

EPIDEMIOLOGICAL PREDICTION OF INFECTION CAUSED BY SOME NON-POLIOENTEROVIRUSES OF COXSACKIE GROUP B IN THE CHILD POPULATION OF AZERBAIJAN IN 2015-2024

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2015-2024 ЙИЛЛАРДА ОЗАРБАЙЖОН БОЛАЛАР АҲОЛИСИДА БАЪЗИ ПОЛИОЭНТЕРОВИРУСЛАР БЎЛМАГАН В ГУРУҲ КОКСАКИ БИЛАН ЧАҚИРИЛГАН ИНФЕКЦИЯЛАРНИНГ ЭПИДЕМИОЛОГИК ПРОГНОЗИ

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ЭПИДЕМИОЛОГИЧЕСКИЙ ПРОГНОЗ ИНФЕКЦИИ, ВЫЗВАННОЙ НЕКОТОРЫМИ НЕПОЛИОЭНТЕРОВИРУСАМИ КОКСАКИ ГРУППЫ В, У ДЕТСКОГО НАСЕЛЕНИЯ АЗЕРБАЙДЖАНА В 2015-2024 гг.

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Резюме. Ушбу мақола 2015-2024 йилларда Озарбайжон болалар аҳолисида баъзи полиоэнтеровируслар бўлмаган В гуруҳ коксаки билан чақирилган инфекцияларнинг эпидемиологик прогнозига бағишланган.

Калит сўзлар: неполиоэнтеровируслар, В гуруҳ Коксаки вируслари, эпидемиологик прогноз, болалар.

Abstract. This article is devoted to the epidemiological prognosis of infection caused by non-polioenterovirus coxsackievirus group b in the child population of Azerbaijan in 2015-2024.

Key words: non-polioenteroviruses, Coxsackie virus group B, epidemiological prediction, children.

After the abolition of poliomyelitis, a dangerous enterovirus infection in a number of countries of the world in the late XX and early XXI centuries, the tendency to activation of other non-polioenterovirus infections is notable for the fact that in many countries this infection is periodically found in the form of epidemic outbreaks [1-3, 7, 10, 11, 14].

Today, the etiological role of various serotypes of non-polioenteroviruses in occurrence of aseptic meningitis, encephalitis, myocarditis, pericarditis, diseases of upper respiratory tract, digestive system, urogenital system, eye, some somatic pathologies, intrauterine, persistent and chronic infections has been proved [4-6, 8, 9, 12, 13, 15-18].

The purpose of this research work is to predict the epidemiology of infection caused by some non-polioenteroviruses of Coxsackie Group B in the child population of Azerbaijan in 2015-2024.

Research materials and methods.

In the research work, the period of some non-polioenteroviruses belonging to Coxsackie Group B -

KB3, KB4 and KB5 serotypes was confirmed by polymerase chain reaction among the child population in Baku during 2006-2010

The research work was affirmed by design - descriptively; by method - clinically; by volume - through generalization; by type - scientifically; by material - retrospectively and prospectively; by term - transversely; by place - laboratorially.

The indicators obtained during the research work were statistically developed on the basis of modern recommendations. Statistical analysis was carried out in MS EXCEL-19 [22] and IBM Statistics SPSS-29 [20] using discriminant and regression methods.

The indicators obtained during the study were statistically developed on the basis of modern recommendations. Statistical analysis was carried out in MS EXCEL-19 [2019] and IBM Statistics SPSS-20 programs [21] using discriminant and regression methods [19].

Regions: according to the application year - by years, 5-year terms; according to passport parameters - by gender, age groups; according to the application period parameters - by the application month, season; according to regional parameters - the by center and regions.

For the purpose of the description of quality indicators, the share amount of intensity indicators for each division (%) and the standard error of these percentages ($\pm mp$), extensibility indicators (for 100,000 population) and their corresponding errors were calculated.

C2-Pirson and T-Studio-Bonferroni criteria were used for comparison of indicators.

Regression analysis was carried out on the basis of previous 15 years (2000-2014) information on extensibility indicators to build the forecast for the next 10 years (2015-2024). Regression analysis was based on simple-linear, polynomial, logarithmic and ARIMA (0,0,0) and ARIMA (1,0,0) (autocorrelation) models. Within the regression equations, the regression equation corresponding to the greatest value of approximation accuracy was evaluated and the rectification interval of 95% of the obtained regression formula was evaluated and the extrusions were statistically evaluated through the Student t-criterion.

The research findings and discussion.

A regression analysis used to predict the prevalence of some nonpolioenteroviruses in Coxsackie Group B for 2015-2024 would show that the incidence rate was on average 100,000 to every 1,152 people. While the 95% confidence interval increased from 2015 (0-6,059) to 2024 (0-13,171), the model's results were statistically correct ($t=3,061$; $p=0,008$). The aproxia accuracy of the forecast model on factual indicators for previous years was $R^2=0.078$ (fig.1).

Using regression analysis in 2015-2024, it was predicted that the spread of Koksaki B3 serotype in the population of Azerbaijan would be stable for every

100,000 population, averagely 0,550. The 95% confidence interval increased from the boundary of 2015 (0-3,225) to the boundary of 2024 (0-7,001), but the results of the model were statistically honest ($t=3,107$; $p=0,008$). The approximation accuracy of the forecast model was $R^2=0.085$ on factual indicators for previous years.

In 2015-2024, it was determined that the prediction of the spread of Coxsackie B4 serotype among the population of Azerbaijan by regression analysis is stable for every

100,000 population on average 0,813. The 95% confidence interval in 2015 and in 2024 was at the 2,163 limit and the results of the model were highly statistically honest ($t=5,016$; $p=0,001$). The approximation accuracy on the actual indicators of the forecast model used for previous years was $R^2=0.0001$.

By the method of regression analysis, the prevalence of Coxsackie B5 serotype among the population in Azerbaijan in 2015-2024 was predicted on average for every 100,000 persons at the level of 0.244 in 2015 and at the level of 0.024 in 2024. While the 95% confidence interval increased from the level of 1,921 in 2015 to the level of 2,650 in 2024, the model's results were statistically exact ($t=4,915$; $p=0,0001$). The approximation accuracy on the actual indicators of the forecast model used for previous years was $R^2=0.344$.

It is known that scientific forecasting implies the possibility of developing an epidemic process among the population over a certain period of time. The ultimate forecasting purpose is not only to say the possibility of occurrence of non-favorable epidemiological situations, but also to plan a complex of pre-emptive measures. Epidemiological forecasting is carried out on the basis of the study and analysis of numerous factors affecting the development of the epidemic process.

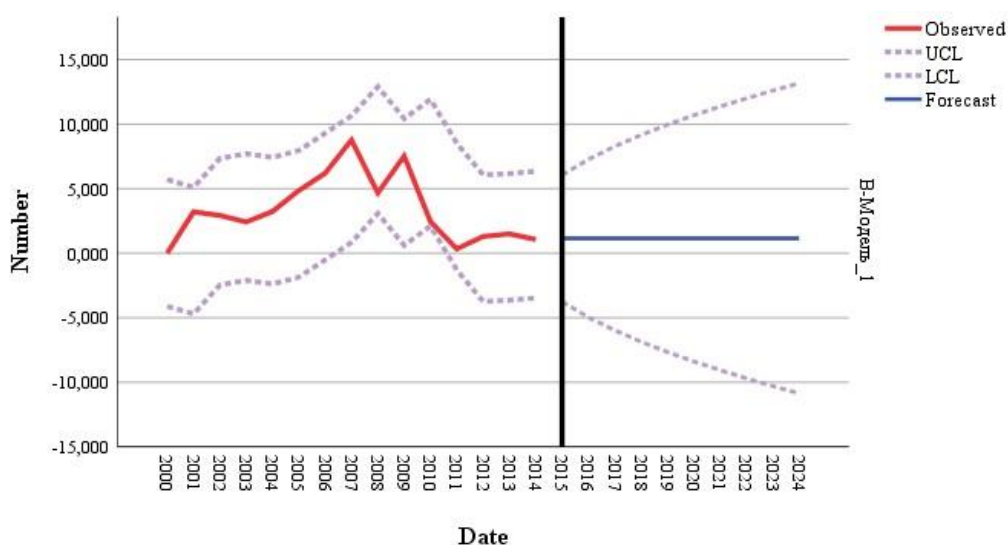


Figure 1. Prognostic model of the spread of some non-polioenteroviruses of Koksaki Group B in the population of the Republic of Azerbaijan in 2015-2024 (for every 100,000 persons)

Table 1. Dissemination of Cocksackie B3 serotype among the population in the Republic of Azerbaijan in 2015-2024

Model Statistics						
Number of Stationary R- Model	Number of Predictors	Model Fit statistics		Ljung -Box Q(18)		
		squared Normalized BIC	Statistics	DF	Sig.	Outliers
B3-Modelğ_1	0	0,085	0,623	0	.	0
Exponential Smoothing Model Parameters						
Model		Estimate	SE	t	Sig.	
B3-Modelğ_1	No Transformation	Alpha (Level) 0,731	0,235	3,107	0,008	

Forecast											
Model		2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
B3-Modelğ_1	Forecast	0,550	0,550	0,550	0,550	0,550	0,550	0,550	0,550	0,550	0,550
	UCL	3,225	3,865	4,399	4,868	5,290	5,678	6,039	6,377	6,697	7,001
	LCL	-2,125	-2,764	-3,299	-3,768	-4,190	-4,578	-4,939	-5,277	-5,597	-5,901

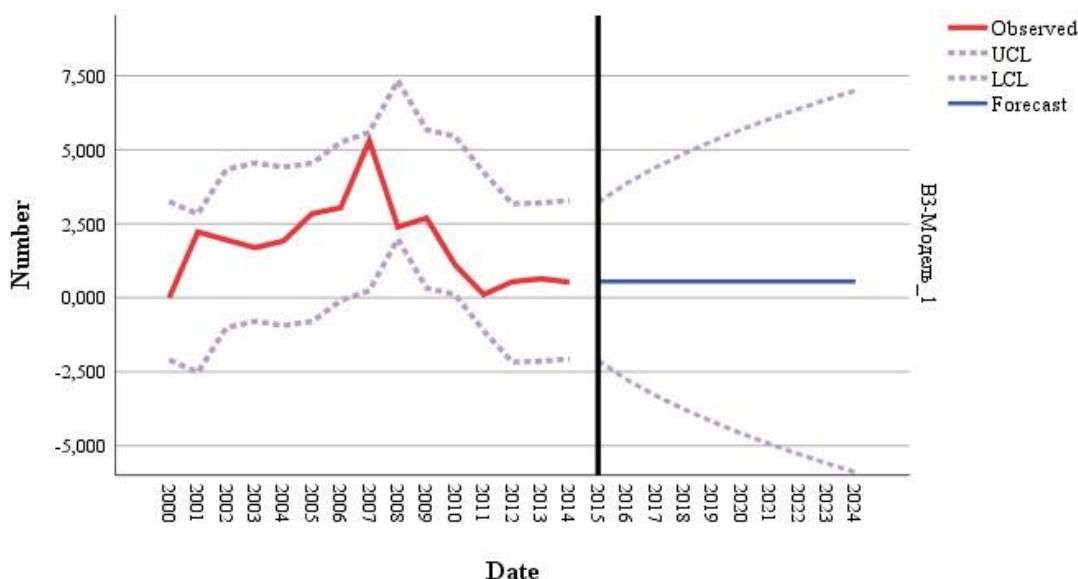


Figure 2. Prognostic model of the spread of Cocksackie B3 serotype among the population of the Republic of Azerbaijan in 2015-2024 (for every 100,000 persons)

At present, sufficient material has been collected on the use of various mathematical methods and approaches to solve epidemiological tasks for the construction of models of the epidemic process. The final result of these studies is, on the one hand, cases of morbidity, and on the other hand, the source of infection is the sensitive organism, etc. it is the determination of dependence between. However, many aspects of forecasting, which include the mathematical epidemiology elements, are still studied little. Thus, the functional dependence between the activity of the epidemic process and the intensity of intestinal viruses detected from environmental objects, especially water bodies, especially during enterovirus infection is not fully opened. Recently, the principles of

"minimal modeling" have attracted attention, which allows us to reflect more significant interactions that the researcher can directly use in his work. K.I. Spynu and etc. reported about a mathematical model to be created to predict serous meningitis morbidity caused by some non-polioenteroviruses, multiple regression analysis with P2R steps.

The results obtained show that the integral indicator (Z) of the spread of Cocksackie B1 virus in water bodies is sufficient to predict short-term incidence of serous meningitis (1988). It should be noted that attempts to determine the dependence between the frequency of morbidity and the detection of intestinal viruses in water bodies have also been made by other researchers.

Table 2. Prevalence of Coxsackie B4 serotype among population in Azerbaijan in 2015-2024
Model Statistics

Model	Model Fit statistics		Ljung -Box Q(18)		Number of Outliers
	Number of Stationary R-Predictors squared	Normalized BIC Statistics	DF	Sig.	
B4-Modelğ_1	0	0,000 -0,750	0	.	0

ARIMA Model Parameters					
	Estimate	SE	t	Sig.	
B4-Modelğ_1	B4 No Transformation Constant	0,813	0,162	5,016	0,000

Forecast										
Model	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
B4-Modelğ_1	Forecast	0,813	0,813	0,813	0,813	0,813	0,813	0,813	0,813	0,813
	UCL	2,160	2,160	2,160	2,160	2,160	2,160	2,160	2,160	2,160
	LCL	-0,533	-0,533	-0,533	-0,533	-0,533	-0,533	-0,533	-0,533	-0,533

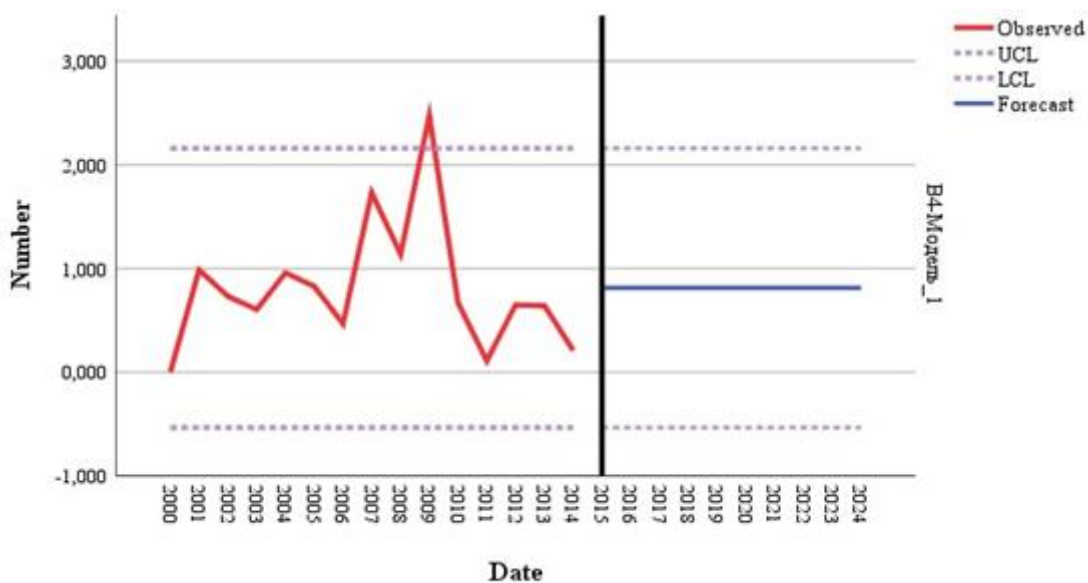


Figure 3. Prognostic model of the spread of Coxsackie B4 serotype among the population of Azerbaijan in 2015-2024 (for every 100,000 persons)

However, at the same time, the authors determined only the correlation between individual indicators of morbidity and the prevalence of enteroviruses in the environment, and did not take into account the interaction between them.

In this view, the research carried out by R.A.Dmitriyeva and others is of great scientific and practical interest. In this research work, it was established that there is a direct correlation between the level of hepatitis morbidity in the controlled area and hepatitis A virus circulating in wastewater and indica-

tors of microbial contamination, including water bodies, centralized and decentralized objects [22].

By conducting a number of adequate mathematical calculations, the authors were able to show the correlation between microbiological indicators of drinking water quality and viral hepatitis A, calculate the specific weight of the impact of hygienic factors on the incidence of viral hepatitis A of the population of controlled areas, as well as show the correlation between alternative hygienic indicators and morbidity indicators.

Table 3. The prevalence of Coxsackie B5 serotype in the population of Azerbaijan in 2015-2024
Model Statistics

Model	Model Fit statistics		Ljung -Box Q(18)	
	Number of Stationary R-Predictors squared	Normalized BIC Statistics	DF	Number of Sig. Outliers
B5-Modelğ_1	0	0,344 -0,311	0	.0

ARIMA Model Parameters		
	Estimate	SE
B5-Modelğ_1	B5 No Transformation AR Lag 1	0,771
		0,157
		4,915
		0,000

2024
0,024

Forecast

Model	2015	2016	2017	2018	2019	2020	2021	2022	2023
B5-Modelğ_1 Forecast	0,244	0,188	0,145	0,112	0,086	0,067	0,051	0,040	0,031
UCL	1,921	2,306	2,486	2,576	2,621	2,642	2,651	2,653	2,652
LCL	-1,433	-1,930	-2,196	-2,352	-2,448	-2,509	-2,548	-2,574	-2,591

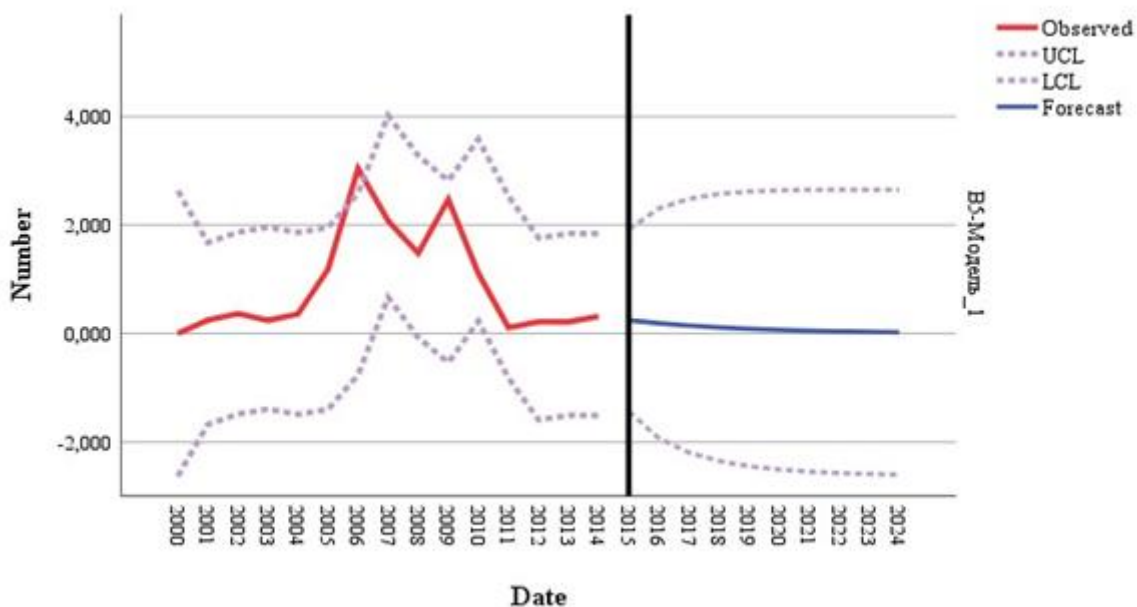


Figure 4. Prognostic model of the spread of Coxsackie B5 serotype in the population of Azerbaijan in 2015-2024 (for every 100,000 persons)

In a number of other published works, the authors attempted to show a direct relationship between the number of viral and the detection of enteroviruses in wastewater. Melnick determined by calculating the amount of virus in faecal and wastewater that a certain type of virus should be 6% virile to detect it in the wastewater of peripheral collectors.

In other experiments carried out by V.A.Kazantseva and S.G.Drozdova with the help of the virus (quandinated variant of poliovirus I) marked by PED, it was possible to determine the re-

moval of this virus by 5-10% of the population for detection of the virus in the wastewater of the central aeration station. It means that by knowing the number of viracists in the period of epidemiological non-satisfactory illusory period it is possible to consider the intensity of the epidemic process.

Some studies have shown that the research of the number of intestinal viruses as a more adequate indicator of the development of the epidemic process is of paramount importance when comparing serous meningitis with the prevalence of enteroviruses in

environmental facilities, especially in order to develop approaches to short-term forecasting of the epidemiological situation [22].

It is known that the improvement of methods for detecting enteroviruses from environmental objects will help to predict the epidemiological situation for serous meningitis or other non-polioenterovirus infection in the short term by applying various mathematical equations, allowing to obtain data on their quantitative and qualitative distribution.

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ЭПИДЕМИОЛОГИЧЕСКИЙ ПРОГНОЗ ИНФЕКЦИИ, ВЫЗВАННОЙ НЕКОТОРЫМИ НЕПОЛИОЭНТЕРОВИРУСАМИ КОКСАКИ ГРУППЫ В, У ДЕТСКОГО НАСЕЛЕНИЯ АЗЕРБАЙДЖАНА В 2015-2024 гг.

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Ибадова Т.И.*

Резюме. Данная статья посвящена эпидемиологическому прогнозу инфекции вызванной неполиоэнтеровирусами коксаки группы в, у детского населения Азербайджана в 2015-2024 гг.

Ключевые слова: неполиоэнтеровирусы, вирус Коксаки группы В, эпидемиологический прогноз, дети.