

## REVIEW

# Marine mollusc extracts—Potential source of SARS-CoV-2 antivirals

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**Summary**

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a novel human coronavirus and the causative agent of coronavirus disease 2019 (Covid-19). There is an urgent need for effective antivirals to treat current Covid-19 cases and protect those unable to be vaccinated against SARS-CoV-2. Marine molluscs live in an environment containing high virus densities ( $>10^7$  virus particles per ml), and there are an estimated 100,000 species in the phylum Mollusca, demonstrating the success of their innate immune system. Mollusc-derived antivirals are yet to be used clinically despite the activity of many extracts, including against human viruses, being demonstrated in vitro. Hemolymph of the Pacific oyster (*Crassostrea gigas*) has in vitro antiviral activity against herpes simplex virus and human adenovirus, while antiviral action against SARS-CoV-2 has been proposed by in silico studies. Such evidence suggests that molluscs, and in particular *C. gigas* hemolymph, may represent a source of antivirals for human coronaviruses.

**KEYWORDS**

human coronaviruses, molluscs, Pacific oyster (*Crassostrea gigas*), SARS-CoV-2 antivirals

## 1 | INTRODUCTION

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a novel human coronavirus which emerged in Wuhan, China during December 2019.<sup>1-3</sup> SARS-CoV-2 is the causative agent of the coronavirus disease 2019 (Covid-19) and as of August 2021, has infected more than 196 million people globally and resulted in over 4.2 million deaths.<sup>4</sup> Although vaccination will likely form the path out of the SARS-CoV-2 pandemic, effective antivirals are still required to treat current Covid-19 cases and protect those unable or unwilling to be vaccinated,<sup>2,5,6</sup> or in whom vaccines have poor efficacy. The efficacy of vaccines and antivirals currently in clinical trials are also threatened by the ongoing emergence of new SARS-CoV-2 variants.<sup>7-9</sup> Since March 2020, several SARS-CoV-2 variants of concern (VOC), including the alpha, beta, gamma and more recently, delta strain have emerged with

discernible changes in epidemiology and transmissibility.<sup>10,11</sup> Immune-modulating agents to control the excessive inflammation seen in Covid-19 will play an important role,<sup>12</sup> and this will be complemented by development of better antiviral drugs. As the science community continues to tackle a moving target, ongoing research to identify novel antiviral compounds against SARS-CoV-2 is crucial.

## 2 | CURRENT STATUS OF SARS-CoV-2 ANTIVIRAL DRUG DISCOVERY

Human coronaviruses are enveloped, single stranded RNA viruses that can further be classified as alpha-coronaviruses (human coronavirus-229E (HCoV-229E) and HCoV-NL63) or beta-coronaviruses (HCoV-OC43, HCoV-HKU1, Middle Eastern

**Abbreviations:** ACE2, angiotensin converting enzyme 2; Adv-5, Adenovirus type 5; Covid-19, coronavirus disease 2019; EBV, Epstein-Barr virus; HCoV, human coronavirus; HIV, human immunodeficiency virus; HSV, herpes simplex virus; MERS, Middle Eastern respiratory syndrome; NRTI, nucleoside reverse transcriptase inhibitor; RNA, ribonucleic acid; RdRp, RNA dependant RNA polymerase; SARS-CoV-2, severe acute respiratory syndrome 2; SOD, superoxide dismutase; SPE, solid phase extraction; VOC, variants of concern.

respiratory syndrome (MERS-CoV), SARS-CoV and SARS-CoV-2).<sup>13</sup> Human coronaviruses contain characteristic spike glycoproteins embedded within the viral envelope.<sup>14</sup> The SARS-CoV-2 spike glycoprotein facilitates entry into host cells by binding to the angiotensin converting enzyme 2 (ACE-2) receptor on the host cell surface.<sup>15</sup> Host proteases, TMPRSS2 and furin have also been established as important enzymes for priming SARS-CoV-2 spike glycoproteins upon binding to ACE2.<sup>15</sup> Blocking of this binding process, along with other stages of the SARS-CoV-2 infectious cycle (viral uncoating, genome replication and virion release) remain targets for development of new antiviral drugs.<sup>16</sup>

An alternative route for SARS-CoV-2 antiviral discovery has been the repurposing of currently approved drugs.<sup>16–18</sup> Remdesivir is a nucleotide prodrug of an adenosine analogue which inhibits the RNA-dependent RNA polymerase (RdRp) of filoviruses.<sup>17</sup> Promising randomised trials<sup>19,20</sup> and *in vitro* studies<sup>21</sup> have led to the approval of remdesivir to treat SARS-CoV-2 infection in Europe and the United States.<sup>17</sup> Despite gaining approval, data from subsequent clinical trials shows remdesivir has failed to emerge as highly efficacious Covid-19 treatment.<sup>22,23</sup> The antimalaria drug hydroxychloroquine showed promising *in vitro* activity against SARS-CoV-2<sup>21</sup> however, it has yielded poor results in randomised clinical trials.<sup>24</sup> Several other repurposing targets have been flagged, including favipiravir, lopinavir-ritonavir, ribavirin, ivermectin and oseltamivir.<sup>16,18,25</sup> Despite repurposing efforts, robust antiviral treatments for SARS-CoV-2 are yet to be identified.

### 3 | MARINE MOLLUSCS AS A SOURCE OF ANTIVIRAL COMPOUNDS

Marine invertebrates represent an almost totally unexploited source of medicinal compounds.<sup>6,26–28</sup> Marine invertebrates lack an adaptive immune system and only have the capacity to elicit innate immune responses,<sup>29–31</sup> despite living in an environment which contains virus particles in the order of  $>10^7$  per ml.<sup>32,33</sup> This demonstrates the success of their innate immunity, which includes the production of potent antiviral compounds.<sup>28,30</sup> The nucleosides spongothymidine and spongouridine, which contain D-arabinose rather than D-ribose, were isolated in the 1950s from the marine sponge, *Tectitethya crypta* (formerly *Cryptoethia crypta*), and this led to the development of the only marine invertebrate derived antiviral drug currently available on the market, vidarabine.<sup>6,28,30</sup> Vidarabine later inspired the design of antiviral drugs, acyclovir, and zidovudine.<sup>28,34</sup> Acyclovir and vidarabine are both nucleoside analogues which inhibit the nucleic acid synthesis of certain herpesviruses<sup>6,35</sup> while zidovudine is a nucleoside reverse transcriptase inhibitor (NRTI) used in treatment of human immunodeficiency virus (HIV).<sup>36</sup> The success of vidarabine, zidovudine and acyclovir exemplify how marine invertebrates not only represent a direct source of antiviral compounds but can also inspire the synthesis of novel antivirals.

Marine organisms of the phylum Mollusca are responsible for much of the diversity among marine invertebrates, and it is estimated

there are over 100,000 species of mollusc,<sup>26</sup> some of which live over 400 years, such as the ocean quahog, *Arctica islandica*.<sup>37</sup> Molluscan antiviral compounds can be sourced exogenously from their algae-based diets,<sup>26</sup> continuously expressed, or transiently expressed in response to viral challenge.<sup>26,38,39</sup> Mollusc derived antivirals are yet to be used clinically despite the activity of many extracts, against human viruses, being demonstrated *in vitro*.<sup>40,41</sup> As listed in Table 1, numerous marine mollusc extracts have been shown to have antiviral activity. The circulatory fluid (hemolymph) and lipophilic digestive gland extract of greenlip abalone (*Haliotis laevis*), has been shown to inhibit herpes simplex virus 1 (HSV-1) in Vero cells.<sup>40</sup> Time-of-addition assays suggested that *H. laevis* hemolymph either inhibited the entry of HSV-1 into Vero cells or was internalised simultaneously with the virus and acted during an early intracellular stage of infection.<sup>40</sup> *Haliotis laevis* lipophilic digestive gland likely inhibits an intracellular stage of HSV-1 infection.<sup>40</sup> Inhibition of HSV-1 has also been observed *in vitro* using extracts from the common cockle (*Cerastoderma edule*), Japanese carpet shell (*Ruditapes philippinarum*), European flat oyster (*Ostrea edulis*), common whelk (*Buccinum undatum*),<sup>41</sup> blacklip abalone (*Haliotis rubra*),<sup>42,43</sup> veined rapa whelk (*Rapanosa venosa*)<sup>44</sup> and the Mediterranean mussel (*Mytilus galloprovincialis*).<sup>45</sup> Early work involving oral administration of aqueous extracts from canned red abalone (*Haliotis rufescens*), in Swiss mice, showed protection against poliovirus and influenza A.<sup>46,47</sup> Antiviral activity against poliovirus has also been observed using paolin II, an extract from the Eastern oyster (*Crassostrea virginica*).<sup>48</sup>

### 4 | PACIFIC OYSTER (*Crassostrea gigas*) HEMOLYMPH—POTENTIAL SARS-CoV-2 ANTIVIRAL?

The Pacific oyster (*Crassostrea gigas*) is an economically important marine mollusc cultured globally.<sup>49</sup> The hemolymph of *C. gigas* has antiviral activity *in vitro*.<sup>49–51</sup> The major *C. gigas* hemolymph protein, cavortin, also exerts an antiviral effect against HSV-1 in Vero cells.<sup>49</sup> The specific mechanism behind cavortin's antiviral activity, along with its bioavailability in cell culture and/or animal models, remains unknown and presents questions for future research. Despite this, a direct virucidal effect of cavortin against HSV-1 has been identified.<sup>49</sup> Time of addition assays have also suggested that cavortin acts on an intracellular stage of HSV-1 infection.<sup>49</sup> Cavortin is a protein of approximately Mr 20,000, containing a single copper/zinc superoxide dismutase (SOD) domain.<sup>52,53</sup> There is evidence to suggest that the SOD activity of cavortin has been lost in evolution and its primary role is as a metal chaperone.<sup>52</sup> Intracellular zinc can inhibit SARS-CoV enzymes: RNA dependent RNA polymerase,<sup>54</sup> 3C-like protease<sup>55</sup> and papain-like protease<sup>56</sup> which are important in viral replication. Zinc may also have potential to act as a therapeutic for SARS-CoV-2.<sup>57–59</sup> The efficacy of zinc as an antiviral for human coronaviruses is improved by coupling with a metal chaperone.<sup>54,58</sup> *C. gigas* has a high zinc content<sup>60</sup> and given the suggested role for cavortin as a metal

TABLE 1 Proposed mode of action for marine mollusc antiviral extracts

Mollusc	Antiviral extract	Mode of action	Virus(s)	Reference(s)
Greenlip abalone ( <i>Haliotis laevis</i> )	Hemolymph	Inhibits viral entry	HSV-1	40,43
	Lipophilic digestive extract	Inhibits intracellular stage of viral infection	HSV-1	40
Blacklip abalone ( <i>Haliotis rubra</i> )	Hemocyanin	Inhibits viral entry	HSV-1	42,65
	Hemolymph	Unknown	HSV-1	43
Red abalone ( <i>Haliotis rufescens</i> )	Aqueous extract	Unknown	Poliovirus, Influenza A	46,47
Pacific oyster ( <i>Crassostrea gigas</i> )	Major hemolymph protein (cavortin)	Inhibits intracellular stage of viral infection	HSV-1	49
		Inhibits viral entry	HSV-1	50
	Hemolymph	Unknown	HSV-1, AdV-5	51
Eastern oyster ( <i>Crassostrea virginica</i> )	Paolin II	Unknown	Poliovirus	48
Mangrove oyster ( <i>Crassostrea rhizophorae</i> )	Hemolymph	Inhibits intracellular stage of viral infection	AdV-5, HSV-1	51
European flat oyster ( <i>Ostrea edulis</i> )	40% SPE-fraction from gill and mantle	Unknown	HSV-1	41
Mediterranean mussel ( <i>Mytilus galloprovincialis</i> )	Myticin C peptide	Inhibits intracellular stage of viral infection	HSV-1, HSV-2	45
Japanese carpet shell ( <i>Ruditapes philippinarum</i> )	40% SPE-fraction	Unknown	HSV-1	41
Common whelk ( <i>Buccinum undatum</i> )	40% SPE-fraction	Unknown	HSV-1	41
Veined rapa whelk ( <i>Rapanosa venosa</i> )	Hemocyanin	Unknown	EBV	44,66
Common cockle ( <i>Cerastoderma edule</i> )	Acidic extract	Unknown	HSV-1	41

Abbreviations: AdV-5, human adenovirus type 5; EBV, Epstein–Barr virus; HSV, herpes simplex virus; SPE, solid phase extraction.

chaperone,<sup>52</sup> it is possible that *C. gigas* cavortin has potential antiviral activity against SARS-CoV-2 and may also act as a metal chaperone which facilitates movement of zinc into host cells.

The discovery of antiviral agents is challenged by the limited number of laboratories which have the appropriate biosafety containment level for working with SARS-CoV-2.<sup>5,61</sup> HCoV-229E is a related coronavirus responsible for mild infections resembling the common cold.<sup>62,63</sup> HCoV-229E can be handled in lesser-rated laboratories making it more accessible for research on human coronaviruses<sup>64</sup> and this virus could be used for initial screening for anti-coronavirus activity. Identification of potential new antiviral compounds against human coronaviruses will have considerable relevance in the current COVID-19 pandemic.

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None.

## CONFLICT OF INTEREST

The authors declare no conflict of interests.

## AUTHOR CONTRIBUTIONS

Peter G. Speck was involved in conception, writing and editing. Rebecca L. Pedler was involved in writing and editing.

## DATA AVAILABILITY STATEMENT

Not applicable.

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