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Research Article

Emergence and Subsiding of the First-wave COVID-19 Pandemic in Pakistan (2020): An Eigenvalue Analysis Based on Synergetics

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Abstract: By November 15, 2020, the COVID-19 pandemic has claimed worldwide 1,300,000 lives. Despite this tragic death toll, several countries managed to make at least their first-waves of the COVID-19 pandemic in their countries to subside to relatively low levels. Pakistan is one of those countries. An analysis of the beginning, middle stage, and ending of the pandemic in Pakistan are presented by combining standard epidemiological modeling and an eigenvalue analysis as used in synergetics. The decay of the effective contact rate throughout the three stages presumably due to intervention measures is demonstrated. Importantly, the sign-switching of the dominant eigenvalue from the beginning to the ending stage is shown that suggests that at least in August and September 2020 the disease-free state (i.e., state free of COVID-19) was stabilized.

Keywords: COVID-19, eigenvalues, synergetics.

1. INTRODUCTION

Within less than one year, by November 15, 2020, the coronavirus disease (COVID-19) claimed 1,300,000 lives [1]. In view of this tragic number, it is worthwhile to study countries like Pakistan in which the first COVID-19 wave during the period from March 2020 to September 2020 subsided from a peak level of almost 7000 daily new infections towards a relatively low level of about 500 daily new infections [2]. In particular, low- and middle-income countries such as Pakistan face particular challenges because they typically lack resources in medical centers and trained medical personnel as compared to high-income countries [3]. According to the World Health Organization (WHO), the COVID-19 pandemic as such originated in the city of Wuhan, China, in December 2019 [4]. The disease geographically expanded rapidly. In particular, Italy was one of the first countries outside Asia that was hit by the virus in an even more dramatic way than China itself [5]. Intervention measures had been put in place in the city of Wuhan, in China as a country, in Italy, and worldwide to stop or slow down the spread of COVID-19. In this context, epidemiological models have been indispensables tools to understand COVID-19 case data and to examine the impact of intervention measures. Susceptible-exposed-infected-recovered (SEIR) models [6,7] and other epidemiological models have been used to study the COVID-19 pandemic for a plenitude of countries around the globe [8,9,10,11,12,13]. However, relatively little attention has been paid to the nonlinear physics underlying the emergence as well as the subsiding of the pandemic in certain countries and regions. Accordingly, the emergence of virus infection in a population corresponds to the evolution of a dynamical system away from an unstable fixed point [14]. The fixed point is characterized by a positive eigenvalue. That is, the linearized dynamical system that describes the infection dynamics close to the fixed point exhibits a particular direction in the state space under consideration in which the dynamics increase exponentially in time. Within the nonlinear physics perspective [15], in general, and the framework of synergetics [16,17], in particular, this eigenvalue determines or dominates the phenomenon under consideration. As such, the synergetic approach addresses the dynamics of systems at unstable fixed points and other kinds of instabilities [16,17]. The synergetics approach

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states that the dynamics of such systems close to the instability under consideration can be completely understood by studying the set of eigenvalues (i.e., the eigenvalue spectrum) of the instability. In this context, a system that exhibits a single positive eigenvalue corresponds to a classical example of a nonlinear system at an unstable fixed point [16,17]. Such classical systems exhibit a single relevant growth rate that describes how quickly the system evolves away from the fixed point (along the aforementioned particular direction) and is given in terms of the positive eigenvalue. A synergetic approach is an interdisciplinary approach that has been applied not only in physics but also in biology, chemistry, biochemistry, sociology, economics [16], and studies on human reactions [17]. However, its application to epidemiology, in general, and to the COVID-19 pandemic, in particular, is still in its infancy [9,18]. For example, using the synergetics framework, recently, a three-stage model for COVID-19 waves has been worked out to show that not only the emergence but also the subsiding of a COVID-19 wave is determined by the aforementioned eigenvalue [18]. More precisely, the study showed for several European countries that their lockdown intervention measures during the Spring months of 2020 resulted in a switch of the positive eigenvalue to a negative one. In doing so, for those countries, the disease-free fixed point was stabilized and the daily new infections decayed towards relatively low levels [18]. That is, the first COVID-19 waves almost subsided in those countries during the summer months of 2020. The epidemiological model used in that study [18] exhibited a relatively small number of eigenvalues (namely: two). In contrast, in the present study, a model involving five relevant eigenvalues will be considered. Moreover, the study [18] focused on European countries that do not face the same kind of challenges as low- and middle-income countries [3]. In contrast, in the present study, the three-stage modeling approach is used to analyze the pandemic in Pakistan from March 2020 to September 2020. It will be argued that a particular key parameter of the infection dynamical system (the so-called effective contact rate) changed throughout the pandemic in Pakistan presumably due to successfully implemented intervention measures. Furthermore, it will be shown that this change of the parameter led to a stabilization of the disease-free fixed point as indicated by a sign switch of the dominant eigenvalue of the fixed point.

2. MATERIALS AND METHODS

To describe the COVID-19 pandemic in Pakistan an epidemiological model was used that involved the class of susceptible (*S*), exposed (*E*), symptomatic infected (I_s), asymptomatic infected (I_a), infected hospitalized (I_h), and quarantined (*Q*) individuals. The model may be considered as an extension of the standard SEIR model. The model equations were given by;

$$\begin{aligned} S' &= -F\,S \\ E' &= F\,S - k_1 E \\ I_s{}' &= \rho\omega E - k_2 I_s \\ I_a{}' &= (1-\rho)\omega E - k_3 I_a \\ I_h{}' &= \eta I_s + \delta Q - k_5 I_h \\ Q' &= \kappa E - k_4\,Q \end{aligned} \tag{1}$$

In Eq. (1) primes denote differential quotients with respect to time. The force F of infection [6] was defined by

$$F = \beta\,\frac{(I_s + \psi I_a + \nu I_h)}{N} \tag{2}$$

All model parameters are positive. They described the proportion of asymptomatic infections (ρ), the incubation period (1/ω), the hospitalization rate of symptomatic infected (η), the hospitalization rate of quarantined (δ), quarantine rate of exposed individuals (κ), and removal rates $k_1,\ldots,k_5$ for individuals of the respective classes. The force of infection involved the effective contact rate (β), and the relative transmissibility of the asymptomatic (ψ) and hospitalized (υ) individuals. The model defined by Eqs. (1) and (2) is a simplified version of the model proposed in [19] and neglects demographic birth and death terms. The reason for this is that the observation period under consideration (March to September) is relatively short [9,11,18]. In this context, the parameter N was the population of Pakistan. As argued before, variations of N during the observation period of interest were assumed to be negligibly small such that N was put to be constant. Importantly, it was assumed that symptomatic cases were detected relatively quickly by health authorities as COVID-19 cases. That is, for sake of simplicity, a separate evolution equation describing a diagnosis step as in Ref. [18] was neglected. Moreover, quarantined individuals who became hospitalized because they developed severe COVID-19 symptoms belonged to the COVID-19 cases as well. Let Pc denote the cumulative population of COVID-19 cases. Then, from Eq. (1) it follows that the rate of change of the cumulative population of COVID-19 cases satisfies

$$P_c' = \rho\omega E + \delta Q \tag{3}$$

For similar considerations see Ref. [18].

The key parameter of the model as defined by Eqs. (1),(2),(3) was the effective contact rate β. As mentioned above, Eq. (1) is identical with the model proposed in [19] except for the demographic terms (compare Eq. (1) of the current study with Eq. (3) of Ref. [19]). The critical contact rate β(crit) is the value of β for which the fixed point changes its stability and, consequently, corresponds to the case for which the so-called basic reproduction number [7,9,10,15,20] equals 1. The basic reproduction number is given in Ref.. [19] (see Eq. (7) in Ref. [19]) and does not depend on the demographic terms. Therefore, it applies to the model defined by Eq. (1) in the current study. Putting the basic reproduction number (defined by Eq. (7) in Ref. [19]) equal to 1 and solving for β, the critical value is given by

$$\beta(crit) = \frac{k_1 k_2 k_3 k_4 k_5}{Z} \tag{4}$$

$$Z = k_4\omega[\rho k_3(\,\eta\nu + k_5) + (1-\rho)k_2 k_5 \psi] + \kappa\delta k_2 k_3 \nu$$

The disease-free fixed point is defined by putting the left-hand sides of Eq. (1) equal to zero and putting S=N. Explicitly, it is given by $(S,E,I_s,I_a,I_h,Q)=(N,0,0,0,0,0)$. For $\beta<\beta$(crit) the disease-free fixed point $(S,E,I_s,I_a,I_h,Q)=(N,0,0,0,0,0)$ is stable, whereas for β> β(crit) it is unstable. In this context, when the disease-free fixed point changes its stability (from unstable to stable), then the infection dynamics changes qualitatively from evolving away from (E, I_s, I_a, I_h, Q) = (0,0,0,0,0) to evolving towards the state (E, I_s, I_a, I_h, Q) = $(0,0,0,0,0)$. Note that the variable S is ignored in these considerations because it can only decay over time. A qualitative change of the dynamics due to the change of the stability of the fixed point is referred to as a bifurcation [16,17].

In the present study, the modeling and eigenvalue analysis was based on the following three stages epidemiological model [18]. In stage 1 (beginning of the pandemic in Pakistan), the COVID-19 infection dynamical system under consideration is characterized by $\beta>\beta$(crit) and a nonlinear (exponential-like) increase of COVID-19 cases. As a reaction to this COVID-19 outbreak, intervention measures (mask-wearing, physical distancing, lockdown, etc.) are implemented that decrease the effective contact rate [8,18,19] such that the system makes a transition from stage 1 to stage 2. In stage 2 (middle stage) the infection dynamical system is at its bifurcation point at which the disease-free fixed point is about to become stable. That is, the system is characterized by $\beta=\beta$(crit) and a linear increase of COVID-19 cases. After stage 2, the intervention measures show their full impact such that the system is characterized by $\beta<\beta$(crit). The system enters stage 3. In stage 3, the disease-free fixed point is stable, the number of daily new infections decays over time, and the pandemic in Pakistan subsides.

In line with those considerations and the key role of the parameter β, the model is defined by Eqs. (1),(2),(3) was fitted to cumulative COVID-19 case data [20] from Pakistan keeping all parameters constants except for β. The constant parameters can be found in Ref. [19]. For sake of completeness, they are listed in Table 1. The parameter fitting procedure for β followed the methodology suggested in Ref. [18]. The time points t_1 and t_2 that denoted the beginnings of stage 2 and stage 3 were varied in intervals prior (t_1) and post (t_2) the half time point t(half) at which COVID-19 cases reached half of the September 30 maximal value (see also the Results section). The parameter β was estimated for stage 1 and stage 3 as the optimal parameter that produced the best model fit given a particular pair of time points (t_1,t_2). For stage 2 the parameter β was fixed at the critical value β(crit), see also Ref. [18]. In total, the four model parameters t_1,t_2, β in stage 1, and β in stage 3 were estimated using COVID-19 case data [20] and β(crit) (i.e., β in stage 2) was computed from Eq. (4).

Once the model parameters t_1,t_2, β in stage 1, β in stage 3, and β(crit) were determined, the eigenvalues of the disease-free fixed point were determined. In line with the general definition

Table 1. Parameters used in Equations (1) and (2) and their values ("/d" means "per day"). All parameters listed here are taken from Ref. [19] (see Table 1 of Ref. [19]; for $k_1,\ldots,k_5$ see the bottom part of page 3 of Ref. [19] and Table 1 of Ref. [19]).

Parameter	Description	Value
N	Total population	220,309,834
ω	Inverse of incubation period	0.2403/d
ρ	Proportion of asymptotic infections	0.2929
η	Hospitalization rate of symptomatic individuals	0.4015/d
δ	Hospitalization rate of quarantined individuals	0.1368/d
κ	Quarantine rate of exposed individuals	0.3922/d
k_1	Removal rate of exposed individuals	0.6325/d
k_2	Removal rate of symptomatic infected individuals	1.0449/d
k_3	Removal rate of asymptomatic infected individuals	0.0806/d
k_4	Removal rate of quarantined individuals	0.6339/d
k_5	Removal rate of hospitalized infected individuals	1.1194/d
ψ	Relative transmissibility of the asymptomatic infected individuals	0.7892
ν	Relative transmissibility of the hospitalized infected individuals	0.6526

of eigenvalues of a dynamical system at a fixed point [16,17], the eigenvalues were defined as the eigenvalues of the 6x6 matrix that describes the linearized dynamical system (1) at the disease-free fixed point (*N,0,0,0,0,0*). Since demographic terms in the evolution equation for the susceptible individuals S were neglected, the disease-free fixed point exhibited a zero eigenvalue related to the sub-dynamics of S(t) [10]. Therefore, the eigenvalue analysis was based on the remaining five state variables E, I_s, I_a, I_h, and Q. Linearizing the infection dynamics defined by Eqs. (1) and (2) at the disease-free fixed point yields the following 5x5 matrix A for those variables

$$A = \begin{pmatrix} -k_1 & \beta & \beta\psi & \beta\upsilon & 0 \\ \varrho\omega & -k_2 & 0 & 0 & 0 \\ (1-\varrho)\omega & 0 & -k_3 & 0 & 0 \\ 0 & \eta & 0 & -k_5 & \delta \\ \kappa & 0 & 0 & 0 & -k_4 \end{pmatrix} \qquad (5)$$

From the matrix, the five eigenvalues of the fixed point were determined.

3. RESULTS AND DISCUSSIONS

Figure 1 presents the COVID-19 case data from Pakistan and the analysis results. Panel A shows the cumulative COVID-19 cases (black circles) during the 7 months (about 210 days) from March 1 to September 30 as reported in the database [20]. The data showed the typically sigmoid, three-stage pattern [18]. A first (accelerating) bend, a linear stage, and a second (de-accelerating) bend. On September 30 about "310,000" cases were reported. The half time point *t*(half) was June 16 (dotted vertical blue line in panel A) with approximately "155,000" cases. By visual inspection, *t*(half) was part of stage 2 characterized by a linear increase. The optimal time parameters were t_l=June 10 for the beginning of stage 2 and t_2=July 1 for the beginning of stage 3 (indicated by dashed vertical blue lines in panels A and B). The solid red line in panel A shows the model fit $P_c(t)$ obtained from Eqs. (1)-(3). The model captured the essential features of the COVID-19 pandemic in Pakistan.

Panel B of Figure 1 shows daily new COVID-19 cases (black circles) as reported in the database [20] and the model fit (solid red line). The three stages of the model are visible. Stage 1 is given by a rapid increase of daily new infections. Stage 2 describes a relatively fast decrease of daily new infections to a plateau. Stage 3 describes the decay of daily new infections from the aforementioned plateau towards the aforementioned low level of about 500 daily cases.

The effective contact rates obtained from the model-based data analysis are presented in Table 2. It was found that β=0.60/d for stage 1, β=β(crit)=0.35/d for stage 2, and β=0.21/d for stage 3. Here and in what follows "/d" means "per day". As predicted, the contact rate was larger than the critical value in stage 1 and dropped below the critical value in stage 3.

Panel C of Figure 1 shows the five eigenvalues in stage 1 and stage 3. For each stage, the eigenvalues were sorted according to their magnitudes. Consequently, for each stage, they form a decreasing spectrum. Importantly, the largest eigenvalue of stage 1 was positive with 0.05/d, indicating that the disease-free fixed point was unstable. In contrast, the largest eigenvalue was negative in stage 3 with -0.03/d, indicating that the fixed point was stabilized presumably due to the implementation of intervention measures. Note that Figure 1 only shows the real parts of eigenvalues. Both for stage 1 and stage 3 the first three eigenvalues (label k=1,2,3) were real-valued. However, two eigenvalues were complex-valued (k=4,5), which implies that they had the same real parts (as can be seen in panel C) but conjugated imaginary parts (not shown in panel C).

Table 2. Model parameter β varying across the three stages ("/d" means "per day").

Stage	β
1	0.60/d
2	0.35/d
3	0.21/d

The results from Pakistan are consistent with previous studies that have explicitly shown that intervention measures can lead to a subsiding of the COVID-19 pandemic in certain countries and regions by reducing effective contact rates [8,12] and switching positive eigenvalues of COVID-19 infection dynamical systems to negative ones [9,18].

Various intervention measures have been put in place in Pakistan during the observation period from March to September 2020. Schools in Pakistan were closed almost during the entire period from March to September [21]. From March 22 to May 9 a strict lockdown was administered involving the closure of shopping areas and restaurants [22,23]. The lockdown restrictions were eased after May 9 [23]. Subsequently, daily new infections increased dramatically (see Figure 1 panel B). The switch from stage 1 to stage 2 around June 10 can not be explained by the aforementioned March 22 to May 9 lockdown measures. Rather, it is plausible to assume that a change in the daily routine of Pakistani people in terms of reducing contacts, practicing physical distancing, wearing face masks, and increased handwashing slowed down the virus spreading. This is consistent with the fact that since the beginning of the pandemic in Pakistan the population has been reached by TV and radio and educated about COVID-19. For example, UNICEF reports that by June 12 a total number of 250.000.000 people (which is more than the 2020 population of Pakistan) had been reached by TV/radio and that 500 new handwashing stations had been established at COVID-19 hotspots [24]. Around June 15 a "smart lockdown strategy" was implemented in Pakistan [25,26]. Lockdown restrictions were put in place in hotspot regions of Pakistan. These restrictions could explain the transition from stage 2 to stage 3 around July 1 suggested by our model-based analysis. Accordingly, the "smart lockdown measures" reduced the nationwide effective contact rate to a sufficiently low value such that the disease-free fixed point became stable.

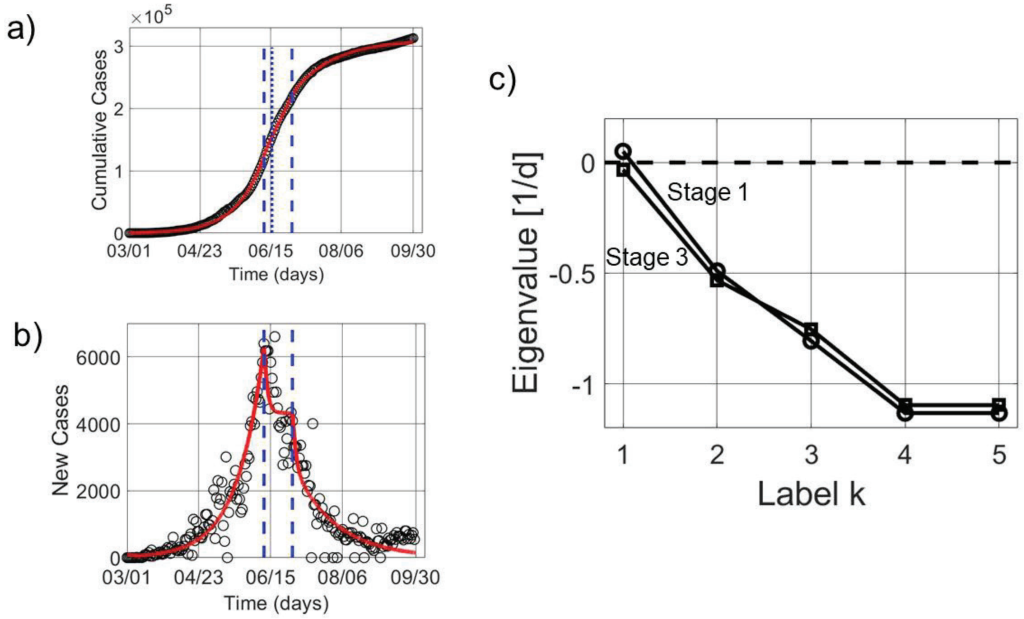

Fig. 1. Model fitting and eigenvalue analysis results.

4. CONCLUSIONS

The analysis supports the notion that the first-wave of the COVID-19 pandemic in Pakistan from March to September 2020 emerged from an unstable fixed point and subsided due to a stabilization of that fixed point. The stabilization was at least in part due to the successful implementation of intervention measures that reduced the frequency of contacts between individuals and the probability of infection in such contacts. However, in the fourth quarter of the year, 2020 Pakistan seems to witness a second COVID-19 wave [27]. The current study suggests that both the Pakistani government and the people living in Pakistan have the tools and intervention mechanisms available to master such a second-wave.

Conflict of interest: The author declares no conflict of interest.

5. REFERENCES

1. World Health Organization. COVID-19 Weekly Epidemiological Update 17 November 2020, https://www.who.int/emergencies/diseases/novel-coronavirus-2019. Accessed Nov 23, 2020.
2. UNICEF. Pakistan COVID-19 Situation Report No 17, https://www.unicef.org/documents/pakistan-covid-19-situation-report-15-september-2020. Accessed Oct 4, 2020.
3. F. Tanveer, A.T. Khalil, M. Ali, and Z.K. Shinwari. Ethics, pandemic and environment; looking at the future of low middle income countries. *International Journal of Equity in Health* 19: article 182 (2020).
4. World Health Organization. Novel coronavirus (2019-nCoV) Situation Report-1, https://www.who.int/emergencies/diseases/novel-coronavirus-2019. Accessed June 17, 2020.
5. Epicentro (Epidemiology for public health), SARS-CoV-2: Infographic 15 June 2020, https://www.epicentro.iss.it/en/coronavirus. Accessed June 17, 2020.
6. K. Rock, S. Brand, J. Moir, and M.J. Keeling. Dynamics of infectious diseases. *Reports on Progress in Physics* 77: article 026602 (2014).
7. M. Munir. Sensitivity and generalized sensitivity studies of the SIR and SEIR Models of computer virus. *Proceedings of the Pakistan Academy of Sciences* A 54: 167-178 (2017).
8. L. Pang, S. Liu, X. Zhang, T. Tian, and Z. Zhao, Transmission dynamics and control strategies of COVID-19 in Wuhan, China. *Journal of Biological Systems* 28: 543–561 (2020).
9. T.D. Frank. COVID-19 order parameters and time constants of Italy and China: a modelling approach based on synergetics. *Journal of Biological Systems* 28: 589-608 (2020).

10. C. Distante, P. Piscitelli, and A. Miani, Covid-19 outbreak progression in Italian regions: Approaching the peak by the end of March in Northern Italy and first week of April in Southern Italy. *Environmental Research of Public Health* 17: article 3025 (2020).
11. K.N. Nabi. Forecasting COVID-19 pandemic: A data-driven analysis. *Chaos, Solitons, and Fractals* 139: article 110046 (2020).
12. M. Gatto, E. Bertuzzo, L. Mari, S. Miccoli, L. Carraro, R. Casagrandi, and A. Rinaldo. Spread and dynamics of the COVID-19 epidemic in Italy: Effects of emergency containment measures. *Proceedings of the National Academy of Sciences* USA 117: article 10484 (2020).
13. Z. Zhao, X. Li, F. Liu, G. Zhu, C. Ma, and L. Wang. Prediction of the COVID-19 spread in African countries and implications for prevention and control: A case study in South Africa, Egypt, Algeria, Nigeria, Senegal and Kenya. *Science of the Total Environment* 729: article 138959 (2020).
14. O. Diekmann, and J.A.P. Heesterbeek. *Mathematical epidemiology of infectious diseases.* John Wiley and Son, Chichester (2000).
15. J. Guckenheimer, and P. Holmes. *Nonlinear oscillations, dynamical systems, and bifurcations of vector fields.* Springer, Berlin (1983).
16. H. Haken. Synergetics. *An introduction.* Springer, Berlin (1977).
17. T. Frank. *Determinism and self-organization of human perception and performance.* Springer, Berlin, (2019).
18. T. D. Frank. COVID-19 interventions in some European countries induced bifurcations stabilizing low death states against high death states: An eigenvalue analysis based on the order parameter concept of synergetics. *Chaos, Solitons, and Fractals* 140: article 110194 (2020).
19. S. Ullah, and M.A. Khan. Modeling the impact of non-pharmaceutical interventions on the dynamics of novel coronavirus with optimal control analysis with a case study. *Chaos, Solitons, and Fractals* 139: article 110075 (2020).
20. COVID-19 tracker, Timeline data from Johns Hopkins Center for Systems Science and Engineering, https://vac-lshtm.shinyapps.io/ncov_tracker/. Accessed Oct 3, 2020.
21. Arab News. Pakistan to start opening schools as coronavirus cases fall, https://www.arabnews.com/node/1730846/world. Accessed Nov 24, 2020.
22. UNICEF. Pakistan COVID-19 Situation Report No 1, https://www.unicef.org/pakistan/reports/covid-19-situation-report-1 Accessed Oct 4, 2020.
23. UNICEF. Pakistan COVID-19 Situation Report No 7, https://www.unicef.org/pakistan/reports/covid-19-situation-report-7 Accessed Oct 4, 2020.
24. UNICEF. Pakistan COVID-19 Situation Report No 10, https://www.unicef.org/pakistan/reports/covid-19-situation-report-10 Accessed Oct 4, 2020.
25. Law Library of US Congress. Smart lockdown imposed across cities of Pakistan as Covid-19 cases grow rapidly, https://www.loc.gov/law/foreign-news/article/pakistan-smart-lockdown-imposed-across-cities-of-pakistan-as-covid-19-cases-grow-rapidly. Accessed Nov 24, 2020.
26. UNICEF Pakistan COVID-19 Situation Report No 11, https://www.unicef.org/pakistan/reports/covid-19-situation-report-11 Accessed Oct 4, 2020.
27. International Monetary Fund. Policy Responses to COVID-19, Pakistan, https://www.imf.org/en/Topics/imf-and-covid19/Policy-Responses-to-COVID-19#P. Accessed Nov 24, 2020.