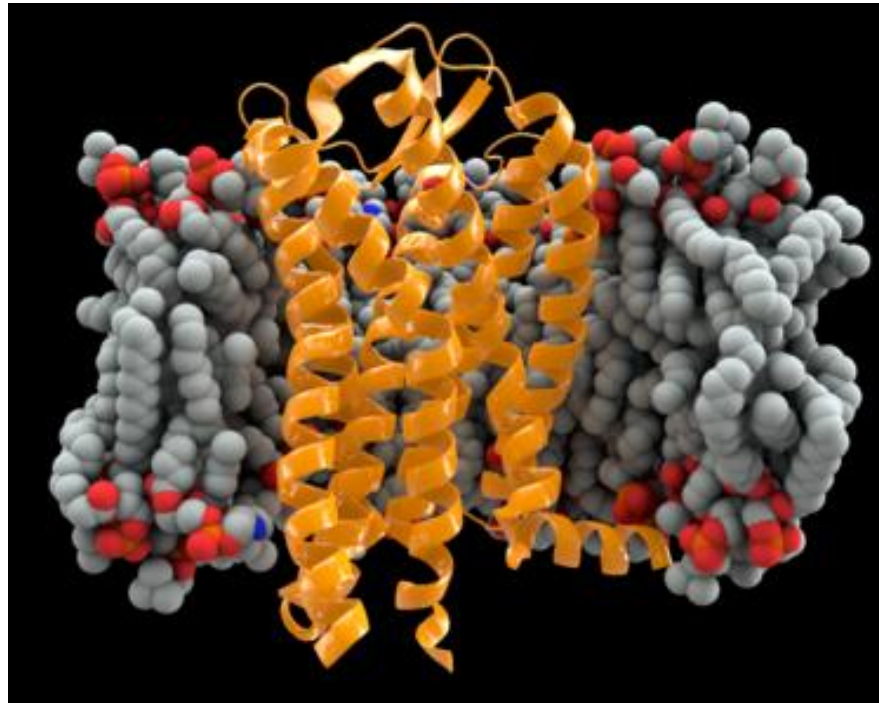


Model organisms and developmental biology

仲寒冰

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Chemokine receptor 5 (CCR5), co-receptor of HIV



About 1% Caucasian carries 2 CCR5 Δ 32, (-/-).

树鼯 (treeshrew)

- 树鼯， *Tupaia belangeri*，树鼯科树鼯属的动物，是介于食虫目和灵长目之间的代表，目前鉴定了 8 个亚种。分布于广西、海南、贵州、云南、四川、西藏等地，和东南亚各国。
- 外形似松鼠，吻尖细，成年时体重 120~150 g。树鼯为昼夜活动的食虫类，栖息活动于灌木林地区，攀缘流窜，行动敏捷。体小，易受惊。
- 2013 年前使用的树鼯大多数为野生捕捉的，年龄及健康状况不详。
- 虽有人在实验室繁殖成功，但量太少，不能满足实验室的应用。实验室大量繁殖，系统了解其正常生理指标，遗传背景及常见病的防治等还有待各个学科的共同努力。

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- 外形似松鼠，~150 g。树鼯为昼夜活动的食虫性动物，行动敏捷。体小，繁殖力强，分布广泛。
- 2013年前使用较少，年龄及健康状况不详。
- 虽有人在实验室繁殖成功，但量太少，不能满足实验室的应用。实验室大量繁殖，系统了解其正常生理指标，遗传背景及常见病的防治等还有待各个学科的共同努力。

乙型病毒性肝炎 Hepatitis B

- 乙肝病毒 (human hepatitis B virus), ~ 3K。
- 感染动物：人，黑猩猩，树鼩。
- 小鼠：可以转基因，但是不感染。
- 1981年，北京第二传染病院资料汇编中，余昌晏等报道树鼩 (treeshrew, *Tupaia*) 可以被人的HBV感染，但在六周以后就出现动物死亡而未持续观察。
- 1981年，《医学研究杂志》刊登中国医学科学院庞其方、万新邦、胥爱源、王祖铭、王桂香、朱宝友、张新生的文章“乙型肝炎病毒 (HBV) 感染树鼩的实验研究”。

Sodium taurocholate cotransporting polypeptide is a functional receptor for human hepatitis B and D virus

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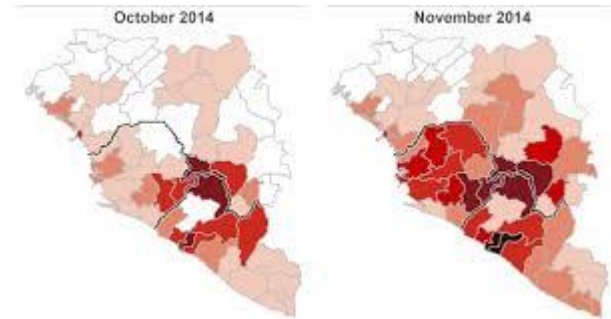
Abstract Human hepatitis B virus (HBV) infection and HBV-related diseases remain a major public health problem. Individuals coinfecting with its satellite hepatitis D virus (HDV) have more severe disease. Cellular entry of both viruses is mediated by HBV envelope proteins. The pre-S1 domain of the large envelope protein is a key determinant for receptor(s) binding. However, the identity of the receptor(s) is unknown. Here, by using near zero distance photo-cross-linking and tandem affinity purification, we revealed that the receptor-binding region of pre-S1 specifically interacts with sodium taurocholate cotransporting polypeptide (NTCP), a multiple transmembrane transporter predominantly expressed in the liver. Silencing NTCP inhibited HBV and HDV infection, while exogenous NTCP expression rendered nonsusceptible hepatocarcinoma cells susceptible to these viral infections. Moreover, replacing amino acids 157–165 of nonfunctional monkey NTCP with the human counterpart conferred its ability in supporting both viral infections. Our results demonstrate that NTCP is a functional receptor for HBV and HDV.

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Ebola virus (埃博拉病毒)



EBOLA MOUSE MODEL

Host genetic diversity enables Ebola hemorrhagic fever pathogenesis and resistance

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Existing mouse models of lethal Ebola virus infection do not reproduce hallmark symptoms of Ebola hemorrhagic fever, neither delayed blood coagulation and disseminated intravascular coagulation nor death from shock, thus restricting pathogenesis studies to nonhuman primates. **Here we show that mice from the Collaborative Cross panel of recombinant inbred mice exhibit distinct disease phenotypes after mouse-adapted Ebola virus infection.** Phenotypes range from complete resistance to lethal disease to severe hemorrhagic fever characterized by prolonged coagulation times and 100% mortality. Inflammatory signaling was associated with vascular permeability and endothelial activation, and resistance to lethal infection arose by induction of lymphocyte differentiation and cellular adhesion, probably mediated by the susceptibility allele *Tek*. These data indicate that genetic background determines susceptibility to Ebola hemorrhagic fever.

A mouse-adapted strain of Ebola virus (MA-EBOV) does not cause hemorrhagic syndrome despite causing lethal disease in laboratory mice, and it cannot be used effectively to study Ebola hemorrhagic fever (EHF) pathogenesis, because the dissimilarity to human disease limits the ability to identify key

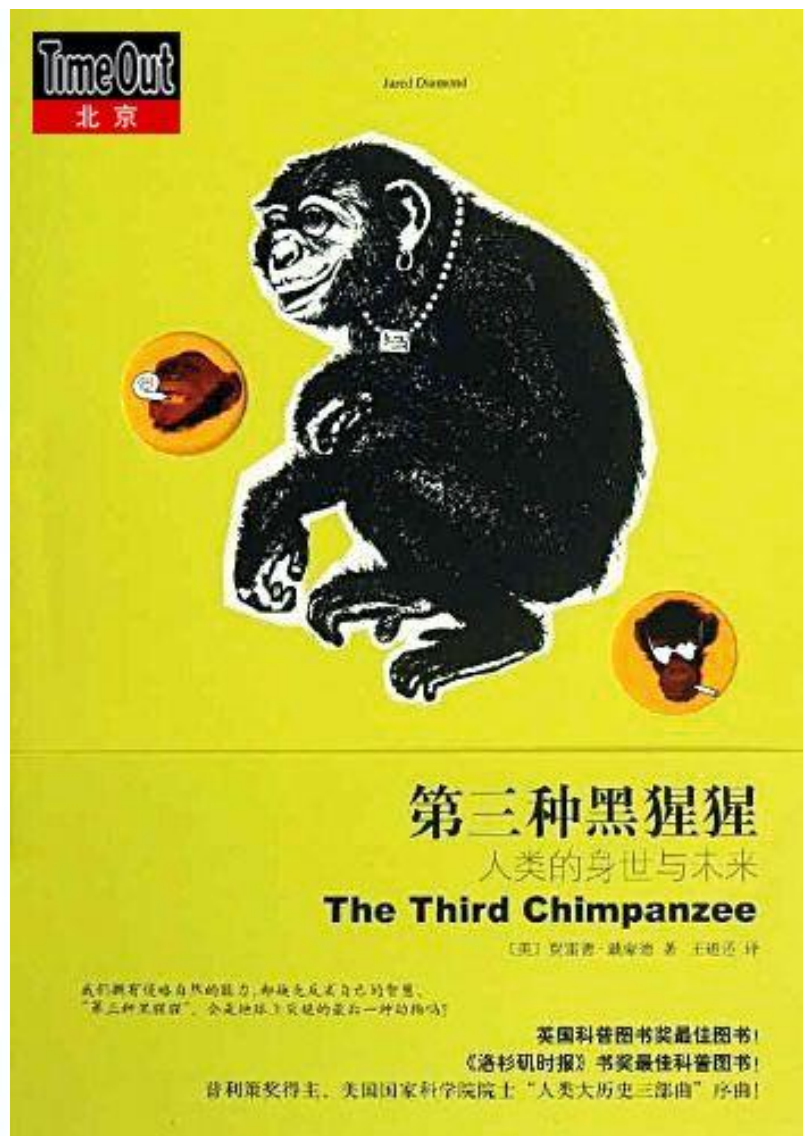
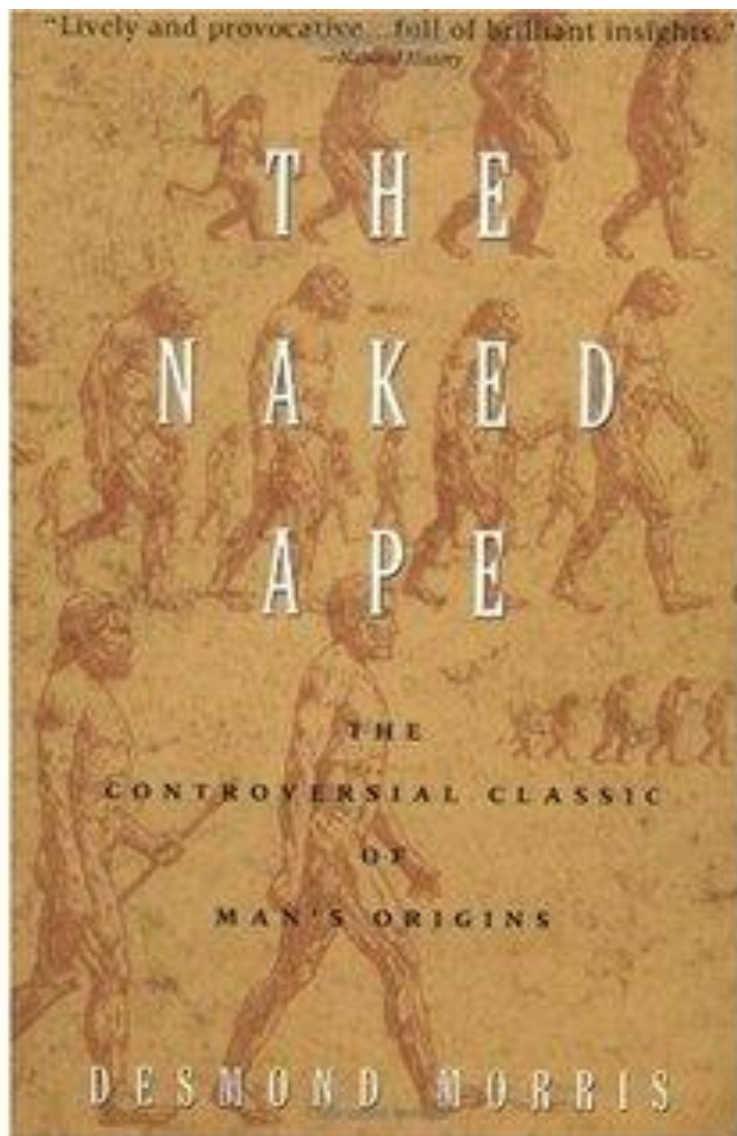
correlates of viral pathogenesis or accurately assess the effect of vaccines or therapeutics. Pathogenesis studies of EHF have thus been restricted to macaques (1–4), guinea pigs (5, 6), and Syrian hamsters (7). Although these models accurately recapitulate most of the disease features of EHF, practical and ethical concerns limit their use, in-

cluding nonreproducible genetic backgrounds, cost, animal availability, and reagent availability. Epidemiologic studies of EBOV infection have identified a range of pathogenic phenotypes, which are not linked to specific mutations in the viral genome (8, 9). This suggests that the host response may determine disease severity after EBOV infection.

We tested the role of host genetics in Ebola virus disease (EVD) using the Collaborative Cross (CC) resource, a genetically diverse panel of recombinant inbred (CC-RI) mice obtained through **a systematic cross of eight inbred founder mouse strains, five of which are classic laboratory strains (C57BL/6J, A/J, 129Sv/SvImJ, NOD/ShiLtJ, and NZO/HuLtJ) and three of which are wild-derived inbred strains (CAST/EiJ, PWK/PhJ, and WSB/EiJ)** (10). The founders represent 90% of the common genetic variation across the three major *Mus musculus* subspecies (*M. m. musculus*, *M. m. domesticus*, and *M. m. castaneus*) (11). Different strains can be crossed with one another to generate CC-RI intercrossed (CC-RIX) F₁ progeny.

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Thanks!

Cat VS Human

	Life stage	Age of cat	Human equivalent
 Tigger 3 months old	Kitten birth to 6 months	0 – 1 month	0 – 1 year
		2 – 3 months	2 – 4 years
		4 months	6 – 8 years
		6 months	10 years
 Sugar 13 months old	Junior 7 months to 2 years	7 months	12 years
		12 months	15 years
		18 months	21 years
		2 years	24 years
 Rosie 3 years old	Prime 3 years to 6 years	3	28
		4	32
		5	36
		6	40
 Nemo 8 years old	Mature 7 years to 10 years	7	44
		8	48
		9	52
		10	56
 George 13 years old	Senior 11 years to 14 years	11	60
		12	64
		13	68
		14	72
 Chinarose 16 years old	Geriatric 15 years+	15	76
		16	80
		17	84
		18	88
		19	92
		20	96
		21	100
		22	104
		23	108
		24	112
		25	116

- 1-month-old kitten = 6-month-old human baby
- 3-month-old kitten = 4-year-old child
- 6-month-old kitten = 10 human years old
- 8-month-old kitten = 15-year-old human
- A 1-year-old cat has reached adulthood, the equivalent of 18 human years
- 2 human years = 24 cat years
- 4 human years = 35 cat years
- 6 human years = 42 cat years
- 8 human years = 50 cat years
- 10 human years = 60 cat years
- 12 human years = 70 cat years
- 14 human years = 80 cat years
- 16 human years = 84 cat years