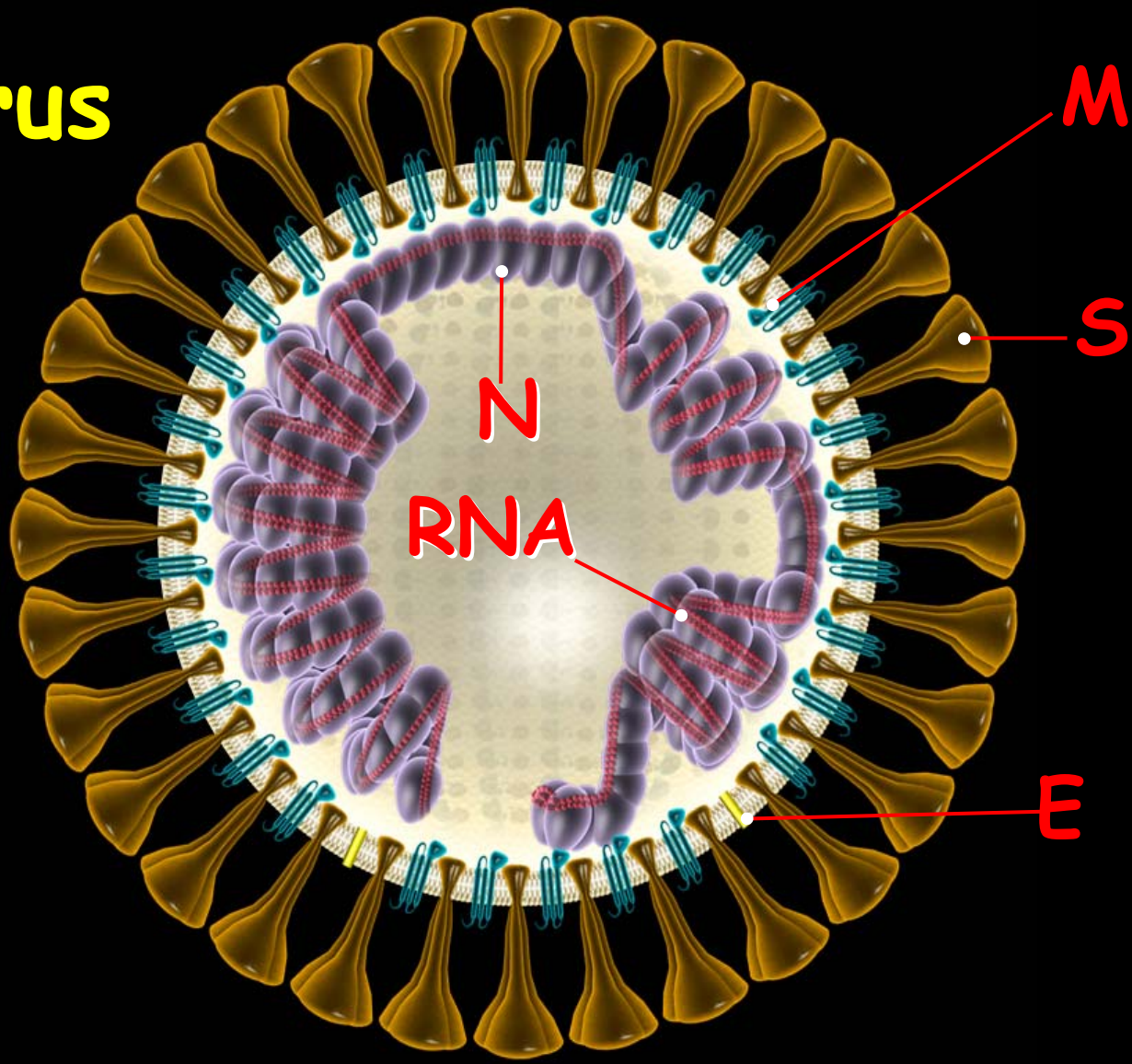
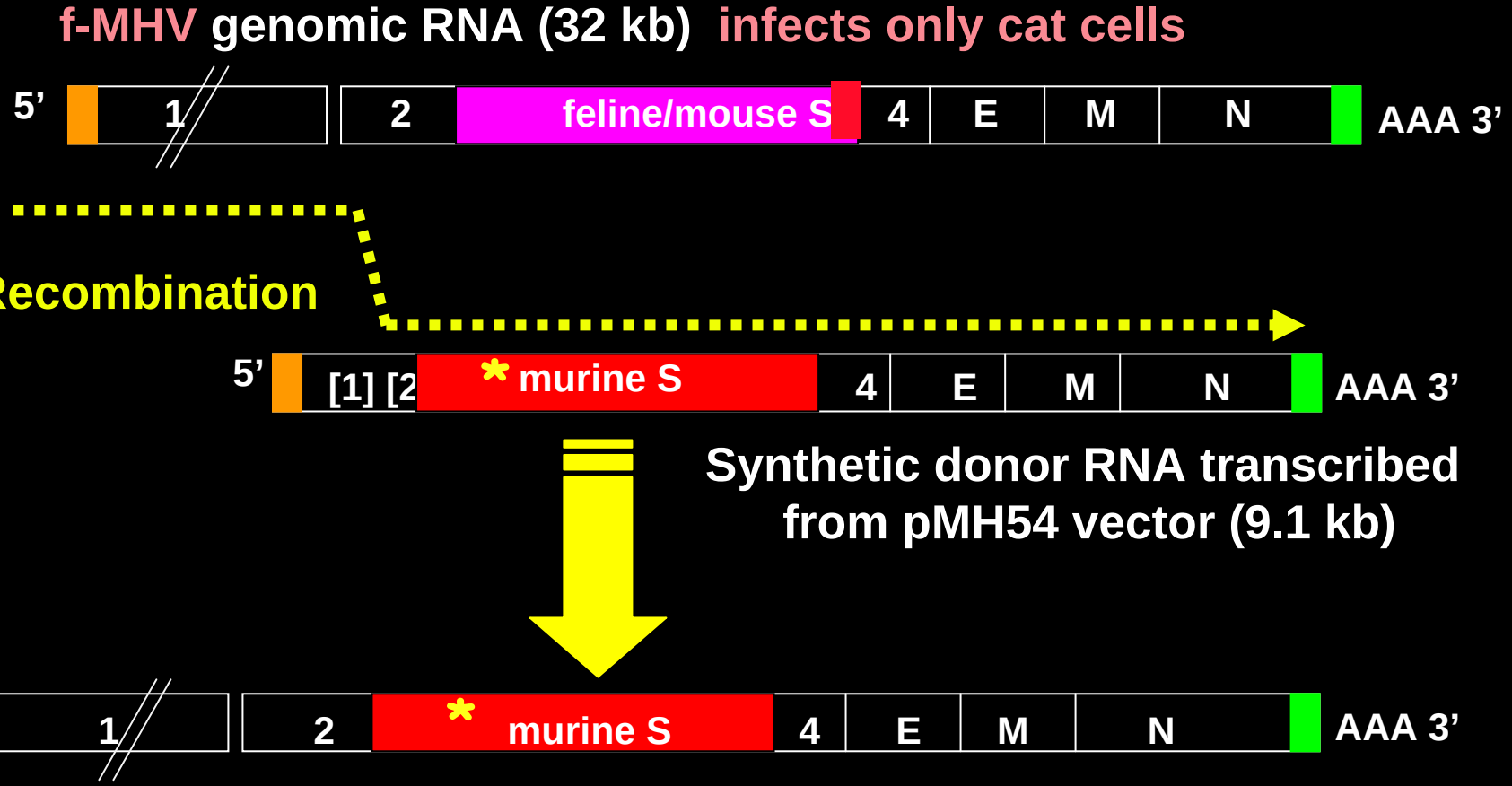
SARS Coronavirus



©jacobsonb@njh.org

30 kb plus sense RNA genome

TARGETED RNA RECOMBINATION IN CORONAVIRUS GENETICS



Kuo et al., J. Virol 74:1393 (2002)

Coronaviruses and host ranges of infection

Genetic Group	Virus	Host with disease
I	HCoV-229E	human
	TGEV	pig
	PRCoV	pig
	PEDV	pig
	FIPV	cat
	FCoV	cat
	CCoV	dog
2	HCoV-OC43	human
	MHV	mouse
	RCoV	rat
	HEV	pig
	BCoV	cattle
2 like	SARS-CoV	human

Coronaviruses and host ranges of infection

Genetic Group	Virus	Host with disease	Other species infectable
I	HCoV-229E	human	cat
	TGEV	pig	cat
	PRCoV	pig	cat
	PEDV	pig	
	FIPV	cat	dog
	FCoV	cat	
	CCoV	dog	cat
2	HCoV-OC43	human	mouse
	MHV	mouse	rat
	RCoV	rat	mouse
	HEV	pig	
	BCoV	cattle	deer, turkey, human
2 like	SARS-CoV	human	palm civet, raccoon dog, monkey, ferret, mouse, hamster

New and emerging viruses

- We cannot predict what virus family will emerge next.
- Each virus family has different reverse genetics techniques.
- Some safety considerations are virus-specific
- Public health needs demand urgent research on new agents.

Communication between investigator and IBC

- Communication must be thorough and efficient

Communication between investigator and IBC

- Communication must be thorough and efficient
- Investigator must know what information is needed to fill out application.

Communication between investigator and IBC

- Communication must be thorough and efficient
- Investigator must know what information is needed to fill out application.
- IBC needs access to up-to-date information to evaluate application.
- Evaluation of risk must be iterative,

Communication between investigator and IBC

- Communication must be thorough and efficient
- Investigator must know what information is needed to fill out application.
- IBC needs access to up-to-date information to evaluate application.
- Evaluation of risk must be iterative, sometimes down-grading BSL level as new information becomes available.