·疾病预防控制·

人群接触和移动模式对传染病传播的影响

李文忻，明博文，余宏杰，张娟娟
复旦大学公共卫生学院流行病学教研室 / 公共卫生安全教育部重点实验室，上海 200032

摘要：人群接触与移动模式，是传染病传播的重要社会行为驱动因素，有助于理解病原体在人与人之间传播，并通过人口流动引起疾病暴发甚至大流行的可能性。定量测量人与人之间的接触模式和移动模式，才能准确理解传染病如何在人际间传播及其空间扩散规律，采取何种干预措施有效。将人群接触与移动数据与传染病动力学建模相结合可显著提高模型预测的准确性，为模拟传染病的传播动态和预测预警提供关键参数。本文综述了国内外人群接触和移动模式相关研究进展，总结了人群接触和移动行为对传染病传播的重要意义，并指出该领域存在的困难与挑战。旨在呼吁加强对人群接触和移动相关研究的重视，为实现传染病的预测预警与精准防控提供重要科学支撑。

关键字：人群接触；人群移动；呼吸道传染病；传染病建模；预测预警与防控
中图分类号：R51 **文献标志码：**A **文章编号：**1003-8507（2025）05-922-09
DOI：10.20043/j.cnki.MPM.202411496

The impact of human contact and mobility patterns on infectious disease transmission

LI Wen-xin, MING Bo-wen, YU Hong-jie, ZHANG Juan-juan
Department of Epidemiology, School of Public Health, Fudan University, Shanghai 200032, China

Abstract: Human contact and mobility patterns are significant social behavioral drivers of infectious disease transmission. They aid in understanding how pathogens spread from person to person and the potential for disease outbreaks or even pandemics due to human mobility. Quantitative measurements of interpersonal contact and mobility patterns are essential for accurately understanding how infectious diseases spread among individuals and their spatial diffusion patterns, as well as for determining effective intervention measures. Integrating human contact and mobility data with infectious disease dynamics modeling can significantly enhance the accuracy of model predictions, providing key parameters for simulating disease transmission dynamics and forecasting alerts. This paper reviews the progress of research on human contact and mobility patterns both domestically and internationally, summarizes the critical importance of these behaviors in the transmission of infectious diseases, and highlights the difficulties and challenges present in this field. The aim is to call for increased attention to research on human contact and mobility, providing crucial scientific support for the prediction, warning, and precise control of infectious diseases.

Keywords: Human contact; Human mobility; Respiratory infectious diseases; Infectious disease modeling; Prediction, warning, and prevention

全球疾病负担研究显示，1990—2021 年，全球人群健康状况总体改善，传染病导致的疾病负担占比虽明显降低，但仍是全球尤其是发展中国家人群发病和死亡的主要原因之一。尤其是下呼吸道感染，从 2010 年至今始终保持全球死因排名前列，2021 年作为新发传染病的新型冠状病毒感染（coronavirus disease 2019，简称“新冠”）全球死因排名位居第二，在全世界造成了严重的健康和经济损失[1]。

传染源、传播途径和易感人群是传染病传播的三个必要环节，复杂多样的驱动因素通过影响以上三个环节影响传染病的流行，主要可以归纳为自然环境因素和社会行为因素两大类，见图 1。在自然因素方面，气候对传染病流行过程中的病原体、传播媒介、易感人群等各环节均有影响，故而呈现地方性和季节性的特点。例如，低温和低湿度能够加强呼吸道病毒的气溶胶传播[2]，在冬季，病毒在飞沫表面停留存活可长达 21 d，而在春秋季只能停留存活 7 d[3]；登革热在夏秋季节高发，与传播媒介伊蚊孳生有关，全球气候变暖促使蚊子活动季节延长、活动区域扩大，继而促使登革热的流行范围从热带、亚热带向温带地区扩展[4-6]；低湿度的干燥环境会导致呼吸道上皮黏膜纤毛运输对气道的清除受阻，损害气道的先天抗病毒防御和组织

基金项目：国家自然科学基金重大研究计划培育项目（92369118）
作者简介：李文忻（1998—），女，硕士在读，研究方向：传染病建模
通信作者：张娟娟，E-mail: zhangjuan@fudan.edu.cn

修复,影响宿主的免疫防御功能[7]。社会因素包括了个体层面的生活方式和群体层面的人群接触和移动行为。个体层面例如居住环境拥挤、室内卫生设施不佳可导致呼吸道及肠道传染病的传播[8];我国部分地区居民喜欢生食或半生食水产品,易引起甲型病毒性肝炎等传染病[9]。群体层面的社会接触和移动行为是传染病人际传播乃至形成大流行的必要因素。以新冠疫情为例,全球各地实施了学校关闭、佩戴口罩、限制人群流动等各类非药物干预措施(non-pharmaceutical interventions,NPIs),有效控制了疫情进展[10-14]。同时这些针对新冠疫情实施的 NPIs 也降低了其他呼吸道传染病的感染发病[15-17],表明了人类社会行为对于传染病传播的直接作用。

量化人群接触和移动模式有助于理解呼吸道传染病的人际传播和空间扩散规律,为公共卫生决策部门制定有效防控策略提供重要科学证据。本文总结了国内外人群接触和移动相关研究进展,讨论其对传染病传播的意义,以及该领域存在的困难与挑战。旨在强调人群接触和移动相关研究的重要性,为传染病的预测预警与精准防控提供科学支撑。

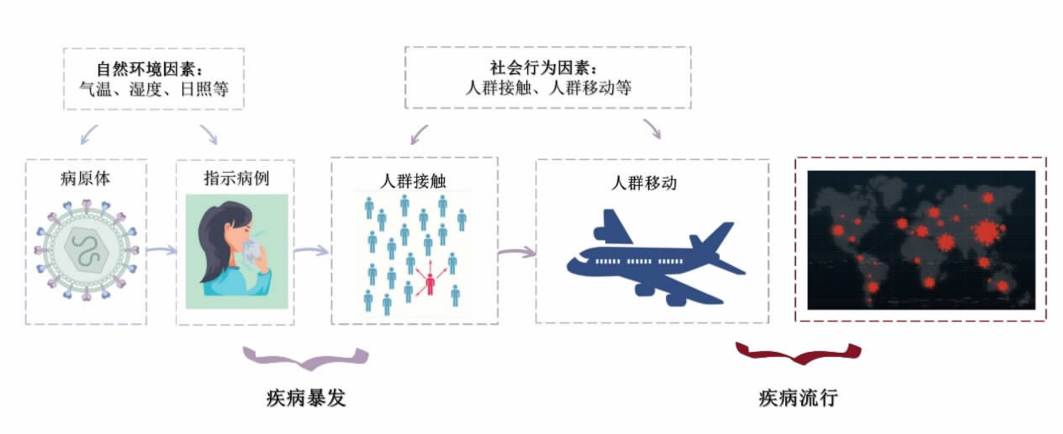

图 1　人群接触和移动模式与传染病传播的关系

Figure 1　Relationship between human contact and mobility patterns and the spread of infectious diseases

1　人群接触

1.1　*人群接触的定义*　人群接触(human contact)的经典定义为 2005—2006 年 Mossong 等人在欧洲八国(比利时、德国、芬兰、英国、意大利、卢森堡、荷兰和波兰)开展全球最早的大规模接触调查(POLYMODE)中的接触定义:三个字以上的对话接触(不包含电话等非面对面的形式)或身体接触(例如握手、拥抱、亲吻等)。此后多篇人群接触研究参考了 POLYMODE 研究的定义[18-25],以便不同研究间的比较。然而,结合研究进展和不同的研究目的,接触的定义也在不断被调整和完善。部分研究在接触类型上调整了接触定义,例如,Ajelli 等人[26]仅将接触定义为五个字以上的对话接触;Ibuka 等人[27]仅将接触定义为两米以内的面对面的对话;Kiti 等人[28]仅将接触定义为身体接触。另有部分研究在纳入身体和对话接触的同时,将对话接触制定了不同空间或时间要求, 例如,Edmunds 等人[29]将人群接触定义为面对面不存在物理屏障及不需要提高音量的超过两个字的对话;Danon 等人[30-32]将对话接触定义为三米以内的对话;Fu 等人[33-34]将对话接触定义为两米以内的对话;Stein 等人[35]将接触定义为两人同处一臂以内的空间且持续时间大于等于 30 s;Waroux 等人[36]将对话接触定义为超过 5 min 的面对面对话;Zhang 等人[37-38]和 Liang 等人[39]在新冠期间的研究将对话接触分为距离一米以内超过三个字的对话和距离大于一米超过三个字的对话。

人群接触的定义需根据所研究的病原体传播的基本特征以及研究目的而定,不同的接触定义可以丰富接触相关疾病的研究范围,但也会导致不同研究间比较的困难性增加。此外,较为复杂的接触定义虽然刻画出病原体传播的具体场景,但在实际现场调查中会增加数据收集的困难。

1.2　*数据收集方式*　目前人群接触调查数据的收集方式主要有电子近距离传感器法和日记法。电子近距离传感法是指一定范围内通过无线电通信测量自动电子传感设备间的距离,从而获得佩戴电子传感设备者间的接触距离[40]。该方法优点是允许记录大量数据且不存在回忆偏移,但缺点在于该方法仅适用于参与者和接触者均佩戴传感器的情况,不适用于大规模调查,并可能会记录一些没有流行病学意义的“接触”数据,例如两位参与者虽然空间距离很近,但实际处于相邻的两个房间。日记法为大部分接触研究运用的数据收集方法,可分为面对面调查[24, 41-42]、电话调查[37-38, 43-44]、纸质自填问卷[18, 22-23, 26-28, 34, 45-46]和网络自填问卷[39, 47-49]。近年来,受新冠疫情的影响,多项接触研究使用了接触追踪应用程序数据[50-52]。没有一种数据收集方式是绝对理想的,不同的数据收集方式可能会

得到不同的数据结果。2017—2018 年上海的人群接触研究表明,调查员访问并填写问卷比研究对象自填问卷平均多报告 1.3 个接触者[19]。另有研究发现纸质问卷相比网络问卷可以记录更多的接触者,并且提前制定调查日期的前瞻性设计会比回顾性设计记录更多接触者[53]。在实际的研究中,研究人员应根据权衡结果的准确性和实际调查的可操作性来选择合适的数据收集方式。对于任何日记法,研究者应该尽可能减少回忆偏倚,比如选择记录离调查日期最近的时间、在问卷中设置自我评价回忆情况的问题并提醒调查对象反复回忆、进行严格的调查员培训等。

1.3　*接触研究结果*　量化人群接触模式的方式有汇总性指标(例如,平均每人每天的接触人数、接触时长等)和构建基于年龄的接触矩阵。接触矩阵计算了不同年龄组的研究对象与各年龄组的接触者的平均每人每天的接触人数和时长,并采用年龄同配性来衡量接触矩阵的规律,同配性越高表示与同龄人接触的概率越高。对于汇总性指标而言,不同研究结果之间由于研究地点、研究设计和研究时间的不同而存在较大差异。早期超过 80%的人群接触模式调查在欧美等高收入国家开展[54],而近年更多接触调查在亚洲和非洲的中低收入国家和地区开展[55]。在中高收入地区中,接触率随着年龄增长而下降,而中低收入地区的各年龄的接触率混合相似。在高收入地区,学校和工作场所内的接触率较高,而低收入地区人群在家庭中的接触率较高,这体现了不同研究地点之间接触模式的差异,这会对传染病传播和公共卫生干预措施的有效性产生实质性的影响。以 POLYMODE 研究为例,欧洲 8 个国家的平均接触人数在 7.95 ~ 19.77 之间不等。而在中国香港,于 2009—2010 年[56]、2012—2013 年[43]和 2015—2016 年[22]进行的三次接触调查的平均每日接触人数分别为 18.0 ~ 18.6、12.5 和 8.1 人,其中最后一次调查未允许记录群组的接触,这可能是其平均人数远低于前两次调查的主要原因。即使是同一国家的不同城市也会有不同的平均每日接触人数,如上海 18.7 人[19]、广州 16.7 人[24]、苏州 19.78 人[25]等。对于接触矩阵,既往研究都观察到了较高的年龄同配性,但不同研究的接触矩阵特征略有差异,例如上海的研究表明祖孙辈之间存在明显的接触混合,而这在欧洲国家的矩阵中却不明显。

1.4　*接触模式对传染病传播的意义*　人群接触模式为传染病动力学模型提供了关键参数,并有助于识别传染病传播过程中的高危人群,制定更精准特异的干预措施。目前研究主要将人群接触模式的结果引入由微分方程构建的仓室模型中估计传染病传播动态,包括流感病毒[57]、呼吸道合胞病毒、新冠病毒等病原体。经典的易感 – 感染 – 恢复(susceptible–-infectious–recovered, SIR)模型最早由 Kermack 等提出,此后研究者们相继提出易感 – 感染(susceptible–infectious,SI)模型、易感 – 感染 – 易感(susceptible–infectious–susceptible,SIS)模型、易感 – 暴露 – 感染 – 恢复(susceptible–exposed–infectious–-recovered,SEIR)模型等[58]。例如,Schmidt–Ott 等人[59]基于 POLYMODE 研究的结果,构建仓室模型发现接触矩阵对欧洲流感发病率具有显著影响;Voirin 等人[60]结合美国的接触矩阵模拟呼吸道合胞病毒的传播以估计尼塞韦单抗对呼吸道合胞病毒的预防作用。在新冠大流行期间,纳入人群接触模式的传染病模型备受关注,新冠疫情暴发初期 Zhang 等人[37–39]在武汉、上海、深圳、长沙进行了三轮接触调查,分别为 2020 年 2 月、3—5 月和 9—11 月,研究疫情和 NPIs 对人群接触模式影响,并利用人群接触模式构建 SIR 模型,评价了 NPIs 对新冠疫情控制的效果,发现人群接触模式随 NPIs 程度的调整而改变,封城可以有效控制新冠病毒在人群中的传播,而学校关闭虽不能阻断新冠病毒的传播但能延迟疫情的达峰时间、降低新增感染率的峰值;Feehan 等人[49]在 2020 年 3—9 月在美国开展的四轮人群接触调查,揭示了新冠大流行期间美国各州人群接触水平变化的异质性,并使用下一代矩阵(next generation matrix,NGM)方法估计了新冠病毒的基本再生数 R_0 变化的异质性;Ge 等人[61]构建了包含年龄结构的仓室模型,结合上海新冠疫情前后的接触变化数据,评估增加社交距离、追踪密切接触者和病例隔离等 NPIs 对控制浙江省第二波新冠疫情的效果;Liu 等人[62]在新型冠状病毒传播中使用了上海市的接触数据,模拟了两种疫苗接种策略的效果。综上所述,研究人群接触模式对于传染病传播的预测预警、干预措施效果评价和疫情精准防控具有重要的科学意义。

2　人群移动

2.1　*人群移动的定义*　人群移动(human mobility)是指人群在不同的地理区域或空间范围内进行的活动。根据时间和空间范围不同,出行通常分为五种类型:(1)日常出行,例如通勤、购物等;(2)周期性出行,例如贸易活动、外出旅游等;(3)季节性出行,例如捕鱼、放牧、外出务工等;(4)长期出行,例如长期在外务工、远距离求学等;(5)人口迁徙,例如农村迁往城市等。越来越多的研究聚焦于国家或城市尺度下的人群移动模式,定量刻画移动模式的特征及其与传染病传播之间的相互作用。

2.2　*数据收集方式*　出行数据来源多样化,常用的

数据来源包括公共交通数据、社会调查数据、人口普查数据、GPS 定位数据、手机信令数据等。研究者可以通过这些数据分析不同时间和空间尺度下的人群移动模式。公共交通数据包括航空[63]、铁路[64]和公共汽车数据[65]等，反映了国家间、城市间以及城市内部较为宏观的人群移动模式，但其覆盖的范围仅限于使用公共交通的人群且多为汇总性数据，无法体现人群特征，比如年龄、性别等。社会调查数据指通过问卷、电话调查或面对面调查收集的关于出行工具、频率、目的地等信息[66–67]，该方法可以获得更丰富的出行信息，但可能存在较大的回忆偏倚以及潜在的自我报告偏倚。人口普查数据指人群定居和迁移模式数据[68–69]，提供了长时间跨度的宏观人口流动数据，但数据受限于更新频次，且很少记录人群的日常出行。GPS 定位数据包括了 GPS 数据记录仪、基于智能手机应用程序的 GPS 数据等，大幅提升了人群移动在时空维度上的精细化，新冠疫情期间有多项基于苹果[70]、谷歌[71]等公司的 GPS 数据的人群移动研究。手机信令数据指基于通信基站信号获取的手机定位数据[72–78]，可高精度高频率地实时测量人群移动，时间跨度大、数据量大，但与 GPS 数据均存在幼儿与老年人口覆盖可能不全面的问题。

2.3　人群移动研究结果　人群移动可以使用出发地–目的地（origin–destination, O–D）矩阵、网络结构指标等进行特征描述。针对 O–D 矩阵，该指标囊括了某一地点内具有特定空间尺度和特定移动目的的人群流量的信息[79]。O–D 矩阵维度取决于研究的空间尺度，包括行政单位尺度，如国家、地区等和栅格尺度。Alexander 等人[80]利用手机通话记录和 O–D 矩阵构建在不同空间尺度、时间尺度下的美国波士顿地区人群通勤模式。Chen 等人[81]基于 O–D 矩阵相关方法表明全球范围内，区域间的航空流动和流感传播风险的变化相关。针对网络特征，单位之间的流通构成了网络。应用于个体，网络为人群接触网络；应用于地点，网络为人群移动网络；应用于交通系统，网络为高铁、机场网络。网络指标通常包括节点度、节点度分布、聚类系数、度相关系数、最短路径长度等指标。现今，大部分研究集中在交通网络特征的探索。Wang 等人[82]计算了中国高铁网络、中国飞机网络和两者耦合网络的网络指标，网络的鲁棒性，发现了中国小城市依赖于周边大城市的交通网络。Hong 等人[83]利用每个航司的飞行网络构建中国多层飞机运输网络，发现中国的航空运输多层网络具有小世界性。Lordan 等人[84]利用 OAG 数据，构建世界范围内七个独立地区内部的航空网络结构特征，发现对重点城市进行隔离时，连接更密集的城市所组成的网络群具有更好的恢复性和鲁棒性。随着研究进展，科学家们对于交通网络已经有了较为深刻的了解。而对精细尺度下人群移动网络的探索较少。Zhang 等人[85]利用手机信令数据刻画了上海市 Omicron BA.2 疫情前后，人群在 1km × 1km 栅格间移动网络的动态变化，表明人群移动网络的结构特征会受到 NPIs 的影响，NPIs 过后，网络结构会逐渐接近 NPIs 实施之前。见图 2。

人群移动模式在研究中体现出一定的规律性，例如出行距离指标多服从幂律分布或指数分布，人群移动多处于家庭、工作地点和社交场所之间[86–87]。人群移动在时间和空间维度上都表现出明显的异质性，例如长假期间人群出行次数和长距离出行会明显增加；城市内部的不同功能区（居民区、商业区等）内的人群移动模式存在差异[88–89]；城市的短途人群移动相较于农村更为频繁[90]；不同人口学特征群体的移动模式存在显著差异[67, 91]。在新冠疫情期间，有多项研究揭示了人群移动模式和疾病传播之间的关联，Chen 等人[92–93]发现在第一波新冠疫情期间，湖北省的人口流出与其他省市的新冠确诊病例数存在正相关；Badr 等人[94–96]发现人群移动的下降与新冠病例增长率的放缓密切相关，多种限制人群移动的 NPIs 是缓解新冠传播的有效方式。Zhang 等人[85]在上海 Omicron BA.2 高峰期间的人群移动研究表明 NPIs 下人们异质性的移动行为变化以及其对新冠疫情动态产生影响。

2.4　人群移动研究对传染病传播的意义　人群移动数据可以用于传染病的建模与预测。目前主要的分析方法有仓室模型、全球流行和移动模型（global epidemic and mobility, GLEAM）以及空间交互模型。在仓室模型方面，Chang 等人[97]在研究中将 SEIR 模型覆盖于每个移动网络之上，探究每个地点的感染率与人群移动性的关系。GLEAM 模型是一种基于个体的随机空间流行方法，通过真实世界数据集成的元人口网络方法，将世界划分为主要交通枢纽为中心的亚种群，在每个亚种群中通过研究疾病的不同阶段（易感、暴露、感染、恢复）进行建模。例如 Chinazzi 等人[98]预测了国内外的旅行限制对疫情传播的影响，模拟了新冠疫情的国际传播。空间交互模型是地理学和空间经济学分析预测人员或货物在不同地理位置间流动的关键工具，可以用于预测人群移动模式，分析疾病传播路径和范围，用于预测和分析传染病传播。例如 Takko 等人[99–100]在新冠疫情期间的不同阶段，基于人群移动数据构建了暴露网络，发现空间交互模型可有效模拟新冠暴露的风险。将空间交互模型与群体或个体水平的传染病模型结合，对于流感[101–102]、麻疹[103]等传染病传播的分析预测均有价值。

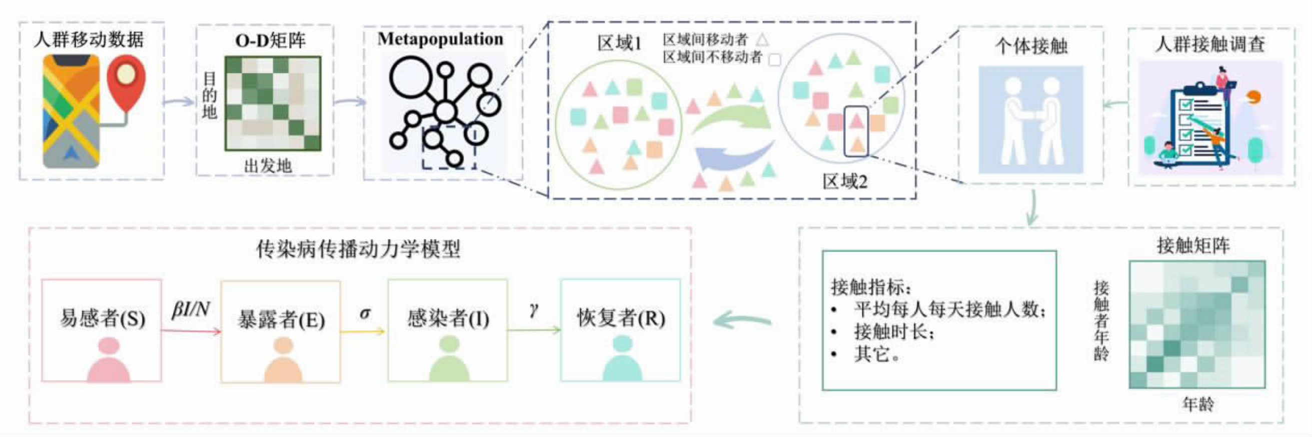

图 2　人群接触和移动模式在传染病传播动力学模型中的应用

Figure 2　Application of human contact and mobility patterns in the dynamic model of infectious disease transmission

3　总结和展望

人群接触和移动模式是呼吸道传染病传播的重要社会驱动因素，定量测量人群接触与移动模式并探索其与呼吸道传染病传播的相互作用至关重要，对传染病预测预警、干预措施效果评价和精准防控具有重要意义。在人群接触方面，主要的数据收集方式是问卷调查，目前相关研究表明不同国家和地区之间人群接触模式具有较大的异质性，有助于特异地构建传染病在当地的传播；在人群移动方面，常用的数据来源包括交通数据、GPS 定位数据和手机信令数据等，目前相关研究表明人群移动模式在不同的时间、空间和人口学上具有异质性。人群接触和移动从两个维度刻画了人类的社会行为，均可为传染病建模提供重要参数，两种研究不同的优缺点对传染病传播研究起到了互补的作用。Tomori 等人[104]在新冠疫情初期的研究比较了接触数据和人群移动数据作为新冠传播动态的早期指标的表现，得出接触调查数据比移动数据在反映感染动态方面更敏感。人群接触模式可以更为直接地反映影响传染病传播的行为变化，但是该数据调查周期长，同时存在回忆偏移和无法覆盖更大的空间尺度等缺陷；人群移动间接反映影响传染病传播的行为变化，但 GPS 定位数据和手机信令数据更新速度快、覆盖不同空间分辨率等优点可以弥补接触研究的不足。然而目前该领域的研究也面对着诸多困难和挑战，例如接触调查需要花费大量的时间和经济成本，并且没有统一的接触定义导致各研究之间缺乏可比性；通过网络 GPS 定位和手机信令数据得到的移动数据可能会存在一定的个人隐私泄露的问题；接触和移动数据的收集和分析往往需要新兴技术和良好的算力参与，同时对跨学科以及研究者的建模能力有较高的要求。

目前人群接触和移动依然存在很多研究空白值得未来进一步探索。首先，对于人群接触研究，在空间上，由于各地经济水平和社会文化的差异，需要继续探索不同类型地区的特定的人群接触模式，以中国的接触研究为例，目前主要集中在东部发达城市，但对于农村地区和西部地区的研究需要未来进一步探索；在时间上，目前接触调查多为横断面设计，然而人群接触模式很可能是随着环境气候[57,105]、节假日[106-107]等多种影响因素而变化，未来需要更多队列研究填补研究空白；在模型参数的构建上，以往研究仅简单地将接触人数的年龄异质性引入传染病传播模型，而往往忽略接触中更为复杂的情况，比如接触的室内外环境、是否戴口罩等等，未来需要在接触调查中收集并探索其对模型预测效果的作用。其次，对于人群移动研究，在空间上，目前大多研究的精度停留在国家或城市间，对于城市内部以及个体层面的移动模式未来仍有待探索；在时间层面，目前研究的时间刻度多为“天”，并且只关注某个特定时间段下的人群移动模式，未来应探索更精细化和动态化的人群移动模式；在数据代表性上，虽然二手数据收集和更新较为容易，但依然存在人群代表性不足、个体出行轨迹不完整等问题，未来建议重点突破数据的代表性、交叉验证及外推技术。最后，人类行为作为传染病传播重要影响因素，接触和移动行为是同时存在、密不可分的，两者之间存在的关联目前却仍不清晰，未来应进一步探索人群接触和出行间的关系，优化人类行为参数在传染病模型中的应用。

利益冲突声明　本研究不存在任何利益冲突

参考文献

[1] GBD 2021 Causes of Death Collaborators. Global burden of 288 causes of death and Life expectancy decomposition in 204 countries and territories and 811 subnational locations, 1990-2021: a systematic analysis for the Global Burden of Disease Study 2021[J]. Lancet, 2024, 403(10440): 2100-2132.

[2] Prévost J, Richard J, Gasser R, et al. Impact of temperature on the

affinity of SARS-CoV-2 Spike glycoprotein for host ACE2 [J]. Journal of Biological Chemistry, 2021, 297(4): 101151.

[3] Kwon T, Gaudreault NN, Richt JA. Environmental stability of SARS-CoV-2 on different types of surfaces under indoor and seasonal climate conditions[J]. Pathogens, 2021, 10(2): 227.

[4] Liyanage P, Tozan Y, Overgaard HJ, et al.Effect of El Nino-Southern oscillation and local weather on aedes dvector activity from 2010 to 2018 in kalutara district,Sri Lanka:a two-stage hierarchical analysis [J]. Lancet Planetary Health, 2022, 6(7): e577-e85.

[5] Oidtman RJ, Lai SJ, Huang ZJ, et al. Inter-annual variation in seasonal dengue epidemics driven by multiple interacting factors in Guangzhou, China[J]. Nature Communications, 2019, 10(1): 1148.

[6] 陈莉华,念鹏英,沈秀莲,等. 云南省 2013-2022 年登革热流行趋势及暴发疫情特征分析 [J]. 中国媒介生物学及控制杂志, 2024,35(1):63-68, 73.
Chen LH, Nian PY, Shen XL, et al. Epidemiological trends and outbreak characteristics of dengue fever in Yunnan Province,China, 2013-2022[J]. Chinese Journal of Vector Biology and Control, 2024, 35(1): 63-68, 73.(In Chinese)

[7] Keetels GH, Godderis L, Van de wiel BJH. Associative evidence for the potential of humidification as a non-pharmaceutical intervention for influenza and SARS-CoV-2 transmission[J]. Journal of Exposure Science & Environmental Epidemiology, 2022, 32(5): 720-726.

[8] Wolf J, Hubbard S, Brauer M, et al. Effectiveness of interventions to improve drinking water, sanitation, and handwashing with soap on risk of diarrhoeal disease in children in low-income and middle-income settings: a systematic review and meta-analysis[J]. Lancet, 2022, 400(10345): 48-59.

[9] Di cola G, Fantilli AC, Pisano MB, et al. Foodborne transmission of hepatitis A and hepatitis E viruses: A literature review [J]. International Journal of Food Microbiology, 2021, 338: 108986.

[10] Brauner JM, Mindermann S, Sharma M, et al. Inferring the effectiveness of government interventions against COVID-19 [J]. Science, 2021, 371(6531): eabd9338.

[11] Zhang JJ, Litvinova M, Wang W, et al. Evolving epidemiology and transmission dynamics of coronavirus disease 2019 outside Hubei province, China: a descriptive and modelling study [J]. Lancet Infectious Diseases, 2020, 20(7): 793-802.

[12] Ge Y, Wu X, Zhang W, et al. Effects of public-health measures for zeroing out different SARS-CoV-2 variants [J]. Nature Communications, 2023, 14(1): 5270.

[13] Liu D, Tai Q, Wang Y, et al. Impact of air temperature and containment measures on mitigating the intrahousehold transmission of SARS-CoV-2:a data-based modelling analysis [J]. BMJ Open, 2022, 12(4): e049383.

[14] Qi Y, Shaman J, Pei S. Quantifying the impact of COVID-19 nonpharmaceutical interventions on influenza transmission in the United States [J]. Journal of Infectious Diseases, 2021, 224 (9): 1500-1508.

[15] Chuang YC, Lin KP, Wang LA, et al. The impact of the COVID-19 pandemic on respiratory syncytial virus infection: a narrative review [J]. Infection and Drug Resistance, 2023, 16: 661-675.

[16] Dhanasekaran V, Sullivan S, Edwards KM, et al. Human seasonal influenza under COVID-19 and the potential Consequences of influenza lineage elimination [J]. Nature Communications, 2022, 13 (1): 1721.

[17] Terliesner N, Unterwalder N, Edelmann A, et al. Viral infections in hospitalized children in Germany during the COVID-19 pandemic: Association with non-pharmaceutical interventions[J]. Front Pediatr, 2022, 10: 935483.

[18] Johnstone-Robertson SP, Mark D, Morrow C, et al. Social mixing patterns within a South African township community: implications for respiratory disease transmission and control [J]. American Journal of Epidemiology, 2011, 174(11): 1246-1255.

[19] Zhang JJ, Klepac P, Read JM, et al. Patterns of human social contact and contact with animals in Shanghai, China [J]. Scientific Reports, 2019, 9(1): 15141.

[20] Horby P, Pham QT, Hens N, et al. Social contact patterns in Vietnam and implications for the control of infectious diseases [J]. PLOS One, 2011, 6(2): e16965.

[21] Hens N, Goeyvaerts N, Aerts M, et al. Mining social mixing patterns for infectious disease models based on a two-day population survey in Belgium[J]. BMC Infectious Diseases, 2009, 9: 5.

[22] Leung K, Jit M, Lau EHY, et al. Social contact patterns relevant to the spread of respiratory infectious diseases in Hong Kong [J]. Scientific Reports, 2017, 7(1): 7974.

[23] Melegaro A, Del Fava E, Poletti P, et al. Social contact structures and time use patterns in the manicaland province of Zimbabwe [J]. PLOS One, 2017, 12(1): e0170459.

[24] Huang YL, Cai XS, Zhang B, et al. Spatiotemporal heterogeneity of social contact patterns related to infectious diseases in the Guangdong Province, China [J]. Scientific Reports, 2020, 10 (1): 6119.

[25] Wang MR, Wang CJ, Gui GP, et al. Social contacts patterns relevant to the transmission of infectious diseases in Suzhou, China following the COVID-19 epidemic [J]. Journal of Health Population and Nutrition, 2024, 43(1): 58.

[26] Ajelli M, Litvinova M. Estimating contact patterns relevant to the spread of infectious diseases in Russia [J]. Journal of Theoretical Biology, 2017, 419: 1-7.

[27] Ibuka Y, Ohkusa Y, Sugawara T, et al. Social contacts, vaccination decisions and influenza in Japan [J]. Journal of Epidemiology and Community Health, 2016, 70(2): 162-167.

[28] Kiti MC, Kinyanjui TM, Koech DC, et al. Quantifying age-related rates of social contact using diaries in a rural coastal population of Kenya[J]. PLOS One, 2014, 9(8): e104786.

[29] Edmunds WJ, O'callaghan CJ, Nokes DJ. Who mixes with whom? A method to determine the contact patterns of adults that May Lead to the spread of airborne infections[J]. Proceedings. Biological Sciences / the Royal Society, 1997, 264(1384): 949-957.

[30] Danon L, House TA, Read JM, et al. Social encounter networks: collective properties and disease transmission[J]. Journal of the Royal Society, Interface / the Royal Society, 2012, 9(76): 2826-2833.

[31] Grijalva CG, Goeyvaerts N, Verastegui H, et al. A household-based study of contact networks relevant for the spread of infectious diseases in the highlands of Peru [J]. PLOS One, 2015, 10 (3): e0118457.

[32] Kifle YW, Goeyvaerts N, Van Kerckhove K, et al. Correction: animal ownership and touching enrich the context of social contacts relevant to the spread of human infectious diseases [J]. PLOS One, 2016, 11

(2): e0148718.

[33] Fu YC, Wang DW, Chuang JH. Representative contact diaries for modeling the spread of infectious diseases in Taiwan [J]. PLOS One, 2012, 7(10): e45113.

[34] Béraud G, Kazmercziak S, Beutels P, et al. The French connection: the first large Population-Based contact survey in France relevant for the spread of infectious diseases [J]. PLOS One, 2015, 10 (7): e0133203.

[35] Stein ML, van Steenbergen JE, Buskens V, et al. Comparison of contact patterns relevant for transmission of respiratory pathogens in Thailand and The Netherlands using respondent-driven sampling[J]. PLOS One, 2014, 9(11): e113711.

[36] Le polain de waroux O, Cohuet S, Ndazima D, et al. Characteristics of human encounters and social mixing patterns relevant to infectious diseases spread by close contact: a survey in Southwest Uganda[J]. BMC Infectious Diseases, 2018, 18(1): 172.

[37] Zhang JJ, Litvinova M, Liang YX, et al. Changes in contact patterns shape the dynamics of the COVID-19 outbreak in China[J]. Science, 2020, 368(6498): 1481-1486.

[38] Zhang JJ, Litvinova M, Liang YX, et al. The impact of relaxing interventions on human contact patterns and SARS-CoV-2 transmission in China[J]. Sci Adv, 2021, 7(19): eabe2584.

[39] Liang YX, Peng C, You Q, et al. Estimating changes in contact patterns in China over the first year of the COVID-19 pandemic: implications for SARS-CoV-2 spread - four cities, China, 2020[J]. China CDC Wkly, 2023, 5(5): 113-119.

[40] Isella L, Romano M, Barrat A, et al. Close encounters in a pediatric ward: measuring face-to-face proximity and mixing patterns with wearable sensors[J]. PLOS One, 2011, 6(2): e17144.

[41] Dodd PJ, Looker C, Plumb ID, et al. Age-and Sex-Specific social contact patterns and incidence of mycobacterium tuberculosis infection [J]. American Journal of Epidemiology, 2016, 183 (2): 156-166.

[42] Quaife M, Torres-Rueda S, Dobreva Z, et al. COVID-19 vaccine hesitancy and social contact patterns in Pakistan: results from a National cross-sectional survey [J]. BMC Infectious Diseases, 2023, 23(1): 321.

[43] Kwok KO, Cowling B, Wei V, et al. Temporal variation of human encounters and the number of locations in which they occur: a longitudinal study of Hong Kong residents [J]. Journal of the Royal Society, Interface / the Royal Society, 2018, 15(138): 20170838.

[44] Quaife M, van Zandvoort K, Gimma A, et al. The impact of COVID-19 control measures on social contacts and transmission in Kenyan informal settlements[J]. BMC Medicine, 2020, 18(1): 316.

[45] Mossong J, Hens N, Jit M, et al. Social contacts and mixing patterns relevant to the spread of infectious diseases [J]. PLOS Medicine, 2008, 5(3): e74.

[46] Leung WTM, Meeyai A, Holt HR, et al. Social contact patterns relevant for infectious disease transmission in Cambodia[J]. Scientific Reports, 2023, 13(1): 5542.

[47] Wambua J, Loedy N, Jarvis CI, et al. The influence of COVID-19 risk perception and vaccination status on the number of social contacts across Europe: insights from the CoMix study [J]. BMC Public Health, 2023, 23(1): 1350.

[48] Reichmuth ML, Heron L, Beutels P, et al. Social contacts in Switzerland during the COVID-19 pandemic: Insights from the CoMix study[J]. Epidemics, 2024, 47: 100771.

[49] Feehan DM, Mahmud AS. Quantifying population contact patterns in the United States during the COVID-19 pandemic [J]. Nature Communications, 2021, 12(1): 893.

[50] Pei S, Kandula S, Cascante Vega J, et al. Contact tracing reveals community transmission of COVID-19 in New York City [J]. Nature Communications, 2022, 13(1): 6307.

[51] Wu M, Li C, Shen Z, et al. Use of temporal contact graphs to understand the evolution of COVID-19 through contact tracing data [J]. Commun Phys, 2022, 5(1): 270.

[52] Qian WC, Cooke A, Stanley KG, et al. Comparing contact tracing through bluetooth and GPS surveillance data: Simulation-Driven approach [J]. Journal of Medical Internet Research, 2024, 26: e38170.

[53] Mccaw JM, Forbes K, Nathan PM, et al. Comparison of three methods for ascertainment of contact information relevant to respiratory pathogen transmission in encounter networks [J]. BMC Infectious Diseases, 2010, 10: 166.

[54] Hoang T, Coletti P, Melegaro A, et al. A systematic review of social contact surveys to inform transmission models of close-contact infections[J]. Epidemiology, 2019, 30(5): 723-736.

[55] Mousa A, Winskill P, Watson OJ, et al. Social contact patterns and implications for infectious disease transmission-a systematic review and meta-analysis of contact surveys[J]. eLife, 2021, 10: e70294.

[56] Kwok KO, Cowling BJ, Wei VW, et al. Social contacts and the locations in which they occur as risk factors for influenza infection[J]. Proceedings. Biological Sciences / the Royal Society, 2014, 281 (1789): 20140709.

[57] Kummer AG, Zhang JJ, Jiang CY, et al.Evaluating seasonal variations in human contact patterns and their impact on the transmission of respiratory infectious diseases [J]. Influenza and Other Respiratory Viruses, 2024, 18(5): e13301.

[58] Vynnycky E, White RG. An introduction to infectious disease modelling[J]. Public Health, 2011, 125(2): 117-121.

[59] Schmidt-Ott R, Schwehm M, Eichner M. Influence of social contact patterns and demographic factors on influenza simulation results[J]. BMC Infectious Diseases, 2016, 16(1): 646.

[60] Voirin N, Virlogeux V, Demont C, et al. Potential impact of nirsevimab on RSV transmission and medically attended lower respiratory tract illness caused by RSV: A disease transmission model[J]. Infectious Diseases and Therapy, 2022, 11(1): 277-292.

[61] Ge Y, Chen ZP, Handel A, et al. The impact of social distancing, contact tracing, and case isolation interventions to suppress the COVID-19 epidemic: A modeling study [J]. Epidemics, 2021, 36: 100483.

[62] Liu HC, Zhang JJ, Cai J, et al. Investigating vaccine-induced immunity and its effect in mitigating SARS-CoV-2 epidemics in China[J]. BMC Medicine, 2022, 20(1): 37.

[63] Findlater A, Bogoch II. Human mobility and the global spread of infectious diseases: a focus on air travel [J]. Trends in Parasitology, 2018, 34(9): 772-783.

[64] Gallotti R, Barthelemy M. The multilayer temporal network of public transport in Great Britain[J]. Sci Data, 2015, 2: 140056.

[65] Ponte C, Carmona HA, Oliveira EA, et al.Tracing contacts to evaluate

the transmission of COVID−19 from highly exposed individuals in public transportation[J]. Scientific Reports, 2021, 11(1): 24443.

[66] Marshall JM, Wu SL, Sanchez C HM, et al. Mathematical models of human mobility of relevance to malaria transmission in Africa[J]. Scientific Reports, 2018, 8(1): 7713.

[67] Garske T, Yu HJ, Peng ZB, et al. Travel patterns in China [J]. PLOS One, 2011, 6(2): e16364.

[68] Wesolowski A, Buckee CO, Pindolia DK, et al. The use of census migration data to approximate human movement patterns across temporal scales[J]. PLOS One, 2013, 8(1): e52971.

[69] Tizzoni M, Bajardi P, Decuyper A, et al.On the use of human mobility proxies for modeling epidemics [J]. PLOS Computational Biology, 2014, 10(7): e1003716.

[70] Strzelecki A. The Apple mobility trends data in human mobility patterns during restrictions and prediction of COVID−19: A systematic review and Meta−Analysis [J]. HEALTHCARE, 2022, 10 (12): 2425.

[71] Cot C, Cacciapaglia G, Sannino F. Mining google and Apple mobility data: temporal anatomy for COVID−19 social distancing[J]. Scientific Reports, 2021, 11(1): 4150.

[72] Deville P, Linard C, Martin S, et al. Dynamic population mapping using Mobile phone data [J]. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111 (45): 15888−15893.

[73] Wesolowski A, Qureshi T, Boni MF, et al. Impact of human mobility on the emergence of dengue epidemics in Pakistan[J]. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112(38): 11887−11892.

[74] Wesolowski A, Metcalf CJ, Eagle N, et al. Quantifying seasonal population fluxes driving rubella transmission dynamics using Mobile phone data [J]. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112(35): 11114−11149.

[75] Wesolowski A, zu Erbach−Schoenberg E, Tatem AJ, et al. Multinational patterns of seasonal asymmetry in human movement influence infectious disease dynamics [J]. Nature Communications, 2017, 8(1): 2069.

[76] Palmer JRB, Espenshade TJ, Bartumeus F, et al. New approaches to human mobility: using Mobile phones for demographic research[J]. Demography, 2013, 50(3): 1105−1128.

[77] Tompkins AM, Mccreesh N. Migration statistics relevant for malaria transmission in Senegal derived from Mobile phone data and used in an agent−based migration model [J]. Geospatial Health, 2016, 11(1 Suppl): 408.

[78] Finger F, Genolet T, Mari L, et al. Mobile phone data highlights the role of mass gatherings in the spreading of cholera outbreaks[J]. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113(23): 6421−6426.

[79] Louail T, Lenormand M, Picornell M, et al. Uncovering the spatial structure of mobility networks [J]. Nature Communications, 2015, 6: 6007.

[80] Alexander L, Jiang S, Murga M, et al. Origin−destination trips by purpose and time of day inferred from Mobile phone data[J]. Transportation Research Part C−Emerging Technologies, 2015, 58: 240−250.

[81] Chen ZY, Tsui JLH, Gutierrez B, et al. COVID−19 pandemic interventions reshaped the global dispersal of seasonal influenza viruses[J]. Science, 2024, 386(6722): eadq3003.

[82] Wang YQ, Lu QY, Cao XB, et al. Travel time analysis in the Chinese coupled aviation and high−speed rail network [J]. Chaos Solitons & Fractals, 2020, 139: 109973.

[83] Hong C, Zhang J, Cao XB, et al. Structural properties of the Chinese air transportation multilayer network [J]. Chaos Solitons & Fractals, 2016, 86: 28−34.

[84] Lordan O, Sallan JM. Core and critical cities of global region airport networks [J]. Physica A−Statistical Mechanics and Its Applications, 2019, 513: 724−733.

[85] Zhang JJ, Tan SY, Peng C, et al. Heterogeneous changes in mobility in response to the SARS−CoV−2 Omicron BA.2 outbreak in Shanghai[J]. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120(42): e2306710120.

[86] González MC, Hidalgo CA, Barabási AL. Understanding individual human mobility patterns[J]. Nature, 2008, 453(7196): 779−782.

[87] Brockmann D, Hufnagel L, Geisel T. The scaling laws of human travel[J]. Nature, 2006, 439(7075): 462−465.

[88] Yang XP, Zhao ZY, Lu SW. Exploring Spatial−Temporal patterns of urban human mobility hotspots [J]. Sustainability−Basel, 2016, 8(7): 674.

[89] Zhang DQ, Wan JF, He ZJ, et al. Identifying Region−Wide functions using urban taxicab trajectories [J]. ACM Transactions on Embedded Computing Systems, 2016, 15(2): 1−19.

[90] Vazquez−Prokopec GM, Bisanzio D, Stoddard ST, et al. Using GPS technology to quantify human mobility, dynamic contacts and infectious disease dynamics in a resource−poor urban environment [J]. PLOS One, 2013, 8(4): e58802.

[91] Pullano G, Valdano E, Scarpa N, et al. Evaluating the effect of demographic factors, socioeconomic factors, and risk aversion on mobility during the COVID−19 epidemic in France under lockdown: a population−based study [J]. Lancet Digital Health, 2020, 2(12): e638−e649.

[92] Chen HJ, Chen Y, Lian ZY, et al. Correlation between the migration scale index and the number of new confirmed coronavirus disease 2019 cases in China[J]. Epidemiology and Infection, 2020, 148: e99.

[93] Xu XL, Wang SH, Dong JH, et al. An analysis of the domestic resumption of social production and Life under the COVID−19 epidemic[J]. PLOS One, 2020, 15(7): e0236387.

[94] Badr HS, Du HR, Marshall M, et al. Association between mobility patterns and COVID−19 transmission in the USA: a mathematical modelling study [J]. The Lancet Infectious Diseases, 2020, 20(11): 1247−1254.

[95] Guo YT, Yu H, Zhang GH, et al. Exploring the impacts of travel−implied policy factors on COVID−19 spread within communities based on multi−source data interpretations[J]. Health & Place, 2021, 69: 102538.

[96] Xia JZ, Yin K, Yue Y, et al. Impact of human mobility on COVID−19 transmission according to mobility distance, location, and demographic factors in the greater Bay Area of China: Population−Based study [J]. JMIR Public Health Surveill, 2023, 9: e39588.

[97] Chang S, Pierson E, Koh PW, et al. Mobility network models of COVID−19 explain inequities and inform reopening [J]. Nature,

2021, 589(7840): 82-87.

[98] Chinazzi M, Davis JT, Ajelli M, et al. The effect of travel restrictions on the spread of the 2019 novel coronavirus (COVID-19) outbreak [J]. Science, 2020, 368(6489): 395-400.

[99] Takko T, Bhattacharya K, Kaski K. Modelling exposure between populations using networks of mobility during COVID-19 [J]. Front Phys-Lausanne, 2023, 11: 63.

[100] Mepparambath RM, Huynh HN, Oon J, et al. The impact of COVID-19 pandemic on the fundamental urban mobility theories using Transit data from Singapore[J]. Transp Res Interdisc, 2023, 21: 100883.

[101] Viboud C, Bj?rnstad ON, Smith DL, et al. Synchrony, waves, and spatial hierarchies in the spread of influenza [J]. Science, 2006, 312 (5772): 447-451.

[102] Engebretsen S, Eng?-Monsen K, Aleem MA, et al. Time-aggregated Mobile phone mobility data are sufficient for modelling influenza spread: the case of Bangladesh [J]. Journal of the Royal Society, Interface / the Royal Society, 2020, 17(167): 20190809.

[103] Bharti N, Xia YC, Bjornstad ON, et al. Measles on the edge: coastal heterogeneities and infection dynamics [J]. PLOS One, 2008, 3(4): e1941.

[104] Tomori DV, R ü bsamen N, Berger T, et al. Individual social contact data and population mobility data as early markers of SARS-CoV-2 transmission dynamics during the first wave in Germany-an analysis based on the COVIMOD study[J]. BMC Medicine, 2021, 19(1): 271.

[105] Nagpal S, Kumar R, Noronha RF, et al. Seasonal variations in social contact patterns in a rural population in North India: Implications for pandemic control[J]. PLOS One, 2024, 19(2): e0296483.

[106] Chen SC, You ZS. Social contact patterns of school-age children in Taiwan: comparison of the term time and holiday periods [J]. Epidemiology and Infection, 2015, 143(6): 1139-1147.

[107] Geenen C, Thibaut J, Laenen L, et al. Unravelling the effect of New Year's Eve celebrations on SARS-CoV-2 transmission[J]. Scientific Reports, 2023, 13(1): 22195.

收稿日期：2024-11-28

（上接第 915 页）

addressing the adverse outcome pathway key event on covalent binding to proteins [EB/OL]. [2025-01-26]. https://www.oecd.org/en/publications/test-no-442c-in-chemico-skin-sensitisation_9789264229709-en.html.

[9] National Institutes of Health. Alternative methods accepted by US agencies [EB/OL]. [2025-01-30]. https://ntp.niehs.nih.gov/whatwestudy/niceatm/accept-methods.

[10] Lee I, Na M, Lavelle M, et al. Predicting points of departure and potency categories for fragrance ingredients by integrating OECD in vitro models[J]. Food and Chemical Toxicology, 2024, 193: 114998.

[11] EURL ECVAM. DB-ALM protocol n° 217: Kinetic Direct Peptide Reactivity Assay (kDPRA) [EB/OL]. [2025-01-26]. http://cidportal.jrc.ec.europa.eu/ftp/jrc-opendata/EURL-ECVAM/datasets/DBALM/LATEST/online/DBALM_docs/217_P_kDPRA_final_27Oct20.pdf.

[12] European Chemicals Agency. Search for chemicals/ regulated substances[EB/OL]. [2025-01-30]. https://echa.europa.eu/.

[13] 彭双清. 21 世纪毒性测试策略[M]. 北京：军事医学出版社，2016.
Peng SQ. Toxicity testing strategy in the 21st century toxicity testing strategy in the 21st century [M]. Beijing: Military Medical Press, 2016.(In Chinese)

[14] Alépée N, Tourneix F, Singh A, et al. Off to a good start? Review of the predictivity of reactivity methods modelling the molecular initiating event of skin sensitization[J]. Altex, 2023, 40(4): 606-618.

[15] 国家药品监督管理局. 国家药监局关于将油包水类化妆品的 pH 值测定方法等 21 项制修订项目纳入化妆品安全技术规范（2015 年版）的通告（2023 年第 41 号）[EB/OL]. [2025-01-30]. https://www.nmpa.gov.cn/xxgk/ggtg/hzhpggtg/jmhzhptg/20230828170520159.html.
National Medical Products Administration. Notice of national medical products administration on the inclusion of 21 revision items such as the determination method of pH value of water-in-oil cosmetics into the Cosmetic Safety Technical Specification (2015 edition) (No. 41 of 2023) [EB/OL]. [2025-01-30]. https://www.nmpa.gov.cn/xxgk/ggtg/hzhpggtg/jmhzhptg/20230828170520159.html. (In Chinese)

[16] Roberts DW. A critical review of the kinetic direct peptide reactivity assay (kDPRA) for skin sensitizer potency assessment - taking it forward[J]. Critical Reviews in Toxicology, 2021, 51(10): 805-819.

[17] Natsch A, Gerberick GF. Integrated skin sensitization assessment based on OECD methods (I): Deriving a point of departure for risk assessment[J]. Altex, 2022, 39(4): 636-646.

[18] Mohoric T, Wilm A, Onken S, et al. Increasing accessibility of bayesian Network-Based defined approaches for skin sensitisation potency assessment[J]. Toxics, 2024, 12(9): 666.

[19] Natsch A, Gerberick GF. Integrated skin sensitization assessment based on OECD methods (II):Hazard and potency by combining kinetic peptide reactivity and the"2 out of 3"Defined Approach[J]. Altex, 2022, 39(4): 647-655.

收稿日期：2024-11-25