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## Accelerating South Africa's indigenous knowledge systems for antiviral drug discovery using computational modelling

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**Description:** This is the review article on using computational modelling to accelerate the drug development process for viral infections based on African indigenous medicinal plant species.

**Background:** Natural products or related drugs such as botanicals or herbal medicines make up approximately 35% of the annual global market, followed by 25% from plants, 13% from microorganisms and 3% from animal sources. The use of indigenous medicinal plant species used on traditional medicines has been used for centuries to treat viral infections. The constant growth of the human population and human interaction with the environment have led to several emerging and re-emerging RNA viruses responsible for diseases and pandemics. Considering the continuous spread of major viral pathogens as well as unpredictable viral outbreaks of emerging or reemerging viral strains, it is essential to ensure preparedness interventions to treat and manage yet another global health crisis.

**Aim:** The review article explores the potential application of computational modelling in identifying antiviral drugs informed by indigenous knowledge systems for future pandemic preparedness by the pharmaceutical industry.

**Methodology:** The South Africa' National Recordal System, which has been developed under the IKS Policy (2007), was used to identify the indigenous medicinal plant species used to treat respiratory diseases. The plants species, *Bulbine frutescens*, *Cyclopia genistoides*, *Harpagophytum procumbens*, *Kigelia Africana*, *Siphonochilus aethopicus*, *Sutherlandia frutescens*, *Trichilia emetic*, *Warburgia salutaris*, *Xysmalobium undulatum* *Lippia javanica* were identified. A systemic review of these plant species was conducted using past literature papers.

**Results:** From the literature, most of these plants have been shown to exhibit a wide range of chemical compounds with potential health benefits as shown in in vitro and in vivo studies for inhibition of the Human Immunodeficiency virus (HIV). The use of the computational modelling in small molecule drug discovery will proficiently accelerate the drug development process thereby impacting on the pharmaceutical industry while ensuring benefit sharing arrangements are released with the communities in terms of the Nagoya Protocol on Access and benefit sharing.

### Student or Postdoc?

No. Not a student nor Postdoc.

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