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Macaque monkeys in Zika virus research: 1947-present

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Abstract

Zika virus was first isolated in 1947 from an exotic rhesus macaque. Nearly 70 years later, the emergence of Zika virus in the Americas and its newly described association with birth defects has motivated the development of captive macaque monkey models of human Zika virus infection. This review describes similarities between macaque and human Zika virus pathogenesis and discusses specific advantages and disadvantages of using macaques instead of other laboratory animal models. In particular, macaques provide an outstanding model for understanding in-utero Zika virus infections that are essential for evaluating preclinical interventions for use in pregnancy.

A brief history of Zika virus

Zika virus (ZIKV) is a mosquito-borne and sexually-transmitted flavivirus that is closely related to dengue virus (DENV) [1–3]. It was first isolated in 1947 in the Zika Forest near Entebbe, Uganda, from the serum of a sentinel rhesus macaque kept there for yellow fever surveillance [1]. ZIKV was subsequently isolated from *Aedes africanus* mosquitoes in 1948 and from humans in 1952 in Uganda and Tanzania [1, 4–6]. Isolated human cases and outbreaks of ZIKV were periodically identified in Africa. In the 1970s and 1980s, ZIKV emerged in Asia [6–9]. ZIKV infection was thought to be largely asymptomatic or to cause only a mild, febrile illness characterized by fever, rash, conjunctivitis, headache, and joint pain. It was not historically associated with widespread outbreaks or epidemics [6, 7, 10].

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Conflicts of interest

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Author declaration

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Then in 2007, a large ZIKV outbreak occurred on Yap Island in the South Pacific [11]. This ZIKV epidemic infected approximately 70% of residents and was the largest ZIKV outbreak ever recorded at the time [11]. Subsequently, ZIKV caused outbreaks throughout the Pacific Islands, including French Polynesia [12–15]. Throughout this period ZIKV was largely ignored by the scientific community; at the beginning of 2013 there were more articles in NCBI PubMed by authors with the surname “Zika” (65) than there were articles with “Zika virus” in the title or abstract (62).¹

The emergence of ZIKV as a global public health emergency in 2016 [16] was therefore surprising. The FIFA Confederations Cup was hosted by Brazil in 2013 and though existing data are not definitive, retrospective phylogenetic analyses suggest that ZIKV was introduced to northeast Brazil at approximately the same time [17], perhaps from visiting players or their supporters. ZIKV spread in northern Brazil, and likely throughout the region, unnoticed for nearly two years until its presence was associated with a surge in reports of febrile rash [18]. From there, ZIKV spread rapidly throughout the Americas, with autochthonous cases identified in 48 countries and territories as of March 2017 [19].

Zika virus Transmission

In the Americas, ZIKV is thought to be primarily transmitted between humans by *Aedes aegypti* (*Ae. aegypti*) mosquitoes [20–24]. This mosquito species has adapted to live in close proximity to humans and transmits a number of important human pathogens including DENV and chikungunya virus (CHIKV) [24, 25]. Rapid human population growth and unprecedented expansion of urban areas has resulted in inadequate water and sewer infrastructure, and has made controlling *Ae. aegypti* populations exceedingly difficult [24]. In addition to vector-borne and vertical transmission, ZIKV is also sexually transmitted [26]. Sexual transmission of ZIKV was first reported in 2011, but received little attention until additional cases were identified during the ongoing outbreak in the Americas [2, 26]. To date, cases of ZIKV sexual transmission have included male-to-male, male-to-female, and female-to-male transmission [2, 27–29]. It is likely that sexual transmission went previously unnoticed in areas with autochthonous transmission, as it is difficult to distinguish between sexual and vector-borne transmission. The contribution of sexual transmission to the epidemiology of ZIKV remains unclear [30]. From an epidemiological perspective, it is important to disentangle vector-borne and sexual transmission, and determine how the mode of transmission influences the pathology of ZIKV infection. To this end, developing a translatable animal model that allows recapitulation of the primary modes of ZIKV transmission is especially important.

Congenital Zika syndrome

Congenital ZIKV infection is associated with a spectrum of adverse outcomes including fetal demise, in utero growth restriction, and a range of brain and neurological defects, including microcephaly (Table 1). Collectively, these outcomes have been designated

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“congenital Zika syndrome (CZS)” [31–33]. Currently, the prevalence of CZS is unclear. A study from Rio de Janeiro found that 42% of infants infected in utero had clinical and/or brain abnormalities [34]. In contrast, despite having thousands of women infected with ZIKV during pregnancy, Puerto Rico has reported only 16 cases of CZS as of this writing [35]. The United States Zika Pregnancy Registry reports an intermediate CZS risk of approximately 5%, with 63 birth defects in 1,311 completed pregnancies as of March 28, 2017 [36]. This discrepancy may be due to the use of different criteria for diagnosing CZS. It may also reflect genuine differences in the outcome severity of congenital ZIKV infection in different populations; for example, pre-existing immunity to DENV, which has been associated with increased ZIKV replication in vitro and more severe pathology mice [37, 38], is much more common in Brazil than in the continental United States. Nonetheless, data are concordant with respect to two key points: first, CZS is the most common pathologic consequence of ZIKV infection and second, CZS severity can range from mild to very severe, and there is currently no way to quantify or mitigate this risk.

Animal Models of Zika virus Infection

It is difficult to study acute ZIKV infection and pathogenesis in humans because a large proportion of infections, up to 80%, are subclinical [11]. In addition, identifying past infection is hindered by serologic cross-reactivity between closely related flaviviruses; serologic tests may not differentiate between ZIKV infection and infection with related flaviviruses, such as DENV or yellow fever virus, or vaccination [39]. Animal models allow for timed infections and thorough analysis of acute viral replication kinetics, even if an infection is subclinical. Animal infections provide a framework within which neurologic complications, viral distribution in tissues, maternal-fetal transmission, and CZS can be studied in detail. To date, descriptions of CZS are limited to a relatively small number of human clinical cases, but further development of animal models may provide a more comprehensive description of the pathology and neurodevelopmental outcomes [31, 32].

ZIKV infection has been modeled in mice, neonatal pigs, chicken embryos, and nonhuman primates [40–56]. Each of these models has strengths and weaknesses making them more or less suited for one or more areas of ZIKV research. For example, mice are relatively inexpensive, have short generation times, and large litters, and may be well-suited for initial vaccine development and therapeutic evaluation studies, but may be less useful for natural history studies because most susceptible mouse strains are interferon deficient and may display exaggerated pathology [41–43]. Differences in placentation (Table 2) and the timing for brain and central nervous system (CNS) development in mice versus humans may also limit the translatability of mouse models for studies of CZS pathophysiology [57, 58]. Although these limitations exist, mouse models of ZIKV infection have been instrumental in identifying potential tissue and cellular targets of ZIKV in vivo [44, 59, 60]. However, studies of ZIKV infection in mice have also reported findings such as testicular atrophy, which has not been reported in human clinical cases to date [61]. Both the chick embryo and neonatal pig models may be very useful for testing therapeutics and/or understanding ZIKV infection outcomes in the early neonatal period respectively, and are relatively inexpensive [49, 55]. However, these ZIKV infection models both bypass the maternal-fetal interface, a potentially important barrier and/or site of virus replication in congenital ZIKV

infections [49, 55, 62]. Animal models that bypass natural barriers in congenital transmission have limited translatability to human infections with regard to the epidemiologic risk of CZS and maternal-fetal transmission of ZIKV.

Nonhuman Primate Models of Zika virus Infection

Given that ZIKV was initially isolated from a rhesus macaque, it is perhaps not surprising that macaques are susceptible to ZIKV in laboratory studies. In the past year, several groups have shown that rhesus, cynomolgus, and pig-tailed macaques can be infected with a variety of ZIKV strains, including isolates from Uganda [52], Thailand [51], French Polynesia [46] [63], Brazil [54], and Puerto Rico [51, 56]. Since African and Asian ZIKV isolates are approximately 90% nucleotide identical, and Asian/American ZIKV isolates are 99% nucleotide identical [52], it is likely that macaques are permissive for infection with all, or nearly all, global ZIKV strains. This is additionally supported by successful infection of macaques with the highly mouse-adapted MR766 ZIKV strain [52].

Zika virus can productively infect macaques via multiple routes. To mimic vector-borne transmission, our initial studies, and those of other groups, infected macaques subcutaneously with doses ranging from 10^2 to 10^6 PFU [46, 47, 51, 53, 63]. Intravenous inoculation has also been successfully utilized to infect macaques [54] and researchers at University of California Davis (UC-Davis) and others are exploring the use of intravaginal and intrarectal transmission to model sexual transmission [71]. Finally, intra-amniotic administration of ZIKV has been used for direct in utero infection of fetuses (Koen Van Rompay, personal communication, April 24, 2017). Thus, all three major routes of transmission -- vector, sexual, and vertical -- can be modelled efficiently in macaques. Moreover, our group recently demonstrated that macaques can also be infected via high-dose application of ZIKV directly to the tonsils, providing evidence for a theoretical risk of transmission via the oropharyngeal mucosa [64]. In addition, we have also shown that feeding ZIKV-infected mosquitoes on macaques is a reliable route of transmission associated with delayed, and modestly higher, peak viremia than needle inoculation in three of four animals [65]. Mosquito challenges may be more widely used in the future in laboratories that have sufficient expertise in mosquito husbandry and containment because it most closely mimics the epidemiology and physiology of human infections. In addition, data from studies of other flaviviruses suggest that vector transmission may differ, sometimes significantly, from experimental modes of transmission [66]. In particular, vector saliva has immune modulatory effects that may influence the progression and pathology of infections [67–69].

Macaques and humans infected with ZIKV are virologically and clinically similar. Plasma viremia typically peaks within the first five days of infection and resolves within 10–14 days. Viral RNA can be detected in lymph nodes after resolution of viremia, though this does not necessarily imply that lymph nodes are sanctuaries for replication-competent virus [54]. Lower titers of viral RNA are detected in other fluids, including urine, saliva, and cerebrospinal fluid. Persistence of ZIKV RNA in semen has not been evaluated in macaques, though in people viral RNA can be detected months after infection [70]. Like most infected people [11], macaques infected with ZIKV do not typically exhibit febrile rash or other

clinical symptoms such as joint pain or swelling, or muscle pain [46]. However, inoculation site rash and joint swelling have been reported by some investigators [56]. Immune responses to ZIKV are robust; rechallenge with homologous or heterologous ZIKV does not cause recrudescent viremia [52]. We are not aware of any ZIKV-associated GBS in macaques, though this is not surprising given the rarity of GBS in people. In addition to natural history studies, nonpregnant macaques have been used to model sexual transmission of ZIKV, study tropism and persistence of ZIKV, characterize clinical isolates of ZIKV, and test ZIKV vaccine platforms [47, 50, 54, 56, 71].

Understanding congenital Zika syndrome in macaques

The similarities between human and macaque ZIKV infection are useful for studying maternal-fetal transmission and CZS. Macaques have been used as models for understanding human pregnancy and disease for decades. This is due, in part, to the 1977 ban on the export of rhesus macaques from India [72]. The vital need for these animals in biomedical research [73] motivated the establishment and expansion of rhesus macaque breeding colonies in the United States. Thousands of macaque pregnancies have been carefully monitored in recent decades, generating a wealth of husbandry, reproductive, and developmental biology knowledge. Macaque gestation is similar to that of humans in its division into trimesters, placentation and blood supply remodeling, and fetal developmental trajectory (Table 2) [57].

To date, two studies have investigated the impact of ZIKV infection on fetal development and outcomes [48, 63]. One of these studies, led by our group, aimed to mimic vector transmitted ZIKV infection during pregnancy using a subcutaneous dose of 10^4 PFU. Two macaques each were infected in the first and third trimesters of pregnancy. Ten days before full gestation, the neonates were delivered by cesarean section and analyzed for fetal injury, growth restriction, and ZIKV infection. All four fetal macaques had pathological abnormalities; both of the first trimester infections exhibited significant injury to the visual system. Ocular pathology correlated with the presence of viral RNA in the optic nerve, among other tissues. Notably, the detection of viral RNA in all four fetuses provides unequivocal evidence of 100% vertical transmission efficiency. While none of the four neonates had microcephaly, all four had below average head circumference and reduced head growth velocity in the last month of pregnancy. These results mirror observational cohorts of human neonates, where microcephaly is rare but other manifestations of CZS are common [34, 74]. This suggests that ZIKV infection of macaques, particularly in the first trimester, consistently causes fetal injury and provides a model for evaluating ZIKV pathogenesis, studying potential cofactors that may increase the severity of in utero ZIKV infection (e.g., preexisting DENV immunity), and evaluating the safety and efficacy of interventions to mitigate fetal pathology (e.g., hyperimmune globulin or monoclonal antibody treatments).

One remarkable feature of ZIKV infections in pregnant macaques is the observation of a prolonged period of detection of plasma viremia that parallels observations that have been made in some women, including an asymptomatic case [75–77]. In nonpregnant humans and monkeys, ZIKV plasma viremia becomes undetectable in approximately two weeks, but in pregnant women, persistent detection of serum or plasma viremia has been described for

more than 10 weeks after clinical symptom onset [77]. Three of four pregnant macaques had prolonged viremia, including one animal who had detectable ZIKV RNA in her plasma for 10 weeks [63]. Additional work is needed to determine the anatomic source of replicating virus during sustained viremia and to assess whether the risk of fetal injury is correlated to the duration of viremia. If it is, longitudinal blood sampling of pregnant women might provide a non-invasive biomarker for fetal CZS risks that cannot be easily visualized via ultrasound.

A second study infected a single pregnant pigtailed macaque at 119 days gestation with a Cambodian ZIKV isolate administered five times at a dose of 10^7 plaque forming units (PFU) per inoculation [48]. This supraphysiologic dose is approximately 5,000 times higher than the dose used in the study described above and is likely much higher than women would encounter naturally. While the dam showed no signs of clinical illness, the fetus developed periventricular lesions and occipital-parietal asymmetry by 10 days post infection (dpi) [48]. At the time of the fetal necropsy that was performed at 162 days' gestation, cerebral white matter hypoplasia, periventricular white matter gliosis, and axonal and ependymal injury were diagnosed [48]. This study demonstrates how high ZIKV challenge dose might be used to evaluate extreme phenotypes including severe neuropathology and microcephaly, however, more data are needed to understand how consistently these phenotypes are observed under experimental conditions.

Although to date, the number of macaque studies ($n = 2$) that have investigated ZIKV infection during pregnancy and CZS are small, the findings in macaques have been similar to findings in human clinical case reports (Table 1) in terms of identification of abnormalities in the ocular system and reduction in head growth trajectory or microcephaly [48] [63]. Further development of the macaque model of ZIKV infection during pregnancy may yield additional similarities to humans in terms of fetal outcomes.

Challenges and opportunities

Zika virus is poised to threaten a generation of pregnancies in the Americas, particularly in regions where its mosquito vectors are abundant. Fortunately, protective immunity can be elicited by natural infection and by vaccination [47, 51, 52]. Within a decade, it is likely that a safe and effective vaccine that protects women from ZIKV will be available. Until such a vaccine is available, it is important to develop a better understanding of ZIKV pathogenesis and countermeasures to protect pregnant women and their babies. The similarities between macaque and human pregnancies and the clinical course of ZIKV provides an opportunity to perform timed infections, ask questions that require invasive sampling, and test high-risk, high reward interventions. The macaque model, however, is not perfect. Studies that require impregnating macaques and intensive follow-up are necessarily very expensive and only possible at facilities with extensive experience and infrastructure to support macaque husbandry. Demand and cost limit the number of animals available for studies, limiting statistical power. For this reason, many aspects of the natural history of ZIKV in pregnancy will likely be resolved more effectively using large observational cohorts of pregnant women than small numbers of pregnant macaques. Nonetheless, the NHP model allows for detailed analyses that are not possible in human infections. NHP studies will be indispensable for

understanding the mechanisms of CZS and for evaluating measures to reduce and eliminate the impacts of this newly recognized disease.

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- of special interest
- of outstanding interest

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Highlights

- Multiple macaque species are susceptible to Zika virus.
- A number of Zika virus strains have been used to infect macaques.
- Different routes of inoculation have all led to productive infections in macaques.
- Zika virus infection has been examined in pregnant and nonpregnant macaques.

Table 1

Clinical features of congenital Zika syndrome (CZS).

Clinical finding	Description	References
abnormal cranial morphology	microcephaly, overlapping cranial sutures, prominent occipital bone, redundant scalp skin, facial disproportion, premature closure of the anterior fontanelle	[31, 33, 74, 78]
brain anomalies	intracranial calcifications, increased fluid spaces, cortical thinning, hypoplasia or absence of the corpus callosum, cerebellar hypoplasia, ventriculomegaly	[31, 33, 78]
ocular anomalies	microphthalmia, coloboma, cataracts, intraocular calcifications, chorioretinal atrophy, optic nerve atrophy, retinal lesions	[31, 33, 79]
congenital contractures	arthrogryposis of one or more joints	[31, 79, 80]
hearing anomalies	sensorineural hearing loss	[31, 33, 81, 82]

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Table 2

Similarities and differences between human, macaque, and mouse gestation.

Feature	Humans	Macaques	Mice	References
gestation easily divided into trimesters	yes	yes	no	[83–86]
hemochorial placentation	yes	yes	yes	[84]
discoid placenta	yes	yes ^a	yes	[83, 84, 87]
trophoblast invasion	yes ^b	yes ^c	no	[84, 88]
remodeling of decidual spiral arteries	yes	yes	no	[84, 88, 89]
unicornuate uterus	yes	yes	no	[84]
primarily singleton gestation	yes	yes	no	[84, 89]
long gestational length ^d	yes	yes	no	[84, 89]

^a bi-discoid placenta is common, but discoid may also occur.

^b extensive invasion.

^c invasion is less extensive than in humans.

^d gestational length >150 days.