

Example Risk Assessment Template: Coronaviruses (DRAFT 6)

Coronaviruses or nucleic acids Factors of interest	Human or animal coronaviruses of mild virulence	Coronavirus that causes serious or fatal diseases of man or animals	Genetically engineered coronaviruses that include wild type and mutant genes from mildly pathogenic coronaviruses, unrelated viruses or cellular genes*	Genetically engineered coronaviruses that include wild type or mutant genes from highly pathogenic coronaviruses, other viruses or cellular genes	cDNA of entire coronavirus genome in vaccinia or BAC that can be amplified <i>in vitro</i>	Plasmid set containing contiguous inserts that can be assembled into an entire full length genome that cannot be amplified <i>in vitro</i>	Infectious coronavirus genomic RNA transcribed <i>in vitro</i> from cDNA in vaccinia or BAC, or transcribed <i>in vivo</i> from infectious cDNA clone	Replication defective coronaviruses
Origin of virus strain (host species, epidemiology, geographic source and passage history)								
Pathogenicity in humans								
Pathogenicity in natural host species								
Pathogenicity in animal model(s)								
Potential for zoonotic reservoir								
Route of transmission or inoculation								

Infectious dose								
Concentration and total volume of infectious virus per experiment								
Agent stability (environmental)								
Genetic stability (ability to recombine with circulating coronaviruses)								
Medical surveillance								
Availability of sensitive diagnostic tests for infection								
Availability of effective prophylaxis or therapeutic intervention								
Training, experience, and skill of at-risk personnel								
Availability of adequate biosafety laboratory facilities and protocols for the proposed project								

* Some genes or mutations might enhance virulence, so this must be considered on a case-by-case basis.