Original Article
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Medical Journal of the Islamic Republic of Iran (MJIRI)

Med J Islam Repub Iran. 2022 (2 Apr);36.29. https://doi.org/10.47176/mjiri.36.29

Family clustering of SARS-CoV-2 in Qazvin, Northwest of Iran

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Received: 10 Aug 2020 Published: 2 Apr 2022

Abstract

Background: Human infection affected by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has been recognized as a global health concern. We report the epidemiological and clinical characteristics of patients with a familial cluster of SARS-CoV-2 from Qazvin province (located in the northwest of Iran).

Methods: In this cross-sectional study, we enrolled 332 hospitalized patients that were confirmed SARS-CoV-2 diseases with laboratory-based (PT-PCR) test in Qazvin province, Iran. Having family infection transmission and subsequently, family clustering of SARS-COV-2 disease was assessed with the Generalized Estimating Equation model in patients.

Results: Crude odds ratio estimates of creating family clustering of SARS-CoV-2 infection was 0.47 times [95% CI: 0.23, 0.98, p=0.045] less for female compared to the males; 2.26 [95% CI: 1.11, 4.58, p=0.024] and 2.69 [95% CI: 1.47, 4.93, p=0.001] for SARS-CoV-2 patients that had digestive and muscle pain in comparison with those did not this mentioned symptoms, respectively. 1.52 [95% CI: 1.05, 2.23, p=0.024] for patients with a longer hospitalization compared with patients that had shorter duration of hospitalization and adjusted odds ratio estimates were 2.13 [95% CI: 1.12, 4.03, p=0.020] for patients who receive public health services in comparison those did not receive public health services.

Conclusion: Our findings confirm the person-to-person transmission of this novel coronavirus in family settings and hospitals, and the reports of infected travelers in other geographical regions. Major gaps in our knowledge about the potential factors in creating family clustering of SARS-CoV-2 infection, epidemiology, duration of human transmission and etc. need fulfillment by future studies.

Keywords: Epidemiology, SARS-CoV-2, COVID-19, Family Clustering, Close Contacts, Iran

Conflicts of Interest: None declared
Funding: The present study was funded by the Qazvin University of Medical Sciences.

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Cite this article as: Hosseinkhani Z, Foroozanfar Z, Zamanian M, Moradzadeh R, Ghandian A, Najari H, Mobaraki K, Ahmadzadeh J, Bagheri H. Family clustering of SARS-CoV-2 in Qazvin, Northwest of Iran *Med J Islam Repub Iran.* 2022 (2 Apr);36:29. https://doi.org/10.47176/mjiri.36.29

Introduction

Since the end of December 2019, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was initially reported in Wuhan City, China (1). In January 2020, SARS-CoV-2 was declared to be a global health emergency by the World Health Organization (WHO) (2). Until August 5, 2020, 18,727,013 confirmed cases and 704,783 deaths of 215 counters had been documented globally (3). Iran confirmed the first case of SARS-CoV-2 in February 2020 in Qom. Currently, 314,786 confirmed case and 17,617 deaths owing to SARS-CoV-2 have been reported

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↑What is "already known" in this topic:
Family clusters with SARS-CoV-2 cases have been confirmed and person-to-person transmission in family settings recognized as a serious threat to public health.

→What this article adds:
This study showed the important factors affecting family clustering among patients of SARS-CoV-2 include receiving government health services, days of hospitalization, and digestive and muscle pain symptoms.

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[DOI: 10.47176/mjiri.36.29]

in Iran (4).

The incubation period of SARS-CoV-2 is reported 2 to 14 days, and in most patients´ symptoms appear within 11.5 days. However, this period may be longer in some patients. People who have been in close contact (contacts of 15 min or more) with confirmed laboratory patients of SARS-CoV-2 should be quarantined for two weeks after the last time that was exposed to the patient (5, 6). Also, people with suspected, probable, or confirmed cases of infection need to be isolated. To make quarantine and isolation to be effective, it is important to know the infectivity of SARS-CoV-2 during the incubation period (7). The disease transmission during the incubation period in SARS-CoV-2 is a challenge for controlling these diseases which can cause family clusters (8).

Family clusters with SARS-CoV-2 cases have been confirmed and person-to-person transmission has been successively reported globally in a hospital and family setting (9). According to the results of other studies, a familial cluster of patients with SARS-CoV-2 had close contact with an asymptomatic family member who was diagnosed and developed symptoms later(8). A study conducted by Jasper Fuk-Woo Chan et al. reported that older age was associated with more systemic symptoms in a family cluster of SARS-CoV-2 (9).

Identifying close contacts and quarantine of family members and close contacts could play an important role in reducing disease transmission and controlling these diseases (9,10). Since the person-to-person transmission in family settings and family clusters is a serious threats to public health (9, 11), determining the factors associated with it in covid-19 disease can help identify high-risk groups for preventive and educational measures in these people. In the current study, we report the epidemiological and clinical findings of patients with a familial cluster of SARS-COV-2 and some of the factors associated with clustering.

Methods

Study Design and Participate

In this cross-sectional study, we enrolled hospitalized in Qazvin province, Iran. We called 322 patients who were hospitalized in Qazvin province hospitals duration SARS-COV-2 epidemic. Inclusion criteria were residence in Qazvin province. All patients with confirmed SARS-CoV-2 diseases with laboratory-based (PT-PCR) tests were included. Exclusion criteria were patients with suspected PT-PCR test and having no inclining to participate in the study.

Data Collection and Tool

Having family infection transmission and subsequently, family clustering of SARS-COV-2 disease was assessed. Besides, we assessed the symptoms of the patients (fever, chill, muscle pain, shortness of breath, dry cough, and digestive disorders), days of hospitalization and family members to identify patterns of infection transmission in family clusters. Traveling history from 14 days before symptoms onset, the number of family members with SARS-CoV-2 infectious, smoking, hookah consumption, history of chronic disease (cancer, diabetes, immunodeficiency, asthma and cardiovascular disease), and receive government health services were assessed. The most important government health services consist of phone tracking with the health workers, home visiting, using recovery room by the patient after discharge from hospital and government disinfection of neighborhood, streets and crowed centers. The interviewer asked the people about the beneficiaries of these services. Patients with the benefit of at least one of the government health services were considered as a consumer. We used a brief checklist for assessing patients´ information.

We also asked about patients´ demographic characteristics such as gender, age, education, job, residence, number of family members. In this study, we obtained the patients' phone numbers from the health center of Qazvin province.

Statistical analysis

Demographic information and health characteristic of the patients were demonstrated as mean, standard deviation, frequency, and percentage. The ratio of gender, education, job, residence, history of chronic disease (cancer, diabetes, immunodeficiency, asthma and cardiovascular disease), symptoms of disease (fever, chill, muscle pain, shortness of breath, dry cough and digestive disorders) was demonstrated for all the patients. Having a family cluster was considered a a dependent variable. We used Generalized Estimating Equation (GEE) to identify the associated factors for having family infection transmission and clustering. The assumptions of GEE (clustering the responses and linear relationship between the covariates) were confirmed. Data were analyzed in bivariate and multiple models. In bivariate analysis, the variables with a p-value lower than 0.2 were selected for the multiple models. Data were analyzed using SPSS software version 23. Type 1 error was considered equal to 0.05 for all analysis. The studies involving human participants were reviewed and verbal informed consent for participation was obtained.

Results

In this study, a total of 322 hospitalized patients with SARS-CoV-2 diagnosis from Feb 23, 2020, to Apr 28, 2020, participated. The mean (SD) age of the participants was 52.25 (17.36) years (range 10-95 years). The most common age group was 45-64 years. There were slightly more males than females among the patients. Half of the patients were illiterate or in primary school. The mean (SD) number of family members was 3.41(1.51) (rang 1-10 people). Fever and muscle pain were the most frequent symptoms of COVID-19 disease, respectively. The mean (SD) of days of the patients´ hospitalization was 5 (4.34) days (rang 0-28 days). Totally 27 family clusters occurred in 322 patients that hospitalized. All of the patients with family clusters were 62 people. The most common number of infection transmissions in family clustering was one infected person. The patients´ demographic characteristics, symptoms of the disease, health care, health behaviors, and days of hospitalization stratified by family cluster are reported in Table 1.

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Table 1. Characteristics of patients with SARS-CoV-2 in Qazvin province, Iran

Characteristics	Patients (N=322)	No family cluster (N=258)	Family cluster (N=62)	P-Value
Age group (yr)				
<=14	1 (0.3)	0 (0)	1 (0.3)	0.157
15-24	10 (3.1)	6 (2.3)	4 (6.5)	
25-44	107 (33.4)	81 (31.4)	26 (41.9)	
45-64	117 (36.1)	100 (38.7)	17 (27.4)	
>=64	85 (26.6)	71 (27.5)	14 (62)	
Gender				
Male	175 (54.7)	146 (56.6)	29 (46.8)	0.164
Female	145 (45.3)	112 (43.4)	33 (53.2)	
Job				
Employee	44 (15.2)	37 (12.8)	7 (2.4)	0.707
Retired	36 (12.4)	28 (9.7)	8 (2.8)	
housewife	136 (46.9)	112 (38.6)	24 (8.3)	
Self-employed	74 (25.5)	57 (19.7)	17 (5.9)	
Education				0.003*
Illiterate	64 (20.0)	56 (17.5)	8 (2.5)	
Primary school	88 (27.5)	73 (22.8)	15 (4.7)	
Middle/High school	50 (15.7)	46 (14.3)	4 (1.2)	
diploma	55 (17.2)	35 (10.9)	20 (6.3)	
University education	63 (19.7)	48 (15)	15 (4.7)	-
Residence				
Urban	217 (67.8)	166 (64.3)	51 (82.3)	0.008
Rural	103 (32.2)	92 (35.7)	11 (17.7)	
History of chronic disease	143 (44.7)	122 (47.3)	21 (33.9)	0.058
Smoking	27 (8.4)	21 (8.1)	6 (9.7)	0.696
Hookah	13 (4.1)	12 (4.7)	1 (1.6)	0.299
Symptoms of disease				
Fever	209 (65.3)	165 (64)	93 (36)	0.298
Chills	165 (51.6)	131 (50.8)	127 (49.2)	0.565
Dry cough	167 (52.2)	138 (53.5)	120 (46.5)	0.342
Shortness breath	97 (30.3)	87 (33.7)	171 (66.3)	0.008
Digestive	68 (21.3)	48 (18.6)	210 (81.4)	0.020
Muscle pain	158 (49.4)	115 (44.6)	143 (55.4)	0.001
Headache	52 (16.3)	43 (16.7)	215 (83.3)	0.680
Travel	19 (5.9)	15 (5.8)	4 (6.5)	0.849
Receive government health services	258 (80.6)	116 (45)	41 (66.1)	0.003
Days of hospitalization				
0-3	133 (41.6)	97 (37.6)	36 (58.1)	0.036
4-6	114 (35.6)	98 (38)	16 (25.8)	
7-10	46 (14.4)	39 (15.1)	7 (11.3)	
>=11	27 (8.4)	24 (9.3)	3 (4.8)	

* Significant at 0.05 level

Table 2 demonstrates the unadjusted and adjusted odds ratio (OR) for factors that had a significant association with having family clustering of COVID-19 patients. As Table 2 shows gender, residence, history of chronic disease and shortness of breath had a significant association with having family clustering in bivariate analysis, but no association was found for each of them in multiple analyses. The multiple analysis showed that the odds of hav-

Table 2. Factors associated with the family cluster: bivariate and multiple analysis

	Unadjusted analysis		Adjusted analysis	
Variables	OR (95% CI)	P value	OR (95% CI)	P value
Gender	0.47 (0.23-0.98)	0.045	…	…
Education				
Illiterate	2.18 (0.85, 5.60)	0.103	1.46 (0.52, 4.09)	0.469
Primary school	1.52 (0.68, 3.395)	0.306	1.284 (0.543, 3.037)	0.569
Middle/High school	3.59 (1.11, 11.63)	0.033	2.88 (0.817, 10.18)	0.100
diploma	0.55 (0.25, 1.2)	0.137	0.560 (0.231, 1.357)	0.199
University education	-	-	-	-
Age	1.31 (0.511, 3.34)	0.157	-	-
Residence	0.389 (0.193, 0.784)	0.008	-	-
History of chronic disease	1.75 (0.981, 3.13)	0.058	-	-
Digestive	0.48 (0.26, 0.89)	0.020	2.26 (1.11, 4.58)	0.024
Shortness breath	2.65 (1.28, 5.46)	0.008	-	-
Muscle pain	0.35 (0.2, 0.64)	0.001	2.69 (1.47, 4.93)	0.001
Days of hospitalization	0.337 (0.10, 1.18)	0.090	1.52 (1.05, 2,23)	0.024
Receive public health services	0.42 (0.23, 0.75)	0.003	2.13 (1.12, 4.03)	0.020

* Significant at 0.05 level
Adjusted variables: gender, education, age, residence, and history of chronic disease

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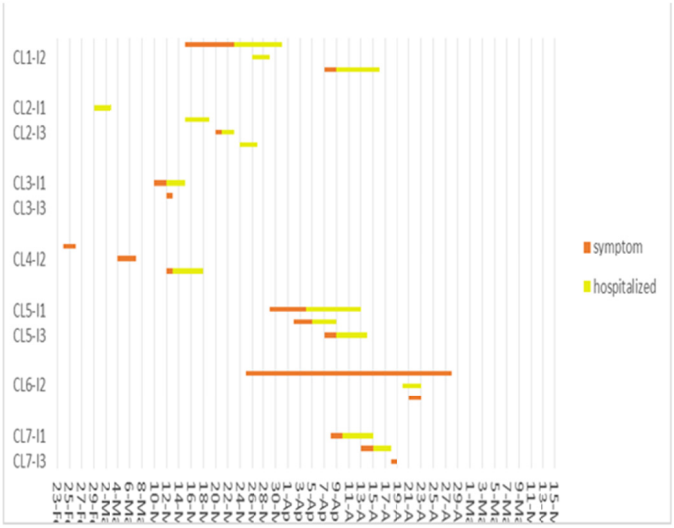

Fig. 1. The pattern of family clustering of patients with more than 2 infected people

ing family clustering among the patients with receive government health services (OR: 2.13, 95% CI (1.12, 4.03)), digestive (OR: 2.26, 95% CI (1.11, 4.58)), muscle pain (OR: 2.69, 95% CI (1.47, 4.93)) and more days of hospitalization (OR: 1.52, 95% CI (1.05, 2.23)) were significantly higher than others. For evaluating the association between symptoms of disease and family clustering, we adjusted demographic characteristics (gender, education, age, residence and history of chronic disease) of the patients.

Figure 1 shows the pattern of family clustering of patients with more than 2 infected people. It confirms a high probability person to person transmission of SARS-CoV-2 in the patient´s family.

Discussion

In this survey, we high-lighted the clinical characteristics and epidemiological of 322 patients with SARS-CoV-2 from Qazvin province, Iran, in 2020. Our finding in Table 1 showed that most patients infected with SARS-CoV-2 during the course of the current study were male and the mean (SD) age of the participants was 52.25 years (the most common age group was 45-64 years). Perhaps one of the reasons for the high prevalence of the SARS-CoV-2 disease in men compared to women is due to the confounding effect of men's jobs. The men are more likely than women to work outside the home, and therefore more exposed. Another reason for this difference probably is that this gender factor, as well as higher frequency in men for most of the diseases, could depend on a general demographic fact of a shorter life expectancy in the men in comparison to the women in Iran and in the world in general. Consistent with our finding the Min Jin et al. (12) have revealed that men and women have the same prevalence for SARS-CoV-2, but men are more at risk for death and other worse outcomes, independent of age. This important issue that men in comparison to women have a higher mortality rate related to SARS-CoV-2 has been reported frequently in most previous studies (12-14). Although all ages are susceptible to catching the SARS-CoV-2, our results (Table 1) consistent with previous reports, suggest that older people are more involved with the SARS-CoV-2 disease. This evidence and behavior of coronavirus as a large number of viruses that cause illnesses ranging from the mild common cold to severe pneumonia which is similar to MERS-CoV (15-20) has been confirmed in previously conducted studies (21, 22). The authors of the study suggested that this issue be separately investigated in further study.

Our research also demonstrated that the mean (SD) of days of the patients´ hospitalization was 5 (4.34) days. The previous studies reported approximately similar results in this regard (23, 24).

We also revealed some potential factors which they had associated with the family cluster (Table 2). Factors such as male gender, having muscle pain, morbid patients with digestive and shortness breath symptoms, higher days of hospitalization, receiving public health services were highlighted for creating family clustering of SARS-CoV-2 infection in the current study (Table 2). Crude odds ratio estimates of creating family clustering of SARS-CoV-2 infection was 0.47 times [95% CI: 0.23, 0.98, p=0.045] less for women compared to the males; 2.26 [95% CI: 1.11, 4.58, p=0.024] and 2.69 [95% CI: 1.47, 4.93, p=0.001] for SARS-CoV-2 patients that had digestive and muscle pain in comparison with those did not this mentioned symptoms, respectively. 1.52 [95% CI: 1.05, 2.23, p=0.024] for patients with a longer hospitalization compared with patients that had a lower duration of hospitalization and adjusted odds ratio estimates was 2.13 [95% CI: 1.12, 4.03, p=0.020] for patients who receive public health services in comparison those did not receive public health services. In China, the family clustering was 31-50% in different close contacts (25). This study is one of the first preliminary studies investigating the role of potential factors in creating family clustering of SARS-CoV-2 infection. Another study introduced family clusters as a

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serious threat to public health, spatially if patients were asymptomatic. It reinforce person-to-person transmission in the family settings (9, 11).

The authors in the current research strongly believe that still there are major gaps in our knowledge about the potential factors in creating family clustering of SARS-CoV-2 infection, epidemiology, origin, duration of human transmission, and clinical spectrum of this aforementioned emerging disease and these gaps needs be fulfillment by future studies.

The limitations of this study consist of: first, for family cluster analysis, only a case series of 322 patients with SARS-CoV-2 was included in this survey, which itself can increase the likelihood of selection bias in the results. Second, because of the urgent circumstances in the world, there was no access to homogeneous and unique data for SARS-CoV-2. It could affect the analysis and probability occurring information bias in the results. However, this is one of the first preliminary studies investigating the role of potential factors in creating family clustering of SARS-CoV-2 infection. Finally, we included all hospitalized patients with confirmed SARS-CoV-2 diseases with laboratory-based (PT-PCR) tests, so only patients with the positive laboratory test results, included in the study and other diagnosis methods were excluded.

Conclusion

In conclusion, factors such as male gender, having muscle pain, morbid patients with digestive and shortness breath symptoms, higher days of hospitalization, receiving public health services significantly ($p<0.05$ for all) had associated with creating family clustering of SARS-CoV-2 infection. Our findings confirm the person-to-person transmission of this novel coronavirus in family settings and hospitals, and the reports of infected travelers in other geographical regions. Major gaps in our knowledge about the potential factors in creating family clustering of SARS-CoV-2 infection, epidemiology, duration of human transmission and etc, need fulfillment by future studies.

Acknowledgment

We thank all patients involved in this study. The authors have special thanks to Qazvin University of Medical Sciences for supporting the present study.

Ethical Approval

This study was approved by the Ethics Committee of Qazvin University Medical Sciences (IR.QUMS.REC.1399.008).

Conflict of Interests

The authors declare that they have no competing interests.

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[DOI: 10.47176/mjiri.36.29]