Original article

Transmission dynamics of novel Coronavirus–SARS-CoV-2 in South Sumatera, Indonesia

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ABSTRACT

SARS-CoV-2 has shaken the world by extremely raising death tolls, illnesses, and economic losses. The virus is transmitted by humans to other humans, spreading to more than 200 countries. This research aims to analyze the transmission dynamics of novel Coronavirus-SARS-CoV-2 in South Sumatera Indonesia. This is epidemiologic research, and the research population is all SARS-CoV-2 patients and those who have close contact with the patients in all districts/cities in South Sumatera. It has been widely known that those that have made contact with patients confirmed positive for SARS-CoV-2 has a risk of getting infected by SARS-CoV-2 by 3.591 higher than those who never have (OR = 3.591, 95% CI: 2.933–4.396). Also, according to the findings, those who have a contact history to patients confirmed positive for SARS-CoV-2 have a risk of getting infected by SARS-CoV-2 by 2.387 higher than those who never have (OR = 2.387, 95% CI: 1.362–4.184). Meanwhile, those who have no idea for having made contact with patients confirmed positive for SARS-CoV-2 has a risk of getting infected by SARS-CoV-2 by 1.082 higher than those who have never a contact history to the SARS-CoV-2 patients (OR = 1.082, 95% CI: 0.622–1.882). To prevent broader transmission, those who have made contact with the SARS-CoV-2 patients need to be quarantined. The findings help us give community health interventions to globally fight this transmittable disease.

1. Introduction

Systemic respiratory disease in humans is the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2).[1,2] SARS-CoV-2 is a communicable disease transmitted by a novel Coronavirus and belongs to a virus family identifiable in animals. Patients infected by SARS-CoV-2 will experience mild to moderate respiratory issues and may recover without any exclusive treatment. However, older people with comorbidities e.g. cardiovascular diseases and cancers may suffer from the severity and even death.[3]

The first COVID-19 case in Indonesia reportedly occurred on March 2nd, 2020, and consistently spread to and increased in other areas. SARS-CoV-2 infects people rapidly and has an incubation period of 5–12 days.[4] SARS-CoV-2 may contract those with mild symptoms and even those without any indication of symptoms.[5,6] You may contract SARS-CoV-2 from those who have been infected through their coughs or sneezes or saliva.[7] The rate of infection spread indicates strong evidence of secondary transmission from humans to humans. This transmission is allegedly triggered by a travel history. For example, 14 cases detected in the US involved a trip to China or close contact with travellers. 3 of the 14 cases were detected in the US citizens transferred from China. Also, 42 cases were identified in passengers transferred from a cruiser which sailed to the centre of the epidemic.[8] To prevent a broader transmission, quarantines should be enacted and cross-country transmission should be prevented.[9] Nevertheless, an inaccurate risk assessment and reporting can increase the potency of SARS-CoV-2 to spread globally.[10] Contact tracing and testing are thus required to lessen the rate of SARS-CoV-2 infection spread.[11]

As it is pivotal to mitigate the spread of SARS-CoV-2, patients with mild symptoms should self-quarantine and must not make a long trip. Human-to-human transmission can incur due to close contact which must be prevented. Therefore, the government should enact a self-quarantine program and travel restriction. Each outbreak provides an opportunity to acquire important information regarding the outbreak so the identification of potential types of exposure has important implications for containment and mitigation strategies. As such, this research aims to investigate the transmission dynamics of SARS-CoV-2 in a population.

2. Methods

The research design used is cross-sectional. The research population is all SARS-CoV-2 patients and those who have made contact with the patients. This research is conducted in all districts/cities in South Sumatera. Data collection was performed in June–September 2020. The data collection instrument used is the instrument for an epidemiological investigation developed by the Indonesia Epidemiological Association in cooperation with the CDD Foundation and inputted to Kobo.humanitarianresponse. Research respondents are all SARS-CoV-2 patients and those who have made close contact and are selected using a total sampling technique.

2.1. Data collection

Sex, occupation, and the history of close contact with SARS-CoV-2 patients are three independent variable variables with two categories, while the history of traveling abroad, visiting local transmission region, visiting health facilities, contact with suspects, contact with patients confirmed positive are divided into three categories. The independent variables comprise three categories which are confirmed cases, probable cases, and suspect cases. The bias which may incur during research is non-response bias from patients. To mitigate the bias impacts, we explain the research objectives and approaches by a means of public figures. Crosschecking the close contacts identified is conducted using the information we acquire from many sources. Besides, households and places which have been visited by patients within the last two weeks before the symptoms appear are also investigated to measure environmental exposure. 2203 samples are inputted in Kobo.humanitarianresponse. The data inputted were cleaned and thereby remaining 2137 respondents proceed to the analysis. Meanwhile, the data which cannot be analyzed are incomplete answers.

2.2. Data analysis

Furthermore, in terms of statistical analysis using a Chi-square test, Simple logistic regression, and double logistic regression, the dependent variables are divided into two categories based on the result of the investigations of confirmed cases and non-confirmed cases. Confirmed-positive cases are cases which have been identified using a Swab test, whereas non-confirmed cases are cases which have not been identified and come with two categories: probable and suspect cases. A Chi-square test is used to compare the dissimilarities between patients confirmed positive for COVID-19 and those not confirmed positive at a significance level of $p < 0.05$. The continue valuable and category are presented as a mean and an absolute number (percentage). Moreover, the double logistic regression analysis is made to examine factors predicting the prevalence of COVID-19 cases. The covariate selection of the final multivariable model is built upon whether the variable has fulfilled the criteria of $p < 0.25$ in the simple logistic regression and whether it constitutes the theoretical/clinical research interests. The variables assessed are sex, occupation, history of traveling abroad, history of visiting health facilities, history of contact with suspects, history of contact with patients confirmed positive for COVID-19, and close contacts.

3. Results

3.1. Patient characteristic

There are 2137 respondents, the majority of whom, 52%, are male. Most respondents are 38.19 years old and work as entrepreneurs (12.7%). (Table 1).

3.2. Predictors of intention to Covid-19

The findings indicate that sex and occupation do not pertain to SARS-CoV-2. Meanwhile, the history of traveling abroad, visiting local transmission areas, visiting health facilities, contact with suspects, contact with patients confirmed positive for COVID-19, and close contacts are deemed as the significant predictors of the SARS-CoV-2 transmission and proceed to the multivariate analysis. Table 2.

In Table 3, the predominant variable predicting the prevalence of SARS-CoV-2 is close contact with patients confirmed positive. Those who have made close contacts with SARS-CoV-2 patients have a risk to get infected by SARS-CoV-2 3591 higher 3.591 than those who have never (OR = 3.591, 95% CI: 2.933–4.396). Besides, those who have made a history of contacts with SARS-CoV-2 patients have a risk to get infected by SARS-CoV-2 2.387 higher than those who have never (OR = 2.387, 95% CI: 1.362–4.184). Meanwhile, those who are unaware of having contacts with SARS-CoV-2 patients have a risk to get infected by SARS-CoV-2 1.082 higher than those who have never made contact with them (OR = 1.082, 95% CI: 0.622–1.882). Model x^2 is 59.7 (degrees of free-dom = 10, p 0.0001) and the Hosmer-Lemeshow test is not significant (p = 0.048), indicating a good model fit. Nagelkerke R^2 is 0.208, which means that 20.8.% variability in the prevalence of COVID-19 by the variables included in the model.

4. Discussion

This research aims to assess the prevalence of SARS-CoV-2 and determine what factors predicting the prevalence of SARS-CoV-2 cases. Respondents infected by SARS-CoV-2 who have made close contact with those infected are the predominant predictors. 45.6% of respondents

Table 1
Characteristic sociodemographic respondence

Sociodemographic characteristics	Finding
Age (years)	
(Mean + Standard deviation)	38.19 + 17.32
Sex	
Male	1111 (52%)
Female	1026 (48%)
Job	
Day laborer	89 (4.2%)
Pharmacist	8 (0.4%)
Accounting	36 (1.7%)
Medical worker	182 (8.5%)
Artist	1 (0.01%)
Factory worker	42 (2%)
Traders	72 (3.4%)
Public service	111 (5.2%)
Institution	90 (4.2%)
Businessman	19 (0.9%)
Fishery	4 (0.2%)
Forestry	3 (0.1%)
Mining	24 (1.1%)
Farmer	79 (3.7%)
Government employees	199 (9.3%)
Information technology	3 (0.1%)
Merchants	1 (0.01)
Army	58 (2.7%)
Transportation	28 (1.3%)
Entrepreneur	271 (12.7%)
Unemployed	817 (38.2%)

Table 2
Predictors of the incidence of SARS-CoV-2.

Variable	Category	Covid-19 cases				p-value
		Confirmed		Unconfirmed (probable + suspect)		
		n	%	n	%	
Sex	Male	681	61.3	430	38.7	0.921
	Female	632	61.6	394	38.4	
Job	Employee	815	61.7	505	38.3	0.751
	unemployed	498	61	319	39	
Abroad travel history	Yes	7	58.3	5	41.7	0.015
	Unknown	17	94.4	1	5.6	
	No	1289	61.2	818	38.8	
Local transmission history	Yes	96	50.8	93	49.2	0.0000
	Unknown	60	92.3	5	7.7	
	No	1157	61.4	726	38.6	
Medical facility visitation history	Yes	195	77.4	57	22.6	0.0000
	Unknown	73	92.4	6	7.6	
	No	1045	57.9	761	42.1	
Contact history with suspect	Yes	138	63.3	80	36.7	0.0000
	Unknown	235	81.6	53	18.4	
	No	940	57.6	691	42.4	
Contact history with confirmed case	Yes	456	72.8	170	27.2	0.0000
	Unknown	189	76.2	59	23.8	
	No					
Close contact	Yes	742	76.2	232	23.8	0.0000
	No	571	49.1	592	50.9	

Table 3
Multivariate analysis of the incidence of SARS-CoV-2.

Risk Factors	Category	β	p-value	OR (95% CI)
History of local transmission area	No			Reff
	Unknown	-1.949	0.000	0.142 (0.049–0.412)
	Yes	-0.812	0.121	0.444 (0.159–1.241)
Medical facility visitation history	No			Reff
	Unknown	-0.759	0.122	0.468 (0.179–1.224)
	Yes	-1.470	0.002	0.230 (0.091–0.579)
Contact history with suspect	No			Reff
	Unknown	-0.833	0.007	0.435 (0.238–0.794)
	Yes	-1.020	0.000	0.361 (0.206–0.632)
Contact history with confirmed case	No			Reff
	Unknown	0.078	0.781	1.082 (0.622–1.882)
	Yes	0.870	0.002	2.387 (1.362–4.184)
Close contact	No			Reff
	Yes	1.278	0.000	3.591 (2.933–4.396)

Notes: OR: Odd Ratio, CI: Confidence Interval.

infected by SARS-CoV-2 admit to having made close contact with SARS-CoV-2 patients. A contact is considered close when those experiencing it is having a contact within 1 m in distance to patients confirmed and suspected positive two days before the appearance of symptoms in the patients confirmed and suspected or two days before the asymptomatic infection sample is collected.[12]

As a preventive effort regarding a broader transmission, quarantine is an obligation for those who have made close contact with SARS-CoV-2 patients. According to clinical tests, the virus needs 1-14-day incubation, but the majority of which takes 3–7 days. Quarantine is supposed to last for 14 days, or within the incubation period of SARS-CoV-2. However, evidence suggests that quarantine may be extended to 21 days.[13] Chen et al. (2020) argue that the dissimilarities in transmission through close contact between the two groups are statistically insignificant.[14] Close contact with SARS-CoV-2 patients may happen in a family and a group of friends, either close friends or working partners. Transmission through close contact within a family is high in prevalence. It may occur between a husband and wife and in a group of people who share a house or plate when eating.[15–18] SARS-CoV-2 has pathogenicity and transmission stronger than SARS-CoV and MERS-CoV.[10] Contacting a patient confirmed positive, being close for 15 of 50 s, and leaving the mask are the factors of infection.[9,19]

SARS-CoV-2 brings about a cluster transmission, especially in a family. The prevalence of MERS transmission between family members is 13–21%, while that of SARS transmission is 22–39%.[20] Although the family member infected has been hospitalized, they might have transmitted the virus to another family member. SARS-CoV-2 can also be transmitted through fesses and the virus can survive within 1–2 days in fesses.[21,22] Our findings also prove that the history of traveling abroad/to other regions (local transmission) may increase the transmission risks. Early detection of imported cases should be activated in the countries which have such potentials. An imported case reportedly incurs in Brazil as one of its citizens travelled to Italy, one of the countries with high cases of SARS-CoV-2.[23] Furthermore, travel restrictions can mitigate the broadened transmission across countries besides the public health interventions and behavioural changes that can facilitate the mitigation.[24,25] This research gives valid evidence which supports the argument that asymptomatic human-to-human SARS-CoV-2 transmission can be through close contact, contact with SARS-CoV-2 patients, trips to other countries, or local transmission. This research allows us to make public health interventions to fight this communicable disease globally.

Ethical statement

Declaration of competing interest

The authors declare that there is no conflict of interests regarding the publication of this paper.

Acknowledgment

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