

## The utility of 2009 H1N1 pandemic data in understanding the transmission potential and estimating the burden of COVID-19 in South Africa to guide mitigation strategies

The coronavirus disease (COVID-19) caused by the severe acute respiratory syndrome coronavirus (SARS-CoV-2) rapidly became a public health emergency of international concern requiring urgent attention. It emerged late in 2019 in China as a respiratory pathogen, with the first epicentres observed in Iran, Spain and northern Italy. At the time of writing there were about 4 525 497 cases and 307 395 deaths worldwide, of which 1 409 452 cases and 85 860 deaths were in the USA, which is the most affected country in absolute terms.<sup>[1]</sup> The COVID-19 pandemic has been marked by extreme heterogeneity in both geography and population across the world. Consequently, leveraging local data aligned to the unique South African (SA) context is critical. Moreover, comprehensive mathematical models should integrate the full complexity of transmission dynamics observed with COVID-19 in the context of rapidly changing individual, social and structural determinants in SA.

From the diagnosis of the first case of SARS-CoV-2 in SA on 5 March 2020 to 16 May, there were 14 355 confirmed cases and 261 deaths.<sup>[2,3]</sup> However, the COVID-19-specific surveillance data employed since March are still severely restricted. The data vary by province and are preliminary, incomplete and not generalisable, with severe restrictions on numbers of available test kits and laboratory capacity. By the time sufficient data are collected and analysed, opportunities for epidemic mitigation may have been lost. Preliminary COVID-19 surveillance data can be strengthened through utilisation of past pandemic data on respiratory pathogens to inform the structure and parameters of current mathematical models and for sustained public health response. We therefore compared the transmission dynamics of SARS-CoV-2 with the lipid-enveloped H1N1 virus called A(H1N1)pdm09 that caused a pandemic resulting in ~575 400 deaths globally in 2009.<sup>[4]</sup> In the USA, where it began, the novel A(H1N1)pdm09 virus resulted in 60.8 million cases, 274 304 hospitalisations and 12 469 deaths from 12 April 2009 to 10 April 2010.<sup>[4]</sup> In SA, the A(H1N1)pdm09 virus resulted in 12 331 confirmed cases and 91 deaths from 14 July to 12 October 2009.<sup>[5]</sup> Recent influenza pandemic proportions of cases in SA have been interestingly low compared with other parts of the world. The population-level morbidity and mortality related to A(H1N1)pdm09 was notably much lower in SA compared with countries in the Northern Hemisphere generally.<sup>[4]</sup> This heterogeneity is also evident in preliminary COVID-19 incidence and mortality data. Although there have been other severe viral epidemics in SA, we confined assessment of the past pandemic transmission dynamics to the most recent influenza pandemic, the 2009 A(H1N1)pdm09, given contextual similarities with COVID-19 in terms of availability of surveillance systems, and medical, technological and social advances.

Although the novel coronavirus is new to the immune systems of humans, similarities with the novel A(H1N1)pdm09 virus were found. In an analysis of the first 100 deaths from A(H1N1)pdm09, most fatalities in SA were in the more affluent population and linked to travel.<sup>[6]</sup> Similarly, the COVID-19 virus first emerged among affluent people who had either travelled internationally or been exposed to individuals who had done so.<sup>[7]</sup> The greatest burden of A(H1N1)pdm09 cases was in the three provinces with the largest metropolitan areas, namely Gauteng, Western Cape and

KwaZulu-Natal.<sup>[5]</sup> Similarly, the highest numbers of cases of COVID-19 to date have been in the same three provinces, with 8 404 cases, representing 58.5% of the country's total, in the Western Cape.<sup>[2]</sup> The latter is attributed to population density, access to healthcare, and testing and tracing strategies. In both A(H1N1)pdm09 and COVID-19, the growth in numbers of cases rapidly transitioned to lower socioeconomic groups owing to challenges related to self-isolation and social distancing in overcrowded settings; lack of affordability of hygiene products; lack of access to potable water and proper sanitation; and food insecurity.<sup>[2,6]</sup> These extreme socioeconomic disparities threaten the survival of vulnerable communities and have serious implications for estimating the potential impact of COVID-19. The incidence of A(H1N1)pdm09 infections declined significantly during the transition from winter to spring in SA, suggesting that winter, which is the typical season for influenza, may have been conducive to spread of the A(H1N1)pdm09 virus.<sup>[5]</sup> Similarly, the colder temperatures in winter may be conducive to spread of the SARS-CoV-2 virus, as is the case for seasonal influenza. As SA enters its influenza season, it is critical for surveillance strategies to evaluate the possible shared risks for both COVID-19 and seasonal influenza, as co-infections could potentially increase disease severity and mortality.

Co-infections with HIV and tuberculosis (TB) during the 2009 A(H1N1)pdm09 epidemic in SA were associated with disease severity and death. The A(H1N1)pdm09 virus mostly killed young adults in SA, with a median age of 33.5 years.<sup>[5]</sup> Fatalities among these young adults were related to TB, HIV, being pregnant, and pre-existing metabolic conditions.<sup>[5]</sup> Although the associations with HIV and TB are not yet clear in the preliminary COVID-19 data, it is highly likely that the estimation of COVID-19's impact would be confounded by these two well-established epidemics. The latter would have serious implications given the fact that SA has the highest burden of HIV in the world; there were 240 000 new HIV infections in 2018, and the country has experienced ~71 000 AIDS deaths annually.<sup>[8]</sup> Furthermore, there were 300 000 new TB infections in same year and 63 000 TB-related deaths (two-thirds of these patients were living with HIV) annually, ~500 per 100 000 people.<sup>[9]</sup> The syndemic of HIV and TB potentiates risk during COVID-19 in two critical ways: potentially increasing severity of the clinical course for those with COVID-19, and also through advertent or inadvertent disruption of services for prevention and treatment programmes. Moreover, these disruptions may be associated with other competing health risks, including vaccinations, cancer screenings, non-communicable diseases and reproductive health programmes, during the COVID-19 crisis.<sup>[10,11]</sup> There may therefore be important and predictable short-, medium- and long-term implications associated with health system disruptions secondary to the COVID-19 crisis in SA.

The contextual factors described here suggest that the impacts of COVID-19 morbidity and mortality in SA may differ from those in other parts of the world. Taken together, these factors suggest the importance of integrating multiple SA-specific parameters in mathematical models that estimate COVID-19 impacts and in optimally scaling up COVID-19 prevention and mitigation strategies. Ultimately, appropriately parameterised mathematical models for

estimating the potential impact of COVID-19 in SA specifically are critical in informing contextually appropriate public health interventions, potential emergency and hospital care resources, policy, and governance.

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*S Afr Med J* 2020;110(7):576-577. <https://doi.org/10.7196/SAMJ.2020.v110i7.14935>