Expression of the Mxra8 receptor promotes alphavirus infection and pathogenesis in mice and Drosophila

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Expression of the Mxra8 Receptor Promotes Alphavirus Infection and Pathogenesis in Mice and Drosophila

Graphical Abstract

Highlights
- Reduced infection of four different alphaviruses is seen in Mxra8-deficient mice
- Reduced CHIKV-induced joint swelling is observed in Mxra8-deficient mice
- D71A mutant CHIKV that lacks binding to Mxra8 is attenuated in wild-type mice
- Ectopic Mxra8 expression is sufficient to enhance CHIKV infection in Drosophila

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In Brief
Zhang et al. use CRISPR-Cas9 gene editing to generate mice with out-of-frame 8- and 97-nucleotide deletions in Mxra8. These mice show markedly reduced infection of CHIKV, MAYV, RRV, and ONNV during the acute phase. These experiments establish a key role for Mxra8 in the pathogenesis of multiple alphaviruses.
Expression of the Mxra8 Receptor Promotes Alphavirus Infection and Pathogenesis in Mice and Drosophila

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SUMMARY

Mxra8 is a recently described receptor for multiple alphaviruses, including Chikungunya (CHIKV), Mayaro (MAYV), Ross River (RRV), and O’nyong nyong (ONNV) viruses. To determine its role in pathogenesis, we generated mice with mutant Mxra8 alleles: an 8-nucleotide deletion that produces a truncated, soluble form (Mxra8<sup>Δ8/Δ8</sup>) and a 97-nucleotide deletion that abolishes Mxra8 expression (Mxra8<sup>Δ97/Δ97</sup>). Mxra8<sup>Δ8/Δ8</sup> and Mxra8<sup>Δ97/Δ97</sup> fibroblasts show reduced CHIKV infection in culture, and Mxra8<sup>Δ8/Δ8</sup> and Mxra8<sup>Δ97/Δ97</sup> mice have decreased infection of musculoskeletal tissues with CHIKV, MAYV, RRV, or ONNV. Less foot swelling is observed in CHIKV-infected Mxra8 mutant mice, which correlated with fewer infiltrating neutrophils and cytokines. A recombinant E2-D71A CHIKV with diminished binding to Mxra8 is attenuated in vivo in wild-type mice. Ectopic Mxra8 expression is sufficient to enhance CHIKV infection and lethality in transgenic flies. These studies establish a role for Mxra8 in the pathogenesis of multiple alphaviruses and suggest that targeting this protein may mitigate disease in humans.

INTRODUCTION

Alphaviruses are single-stranded, positive-polarity enveloped RNA viruses that are among the most important arthropod-transmitted viruses causing disease in humans and other animals (Powers et al., 2001). Alphaviruses are classified into two groups, Old World and New World, based on their genetic relatedness and historical boundaries. Old World alphaviruses include Chikungunya (CHIKV), Mayaro (MAYV), O’nyong’nyong (ONNV), Ross River (RRV), Sindbis (SINV), and Semliki Forest (SFV) viruses, several of which cause epidemic debilitating acute and chronic polyarthritis affecting millions of people globally. New World viruses, which include Eastern (EEEV), Venezuelan (VEEV), and Western (WEEV) equine encephalitis viruses, propagate through enzootic and epizootic cycles and can infect neuronal cells in the brain, resulting in encephalitis and death. With recent global spread, some Old World alphaviruses (e.g., CHIKV) now circulate in both hemispheres. Despite their epidemic potential, there are no licensed therapies or vaccines for any alphavirus infection.

The alphavirus genomes encode four non-structural and five structural proteins using two open reading frames and have a 5’ cap and a 3’ poly(A) tail (Strauss et al., 1994). The non-structural proteins are synthesized from the 49S genomic RNA and are required for virus translation, replication, and immune evasion; the structural proteins (capsid [C] and envelope [E3-E2-6K-E1]) are synthesized from a 26S subgenomic RNA. The alphavirus envelope glycoprotein contains a hydrophobic peptide that participates in pH-dependent endosomal fusion (Lescar et al., 2001). The E2 envelope glycoprotein binds to attachment and entry factors (Smith et al., 1995; Zhang et al., 2005), which facilitates clathrin-dependent endocytosis (DeTulleo and Kirchhausen, 1998; Lee et al., 2013). The E3 protein is necessary for the folding of p62 (precursor to E2) and the formation of the E2-E1 heterodimer (Carleton et al., 1997; Mulvey and Brown, 1995) but is cleaved during the maturation process in the trans-Golgi network (Heidner et al., 1996). Mature alphaviruses form at the plasma membrane and contain a single copy of genomic RNA and a lipid bilayer with 240 embedded E2-E1 heterodimers assembled into 80 trimERIC spikes that have T = 4 icosahedral symmetry (Cheng et al., 1995; Kostyuchenko et al., 2011; Paredes et al., 1993; Voss et al., 2010). Despite studying alphaviruses for >50 years, the basis for their cellular and tissue tropism is not fully understood. Attachment factors such as laminin receptor and heparan sulfate have been shown to enhance viral infection for certain alphaviruses (Gardner et al., 2011; Kilimstra et al., 1998; Wang et al., 1992). Natural resistance-associated macrophage protein (NRAMP2)
has been described as a cellular receptor for SINV but not for CHIKV or RRV (Rose et al., 2011). The protein prohibitin has been suggested as a CHIKV receptor (Wintachai et al., 2012) but corroborating studies are lacking. In addition, the cell surface proteins T cell immunoglobulin (Ig) and mucin-domain containing protein 1 (TIM-1) and TAM family member AXL, which engage phosphatidylserine ligands, may promote CHIKV infection (Jemioly et al., 2013). We recently used a genome-wide CRISPR-Cas9-based screen in mouse cells to identify the two Ig-like domain containing plasma membrane molecule Mxra8 (also called DICAM, Asp3, and Limitrin) as a cellular entry receptor for multiple arthritogenic alphaviruses, including CHIKV, RRV, MAYV, and ONNV (Zhang et al., 2018). The human ortholog MXRA8 also bound to CHIKV and other alphaviruses and facilitated the infection of human fibroblasts, skeletal muscle cells, and chondrocytes. Mxra8 bound directly to CHIKV particles and enhanced attachment and internalization into cells, and Mxra8–Fc fusion protein or anti-Mxra8 monoclonal antibodies (mAbs) blocked CHIKV infection of both mouse and human cells.

Here, to examine the role of Mxra8 in alphavirus pathogenesis, we used CRISPR-Cas9 gene editing to generate mice with out-of-frame 8 (D8) and 97 (D97) nucleotide (nt) deletions in Mxra8. These mice were born in normal Mendelian frequencies and showed no defects in development, growth, or fecundity. The Δ8 and Δ97 deletions in Mxra8 produced a truncated, soluble form of the ectodomain or no intact protein, respectively. In cell culture, murine embryonic fibroblasts (MEFs) from the Mxra8Δ8/Δ8 and Mxra8Δ97/Δ97 mice had markedly reduced infection by CHIKV compared to wild-type (WT) MEFs. The inoculation of Mxra8Δ8/Δ8 or Mxra8Δ97/Δ97 mice with CHIKV, MAYV, RRV, or ONNV resulted in markedly diminished, yet not abolished, infection of musculoskeletal tissues. Thus, cell surface expression of Mxra8 is required for optimal infection by multiple alphaviruses in vivo, although alternative cell entry pathways exist. In the context of CHIKV infection, mutation and loss of function of Mxra8 were associated with reduced neutrophil infiltration, decreased inflammation, diminished joint swelling, and lower levels of viral RNA at 28 days post-infection (dpi). Reciprocally, a recombinant mutant CHIKV (D71A), which shows loss of binding to Mxra8, specifically showed reduced infection in WT mice compared to the parental virus, although the two replicated equally, albeit at lower levels, in Mxra8Δ8/Δ8 mice. Moreover, in Drosophila, which lack endogenous expression of Mxra8 or any apparent ortholog, ectopic expression of Mxra8 transgenes resulted in increased CHIKV infection and lethality. Overall, these experiments establish that the entry receptor Mxra8 is required for optimal in vivo infection, dissemination, and pathogenesis of multiple alphaviruses.

RESULTS

Generation of Mxra8-Deficient Mice
Since the mouse Mxra8 gene locus has two full-length transcripts and a short putative transcript near its 3’ end (Figure 1A), we designed two single guide RNAs (sgRNAs) to target a conserved region in all isoforms for CRISPR-Cas9 gene editing (Figures 1A and 1B). After screening the guide sequences for...
minimal off-target effects, each sgRNA was complexed with the WT Cas9 protein and introduced into day 0.5 C57BL/6J embryos (embryonic day [E] 0.5) via electroporation; two out-of-frame deletion variants (Δ8 and Δ97 nt) were identified by sequencing DNA isolated from pups (Figures 1B and S1A). These mice were backcrossed twice to establish germline transmission and bred to either heterozygosity (Mxra8<sup>+/−</sup>) or homozygosity (Mxra8<sup>−/−</sup> and Mxra8<sup>−/−</sup>Δ8) for experimentation. Both Mxra8<sup>−/−</sup>Δ8 and Mxra8<sup>−/−</sup>Δ97 lines showed normal development, growth characteristics, and fecundity.

The Δ8 and/or Δ97 deletion variants could express truncated, soluble forms of Mxra8 due to our targeting of a downstream common exon within the Ig-like domain 2 of Mxra8 (Figure 1B). Regardless, we hypothesized that they may mitigate alphavirus replication because cell surface receptor-dependent internalization is required for infection (Hoornweg et al., 2016). To evaluate this possibility, we generated primary MEFs from WT, Mxra8<sup>−/−</sup>Δ8, and Mxra8<sup>−/−</sup>Δ97 mice and performed western blotting on the cell lysates and supernatants with two anti-Mxra8 mAbs (Zhang et al., 2018). In the cell lysate, a ~52-kDa Mxra8 band was apparent in WT cells, and a ~34-kDa band was present in Mxra8<sup>−/−</sup>Δ8 cells; no specific band was detected in Mxra8<sup>−/−</sup>Δ97 cell lysate (Figure 1C). A ~34-kDa band also was detected in the Mxra8<sup>−/−</sup>Δ8 MEF supernatant but not in that from WT or Mxra8<sup>−/−</sup>Δ97 cells (Figure 1D). The western blotting results were consistent with the deletion sites: the Δ8 deletion causes a truncation of 12 amino acids C-terminal to the last β strand of domain 2, whereas the Δ97 deletion results in a truncation of the G-strand in domain 2, which is predicted to compromise the integrity of the Ig-like fold (Basore et al., 2019; Song et al., 2019) (Figure 1B). Surface expression of Mxra8 was absent in both Mxra8<sup>−/−</sup>Δ8 and Mxra8<sup>−/−</sup>Δ97 cells, as determined by flow cytometry (Figure S1B). To assess whether the deletions in Mxra8 affected CHIKV infectivity in cell culture, we performed multi-step growth analysis with WT, Mxra8<sup>−/−</sup>Δ8, and Mxra8<sup>−/−</sup>Δ97 primary MEFs. CHIKV infection was reduced in both Mxra8<sup>−/−</sup>Δ8 and Mxra8<sup>−/−</sup>Δ97 MEFs compared to WT cells (Figure 1E), confirming the loss-of-function phenotype in cells expressing a truncated, soluble variant or no Mxra8 protein at all.

We next examined which cell types and tissues expressed Mxra8 in WT mice. A prior study generated a rabbit polyclonal serum against the 192 N-terminal amino acids of DICAM (an alias of Mxra8) for immunohistochemistry and reported Mxra8 expression on epithelial, myeloid, and mesenchymal cells (Jung et al., 2008). Despite numerous attempts, we were unable to reproduce these findings on either fixed or frozen tissue sections with anti-Mxra8 mAbs, affinity-purified rabbit polyclonal IgG against the Mxra8 ectodomain, or polyclonal rabbit serum elicited against the same 192 N-terminal amino acids of Mxra8. In lieu of these results, we performed RNA in situ hybridization (ISH) in musculoskeletal-associated tissues, a relevant site of arthritogenic alphavirus infection, with Mxra8-specific and -negative control probes. Mxra8 mRNA was detected in skin fibroblasts, bone marrow, and synovium (Figure S2A), which is consistent with expression patterns observed from mouse RNA Atlas data (https://oncogene.c3.str Canc.org/atlas.gs.washington.edu/mouse.rna/genes). We also measured Mxra8 mRNA levels in tissues of uninfected and CHIKV-infected mice using qRT-PCR (Figures S2B and S2C). Roughly equivalent expression was detected in musculoskeletal tissues and visceral organs, with slightly lower levels measured in lymph nodes.

**Impact of Mxra8 on Acute CHIKV Infection In Vivo**

To begin to define the contribution of Mxra8 in alphavirus pathogenesis, we inoculated CHIKV (Asian strain AF15561) subcutaneously in the feet of WT and Mxra8 mutant mice. To monitor viral spread at the earliest stages of infection, we measured CHIKV titers in the ipsilateral (to the site of virus injection) ankle at 12 h post-infection (hpi) and viremia at 1 and 2 dpi. Reduced levels of CHIKV infection were observed 12 hpi in the ipsilateral ankle of Mxra8<sup>−/−</sup>Δ8 compared to WT mice (5-fold, p < 0.01) (Figure 2A). Consistent with these data, lower levels of CHIKV RNA were detected in the serum of Mxra8<sup>−/−</sup>Δ8 mice at 1 and 2 dpi (5- to 16-fold, p < 0.05) (Figure 2B). Next, we measured the amount of infectious virus and foot swelling in WT, Mxra8<sup>−/−</sup>Δ8, Mxra8<sup>−/−</sup>Δ97, and Mxra8<sup>−/−</sup>Δ97 mice at 3 dpi, a time point that corresponds to the first peak of clinical disease in mice (Morrison et al., 2011). Notably, ipsilateral foot swelling at 3 dpi was nearly abrogated in both Mxra8<sup>−/−</sup>Δ8 and Mxra8<sup>−/−</sup>Δ97 mice and reduced in heterozygous Mxra8<sup>−/−</sup>Δ8 compared to the WT mice (Figures 2C and 2G). Smaller differences (2- to 4-fold, p < 0.05) in viral titers were observed in the ipsilateral ankle of Mxra8<sup>−/−</sup>Δ8 and Mxra8<sup>−/−</sup>Δ97 mice at 3 dpi compared to WT mice, and no difference was observed in the Mxra8<sup>−/−</sup>Δ8 mice (Figures 2D and 2H). However, larger reductions in viral burden were observed in the ipsilateral calf muscle (11- to 45-fold, p < 0.001), contralateral ankle (30- to 50-fold, p < 0.001), and contralateral calf muscle (5- to 15-fold, p < 0.01) in Mxra8<sup>−/−</sup>Δ8 and Mxra8<sup>−/−</sup>Δ97 mice compared to WT mice (Figures 2D, 2E, 2H, and 2I). We observed a trend toward a reduction in virus titers in the calf muscles of Mxra8<sup>−/−</sup>Δ8 mice at 3 dpi. We expanded the time course and examined viral infection at 7 dpi, which represents the second peak of clinical disease in mice. Decreases in CHIKV titers were observed in the ipsilateral ankle of Mxra8<sup>−/−</sup>Δ8 compared to WT mice at 7 dpi (18-fold, p < 0.01) (Figure 2F). To define the role of Mxra8 in CHIKV tropism, we performed RNA ISH on the ipsilateral and contralateral ankles at 3 dpi. Relatively minor differences were observed with viral RNA ISH in the ipsilateral ankle (Figure 2M), which is consistent with the small reduction in viral titers (Figures 2D and 2H). However, in the contralateral ankle, CHIKV RNA was detected readily in the dermis, synovium, and muscle cells of WT but not Mxra8<sup>−/−</sup>Δ8 mice (Figure 2M).

We also infected WT and Mxra8<sup>−/−</sup>Δ8 mice with CHIKV LR 2006, an East/Central/South African strain that showed less dependence on the Mxra8 entry pathway in cell culture (Zhang et al., 2018). Nonetheless, we observed similar in vivo results with CHIKV LR 2006 and AF15561 strains. Decreased swelling and reduced virus titers in the ipsilateral and contralateral ankles and calf muscles were observed in CHIKV LR 2006-infected Mxra8<sup>−/−</sup>Δ8 mice, and spread to tissues distal from the site of inoculation was greatly diminished (Figures 2J–2L). To evaluate whether the soluble, truncated Mxra8 protein generated from the 8-nt frameshift deletion had any effect on CHIKV infection, Mxra8<sup>−/−</sup>Δ8 mice were administered PBS, an isotype control mAb, or two anti-Mxra8 blocking mAbs (1G11.E6 + 7F1.D8) (Zhang et al., 2018) 12 h pre-CHIKV inoculation. At 3 dpi, no
differences in viral load were detected in the ipsilateral and contralateral ankles and calf muscles of Mxra8D8/D8 mice treated with PBS or the control or anti-Mxra8 mAbs (Figure S3); these data suggest that soluble Mxra8 did not independently affect CHIKV infection. Overall, these experiments establish the following: (1) Mxra8D8/D8 (truncated, soluble protein) and Mxra8D97/D97 (protein null) mice phenocopy each other in the context of CHIKV infection and joint swelling, (2) small differences in CHIKV infection are observed with Mxra8 haploinsufficiency, (3) the absence of Mxra8 modulates virus spread to a greater extent than replication at the local site of injection, (4) two CHIKV strains with varying Mxra8 dependency in cell culture showed similar clinical and virological phenotypes in Mxra8 mutant mice.

Our subcutaneous inoculation model suggests that Mxra8 has a greater role in CHIKV dissemination than local infection. We
speculated this could reflect a cell type-specific Mxra8-independent entry pathway in the tissues of the foot or unique growth kinetics of CHIKV in the absence of early innate immune responses. To begin to address this question, we inoculated intravenously WT and Mxra8−/− mice with CHIKV-AF15561 and monitored infection at 1 and 3 dpi. Notably, reduced virus titers were observed in both the ankles and calf muscles of Mxra8−/− compared to WT mice (Figures 3A and 3B). The disparity in infection of ipsilateral and contralateral ankles in WT and Mxra8 mutant mice after subcutaneous and intravenous inoculation suggests that additional factors (e.g., local innate immunity) may modulate the kinetics of CHIKV growth.

Impact of Mxra8 on Other Arthritogenic Alphavirus Infections In Vivo

We next evaluated MAYV, RRV, and ONNV infection in Mxra8 mutant mice. Similar to results observed with CHIKV, reductions in MAYV-induced foot swelling were observed in Mxra8−/− compared to WT mice at 3 dpi (Figure 4A). We also observed a phenotype with MAYV spread, as there was a significant decrease in virus titers in the ipsilateral calf muscle (14-fold, p < 0.0001), draining lymph node (9-fold, p < 0.01), contralateral ankle (10-fold, p < 0.05), and contralateral calf muscle (4-fold, p < 0.01), but not in the ipsilateral ankle (4-fold, p > 0.05) at 3 dpi (Figures 4B–4D). In an ONNV infection model, which does not cause joint swelling (Morrison et al., 2006), we observed reduced virus titers in the ipsilateral ankle (15-fold, p < 0.0001), ipsilateral calf muscle (6-fold, p < 0.01), contralateral ankle (11-fold, p < 0.0001), and contralateral calf muscle (4-fold, p < 0.01) of Mxra8−/− mice at 3 dpi (Figures 4E and 4F). In an ONNV infection model, virus titers in the ipsilateral ankle were reduced (7-fold, p < 0.01) in Mxra8−/− compared to WT mice at 1 dpi (Figure 4G); later time points and other tissues were not analyzed, as ONNV infection is rapidly controlled by interferon (IFN) responses in immunocompetent mice (Fox et al., 2015; Seymour et al., 2013).

Impact of Mxra8 on Subacute Alphavirus Infection and Persistence

Subcutaneous CHIKV infection in mice results in prolonged foot swelling lasting 2–3 weeks and persistent viral RNA in joint-associated tissues for months, which is associated with the histopathological evidence of synovitis, arthritis, and tendonitis (Hawman et al., 2013). We tested the impact of Mxra8 on ankle swelling during the first month of infection. Compared to WT animals, Mxra8−/− mice inoculated with CHIKV-AF15561 showed markedly reduced foot swelling during the first two peaks of swelling at 2–3 dpi and 6–8 dpi, respectively (Figure 5A). At 28 dpi, lower levels (12-fold, p < 0.0001) of CHIKV RNA were detected in the ipsilateral ankle of Mxra8−/− mice (Figure 5B). To corroborate these results, anti-Mxra8-blocking mAbs (Zhang et al., 2018) were administered via an intraperitoneal route to WT mice at 12 h pre- (Figure 5C) or post- (Figure 5D) infection and subsequently every 4 days. Similar to results with Mxra8−/− mice, reduced foot swelling was also observed with either prophylactic or therapeutic administration of anti-Mxra8 mAbs.

CHIKV-Induced Inflammation in Mxra8−/− Mice

Given the reduction in swelling of the ipsilateral ankles of Mxra8−/− mice, we analyzed the impact of Mxra8 on immune cell accumulation at 3 and 7 dpi, which corresponds to the infiltration of myeloid cells (monocytes and neutrophils) and pathogenic CD4+ T cells (Haist et al., 2017; Poo et al., 2014; Teo et al., 2013), respectively, in mice (Figure 6). In uninfected mice (day 0), as expected, relatively few CD45+ leukocytes were present in the joint homogenates; however, we did observe small reductions in some cell types (e.g., neutrophils, macrophages, dendritic cells) at baseline in Mxra8−/− mice compared to WT mice (Figure 6B). At 3 dpi, despite the large differences in tissue swelling and edema (Figure 6A), the numbers of most immune cell populations had increased and were similar between WT and Mxra8-mutant mice (Figures 6C and S4); however, differences were observed in the number of neutrophils (2-fold decrease, p < 0.05) and dendritic cells (3-fold increase, p < 0.001) in Mxra8−/− mice. At 7 dpi, similar results were observed with a decrease in neutrophils (5-fold, p < 0.0001) and an increase in dendritic cells (2-fold, p < 0.05) in Mxra8−/− mice (Figure 6D).

To gain further insight into the effect of Mxra8 on CHIKV-induced joint inflammation, we profiled cytokines and chemokines in ipsilateral ankles at 3 and 7 dpi in WT and Mxra8−/− mice. Although many were undetectable (e.g., interleukin-2 [IL-2], IL-3, IL-4, IL-5, IL-13, and IL-17), several pro-inflammatory cytokines and chemokines were reduced in the joint homogenates of Mxra8−/− mice, including IL-1β (7 dpi), IL-6 (3 dpi), IL-12 (p40) (7 dpi), IFN-γ (7 dpi), tumor necrosis factor α (TNF-α) (7 dpi), granulocyte colony-stimulating factor (G-CSF) (3 and 7 dpi), granulocyte-macrophage CSF (GM-CSF) (3 and 7 dpi),
monocyte chemoattractant protein 1 (MCP-1) (7 dpi), macrophage inflammatory protein 1α (MIP-1α) (7 dpi), MIP-1β (3 and 7 dpi), RANTES (7 dpi), and CXCL1 (7 dpi) (Figures 6E and S5). Thus, even the moderate reductions in CHIKV virus titers in the ipsilateral foot at 3 and 7 dpi were associated with marked decreases in levels of multiple pro-inflammatory mediators, which likely affected the clinical swelling phenotype.

A Mutant CHIKV with Diminished Mxra8 Binding Is Attenuated Specifically in WT Mice

Two groups recently showed that Mxra8 binds to CHIKV by wedging into a cleft created by two adjacent E2-E1 heterodimers within a trimeric spike (Basore et al., 2019; Song et al., 2019). Several solvent-exposed residues in the A domain of E2 (e.g., D71) were predicted to form key contacts with Mxra8 directly (Figure 7A), and E2-6K-E1 expression constructs with these mutations decreased Mxra8 binding in transfection experiments in cells (Zhang et al., 2018). As an independent method of determining the contribution of Mxra8 to CHIKV pathogenesis, we generated the D71A mutation in CHIKV (AF15561 strain background). We confirmed that the mutant CHIKV had a diminished ability to bind Mxra8 in a modified virus capture ELISA (Figure 7B). Subsequently, we inoculated WT and D71A CHIKV into WT and Mxra8D8/D8 mice. At 3 dpi, compared to the parental WT virus, D71A CHIKV showed reduced infection in the ipsilateral and contralateral ankles (5- to 14-fold, p < 0.01) and the ipsilateral and contralateral ankles and calf muscles at 12 h (G) and 3 dpi (B-F) were harvested for virus titration by FFU assay (two experiments; n = 9–15; two-tailed Mann-Whitney test; **p < 0.01, ***p < 0.001, and ****p < 0.0001; ns, not significant).

A BLAST alignment of Mxra8 revealed orthologs in mammals, birds, reptiles, and fish but none in invertebrate animals (Zhang et al., 2018), even though the transmission of arthritogenic alphaviruses requires an amplification stage in mosquito hosts. Although our experiments in mice establish that Mxra8 expression is necessary for optimal infection and pathogenesis, we set out to determine whether it would be sufficient to enhance infection in vivo. To test this, we created transgenic flies that ectopically express mouse Mxra8 (Figure 7D). Uninfected flies expressing Mxra8 showed no difference in survival rates compared to transgenic control flies. As in mosquitoes, infection of WT flies with arboviruses such as CHIKV (strain 181/25) have no impact on mortality (Figure 7E). In comparison, Mxra8-expressing flies infected with CHIKV showed greater mortality rates, and this phenotype was associated with higher levels in viral RNA in whole flies (Figures 7E and 7F). Thus, ectopic expression of Mxra8 in flies is sufficient to enhance infection and disease in invertebrate animals that do not normally succumb to infection and lack this alphavirus receptor.

**DISCUSSION**

In a prior study, we defined the cell surface protein Mxra8 as an entry receptor for CHIKV and other related arthritogenic alphaviruses (Zhang et al., 2018). Here, we assessed the role of Mxra8 in alphavirus infection using genetically engineered Mxra8 mutant mice to study tissue tropism, viral pathogenesis, and the ensuing immune response. Introduction of either 8- or 97-nt frameshift deletions in domain 2 of mouse Mxra8, which generated a soluble protein or no protein at all, resulted in markedly reduced foot swelling and dissemination of CHIKV. Haploinsufficiency was observed, as less swelling and reduced viral burden occurred in CHIKV-infected Mxra8D8/D8 mice. Associated with the reductions in CHIKV infection were diminished accumulation of neutrophils and lower levels of pro-inflammatory cytokines in animals expressing intact forms of Mxra8.
musculoskeletal-associated tissues. Loss of cell surface Mxra8 expression also mitigated CHIKV persistence and resulted in the reduced infection of MAYV, RRV, and ONNV, three additional emerging arthritogenic alphaviruses. Compared to a parental WT virus, a recombinant CHIKV (D71A) encoding a loss-of-Mxra8-binding substitution was attenuated specifically in WT but not Mxra8<sup>−/−</sup> mice. Moreover, ectopic expression of Mxra8 in transgenic Drosophila was sufficient to increase CHIKV replication and mortality. Overall, these experiments establish a key role for Mxra8 in the infection, dissemination, and pathogenesis of multiple related arthritogenic alphaviruses in vivo.

The physiological function of Mxra8 is not fully understood. Mxra8 was first called adipocyte-specific protein 3 (ASP3), as it is upregulated during adipocyte differentiation and expressed in mesenchymally derived cells (Jung et al., 2004). High levels of mRNA expression of its bovine ortholog were observed in skeletal muscle tissue with high marbling and fat content (Clark et al., 2011). Mxra8 was also called limitrin, because of its expression in the glia limitans and speculated function in maintaining the blood-brain barrier (Yonezawa et al., 2003). Given its predicted Ig-like domains and cell surface expression pattern, Mxra8 was called DICAM (Jung et al., 2008) and shown in vitro to bind to the vβ7 integrin, resulting in attenuated vβ7 signaling and suppression of osteoclast differentiation and angiogenesis (Han et al., 2013; Jung et al., 2008, 2012). Mxra8 RNA in fibroblasts and cells in the synovium, which is consistent with the targets and tropism of arthritogenic alphavirus infection in musculoskeletal-associated tissues (Morrisson et al., 2006, 2011; Sourisseau et al., 2007). Nonetheless, despite repeated attempts with multiple monoclonal and polyclonal antibodies, we were unable to detect reliably the Mxra8 protein expression pattern in tissues that one group has reported (Jung et al., 2008, 2012). The generation of Mxra8 reporter gene mice may be required to fully delineate its expression pattern and elucidate its possible functions in connective tissues and other sites.

One prominent phenotype we observed was the nearly abolished joint swelling despite rather modest reductions in CHIKV burden at day 3 in the ipsilateral ankle of Mxra8-deficient mice when the virus was administered in the foot at a proximal site. These results are consistent with our prior study using function-blocking mAbs against Mxra8 (Zhang et al., 2018). At this early time point in CHIKV pathogenesis in mice, the host innate immune response exerts a dominant function in modulating inflammation, and this is mediated in part by vasoactive cytokines and infiltrating monocytes and neutrophils (Fox et al., 2019; Poo et al., 2014). In joint-associated tissues of CHIKV-infected Mxra8-deficient mice, we detected reduced numbers of neutrophils and increased dendritic cells, the latter of which express regulatory receptors that can mitigate CHIKV-induced
arthritis and edema (Long et al., 2013); some of this difference in foot swelling after CHIKV infection could have been affected by the slight differences in immune cell numbers in musculoskeletal tissues observed at baseline between WT and Mxra8-deficient mice. Associated with this were reduced tissue homogenate levels of several pro-inflammatory mediators, including IL-6, G-CSF, GM-CSF, and MIP-1β, in Mxra8-deficient compared to WT mice. The basis for the ostensible discrepancy between

Figure 6. Analysis of Inflammation in the Musculoskeletal Tissues of Mxra8Δ/Δ Mice after CHIKV Infection

(A–D) WT and Mxra8Δ/Δ mice were inoculated subcutaneously in the foot with 10^5 FFU of CHIKV-AF15561. (A) At 3 dpi, ipsilateral feet were collected, fixed, decalcified, paraffin embedded, sectioned, and stained with H&E. Scale bar, 100 μm; representative images are shown from n = 4 mice from two experiments. Arrows indicate tissue edema. At days 0 (B) (uninfected), 3 (C), and 7 (D) post-infection, cells from ipsilateral feet were harvested and analyzed for numbers of leukocytes (CD45+), monocytes (CD11b+CD11c−/Ly6G−Ly6C+), neutrophils (CD11b+CD11c−/Ly6G+), natural killer (NK) cells (CD3−NK1.1+), macrophages (CD11b+CD11c−/Ly6G−Ly6C−/F4/80+), monocyte-derived dendritic cells (DCs) (CD11b−CD11c+Ly6G−Ly6C−/MHCII+), CD4+ T cells (CD3+CD4+), and CD8+ T cells (CD3+CD8+) by flow cytometry (see Figure S4 for gating scheme, two experiments; n = 8–10; two-tailed Mann-Whitney test; *p < 0.05, **p < 0.01, ***p < 0.001, and ****p < 0.0001; ns, not significant).

(E) At 3 and 7 dpi, ipsilateral ankles from WT and Mxra8Δ/Δ mice were harvested, homogenized, and the indicated cytokines or chemokines were measured (two experiments; n = 8–10, mean ± SD; two-way ANOVA with Sidak’s test; *p < 0.05; **p < 0.01; ****p < 0.0001; ns, not significant). See also Figures S4 and S5.
the marked effect of Mxra8 expression on foot swelling and the smaller effect on CHIKV infection warrants further study. Possible explanations include a non-linear relation between infection and joint inflammation; an independent effect of Mxra8 signaling on inflammation; or local interactions between CHIKV, Mxra8, and the innate immune response in the foot. However, when we inoculated CHIKV via an intravenous route, equivalent reductions in viral burden were observed in both ankles, suggesting that the tropism of the virus in the foot and associated musculoskeletal tissues can vary, depending on the pathogenesis sequence.

Our prior studies in cell culture with CHIKV suggested that while Mxra8 was a dominant receptor for entry and infection, a second, Mxra8-independent pathway must exist because low levels of infection were observed in gene-edited fibroblasts for Mxra8 or in other cell types that endogenously do not express Mxra8 (Zhang et al., 2018). Our infection studies in Mxra8<sup>D8/D8</sup> or Mxra8<sup>D97/D97</sup> mice are consistent with this observation. Although markedly reduced infection was measured in the gene-edited mice, alphavirus replication clearly occurred in the absence of Mxra8 expression. Both strains of CHIKV (Asian AF15561 and East/Central/South African LR 2006) showed equivalent loss-of-infection phenotypes in vivo, even though we previously observed a differential Mxra8 dependence in NIH 3T3 cells. The basis for this apparent discrepancy between cell culture and mouse data remains uncertain, although it could be due to differences in the cell type-specific expression of the Mxra8-independent ligand in culture and in vivo. The identity of the alternative, Mxra8-independent entry ligand also remains unknown, and the precise function of Mxra8 in attachment, entry, and trafficking of alphavirus virions remains to be established.

Possible alternative binding ligands that require future investigation include heparan sulfate proteoglycans (Gardner et al., 2011; Klimstra et al., 1998; Silva et al., 2014), prohibitin (Wintachai et al., 2012), NRAMP2 (Rose et al., 2011), and TIM and TAM family members proteins that bind phosphatidylserine moieties (Jemielity et al., 2013). The ability to cross putative ligand-deficient mice onto a Mxra8-deficient background or treat such animals with Mxra8 function blocking mAbs may help to elucidate the residual entry pathway of CHIKV and possibly other alphaviruses. Alternatively, genetic screens (small interfering RNA [siRNA], small hairpin RNA [shRNA], or CRISPR-based) can be performed in Mxra8-deficient cells with a loss-of-CHIKV infection readout to define the residual pathway of entry.

Figure 7. Loss- and Gain-of-Function Effects of Mxra8 in Mice and Drosophila
(A) Structural representation of the CHIKV E2-D71 residue (red) on the cryoelectron microscopy (cryo-EM) model of Mxra8 bound to CHIKV (PDB 6NK6). Color scheme: Mxra8, purple; CHIKV E2, cyan; and CHIKV E1, gray. Inset: magnified view of the Mxra8-CHIKV E2-D71 interface.
(B) Loss of binding to Mxra8 by D71A mutation in CHIKV. WT and D71A CHIKV were captured with mouse CHK-152 (anti-E2) and CHK-166 mAb (anti-E1). After washing, Mxra8-Fc (human IgG1 Fc) was added and binding was measured. Equivalent amounts of WT and D71A CHIKV were captured on the microtiter plate as determined by the binding of humanized CHIK-152. Humanized E16 (anti-West Nile virus [WNV] E) served as a negative control. Results are the mean of three experiments performed in triplicate (Mann-Whitney test: ***p < 0.0001).
(C) WT and Mxra8<sup>Δ8,Δ8</sup> mice were inoculated subcutaneously in the foot with 10<sup>3</sup> FFU of CHIKV-AF15561 (WT or D71A mutant). At 3 dpi, tissues were harvested for virus titration by FFU assay (two experiments; n = 8; two-tailed Mann-Whitney test; *p < 0.05, **p < 0.01, and ***p < 0.001; ns, not significant).
(D–F) Transgenic flies expressing mouse Mxra8 have increased susceptibility to CHIKV infection. (D) Flies of the indicated genotypes were analyzed for the ectopic expression of Mxra8 by western blotting. (E) The indicated flies were either uninfected or challenged with CHIKV (strain 181/25) and monitored daily for mortality. Data are pooled from three experiments and the number of flies are indicated (log rank test; **p < 0.01). (F) Groups of 15 flies of the indicated genotype were inoculated with CHIKV, and total RNA was collected at 7 dpi. Viral RNA was quantified by qRT-PCR, normalized to the housekeeping gene rp49, and shown relative to control (Act > +). Means ± SEMs are shown for four experiments (unpaired t test; *p < 0.05).
The existence of a second entry pathway for CHIKV in mammals is consistent with the observation that lower organisms, such as mosquitoes, which do not encode an Mxra8 ortholog, transmit this virus in nature. The identity of this secondary entry receptor for CHIKV in mammals and its possible relation to the one in insects remains to be defined. Nevertheless, ectopic expression of Mxra8 rendered flies more susceptible to infection with increased replication and mortality. For mosquito transmission, arboviruses must replicate to high enough titer for efficient transfer to vertebrates during a blood meal, but not so high that pathogenesis occurs in the infected mosquito. The loss of innate immune control of arboviruses in insects leads to increased replication and mortality (Liu et al., 2018; Merkling and van Rij, 2013). Our data suggest that higher levels or ectopic expression of receptors in insects also can shift this balance away from controlled levels of arbovirus infection.

In summary, we generated Mxra8 mutant mice by introducing out-of-frame deletions within and adjacent to the second Ig-like domain. Where the 8-nt deletion resulted in a truncated, soluble Mxra8, the 97-nt deletion was a protein null. Both mice showed marked reductions in CHIKV infection and swelling and appeared to phenocopy each other. Similar results were observed in the Mxra8<sup>D8/D8</sup> mice after inoculation with three other arthropod alphaviruses, MAYV, RRV, and ONNV. No obvious developmental or growth defects were observed in our two founder lines, which is consistent with an Mxra8-deficient mouse generated by another laboratory studying experimental colitis (Han et al., 2019). Although future studies are required to define fully the endogenous functions of Mxra8, its transient blockade with antibodies or small molecules could represent a plausible therapeutic strategy to prevent or treat infections by multiple globally emerging arthritogenic alphaviruses with epidemic potential.

**SUPPLEMENTAL INFORMATION**

Supplemental Information can be found online at https://doi.org/10.1016/j.celrep.2019.07.105.

**ACKNOWLEDGMENTS**

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**AUTHOR CONTRIBUTIONS**

R.Z., J.T.E., E.S.W., P.D., S.C., and M.S.D. designed the experiments. R.Z., J.T.E., E.S.W., P.D., L.J.A., and G.H. performed the in vivo and mammalian cell culture experiments. A.S.K. performed the structural analysis and the Mxra8 binding assays. B.G. performed the experiments with transgenic flies. R.Z. and M.S.D. wrote the initial draft of the manuscript, with the other authors providing comments and edits to the final version.

**DECLARATION OF INTERESTS**

M.S.D. is a consultant for Inbios and Atreca and serves on the Scientific Advisory Board of Moderna.

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## STAR★METHODS

### KEY RESOURCES TABLE

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Note: Additional data continues on the next page.
LEAD CONTACT AND MATERIALS AVAILABILITY

Further information and requests for resources and reagents should be directed to and will be fulfilled by the Lead Contact author Michael S. Diamond (diamond@wusm.wustl.edu). All plasmids, antibodies, cells, viruses, and mouse lines developed for this study are available under Material Transfer Agreements from Washington University.

EXPERIMENTAL MODEL AND SUBJECT DETAILS

Viruses
The following viruses were used in the study: CHIKV (LR 2006, AF15561, and 181/25), RRV (T48), MAYV (BeH407), and ONNV (MP30). All viruses were propagated in Vero cells and titrated by focus-forming assays, as described previously (Zhang et al., 2018). The CHIKV AF15561 D71A mutant was generated by overlapping PCR. The genomic RNA was transcribed \textit{in vitro} from cDNA using the \textit{mMESSAGE mMACHINE SP6 Transcription Kit} (ThermoFisher scientific, AM1340), purified, and electroporated into BHK21 cells to rescue the virus. The mutant virus was passaged once in Vero cells and titrated by focus-forming assay (Zhang et al., 2018). The region encompassing the structural genes (C-E3-E2-6K-E1) was confirmed by sequencing before use.

Generation of Mxra8 deficient mice
The sequence of Mxra8 locus (NC_000070.6) was obtained from NCBI, and two sgRNAs targeting the common exon were designed based on the RefSeq annotations, which have two nearly identical transcripts and one short, putative transcript. The two sgRNAs also were selected based on their low off-target profile and absence of single nucleotide polymorphisms: sgRNA-1, 5’-GGAA GACTCGGCGCTCGTGG-3’; sgRNA-2, 5’- CTGTGACCAGACCCATTGCC-3’. The two gRNAs containing the scaffold were generated \textit{in vitro} synthesis (HiScribe T7 In Vitro Transcription Kit, New England BioLabs) followed by cleanup purification (MEGAclear Transcription Clean-Up Kit, Thermo Fisher). Guide RNAs and Cas9 protein were complexed and electroporated into BHK21 cells to rescue the virus. The mutant virus was passaged once in Vero cells and titrated by focus-forming assay (Zhang et al., 2018). The region encompassing the structural genes (C-E3-E2-6K-E1) was confirmed by sequencing before use.

Mouse experiments
Experiments were carried out in accordance with the recommendations in the Guide for the Care and Use of Laboratory Animals of the National Institutes of Health after approval by the Institutional Animal Care and Use Committee at the Washington University School of Medicine (Assurance number A3381-01). Four week-old WT, Mxra8	extsuperscript{−/−}, Mxra8	extsuperscript{+/−}, and Mxra8	extsuperscript{397/397} male or female
C57BL/6J mice were inoculated subcutaneously in the footpad with 10^3 FFU of CHIKV (AF15561 or LR 2006 strains), MAYV, RRV, or ONNV. At 12 h, day 1, 2, 3, or 7 post-infection, animals were euthanized, and after extensive perfusion with PBS, indicated tissues were collected. Ipsilateral ankle joint swelling (width x height) was monitored using digital calipers as previously described (Hawman et al., 2013). To assess the long-term effect of CHIKV infection, the ipsilateral feet were collected for viral RNA quantification. Similarly, for antibody pre- or post-treatment experiments, 300 μg of purified Armenian hamster mAbs (1G11.E6 + 7F1.D8) or isotype control (Bio X Cell # BE0260) in PBS were administered via an intraperitoneal route to four-week-old WT male C57BL/6 mice either 12 h before or after subcutaneous inoculation in the footpad with 10^5 FFU of CHIKV-AF15561. The mice also were administered mAbs at 4 and 8 dpi, and joint swelling was measured for 12 days. For intravenous inoculation experiments, mice were injected via the tail vein with 10^6 FFU of CHIKV AF15561, and tissues were harvested at 1 and 3 dpi for viral burden analysis. Blinding and randomization were not performed.

**Fly infections**

Mouse Mxra8 (NM_024263) gene sequences was codon-optimized for *Drosophila*, synthesized with a *Drosophila* Kozak-like sequence (CAAA) and a 3’ FLAG tag, and inserted into a NotI and XhoI digested pUASTattB vector using In-Fusion Cloning. Transgenic flies were generated after integrating the Mxra8 transgene into Chromosome 2 attB (Rainbow Transgenics). Flies were verified, with 3 Mxra8 sequence (CAAA) and a 3’ formaldehyde (PFA) for 24 h. Tissues were decalcified in 14% EDTA free acid for two weeks and embedded in paraffin. Tissue

**METHOD DETAILS**

**Viral growth kinetics analysis**

Primary MEFs (sex unknown) were generated from E15 to E16 mouse embryos and maintained in DMEM supplemented with 10% FBS, non-essential amino acids, and penicillin and streptomycin. Cells in 12-well plates were inoculated with CHIKV AF15561 at a multiplicity of infection (MOI) of 0.01 for 1 h, washed twice and maintained in culture medium supplemented with 2% FBS. Supernatants were harvested and concentrated using Amicon Ultra-15 Centrifugal Filter Units (EMD Millipore #UFC900324). Concentrated supernatants were added to RIPA buffer (1X final) for western blotting analysis as described above.

**Mxra8 ELISA binding assay**

Maxisorp ELISA plates were coated with 2 μg/ml of anti-CHIKV mAbs CHK-152 and CHK-166 (Pal et al., 2013) overnight in sodium bicarbonate buffer (pH 9.3). Plates were washed four times with 1X PBS and blocked for 1 h at 25°C with 4% BSA. CHIKV AF15561 wild-type and D71A mutant viruses were diluted to 10^6 FFU/ml in 2% BSA and added to plates (50 μl/well) for 1 h at 25°C. Plates were washed five times with PBS and incubated with 10 μg/ml of Mxra8-Fc (mouse Mxra8 fused to human IgG1 Fc region), humanized CHIK-152, or humanized anti-WNV E16 (negative control) (Oliphant et al., 2005; Pal et al., 2013). Plates were washed, incubated with horseradish peroxide conjugated goat anti-human IgG (H + L) (1:5000 dilution, Jackson ImmunoResearch #109-035-088) for 1 h at 25°C, and washed again. Plates then were developed with 3,3’-5,5’ tetramethylbenzidine substrate (Thermo Fisher) and 2N H2SO4 and read at 450 nM using a TriStar Microplate Reader (Berthold).

**Western blotting**

Primary MEFs (10^6 cells, sex unknown) were harvested using TrypLE (Thermo Fisher #12605010) and lysed in 45 μL of RIPA buffer (Cell Signaling #9806S) containing protease inhibitors (Sigma Aldrich #S8830). Samples were prepared in LDS buffer (Life Technologies) under reducing (50 mM dithiothreitol) conditions. After a 70°C incubation for 10 min, samples were electrophoresed using 12% Bis-Tris gels in MOPS running buffer (Life Technologies). Proteins were transferred to PVDF membranes using an iBlot2 Dry Blotting System (Life Technologies). Membranes were blocked with 5% non-fat dry powdered milk, and probed with hamster anti-Mxra8 mAbs (3G2.F5 or 9G2.D6, 0.5 μg/ml). Western blots were incubated with Peroxidase AffiniPure goat anti-Armenian hamster IgG (H + L) (Jackson ImmunoResearch #109-035-088) for 1 h at 25°C, and washed again. Plates then were developed with 3,3’-5,5’ tetramethylbenzidine substrate (Thermo Fisher) and 2N H2SO4 and read at 450 nM using a TriStar Microplate Reader (Berthold).

**Histology and RNA*in situ* hybridization**

Four week-old WT and Mxra8^3β/3β male mice were inoculated subcutaneously in the foot with 10^7 FFU of CHIKV AF15561. At 3 dpi, animals were euthanized and perfused extensively with PBS. Ipsilateral and contralateral feet were harvested and fixed in 4% paraformaldehyde (PFA) for 24 h. Tissues were decalcified in 14% EDTA free acid for two weeks and embedded in paraffin. Tissue
sections were stained with hematoxylin and eosin to assess tissue morphology. To determine sites of CHIKV infection, RNA in situ hybridization was performed using the RNAscope 2.5 HD Assay (Brown Kit) according to the manufacturer’s instructions (Advanced Cell Diagnostics). Briefly, sections were deparaffinized, treated with H2O2 and Protease Plus prior to probe hybridization. A probe specifically targeting the CHIKV RNA (strain AF15561) (Advanced Cell Diagnostics, #481981) was custom-designed and used for ISH experiments. Tissues were counterstained with Gill’s hematoxylin. To assess the cell types that express Mxra8 RNA in naïve mice, in situ hybridization was performed using the RNAscope 2.5 HD Assay (Red Kit). A probe specifically targeting Mxra8 (NM_024263.4) (Advanced Cell Diagnostics, #520711) was custom-designed. A negative control probe (#320751) was used in parallel. Tissue sections were visualized using a Nikon Eclipse microscope equipped with an Olympus DP71 color camera.

qRT-PCR
RNA from serum and tissues was extracted with the Viral RNA Mini Kit and RNeasy Mini Kit (QIAGEN), respectively. Viral RNA levels were determined using the TaqMan® RNA-to-Ct 1-Step Kit (Thermo Fisher #4392938) on QuantStudio 6 Flex instrument. A standard curve was produced using serial 10-fold dilutions of CHIKV RNA extracted from the viral stock. Viral burden was expressed on a log10 scale as viral focus-forming unit (FFU) equivalents per g of tissue or ml of serum. Primers and probes used are as follows: CHK181/AF Fwd: 5’-TCGACGCGCCCATTTAA-3’; CHK181/AF Rev: 5’-ATCGAATGCACCGCACACT-3’; CHK181/AF Probe: 5’-56-FAM/AC
CAGCCTG/ZEN/CACCCACTCTCAGAC/3IABkFQ/-30; GAPDH (Mm.PT.39a.1 predesigned set, IDT); and Mxra8 (Mm.PT.58.42796673, predesigned set, IDT).

Flow cytometry
To analyze immune cells in the musculoskeletal tissues at 3 and 7 dpi, ipsilateral feet were perfused extensively, skinned, disjointed from the tibia, and digested in RPMI 1640 medium supplemented with 10% FBS, 15 mM HEPES, 0.5 mg/ml of collagenase (Sigma, C0130) and 10 ug/ml of DNase I (Sigma, D5025) for 1 h at 37°C. Digested tissue was passed through a 70 μm strainer, and cells were separated by centrifugation and washed with PBS supplemented with 2% FBS and 2 mM EDTA. Cells were stained with a Fixable Viability Dye eFluor 506 (eBioscience, 65-0866-14) and incubated with the following antibodies for 1 h at 4°C: CD16/32 (Biolegend, 101301, 1:200), CD11b PE-Dazzle 594 (Biolegend, 101256, 1:200), Ly6G PerCP-Cy5.5 (Biolegend, 127616, 1:400), Ly6C Pacific Blue (BioLegend, 128014, 1:200), F4/80 APC (Thermo Fisher, 17-4801-82, 1:200), CD11c PE-Cy7 (BD Biosciences, 558079, 1:200), I-A/I-E (MHC class II) Alexa Fluor 700 (BioLegend, 107622, 1:200), NK-1.1 PE (BioLegend, 108708, 1:200), CD3 BV786 (BD Biosciences, 564380, 1:200), CD8 PerCP-Cy5.5 (BioLegend, 100734, 1:200), CD4 BV786 (BioLegend, 100552, 1:200), B220 BV711 (BioLegend, 103255, 1:200). Cells were analyzed using a BD X20 Fortessa flow cytometer, and all data were processed using FlowJo software (FlowJo, LLC).

Structural analysis of Mxra8 truncation mutants and CHIKV E2-D71 residue
The truncated forms of Mxra8 generated by the 8- or 97-bp frameshift deletions were modeled from the atomic coordinates of mouse Mxra8 (PDB 6NK3 ((Basore et al., 2019)) using PyMOL (Version 2.1.0, Schrodinger). The CHIKV E2-D71 residue was visualized on the Mxra8-bound CHIKV VLP cryo-EM model (PDB 6NK6) using PyMOL.

Cytokine and chemokine analysis
Mice were inoculated subcutaneously with 10^3 FFU of CHIKV, and the ipsilateral feet were collected at 3 and 7 dpi. Tissues were homogenized in DMEM supplemented with 2% FBS with a MagNA lyser (Roche) and analyzed for cytokine and chemokine levels using a Bio-Plex Pro Mouse Cytokine 23-plex Assay kit (Bio-Rad, #m60009rdpd) according to the manufacturer’s instructions.

QUANTIFICATION AND STATISTICAL ANALYSIS
Data analysis
Statistical significance was assigned when p values were < 0.05 using Prism Version 8 (GraphPad). Analysis of levels of joint swelling, viral burden, cytokines and chemokines, and immune cell infiltration was determined by Mann-Whitney, one-way ANOVA, Kruskal-Wallis ANOVA, or unpaired t test depending on the data distribution and the number of comparison groups. The specific tests and numbers of experiments are indicated in the Figure legends.

DATA AND CODE AVAILABILITY
The published article includes all data generated or analyzed during this study. Original source data for Figures in the paper are available upon request to the Lead Contact author. No proprietary software was used in the data analysis.
Supplemental Information

Expression of the Mxra8 Receptor Promotes Alphavirus Infection and Pathogenesis in Mice and Drosophila

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Figure S1. Sequence alignment and surface expression of Mxra8, Related to Figure 1. (A) Sequence alignment of Mxra8 with 8- and 97-nt deletions. The deleted nucleotides are indicated by dashes. (B) Surface staining of Mxra8 in WT, Mxra8ΔΔ8, and Mxra8ΔΔ97 primary MEFs. Live cells were stained with anti-Mxra8 hamster mAbs (4E7.D10) (1 µg/ml) at 4°C for 25 min. After washing, cells were stained with 2 µg/ml of Alexa 647-conjugated goat anti-Armenian hamster IgG, processed and subjected to flow cytometry analysis. Data are representative of two experiments.
Figure S2. Mxra8 RNA expression in naïve and CHIKV-infected mice, Related to Figure 1. A. A probe specifically targeting the Mxra8 mRNA (left panels: NM_024263.4; Advanced Cell Diagnostics, #520711) was custom-designed and observed in the staining as red dots. A negative control probe is included as comparison (right panels). Scale bar, 50 µm; representative images are shown from three mice from two experiments. Black arrows indicate cells that are positive for Mxra8 RNA. B-C. The indicated mouse tissues were harvested from uninfected (B) or CHIKV-infected (day +3, C) C57BL/6 mice, and RNA was extracted and processed by qRT-PCR. The levels of Mxra8 RNA were normalized to GAPDH levels. Data are from two experiments (n = 6), and bars indicate median values.
Figure S3. CHIKV infection in Mxra8\textsuperscript{Δ8/Δ8} mice pretreated with anti-Mxra8 blocking antibodies, Related to Figure 2. Mice were treated via an intraperitoneal injection with PBS, isotype control hamster mAb (300 µg total), or a cocktail (300 µg total) of anti-Mxra8 mAbs (1G11.E6 + 7F1.D8). Twelve hours later, mice were inoculated subcutaneously in the foot with $10^3$ FFU of CHIKV-AF15561. At 3 dpi, ipsilateral (A) and contralateral (B) ankles and calf muscles were collected for virus titration by focus-forming assay (two experiments; n = 8; one-way ANOVA with Tukey’s test; ns, not significant).
Figure S4. Flow cytometry gating scheme for infiltrating immune cells, Related to Figure 6. WT and 
*Mxra8* Δ/Δ mice were inoculated subcutaneously in the foot with $10^3$ FFU of CHIKV-AF15561. At 3 and 7 dpi, 
single cell suspensions from the ipsilateral feet were harvested for flow cytometry analysis. (A) Gating scheme for 
myeloid and NK cells (monocytes, neutrophils, NK cells, macrophages, and dendritic cells). (B) Gating scheme for 
CD4$^+$ T cells, CD8$^+$ T cells. The plots are representative of two independent experiments.
Figure S5. Cytokine and chemokine analysis, Related to Figure 6. WT and Mxra8Δ/Δ mice were inoculated subcutaneously in the foot with $10^3$ FFU of CHIKV-AF15561. At 3 and 7 dpi, ipsilateral ankles were harvested, homogenized, and the indicated cytokines or chemokines were measured (two experiments; n = 8-10, mean ± SD; two-way ANOVA with Sidak’s test; *, P < 0.05; **, P < 0.01; ****, P < 0.0001; ns, not significant).