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Prevalence of human infection with respiratory adenovirus in China: a systematic review and meta-analysis --Manuscript Draft--

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Short Title:	Prevalence of human infection with respiratory adenovirus in China
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Keywords:	Human adenovirus; China; respiratory tract infections; meta-analysis
Abstract:	Abstract Background Human adenovirus (HAdV) is a major pathogen that causes acute respiratory tract infections (ARTI) and is frequently associated with outbreaks. The HAdV prevalence and the predominant types responsible for ARTI outbreaks remains obscure in China. Methods A systematic review was performed to retrieve literature that reported outbreaks or etiological surveillance of HAdV among ARTI patients in China from 2009 to 2020. Patient information was extracted from the literature to explore the epidemiological characteristics and clinical manifestations of the infection of various HAdV types. The study is registered with PROSPERO, CRD42022303015. Results A total of 950 articles (91 about outbreaks and 859 about etiological surveillance) meeting the selection criteria were included. Predominant HAdV types from etiological surveillance studies differed from those in outbreak events. Among 859 hospital-based etiological surveillance studies, positive detection rates of HAdV-3 (32.73%) and HAdV-7 (27.48%) were significantly higher than other virus types. While nearly half (45.71%) of outbreaks were caused by HAdV-7 with an overall attack rate o 22.32% among the 70 outbreaks for which the HAdVs were typed by the meta- analysis. Military camp and school were main outbreak settings with significantly different seasonal pattern and attack rate, where HAdV-55 and HAdV-7 were identified as the leading type, respectively. Clinical manifestations mainly depended on the HAdV types and patient's age. HAdV-55 infection tends to develop into pneumonia with poorer prognosis, especially in children <5 years old. Conclusions This study improves the understanding of epidemiological and clinical features of HAdV infections and outbreaks with different virus types, and helps to inform future surveillance and control efforts in different settings.
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1	Prevalence	of human	infection	with	respiratory	adenovi	rus in	China:
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2 a systematic review and meta-analysis

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17 Abstract

18	Background Human adenovirus (HAdV) is a major pathogen that causes acute
19	respiratory tract infections (ARTI) and is frequently associated with outbreaks. The
20	HAdV prevalence and the predominant types responsible for ARTI outbreaks remains
21	obscure in China.
22	Methods A systematic review was performed to retrieve literature that reported
23	outbreaks or etiological surveillance of HAdV among ARTI patients in China from
24	2009 to 2020. Patient information was extracted from the literature to explore the
25	epidemiological characteristics and clinical manifestations of the infection of various
26	HAdV types. The study is registered with PROSPERO, CRD42022303015.
27	Results A total of 950 articles (91 about outbreaks and 859 about etiological
28	surveillance) meeting the selection criteria were included. Predominant HAdV types
29	from etiological surveillance studies differed from those in outbreak events. Among
30	859 hospital-based etiological surveillance studies, positive detection rates of HAdV-
31	3 (32.73%) and HAdV-7 (27.48%) were significantly higher than other virus types.
32	While nearly half (45.71%) of outbreaks were caused by HAdV-7 with an overall
33	attack rate of 22.32% among the 70 outbreaks for which the HAdVs were typed by
34	the meta-analysis. Military camp and school were main outbreak settings with
35	significantly different seasonal pattern and attack rate, where HAdV-55 and HAdV-7
36	were identified as the leading type, respectively. Clinical manifestations mainly

37	depended on the HAdV types and patient's age. HAdV-55 infection tends to develop
38	into pneumonia with poorer prognosis, especially in children <5 years old.
39	Conclusions This study improves the understanding of epidemiological and clinical
40	features of HAdV infections and outbreaks with different virus types, and helps to
41	inform future surveillance and control efforts in different settings.
42	

Keywords: Human adenovirus; China; respiratory tract infections; meta-analysis.

44 Author Summary

45	In this systematic review, we made an exhaustive search of published literature
46	that reported outbreaks or etiological surveillance of HAdV among ARTI patients in
47	China from 2009 to 2020. A total of 950 studies were included in this study, and we
48	explored the epidemiological characteristics and clinical manifestations of the
49	infection of various HAdV types. Positive detection rates of HAdV-3 (32.73%) and
50	HAdV-7 (27.48%) were significantly higher than other virus types according to the
51	hospital-based etiological surveillance studies. Nearly half (45.71%) of outbreaks
52	were caused by HAdV-7 with an overall attack rate of 22.32% among the 70
53	outbreaks for which the HAdVs were typed by the meta-analysis. Military camp and
54	school were main outbreak settings with significantly different seasonal pattern and
55	attack rate, where HAdV-55 and HAdV-7 were identified as the leading type,
56	respectively. Clinical manifestations mainly depended on the HAdV types and
57	patient's age. HAdV-55 infection tends to develop into pneumonia with poorer
58	prognosis, especially in children <5 years old. This study will help improve the
59	epidemiological and clinical understanding of different HAdV types of human
60	infections and thus will promote the targeted surveillance and measures to control and
61	prevent HAdV infection.

62 Introduction

63	Infection with human adenovirus (HAdV) causes a broad spectrum of clinical
64	illnesses, e.g., pharyngoconjunctival fever, keratoconjunctivitis, pneumonia,
65	hemorrhagic cystitis, gastroenteritis, acute respiratory disease, cardiomyopathy, and
66	encephalitis, which varies depending on the infected virus types and is severer among
67	immunocompromised patients such as organ transplant patients [1]. Even unexplained
68	liver injury or hepatitis was reported by two recent independent studies with UK
69	children with HAdV- 2 infection, suggesting that HAdV-2 may trigger liver damage
70	through the immune mechanisms of genetically predisposed children[2, 3]. There are
71	at least 113 recognized HAdV types (http://hadvwg.gmu.edu/), which are assigned to
72	seven subgroups (A-G) according to biophysical, biochemical, and genetic
73	characteristics, with marked differences in tissue tropism and clinical
74	manifestations[4]. Species C, species B, subspecies B1 and B2 were the most
75	common HAdV types found in respiratory samples among pediatric patients with
76	ART <mark>I[</mark> 5, 6].
77	In recent years, new serotypes or subspecies were increasingly recognized by
78	using phylogenetic analysis, which arise from genome recombination between the
79	hexon gene, fiber, and penton genes. For any of the emerging new types or
80	recombinant strains, there is a high potential of spreading widely and causes epidemic
81	outbreaks, due to the lack of herd immunity and specific vaccine intervention, posing
82	severe threats to public health[7-10]. Acute respiratory infection caused by HAdV is

83	the leading cause of morbidity in military forces worldwide. Since 1971, U.S. military
84	recruits have been vaccinated with oral HAdV-4 and HAdV-7 vaccines, which has
85	significantly decreased the epidemics of HAdV in the military[1, 11].
86	In recent years, there has been an increase in studies from hospital-based
87	etiological surveillance, reflecting a growing awareness of the importance of HAdV
88	as respiratory pathogens. A global study concluded that adenovirus infections
89	accounted for 5–10% of respiratory infections in children and 1–7% in adults, and
90	caused pneumonia in up to 20% of newborns and infants. In patients with severe
91	HAdV pneumonia, the mortality rate may exceed 50%[12]. The positive detection rate
92	of adenovirus was 3.9% and the mortality rate was 3% from 2004 to 2018 among
93	inpatients hospitalized due to severe acute respiratory infection[13]. Studies in
94	mainland China have shown that positive detection rate of adenovirus among ARTI
95	patients was approximately 5.8%-13%, and the main affected groups were children
96	and young adults[14]. Studies showed that the positive detection rate of adenovirus
97	was 5.64% among hospitalized children with ARTI in Beijing from 2017 to 2018 and
98	6.9% in Zhejiang from 2018 to 2019[15, 16]. In general, there is still a lack of data on
99	the HAdV prevalence and the predominant virus types responsible for ARTI sporadic
100	outbreaks or epidemics in China.
101	Here we conduct a systematic review and meta-analysis of all published research
102	articles on outbreak investigation and etiological surveillance of HAdV associated

103 with cases of respiratory infection in China at the nation-wide level from 2009 to

104 2020 to evaluate the HAdV prevalence, virus types, seasonality, as well as to

105 characterize patients' demographic and clinical data. This information might help to

106 comprehensively understand the epidemic patterns of HAdV in China and support the

107 adoption of targeted prevention and control measures.

108

109 Materials and Methods

110 This review was conducted according to the Preferred Reporting Items for

111 Systematic Reviews and Meta-Analyses (PRISMA) statement (data in S1 File), and

112 has been registered with the international prospective register of systematic reviews

113 (PROSPERO) (International Prospective Register of Ongoing Systematic Reviews)

114 (CRD42022303015)[17].

115 Search strategy and selection criteria

- 116 Literature search was performed from the major databases including the PubMed
- 117 database (https://pubmed.ncbi.nlm.nih.gov/), China National Knowledge
- 118 Infrastructure (CNKI) (http://www.cnki.net/), Chongqing VIP Chinese Science and
- 119 Technology Journal Database (CQVIP) (http://www.cqvip.com) and Wanfang
- 120 databases (http://www.wanfangdata.com.cn/), with the keywords ('HAdV' OR
- 121 'adenovirus' [Title/Abstract]) AND ('respiratory' [Title/Abstract] OR 'pneumonia'
- 122 [Title/Abstract]), AND ('China' OR 'the mainland of China' OR 'Chinese mainland'
- 123 OR 'Taiwan' OR 'Hong Kong' OR 'Macau' OR 'Macao' [Title/Abstract]) (Table 1 in S2

File). All the articles published between January 2009 and March 2021 were searchedwithout language limitations.

126	We included studies of human infection with HAdV, across all settings (i.e.,
127	hospital, community, long-term care) and among all age groups (pediatric and adult
128	patients). We included etiological surveillance studies and outbreak investigation, but
129	excluded reviews, editorials, letters, case studies, randomized controlled trials and
130	experimental studies. Studies were eligible if they explicitly described the total
131	number of individuals tested and those that were positive for HAdV infections in
132	humans. The following articles were excluded: (1) drug, vaccine trials, mechanism
133	studies, animal experiments or reviews for HAdV; (2) etiological surveillance studies
134	with sampling size <100 for laboratory test or HAdV positive detection <10; (3)
135	describing cases imported from abroad after international travel; (4) lacking
136	information about methods of laboratory diagnosis, specimens tested; (5) evaluations
137	on laboratory methods for HAdV; (6) study period beyond the duration from 2009 to
138	2020 (Table 2 and Table 3 in S2 File).
139	Titles and abstracts of the retrieved studies were screened using Endnote X9
140	independently by two reviewers (MCL and TTL) to identify studies potentially
141	eligible for inclusion, and then the full texts were retrieved and independently
142	assessed for eligibility. Discrepancies between reviewers were resolved by consensus
143	or a third reviewer (QX). Studies potentially describing overlapping data were noted

and the duplication were removed (e.g., same hospital and population during anoverlapping time period).

146 **Data extraction and variable definition**

147 One of the authors (MCL) extracted data from included studies using a 148 standardized data collection form. The following variables were collected: reference 149 ID, author, publication year, study sites, start and end dates, name(s) of healthcare 150 facility; study design (etiological surveillance study, outbreak investigation), outbreak 151 setting (school/daycare, healthcare comprised of hospitals and long-term care 152 facilities, military camps, swimming pools), age group, patient population, mean or 153 median age, gender proportion, laboratory test methods (molecular, serological) and type of HAdV, sample size, absolute number or rate of positive detection, presence of 154 155 clinical symptoms or syndromes of patients if reported (Table 4 and Table 5 in S2 156 File). For quality assurance, another two authors (QX, TW) randomly sampled 25% of 157 recorded data to confirm accuracy and completeness. 158 For definition of outbreak event, all those recognized and reported outbreaks 159 related to HAdV by health agencies were included. Otherwise, an outbreak event was 160 defined as a number of clustered HAdV cases with a higher incidence than the 161 average or expected incidence for a region where the cases occur[18]. All the events 162 had to be laboratory confirmed, e.g., etiological pathogen determined to be HAdV by 163 molecular methods (PCR) or serological methods (ELISA, IFA), while those

164 outbreaks reporting suspected HAdV without laboratory confirmation for HAdV were

165	not included in the analysis. For outbreak investigation, we extracted additional
166	information regarding the exact date of outbreak, attack rate, numbers of primary
167	cases and persons at risk, and number of secondary cases if available. For articles
168	reporting more than one outbreak, data were separately extracted for each outbreak.
169	For outbreaks reported in multiple publications, we included the one that reported
170	more detailed data.
171	Four age groups were defined for comparison, including children (<5 years old),
172	adolescent (5–17 years old), adult (18–59 years old), and the elderly (\geq 60 years old).
173	When a study did not mention any age information, the all-age group was specified.
174	Seven regions were defined according to the ecoclimatic characteristics, i.e.,
175	Northeast China, North China, Inner Mongolia-Xinjiang, Qinghai-Tibet, Southwest
176	China, Central China, and South China[19].
177	Meta-analysis
1 = 0	

178 We performed the meta-analysis to evaluate demographic characteristics of 179 patients, attack rate, or positive detection rate for HAdV. Briefly, the pooled 180 proportion and 95% CI were estimated using the inverse variance combined with 181 fixed effects or random effects models depending on the degree of the heterogeneity 182 between studies. Heterogeneity was quantified using the statistic Higgin's I², when its 183 value was greater than 50%, random effects model was used, otherwise, fixed effects 184 model was applied[20]. We performed the meta-analysis to estimate the clinical 185 manifestations that were related to different HAdV types, based on the 105 articles

186	with a study size more than 20 patients and reporting the information of clinical
187	manifestation. For those clinical manifestations which were reported only in one
188	study, the proportion was calculated without a 95% CI estimated (Data in S3 File). All
189	maps were produced by using the ArcGIS 10.7 software. The Meta program package
190	in R 4.1.2 software was used to merge the rates and draw forest plots. All analyses
191	were conducted with R 4.1.2 software.

192

193	Results
195	ILLSUILS

Temporal and spatial features of publications and patients 194

195 A total of 5,056 studies published from January 2009 to March 2021 were

- 196 identified, 3,874 studies underwent title and abstract screening after duplicate
- removal, among which 1,329 were assessed via full-text screening. We included 950 197
- 198 studies (881 in Chinese and 69 in English) in the final analysis, comprised of 859
- 199 etiological surveillance studies involving 119,838 patients and 91 outbreak
- 200 investigations involving 15,940 patients (Fig 1, Data in S4 File).
- 201

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202
Fig 1. Flow diagram of the literature review. Literature search was performed from
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- 203 the major databases including the PubMed database
- (https://pubmed.ncbi.nlm.nih.gov/), China National Knowledge Infrastructure (CNKI) 204
- (http://www.cnki.net/), Chongqing VIP Chinese Science and Technology Journal 205

206 Database (CQVIP) (http://www.cqvip.com) and Wanfang databases

207 (http://www.wanfangdata.com.cn/).

208

209	Of the 91 articles reporting 97 outbreak events, 68 (74.73%) were published
210	between 2014–2019, with the highest number of articles published in 2014 (14
211	articles), followed by 2017 (13) (Fig 2A). Of the 859 etiological surveillance studies,
212	594 (69.15%) were published during 2015–2020, with the largest number published in
213	2015 (135 articles), followed by 2016 (103) (Fig 2C).
214	
215	Fig 2. Temporal pattern of reported outbreaks and etiological surveillance as
216	well as the HAdV types in China. (A) number of articles about reported outbreak
217	events over publication year; (B) number of reported outbreaks according to each
218	HAdV type group over publication year; (C) number of articles about etiological
219	surveillance of HAdV over publication year; (D) number of patients reported in
220	etiological surveillance according to each HAdV type group over publication year.
221	Other in the panel D indicate those rarely seen HAdV types, including HAdV-21 (30
222	patients), HAdV-57 (18), HAdV-31 (5), HAdV-50 (2), HAdV-12 (1), HAdV-35 (1),
223	and HAdV-104 (1). Deadline for literature search is March 2021.
224	
225	A comparable number of outbreaks took place in Northern and Southern China

226 (Table 1). The geographic discrepancy of seasonal timing was shown for the

227	outbreaks, with most of the outbreak events occurring in the winter season in
228	Northern China (28/46), while a dual seasonal timing was observed in Southern
229	China, at the turn of spring and summer and winter separately (44/51) (Fig 3A). The
230	overall attack rate was estimated to be 15.91% (95% CI: 13.85-17.98). A higher
231	attack rate was observed in Northern China than in Southern China (19.01%, 95% CI:
232	14.42–23.60 versus 13.53%, 95% CI: 11.28–15.77). When the outbreak settings were
233	compared, the highest attack rate was observed in military camps (23.55%, 95%
234	CI:18.02–29.07), followed by swimming pools (22.47%, 95% CI: 12.49–32.45),
235	hospitals (19.75%, 95% CI: 8.64–30.86) and schools (6.19%, 95% CI: 4.92–7.46)
236	(Fig 3B). In contrast with the outbreak events, the etiological surveillance studies
237	among ARTI patients reported comparable interregional positive rate (4.13%, 95%
238	CI: 3.95–4.31 in Southern China, 4.15%, 95% CI: 3.95–4.34 in Northern China), and
239	the overall positive detection rate was estimated to be 4.21% (95% CI: 4.07–4.34)

240 (Fig 3C, Table 6 and Table 10 in S2 File).

241 Table 1. Attack rate and positive detection rate of HAdV by areas, seasons, patients' ages, settings and virus types based on meta-

242 analysis.

	Outbreak events			Etiological surveillance			
-	Number of articles	Genera	Attack rate by meta-		Genera	Positive detection rate by meta	
	(No. of outbreaks)	Cases	analysis % (95% CI)*	Number of articles	Cases	analysis % (95% CI)	
Number	91 (97)	15,940	15.91 (13.85, 17.98)	859	119,838	4.21(4.07, 4.34)	
Mortality	4 (4)	4	-	9	37	-	
Areas**							
Northern	44 (46)	9,182	19.01 (14.42, 23.60)	283	19,955	4.15 (3.95, 4.34)	
Southern	48 (51)	6,758	13.53 (11.28, 15.77)	584	97,162	4.13 (3.95, 4.31)	
Season							
Spring	19 (20)	899	5.92 (4.47, 7.36)	39	2,047	5.21 (4.35, 6.07)	
Summer	16 (17)	440	16.76 (12.47, 21.04)	39	1,780	4.64 (3.82, 5.47)	
Autumn	16 (17)	394	5.71 (3.41, 8.01)	36	1,278	3.62 (2.95, 4.29)	
Winter	40 (43)	8,453	22.65 (16.33, 28.96)	37	2,042	3.54 (2.83, 4.24)	
Age							
Children	6 (6)	121	12.78 (7.95, 17.62)	174	10,671	4.04 (3.76, 4.31)	
Adolescent	40 (43)	2,042	6.52 (5.5, 7.55)	8	531	4.45 (2.55, 6.36)	
Adult	44 (47)	13,734	23.56 (18.31, 28.8)	28	1,219	3.44 (2.76, 4.12)	
The elderly	0 (0)	0		9	229	2.81 (1.84, 3.78)	
All-age groups	1 (1)	43	25.29	644	107,188	4.29 (4.12, 4.45)	
Settings							
School	41 (43)	3,386	6.19 (4.92, 7.46)	0	0		

Military camp	37 (40)	11,849	23.55 (18.02, 29.07)	0	0	
Hospital	5 (5)	142	19.75 (8.64, 30.86)	859	119,838	4.21(4.07, 4.34)
Swimming	9 (9)	563	22.47 (12.49, 32.45)	0	0	
pool	9 (9)	505	22.47 (12.49, 32.45)	0	0	
Types†						
HAdV-1	0 (0)	0	-	40	466	6.70 (5.39, 8.01)
HAdV-2	0 (0)	0	-	44	772	8.90 (7.31, 10.50)
HAdV-3	9 (11)	711	5.55 (2.63, 8.48)	60	2,869	32.73 (22.13, 43.34)
HAdV-4	7 (7)	150	8.75 (0.00, 21.30)	30	137	2.07 (1.41, 2.74)
HAdV-5	0 (0)	0	-	38	249	3.55 (2.78, 4.32)
HAdV-6	0 (0)	0	-	21	83	1.97 (1.23, 2.70)
HAdV-7	30 (32)	7,048	22.32 (14.78, 29.86)	59	2,518	27.48 (17.04, 37.91)
HAdV-11	0 (0)	0	-	4	186	16.14 (1.89, 30.40)
HAdV-14	3 (4)	92	8.83 (6.31, 11.35)	12	43	2.01 (0.92, 3.09)
HAdV-21	0 (0)	0	-	7	30	0.87 (0.17, 1.57)
HAdV-31	0 (0)	0	-	4	5	0.33 (0.00, 0.73)
HAdV-55	16 (16)	4,043	27.18 (19.16, 35.20)	25	258	4.70 (3.40 , 6.00)
HAdV-57	0 (0)	0	-	8	18	1.01 (0.51, 1.50)

* 53 outbreaks recording attack rate were included in the total; 2, 26, 24 and 1 outbreaks recording attack rate were included in the children, adolescent, adult, and all age groups, respectively;

244 13, 8, 6 and 25 outbreaks recording attack rate were included in the spring, summer, autumn and winter groups, respectively; 25 and 28 outbreaks recording attack rate were included in the

Northern and Southern groups, respectively; 22, 2, 6 and 23 outbreaks recording attack rate were included in the military, hospital swimming pool and school groups, respectively; 4, 2, 17, 1

and 9 outbreaks recording attack rate were included in the HAdV-3, HAdV-4, HAdV-7, HAdV-14 and HAdV-55 groups, respectively.

247 ** Of the 848 articles mentioning locations, 19 mentioned both Northern and Southern China.

248 *†*HAdV type with case number > 5 were included, other rarely seen types including HAdV-50 (2 cases), HAdV-12 (1), HAdV-35 (1), and HAdV-104 (1).

249	Fig 3. Attack rate of HAdV in outbreaks and positive detection rate of HAdV in
250	etiological surveillance over months based on the meta-analysis. (A) attack rate by
251	region; (B) attack rate by settings; (C) positive detection rate by regions; (D) attack
252	rate by age groups. The bars in panels A, B, and D indicate the number of outbreaks,
253	and the intervals indicate the attack rate and 95% CI. The bars on panel C indicate the
254	case number in etiological surveillance, and the intervals indicate the positive
255	detection rate and 95% CI.

257 **Demographic characteristics of patients**

258 The highest number of outbreak events was observed in the adult group (47),

- followed by adolescents (43) and children (6). The highest attack rate was shown in
- 260 adults (23.56%, 95% CI: 18.31–28.80), followed by children (12.78%, 95% CI: 7.95–
- 261 17.62) and adolescents (6.52%, 95% CI: 5.50–7.55). An age pattern of HAdV
- 262 infection was shown from the etiological surveillance data, with higher positive rate
- 263 observed in children (4.04%, 95% CI: 3.76–4.31) and adolescents (4.45%, 95% CI:
- 264 2.55–6.36) than those of the two older groups (Table 1). Seasonal pattern differed
- between age groups. For children and adolescent, over half of the outbreaks occurred
- in autumn and spring (29 of 49 outbreaks), while for adult groups, most outbreaks
- 267 occurred in winter (38/47) (Fig 3D, Table 11 in S2 File).

Among 97 outbreaks that reported settings, the highest number was reported in

269 schools (44.33%, 43/97), followed by military camps (41.24%, 40/97), swimming

277	Temporal and geographic pattern of HAdV types in China
276	(Table 1).
275	infection were reported from 13 articles, with an overall case fatality rate of 0.03%
274	terms as expected (69.77%, 30/43). A total of 41 deaths with confirmed HAdV
273	8/9), while school outbreaks usually occurred in spring and autumn during school
272	(85.00%, 34/40), and most swimming pool outbreaks occurring in summer (88.89%,
271	the outbreak settings, with most of the military camps outbreaks occurring in winter
270	pools (9.28%, 9/97), and hospitals (5.15%, 5/97). The seasonality depended largely on

Sequence information was available for 70 outbreak events involving 12,044 279 cases and 67 etiological surveillance studies involving 7,639 cases. The most common 280 type responsible for outbreak events was HAdV-7, accounting for 45.71% (32/70) of 281 the total number of outbreaks for which HAdV typing was performed, followed by 282 HAdV-55 (16/70), HAdV-3 (11/70), HAdV-4 (7/70), and HAdV-14 (4/70). HAdV-7 283 had the highest number of reported outbreaks in 2014, 2015 and 2017, while HAdV-284 55 (5) had the highest proportion of reported outbreaks in 2018 (Fig 2B). The case

278

285 numbers involved in outbreaks caused by HAdV-7, HAdV-55 and HAdV-3 were

7,048, 4,043 and 711, respectively, based on which the attack rate of HAdV-55 was 286

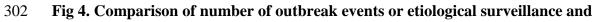
estimated to be 27.18% (95% CI: 19.16-35.20), which was significantly higher than 287

288 that of HAdV-7 (22.32%, 95% CI: 14.78-29.86) and HAdV-3 (5.55%, 95% CI: 2.63-

289 8.48) (Table1). A difference of the predominant HAdV type in outbreak events was

290 shown between Northern China and Southern China. Among all the outbreaks

291	reporting HAdV types and study sites, HAdV-55 (12 events involving 3,841 cases)
292	and HAdV-7 (17 events involving 2,614 cases) were predominant in Northern China,
293	while HAdV-7 (15 events involving 4,434 cases), HAdV-3 (seven events involving
294	640 cases), and HAdV-55 (four events involving 202 cases) were predominant in
295	Southern China (Fig 4A). According to the ecological regions of China, we found that
296	HAdV-55 was the dominant HAdV type for outbreak events in four regions including
297	Inner Mongolia-Xinjiang, North China, Qinghai-Tibet, and South China, while
298	HAdV-7 was the dominant type in the others including Northeast China and Central
299	China, except for one region(Southwest China) without reporting outbreaks with
300	HAdV typing information (Fig 1 in S2 File).
301	



303 case number with HAdV types by region, age, and setting. (A) outbreaks in

304 different regions; (B) etiological surveillance in different regions; (C) outbreaks in

305 different age groups; (D) outbreaks in different settings. Solid circles in panels A, C,

306 and D indicate the number of outbreaks, and hollow circles indicate the number of

- 307 cases. Solid circles in panel B indicate the number of etiological surveillances, and
- 308 hollow circles indicate the number of cases.

309

310	The predominant HAdV types differed from those in outbreak events. The most
311	common type was HAdV-3 (2,869 cases), followed by HAdV-7 (2,518), HAdV-2

- 312 (772), HAdV-1 (466), HAdV-55 (258), and HAdV-5 (249). Both HAdV-3 and
- 313 HAdV-7 had been shown an increasing pattern in the number of reported cases during
- the study period (Fig 2D). The positive rate of HAdV-3 was determined as 32.73%
- 315 (95% CI: 22.13–43.34), which was significantly higher than that of HAdV-7
- 316 (27.48%), HAdV-11 (16.14%), HAdV-2 (8.90%), HAdV-1 (6.70%), HAdV-55
- 317 (4.70%), and. HAdV-5 (3.55%). Both HAdV-3 and HAdV-7 were the common types
- 318 identified in Northern and Southern China (Fig 4B, Table1).
- 319 Among 70 outbreaks providing information on age and HAdV type, HAdV-7
- 320 (25) and HAdV-55 (15) were responsible for all the 40 outbreaks reported in the adult
- 321 group; HAdV-7 (3) and HAdV-4 (3) were determined in the six outbreaks reported
- 322 from children, while a higher diversity of types was observed in the 24 outbreaks
- 323 reported in the adolescent group, including HAdV-3 (11), HAdV-4 (4), HAdV-7 (4),
- HAdV-14 (4), and HAdV-55 (1) (Fig 4C). Among the 70 outbreaks with reported
- 325 settings and types, HAdV-7 (21) and HAdV-55 (12) were responsible for all the 33
- 326 outbreaks in military camps, which involved 5,111 and 3,674 cases, respectively.
- 327 HAdV-55 (3 outbreaks) and HAdV-7 (2) were responsible for the five outbreaks in
- 328 hospitals, with 113 and 29 cases involved respectively. HAdV-3 (2 outbreaks),
- 329 HAdV-4 (1), and HAdV-7 (2) were determined to be responsible for the five
- 330 swimming pool outbreaks, with 199, 147, and 9 cases involved respectively. Five
- HAdV types were responsible for the 28 outbreaks in schools, including HAdV-3 (9),

332	HAdV-7	(7), HAdV-4	(6), HAdV	-14 (4), and	HAdV-55 (2), with 1, 7	761 cases
-----	--------	-------------	-----------	--------------	------------	--------------	-----------

infected with HAdV-7 and 512 cases with HAdV-3 infection (Fig 4D).

- 334 Clinical manifestations
- Altogether, 105 articles with HAdV cases greater than 20 were included in the
- analysis of clinical manifestations. Among children with HAdV infection, cough was
- the most prevalent symptom, identified in 76.47% of the cases, followed by
- pneumonia (66.56%), expectoration (56.28%), respiratory failure (11.05%), breathing
- difficulties (34.69%), running nose (29.58%), vomiting (25.00%), and diarrhea
- 340 (16.87%). Among adolescents, tonsillar enlargement (70.89%), pneumonia (21.69%)
- and vomiting (15.43%) were frequently seen. Among adults, less diverse clinical
- 342 presentations were seen, including expectoration (31.19%), running nose (8.05%) and
- 343 vomiting (4.60%) (Fig 5A, Table 12 in S2 File).
- 344

345 Fig 5. Clinical manifestations of HAdV infection by age groups and virus types.

- 346 (A) for different age groups; (B) for different virus types. The bars indicate the
- 347 number of articles, and the intervals indicate the proportion of patients with the
- 348 clinical manifestation and 95% CI based on the meta-analysis.
- 349
- 350 Compared with the infection of HAdV-55 and HAdV-7, HAdV-3 infection was
- related to higher frequency of cough (79.91%), running nose (20.59%) and vomiting
- 352 (20.59%). HAdV-55 infection was related to higher frequency of tonsillar

353	enlargement (96.91%), pneumonia (27.91%), while lower occurrence of cough
354	(56.61%), expectoration (45.10%), running nose (6.90%), and vomiting (3.37%),
355	diarrhea (1.50%), compared with the infection of HAdV-3 and HAdV-7. HAdV-7
356	infection was related to higher presence of expectoration (60.59%), breathing
357	difficulties (26.80%), compared with the infections of HAdV-3 and HAdV-55 (Fig
358	5B, Table 13 in S2 File).

360 **Discussion**

361 The current study provided a most comprehensive and up to date estimation on 362 the attack rate/positive rate of HAdV as well as the dominant virus types, that differed across age, setting and seasons. Attack rates were significantly higher in outbreaks 363 364 related to military camps and in the winter season. HAdV-55, HAdV-7 and HAdV-3 365 were the major causative agents in the outbreak events. Outbreaks in military camps 366 were more likely to be associated with HAdV-7 and HAdV-55, while outbreaks in 367 other setting were associated with more HAdV genotypes, particularly for the school 368 outbreaks. This was also in line with the higher diversity of virus types in the 369 adolescent group, who constituted the major part of school outbreaks. These virus 370 typing results contrasted with the etiological surveillance studies where HAdV-3 and 371 HadV-7 were the most frequently determined when an all-age group was studied. The 372 current surveillance finding was highly consistent with the prior epidemiological

373	investigation performed in China, where HAdV-3 and HAdV-B7 were the most
374	frequently detected among acute respiratory distress syndrome patients[21-24].
375	We found that school-related outbreaks were associated with the lowest attack
376	rate, suggesting either a less confined space that limited the transmission or the lower
377	transmission capacity relate to different HAdV types. We also revealed a different
378	situation from that shown in other countries, for example, in the American troops,
379	HAdV-4, HAdV-B7 and HAdV-B14 act as the predominant strains sequentially
380	isolated from the outbreaks[7, 25-27]. HAdV vaccination program against the two-
381	outbreak-related virus types in this high-risk population is urgently needed. Our meta-
382	analysis showed that overall attack rate of adenovirus infection in outbreaks was
383	estimated at 15.91% (95% CI: 13.85–17.98), which is comparable with the outbreak
384	among college students in Pennsylvania, USA, of which a 15% (44/288) attack rate
385	was reported based on the test of nasopharyngeal swabs for HAdV[28].
386	Our study for the first time revealed a clear seasonal pattern for the outbreak
387	events. The school outbreaks occurred mostly at the beginning of new school years,
388	while the military outbreaks mainly occurred at the recruit training seasons. A Korean
389	study from 2013 to 2018 showed that HAdV was the most frequently detected
390	respiratory virus in military recruits (6,646/14,630, 45.4%)[29]. HAdV has been
391	implicated in over half of the febrile respiratory illness cases reported at recruit
392	training center clinics.

393	A total of 17 virus types involving respiratory adenovirus infection have been
394	reported in China, of which HAdV-3, HAdV-7 and HAdV-55 were predominant.
395	Outbreaks were dominated by HAdV-7 and HAdV-55, while other types included
396	HAdV-3, HAdV-4 and HAdV-14. The main virus types of outbreaks differ in
397	different settings, with school outbreaks having more types, including HAdV-7,
398	HAdV-55, HAdV-3, HAdV-4 and HAdV-14, with HAdV-3 and HAdV-7
399	predominating; swimming pool outbreaks having mainly HAdV-3, HAdV-7 and
400	HAdV-4, mainly in summer; hospital outbreaks and military outbreaks having mainly
401	HAdV-7 and HAdV-55. The virus types of outbreaks vary by age groups, HAdV-7
402	and HAdV-4 are dominant in children, HAdV-7 and HAdV-55 are dominant in adults,
403	and more virus types are shown in adolescents, including HAdV-7, HAdV-55, HAdV-
404	3, HAdV-4, and HAdV-14. There are more virus types detected in etiological
405	surveillance, including HAdV-3, HAdV-7, HAdV-2, HAdV-1, HAdV-55, HAdV-5,
406	etc. The most common types are HAdV-3 and HAdV-7 with an increasing trend along
407	the year, which may be related to both the increasing number of infections and rising
408	levels of surveillance. Differences in the main HAdV types in outbreak investigations
409	and etiological surveillance reports suggest that HAdV-55 is more infectious and
410	more likely to lead to outbreaks, whereas HAdV-3 is less infectious than HAdV-55
411	and HAdV-7 and is easily detected during hospital-based surveillance. This may be
412	because HAdV-55 is more symptomatic, more contagious and more likely to be
413	reported. A study has shown that HAdV-7 replicates more robustly than HAdV-3, and

414 promotes an exacerbated cytokine response, causing a more severe airway

415	inflammation[30]. In our study, the mortality rate of adenovirus infection in patients
416	with respiratory infections was about 0.03%, while a study in Rio Grande Do Sul,
417	Brazil showed a higher mortality rate (3%) among hospitalized patients with severe
418	acute respiratory infection, which might be caused by a lower proportion of patients
419	with severe respiratory infection in our study[13].
420	Overall, adenovirus circulates throughout the year, with slightly higher numbers
421	reported during the summer and winter. Previous studies have shown that HAdV
422	detection rates are positively associated with the monthly mean temperature and
423	sunshine duration, and negatively associated with wind speed[31]. In our study, the
424	main prevalent adenovirus types were HAdV-3, HAdV-7 and HAdV-55 in China,
425	with other more frequent types such as HAdV-2, HAdV-4, HAdV-1 and HAdV-5.
426	The main outbreak sites were schools and the military, with higher attack rates in the
427	north than in the south. The prevalent virus typing varies between countries and
428	regions. Species B, C and D are the most common adenoviruses worldwide, of which
429	species B and C could cause respiratory infections. For species B, a low prevalence of
430	HAdV-7, HAdV-11 and HAdV-35 was reported globally, however, it is high
431	prevalence for HAdV-35 in some counties from Africa with a positive detection rate
432	of about 20% among HIV-infected patients, and a high prevalence of HAdV-7 was
433	reported in China, United States and Belgium. For species C, HAdV-5 was the widely
434	distributed species, and HAdV-2 usually had a high positive detection rate among

435	healthy individuals and HIV-infected patients in China and developed countries[5].
436	An epidemiologic study based on HAdV molecular typing was conducted in the
437	Korean military from January 2013 to April 2014, and HAdV-55 (42.0%) was the
438	most frequently identified strain, followed by HAdV-4 (13.0%), HAdV-5 (1.4%), and
439	HAdV-6 (1.4%)[32]. HAdV-55 is a recently identified pathogen, which evolved from
440	recombination between adenovirus 11 and 14[33, 34]. It was initially described as
441	serotype 11a and was later re-labeled as HAdV-55 because of its recombinant
442	genome[33], which is mainly found in China and Korea[35].
443	The clinical presentation varies by age group and by virus type. Most adenovirus
444	respiratory infections are light to moderate and self-limited; however, sometimes they
445	may cause life-threatening conditions, comorbidities, and serious sequelae. The rate of
446	pneumonia is higher in children than in other age groups. In addition, the children are
447	more likely to have breathing difficulties. Attention should be paid to the occurrence
448	of adenovirus pneumonia in children. The main symptoms are fever and tonsil
449	enlargement in adolescents while the main symptoms are cough and tonsil
450	enlargement in adults. Adolescents and adults have a stronger immune system and the
451	symptoms are mainly mild. Compared to other virus types, HAdV-55 is more likely to
452	cause pneumonia and has a high prevalence in the military camps, so attention should
453	be paid to the prevention and control of adenovirus in the military camps.
454	There were two main limitations to this study. First, inherent to systematic
455	reviews, our study was influenced by publication bias. Most outbreaks are reported by

456	passive surveillance which may not be as comprehensive as in active surveillance, and
457	are also subject to reporting biases. Secondly, as our data came from different studies,
458	and did not have the same variables. This may have increased the likelihood of
459	misclassification bias, also limited the number of variables that can be used for
460	analysis.
461	Despite of these limitations, we have disclosed the prevalence of human
462	infection with respiratory adenovirus and the major genotypes that differed over time,
463	by location, and by demographical characteristics, e.g., patients' age. Comparing and
464	contrasting the features across diverse settings can help to attain an enhanced
465	epidemiological and clinical understanding of human infections with different HAdV
466	types, and thus enhancing the accuracy of HAdV surveillance systems.

468 Author Contributors

The author contributions are as follows. LQF and WL conceived, designed, and supervised the study. MCL, QX, TTL, TW, BGJ and CLL searched, screened, and assessed the publications. MCL and TTL created data extraction forms and extracted and analyzed the data. QX, TW, BGJ, CLL and XAZ helped with checking data and constructed the figures. QX, TW, BGJ and CLL provided statistical and clinical expertise in data analysis. MCL and QX wrote the drafts of the manuscript. MCL and QX interpreted the findings. LQF and WL commented on and revised drafts of the 476 manuscript. All authors read the manuscript, provided feedback, and approved the

477 final version.

478

479 Data Availability Statement

480 All relevant data are within the manuscript and its Supporting Information files.

481

482 **Declaration of interests**

483 We declare no competing interests.

484

485 Financial Disclosure

486 Natural Science Foundation of China (No. 81825019) was awarded to WL. The

487 funders had no role in study design, data collection and analysis, decision to publish,

488 or preparation of the manuscript.

489

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492 collected the data.

493

494 **Reference**

495 1. Lynch JP 3rd, Fishbein M, Echavarria M. Adenovirus. Semin Respir Crit Care

496 *Med.* 2011;**32**(4):494-511.

- 497 2. Antonia Ho, Richard Orton, Rachel Tayler, et al. Adeno-associated virus 2
- 498 infection in children with non-A-E hepatitis. *medRxiv*, 2022.07.19.22277425
- 499 [Preprint]. 2022 [cited 2022 Oct 9]. Available from:
- 500 https://www.medrxiv.org/content/10.1101/2022.07.19.22277425v1.
- 501 3. Morfopoulou, S. et al. Genomic investigations of acute hepatitis of unknown
- 502 aetiology in chilfren. *medRxiv*, 2022.07.28.22277963 [Preprint]. 2022 [cited 2022 Oct
- 503 9]. Available from:
- 504 https://www.medrxiv.org/content/10.1101/2022.07.28.22277963v1.
- 505 4. Seto D, Chodosh J, Brister JR, Jones MS. Members of the adenovirus research
- 506 community. Using the whole-genome sequence to characterize and name human
- 507 adenoviruses. *J Virol*. 2011;**85**(11):5701-5702.
- 508 5. Mennechet FJD, Paris O, Ouoba AR, et al. A review of 65 years of human
- adenovirus seroprevalence. *Expert Rev Vaccines*. 2019;18(6):597-613.
- 510 6. Barrero PR, Valinotto LE, Tittarelli E, Mistchenko AS. Molecular typing of
- 511 adenoviruses in pediatric respiratory infections in Buenos Aires, Argentina (1999-
- 512 2010). *J Clin Virol*. 2012;**53**(2):145-150.
- 513 7. Ryan MA, Gray GC, Smith B, McKeehan JA, Hawksworth AW, Malasig MD.
- 514 Large epidemic of respiratory illness due to adenovirus types 7 and 3 in healthy young
- 515 adults. Clin Infect Dis. 2002;**34**(5):577-582.

516	8. Kajon AE, Lu X, Erdman DD, et al. Molecular epidemiology and brief history of
517	emerging adenovirus 14-associated respiratory disease in the United States. J Infect
518	Dis. 2010; 202 (1):93-103.

- 519 9. Mi Z, Butt AM, An X, et al. Genomic analysis of HAdV-B14 isolate from the
- 520 outbreak of febrile respiratory infection in China. *Genomics*. 2013;**102**(5-6):448-455.
- 521 10. Lu G, Peng X, Li R, et al. An outbreak of acute respiratory infection at a training
- 522 base in Beijing, China due to human adenovirus type B55. *BMC Infect Dis*.
- 523 2020;**20**(1):537.
- 524 11. Hoke CH Jr, Snyder CE Jr. History of the restoration of adenovirus type 4 and
- 525 type 7 vaccine, live oral (Adenovirus Vaccine) in the context of the Department of
- 526 Defense acquisition system. *Vaccine*. 2013;**31**(12):1623-1632.
- 527 12. Lynch JP 3rd, Kajon AE. Adenovirus: Epidemiology, global spread of novel
- 528 serotypes, and advances in treatment and prevention. Semin Respir Crit Care Med.
- 529 2016;**37**(4):586-602.
- 530 13. Pscheidt VM, Gregianini TS, Martins LG, Veiga ABGD. Epidemiology of human
- adenovirus associated with respiratory infection in southern Brazil. Rev Med Virol.

532 2021;31(4):e2189.

- 533 14. Mao NY, Zhu Z, Zhang Y, Xu WB. Current status of human adenovirus infection
- 534 in China. World J Pediatr. 2022;18(8):533-537.

- 535 15. Yao LH, Wang C, Wei TL, Wang H, Ma FL, Zheng LS. Human adenovirus
- among hospitalized children with respiratory tract infections in Beijing, China, 2017-
- 537 2018. *Virol J.* 2019;**16**(1):78.
- 538 16. Wang C, Liu J, Mi Y, Chen J, Bi J, Chen Y. Clinical features and epidemiological
- analysis of respiratory human adenovirus infection in hospitalized children: a cross-
- 540 sectional study in Zhejiang. *Virol J.* 2021;**18**(1):234.
- 541 17. Page MJ, McKenzie JE, Bossuyt PM, et al. The PRISMA 2020 statement: an
- 542 updated guideline for reporting systematic reviews. *BMJ*. 2021;**372**:n71.
- 543 18. Porta M. A dictionary of epidemiology, 5th edn. *J Epidemiol Community Health*
- 544 2006;**60**:653.
- 545 19. Wang LP, Zhou SX, Wang X, et al. Etiological, epidemiological, and clinical
- features of acute diarrhea in China. *Nat Commun.* 2021;**12**(1):2464.
- 547 20. Rowe WP, Huebner RJ, Gilmore LK, Parrott RH, Ward TG. Isolation of a
- 548 cytopathogenic agent from human adenoids undergoing spontaneous degeneration in
- 549 tissue culture. *Proc Soc Exp Biol Med.* 1953;**84**(3):570-573.
- 550 21. Deng J, Qian Y, Zhao LQ, Zhu RN, Sun Y, Tian R. Identification and typing of
- adenovirus from acute respiratory infections in pediatric patients in Beijing from 2003
- 552 to 2012. *Chinese journal of virology*. 2013;**29**(6):615-20. Chinese.
- 553 22. Jin Y, Zhang RF, Xie ZP, et al. Prevalence of adenovirus in children with acute
- respiratory tract infection in Lanzhou, China. *Virol J.* 2013;**10**:271.

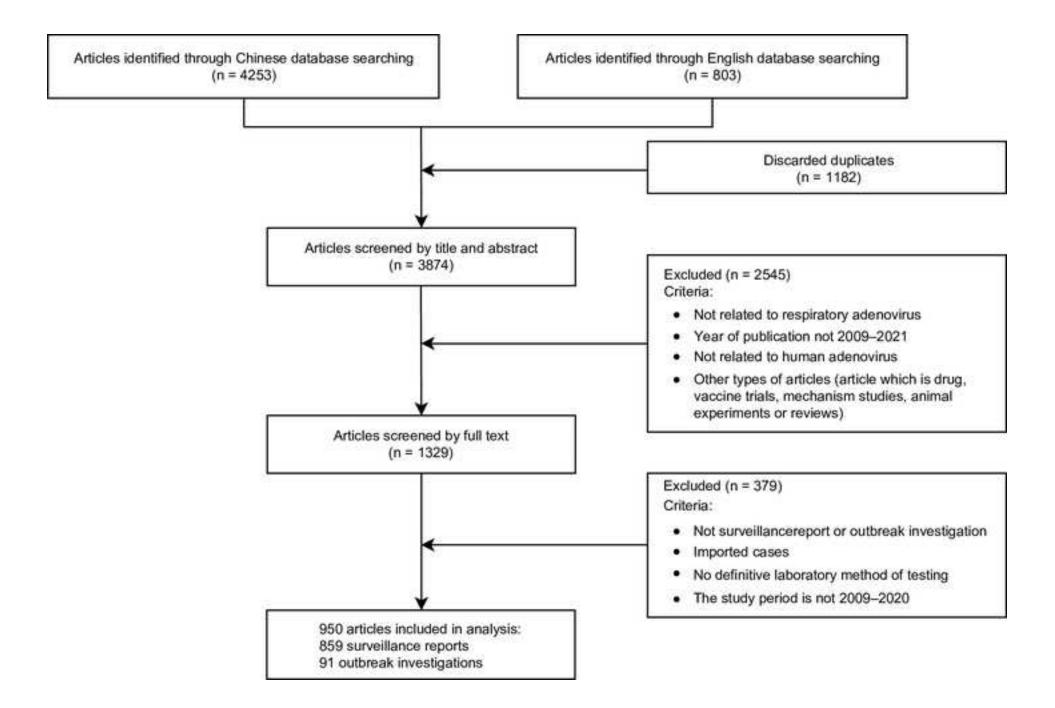
555	23. Lu QB,	Tong YG	, Wo Y, et al. I	Epidemiology	⁷ of human	adenovirus	and molecular
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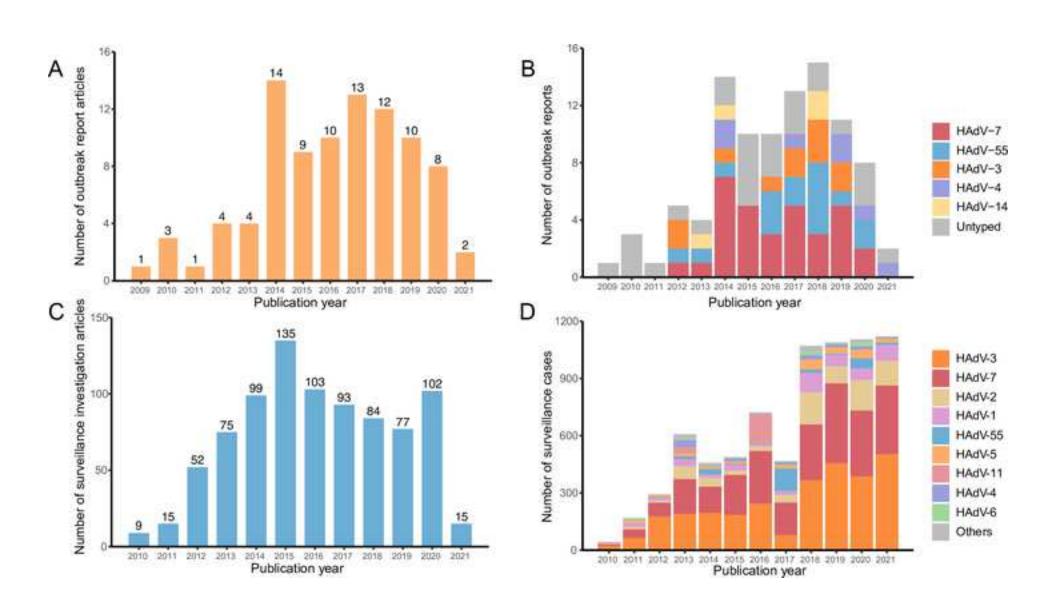
- 556 characterization of human adenovirus 55 in China, 2009-2012. Influenza Other Respir
- 557 Viruses. 2014;**8**(3):302-308.
- 558 24. Cao B, Huang GH, Pu ZH, et al. Emergence of community-acquired adenovirus
- type 55 as a cause of community-onset pneumonia. *Chest.* 2014;**145**(1):79-86.
- 560 25. Kolavic-Gray SA, Binn LN, Sanchez JL, et al. Large epidemic of adenovirus type
- 561 4 infection among military trainees: epidemiological, clinical, and laboratory studies.
- 562 *Clin Infect Dis.* 2002;**35**(7):808-818.
- 563 26. Binder AM, Biggs HM, Haynes AK, et al. Human adenovirus surveillance -
- 564 United States, 2003-2016. *MMWR Morb Mortal Wkly Rep.* 2017;**66**(39):1039-1042.
- 565 27. Kajon AE, Lamson DM, St George K. Emergence and re-emergence of
- respiratory adenoviruses in the United States. *Curr Opin Virol.* 2019;**34**:63-69.
- 567 28. Biggs HM, Lu X, Dettinger L, Sakthivel S, et al. Adenovirus-associated influenza-
- 568 like illness among college students, Pennsylvania, USA. *Emerg Infect Dis.*
- 569 2018;**24**(11):2117-2119.
- 570 29. Ko JH, Woo HT, Oh HS, et al. Ongoing outbreak of human adenovirus-associated
- 571 acute respiratory illness in the Republic of Korea military, 2013 to 2018. Korean J
- 572 *Intern Med.* 2021;**36**(1):205-213.
- 573 30. Fu Y, Tang Z, Ye Z, et al. Human adenovirus type 7 infection causes a more
- severe disease than type 3. *BMC Infect Dis.* 2019;**19**(1):36.

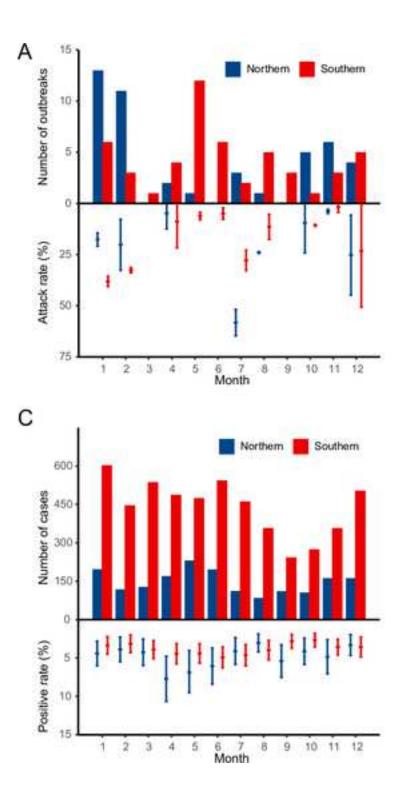
- 575 31. Tian JY, Hu AH, Pan JG, et al. An outbreak of acute respiratory tract infection
- 576 caused by adenovirus serotype 7 in a military camp in Shanxi province. J Pre Med
- 577 *Chin PLA*. 2014;**32**:203–205.
- 578 32. Heo JY, Noh JY, Jeong HW, et al. Molecular epidemiology of human adenovirus-
- 579 associated febrile respiratory illness in soldiers, South Korea. Emerg Infect Dis
- 580 2018;**24**(7):1221-1227.
- 581 33. Yang Z, Zhu Z, Tang L, et al. Genomic analyses of recombinant adenovirus type
- 582 11a in China. *J Clin Microbiol* 2009;**47**(10):3082-3090.
- 583 34. Walsh MP, Seto J, Jones MS, et al. Computational analysis identifies human
- adenovirus type 55 as a re-emergent acute respiratory disease pathogen. J Clin
- 585 *Microbiol* 2010;**48**(3):991-993.
- 586 35. Hang J, Kajon AE, Graf PCF, et al. Human adenovirus type 55 distribution,
- regional persistence, and genetic variability. *Emerg Infect Dis* 2020;**26**(7):1497-1505.

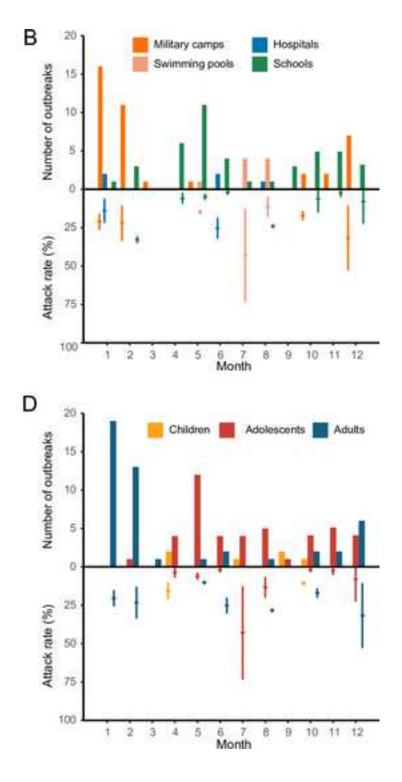
589 Supporting information

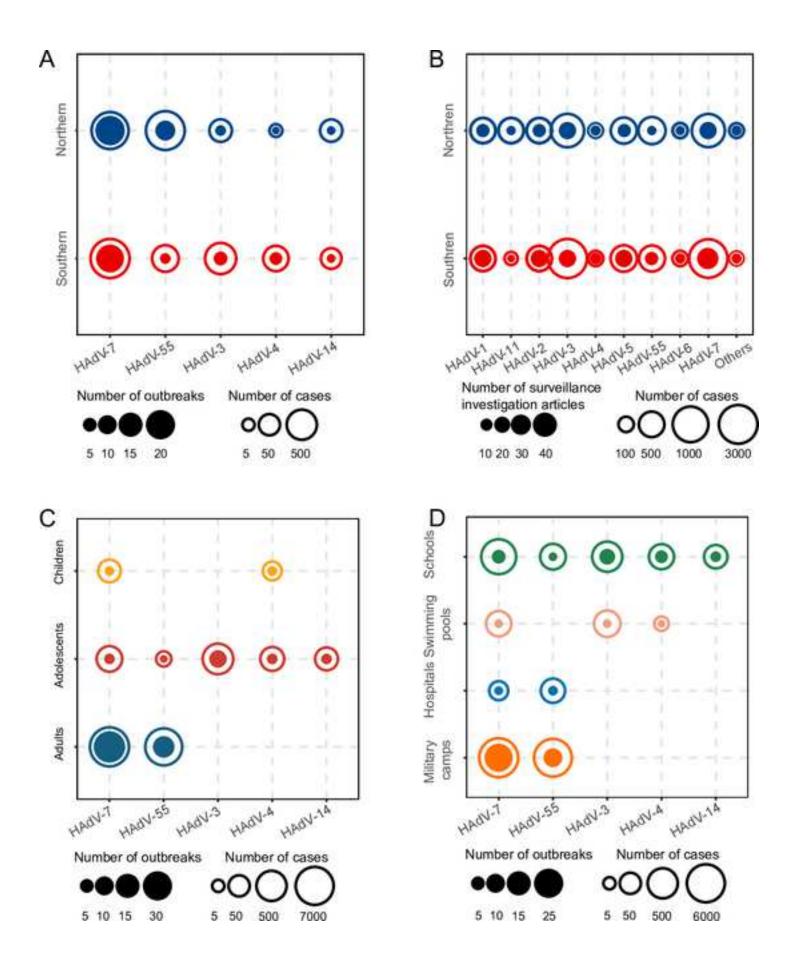
- 590 S1 File. PRISMA checklist.
- 591 S2 File. Supplementary appendix.
- 592 S3 File. Forest plot.
- 593 S4 File. List of references.

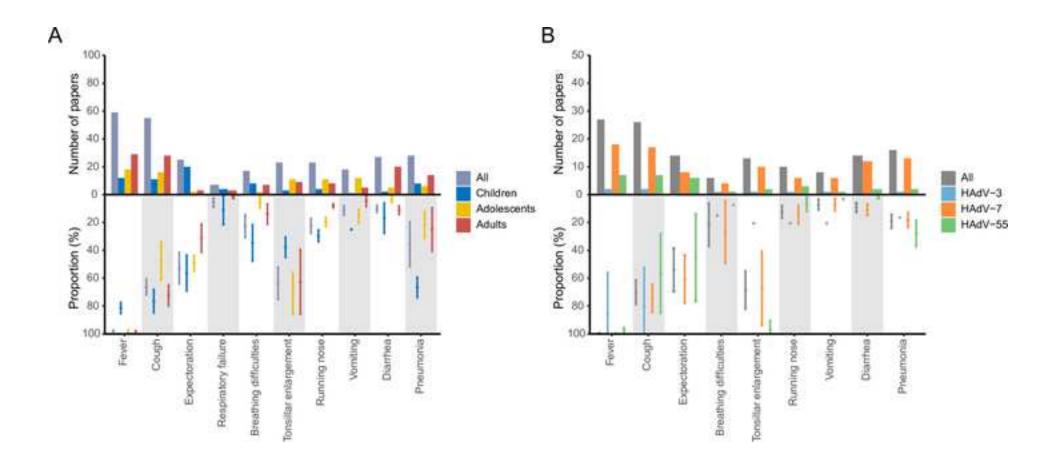












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Responses to the reviewers' comments Title

Reviewer #1:

It would be good to clarify if this article is a prevalence study or not.

[Response] We appreciate the reviewer's helpful suggestion. We have added the prevalence study to the title as: "Prevalence of human infection with respiratory adenovirus in China: a systematic review and meta-analysis". (Page 1, Lines 1–2)

Abstract

Reviewer #1:

Methods should be written in more detail about the study design, sampling, and clinical manifestation.

[Response] Thanks for the reviewer's suggestions. We have supplemented the study design, sampling, and clinical manifestation in the Abstract as: "A systematic review was performed to retrieve literature that reported outbreaks or etiological surveillance of HAdV among ARTI patients in China from 2009 to 2020. Patient information was extracted from the literature to explore the epidemiological characteristics and clinical manifestations of the infection of various HAdV types. The study is registered with PROSPERO, CRD42022303015". (Page 2, Lines 24–28)

Introduction

Reviewer #1:

1. The introduction needs to be improved by adding some information about the global prevalence, mortality, morbidity, and burden of HAdV both worldwide and in China. [Response] Many thanks for the reviewer's helpful suggestions. We have supplemented the information about the global prevalence, mortality, morbidity, and burden of HAdV both worldwide and in China as: "A global study concluded that adenovirus infections accounted for 5-10% of respiratory infections in children and 1–7% in adults, and caused pneumonia in up to 20% of newborns and infants. In patients with severe HAdV pneumonia, the mortality rate may exceed 50%[12]. The positive detection rate of adenovirus was 3.9% and the mortality rate was 3% from 2004 to 2018 among inpatients hospitalized due to severe acute respiratory infection[13]. Studies in mainland China have shown that positive detection rate of adenovirus among ARTI patients was approximately 5.8%–13%, and the main affected groups were children and young adults[14]. Studies showed that the positive detection rate of adenovirus was 5.64% among hospitalized children with ARTI in Beijing from 2017 to 2018 and 6.9% in Zhejiang from 2018 to 2019[15,16]". (Page 6, Lines 129-139)

2.Page 4, line 75: "Here we conduct a systematic review of all published research..." isn't that a systematic review and meta-analysis?

[Response] Thanks. We have corrected this sentence as "Here we conduct a systematic review and meta-analysis of all published research articles on

outbreak investigation and etiological surveillance of HAdV among ARTI patients in China at the nation-wide level from January 2009 to 2020, to evaluate the HAdV prevalence, types, seasonality, as well as to characterize patients' demographic and clinical data". (Page 6, Line 142–156)

Methods

Reviewer #1:

1.Page 5, line 109: Part 6 of the exclusion criteria says "Study period beyond the duration 2009-2020" while the authors indicated data extraction was conducted between Jan 2009 and Mar 2021. Also, in Appendix1 study period is 2009-2021 but in table S3 it is from 2009 to 2020. Please explain the difference.

[Response] Thanks for the reviewer's helpful comments. We extracted the literature in March 2021 for the study period from 2009 to 2020. We have addressed this issue throughout the manuscript.

2.In appendix1 figure S1, I can't see the distribution of adenovirus typing pie chart for southwest China on the map!

[Response] Many thanks for the reviewer's helpful comments. Few studies reported the status of respiratory adenovirus infections in Southwest China, where no data has been reported on the adenovirus typing. We have supplemented the information in the notes of fig 1 in S2 File.

3. There is not enough information about how the quality assessment was done! Please state the exact method that has been used, provide a complete checklist of risk of bias as an appendix, and address the references.

[Response] We appreciate the reviewer's valuable suggestions. Our exclusion criteria partially accounted for the quality of studies, e.g., The study requires an adequate sample size, complete outcome data, complete laboratory testing standards, specific testing criteria. To evaluate the methodological quality of the studies, two reviewers (MCL and TTL) independently assessed each study potentially eligible for inclusion. Discrepancies between reviewers were resolved by consensus or a third reviewer (QX). One of the authors (MCL) extracted data from included studies using a standardized data collection form. For quality assurance, another two authors (QX, TW) randomly sampled 25% of recorded data to confirm accuracy and completeness. We followed the PRISMA checklist to complete the meta-analysis. S4 File contains all included literature, and the full checklist has been provided in S1 File.

4.Page 6, lines 131-133: "an outbreak event was defined..." is there any reference for this definition?

[Response] Thanks for the reviewer's helpful comments. We have supplemented a reference (Ref. 18) for this definition.

5. Please report sensitivity and specificity of laboratory determination methods that

have been used.

[Response] Thanks for the reviewer's valuable suggestion. It is pity that the information about sensitivity and specificity of laboratory determination methods is not available due to the data were from the literature, of which the related information was not reported.

Reviewer #2:

The hypothesis and objectives of the work are clearly stated. The selection of the articles is carried out properly. Statistical analyzes are adequate. [Response] Many thanks for the reviewer's positive comments.

Reviewer #3:

The study is a systematic review and meta-analysis about human adenovirus (HAdV) infection associated with respiratory disease in China. The methodology is in accordance with a systematic review and met analysis article.

[Response] Many thanks for the reviewer's positive comments.

Results

Reviewer #1:

There could have been data from HAdV vaccination in China among all age groups and a proper comparison of HAdV incidence between vaccinated and non-vaccinated individuals.

[Response] Many thanks for the reviewer's helpful suggestion. However, there is no available adenovirus vaccine in China up to now, and all patients in this study were considered not to be vaccinated.

There could have been information about the most common type of HAdV separated by year from fig2B and fig2C.

[Response] Many thanks for the reviewer's helpful suggestions. We have supplemented a detailed description about the most common type of HAdV as: "The most common type responsible for the outbreak events was HAdV-7, accounting for 45.71% (32/70) of all outbreaks with information about HAdV typing, followed by HAdV-55 (16/70), HAdV-3 (11/70), HAdV-4 (7/70), and HAdV-14 (4/70). HAdV-7 had the highest number of reported outbreaks in 2014, 2015 and 2017, while HAdV-55 (5) had the highest proportion of reported outbreaks in 2018 (Fig 2B)." (Page 17, Lines 473–478) "Both HAdV-3 and HAdV-7 had been shown an increasing pattern in the number of reported cases during the study period (Fig 2D)". (Page 19, Lines 527–529)

Reviewer #2:

The results section describes very well the analysis carried out considering three different age ranges, and important to describe.

The graphs are well designed and display the results in an easy to view manner. The comparative table is correct and presents valuable information comparing outbreaks and surveillance.

[Response] Many thanks the reviewer's positive comments.

Reviewer #3:

A total of 5056 studies were identified, of which 950 articles met the inclusion criteria and were analyzed in the study. The study analyzed both articles from outbreak studies as well as from surveillance studies.

Presentations of results could be improved, especially concerning use of expressions and words not well explained in the text, grammar errors that make the text hard to understand, including in Figure legends.

[Response] Many thanks for the reviewer's helpful suggestions. We have a senior author with fluent English check the language throughout the manuscript carefully, and the presentations of results and figure legends have been improved in the revised manuscript.

Discussion

Reviewer #1:

Page 17 line 3: "The prevalent typing varies..." presented common HAdV types in the United States from 2003-2016. It would be better if authors used the same time period for comparison as the current study. And please mention the most common types globally not just one country like the USA.

[Response] We appreciate the reviewer's helpful suggestion. We have added a corresponding description in the discussion as: "The prevalent virus typing varies between countries and regions. Species B, C and D are the most common adenoviruses worldwide, of which species B and C could cause respiratory infections. For species B, a low prevalence of HAdV-7, HAdV-11 and HAdV-35 was reported globally, however, it is high prevalence for HAdV-35 in some counties from Africa with a positive detection rate of about 20% among HIV-infected patients, and a high prevalence of HAdV-7 was reported in China, United States and Belgium. For species C, HAdV-5 was the widely distributed species, and HAdV-2 usually had a high positive detection rate among healthy individuals and HIV-infected patients in China and developed countries[5]". (Page 24, Line 690–704)

Reference

Reviewer #1: Please add journal issue after volume number. [Response] Thanks. Done as suggested. Reference order could have been reported by year, but it looks fine this way. [Response] Thanks. We have revised the order of references according to the year of publication (Data in S4 File).

Minor issues

Reviewer #1: There is no line number after page 10. [Response] Thanks. Done as suggested.

Page 11, first paragraph line 5: rat \Diamond rate [Response] Many thanks for the reviewer's correction. We have made this correction as suggested.

Reviewer #2: The discussion is correct, with updated bibliography. The results support the discussion and the conclusion reached by the authors. The limitations of the study are clearly stated in the discussion. [Response] Thanks for the reviewer's positive comments.

Reviewer #3: The study discusses the analyses performed and its findings, comparing with studies from some other countries. I suggest including a discussion about mortality associated with HAdV infection, comparing findings of the study (0.03 mortality) with other studies, for example the study by Pscheidt et al. (2020 https://doi.org/10.1002/rmv.2189) that found 3% fatalities among patients hospitalized with severe respiratory infection and who were HAdV-positive. [Response] Many thanks for the reviewer's helpful suggestions. We have supplemented the discussion about the mortality associated with HAdV infection, comparing findings of our study with other studies as: "In our study, the mortality rate of adenovirus infection in patients with respiratory infections was about 0.03%, while a study in Rio Grande Do Sul, Brazil showed a higher mortality rate (3%) among hospitalized patients with severe acute respiratory infection, which might be caused by a lower proportion of patients with severe respiratory infection in our study[13]." (Page 24, Line 678–682)

Summary and General Comments

Reviewer #1: The manuscript "Human infection with respiratory adenovirus in China: a systematic review and meta-analysis" is a review of 950 articles that describes Human adenovirus (HAdV) prevalence, predominant types, clinical manifestation among different age groups and settings, national wide. The objective is interesting, although it needs some revisions before acceptance.

[Response] We appreciate the reviewer's positive comments and helpful suggestions.

Reviewer #2: The manuscript entitled "Human infection with respiratory adenovirus in China: a systematic review and meta-analysis", authored by Mei-Chen Liu et al, described the epidemiological and clinical features of HAdV infections in China, from January 2009 to March 2021. In addition, the genetic and epidemiological characteristics of HAdVs were investigated.

I want to emphasize that the work is very well written and concisely covers all the epidemiological characteristics of HAdV respiratory infections.

The work carried out is a very important contribution to the knowledge of the classical and molecular epidemiology of HAdV in China and also provides valuable information worldwide.

[Response] Many thanks for the reviewer's positive comments.

Reviewer #3: The study is interesting and is worth publication, however thorough English revision is necessary. I recommend revision by a native English speaker. Main comments and corrections were made in the pdf file, attached.

[Response] Many thanks for the reviewer's positive comments and corrections. We have a senior author with fluent English check the language carefully. Revised Article with Changes Highlighted

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