[53] SONEJA S, JIANG CS, ROMEO UPPERMAN C, MURTUGUDDE R, MITCHELL CS, BLYTHE D, SAPKOTA AR, SAPKOTA A. Extreme precipitation events and increased risk of campylobacteriosis in Maryland, U.S.A[J]. Environmental Research, 2016, 149: 216-221.

[54] POWERS JE, MUREITHI M, MBOYA J, CAMPOLO J, SWARTHOUT JM, PAJKA J, NULL C, PICKERING AJ. Effects of high temperature and heavy precipitation on drinking water quality and child hand contamination levels in rural Kenya[J]. Environmental Science & Technology, 2023, 57(17): 6975-6988.

[55] HINES JZ, JAGGER MA, JEANNE TL, WEST N, WINQUIST A, ROBINSON BF, LEMAN RF, HEDBERG K. Heavy precipitation as a risk factor for shigellosis among homeless persons during an outbreak—Oregon, 2015–2016[J]. Journal of Infection, 2018, 76(3): 280-285.

[56] LEE D, CHANG HH, SARNAT SE, LEVY K. Precipitation and salmonellosis incidence in Georgia, USA: interactions between extreme rainfall events and antecedent rainfall conditions[J]. Environmental Health Perspectives, 2019, 127(9): 97005.

[57] KUHN KG, NYGÅRD KM, GUZMAN-HERRADOR B, SUNDE LS, RIMHANEN-FINNE R, TRÖNNBERG L, JEPSEN MR, RUUHELA R, WONG WK, ETHELBERG S. *Campylobacter* infections expected to increase due to climate change in Northern Europe[J]. Scientific Reports, 2020, 10(1): 13874.

[58] FITZGERALD C. *Campylobacter*[J]. Clinics in Laboratory Medicine, 2015, 35(2): 289-298.

[59] QADRI F, KHAN AI, FARUQUE ASG, BEGUM YA, CHOWDHURY F, NAIR GB, SALAM MA, SACK DA, SVENNERHOLM AM. Enterotoxigenic *Escherichia coli* and *Vibrio cholerae* diarrhea, Bangladesh, 2004[J]. Emerging Infectious Diseases, 2005, 11(7): 1104-1107.

[60] KUHN KG, FALKENHORST G, EMBORG HD, CEPER T, TORPDAHL M, KROGFELT KA, ETHELBERG S, MØLBAK K. Epidemiological and serological investigation of a waterborne *Campylobacter jejuni* outbreak in a Danish town[J]. Epidemiology and Infection, 2017, 145(4): 701-709.

[61] HEMPHILL A, MÜLLER N, MÜLLER J. Comparative pathobiology of the intestinal protozoan parasites *Giardia lamblia*, *Entamoeba histolytica*, and *Cryptosporidium parvum*[J]. Pathogens, 2019, 8(3): 116.

[62] BOURLI P, ESLAHI AV, TZORAKI O, KARANIS P. Waterborne transmission of protozoan parasites: a review of worldwide outbreaks - an update 2017–2022[J]. Journal of Water and Health, 2023, 21(10): 1421-1447.

[63] MA JY, LI MY, QI ZZ, FU M, SUN TF, ELSHEIKHA HM, CONG W. Waterborne protozoan outbreaks: an update on the global, regional, and national prevalence from 2017 to 2020 and sources of contamination[J]. Science of the Total Environment, 2022, 806: 150562.

[64] COFFEY R, BENHAM B, KROMETIS LA, WOLFE ML, CUMMINS E. Assessing the effects of climate change on waterborne microorganisms: implications for EU and U.S. water policy[J]. Human and Ecological Risk Assessment, 2014, 20(3): 724-742.

[65] BOXALL ABA, HARDY A, BEULKE S, BOUCARD T, BURGIN L, FALLOON PD, HAYGARTH PM, HUTCHINSON T, KOVATS RS, LEONARDI G, LEVY LS, NICHOLS G, PARSONS SA, POTTS L, STONE D, TOPP E, TURLEY DB, WALSH K, WELLINGTON EMH, WILLIAMS RJ. Impacts of climate change on indirect human exposure to pathogens and chemicals from agriculture[J]. Environmental Health Perspectives, 2009, 117(4): 508-514.

[66] DARAEI H, OLIVERI CONTI G, SAHLABADI F, THAI VN, GHOLIPOUR S, TURKI H, FAKHRI Y, FERRANTE M, MORADI A, MOUSAVI KHANEGHAH A. Prevalence of *Cryptosporidium* spp. in water: a global systematic review and meta-analysis[J]. Environmental Science and Pollution Research International, 2021, 28(8): 9498-9507.

[67] GERTLER M, DÜRR M, RENNER P, POPPERT S, ASKAR M, BREIDENBACH J, FRANK C, PREUßEL K, SCHIELKE A, WERBER D, CHALMERS R, ROBINSON G, FEUERPFEIL I, TANNICH E, GRÖGER C, STARK K, WILKING H. Outbreak of *Cryptosporidium hominis* following river flooding in the city of Halle (Saale), Germany, August 2013[J]. BMC Infectious Diseases, 2015, 15: 88.

[68] HOWE AD, FORSTER S, MORTON S, MARSHALL R, OSBORN KS, WRIGHT P, HUNTER PR. *Cryptosporidium* oocysts in a water supply associated with a cryptosporidiosis outbreak[J]. Emerging Infectious Diseases, 2002, 8(6): 619-624.

[69] IKIROMA IA, POLLOCK KG. Influence of weather and climate on cryptosporidiosis: a review[J]. Zoonoses and Public Health, 2021, 68(4): 285-298.

[70] SOUZA NR, METCALF JS. Cyanobacterial toxins and their effects on human and animal health[M]//Handbook of Algal Science, Technology and Medicine. Amsterdam: Elsevier, 2020: 561-574.

[71] LAWTON LA, ROBERTSON PKJ, CORNISH BJPA, MARR IL, JASPARS M. Processes influencing surface interaction and photocatalytic destruction of *Microcystins* on titanium dioxide photocatalysts[J]. Journal of Catalysis, 2003, 213(1): 109-113.

[72] 夏江，施之新. 武汉市饮用水中浮游藻类的调查[J]. 环境与健康杂志, 2005(4): 287-288.

XIA J, SHI ZX. Survey on algae in drinking water in Wuhan[J]. Journal of Environment and Health, 2005, 22(4): 287-288

[73] PIP E, ALLEGRO E. Nearshore fluctuations in water chemistry, microcystins and coliform bacteria during the ice-free season in Lake Winnipeg, Manitoba, Canada[J]. Ecohydrology & Hydrobiology, 2010, 10(1): 35-43.

[74] PHAM LT, TRAN YTH, TRAN TT, BUI HM, LE LT, DAO ST, NGUYEN DT. Ecological and human health risk assessments of cyanotoxins and heavy metals in a drinking water supply reservoir[J]. Journal of Water and Health, 2023, 21(8): 1004-1016.

[75] 俞顺章，赵宁，资晓林，陈刚，董传辉，连民，刘颖，穆丽娜. 饮水中微囊藻毒素与我国原发性肝癌关系的研究[J]. 中华肿瘤杂志, 2001, 23(2): 96-99.

YU SZ, ZHAO N, ZI XL, CHEN G, DONG CH, LIAN M, LIU Y, MU LN. The relationship cyanotoxin (microcystin, MC) in pond-ditch water and primary liver cancer in China[J]. Chinese Journal of Oncology, 2001, 23(2): 96-99 (in Chinese).

[76] LI D, LIU SL, YANG Y, GUO L, LYU BY, YANG RJ, ZHANG XX, WANG YL, YANG F, CHEN QB. Metal-algae interaction contributes to the water environment heterogeneity in an urbanized river[J]. Ecological Indicators, 2022, 139: 108875.

[77] 张胜花，常军军，孙珮石. 水体藻类磷代谢及藻体磷矿化研究进展[J]. 生态环境学报, 2013, 22(7): 1250-1254.

ZHANG SH, CHANG JJ, SUN PS. Phosphorus cycle of algae during its growth and death process: phosphorus uptake and release[J]. Ecology and Environmental Sciences, 2013, 22(7): 1250-1254 (in Chinese).

[78] 李飞鹏，陈蒙蒙，贾玉宝，张海平，陈玲. 气象因素对封闭浅水湖泊浮游藻类生长和分布影响[J]. 水生态学杂志, 2019, 40(5): 55-62.

LI FP, CHEN MM, JIA YB, ZHANG HP, CHEN L. Effects of meteorological factors on growth and distribution of phytoplankton in an enclosed shallow lake[J]. Journal of Hydroecology, 2019, 40(5): 55-62 (in Chinese).

[79] REICHWALDT ES, GHADOUANI A. Effects of rainfall patterns on toxic cyanobacterial blooms in a changing climate: between simplistic scenarios and complex dynamics[J]. Water Research, 2012, 46(5): 1372-1393.

[80] LI B, ZHANG T. Mass flows and removal of antibiotics in two municipal wastewater treatment plants[J]. Chemosphere, 2011, 83(9): 1284-1289.

[81] LI C, CHEN JY, WANG JH, MA ZH, HAN P, LUAN YX, LU AX. Occurrence of antibiotics in soils and manures from greenhouse vegetable production bases of Beijing, China and an associated risk assessment[J]. Science of the Total Environment, 2015, 521: 101-107.

[82] LI XW, SHI HC, LI KX, ZHANG L, GAN YP. Occurrence and fate of antibiotics in advanced wastewater treatment facilities and receiving rivers in Beijing, China[J]. Frontiers of Environmental Science & Engineering, 2014, 8(6): 888-894.

[83] SU HC, YING GG, TAO R, ZHANG RQ, ZHAO JL, LIU YS. Class 1 and 2 integrons, *sul* resistance genes and antibiotic resistance in *Escherichia coli* isolated from Dongjiang River, South China[J]. Environmental Pollution, 2012, 169: 42-49.

[84] ZHANG XX, ZHANG T, FANG HHP. Antibiotic resistance genes in water environment[J]. Applied Microbiology and Biotechnology, 2009, 82(3): 397-414.

[85] BAI Y, RUAN XH, XIE XC, YAN ZY. Antibiotic resistome profile based on metagenomics in raw surface drinking water source and the influence of environmental factor: a case study in Huaihe River Basin, China[J]. Environmental Pollution, 2019, 248: 438-447.

[86] SHAO SC, HU YY, CHENG JH, CHEN YC. Research progress on distribution, migration, transformation of antibiotics and antibiotic resistance genes (ARGs) in aquatic environment[J]. Critical Reviews in Biotechnology, 2018, 38(8): 1195-1208.

[87] ZHANG L, JI L, LIU X, ZHU X, NING K, WANG Z. Linkage and driving mechanisms of antibiotic resistome in surface and ground water: their responses to land use and seasonal variation[J]. Water Research, 2022, 215: 118279.

[88] LARSSON DGJ, FLACH CF. Antibiotic resistance in the environment[J]. Nature Reviews Microbiology, 2022, 20(5): 257-269.

[89] SHEN XX, JIN GQ, ZHAO YJ, SHAO XH. Prevalence and distribution analysis of antibiotic resistance genes in a large-scale aquaculture environment[J]. Science of the Total Environment, 2020, 711: 134626.

[90] LEE J, BECK K, BÜRGMANN H. Wastewater bypass is a major temporary point-source of antibiotic resistance genes and multi-resistance risk factors in a Swiss river[J]. Water Research, 2022, 208: 117827.

[91] BENGTSSON-PALME J, KRISTIANSSON E, LARSSON DGJ. Environmental factors influencing the development and spread of antibiotic resistance[J]. FEMS Microbiology Reviews, 2018, 42(1): fux053.

[92] KARKMAN A, JOHNSON TA, LYRA C, STEDTFELD RD, TAMMINEN M, TIEDJE JM, VIRTA M. High-throughput quantification of antibiotic resistance genes from an urban wastewater treatment plant[J]. FEMS Microbiology Ecology, 2016, 92(3): fiw014.

[93] WELSH RM, SEXTON DJ, FORSBERG K, VALLABHANENI S, LITVINTSEVA A. Insights into the unique nature of the East Asian clade of the emerging pathogenic yeast *Candida auris*[J]. Journal of Clinical Microbiology, 2019, 57(4): e00007-19.

[94] GIRONES R, FERRÚS MA, ALONSO JL, RODRIGUEZ-MANZANO J, CALGUA B, de ABREU CORRÊA A, HUNDESA A, CARRATALA A, BOFILL-MAS S. Molecular detection of pathogens in water: the pros and cons of molecular techniques[J]. Water Research, 2010, 44(15): 4325-4339.

[95] GU W, DENG XD, LEE M, SUCU YD, AREVALO S, STRYKE D, FEDERMAN S, GOPEZ A, REYES K, ZORN K, SAMPLE H, YU GX, ISHPUNIANI G, BRIGGS B, CHOW ED, BERGER A, WILSON MR, WANG C, HSU E, MILLER S, et al. Rapid pathogen detection by metagenomic next-generation sequencing of infected body fluids[J]. Nature Medicine, 2021, 27(1): 115-124.

[96] GALLAGHER T, PHAN J, WHITESON K. Getting our fingers on the pulse of slow-growing bacteria in hard-to-reach places[J]. Journal of Bacteriology, 2018, 200(24): e00540-18.

[97] AW TG, ROSE JB. Detection of pathogens in water: from phylochips to qPCR to pyrosequencing[J]. Current Opinion in Biotechnology, 2012, 23(3): 422-430.

[98] SHANNON KE, LEE DY, TREVORS JT, BEAUDETTE LA. Application of real-time quantitative PCR for the detection of selected bacterial pathogens during municipal wastewater treatment[J]. Science of the Total Environment, 2007, 382(1): 121-129.

[99] LEE DY, SHANNON K, BEAUDETTE LA. Detection of bacterial pathogens in municipal wastewater using an oligonucleotide microarray and real-time quantitative PCR[J]. Journal of Microbiological Methods, 2006, 65(3): 453-467.

[100] 邓闵, 李露, 宋康. 水环境中致病菌快速检测技术及应用研究进展[J]. 环境科学研究, 2023, 36(10): 1835-1844.
DENG M, LI L, SONG K. Rapid molecular biology detection and risk assessment of waterborne pathogens: a review[J]. Research of Environmental Sciences, 2023, 36(10): 1835-1844 (in Chinese).

[101] LAN W, LIU HY, WENG R, ZENG YX, LOU J, XU HX, YU YS, JIANG Y. Microbial community of municipal drinking water in Hangzhou using metagenomic sequencing[J]. Environmental Pollution, 2024, 342: 123066.

[102] RIMOLDI SG, BRIOSCHI D, CURRELI D, SALARI F, PAGANI C, TAMONI A, LONGOBARDI C, BOSARI R, RIZZO A, LANDONIO S, COEN M, PASSERINI M, GISMONDO MR, GORI A, MANZOTTI A. Traditional cultures versus next generation sequencing for suspected orthopedic infection: experience gained from a reference centre[J]. Antibiotics, 2023, 12(11): 1588.

[103] TUO JH, SHEN Y, JIA SY, LIU SN, ZHANG QF, WANG DP, HE XW, LIU P, ZHANG XX. HPB-Chip: an accurate high-throughput qPCR-based tool for rapidly profiling waterborne human pathogenic bacteria in the environment[J]. Water Research, 2024, 260: 121927.

[104] YANG Y, CHE Y, LIU L, WANG CX, YIN XL, DENG Y, YANG C, ZHANG T. Rapid absolute quantification of pathogens and ARGs by nanopore sequencing[J]. Science of the Total Environment, 2022, 809: 152190.

[105] LOU EG, FU YL, WANG Q, TREANGEN TJ, STADLER LB. Sensitivity and consistency of long- and short-read metagenomics and epicPCR for the detection of antibiotic resistance genes and their bacterial hosts in wastewater[J]. Journal of Hazardous Materials, 2024, 469: 133939.

[106] WEI ZY, FENG K, WANG ZJ, ZHANG Y, YANG M, ZHU YG, VIRTA MPJ, DENG Y. High-throughput single-cell technology reveals the contribution of horizontal gene transfer to typical antibiotic resistance gene dissemination in wastewater treatment plants[J]. Environmental Science & Technology, 2021, 55(17): 11824-11834.

[107] 王尚, 冯凯, 李瞳, 王洁, 顾松松, 杨兴盛, 李春格, 邓晔. 环境病原微生物研究数据库及数据挖掘方法[J]. 生物技术通报, 2024, 40(10): 221-232.
WANG S, FENG K, LI T, WANG J, GU SS, YANG XS, LI C, DENG Y. Database and data mining methods[J]. Biotechnology Bulletin, 2024, 40(10): 221-232 (in Chinese).

[108] LI T, FENG K, WANG S, YANG XS, PENG X, TU QC, DENG Y. Beyond water and soil: air emerges as a major reservoir of human pathogens[J]. Environment International, 2024, 190: 108869.

[109] DJIKENG A, KUZMICKAS R, ANDERSON NG, SPIRO DJ. Metagenomic analysis of RNA viruses in a fresh water lake[J]. PLoS One, 2009, 4(9): e7264.

[110] ROSARIO K, NILSSON C, LIM YW, RUAN YJ, BREITBART M. Metagenomic analysis of viruses in reclaimed water[J]. Environmental Microbiology, 2009, 11(11): 2806-2820.

[111] GALE P. Developments in microbiological risk assessment for drinking water[J]. Journal of Applied Microbiology, 2001, 91(2): 191-205.

[112] HAAS CN, ROSE JB, GERBA CP. Quantitative Microbial Risk Assessment[M]. 2nd edition. New York: John Wiley & Sons, Inc, 2014.

[113] EISENBERG JNS, MOORE K, SOLLER JA, EISENBERG D, JR COLFORD JM. Microbial risk assessment framework for exposure to amended sludge projects[J]. Environmental Health Perspectives, 2008, 116(6): 727-733.

[114] ROSE JB, HAAS CN, REGLI S. Risk assessment and control of waterborne giardiasis[J]. American Journal of Public Health, 1991, 81(6): 709-713.

[115] HAAS CN, ROSE JB, GERBA C, REGLI S. Risk assessment of virus in drinking water[J]. Risk Analysis, 1993, 13(5): 545-552.

[116] ZWIETERING MH, van GERWEN SJC. Sensitivity analysis in quantitative microbial risk assessment[J]. International Journal of Food Microbiology, 2000, 58(3): 213-221.

[117] DUNN G, HARRIS L, COOK C, PRYSTAJECKY N. A comparative analysis of current microbial water quality risk assessment and management practices in British Columbia and Ontario, Canada[J]. Science of the Total Environment, 2014, 468: 544-552.

[118] HOFSTRA N, BOUWMAN AF, BEUSEN AHW, MEDEMA GJ. Exploring global *Cryptosporidium* emissions to surface water[J]. Science of the Total Environment, 2013, 442: 10-19.

[119] CAO SK, JIANG YY, YUAN ZY, YIN JH, XU M, XUE JB, TANG LH, SHEN YJ, CAO JP. Quantitative microbial risk assessment of *Cryptosporidium* and *Giardia* in public drinking water in China[J]. Biomedical and Environmental Sciences, 2021, 34(6): 493-498.

[120] HUANG Q, HUANG S, LI B, XIONG YH, KUANG WJ, XIAO SX, YI JH, ZHAO F, XIAO GS. Spatially explicit model of the *Cryptosporidium* and *Giardia* disease burden from surface and ground waters in urban and rural areas of the Three Gorges Reservoir watershed in Chongqing, China[J]. Environmental Science and Pollution Research International, 2023, 30(13): 37127-37142.

[121] YAN C, WAN WD, WANG RN, LAI TN, ALI W, HE SS, LIU S, LI X, AHMAD NASIR Z, COULON F. Quantitative health risk assessment of microbial hazards from water sources for community and self-supply drinking water systems[J]. Journal of Hazardous Materials, 2024, 465: 133324.

[122] HAMILTON KA, HAMILTON MT, JOHNSON W, JJEMBA P, BUKHARI Z, LeCHEVALLIER M, HAAS CN, GURIAN PL. Risk-based critical concentrations of *Legionella pneumophil*a for indoor residential water uses[J]. Environmental Science & Technology, 2019, 53(8): 4528-4541.

[123] 史亮亮, 陆韻, 陈梦豪, 刘刚. 病原微生物基准对再生水检测的指导意义[J]. 环境工程, 2021, 39(3): 22-28.
SHI LL, LU Y, CHEN MH, LIU G. Guiding significance of microbial benchmark in reclaimed water detection[J]. Environmental Engineering, 2021, 39(3): 22-28 (in Chinese).

[124] 生活饮用水卫生标准: GB 5749—2022[S]. 北京: 中国标准出版社, 2022.
Standards for Drinking Water Quality: GB 5749—2022[S]. Beijing: Standards Press of China, 2022 (in Chinese).

[125] 生活饮用水标准检验方法: GB/T 5750—2023[S]. 北京: 中国国家标准化管理委员会, 2023.
Standard Testing Methods for Drinking Water: GB/T 5750—2023[S]. Beijing: National Standardization Management Committee of China, 2023 (in Chinese).