Mass culling of minks to protect the COVID-19 vaccines: is it rational?

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Abstract

The Danish Government announced the culling of 17 million minks in rearing after the report of mink-specific mutations of severe acute respiratory syndrome coronavirus 2 in humans. The rationale behind this decision is that these mutations might negatively impact the deployment of anti-coronavirus disease 2019 vaccines. Is it a precautionary attitude or a panic-driven overreaction?

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To the Editor,

The Danish Government released on Wednesday 4 November 2020 a statement, relayed by WHO on 6 November 2020 [1], that the 17 million minks present within all mass-rearing facilities in Denmark would be culled. This decision was based on the identification in September 2020 of a novel variant of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in 12 people in North Jutland, Denmark. This variant was also found in a mink-rearing facility. The 12 individuals were linked to the mink rearing. This variant was considered as bearing mink-

related mutations. Fearing that these mutations may be a threat to the human population and that they might interfere with future anti-SARS-CoV-2 vaccines, the decision was taken to cull all of the 17 million minks in Denmark. These mutations have not been made public and there is no evidence yet that the mutations observed in the minks in Denmark will affect the development of vaccines in humans. A rational attitude would be to isolate those minks while more information is gathered on the true meaning of the mutations observed. SARS-CoV-2, like other coronaviruses and RNA viruses, is evolving through a quasispecies mechanism [2-4]. A main characteristic of the quasispecies evolutionary process is the generation of postinfection mutations under positive selective pressure, i.e. host-driven viral evolution [5]. Therefore, mutations are not pre-existing but instead are acquired after infection and are specific to the host, usually allowing the virus to escape host defence mechanisms [6,7]. SARS-CoV-2 can infect both humans and minks, each one being a source of infection [8]. SARS-CoV-2 variants reported in minks in Denmark [1] are very likely to be 'mink signatures', i.e. adaptation to the host. In turn, humans infected with a virus coming from minks are most likely to force the virus to mutate to evade the human immune defence system. Mutations in humans will therefore be different from those in minks.

Mink is not the only species outside humans to be infected by SARS-CoV-2. Many other wild animals such as bats, pangolins, palm civets, ferrets, monkeys, turtles, snakes and even whales can potentially be infected because they bear a compatible angiotensin-converting enzyme 2 receptor [9]. However, this is not limited to wild animals and several domestic species display the same trait, including cats, dogs, pigs, sheep, cows, water buffalo, goats and pigeons [9]. These wild and domestic animals present the same risk of infecting humans back with SARS-CoV-2. Coronavirus disease 2019 has been clearly shown in cats and dogs, which are humans' closest companions [10]. Should we take the same decision as with minks and cull them? This would be irrational behaviour. Minks might show specific mutations because of the mass-rearing conditions and containment, which generate a high population density, a high rate of contacts and fast frequency increase of viral genotypes that have evolved in the host. The spillover model of pre-existing adapted 'humanactive' genotypes in the wild has never been demonstrated and another model, the circulation model, has been proposed to explain the in-host evolution of 'human-active' mutations after transmission and circulation of the virus in humans [9].

Fear is commonly observed in the face of a pandemic. However, fear and panic should not be the drivers because they lead to irrational reactions. Culling millions of animals with no evidence of actual danger but simply on the basis of fear is setting up a dangerous precedent. The risk is high then to consider that the safest way of protecting humans from any zoonosis would be to eradicate the animals around. Humans are exposed to diseases. It is a natural process that we cannot deny and we cannot avoid. The right attitude is not to cull and eradicate all putative threats as a precaution but instead, as we occupy all the planet with a very large and still growing population, to ask ourselves how human activities impact the emergence and diffusion of infectious diseases. Human activities are the real drivers of epidemics and pandemics. The rational behaviour would then be to organize these activities properly to reduce that risk instead of building a safety dome by eradicating all supposed sources of infection.

Ethics declarations

No human samples or clinical data were used.

Author contributions

RF and CAD contributed equally to the manuscript. Both authors participated in the writing and correction of the manuscript. Both authors read and agreed with the manuscript.

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Conflicts of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

References

- WHO. Available from: https://www.who.int/csr/don/06-november-2020-mink-associated-sars-cov2-denmark/en/; 2020.
- [2] Karamitros T, Papadopoulou G, Bousali M, Mexias A, Tsiodras S, Mentis A. SARS-CoV-2 exhibits intra-host genomic plasticity and lowfrequency polymorphic quasispecies. J Clin Virol 2020;131:104585.
- [3] Xu D, Zhang Z, Wang FS. SARS-associated coronavirus quasispecies in individual patients. N Engl J Med 2004;350:1366–7.
- [4] Jary A, Leducq V, Malet I, Marot S, Klement-Frutos E, Teyssou E, et al. Evolution of viral quasispecies during SARS-CoV-2 infection. Clin Microbiol Infect 2020. https://doi.org/10.1016/j.cmi.2020.07.032. Epub ahead of print.
- [5] Cali L, Wang B, Mikhail M, Gill MJ, Beckthold B, Salemi M, et al. Evidence for host-driven selection of the HIV type I vpr gene in vivo during HIV disease progression in a transfusion-acquired cohort. AIDS Res Hum Retrovir 2005;21:728–33.
- [6] Martínez MA, Martrus G, Capel E, Parera M, Franco S, Nevot M. Quasispecies dynamics of RNA viruses. In: Witzany G, editor. Viruses: essential agents of life. Dordrecht: Springer; 2012. p. 21–42.
- [7] Woo HJ, Reifman J. A quantitative quasispecies theory-based model of virus escape mutation under immune selection. Proc Natl Acad Sci USA 2012;109:12980–5.
- [8] Munnink BBO, Sikkema RS, Nieuwenhuijse DF, Molenaar RJ, Munger E, Molenkamp R, et al. Jumping back and forth: anthropozoonotic and zoonotic transmission of SARS-CoV-2 on mink farms. bioRxiv 2020. https://doi.org/10.1101/2020.09.01.277152.
- [9] Frutos R, Serra-Cobo J, Chen T, Devaux CA. COVID-19: time to exonerate the pangolin from the transmission of SARS-CoV-2 to humans. Infect Genet Evol 2020;84:104493.
- [10] Leroy EM, Gouilh MA, Brugère-Picoux J. The risk of SARS-CoV-2 transmission to pets and other wild and domestic animals strongly mandates a one-health strategy to control the COVID-19 pandemic. One Health 2020;10:100133.