



Evaluation of anthropogenetic predisposition in relation potentiate risk factors in COVID-19 patients

Kristina Virijejić^{1*}, Olivera Milošević-Djordjević^{1,2}, Ljiljana Mirkov³, Jovana Tubić Vukajlović¹,
Aleksandra Marković¹, Marina Radović Jakovljević¹, Darko Grujičić¹

¹University of Kragujevac, Faculty of Science, Department of Biology and Ecology, Kragujevac, Serbia; ²University of Kragujevac, Serbia, Faculty of Medical Sciences, Department of Genetics, Kragujevac, Serbia; ³Health Care Center, Kragujevac, Serbia

*Corresponding author, E-mail: kristina.virijejić28@gmail.com

AIM

The aim of this study was to analyze the homozygous-recessive characteristics (HRCs) in the COVID-19 patients, regarding gender, forms of the disease (milder and severe symptoms), risk factors (RF) such as hypertension, diabetes mellitus, hyperlipidemia, and smoking habits, and distributions of the ABO blood groups compared to healthy controls.

MATERIAL AND METHODS

The study was performed using an HRC test when we analyzed 20 HRCs in a sample of 200 individuals: 100 patients of both genders average age 45.29 ± 14.99 , and 100 controls of both genders average age 46.29 ± 15.38 .

RESULTS

Our results showed that the average value of HRC in patients was significantly higher compared to controls ($X_{hrc}/20P = 7.09 \pm 1.51$, $X_{hrc}/20C = 4.54 \pm 1.83$; $p < 0.001$). As for the form of the disease, average value of HRC in patients with severe symptoms was significantly higher (Fig. 1). In patients, four HRC were more common, and that are continuous frontal hairline, digital index, top joint of the thumb $> 45^\circ$, and mid-phalangeal hair absence (Table 1). Our results indicated that the average value of HRC was significantly different in patients regarding the number and presence of RFs. Binary logistic regression analysis confirmed that patients with 5 or more HRC (cut-off 5) had a 2.5 times higher risk to get sick ($OR = 2.520$; $CI = 1.95-3.27$; $p < 0.0005$) (Fig. 2).

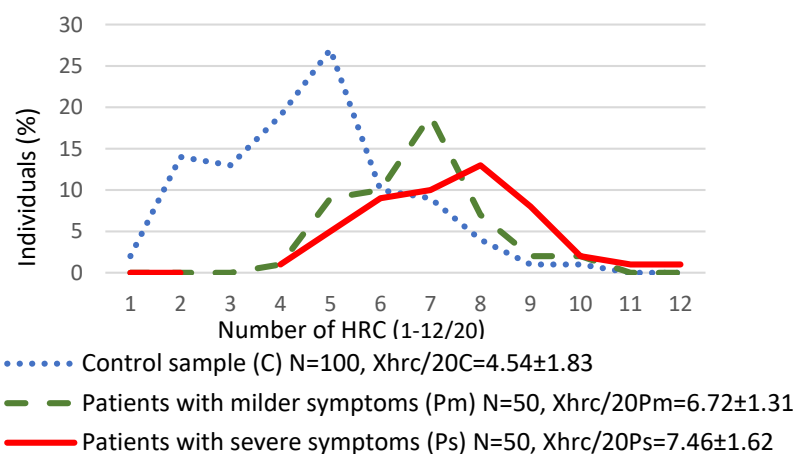


Fig. 1. Distribution of HRC in COVID-19 patients with milder and severe symptoms and the control sample

Table 1. Frequencies of homozygous-recessive characteristics among COVID-19 patients and controls

No.	Homozygous-recessive characteristics	COVID-19 patients; sample; N=100		χ^2
		Total (%)	Control patients; sample; N=100 Total (%)	
1.	Blond hair	15 (15)	17 (17)	0.22
2.	Continuous frontal hairline	70 (70)	39 (39)	24.64*
3.	Straight hair	71 (71)	54 (54)	5.35
4.	Double hair whorl	10 (10)	14 (14)	1.14
5.	Blue eyes	42 (42)	30 (30)	4.80
6.	Attached ear lobe	73 (73)	50 (60)	10.58
7.	Ear without Darwinian notch	50 (50)	29 (29)	15.21
	Inability to			
8.	Longitudinally Tongue Roll	28 (28)	22 (22)	1.28
9.	Guttural "r"	4 (4)	10 (10)	9.00
10.	Daltonisms	2 (2)	0 (0)	2
11.	Right thumb over left thumb (hand claspings)	48 (48)	30 (30)	10.8
12.	Top joint of the thumb $> 45^\circ$	56 (56)	25 (25)	38.44*
13.	Left-handedness	5 (5)	4 (4)	0.2
14.	Digital index	73 (73)	30 (30)	80.03*
15.	Mid-phalangeal hair absence	59 (59)	21 (21)	24.47*
16.	Soft hair	73 (73)	58 (58)	3.08
17.	Retraction of anterior teeth	3 (3)	2 (2)	0.33
18.	Retracted chin	3 (3)	3 (3)	0
19.	Proximal thumb hyperextensibility	4 (4)	9 (9)	6.25
20.	Inability to transversally Tongue Roll	13 (13)	8 (8)	1.23

$\Sigma \chi^2 = 239.05^*$; $df = 19$; $p < 0.001$

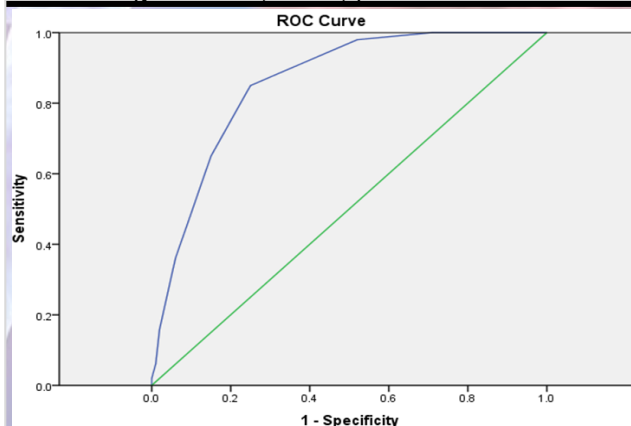


Fig. 2. Receiver operating characteristics (ROC) curve for HRC (The area under the ROC curve (95% CI) was 0.857 (0.806-0.909, $p < 0.0005$))

CONCLUSION

Our results indicate a higher degree of genetic homozygosity in the group of patients in relation to healthy individuals.

ACKNOWLEDGEMENTS

This work was supported by the Serbian Ministry of Education, Science and Technological Development (Agreement No. 451-03-68/2022-14/ 200122).