

# CCR2 deficiency promotes exacerbated chronic erosive neutrophil-dominated chikungunya virus arthritis

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1	CCR2 Deficiency Promotes Exacerbated Chronic Erosive Neutrophil-Dominated
2	Chikungunya Virus Arthritis
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4	Running title; CCR2 Deficiency Exacerbates Chikungunya Arthritis
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ABSTRACT

27	Chikungunya virus (CHIKV) is a member of a globally distributed group of arthritogenic
28	alphaviruses, that cause weeks to months of debilitating polyarthritis/arthralgia, which is
29	often poorly managed with current treatments. The arthritic disease is usually characterised
30	by high levels of the chemokine CCL2 and a prodigious monocyte/macrophage infiltrate.
31	Several inhibitors of CCL2 and its receptor CCR2 are in development and may find
32	application for treating certain inflammatory conditions, including autoimmune and viral
33	arthritides. Herein we used CCR2 <sup>-/-</sup> mice to determine the effect of CCR2 deficiency on
34	CHIKV infection and arthritis. Although there were no significant changes in viral load or
35	RNA persistence, and only marginal changes in anti-viral immunity, arthritic disease was
36	substantially increased and prolonged in CCR2 <sup>-/-</sup> mice when compared with wild-type mice.
37	The monocyte/macrophage infiltrate was replaced in CCR2 <sup>-/-</sup> mice by a severe neutrophil
38	(followed by an eosinophil) infiltrate, and was associated with changes in expression of
39	multiple inflammatory mediators (including CXCL1, CXCL2, G-CSF, IL-1 $\beta$ , IL-10). Loss
40	of anti-inflammatory macrophages and their activities (eg efferocytosis) was also implicated
41	in the exacerbated inflammation. Clear evidence of cartilage damage was also seen in
42	CHIKV infected CCR2 <sup>-/-</sup> mice, a feature not normally associated with alphaviral arthritides.
43	Although recruitment of CCR2 <sup>+</sup> monocyte/macrophages can contribute to inflammation, they
44	also appear to be critical for preventing excessive pathology and resolving inflammation
45	following alphavirus infection. Caution might thus be warranted when considering
46	therapeutic targeting of CCR2/CCL2 for the treatment of alphaviral arthritides.
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### 48 Importance statement

49	Herein we describe the first analysis of a viral arthritis in mice deficient for chemokine
50	receptor CCR2. CCR2 is thought to be central to the monocyte/macrophage dominated
51	inflammatory arthritic infiltrates seen after infection with arthritogenic alphaviruses, such as
52	chikungunya virus. Surprisingly, the viral arthritis caused by chikungunya virus in CCR2
53	deficient mice was more severe, prolonged and erosive, and neutrophil dominated, with viral
54	replication and persistence not significantly affected. Monocytes/macrophages recruited by
55	CCL2 thus also appear to be important for both preventing even worse pathology mediated
56	by neutrophils, and for promoting resolution of inflammation. Caution might thus be
57	warranted when considering use of therapeutic agents that target CCR2/CCL2 or
58	inflammatory monocyte/macrophages for treating alphaviral (and perhaps other viral)
59	arthritides. Individuals with diminished CCR2 responses (due to drug treatment or other
60	reasons) may also be at risk of exacerbated arthritic disease following an alphaviral infection.
61	
62	

63	Although many viruses can cause arthritis (56), few do so with the reliability of the
64	arthritogenic alphaviruses, where symptomatic infection of adults is nearly always associated
65	with rheumatic disease. This group of globally distributed, mosquito borne, positive-strand
66	RNA viruses include the Australasian Ross River virus and Barmah Forest virus, the African
67	o'nyong-nyong virus, the American Mayaro virus, the Sindbis virus family (which includes
68	the Scandinavia Ockelbo and Pogosta viruses), and chikungunya virus (CHIKV) (54, 55).
69	CHIKV has caused sporadic outbreaks every 2-50 years, which have generally been restricted
70	to Africa and Asia. However, in 2004-2012, CHIKV caused the largest outbreak ever
71	recorded for this virus, with an estimated 1.4-6.5 million patients and imported cases reported
72	in nearly 40 countries, including USA, Japan and several European countries (7, 54, 59).
73	CHIKV disease, and alphaviral rheumatic disease generally, is usually self-limiting and
74	characterised by acute and chronic symmetrical peripheral polyarthralgia/polyarthritis, with
75	acute disease often also associated with fever, myalgia and/or rash. Arthropathy can be
76	debilitating, usually lasts weeks to months, is generally not erosive, but can be protracted (54,
77	55).
78	Chemokine (C-C motif) receptor 2 (CCR2) is the receptor for a number of C-C motif
79	chemokines, including CCL2, which is also known as monocyte chemotactic protein-1
80	(MCP-1). CCL2 recruits monocytes, basophils and T-cells to sites of inflammation and has
81	been implicated as an important mediator in a range of inflammatory diseases including inter
82	alia rheumatoid arthritis (RA), multiple sclerosis, atherosclerosis, asthma, neuropathic pain
83	(53), obesity, diabetes (37) and cancer (66). A range of therapeutic agents that target CCR2
84	or CCL2 are being developed (37, 53, 66), although initial trial results for CCR2 blockade in
85	RA patients have been disappointing (23). Nevertheless, CCR2/CCL2 inhibition may
86	ultimately find utility in the treatment of a range of conditions (37, 53, 66). Elevated CCL2
87	and monocyte/macrophage infiltrates are also prominent features in several viral arthritides,

88	and are well described for alphaviral arthropathies (56), including CHIKV disease in mice,
89	monkeys and humans (13, 22, 54). Treatments with anti-CCL2 antibody or bindarit, a new
90	drug purported to target CCL2 production, were shown to be effective at ameliorating
91	rheumatic disease in CHIKV and Ross River virus mouse models (43, 44). As CCL2
92	generally appears to have no direct anti-viral activity (15, 26, 44, 56), targeting this
93	chemokine and/or its receptor would appear attractive for treatment of viral arthritides.
94	The inflammation biology of CCR2/CCL2 has emerged to be complicated. Collagen-
95	induced arthritis in CCR2 <sup>-/-</sup> mice is more severe with increased macrophage and neutrophil
96	infiltrates (39, 40), whereas in other arthritis models, inhibition of CCL2 ameliorated disease
97	(14, 50). CCR2 deficiency was associated with reduced monocyte/macrophage infiltration in
98	some settings (3, 38, 47), but not others (12, 39). More neutrophil infiltrates were seen in
99	CCR2 <sup>-/-</sup> mice in certain settings (12, 33, 39), unchanged in some (10), less in others (51). For
100	dengue and influenza infections in CCR2 <sup>-/-</sup> mice the viral load was unchanged, and the
101	pathology was attenuated (15, 26). In contrast, cytomegalovirus and West Nile virus
102	infections in these mice resulted in increased viral loads and pathology (17, 25).
103	Given the recent outbreak of CHIKV and the interest in using CCR2/CCL2 blockers for
104	alphaviral arthritides and other diseases, we sought to determine the effect of CCR2
105	deficiency in CHIKV arthritis using a recently established adult mouse model, which mimics
106	many aspects of human disease (13).
107	
108	MATERIALS AND METHODS
109	Ethics statement. Animals were handled in accordance with National Health and Medical
110	Research Council (Australia) guidelines. Animals were kept in the modern Optimice caging

111 system (Centennial, CO, USA). All animal experimentation was approved by the QIMR

112 Berghofer animal ethics committee.

113 Virus isolates and preparation. The Reunion Island (LR2006-OPY1) CHIKV isolate 114 was prepared as described (13). The virus preparations had undetectable endotoxin and mycoplasma contamination (19, 21). As CHIKV is a biosafety level 3 pathogen, all work 115 with infectious virus was conducted in the BSL3 facility at QIMR Berghofer. 116 117 Mouse infection, arthritis and antibody monitoring. Female 6-10 week old mice were 118 inoculated s.c. into each hind foot with CHIKV (LR2006-OPY1) (viral dose of 10<sup>4</sup> CCID<sub>50</sub> in 119 40 µl medium) and tissue viral titres and viraemia determined as described (13). Arthritis 120 was monitored by measuring the height and width of the metatarsal area of the hind feet using 121 digital calipers. The data is presented as a group average of the percentage increase in foot 122 height x width for each foot compared with the same foot on day 0 (42). C57BL/6 mice were supplied by Animal Resources Centre (Perth, Australia). CCR2<sup>-/-</sup> mice on a C57BL/6 123 124 background (3) were bred in-house at QIMR Berghofer. Antibody responses were 125 determined using isotope-specific ELISA using inactivated whole CHIKV as antigen as 126 described (62). 127 Quantitative real-time reverse transcription PCR (qRT-PCR) analyses. RNA 128 isolation from feet, cDNA preparation and quantitative real-time PCR analyses were 129 performed as described (13). The qRT-PCR analyses used 1  $\mu$ l ( $\approx$ 50 ng) of cDNA, 10  $\mu$ l of SYBR green Super mix-UDG (Invitrogen), 1  $\mu$ l of the kit's BSA solution, 6  $\mu$ l H<sub>2</sub>O, and 1  $\mu$ l 130 of 10 µM of forward and reverse primers. Each sample was analyzed in duplicate and 131 132 normalized to RPL13A mRNA levels (13). Primer sequences are shown in Table S1 in the 133 supplemental material. 134 Histology and immunohistochemistry. H&E, F4/80 and ApoTag staining (Millipore, 135 Temecula, US) was undertaken as described previously (13, 34). Anti-Ly6G staining was 136 undertaken using rat anti-mouse Ly6G (Abcam, Cambridge, MA, USA; #NMP-R14) and was 137 detected in the same way as for F4/80. Leder (Naphthol AS-D Chloroacetate, Sigma, USA),

138 Chromotrope 2R (ProSciTech, Thuringowa, Australia) and Safranin O staining (BDH 139 Laboratory Supplies, Poole, UK) used standard protocols. Stained whole foot sections were 140 digitally scanned using Scan Scope XT digital slide scanner (Aperio, Vista, CA). Image analyses of whole foot sections in duplicate were undertaken using Aperio ImageScope 141 142 Software (v10) and the Positive Pixel Count v9 algorithm using default "Strong" settings. 143 MK0812 treatment. MK0812 (Amandis Chemical, China) was dissolved in chloroform 144 (5% in PBS final) and administered i.p. 30 mg/kg, daily days 1-6 post infection. Control 145 mice received 5% chloroform in PBS. Microarray analyses. Microarray analysis, identification of differentially expressed 146 147 genes (DEGs) and Ingenuity Pathway Analyses (IPA) were performed as described previously (34). DEGs were obtained for day 7 post-infection relative to day 0, separately for 148 WT and CCR2<sup>-/-</sup> mice, using pooled RNA samples from feet of 4-6 mice for each time point 149 150 and mouse strain. Genes with low expression levels in the microarray analysis (log2 151 expression < 7) for both days 0 and 7 were removed. Gene set enrichment analysis (GSEA) 152 was undertaken as described (34) using publicly available microarray raw data files from 153 studies of synovial biopsies from healthy patients and patients with RA (GSE1919). Human 154 genes were converted into mouse homologs utilizing the NCBI Homolo-Gene annotation 155 (available at http://www.ncbi.nlm.nih.gov/homologene). 156 Statistics. Analysis was performed using IBM SPSS Statistics (version 19). The t test 157 was used if the difference in the variances was <4, skewness was >-2, and kurtosis was <2. 158 Where the data was non-parametric and difference in variances was < 4 the Mann Whitney U 159 test was used, if > 4 the Kolmogorov-Smirnov test was used. 160 161 RESULTS Foot swelling in CHIKV infected wild-type and CCR2<sup>-/-</sup> mice. After CHIKV infection of 162

163	adult wild-type (WT) mice, a clearly discernable foot swelling is observed, which peaks on
164	day 6/7 and largely resolves by day 10-14 (Fig. 1A, black squares) as reported previously
165	(13). The same CHIKV infection of $CCR2^{-/-}$ mice resulted in a nearly 2 fold higher mean
166	peak foot swelling (Fig. 1A, day 6), with differences clearly observable by eye (Fig. 1B).
167	The swelling in CCR2 <sup>-/-</sup> mice also resolved much more slowly, returning to normal after day
168	40 (Fig. 1A). Foot swelling in CCR2 <sup>-/-</sup> mice was significantly higher than WT mice for all
169	time points from day 3 to 31.5 (Fig. 1A). Area under the curve calculations show that CCR2 <sup>-</sup>
170	<sup>/-</sup> mice experience >4 fold more foot swelling than WT mice (not shown).
171	Virus and viral RNA in WT and CCR2 <sup>-/-</sup> mice. No consistent and/or significant
172	differences were seen between WT and CCR2 <sup>-/-</sup> mice following CHIKV infection in (i)
173	viraemia (Fig. 1C), (ii) virus titres in feet, muscle, spleen, and lymph node (Fig. 1D), or (iii)
174	viral RNA levels in feet (Fig. 1E). CCR2 deficiency thus does not appear to have a
175	significant effect on CHIKV replication or persistence of CHIKV RNA (54). The increased
176	and more protracted disease seen in CCR2 <sup>-/-</sup> mice (Fig. 1A), was thus not due to an increase
177	in viral replication or increased persistence of viral RNA in these mice.
178	Histology and immunohistochemistry of the cellular infiltrates in the arthritic feet
179	of WT and CCR2 <sup>-/-</sup> mice. Histological examination of arthritic feet in WT mice shows a
180	predominance of mononuclear cell infiltrates on day 6 (the day of peak arthritis) as described
181	previously (13). This could be clearly seen by H&E staining of muscle (compare Fig. 2A
182	with 2B and 2C). Staining of foot sections with F4/80 antibody (a monoclonal antibody
183	recognising mouse monocyte/macrophages), also showed a large number of infiltrating
184	$F4/80^+$ cells (Fig. 2D) as reported previously (13). Leder staining (Fig. 2E) showed that
185	neutrophils were largely absent from infiltrates in day 6 feet of WT mice (Fig. 2E). ApoTag
186	staining revealed some apoptosis primarily in cells with monocytic and fibroblastic
187	morphology (Fig. 2F). Chromotrope2R staining (Fig. 2F) showed that eosinophils were

#### 188 largely absent (Fig. 2G).

The cellular infiltrates in the feet of CCR2<sup>-/-</sup> mice were quite distinct from those seen in 189 WT mice. H & E staining showed a predominance of neutrophils (compare Fig. 2H with 2I 190 and 2J), (many with hyper-segmented nuclei), with few F4/80<sup>+</sup> cells detected in the infiltrates 191 192 (Fig. 2K). Prodigious neutrophil infiltrates were also clearly seen by Leder staining (Fig. 193 2L). ApoTag staining was more widespread, with frequent staining of cytoplasmic debris 194 (Fig. 2M, left), suggestive of secondary necrosis. ApoTag staining was often also present in 195 cells with polymorphonuclear morphology (Fig. 2M, right). The latter suggests inflammatory 196 neutrophils undergoing apoptosis, a well described phenomena in inflammation biology (2). 197 Chromotrope2R staining also revealed that a large number of eosinophils were present in the arthritic infiltrates in CCR2<sup>-/-</sup> feet on day 21 post-infection (Fig. 2L). 198 199 Quantitation of histology and immunohistochemistry of the cellular infiltrates in the arthritic feet of WT and CCR2<sup>-/-</sup> mice. To quantitate the features described above, the 200 201 indicated number of feet were processed and stained in parallel, and slides were digitally 202 scanned (Aperio) and analysed using the Positive Pixel Count algorithm (Fig. 3). F4/80 203 staining increased substantially in WT feet on day 6 post-infection (as reported previously (13)). This did not occur in CCR2<sup>-/-</sup> feet, with F4/80 staining significantly higher in WT feet 204 compared with CCR2<sup>-/-</sup> feet at this time (Fig. 3A). These data support the widely expressed 205 206 view that the prodigious monocyte/macrophage infiltrate seen in WT mice after infection 207 with arthritogenic alpaviruses is dependent on CCL2/CCR2 expression (13, 22, 24, 43, 44, 54, 56). We cannot formally exclude the possibility that the reduced monocyte/macrophage 208 recruitment in CCR2<sup>-/-</sup> mice is, at least in part, due to the reduced level of circulating 209

210 monocytes in these animals (25). However, pixel count of F4/80 staining of feet day 6 post

211 infection after adoptive transfer (prior to infection) of WT CCR2<sup>+/+</sup> splenocytes (3x10<sup>7</sup>) into

212 CCR2<sup>-/-</sup> mice gave a mean value of  $0.172 \pm \text{SE } 0.02$  Brown pixels/ $\mu$ m<sup>2</sup> (settings as in Fig.

213	3A), whereas after adoptive transfer of CCR2 <sup>-/-</sup> splenocytes into CCR2 <sup>-/-</sup> mice this value was
214	$0.119 \pm \text{SE } 0.006 \text{ Brown pixels/}\mu\text{m}^2$ (i.e. very similar to CCR2 <sup>-/-</sup> mice on day 6, see Fig. 3A)
215	(data not shown). The difference between the two adoptive transfer groups was significant
216	(p=0.015, n=8 feet from 4 mice per group). Pixel counts of Ly6C staining of the same feet
217	also indicated a $\approx 25\%$ reduction in neutrophil infiltration in CCR2 <sup>-/-</sup> mice given WT cells, but
218	this only approached significance (p=0.057) (data not shown).
219	F4/80 staining increased significantly in CCR2 <sup>-/-</sup> feet on days 21 and 29 post infection
220	(Fig. 3A). Rather than being associated with monocyte/macrophages, these increases were
221	likely associated with infiltrating eosinophils (see below), which also stain with F4/80
222	antibody (data not shown) as reported previously (30).
223	Leder staining showed a dramatic increase in CCR2 <sup>-/-</sup> feet on day 6 post-infection and
224	was still significantly elevated on day 14, consistent with the increase in neutrophils seen by
225	H&E staining (Fig. 3B). In WT mice Leder staining was slightly elevated day 6, but was
226	substantially lower than in CCR2 <sup>-/-</sup> feet on days 6 and 14 (Fig. 3B). Immunohistochemistry
227	using a neutrophil-specific anti-Ly6G antibody and image analysis confirmed the stark and
228	significant contrast in neutrophil infiltrate between WT and CCR2 <sup>-/-</sup> feet on day 6 (data not
229	shown). To investigate how important neutrophils were for the increased foot swelling seen
230	in these mice (Fig. 1A), neutrophils were depleted using an anti-Ly6G antibody (administered
231	day 4, 5, and 6 post infection; 0.3 mg per day), with a $\approx$ 85% reduction in circulating
232	neutrophil numbers achieved on day 7. However, this led to slightly increased foot swelling
233	(days 5-7), with widespread haemorrhage and edema evident (data not shown). Neutrophil
234	depletion in CCR2 <sup>-/-</sup> mice post CHIKV infection thus appears to promote a new pathology
235	(42), complicating any analysis of the arthritogenic role of neutrophils using this approach.
236	ApoTag staining of apoptotic cells was significantly higher in CCR2 <sup>-/-</sup> feet on day 6, and
237	was also significantly elevated on day 14, whereas in WT mice there was no significant

difference between any of the time points shown (34) (Fig. 3C). Chromotrope2R staining
(eosinophils) was slightly elevated on days 6 and 14 in WT mice, but was substantially
elevated in CCR2<sup>-/-</sup> mice on day 21 and 29 (Fig. 3D).

In summary, the increased and prolonged arthritic disease seen in CCR2<sup>-/-</sup> mice was 241 242 associated with loss of infiltrating monocytes/macrophages, a severe neutrophil infiltrate 243 followed by an eosinophil infiltrate, with more apoptotic cells also seen during peak disease. 244 Treatment with a CCR2 antagonist. To determine whether treatment with a CCR2 antagonist might have a similar effect on neutrophil infiltration as that seen in CCR2<sup>-/-</sup> mice, 245 WT mice were treated with MK0812, a CCR2 antagonist tested (without clinical benefit) in 246 247 rheumatoid arthritis patients (65). The drug has been shown to reduce the peripheral blood 248 monocyte frequency and monocyte recruitment to sites of inflammation in animal models 249 (31, 63). On day 6 post-infection a significant increase in Ly6G staining was seen in feet of 250 WT mice treated with MK0812, when compared with control treatment (Fig. 3E). This 251 observation supports the view that reduction in CCR2 signalling can lead to increased 252 neutrophil infiltration following CHIKV infection. Cartilage damage in CHIKV infected CCR2<sup>-/-</sup> mice. In contrast with most 253 254 autoimmune arthritides, alphaviral arthritides (and most viral arthritides (56)) are generally 255 not associated with joint damage (54). Joint damage was also not seen in CHIKV-infected WT mice in the current study (6/6 feet examined) (Fig. 4A), or in previous studies (13, 42) or 256 257 in CHIKV-infected monkeys (22). However, H&E staining of joints from CHIKV-infected CCR2<sup>-/-</sup> mice day 45 post-infection often showed (in 6/6 feet examined) loss of chondrocytes 258 259 with empty lacunae in one or more foot joints (Fig. 4, arrows). Clear signs of cartilage damage at the articular surfaces (never seen in WT mice) was also occasionally observed in 260 261 CCR2<sup>-/-</sup> mice (twice in 6 feet) (Fig. 4B, arrowhead). Loss of cartilage collagen (as revealed 262 by Safranin O staining) was not observed in WT mice (Fig. 4C), but was clearly seen in at

least 1, occasionally 2, joints per foot in CCR2<sup>-/-</sup> mice (6 feet examined) (Fig. 4D, blue areas
indicated by arrows). CCR2 deficiency thus increased the severity of CHIKV arthritis, with
cartilage damage clearly apparent.

#### Anti-viral Th1/Th2/Th17 responses in CHIKV-infected WT and CCR2<sup>-/-</sup> mice.

267 CHIKV infections induce a strongly Th1-biased immune response (13, 22), with CCR2<sup>-/-</sup>

268 mice reported to have impaired Th1 responses (3, 18, 46). However, analysis of the anti-

- 269 CHIKV IgG2c (Th1) and IgG1 (Th2) titres (48, 62), illustrated that the dominant IgG2c
- 270 responses were not significantly different in CCR2<sup>-/-</sup> mice (Fig. 5A). Anti-CHIKV-specific
- 271 IgG1 levels were, however, significantly elevated in CCR2<sup>-/-</sup> mice (Fig. 5A), perhaps

272 consistent with the increased eosinophilia seen in these mice (Fig. 3D). Serum IFNγ levels

273 (measured as described (13)) and neutralizing antibody levels (measured as described (62))

274 were not significantly different between WT and CCR2<sup>-/-</sup> mice (data not shown).

275 qRT-PCR analysis of T-bet, a key transcription factor for Th1 cells (27), showed a clear

276 increase in WT mice on day 6 (peak arthritis) (Fig. 5B, T-bet), consistent with the

277 arthritogenic role of CD4 T cells and IFNy reported previously (34). However, T-bet mRNA

278 induction and levels were not significantly different (from WT mice) in CCR2<sup>-/-</sup> mice (Fig.

279 5B, T-bet), supporting the view that anti-CHIKV Th1 responses were not significantly

280 impaired in CCR2<sup>-/-</sup> mice.

281 Expansion of Th17 cells were reported to be responsible for the increase in neutrophil

282 infiltration and exacerbated arthritic disease seen in collagen-induced arthritis in CCR2<sup>-/-</sup>

283 mice (40). However, no significant increases in RORYT mRNA were observed in either

284 mouse strain on day 6 post-infection (Fig. 5B, RORYT). RORYT is a key transcription factor

285 for Th17 cells (41).

286 Changes in inflammatory mediators in the arthritic feet of CCR2<sup>-/-</sup> mice. Increased

287 neutrophil infiltrates in CCR2<sup>-/-</sup> mice have been associated with elevated levels of (i)

288	neutrophil-attracting chemokines CXCL1 (KC) and/or CXCL2 (macrophage inflammatory
289	protein 2-alpha) (12, 33, 39), and/or (ii) G-CSF (47), a key growth factor for neutrophil
290	development and recruitment involved in inflammatory arthritis (11). IL-1 $\beta$ can also
291	promote neutrophil recruitment (45), and IL-10 can inhibit neutrophil recruitment (1). qRT-
292	PCR analyses showed that significantly more CXCL1, CXCL2, G-CSF and IL-1 $\beta$ , and less
293	IL-10, was present in the arthritic feet of CCR2 <sup>-/-</sup> mice (Fig. 5C), suggesting multiple
294	mediators were involved in the switch from the predominantly monocyte/macrophage to
295	neutrophil infiltrates. (Serum IL-10 was also elevated earlier in the course of infection in WT
296	mice – data not shown). qRT-PCR analysis also showed that Arg-1 expression (a marker of
297	M2 macrophages), although up-regulated in WT feet as expected (52), was not up-regulated
298	in CCR2 <sup>-/-</sup> feet (Fig. 5C, Arg-1). M2 macrophages are associated with resolution of
299	inflammation (2).
300	Global gene expression changes induced by CHIKV infection. Microarray analysis
300 301	Global gene expression changes induced by CHIKV infection. Microarray analysis was undertaken to determine what genes were up- and down-regulated in the arthritic feet of
300 301 302	<b>Global gene expression changes induced by CHIKV infection.</b> Microarray analysis was undertaken to determine what genes were up- and down-regulated in the arthritic feet of CHIKV-infected WT and CCR2 <sup>-/-</sup> mice. The genes up- or down-regulated on day 7 post-
<ul><li>300</li><li>301</li><li>302</li><li>303</li></ul>	<b>Global gene expression changes induced by CHIKV infection.</b> Microarray analysis was undertaken to determine what genes were up- and down-regulated in the arthritic feet of CHIKV-infected WT and CCR2 <sup>-/-</sup> mice. The genes up- or down-regulated on day 7 post-infection (one day after peak arthritis to capture genes associated with resolution initiation)
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<ul> <li>300</li> <li>301</li> <li>302</li> <li>303</li> <li>304</li> <li>305</li> </ul>	Global gene expression changes induced by CHIKV infection. Microarray analysis was undertaken to determine what genes were up- and down-regulated in the arthritic feet of CHIKV-infected WT and CCR2 <sup>-/-</sup> mice. The genes up- or down-regulated on day 7 post- infection (one day after peak arthritis to capture genes associated with resolution initiation) relative to day 0 were determined for both mouse strains. A total of 2406 genes were up- or down-regulated following CHIKV infection in WT and/or CCR2 <sup>-/-</sup> mice. When the fold up-
<ul> <li>300</li> <li>301</li> <li>302</li> <li>303</li> <li>304</li> <li>305</li> <li>306</li> </ul>	Global gene expression changes induced by CHIKV infection. Microarray analysis was undertaken to determine what genes were up- and down-regulated in the arthritic feet of CHIKV-infected WT and CCR2 <sup>-/-</sup> mice. The genes up- or down-regulated on day 7 post- infection (one day after peak arthritis to capture genes associated with resolution initiation) relative to day 0 were determined for both mouse strains. A total of 2406 genes were up- or down-regulated following CHIKV infection in WT and/or CCR2 <sup>-/-</sup> mice. When the fold up- or down-regulation of these differentially expressed genes (DEGs) was compared between
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<ul> <li>300</li> <li>301</li> <li>302</li> <li>303</li> <li>304</li> <li>305</li> <li>306</li> <li>307</li> <li>308</li> </ul>	Global gene expression changes induced by CHIKV infection. Microarray analysis was undertaken to determine what genes were up- and down-regulated in the arthritic feet of CHIKV-infected WT and CCR2 <sup>-/-</sup> mice. The genes up- or down-regulated on day 7 post- infection (one day after peak arthritis to capture genes associated with resolution initiation) relative to day 0 were determined for both mouse strains. A total of 2406 genes were up- or down-regulated following CHIKV infection in WT and/or CCR2 <sup>-/-</sup> mice. When the fold up- or down-regulation of these differentially expressed genes (DEGs) was compared between WT and/or CCR2 <sup>-/-</sup> mice, 81% showed less than 2 fold difference, illustrating that most genes were similarly regulated in feet day 7 post-infection in the two mouse strains. However,
<ul> <li>300</li> <li>301</li> <li>302</li> <li>303</li> <li>304</li> <li>305</li> <li>306</li> <li>307</li> <li>308</li> <li>309</li> </ul>	<b>Global gene expression changes induced by CHIKV infection.</b> Microarray analysis was undertaken to determine what genes were up- and down-regulated in the arthritic feet of CHIKV-infected WT and CCR2 <sup>-/-</sup> mice. The genes up- or down-regulated on day 7 post- infection (one day after peak arthritis to capture genes associated with resolution initiation) relative to day 0 were determined for both mouse strains. A total of 2406 genes were up- or down-regulated following CHIKV infection in WT and/or CCR2 <sup>-/-</sup> mice. When the fold up- or down-regulation of these differentially expressed genes (DEGs) was compared between WT and/or CCR2 <sup>-/-</sup> mice, 81% showed less than 2 fold difference, illustrating that most genes were similarly regulated in feet day 7 post-infection in the two mouse strains. However, consistent with the histological analyses, monocyte/macrophage-associated genes and
<ul> <li>300</li> <li>301</li> <li>302</li> <li>303</li> <li>304</li> <li>305</li> <li>306</li> <li>307</li> <li>308</li> <li>309</li> <li>310</li> </ul>	<b>Global gene expression changes induced by CHIKV infection</b> . Microarray analysis was undertaken to determine what genes were up- and down-regulated in the arthritic feet of CHIKV-infected WT and CCR2 <sup>-/-</sup> mice. The genes up- or down-regulated on day 7 post- infection (one day after peak arthritis to capture genes associated with resolution initiation) relative to day 0 were determined for both mouse strains. A total of 2406 genes were up- or down-regulated following CHIKV infection in WT and/or CCR2 <sup>-/-</sup> mice. When the fold up- or down-regulation of these differentially expressed genes (DEGs) was compared between WT and/or CCR2 <sup>-/-</sup> mice, 81% showed less than 2 fold difference, illustrating that most genes were similarly regulated in feet day 7 post-infection in the two mouse strains. However, consistent with the histological analyses, monocyte/macrophage-associated genes and pathways were more up-regulated/significant in WT feet, and neutrophil-associated genes

312 supplemental material). CHIKV infection-associated induction of multiple chemokines and

313 chemokine receptors was also different in the two mouse strains, with these differences again 314 consistent with the contrasting cellular infiltrates in WT and  $CCR2^{-/-}$  mice (see Table S2 in 315 the supplemental material).

To gain a better understanding of the differences in infection-associated gene regulation 316 between CCR2<sup>-/-</sup> and WT mice, the differences in fold changes in gene expression between 317 318 the two strains for all 2406 DEGs was expressed as a ratio. For 181 genes (7.5% of all DEGs) the "the fold change in CCR2<sup>-/-</sup> feet" divided by "the fold change in WT feet" was 319 >1.5 (Fig. 6, top left). For 920 genes (38% of all DEGs) "the fold change in WT feet" 320 divided by "the fold change in CCR2<sup>-/-</sup> feet" was >1.5. The former 181 genes thus represent 321 genes that were more induced in CCR2-1- mice than in WT mice, and the latter 920 genes 322 represent genes that were less induced in CCR2<sup>-/-</sup> mice than in WT mice. IPA analysis of the 323 181 genes more induced in CCR2<sup>-/-</sup> mice, revealed canonical pathways associated with 324 325 granulocyte, IL-17A in autoimmunity, RA, and inflammation (Fig. 6, IPA pathways, top; see 326 Table S3 in the supplemental material). Although autoimmune pathways were identified (consistent with the worse pathology). CCR2<sup>-/-</sup> mice did not develop anti-nuclear antibodies 327 (data not shown). IPA analysis of the 920 genes less induced in CCR2<sup>-/-</sup> feet revealed 328 329 canonical pathways associated with monocyte/macrophage, pattern recognition, 330 autoimmunity, B and T cell (mostly Th cell), NK cell, muscle and inflammation pathways 331 (Fig. 6, IPA pathways, bottom; see Table S4 in the supplemental material). Many of these 332 pathways are consistent with the aforementioned changes in infiltrates and inflammation. The identification of muscle pathways likely reflects increased muscle damage (34) in CCR2<sup>-</sup> 333 <sup>/-</sup> feet. The identification of NK, T and B cell pathways in this gene set also suggests reduced 334 recruitment of these cells (13) into the infected feet in CCR2<sup>-/-</sup> mice; T cells can also express 335 336 CCR2 (5).

337 The same 181 and 920 gene sets were subjected to Ingenuity upstream regulator analysis.

338	STAT1 and 3 were identified as upstream regulators in both gene sets (see Tables S6 and S7
339	in the supplemental material), consistent with STAT1 and 3 regulating a distinct set of genes
340	in monocyte/macrophages and neutrophils (16). Several muscle-associated upstream
341	regulators were identified in the 181 gene set (with negative z-scores) and in the 920 gene set
342	(with positive z-scores), again indicating increased muscle damage in $CCR2^{-/-}$ feet. NF- $\kappa B$
343	pathways were prominent upstream regulators identified in the 181 gene set (see Table S5 in
344	the supplemental material), consistent with the NF- $\kappa$ B-dependent expression of the multiple
345	chemokines and proinflammatory mediators seen in this gene set. Perhaps surprising (given
346	no change in viral loads - Fig. 1C,D,E) was the identification of STAT1, IRF1, IRF3 and
347	IRF7 as upstream regulators in the 920 genes less induced in CCR2 <sup>-/-</sup> mice (see Table S6 in
348	the supplemental material). Reduced STAT1 signalling is perhaps consistent with the
349	slightly lower IFN $\alpha/\beta$ receptor and IFN $\gamma$ expression in CCR2 <sup>-/-</sup> feet. Reduced interferon
350	signalling is also supported by a smaller overall fold up-regulation of interferon-associated
351	genes in CCR2 <sup>-/-</sup> feet (see Fig. S2 in the supplemental material).
352	Comparison of gene expression profiles of feet from CHIKV infected CCR2 <sup>-/-</sup> and
353	WT mice and synovial biopsies from human RA patients. The DEGs identified for CCR2 <sup>-</sup>
353 354	WT mice and synovial biopsies from human RA patients. The DEGs identified for CCR2 <sup>-</sup> /- mice and the DEGs identified for WT mice (both comparing day 7 with day 0) were each
353 354 355	WT mice and synovial biopsies from human RA patients. The DEGs identified for CCR2 <sup>-</sup> <sup>/-</sup> mice and the DEGs identified for WT mice (both comparing day 7 with day 0) were each separately compared with a publicly available gene set from a microarray study of RA
353 354 355 356	WT mice and synovial biopsies from human RA patients. The DEGs identified for CCR2 <sup>-</sup> <sup>/-</sup> mice and the DEGs identified for WT mice (both comparing day 7 with day 0) were each separately compared with a publicly available gene set from a microarray study of RA patients (34). Gene set enrichment analysis (GSEA) software was used to determine whether
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<ol> <li>353</li> <li>354</li> <li>355</li> <li>356</li> <li>357</li> <li>358</li> <li>359</li> </ol>	WT mice and synovial biopsies from human RA patients. The DEGs identified for CCR2 <sup>-/-</sup> mice and the DEGs identified for WT mice (both comparing day 7 with day 0) were each separately compared with a publicly available gene set from a microarray study of RA patients (34). Gene set enrichment analysis (GSEA) software was used to determine whether the rank-ordered list of genes in the RA study (i.e. genes ranked by their fold change in expression in RA patients relative to healthy individuals) were enriched in the DEGs identified in CCR2 <sup>-/-</sup> and WT mice. Nominal p values and false discovery rates (FDR) are
<ol> <li>353</li> <li>354</li> <li>355</li> <li>356</li> <li>357</li> <li>358</li> <li>359</li> <li>360</li> </ol>	WT mice and synovial biopsies from human RA patients. The DEGs identified for CCR2 <sup>-/-</sup> mice and the DEGs identified for WT mice (both comparing day 7 with day 0) were each separately compared with a publicly available gene set from a microarray study of RA patients (34). Gene set enrichment analysis (GSEA) software was used to determine whether the rank-ordered list of genes in the RA study (i.e. genes ranked by their fold change in expression in RA patients relative to healthy individuals) were enriched in the DEGs identified in CCR2 <sup>-/-</sup> and WT mice. Nominal p values and false discovery rates (FDR) are provided for comparisons of both up- and down-regulate genes (Fig. 6B). In all cases there
<ul> <li>353</li> <li>354</li> <li>355</li> <li>356</li> <li>357</li> <li>358</li> <li>359</li> <li>360</li> <li>361</li> </ul>	WT mice and synovial biopsies from human RA patients. The DEGs identified for CCR2 <sup>-/-</sup> mice and the DEGs identified for WT mice (both comparing day 7 with day 0) were each separately compared with a publicly available gene set from a microarray study of RA patients (34). Gene set enrichment analysis (GSEA) software was used to determine whether the rank-ordered list of genes in the RA study (i.e. genes ranked by their fold change in expression in RA patients relative to healthy individuals) were enriched in the DEGs identified in CCR2 <sup>-/-</sup> and WT mice. Nominal p values and false discovery rates (FDR) are provided for comparisons of both up- and down-regulate genes (Fig. 6B). In all cases there was significant enrichment, suggesting the high degree of similarity between the gene

363 retained for CCR2<sup>-/-</sup> mice. (Previous analyses (34) used a consensus signature from 2

364 CHIKV isolates, whereas the data in Fig. 6B represents an analysis for the Reunion Island

365 isolate alone to allow comparison with data from CCR2<sup>-/-</sup> mice).

366

#### 367 **DISCUSSION**

368 This paper describes the first analysis of a viral arthritis in CCR2<sup>-/-</sup> mice, and illustrates that

369 deficiency in this gene results in a more severe, prolonged and erosive arthritis. The

370 prodigious monocyte/macrophage infiltrate seen in WT mice was almost entirely replaced by

371 a neutrophil infiltrate in CCR2<sup>-/-</sup> mice, with this switch associated with dysregulation of a

372 range of inflammatory and anti-inflammatory pathways. Recruitment of CCR2<sup>+</sup> monocytes

373 during CHIKV arthritis, although likely contributing to acute inflammatory disease (54, 56),

thus also protects against even worse neutrophil-mediated pathology.

375 CXCL1, CXCL2, G-CSF, and IL-1 $\beta$  were increased in the arthritic feet of CCR2<sup>-/-</sup> mice,

376 whereas IL-10 was decreased, suggesting multiple mediators were involved in promoting

377 neutrophil recruitment (1, 11, 12, 33, 39, 45, 47). The reduction in IL-10 and lack of Arg-1

378 induction, also suggests a paucity of (CCR2<sup>+</sup> derived) M2 and resolving macrophages and

379 their anti-inflammatory activities in  $CCR2^{-/-}$  mice. This contention is supported by array data

380 that shows less up-regulation of a number of M2 and resolving macrophage markers in

381 CCR2<sup>-/-</sup> feet (eg TGF $\beta$ , Ym1, Msr1) (see Fig. S3 in the supplemental material). M2

382 macrophages have high efferocytosis activity, with efferocytosis a key driver of inflammation

383 resolution (2). The increase in ApoTag staining in CCR2<sup>-/-</sup> mice also suggests that

384 efferocytosis is compromised in these mice, with CCL2 having previously been shown to

385 promote efferocytosis (57). Evidence for secondary necrosis is also present in CCR2<sup>-/-</sup> feet

386 (Fig. 2M), and usually occurs when efferocytosis is compromised. Secondary necrosis itself

387 promotes inflammation by releasing a number of soluble inflammatory mediators (32).

The eosinophil infiltration that follows the neutrophil infiltration in CCR2<sup>-/-</sup> mice may be promoted by the tissue damage induced by the neutrophils and/or secondary necrosis, and may help down-regulate the inflammatory response in these animals (29). Eosinophilic arthritis has been reported previously, and is usually associated with a benign course of disease (60).

Exactly how CCR2<sup>+</sup> monocytes recruited during CHIKV infection, and/or the 393 394 macrophages that develop from them (and/or other CCR2<sup>+</sup> cells), might prevent excessive 395 neutrophil infiltration and pathology in WT mice remains unclear. IL-10 may be involved 396 (1), but is unlikely to be the only player, with foot swelling and neutrophil infiltration only slightly elevated (the latter not significantly) in IL-10<sup>-/-</sup> mice (data not shown). Treatment of 397 CCR2<sup>-/-</sup> mice with Anakinra (an IL-1 receptor antagonist) had no significant affect on peak 398 399 foot swelling (data not shown). Anti-inflammatory macrophages might suppress neutrophil 400 recruitment by inter alia secreting (i) a series of proresolving lipid mediators (49) and/or (ii) 401 proteases that cleave neutrophil-attracting chemokines (36). The reduction in interferon signalling seen CCR2<sup>-/-</sup> mice may also be involved as loss of IFN $\alpha/\beta$  receptor signalling has 402 403 been shown to promote production of neutrophil-recruiting cytokines/chemokines in a 404 number of infections (6, 64). Treg cells may be involved as (i) depletion of  $CCR2^+$  Tregs has 405 been shown to exacerbate collagen-induced arthritis (5), (ii) anti-inflammatory macrophages can promote Treg expansion via TGF $\beta$  and IL-10 (28, 36), (iii) T cells are important in 406 driving CHIKV arthritis (34), and (iv) Th cell pathways were decreased in CCR2<sup>-/-</sup> mice (Fig. 407 6), with the microarray analysis unable to differentiate between Th and Treg cells. The 408 increased IgG1 responses in CCR2<sup>-/-</sup> mice also supports the view that T cell activities were 409 410 altered in CHIKV-infected CCR2<sup>-/-</sup> mice. Further work is needed before the mechanisms and 411 cells involved and their relative importance are fully elucidated, with other cell types (eg 412 myeloid-derived suppressor cells (36)) potentially also involved. What does emerge from

413	these studies is that in CHIKV arthritis (and perhaps other viral arthritides (56)),
414	inflammation-recruited CCR2 <sup>+</sup> monocyte/macrophages appear to be important for limiting
415	neutrophil recruitment into the infected and inflamed joint tissues. This contrasts with
416	observations in other arthritis models where these cells promote neutrophil recruitment (61).
417	Treatment of WT mice with clodronate (one day prior to CHIKV infection) to deplete
418	monocyte/macrophages was previously shown to reduce foot swelling day 6/7 after CHIK
419	infection (13); data that would seem at odds with the observations presented herein.
420	However, the recent recognition that CD4 T cells and IFN $\gamma$ play important roles in driving
421	arthritis in this CHIKV mouse model (34), and the ability of clodronate treatment to suppress
422	Th1 responses (4), might suggest the observation above (13) has more to do with reduced
423	Th1 responses than reduced monocyte/macrophage infiltration (9). (Th1 responses were not
424	significantly affected in CHIKV infected CCR2 <sup>-/-</sup> mice). Clodronate treatment of WT mice
425	also extended the viraemia (13), whereas viraemia was not significantly different in CCR2 <sup>-/-</sup>
426	and WT mice. Clodronate treatment was recently shown to affect germinal centres (35), with
427	compromised antibody responses perhaps explaining the extended viraemia (13).
428	The reduction in interferon signalling in CCR2 <sup>-/-</sup> mice was surprising as IFN $\alpha/\beta$ receptor,
429	STAT1, IRF3 and IRF7-associated signalling (but not IFN $\gamma$ (34)) are important for anti-viral
430	activity against CHIKV (42), and viral titres and RNA levels were unchanged in CCR2-/-
431	mice (Fig. 1C,D,E). Macrophages are, whereas neutrophils are generally not, infected with
432	CHIKV, so viral RNA-mediated IRF3 and IRF7 stimulation via the cytoplasmic IPS-1
433	pathway (42) would not occur in neutrophils. In contrast to monocytes/macrophages,
434	neutrophil TLR3 expression is also low, both in humans (58) and mice
435	(http://www.immgen.org/databrowser/index.html), with TLR3 signalling (upstream of IRF3
436	and 7) known to be active during CHIKV infection (42). Conceivably, the reduced interferon
437	signalling thus simply reflects fewer CCR2 <sup>+</sup> monocytes/macrophages being infected and

- responding to infection in CCR2<sup>-/-</sup> feet, with infection of these cells making a relatively minor
  contribution to overall viral load (Fig. 1C,D,E). One might speculate that resident tissue
  macrophages (whose recruitment is CCR2-independent) may be a more important target of
  CHIKV infection and/or persistence (22, 52).
- The increase in IL-17 pathway activation in CHIKV infected CCR2<sup>-/-</sup> feet did not appear 442 to be due to increased levels of Th17 cells (as was reported for in collagen-induced arthritis 443 444 (40)). Recently, immune complexes present during acute arthritis were shown to induce IL-445 17 production by neutrophils (20). Similar levels of neutralising antibody responses were raised against CHIKV in WT and CCR2-/- mice (data not shown), so immune complexes are 446 likely to be present in CCR2<sup>-/-</sup> mice and may thus be responsible for triggering IL-17 447 448 production by the infiltrating neutrophils. 449 The widespread dysregulation of inflammatory processes observed in CHIKV infected CCR2<sup>-/-</sup> mice, suggests care might be warranted when considering therapeutic agents that 450
- 451 target CCR2/CCL2 for treating alphaviral arthritides (44) (and perhaps other arthritides (12)).
- 452 The association of (i) neutrophil-recruiting chemokines, IL-8 (homologue of murine CXCL1)
- 453 and CCL3, both elevated in CCR2<sup>-/-</sup> mice (see Table S2 in the supplemental material), and
- 454 (ii) IL-6, which was higher in the serum of CCR2<sup>-/-</sup> than WT mice post infection (data not
- 455 shown), with chronic human CHIKV arthropathy (8), perhaps adds to these concerns.
- 456 Complications might also arise when patients who are being treated with such agents (for
- 457 other conditions) become infected with an arthritogenic alphavirus.
- 458

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467

468

#### 472 FIGURE LEGENDS

473

FIG 1. Disease, virus replication and RNA persistence. (A) The mean percentage increase 474 in foot swelling over time for wild-type (WT) (n=16 feet, 8 mice) and CCR2<sup>-/-</sup> mice (n=14 475 476 feet, 7 mice). Asterisks (\*) indicates significant differences (p<0.01) by t test or 477 Kolmogorov-Smirnov test; the choice of test at each time point was dependent on the 478 skewness, kurtosis and variance of the data being compared (see Statistics in Materials and 479 Methods). (A single experiment, representative of 3 repeat experiments is shown). (B) Images of WT and CCR2<sup>-/-</sup> feet on day 0 and day 6 (peak arthritis). (C) Peripheral blood 480 viremia (n=7 for CCR2<sup>-/-</sup> mice, n=8-14 for WT mice). (D) Virus titres in the indicated tissues 481 482 at the indicated times post infection (n=3-6 mice per time point) (NT - not tested). (E) qRT-483 PCR analyses of CHIKV RNA in feet. Feet were taken at the indicated times (n=3-6) and the 484 level of CHIKV positive-stand RNA determined using qRT-PCR analyses and primers 485 specific for E1 (a major CHIKV structural protein); data was normalised to RPL13A mRNA 486 levels. 487 FIG 2. Histology and immunohistochemistry of rheumatic lesions in CHIKV infected WT 488

and CCR2<sup>-/-</sup> mice. (A-G) WT mice. (H-N) CCR2<sup>-/-</sup> mice. (A, H) H&E staining of muscle
from uninfected mice. (B and I) H&E staining of muscle day 6 post infection. (C, J) high
magnification of H&E staining of muscle day 6 post-infection. (D, K) F4/80 antibody
(monocyte/macrophage) staining of connective tissue day 6 post-infection. (E, L) Leder
staining (neutrophils) of connective tissue day 6 post-infection. (F, M) ApoTag staining
(apoptotic cells) day 6 post-infection (F, two images, M, three images). (G, N)
Chromotrope2R staining (eosinophils) of connective tissue day 21 post-infection.

497	FIG 3. Histology quantitation. (A) Image analysis (strong brown) of F4/80 staining of
498	whole foot sections from WT and CCR2 <sup>-/-</sup> mice at the indicated times post-infection. Dotted
499	line indicates upper limit of non-specific staining in control slides. (n=3-5 feet from different
500	mice per time point and mouse strain, 2 sections per foot analysed). Statistics by
501	Kolmogorov-Smirnov test. (B) Image analysis (strong red) of Leder staining of whole foot
502	sections of WT and CCR2 <sup>-/-</sup> mice at the indicated times post-infection. (n as above).
503	Statistics by Kolmogorov-Smirnov, Mann Whitney U or t tests. (C) Image analysis (strong
504	brown) of ApoTag staining of whole foot sections of WT and CCR2 <sup>-/-</sup> mice at the indicated
505	times post-infection. (n as above). Statistics by Kolmogorov-Smirnov tests. (D) Image
506	analysis (strong red) of Chromotrope2R staining of whole foot sections of WT and CCR2 <sup>-/-</sup>
507	mice at the indicated times post-infection. (n as above). Statistics by Kolmogorov-Smirnov
508	or Mann Whitney U tests. (E) WT mice were treated with the CCR2 antagonist MK0815 or
509	diluent (Control) after CHIKV infection and feet stained with anti-Ly6G (a neutrophil
510	specific marker), followed by image analysis. Statistics by Kolmogorov-Smirnov test ( $n=4/6$
511	feet per group).
512	
513	FIG 4. Cartilage damage in CCR2 <sup>-/-</sup> feet. (A) H & E staining of joint from WT mouse day
514	45 post-infection (SS – synovial space). (B) H & E staining of joint from $CCR2^{-/-}$ mouse day
515	45 post-infection. Arrows indicate empty chondrocytic lacunae within the hyaline cartilage.
516	Arrowheads show cartilage damage at the articular surface. (C) Safranin O staining
517	(cartilage) of joint from WT mouse day 45 post-infection. (D) Safranin O staining (cartilage)
518	of joint from CCR2 <sup>-/-</sup> mouse day 45 post-infection. Arrows show loss of red collagen
519	staining (replaced by blue staining) at the articular surfaces.

520

521 FIG 5. Immune and inflammatory mediator responses. (A) CHIKV-specific IgG2c and

522	IgG1 titres 7 weeks post-infection as determined by ELISA. Statistics by Mann Whitney U
523	test (n=5 mice per group assayed in duplicate). (B) qRT-PCR analysis of T-bet (Th1 T cell
524	transcription factor) and RORyT (Th17 transcription factor) at the indicated times post-
525	infection. Figure legend as in A. Statistics by Kolmogorov-Smirnov tests (n=4/5 mice and
526	feet per group and time point assayed in duplicate). (C) qRT-PCR analysis of the indicated
527	species at the indicated times post-infection. Figure legend as in A. Statistics by
528	Kolmogorov-Smirnov or t tests (n=4/5 mice and feet per group and time point assayed in
529	duplicate).
530	
531	FIG 6. Microarray analysis of arthritic feet from WT and CCR2 <sup>-/-</sup> mice. (A) Genes
532	differentially expresses on day 7 post infection (compared to day 0) for WT and CCR2 <sup>-/-</sup> feet
533	were determined by microarray analysis. 2406 differentially expressed genes were up or
534	down-regulated in WT and/or CCR2 <sup>-/-</sup> feet. For 181 of these genes "fold change in CCR2 <sup>-/-</sup>
535	mice"/"fold change in WT mice" was >1.5 fold (top left); (for 603 DEGs this ratio was >1).
536	For 920 of these genes the "fold change in WT mice"/"fold change in CCR2 <sup>-/-</sup> mice" was
537	>1.5 fold (bottom right); (for 1794 genes this ratio was >1, for 9 the ratio was =1). IPA
538	canonical pathway analyses of the 181 genes more induced in CCR2 <sup>-/-</sup> feet (top right) and the
539	920 genes less induced in CCR2 <sup>-/-</sup> feet (bottom left) are shown, with pathways grouped into
540	themes. Pathway details are shown in Tables S3 and S4 in the supplemental material.
541	(B) Comparison of gene signatures of chikungunya virus (CHIKV) arthritis in WT and
542	CCR2 <sup>-/-</sup> mice with a gene signature from RA patients. Gene Set Enrichment Analysis
543	showed statistically significant enrichment of up-regulated genes (UP CCR2 <sup>-/-</sup> 163 genes and
544	UP WT 341 genes in "core enrichment"; overlap 150) and down-regulated genes (DOWN
545	CCR2 <sup>-/-</sup> 82 genes and DOWN WT 76 genes in "core enrichment") from CHIKV arthritis in
546	the up- and down-regulated genes, respectively, identified in synovial biopsies from RA

547 patients. FDR, false discovery rate.

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Figure 4





