Searching for animal models and potential target species for emerging pathogens: Experience gained from Middle East respiratory syndrome (MERS) coronavirus

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Abstract

Emerging and re-emerging pathogens represent a substantial threat to public health, as demonstrated with numerous outbreaks over the past years, including the 2013–2016 outbreak of Ebola virus in western Africa. Coronaviruses are also a threat for humans, as evidenced in 2002/2003 with infection by the severe acute respiratory syndrome coronavirus (SARS-CoV), which caused more than 8000 human infections with 10% fatality rate in 37 countries. Ten years later, a novel human coronavirus (Middle East respiratory syndrome coronavirus, MERS-CoV), associated with severe pneumonia, arose in the Kingdom of Saudi Arabia. Until December 2016, MERS has accounted for more than 1800 cases and 35% fatality rate. Finding an animal model of disease is key to develop vaccines or antivirals against such emerging pathogens and to understand its pathogenesis. Knowledge of the potential role of domestic livestock and other animal species in the transmission of pathogens is of importance to understand the epidemiology of the disease. Little is known about MERS-CoV animal host range. In this paper, experimental data on potential hosts for MERS-CoV is reviewed. Advantages and limitations of different animal models are evaluated in relation to viral pathogenesis and transmission studies. Finally, the relevance of potential new target species is discussed.

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Keywords: Animal model, Coronavirus (CoV), Emerging pathogen, Middle East respiratory syndrome (MERS), Reservoir

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Abbreviations: BSL, biosafety level; DPP4, dipeptidyl peptidase-4; FDA, Food and Drug Administration; HCoV, human coronaviruses; hDPP4, human dipeptidyl peptidase-4; MERS-CoV, Middle East respiratory syndrome coronavirus; NHP, Nonhuman primates; PI, post-inoculation; RDB, receptor binding domain; SARS-CoV, severe acute respiratory syndrome coronavirus; URT, upper respiratory tract; WHO, World Health Organization.

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1. Introduction

Over the past years, outbreaks of zoonotic diseases and growing resistance against antibiotics have emphasized the need for interdisciplinary collaboration between human health, veterinary medicine and environmental sciences, a concept commonly known as “One health” [1]. Most of emerging diseases are zoonotic [2]. For instance, the human flu pandemics have originated in domestic animals and wildlife, and have been driven by ecological, behavioral, or socioeconomic changes [3]. In these cases, the reaction time between detection of a new outbreak and application of medical countermeasures are critical in terms of epidemic control. To understand the potential role that animal sources could play in virus dissemination and the epidemiology of the disease, surveillance studies, as well as experimental infections in potential target species, are required. Furthermore, after having identified the novel or re-emerged virus responsible of the outbreak, it is important to rapidly provide an accurate diagnosis as a basis for quarantine measures. It is also imperative to focus on the search for new vaccines and treatments for highly pathogenic viruses, especially for those that represent a threat to human and animal health, particularly livestock.

Until the beginning of the last decade, human coronaviruses (HCoV) infections were considered to be restricted to the upper respiratory tract (URT), with low mortality rate, and recognized as the second ranked cause of the common cold after rhinoviruses [4]. However, in the late-2002, the severe acute respiratory syndrome coronavirus (SARS-CoV) emerged in China. It rapidly spread worldwide with more than 8000 causalities and a lethality rate of 10% [5]. Ten years later, a novel HCoV associated with severe pneumonia emerged in the Kingdom of Saudi Arabia [6]. The new CoV was named Middle East respiratory syndrome coronavirus (MERS-CoV), and by March 2014, a total of 207 cases and 45% fatalities were recorded. One month later, only in April 2014, an increase in human cases was registered with at least 217 more infected people and 38 fatalities. More recently, as of December 2016, 1842 cases of MERS-CoV have been reported to the World Health Organization (WHO), including at least 652 deaths [7].

Besides coronaviruses, highly pathogenic viruses belonging to other families represent a threat to either human or animal health, or both. One of the most recent examples is the outbreak of Ebola virus (Filoviridae) in West Africa, which started in December of 2013 in Guinea and evolved as the largest Ebola outbreak recorded with more than 28,600 cases [8]. Furthermore, during recent years, outbreaks caused by other emerging viral pathogens from Arenaviridae, Bunyaviridae, and Flaviviridae families among others, disturbed public and private health, social networks and the economies of the affected countries [9, 10]. Prevention and control of emerging and reemerging viral diseases is efficient when several actions are combined: i.e. creating diagnostic networks and surveillance programs, training medical and veterinary staff, informing the population about sanitary measures, and also promoting research on prophylaxis, treatments and on the causative agent pathogenesis. Regarding the last point, animal models are crucial to study the viral and host factors contributing to the disease as well as transmission outcomes of virus infection and to allow pre-clinical testing of antiviral drugs and vaccines. Non-human primates (NHP) are the preferred models for pathogenesis studies, and potential vaccine and treatment testing, as they better translate to humans [11]. However, working with NHP is costly, with limited availability, and raises ethical problems. Therefore small-animal models are usually the first choice for drug screening. The United States Food and Drug Administration’s (FDA) Animal Rule provides guidelines concerning the appropriateness of animal models for licensing purposes [12]. Additionally, by controlling the disease in animal reservoirs and/or in intermediate hosts, virus transmission to humans can be significantly reduced [13, 14]. This is particularly true for domestic or feral animals for which efficient vaccines and vaccination strategies can be implemented [15]. Therefore, in cases of new pathogenic virus outbreaks, the search for natural hosts or potential target animals (as opposed to laboratory animals) seems to be relevant not only to implement prophylactic solutions but also to improve the preparedness for an eventual global extension of diseases. Nowadays, this task is rendered possible by the availability of improved biosafety levels 3 and 4 (BSL3 and 4) animal facilities, which can accommodate large animal experimentation with such highly virulent pathogens [16].

In this article, the current situation of comprehension on potential hosts for MERS-CoV is reviewed. Based on the coronaviruses experience, benefits and limitations of these species as animal models and transmission studies are discussed.

2. Animal models for MERS research

Several review articles have described and discussed animal models for MERS-CoV infection [17–20]. In this section, the current status of animal models for MERS disease reproduction is briefly summarized.

After the identification of MERS-CoV in 2012 [6], the efforts were directed to develop an animal model to study pathogenesis and to test the efficacy of vaccines and/or treatments in vivo. Similar to SARS-CoV, rhesus macaques have demonstrated susceptibility to MERS-CoV [21–23]. A work led by Munster demonstrated that the common marmoset is also suitable as a MERS-CoV model [24]. They showed that this model recapitulates the disease observed in humans; therefore, findings in the evaluation of potential therapeutic strategies might be implemented in humans. However, small animals are required for controlled, large and comprehensive studies. While, at first, experiences with SARS-CoV turned out to be very helpful for the research on MERS-CoV, the development of a small animal model for MERS was a more difficult task [18, 19]. Raj and collaborators rapidly identified dipeptidyl peptidase-4 (DPP4) as the functional receptor for MERS-CoV [25], and DPP4 is present in lung cells of many rodents. Thus, rodents were expected to be susceptible for MERS-CoV. However, and as predicted by the crystal structure analysis of the MERS-CoV receptor binding domain (RBD) with the human DPP4 (hDPP4) extracellular domain [26], so far, no rodent model is naturally permissive for MERS-CoV infection. In Syrian hamster, the DPP4 receptor was shown to be expressed on bronchiolar epithelium, but inoculation of MERS-CoV via aerosols or intratracheal routes with different doses did not lead to productive infection [27]. Wild type and immune-deficient mice were also tested for MERS-CoV infection without success [28]. Since then, several groups have been focused on new strategies to develop a small animal model susceptible to MERS-CoV infection. It was found that mouse cells could be made permissive for MERS-CoV when expressing hDPP4. Consequently, the hDPP4 was transduced into mouse lungs using an adenovirus vector, which resulted in animals susceptible to MERS-CoV infection. These mice exhibited pneumonia and extensive inflammatory–cell infiltration with the presence of virus in the lungs [29]. Recently, a transgenic mouse model expressing hDPP4, highly susceptible to MERS-CoV infection and able to display systemic lesions, has been developed [30]. As demonstrated for several diseases, transgenic animal models have become an important tool to improve medical research [31]. On the other hand, glycosylation of the murine DPP4 is a major factor impacting the receptor function by blocking the binding to MERS-CoV [32]. Therefore, the modification of the mouse genome to match the sequence in the hDPP4 made this species susceptible to MERS-CoV infection [33]. Accordingly, these newly established mice models are useful to evaluate the efficacy of vaccines and therapeutic agents against MERS-CoV infection [30, 34–36]. VelocImmune and Velocogene technologies have been used to develop a humanized mouse model for MERS-CoV infection [36]; these methodologies can be also applied for other pathogens in future emerging epidemics.

3. MERS-CoV animal reservoir and the role of domestic animals

Researchers worldwide have identified several animal species which could have a role in the transmission of MERS-CoV to humans (summarized in Fig. 1). Bats have been suggested to be the reservoir for MERS-
CoV, but RNA of MERS-like CoVs (and no MERS-CoV) has been found in several bat families (Vespertilionidae, Molossidae, Nycteridae and Emballonuridae) in Africa, America, Asia and Europe [37,38]. Recently, an experimental infection with Jamaican fruit bats (Artibeus jamaicensis) confirmed that MERS-CoV can replicate in bats [39]. However, MERS-CoV strains causing disease in humans have not been so far identified in bats. The presence of MERS-CoV neutralizing antibodies has been reported in dromedary camels (Camelus dromedaries) [40,41] and, more recently, a link between MERS-CoV infection in camels and a human infection in Qatar has been suggested [42–45]. Most importantly, the MERS-CoV strain that caused the 2015 human outbreak was found in dromedary camels; in fact, phylogenetic analyses indicate that MERS-CoV was generated in this species by recombination [46]. In addition, Adney and collaborators have provided experimental evidence to support the role of dromedary camels as a MERS-CoV reservoir [47]. Recently, evidence was provided that other members of the Camelidae family such as alpaca (Vicugna pacos) and llama (Lama glama), are also susceptible to MERS-CoV [48–50]. Field studies with alpacas performed in Qatar confirmed this finding [51]. A recently published experimental study has demonstrated that domestic pigs are also susceptible to MERS-CoV infection, suggesting the possibility of MERS-CoV circulation in other unsuspected animal species such suidae [50]. While DPP4 in silico predictions and in vitro studies suggested that other livestock species such as goats, sheep, or horses could be susceptible to MERS-CoV infection, experimental data suggested the opposite [50]. Each natural and potential host for MERS-CoV infection is discussed below in detail and summarized in Tables 1 and 2.

3.1. Camelids

Dromedary camels are the main source of MERS-CoV zoonotic transmission (reviewed in [52]). In experimental intranasal inoculations with MERS-CoV, only mild clinical signs (i.e. nasal discharge) with URT infection were observed. Viral RNA was detected in nasal swabs, in upper and lower respiratory tracts, and also in extra-pulmonary tissues (i.e. lymph nodes, tonsil, intestine, liver, adrenal gland, etc.). In contrast, infectious virus was only detected in the URT, trachea, large bronchus and tracheobronchial lymph node. Gross lesions were not observed in dromedary camels, but inflammation in the nasal cavity, trachea and bronchus was present. The virus replication in dromedaries was only detected in epithelial cells in the URT [47,53].

Llamas and alpacas, also known as domestic new world camelids, developed a similar clinical-pathological picture to that of dromedaries after experimental MERS-CoV infection. In both species the virus was inoculated via intranasal route, and either no clinical signs (alpacas) or mild mucus secretion (llamas) was observed. MERS-CoV was detected in nasal swabs, and in the URT and trachea of both llamas and alpacas. None of the species showed lesions macroscopically, but microscopically mild to severe rhinitis was detected in alpacas as well as metaplasia of the epithelium of the turbinate in alpacas. Similar to dromedaries, the epithelial cells in the URT were the main target cells for virus replication. Concomitant to an antibody response, the virus was cleared from the URT 7 to 10 days after experimental infection [48–50].

3.2. Non-camelid domestic species

After intranasal inoculation of MERS-CoV, only mild excretion of mucus was observed in 6 to 8-week old domestic pigs [50]. Viral RNA was detected in nasal swabs, in the URT, trachea and bronchus. Although gross lesions were not present in pigs, they showed mild to moderate rhinitis, with virus replication observed in the epithelial cells in the URT. Shedding of MERS-CoV was detected in nasal swabs from days 1 to 10 PI, but infectious virus was only detected until day 4 PI. Viral RNA was also detected in the URT, trachea and bronchus [50].
New Zealand white rabbits did not exhibit clinical signs or significant gross lesions at necropsy after experimental MERS-CoV inoculation; thus, they were considered an animal model of asymptomatic infection [54]. Similar to pigs, mild to moderate rhinitis with necrosis was observed, and respiratory epithelial cells in the URT were identified as the target cells for MERS-CoV replication. Viral RNA was present in nasal swabs, and upper and lower respiratory tracts. Infectious virus was also detected in nasal swabs up to 7 days PI [54].

3.3. Non-human primates

The rhesus macaque was used as the first animal model developed for MERS-CoV infection, showing mild to moderate respiratory disease from day 1 to 4 PI after intratracheal inoculation [21]. Gross lesions were present only in the lung, consisting in congestion and presence of nodules, and the main observed microscopical lesion was interstitial pneumonia. Although MERS-CoV RNA was detected in nasal swabs, bronchoalveolar lavage samples, oropharyngeal swabs; PFU, plaque-forming units; PSG, parotid salivary gland; RNA, ribonucleic acid; TCID50/IT, 5.5 × 10^7; TCID50/IN, 5 × 10^6 TCID50; TCID50, 50% tissue culture infectious dose; URT, upper respiratory tract.

### Table 1
Summary of MERS-CoV shedding and presence of virus in different tissues in the potential animal reservoirs for MERS-CoV after experimental inoculation.

| Species | Route and dose of inoculation | MERS-CoV shedding | MERS-CoV RNA in tissues | MERS-CoV antigen in tissues | References |
|---------|-------------------------------|-------------------|-------------------------|-----------------------------|------------|
| Camelids | Dromedary camels (Camelus dromedarius) | IT, IN, conjunctival or IN only; 10^7 TCID50 | Viral RNA in NS (1 to 13 dpi) | URT, LRT, tracheal LN, pulmonary LN, cervical LN, tonsil, PSG, intestine, liver, spleen, kidney, heart, adrenal | ND [47,53] |
| | Alpacas (Vicugna pacos) | IN; 10^7 PFU in 3 mL saline solution | Infectious virus in NS (1 to 5 dpi) | Nasal respiratory epithelial cells | ND [48,49] |
| | Llamas (Lama glama) | IN; 10^7 TCID50 in 3 mL saline solution | Viral RNA in NS (1 to 15 dpi) | Nasal respiratory epithelial cells | ND [50] |
| Non-camellid domestic species | Domestic pig (Sus scrofa domesticus) | IN; 10^7 TCID50 in 3 mL saline solution | Viral RNA in NS (1 to 10 dpi) | URT, trachea and bronchus | ND [50] |
| | Rabbit (Oryctolagus cuniculus) | IN (1 × 10^6 TCID50), IT (4 × 10^5 TCID50) | Viral RNA in NS (1 to 10 dpi) | Mainly in URT, LRT nasal respiratory and bronchiolar epithelial cells | ND [54] |
| NHP | Rhesus macaques (Macaca mulatta) | IT, OC, oral, IN; 7 × 10^6 TCID50/IT, 6.5 × 10^5 TCID50 | Viral RNA in NS, BAL samples, and few OS | URT, lung, mediastinal LN | Lung [21–23] |
| | Common marmoset (Callithrix jacchus) | OC, oral, IT, IN; 5 × 10^5/IT, 5 × 10^5 TCID50 | Viral RNA in NS and OS | URT, lung, mediastinal LN, blood | Nasal mucosa, trachea, lung [24,55] |

Abbreviations: BAL, bronchoalveolar lavages; dpi, days post inoculation; IN, intranasal; IT, intratracheal; LN, lymph node; LRT, lower respiratory tract; M, macrophages; ND, non-detected; NHP, non-human primates; NS, nasal swabs; OC, ocular; OS, oropharyngeal swabs; PFU, plaque-forming units; PSG, parotid salivary gland; RNA, ribonucleic acid; TCID50; 50% tissue culture infectious dose; URT, upper respiratory tract.

The rhesus macaque was used as the first animal model developed for MERS-CoV infection, showing mild to moderate respiratory disease from day 1 to 4 PI after intratracheal inoculation [21]. Gross lesions were present only in the lung, consisting in congestion and presence of nodules, and the main observed microscopical lesion was interstitial pneumonia. Although MERS-CoV RNA was detected in nasal swabs, bronchoalveolar lavage samples, oropharyngeal swabs, and also in some upper and lower respiratory tract tissue samples, infectious virus was only isolated from the lungs. MERS-CoV replication occurred in type I and II pneumocytes, and viral antigen co-localized with sites of pneumonia [21]. Macaques represent a useful model to study mild MERS-CoV infection because they develop a transient respiratory disease similar to humans.

On the other hand, common marmosets exhibited moderate to severe respiratory disease from 1 to 13 days after inoculation of MERS-CoV through multiple routes (ocular, oral, intratracheal and intranasal) [24]. Similar to macaques, gross findings were present only in the lung.

### Table 2
Summary of clinical signs, pathological findings and target cells in tissues of natural and potential reservoir hosts for MERS-CoV infection as experimental animal models.

| Species | Clinical signs | Gross findings | Histopathological lesions | Target cells in tissues | References |
|---------|----------------|----------------|--------------------------|-------------------------|------------|
| Camelids | Dromedary camels (Camelus dromedarius) | Mild respiratory disease, nasal discharge | Not present | Multifocal moderate rhinitis, tracheitis and bronchitis with epithelial necrosis. Hyperplasia of lymph nodes and tonsil | Respiratory epithelial cells in the URT [47,53] |
| | Alpacas (Vicugna pacos) | Not observable | Not present | Squamous metaplasia of the epithelium of the turbinates. Hypertrophy and hyperplasia of lymph nodes | Respiratory epithelial cells in the URT [48,49] |
| | Llamas (Lama glama) | Mild mucus secretion in one nostril | Not present | Mild to severe rhinitis | Respiratory epithelial cells in the URT [50] |
| Non-camellid domestic species | Domestic pig (Sus scrofa domesticus) | Mild excretion of mucus in the nose | Not present | Mild to severe rhinitis | Respiratory epithelial cells in the URT [50] |
| | Rabbit (Oryctolagus cuniculus) | Not observable | Not present | Focal mild to moderate rhinitis with necrosis | Respiratory epithelial cells in the URT [54] |
| NHP | Rhesus macaques* (Macaca mulatta) | Fever, mild to moderate respiratory disease | Lung congestion and nodules in lung | Multifocal mild-to-moderate interstitial pneumonia | Type I and II pneumocytes and alveolar macrophages [21,22,23] |
| | Common marmoset* (Callithrix jacchus) | Mild to severe respiratory disease | Congestion of bronchioles | Diffuse interstitial infiltration in lower lung lobes, bronchointerstitial pneumonia | Type I pneumocytes and alveolar macrophages [24] |

Abbreviations: NHP, non-human primates; URT, upper respiratory tract.

* Also animal models of disease (translation to human).
and correlated with moderate to severe bronchointerstitial pneumonia. MERS-CoV antigen was detected by immunohistochemistry in both type I and II pneumocytes and alveolar macrophages, but the virus replicated only in type I pneumocytes and macrophages. Similar results were observed in marmosets after inoculation of MERS-CoV only via intratracheal route [55]. However, the outcome of MERS-CoV infection in marmosets has been controversial after the publication of a recent study by Johnson and collaborators, which demonstrated no lethality after intratracheal inoculation [56]. The outcome of experimental infections in both species is reviewed in recent publications [17–20].

4. Advantages and disadvantages of animal hosts used for MERS-CoV experimental infection

As described in the previous section, a number of animal species have been described as either natural reservoir (dromedary camel) or potential intermediate hosts of MERS-CoV, each one with its benefits and limitations (Table 3) when used as experimental infection models. Camelids (dromedary camels, alpacas and llamas), non-camelid domestic species (pigs and rabbits), and NHP (rhesus macaques and common marmosets) have been experimentally demonstrated to be susceptible to MERS-CoV infection, but with differences among them [21–24,47–50,53,54]. Experiments with dromedary camels, the natural MERS-CoV host, and probably the first target for controlling MERS through vaccination [53], are costly and represent a high security risk for animal caretakers because of the difficulty in handling these animals under appropriate biosafety conditions. The main advantages of using the llama or alpaca models are that both belong to the family Camelidae, have smaller size, more gentle behavior, and are more available at a commercial level than dromedary camels; importantly, specific reagents for immune monitoring have been developed for new world camels [57]. Therefore, they may be useful surrogates for dromedaries under experimental conditions. However, both models are quite expensive and require large and complex BSL3 facilities. In contrast to camels, other domestic species such as pigs and rabbits are readily available, with lower cost and easier handling. Additionally, an extensive panel of specific-immunological reagents is available for these species. When compared to camels, however, lower MERS-CoV titers were detected in nasal cavities and tissue samples of pigs and rabbits during the infection. Furthermore their usefulness as animal models for transmission studies has not yet been addressed.

Contrary to the mentioned species, both macaques and common marmosets develop clinical disease relatively similar to humans. In that respect, phylogenetically-related species as babbons [58], which live in Africa and Arabic Peninsula, might also play a role in the transmission of the virus. However, little attention has been paid to these species since no sero-epidemiology has been documented. There are important limitations when working with NHP models, namely the complex husbandry requirements that lead to substantially increased costs, some controversy results among different groups. Besides practical considerations, human-specific immunological reagents cross-react with NHP species and are widely available.

5. Conclusion and future steps

As summarized in this review, several species of animals are susceptible to experimental MERS-CoV infection; thus, they might act as potential intermediate hosts of the disease. However, the presence of viral RNA and/or specific antibodies against the virus has been only demonstrated in the field in dromedaries and alpacas [41,51]. At the light of recent experimental studies, it seems that the list of potential host targets for MERS-CoV is not closed. MERS surveillance programs should be implemented in endemic areas in animal species for which experimental evidence of susceptibility has been provided and species closely related to them.

Table 3

| Species | Advantages | Limitations |
|---------|------------|-------------|
| Camelids | Natural host for MERS-CoV | Expensive and limited availability |
| | Efficient animal-to-animal transmission (field studies) | Complex husbandry requirements (large BSL3 facilities) |
| | Potential surrogates for dromedaries under experimental conditions (potential hosts for MERS-CoV) | Expensive and limited availability |
| | Efficient animal-to-animal transmission (experimental) | Complex husbandry requirements (large BSL3 facilities) |
| | Potential surrogates for dromedaries under experimental conditions (potential hosts for MERS-CoV) | Complex husbandry requirements (large BSL3 facilities) |
| | Relative low cost and readily available | No animal-to-animal transmission studies available |
| Non-camelid domestic species | Ease handling | Complex husbandry requirements (large BSL3 facilities) |
| | Potential surrogates for dromedaries under experimental conditions (potential hosts for MERS-CoV) | Limited transmission (only via direct contact, and during few days) |
| | Animal-to-animal transmission (experimental) | Lower viral titers in NS and tissues upon infection |
| | Pig-specific immunological reagents are available | No animal-to-animal transmission studies available |
| | Low cost and readily available | Lower viral titers in NS and tissues upon infection |
| | Ease handling | |
| | Potential surrogates for dromedaries under experimental conditions (potential hosts for MERS-CoV) | |
| | Rabbit-specific immunological reagents are available | |
| | Human-specific immunological reagents are widely available | |
| | Clinical disease similar to humans: translational research (for intra species transmission) | |
| NHP | Some human-specific immunological reagents cross-react | Expensive and limited availability |
| | Clinical disease similar to humans: translational research (for intra species transmission) | Complex husbandry requirements (large BSL3 facilities) |

Abbreviations: BSL3, biosafety level 3; MERS-CoV, Middle East respiratory syndrome; NHP, non-human primates; NS, nasal swabs.
SARS and MERS outbreaks taught us many lessons, and one of the most important is that, even in the absence of an overt threat, there is the possibility of the re-emergence of a virus or other similar viruses. On the other hand, and since the first case of MERS, continuous new cases have been described in different countries around the world [59–62]. This undermines the importance of the development of animal models closer to the natural host targets. The key role of domestic animals and wildlife in the transmission of MERS-CoV should be further elucidated; meanwhile, countermeasures against deadly coronaviruses must be further explored since the risk of a global outbreak is not negligible. Noteworthy, after more than a decade of SARS and five years of MERS epidemics, there are still no licensed preventive or therapeutic drugs available that could be used in case of an eventual re-emergence of SARS or MERS. This scenario is not the outcome of technical issues, since effective vaccine prototypes against those pathogens are already available [53,63,64]. In case of MERS-CoV, vaccination of dromedary camels, the main source of zoonotic transmission, might be useful to control the spread of MERS [53]. However, when developing a vaccine, besides testing the protection efficacy, researchers need to think about social problems such as the reticence of camel owners to vaccinate their animals. Thus, the development of a dual vaccine able to protect against both, MERS-CoV and camelpox virus (an endemic disease in the Middle East, Africa and Asia) might be an ideal solution [53]. Recently, another dual-vaccine for humans and animals against MERS-CoV and rabies virus has been designed [65]. Political aspects have also a key role in the release of a vaccine into the market. Unless the requirements and timings for vaccine licensing procedures are facilitated, pharmaceutical companies will unlikely invest in their development taking into account the current market demand. Moreover, fragmentation of intellectual property rights may also adversely affect the development of vaccines to combat those infections [66].

Conflicts of interest

None.

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