Hilla University College Journal For Medical Science

Volume 2 | Issue 4 Article 4

2024

Evaluation of Foot and Mouth Disease (coxsackie virus) Infections among Sheep, Goats and Humans in Baquba District/ Diyala Iraq

Safa Ibrahim Jaber
College of Health and Medical Techniques, Middle Technical University Baghdad, Iraq,
safa.ibrahim@mtu.edu.iq

How to Cite This Article

Jaber, Safa Ibrahim (2024) "Evaluation of Foot and Mouth Disease (coxsackie virus) Infections among Sheep, Goats and Humans in Baquba District/Diyala Iraq," *Hilla University College Journal For Medical Science*: Vol. 2: Iss. 4, Article 4.
DOI: https://doi.org/10.62445/2958-4515.1036

ORIGINAL STUDY

Hilla Univ Coll J Med Sci

Evaluation of Foot and Mouth Disease (coxsackie virus) Infections among Sheep, Goats and Humans in Baquba District/Diyala Iraq

Safa Ibrahim Jaber

College of Health and Medical Techniques, Middle Technical University Baghdad, Iraq

Abstract

Foot-and-mouth disease (Coxsackievirus) is a serious infection that affects animals such as sheep, goats, and cattle. The study was conducted from 1st February to 1st July 2024 / in Baquba district. The results showed that the prevalence rate of Coxsackievirus infections was the highest 11 (73.3) in the age group (1–9) years. The Anti-Human Coxsackievirus IgM showed a variance value of (52.315) with highly significant changes (P < 0.01). The Anti-Human Coxsackievirus IgG showed a variance value of (20.603) with highly significant change (P < 0.01). The Anti-Sheep Coxsackievirus IgM showed a variance value of (29.687) with highly significant changes (P < 0.01). The Anti-sheep Coxsackievirus IgG showed a variance value of (39.479) with highly significant change (P < 0.01). Furthermore, the Anti-Goat Coxsackievirus IgM showed a variance value of (21.429) with highly significant change (P < 0.01), and the Anti-Goat Coxsackievirus IgG showed a variance value of (26.613) with highly significant change. The results also showed a weak negative correlation (r = 1, −.011, .142) between the human Coxsackievirus and (sheep, goat) Coxsackievirus type in regard to IgM levels respectively, and these correlations were non-significant (p = 0, .507, .954) respectively. The results of this study reported a weak positive correlation (r = .126, .310, −.014) between the levels of Human-IgG Coxsackievirus and (Sheep, Goats) IgG respectively (P = .507, .954, .940), with statistically non-significant differences. The Anti-Cattle Coxsackievirus IgM concentration was 0.0% and Specificity 43.3% at a Cut-off <1.62, but he Anti-sheep concentration IgG was 0.0% and Specificity 43.3% in Cut-off <0.96. In addition, the Anti-Goat Coxsackievirus IgM concentration was 0.0% and Specificity 36.7% at Cut-off <1.22, and the Anti-Goat concentration IgG concentration was 0.0% and Specificity 10.0% at a Cut off <0.61.

Keywords: Coxsackie virus, Cattle, Goats, Foot and Mouth Disease, Iraq

1. Introduction

Foot-and-mouth disease (FMD) or hoof-and-mouth disease (HMD) is an infectious and sometimes fatal viral disease that affects cloven-hoofed animals, including domestic and wild bovids. The virus causes a high fever lasting two to six days, followed by blisters inside the mouth and near the hoof that may rupture and cause lameness [1].

Humans can be infected with FMD through contact with infected animals, but this is extremely rare. Some cases were caused by laboratory accidents. Because the virus that causes FMD is sensitive to stomach acid, it cannot spread to humans via consumption of infected meat, except in the mouth before the meat is swallowed [2]. Symptoms of FMD in humans include malaise, fever, vomiting, red ulcerative lesions (surface-eroding damaged spots) of the oral tissues, and sometimes vesicular lesions (small blisters) of the skin. According to a newspaper report, FMD killed two children in England in 1884, supposedly due to infected milk [3].

The Foot and mouth disease is included in the Office International des Epizooties (OIE) list of diseases i.e. (OIE Animal Health Code, OIE Bulletin), which indicates that it is a communicable disease and is of a

Received 30 September 2024; accepted 8 October 2024.
Available online 30 December 2024

E-mail address: safa.Ibrahim@mtu.edu.iq (S. I. Jaber).

https://doi.org/10.62445/2958-4515.1036

socio-economic significance in certain countries and significantly affects international trade [4]. The disease is capable of spreading quickly via air or through direct or indirect contact with an infected animal or a material [5]. The major mode of its transmission is by virus particle inhalation via direct contact with the breath of an acutely-infected animal [6].

The disease may also be transmitted indirectly through contaminated environments when foot-and-mouth disease virus (FMDV) can live for long periods under favorable circumstances [7]. A temperature below 50° C, relative humidity >55% and a neutral pH are ideal circumstances for the virus to survive [8]. It has been observed that airborne transmission is also involved in the disease transmission over both long distances (regarded as up to 50 km over land and 200 km over water) and short distances (within a premise and a neighboring premise within 2 km proximities) [4]. Although airborne transmission is extensively studied for (FMDV), there is still a gap in our information on the practical methods for controlling FMD and on how modern applications, instrumentation, and modeling can help our understanding of airborne FMD transmission. This study aimed to revisit our current knowledge and identify gaps that can directly inform and aid future studies in this area [9].

The highly infectious viral hand, foot, and mouth disease (HFMD) causes blister-like rashes on a child's feet and hands and painful sores in their mouth. Babies and children <5 years old are most frequently affected by the disease. The HFMD disease is usually mild and disappears on its own within (7–10) days. The single-stranded RNA virus (Genus *Aphthovirus*, family Picornaviridae) causes foot-and-mouth disease, which affects cloven-hoofed animals [10]. Since FMDV has no external membrane, it is destroyed quickly in circumstances of pH <5.0 and pH >11.0. The viability of the virus is drastically reduced when it is exposed to a relative humidity of ≤60% or when it is placed at 56°C for 30 minutes. Seven FMDV types are present: A, O, C, SAT1, 2, 3 as well as Asia 1 [6.11]. The characterization of individual virus strains has been enabled by the development of molecular methods [12]. This study aimed to evaluate the foot and mouth disease among cattle, goats and humans in Baquba district, Diyala, Iraq.

2. Materials and methods

2.1. Study design and subjects

In the current study, blood specimens (5 ml) were taken from 30 people infected with Coxsackievirus residing in Transient Diseases Hospital / Baquba, Diyala lraq. Also, blood specimens were taken from 30 sheep and 30 goats at the veterinary medical clinics in Baquba District. In addition, 15 blood specimens were taken from healthy persons.

Also, 15 specimens were taken from healthy sheep and 15 specimens from healthy goats as controls during the period from 1st February to 1st July 2024 in Baquba District, Diyala, Iraq. The ELISA kit from MyBioSorces company was used to estimate the Coxsackievirus IgG and IgM in the specimens.

Table 1. Prevalence of Coxsackievirus according to ages and Residency.

Age groups	Patients No (%)	Control No (%) Age groups	
(1–9)	11 (73.3)	(12–19)	11 (73.3)
(10–29)	3 (20.0)	(20–29)	3 (20.0)
(30≥40)	1 (6.7)	(30≥40)	1 (6.7)
Total	15 (100.0)	Total	15 (100.0)
Residence	No (%)	No (%)	
Urban	6 (25.0)	16 (53.3)	
Rural	24 (75.0)	14 (46.7)	
Total	30 (100.0)	30 (100.0)	

2.2. Statistical analysis

Statistical analysis was carried out using Statistical Package for the Social Sciences (SPSS) version 23.0 (SPSS, IBM Company, Chicago, IL 60606, USA) which included the t-test. The ($P < 0.05$) was considered significant.

3. Results

The results in (Table 1) showed that the prevalence rate of Coxsackievirus infections was the highest at 11 (73.3%) in the age group (1–9) years, then 3 (20.0%) in the age group (10–29) years followed by 1 (6.7%) in the age group (30–≥40) years, while the distribution of Coxsackievirus infections in the rural area was 24 (80%) and 6 (20%) the urban area.

The range of Human Coxsackievirus IgM was 5.42 with Minimum statistical 1.08 and Maximum statistical 6.50 compared to the healthy individual whose range was .74, with Minimum statistical .01 and Maximum .75. Also, the range of Human Coxsackievirus IgG was 2.15 with Minimum statistical .25 and Maximum statistical 2.40 compared to the healthy individuals whose range was .99, with Minimum statistical .01 and Maximum 1.00. However, the range of sheep Coxsackievirus IgM was5.49 with Minimum statistical 1.01 and Maximum statistical 6.50 compared to the healthy control whose range was .65, with Minimum statistical .01 and Maximum .66, and the range of sheep CCHF IgG was 2.25 with Minimum

Table 2. Descriptive Statistics of Coxsackievirus in Cattle, Goats and Humans.

	Patients			Control		
	Range	Minimum	Maximum	Range	Minimum	Maximum
Human IgM	5.42	1.08	6.50	.74	.01	.75
Human IgG	2.15	.25	2.40	.99	.01	1.00
Cattle IgM	5.49	1.01	6.50	.65	.01	.66
Cattle IgG	2.25	.25	2.50	.65	.01	.66
Goats IgM	3.59	1.01	4.60	.87	.01	.88
Goats IgG	2.40	.10	2.50	.68	.01	.69

statistical .25 and Maximum statistical 2.50 compared to the healthy control.

The results also revealed that the range .65, with Minimum statistical .01and Maximum .66. The range of Goats Coxsackievirus IgM was 3.59 with Minimum statistical 1.01 and Maximum statistical 4.60 compared to the healthy control, while the range was .87, with Minimum statistical .01 and Maximum .88, and the range of Goats Coxsackievirus IgG was 2.40 with Minimum statistical .10 and Maximum statistical 2.50 compared to the healthy control, the range .68, with Minimum statistical .01 and Maximum .69 as shown in (Table 2).

Table 3 illustrates that the Anti-Human Coxsackievirus IgM showed a variance value of (52.315) with highly significant changes ($P < 0.01$). The Anti-Human Coxsackievirus IgG showed a variance value of (20.603) with highly significant change ($P < 0.01$). Also the Anti-sheep Coxsackievirus IgM showed a variance value of (29.687) with highly significant changes ($P < 0.01$). The Anti-sheep Coxsackievirus IgG showed a variance value of (39.479) with highly significant change ($P < 0.01$). Furthermore, the Anti-Goat Coxsackievirus IgM showed a variance value of (21.429) with highly significant change ($P < 0.01$), and the Anti-Goat Coxsackievirus IgG showed a variance value of (26.613) with highly significant change.

The results of this study showed that there were weak negative correlations ($r = 1, -.011, .142$) between the human Coxsackievirus and (sheep, Coat Coxsackievirus type with the levels of IgM respectively) and these correlations were non-significant P-value (0,.507, .954) respectively. The results of this study reported weak positive correlations ($r = .126, .310, -.014$) between the levels of Human-IgG Coxsackievirus and (sheep, Goatt) IgG respectively (P-value = .507, .954, .940), and these correlations were statistically non-significant for the three above-mentioned tests (P-value ≥ 0.05), as shown in (Table 4).

Table 3. Comparison between Anti-Coxsackievirus IgM and Anti Coxsackievirus IgG among Study groups.

Parameters	F	P-Value	C.S.
Human IgM	52.315	.000	P < 0.01 (HS)
Human IgG	20.603	.000	P < 0.01 (HS)
Cattle IgM	29.687	.000	P < 0.01 (HS)
Cattle IgG	39.479	.000	P < 0.01 (HS)
Goats IgM	21.429	.000	P < 0.01 (HS)
Goats IgG	26.613	.000	P < 0.01 (HS)

Results of the ROC test in Table 5 and Fig. 1 revealed that the Sensitivity of Anti-human Coxsackievirus IgM concentration was 0.0% and Specificity 46.7% in a Cut off <1.71. Also, the Sensitivity of Anti-human Coxsackievirus IgG concentration was 0.0% and Specificity 16.7% in Cut off <0.90. The Anti-Cattle Coxsackievirus IgM concentration was 0.0% and Specificity 43.3% in Cut off <1.62. But the Anti-sheep concentration IgG was 0.0% and Specificity 43.3% in Cut off <0.96. In addition, the Anti-Goat Coxsackievirus IgM concentration was 0.0% and Specificity 36.7% in Cut off <1.22, and the Anti-Goat concentration IgG concentration was 0.0% and Specificity 10.0% in Cut off <0.61.

4. Discussion

Coxsackievirus is a risky infection that infects animals like sheep, goats, and humans. The results showed that the prevalence rate of Coxsackievirus infections was the highest at 11 (73.3%) in the age group (1–9) years, then 3 (20.0%) in the age group (10-29) years followed by 1 (6.6%) in the age group (30-≥40) years. These finding agreed with (Kordi *et al.*, 2024), who found that the age group 1–10 years is more affected because children are more susceptible to this virus [13]. The distribution of Coxsackievirus infections in the rural was 24 (80%) and in the urban was 6 (20%), with highly significant variation. Zhu *et al.*, reported that the people of the rural area are the most infected with the Foot and Mouth virus [14]. The variance of Anti-Human Coxsackievirus IgM was (F = 52.315) with highly significant changes, and these results matched with Rodríguez-Habibe *et al.* who showed that the Anti-Human Coxsackievirus IgM should be higher in people in the acute phase of infection with Foot-and-Mouth disease [15].

Table 4. Correlations between Coxsackievirus antibodies among study groups.

		Human IgM	Human IgG	Cattle IgM	Cattle IgG	Coats IgM	Goats IgG
Human IgM	r	1					
	P-Value						
Human IgG	r	.126	1				
	P-Value	.507					
Sheep IgM	r	−.011	−.016	1			
	P-Value	.954	.935				
Cattle IgG	r	.310	.048	.178	1		
	P-Value	.096	.800	.347			
Coats IgM	r	.142	−.153	−.120	.058	1	
	P-Value	.453	.420	.529	.759		
Goats IgG	r	−.014	.061	.114	.095	.020	1
	P-Value	.940	.748	.549	.617	.917	

Table 5. ROC Curve of Anti-CCHF antibodies among study groups.

Test Result Variable(s)	Area	Asymptotic Sig.	Cut point	Sensitivity	Specificity
Human IgM	.000	.000	<1.71	0.0%	46.7%
Human IgG	.013	.000	<0.90	0.0%	16.7%
Cattle IgM	.000	.000	<1.62	0.0%	43.3%
Cattle IgG	.016	.000	<0.96	0.0%	30.0%
Goats IgM	.000	.000	<1.22	0.0%	36.7%
Goats IgG	.032	.000	<0.61	67.0%	10.0%

The variance of Anti-Human Coxsackievirus IgG was (20.603) with highly significant changes. Cui *et al.* reported that the chronic case of infection in Foot-and-Mouth disease is also very high, as is the case of acute infection, because both acute and chronic cases have similar antibody concentrations [16]. The variance of Anti-sheep Coxsackievirus IgM was (29.687) with highly significant changes. Zecconi revealed that

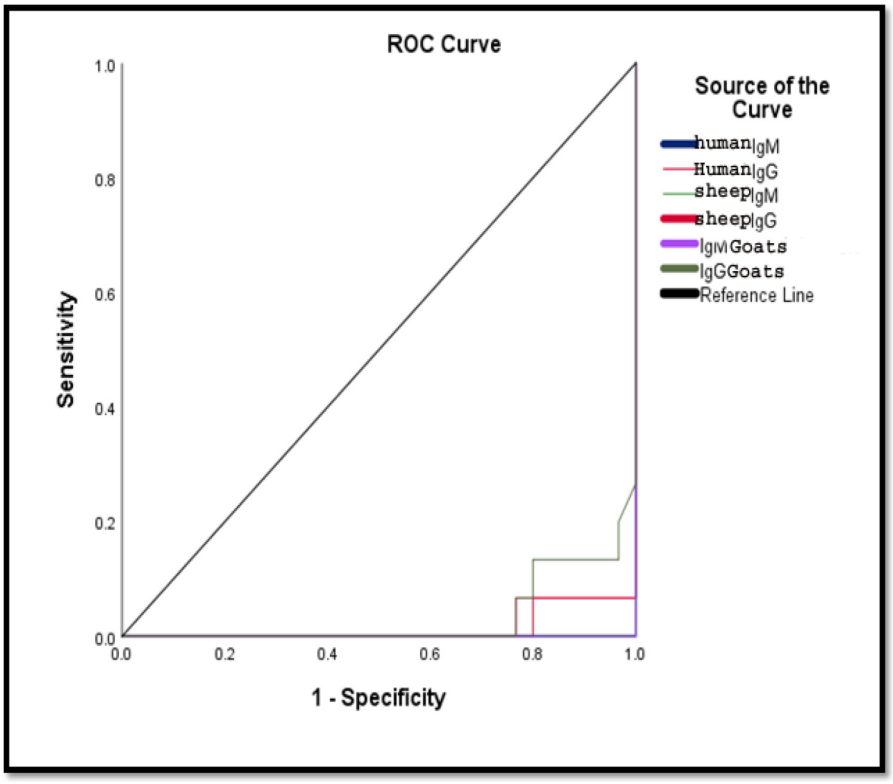

Fig. 1. Roc Curve of Anti-Coxsackievirus antibodies among study groups.

in severe cases of infectious foot and mouth disease in sheep, the antibodies, which are of the IgM type, are at a high level [17].

The variance of Anti-sheep Coxsackievirus IgG showed highly significant changes. Zecconi stated that chronic infections remain high for a long period in these sheep [17]. The variance of Anti-Goat Coxsackievirus IgM showed highly significant change. The variance of Anti-Goats Coxsackievirus IgG showed highly significant change. These findings were in a harmony with (Liu *et al.*, 2016) who showed that both acute infections and chronic infections are high in goats, especially since the incubation period may be long because the diagnosis may not be early in these domestic animals [18].

Furthermore, there were weak negative correlations (r = 1, −.011, .142) between the human Coxsackievirus and (sheep, Coat) Coxsackievirus type with the levels of IgM respectively. These correlations were non-significant P-value (0,.507, .954) respectively. Aslam and Alkheraije found that there is a weak or weakly positive relationship between foot infections in humans and sheep, as well as between humans and goats P-value ≥0.05 [19]. Also Ullah *et al.* proved that there is a weak statistical relationship between infections, whether in humans or animals [20]. According to the results, it was found that there were highly significant differences between the people infected with Coxsackievirus compared to the control groups, and they were as follows: the Anti-Human Coxsackievirus IgM (F = 52.315), the Anti-Human Coxsackievirus IgG (F = 20.603), the Anti-sheep Coxsackievirus IgM (F = 29.687). The Anti-sheep Coxsackievirus IgG (F = 39.479). Also the Anti-Goats Coxsackievirus IgM (F = 21.429). Furthermore, the Anti-Goats Coxsackievirus IgM (F = 21.429) and the Anti-Goats Coxsackievirus IgG (F = 26.613), P < 0.01 (HS) respectively. These results were inconsistent with Dubie and Negash, who found that there are high levels of antibody concentrations in the acute condition, IgM in humans and animals, with Foot, Hand, and Mouth diseases, and the levels of IgG in the chronic conditions are present in advanced stages [21]. The results of this study were compatible with Das *et al.* who reported that there were highly important differences among animals and human P < 0.01 [22].

5. Conclusion

According to the results, it was found that there were very significant differences between the people infected with Coxsackievirus compared to the control groups, regarding Anti-Human Coxsackievirus IgM, Anti-Human Coxsackievirus IgG, Anti-sheep Coxsackievirus IgM, Anti-sheep Coxsackievirus IgG, Anti-Goat Coxsackievirus IgM, and Anti-Goat Coxsackievirus IgG.

Ethical issue

The ethical approval for this study is according to 4/12 in 7/8/2024 and the study approved by scientific committee in the college.

Financial funding

The research done by personal fund.

Conflicts of interest

None.

References

1. Kim H, Choi K. Investigation of disinfectants for foot-and-mouth disease in the Republic of Korea, Fenner's Veterinary Virology (Fifth Edition). 2020.
2. Capella GL. Foot and mouth disease in human beings. The Lancet. 2001;358(9290):1374.
3. López A. Control of foot and mouth disease: the experience of the Americas. Revue Scientifiqueet Technique (International Office of Epizootics). 2002;21(3):695–8.
4. Kharatyan S, Sargsyan K, Elbakyan H, *et al.* Evaluation of the effectiveness of foot-and-mouth disease vaccination of animals in the buffer zone of the Republic of Armenia in 2016–2020. BMC Vet Res. 2023;19:176. doi: 10.1186/s12917-023-03728-8.
5. Gordon LG. A scoping review of foot-and-mouth disease risk, based on spatial and spatio-temporal analysis of outbreaks in endemic settings. Wily Journal 2022. doi: 10.1111/tbed.14769.
6. Brown E Nelson N Gubbins S, Colenutt C. Airborne Transmission of Foot-and-Mouth Disease Virus: A Review of Past and Present Perspectives. Viruses. 2022;14(5):1009. doi: 10.3390/v14051009.
7. Ellis J, Brown E, Colenutt C, *et al.* Inferring transmission routes for foot-and-mouth disease virus within a cattle herd using approximate Bayesian computation. Epidemics. 2024;46:100740.
8. Bartley LM, Donnelly CA, Anderson RM. Review of foot-and-mouth disease virus survival in animal excretions and on fomites. The Veterinary Record. 2002;151(22):667–9. doi: 10.1136/vr.151.22.667.
9. Brown E, Nelson N, Gubbins S, Colenutt C. Airborne transmission of foot-and-mouth disease virus: a review of past and present perspectives. Viruses. 2022;14(5):1009. doi: 10.3390/v14051009.
10. Hwang SY, Shin SH, Kim HM, *et al.* Evaluation of Vaccine Strains Developed for Efficient, Broad-Range Protection against Foot-and-Mouth Disease Type O. Vaccines. 2023;11(2):271. doi: https://doi.org/10.3390/vaccines11020271.
11. Caridi F, Vázquez-Calvo A, Sobrino F. The pH Stability of Foot-and-Mouth Disease Virus Particles Is Modulated by Residues Located at the Pentameric Interface and in the N Terminus of VP1. J Virol. 2015;89(10):5633–5642. doi: 10.1128/JVI.03358-14.
12. Bandaw T, Gebremeskel HF, Muluneh A, *et al.* Seroprevalence and molecular detection of foot and mouth disease virus in cattle in selected districts of Wolaita Zone, Southern Ethiopia. Scientific Reports. 2024;14, Article number: 7929.
13. Kordi R, Chang J, Hicar MD. Seasonal Testing, Results, and Effect of the Pandemic on Coxsackievirus Serum Studies. Microorganisms. 2024;12(2):367. doi: 10.3390microorganisms12020367.

14. Zhu P, Ji W, Li D, *et al.* Current status of hand-foot-and-mouth disease. J Biomed Sci. 2023;30:15. doi: 10.1186/s12929-023-00908-4.
15. Rodríguez-Habibe I, Celis-Giraldo C, Patarroyo ME. *et al.* A Comprehensive Review of the Immunological Response against Foot-and-Mouth Disease Virus Infection and Its Evasion Mechanisms. Vaccines (Basel). 2020;8(4):764. doi: 10.3390/vaccines8040764.
16. Cui X, Wang Y, Maqbool B, *et al.* Early IgG Response to Foot and Mouth Disease Vaccine Formulated with a Vegetable Oil Adjuvant. Vaccines (Basel). 2019;7(4):143. doi: 10.3390/vaccines7040143.
17. Zecconi A. Features in Sheep with IgG and IgM Antibodies against *Borrelia burgdorferi sensu lato*. Pathogens. 2021;10(2):164. doi: 10.3390/pathogens10020164.
18. Liu D, Xu L, Zhu R, *et al.* Development of an efficient neutralization assay for Coxsackievirus A10. Appl Microbiol Biotechnol. Springer Link J. 2019;103:1931–1938.
19. Aslam M, Alkheraije KA. The prevalence of foot-and-mouth disease in Asia. Front Vet Sci. 2023;10:1201578. doi: 10.3389/fvets.2023.1201578.
20. Ullah M, Li Y, Munib K, *et al.* Sero-Epidemiology and Associated Risk Factors of Foot-and-Mouth Disease (FMD) in the Northern Border Regions of Pakistan. Vet. Sci. 2023;10(5):356. doi: https://doi.org/10.3390/vetsci10050356.
21. Dubie T, Negash W. Seroprevalence of bovine foot and mouth disease (FMD) and its associated risk factors in selected districts of Afar region, Ethiopia. Vet Med Sci. 2021;7(5):1678–1687. doi: 10.1002/vms3.574.
22. Das S, Pal S, Rautaray SS, *et al.* Estimation of foot-and-mouth disease virus sero-prevalence rates using novel computational approach for the susceptible bovine population in India during the period 2008–2021. Scientific Report. 2023;13:22583. doi: 10.1038/s41598-023-48459-w.