DRAFT

HIGH LEVEL SUMMARY OF EMERGING VIRAL THREATS TO HUMAN HEALTH

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Overview

Viruses from 28 different families (10 DNA, 18 RNA) are known to infect mammals (Table 1).

Viruses from 27 of these families can infect humans.

Viruses from 22 of these families are capable of epidemic spread in human populations.

Viruses from 22 of these families have been associated with human deaths.

We stress that the wide taxonomic distribution of these traits makes it unwise to rule out a potential future public health threat from any broad category of mammal or bird viruses. Here, however, we limit discussion to three categories of viruses:

1) Clear and present danger
2) Concern
3) Gaps

We do not discuss viruses for which effective vaccines are already available (e.g. MMR, polio, rotavirus, rabies). However, we note the possibility of vaccine escape.

Nor do we discuss endemic viruses long identified as candidates for vaccine development (e.g. HIV, RSV).

Clear and present danger

This category covers taxa containing viruses that are well-recognised public health threats and where (better) vaccines are needed.

Filoviridae, including the ebolaviruses and Marburg virus. These cause haemorrhagic fevers and are transmitted by contact. Most, but not all, are associated with severe disease in humans.

Coronaviridae, including the severe respiratory infections SARS CoV and MERS CoV. We note that although there are not currently any vaccines available against human coronaviruses there are vaccines for animal coronaviruses (canine CoV and porcine epidemic diarrhoea virus).

Orthomyxoviridae, the human influenza viruses, plus the avian influenzas. Vaccine reformulation is a long-standing issue. Antivirals have the advantage of being effective against a broader spectrum of influenza viruses than strain-specific vaccines.