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EPIDEMIOLOGICAL PREDICTION OF INTESTINAL INFECTION CAUSED BY SOME NON-POLIOENTEROVIRUSES OF COXSACKIE GROUP A AMONG THE POPULATION OF AZERBAIJAN FOR 2015–2024

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Background. *Despite significant achievements in research and diagnostic practice, as well as in the field of Molecular and Biological Technology, the problem of non-polioenterovirus infections is still at the stage of serious research.*

Purpose. *The purpose of the study epidemiological prevalense for some non-polioenteroviruses of Coxsackie group A among the population of Azerbaijan for 2015-2024.*

Materials and methods. *In the study, the period of some non-polioenteroviruses belonging to Coxsackie group A – KA18, KA20 and KA21 serotypes was confirmed by polymerase chain reaction among the population in Baku during 2006-2010.*

The study was affirmed by design-descriptively; by method – clinically; by volume – by generalization; by type – scientifically; by material – retrospectively and prospectively; by term – transversely; by place – clinically.

Statistical analysis was carried out in MS EXCELL-2019 and IBM Statistics SPSS-26 using determinant and regression methods (ARIMA).

Results. *On the basis of results of study the statistical reliability of prognostic model showing prediction of stabil appearing level of intestinal infection caused by some non-polioenteroviruses of Coxsackie group A (KA18, KA20 and KA21) among the child population of Azerbaijan for 2015-2024 have been determined.*

Practical implications. *The results of investigation show the advisability of the using of ARIMA models for epidemiological prediction of intestinal infection caused by Coxsackie group A among the population in Azerbaijan.*

Keywords: *non-polioenteroviruses; Coxsackie virus group A; epidemiological prediction; population of Azerbaijan, intestinal infection*

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This infection is considered to be an uncontrolled one due to insufficient polymorphism of non-polioenterovirus infection, lack of specific dependence on the Serological type of causative agents, the presence of asymptomatic forms, long-term viral infection, and the absence of specific methods of prevention [2; 5; 6; 9; 11].

Despite significant achievements in research and diagnostic practice, as well as in the field of Molecular and Biological Technology, the problem of non-polioenterovirus infections is still at the stage of serious research [4; 7; 8; 10; 12].

In the 1960s in the Republic of Azerbaijan the research was carried out to study the spread of poliomyelitis, its findings being that during paralytic and non-paralytic forms of the disease non-polioenteroviruses B1, B3, B5 and B6 included in the Coxsackie Group are excluded from the patients' intestines [3].

Serological and virological diagnosis of non-polioenterovirus infection has been carried out in the Republic of Azerbaijan since 1999. A few serotypes of non-polioenteroviruses being natural for Coxsackie A and B, ECHO group in children and adults were isolated and identified, and certain epidemiological features of their non-polioenteroviruses were studied [12-16].

The purpose of this study is to predict the epidemiological prevalense for some non-polioenteroviruses of Coxsackie Group A among the population of Azerbaijan for 2015-2024.

Research materials and methods

In the study, the period of some non-polioenteroviruses belonging to Coxsackie Group A - KA18, KA20 and KA21 serotypes was confirmed by polymerase chain reaction among the population in Baku during 2006-2010.

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

The indicators obtained during the study were statistically developed on the basis of modern recommendations. Statistical analysis was carried out in MS EXCELL-19 [19] and IBM Statistics SPSS-26 [18] using discriminant and regression methods.

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), extensibility indicators (for 100,000 population) and their corresponding errors were calculated. χ^2-Pirson and T-Studio-Bonferroni criteria were used for comparison of indicators.

Regression analysis was carried out on the basis of previous information over 15 years (2000-2014) 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 (autocorrelation) models (ARIMA – auto regressive integrated moving averace). 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 Stüdent t-criterion.

The research findings and discussion. Fig. 1 shows the prognostic model of the spread of some non-polioenteroviruses of Coxsackie Group A in the population of the Republic of Azerbaijan in 2015-2024.

The regression analysis allows to predict the prevalence of some non-polioenteroviruses in Coxsackie Group A for every 100.000 population at an average stable level of 0.266. While the 95% confidence interval (EI) increased from 2015 (0-4,626) to 2024 (0-7,774), the model results were statistically correct (t=2,004; p=0,065). At the same time, the forecast model approximation accuracy on actual indicators for previous years was equal to R2=0.307 (Fig. 1).

Table 1.

The prevalence of Coxsackie Group A non-polienteroviruses among the population in Azerbaijan in the period 2015-2024

Model Statistics							
		Model Fitstatistics		Ljung-Box Q(18)			
Model	Number of Predictors	Stationary R-squared	Normalized BIC	Statis-tics	DF	Sig.	Number of Outliers
A-Model_1	0	0,307	1,599	.	0	.	0

Exponential Smoothing Model Parameters						
Model			Estimate	SE	t	Sig.
A-Model_1	NoTransformation	Alpha (Level)	0,467	0,233	2,004	0,065

Forecast											
Model		2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
A-Model_1	Forecast	0,266	0,266	0,266	0,266	0,266	0,266	0,266	0,266	0,266	0,266
	UCL	4,626	5,078	5,492	5,875	6,234	6,572	6,893	7,199	7,492	7,774
	LCL	-4,093	-4,546	-4,959	-5,343	-5,701	-6,039	-6,360	-6,667	-6,960	-7,242

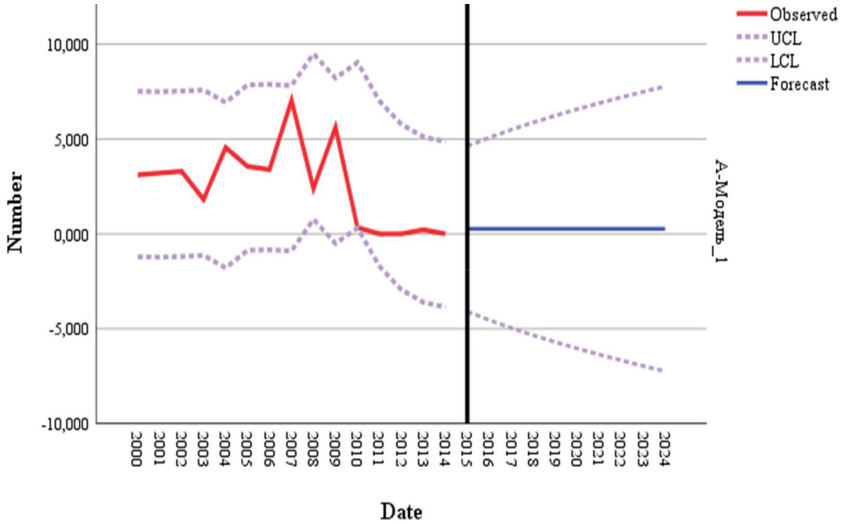

Fig. 1. Prognostic model of the spread of some Coxsackie Group A non-polioenteroviruses in the population of the Republic of Azerbaijan in 2015-2024 (each 100.000 persons)

Table 2.

The spread of the Coxsackie A18 serotype among the population of Azerbaijan in the period 2015-2024

Model Statistics							
	Number of Predictors	Model Fitstatistics		Ljung-Box Q(18)			Number of Outliers
Model		Stationary R-squared	Normalized BIC	Statistics	DF	Sig.	
A18-Model_1	0	0,261	0,304	.	0	.	0

Exponential Smoothing Model Parameters						
Model			Estimate	SE	t	Sig.
A18-Model_1	NoTransformation	Alpha (Level)	0,503	0,235	2,139	0,051

Forecast											
Model		2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
A18-Model_1	Forecast	0,108	0,108	0,108	0,108	0,108	0,108	0,108	0,108	0,108	0,108
	UCL	2,390	2,662	2,909	3,135	3,345	3,543	3,730	3,908	4,077	4,240
	LCL	-2,173	-2,445	-2,692	-2,918	-3,129	-3,326	-3,513	-3,691	-3,861	-4,023

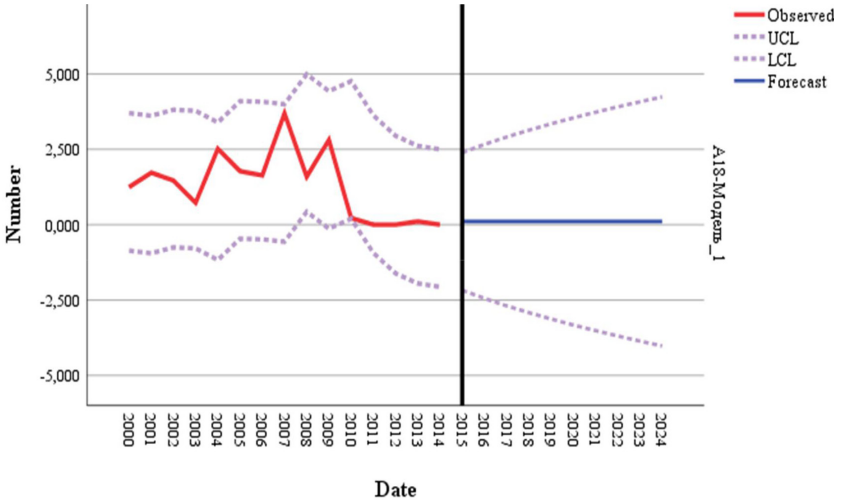

Fig. 2. Prognostic model of the spread of the KA18 serotype in the population of the Republic of Azerbaijan in the period2015-2024 (per 100,000 persons)

The prediction of the prevalence of Coxsackie A18 serotype among the population by regression analysis for 2015-2024 showed that every 100,000 people on average had the stable level of 0,108. While 95% confidence interval increased from 2015 (0-2,390) to 2024 (0-4, 240), the model's results were statistically correct (t=2,139; p=0.051).

The approximation accuracy of the forecast model on factual indicators for previous years was equal to R2=0.261 (Fig. 3).

Table 3.

The spread of the Coxsackie A20 serotype in the population of Azerbaijan in 2015-2024

Model Statistics							
Model	Number of Predictors	Model Fitstatistics		Ljung-Box Q(18)			Number of Outliers
		Stationary R-squared	Normalized BIC	Statistics	DF	Sig.	
A20-Model_1	0	0,358	0,100	.	0	.	0

Exponential Smoothing Model Parameters						
Model			Estimate	SE	t	Sig.
A20-Model_1	NoTransformation	Alpha (Level)	0,366	0,225	1,628	0,126

Forecast											
Model		2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
A20-Model_1	Forecast	0,323	0,323	0,323	0,323	0,323	0,323	0,323	0,323	0,323	0,323
	UCL	2,383	2,517	2,643	2,762	2,876	2,985	3,090	3,191	3,289	3,383
	LCL	-1,737	-1,870	-1,996	-2,116	-2,230	-2,339	-2,444	-2,545	-2,642	-2,737

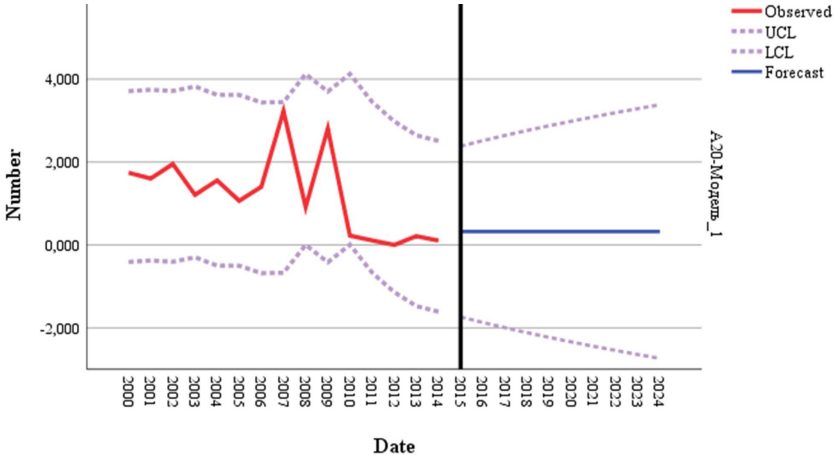

Fig. 3. Prognostic model of the spread of KA-20 serotype in the population of the Republic of Azerbaijan in 2015-2024 (each 100.000 persons)

In 2015-2024, the prognostic model of the distribution of Coxsackie A20 serotype in Azerbaijan made it possible to predict this serotype on average stably at the level of 0.323 per 100.000 people of the population. 95% confidence interval increased from (0-2,383) level in 2015 to (0-3,383) level in 2024, but the results of the model were statistically correct (t=1,628; p=0,126). The approximation accuracy of the forecast model on actual indicators for previous years was equal to R2=0,358 (Fig. 3).

Table 4.

The spread of the Coxsackie A18 serotype among the population of Azerbaijan in the period 2015-2024

Model Statistics							
Model	Number of Predictors	Model Fitstatistics		Ljung-Box Q(18)			Number of Outliers
		Stationary R-squared	Normal-ized BIC	Statis-tics	DF	Sig.	
A21-Model_1	0	0,532	-3,363	.	0	.	1

ARIMA Model Parameters							
				Esti-mate	SE	t	Sig.
A21-Model_1	A21	NoTransformation	Constant	0,093	0,042	2,230	0,044

Outliers						
			Estimate	SE	t	Sig.
A21-Model_1	2005	Innovational	0,618	0,161	3,842	0,002

Forecast											
Model		2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
A21-Model_1	Forecast	0,093	0,093	0,093	0,093	0,093	0,093	0,093	0,093	0,093	0,093
	UCL	0,428	0,428	0,428	0,428	0,428	0,428	0,428	0,428	0,428	0,428
	LCL	-0,243	-0,243	-0,243	-0,243	-0,243	-0,243	-0,243	-0,243	-0,243	-0,243

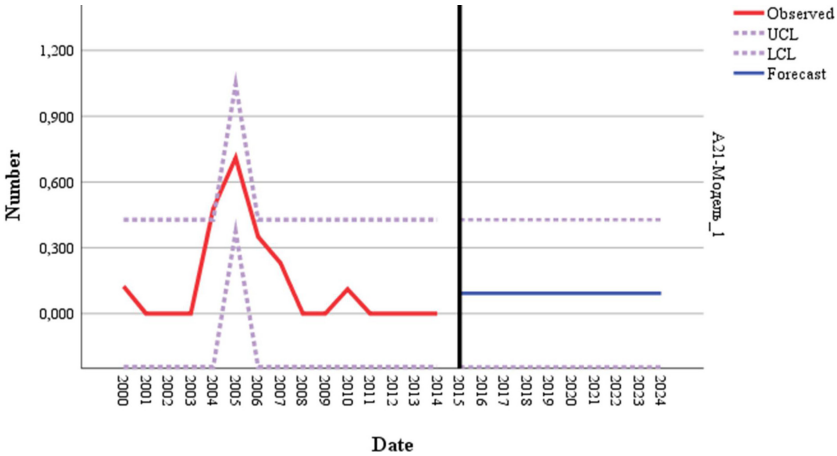

Fig. 4. Prognostic model of the spread of the KA21 serotype in the population of the Republic of Azerbaijan in 2015-2024 (each 100.000 persons)

An analysis of the prognostic model of the spread of the KA2015 serotype among the population in Azerbaijan in 2024-21 showed that on average, the incidence rate is specified to be 100,000 to 0,093 per person. 95% confidence intervals were defined in 2015 (0-0,428) and 2024 (0-0,428), but the results of the model were statistically correct (t=3,842; p=0.002). The approximation accuracy of the forecast model on actual indicators for previous years was R2=0.532 (Fig. 4).

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.

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. However, many aspects of forecasting, which include the mathematical epidemiology elements, have been insufficiently studied. 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 et al. reported 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 Coxsackie B1 virus in water bodies is sufficient to predict short-term incidence of serous meningitis. It should be noted that there have been attempts madeby other researchers to determine the dependence between the frequency of morbidity and the detection of intestinal viruses in water bodies. However 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 [17].

The results of investigation show the advisability of the using of ARIMA models for epidemiological prediction of intestinal infection caused by Coxsackie group A among the population in Azerbaijan.

The authors declare no conflict of interests.
There is no the sponsor supporting.

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