ARTICLE

Critical role of chemokine (C-C motif) receptor 2 (CCR2) in the KKAy⁺Apoe^{-/-} mouse model of the metabolic syndrome

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Received: 31 May 2011 / Accepted: 3 June 2011 / Published online: 21 July 2011 © Springer-Verlag 2011

Abstract

Aims/hypothesis Chemokines and their receptors such as chemokine (C-C motif) receptor 2 (CCR2) may contribute to the pathogenesis of the metabolic syndrome via their effects on inflammatory monocytes. Increased accumulation of CCR2-driven inflammatory monocytes in epididymal fat pads is thought to favour the development of insulin resistance. Ultimately, the resulting hyperglycaemia and dyslipidaemia contribute to development of the metabolic syndrome complications such as cardiovascular disease and diabetic nephropathy. Our goal was to elucidate the role of

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Electronic supplementary material The online version of this article (doi:10.1007/s00125-011-2248-8) contains peer-reviewed but unedited supplementary material, which is available to authorised users.

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CCR2 and inflammatory monocytes in a mouse model that resembles the human metabolic syndrome.

Methods We generated a model of the metabolic syndrome by backcrossing $KKAy^+$ with $Apoe^{-/-}$ mice $(KKAy^+Apoe^{-/-})$ and studied the role of CCR2 in this model system.

Results KKAy⁺Apoe^{-/-} mice were characterised by the presence of obesity, insulin resistance, dyslipidaemia and increased systemic inflammation. This model also manifested two complications of the metabolic syndrome: atherosclerosis and diabetic nephropathy. Inactivation of Ccr2 in KKAy⁺Apoe^{-/-} mice protected against the metabolic syndrome, as well as atherosclerosis and diabetic nephropathy. This protective phenotype was associated with a reduced number of inflammatory monocytes in the liver and muscle, but not in the epididymal fat pads; circulating levels of adipokines such as leptin, resistin and adiponectin were also not reduced. Interestingly, the proportion of inflammatory monocytes in the liver, pancreas and muscle, but not in the epididymal fat pads, correlated significantly with peripheral glucose levels.

Conclusions/interpretation CCR2-driven inflammatory monocyte accumulation in the liver and muscle may be a critical pathogenic factor in the development of the metabolic syndrome.

Keywords Animal-mouse · Basic science · Cardiac complications · Experimental immunology · KO mice · Metabolic syndrome · Nephropathy

Abbreviations

CCL2 Chemokine (C-C motif) ligand 2 CCR2 Chemokine (C-C motif) receptor 2 GSK-3 β Glycogen synthase kinase 3 β

GTT Glucose tolerance test

HFD High-fat diet

ITT Insulin tolerance test LPS Lipopolysaccharide

pGSK-3β Phosphorylation of GSK-3β

STAT3 Signal transducer and activator of transcription 3

Introduction

The metabolic syndrome, a condition that affects 47 million Americans [1], clinically manifests as insulin resistance, atherogenic dyslipidaemia (high triacylglycerol, hypercholesterolaemia with low HDL-cholesterol and/or high LDL-cholesterol), hypertension, obesity and increased systemic inflammation. Complications of the metabolic syndrome include coronary artery disease [2] caused by worsening of atherosclerosis, and diabetic nephropathy [3], the most common cause of end-stage renal disease worldwide [4].

Systemic inflammation as well as local effects of inflammatory cells are thought to play an important role in the development of processes related to the metabolic syndrome, such as insulin resistance and atherogenesis [5]. Chemokines and their receptors are vital to the recruitment of leucocytes and many other inflammatory processes [6]. For example, chemokine (C-C motif) receptor 2 (CCR2) is indispensable for adequate monocyte/macrophage trafficking and activation [7, 8]. This role of CCR2 may be important in the emergence of the metabolic syndrome, as indicated by the finding that mice in which CCR2 is genetically ablated or pharmacologically blocked were protected against development of insulin resistance and obesity, presumably by decreasing monocyte infiltration into fat [9, 10]. Insights derived from other rodent models also suggest that defective macrophage migration induced by modulating the CCR2 ligand, chemokine (C-C motif) ligand 2 (CCL2, also known as MCP-1), may influence atherosclerosis [11] and diabetic nephropathy [12]. However, no single current animal model captures the complex phenotype seen in humans with the metabolic syndrome (Electronic supplementary material [ESM] Table 1).

We therefore generated a murine model of the metabolic syndrome by backcrossing KKAy+ mice (a polygenic model of type 2 diabetes [13]) with atherosclerosis-prone Apoe^{-/-} mice [14]. KKAy+Apoe^{-/-} mice progressively developed obesity, insulin resistance, dyslipidaemia and complications of the metabolic syndrome such as atherosclerosis and diabetic nephropathy. We also found that Ccr2 inactivation in KKAy+Apoe^{-/-} mice protected against the metabolic syndrome-defining features and complications. Interestingly, after excluding several confounding factors, we found that the protective effect of Ccr2 ablation is possibly linked to reduced accumulation of inflammatory monocytes in the muscle and liver, but not in the epididymal fat pads.

Methods

Mice, diet and induction of chronic inflammation

KKAv⁺ mice (stock KK-Ay/TaJcl) were purchased from CLEA Japan (Tokyo, Japan). KKAy⁺ mice were crossed with Apoe-/- mice for two to three generations until a sufficient number of mice with the genotype KKAv Apoe or KKAy⁺Apoe^{-/-} were obtained. KKAy⁻Apoe^{-/-} or KKAy⁺Apoe^{-/-} mice were further bred with Apoe^{-/-}Ccr2^{-/-} mice (C57BL/6J background). Our laboratory and others have described the generation and backcrossing procedures of the later two strains [15-17]. The resulting intercross mating produced the experimental animal groups. Ccr2 and Apoe genotypes were confirmed by PCR, as previously described [15]. Visual inspection of the coat colour further verified the Ay (agouti) allele transmission, with yellow coat identifying positive (Ay^{+}) transmission, whereas black coat indicated negative (Ay⁻) allele transmission. KKAy⁻Apoe^{-/-} and KKAy⁻Apoe^{-/-}Ccr2^{-/-} littermates served as controls for all Ay^+ mice.

All data sets presented here were derived from mice at 25 ± 5 weeks of age. All animals were kept under pathogen-free conditions and the Institutional Animal Care and Use Committee of the University of Texas Health Science Center at San Antonio (UTHSCSA) approved all protocols.

Mice genotype, dual energy X-ray absorptiometry (DEXA) scan, stains in kidneys, blood pressure analysis, electron microscopy, Akt phospho 7-plex panel and Ingenuity pathway analysis are described in more detail in the ESM Methods.

Weight analyses and food intake

Mice were followed for 8 to 10 weeks, fed with a normal diet and had body weights recorded weekly by an investigator blind to the experimental groups. A second experimental set of animals was individually housed in metabolism cages for 3 to 4 days for acclimatisation, after which food and water intake was recorded every 24 h for four consecutive days.

Metabolic variables

Blood samples were obtained to determine glucose levels using a glucose monitor (Ascencia Elite; Bayer, Mishawaka, IN, USA) and cholesterol levels (Vetometer II; Kacey, Asheville, NC, USA). Serum ELISA (performed following manufacturers' instructions) was done to measure levels of insulin (Crystal Chem, Downers Grove, IL, USA), TNF α and IL-6 (eBiosciences, San Diego, CA, USA), and leptin, resistin and adiponectin (Alpha Diagnostics, San Antonio, TX, USA) in sera. Triacylglycerol levels were



assessed with a Trace Infinity reagent (Thermo Scientific, Waltham, MA, USA). For details on insulin tolerance test (ITT) and glucose tolerance test (GTT), see ESM Methods.

Serum creatinine was measured using HPLC. Briefly, 1 ml acetonitrile was added to 10 μ l serum, incubated for 20 min, mixed and centrifuged for 15 min at 16,400 g after which the sample was concentrated by speed vac. Before use, the sample was re-suspended with 120 μ l of the mobile phase (5 mmol/l sodium acetate pH 5.1) and 25 μ l was injected into the machine.

Urine albumin and creatinine collected in metabolism cages were analysed by ELISA (Exowell, Philadelphia, PA, USA), following the manufacturer's protocol.

Immunohistochemistry and histomorphometric analysis

Sections of atherosclerotic plaques were stained with the ER-HR3 marker for macrophages, as previously described [18]. For macrophage staining in liver, F4/80 antibody was used (clone A1-3; AbD Serotec, Raleigh, NC, USA). Percentage of stained area was determined using ImageJ software (National Institutes of Health, Bethesda, MD, USA).

Histomorphometric analysis of atherosclerotic plaques at the level of the aortic root was performed as previously described [18]. For the histomorphometric analysis of the kidneys, glomerular volume was calculated according to the formula: $GV=(\beta/\kappa)\times (GA)^{3/2}$, where GV is glomerular volume, $\beta=1.38$, $\kappa=1.1$ and GA is glomerular area, as described by Pagtalunan et al. [19].

Flow cytometry

Mice were perfused with 15 ml cold PBS prior to organ removal and single cell suspensions were prepared as described by Soos et al. [20]. Cell suspensions were stained with diverse combinations of antibodies including CD11b APC, Ly6C FITC and Ly6G PE or isotype-matched antibodies (BD Biosciences, San Jose, CA, USA), and analysed on a FACScalibur with Cell Quest software (BD Biosciences).

Statistical analysis

For brevity, data presented compare $KKAy^+Apoe^{-/-}$ and $KKAy^+Apoe^{-/-}$ Ccr2 $^{-/-}$ mice. However all experimental groups were included as controls in each experiment. Data represent the mean \pm SD; statistical analysis was performed with Stata (StataCorp, College Station, TX, USA) or SPSS (Chicago, IL, USA) statistical software. Based on the number of groups and their distribution (normally distributed or not), non-paired t test, one-way ANOVA, Kruskal–Wallis, Mann–Whitney or Fisher's exact tests were performed. Statistical significance was accepted at p<0.05.



Murine model of the metabolic syndrome

Weight gain KKAy⁺Apoe^{-/-} and KKAy⁺Apoe^{-/-} Ccr2^{-/-} mice, and their respective controls (KKAy⁻Apoe^{-/-} and KKAy⁻Apoe^{-/-} Ccr2^{-/-} littermates) were followed for up to 10 weeks, during which weight and food intake were assessed. Weight in KKAy⁺Apoe^{-/-} mice increased over time and was significantly higher than in controls (Table 1, ESM Fig. 1a). Notably, Ccr2 inactivation in KKAy⁺Apoe^{-/-} mice significantly ameliorated the total weight gained after 10 weeks of follow-up (Table 1, ESM Fig. 1a). Comparable food intake in KKAy⁺Apoe^{-/-} and KKAy⁺Apoe^{-/-} Ccr2^{-/-} mice suggested that mechanisms other than energy intake accounted for weight differences (Fig. 1b).

Glucose and insulin resistance Inactivation of *Ccr2* in KK*Ay*⁺*Apoe*^{-/-} mice blunted the development of hyperglycaemia and hyperinsulinaemia that were observed at 10 weeks of follow-up (Table 1). Furthermore, using the HOMA of insulin resistance, we found that inactivation of *Ccr2* protected against insulin resistance in KK*Ay*⁺*Apoe*^{-/-} mice. This notion was substantiated further by results from ITT (Fig. 1c) and GTT (Fig. 1d).

Differences in fasting glucose between KK $Ay^+Apoe^{-/-}$ (n=10) and $Ccr2^{-/-}$ (n=8) mice remained significant even after accounting for the weight differences. A multivariate analysis that included age, sex and weight as covariates revealed that Ccr2 inactivation was associated with significantly lower levels of glucose in KK $Ay^+Apoe^{-/-}$ mice (8.1±0.6 vs 7.0±0.6 mmol/l for KK $Ay^+Apoe^{-/-}$ vs KK $Ay^+Apoe^{-/-}$ Ccr2 $^{-/-}$, p=0.002; data not shown).

 Table 1
 Metabolic variables

KKAy ⁺ Apoe	p value	
Ccr2 ^{+/+}	Ccr2 ^{-/-}	
45.0±6.0	29.0±5.0	0.01
2.5 ± 0.6	1.9 ± 0.5	0.21
13.5 ± 7.5	10.6 ± 4.5	0.01
219.2 ± 4.0	151.5 ± 4.0	0.03
19.0 ± 0.2	10.3 ± 0.1	0.04
7.6 ± 0.6	7.5 ± 0.5	0.92
1.3 ± 0.2	1.3 ± 0.3	0.90
	Ccr2 ^{+/+} 45.0±6.0 2.5±0.6 13.5±7.5 219.2±4.0 19.0±0.2 7.6±0.6	$\begin{array}{cccc} 45.0\pm6.0 & 29.0\pm5.0 \\ 2.5\pm0.6 & 1.9\pm0.5 \\ 13.5\pm7.5 & 10.6\pm4.5 \\ 219.2\pm4.0 & 151.5\pm4.0 \\ 19.0\pm0.2 & 10.3\pm0.1 \\ 7.6\pm0.6 & 7.5\pm0.5 \end{array}$

Values are mean \pm SD

Mice were 20 ± 5 weeks of age; each group contained n=3-5 mice (one representative experiment of three performed is shown)

 $HOMA-IR,\ HOMA\ of\ insulin\ resistance\ (determined\ using\ a\ web\ calculator\ found\ at\ www.hepcnomads.co.uk/HOMACalc.htm)$



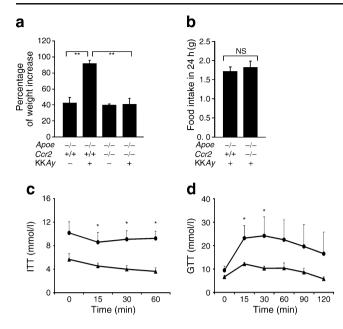


Fig. 1 Weight and glucose analysis. **a** Percentage of weight increase was determined by comparing the mean weight in each group, following the mice from week 10 to 18. Ccr2 inactivation in the pathogenic KK $Ay^+Apoe^{-/-}$ mice led to a significant reduction in the percentage of weight gain. **b** Food intake during 24 h periods was quantified for four consecutive days; no difference was seen between KK $Ay^+Apoe^{-/-}$ and KK $Ay^+Apoe^{-/-}$ ccr2 $^{-/-}$ mice. **a**, **b** Data are representative of experiments performed three times; n=3-5. Significant decrease in ITT (**c**) and GTT (**d**) values for KK $Ay^+Apoe^{-/-}$ Ccr2 $^{-/-}$ mice (black circles) at 12 weeks of age; n=3-5 per group. *p<0.05 vs KK $Ay^+Apoe^{-/-}$ Ccr2 $^{-/-}$ value at the same time point; **p<0.001

Dyslipidaemia While genetic inactivation of *Apoe* is associated with significantly higher total cholesterol levels but normal triacylglycerol [14], the *Ay*⁺ phenotype is associated with hypertriacylglycerolaemia [21, 22]. Consistent with this notion, we found that KK*Ay*⁺*Apoe*^{-/-} mice displayed hypercholesterolaemia and hypertriacylglycerolaemia compared with KK*Ay*⁻*Apoe*^{-/-} mice (data not shown). *Ccr2* inactivation did not affect triacylglycerol or cholesterol levels, as they were comparable between KK*Ay*⁺*Apoe*^{-/-} and KK*Ay*⁺*Apoe*^{-/-} *Ccr2*^{-/-} mouse groups (Table 1).

Blood pressure Previous reports had suggested that $KKAy^+$ mice had higher blood pressure than C57BL/6J controls [23, 24]. However, we found that $KKAy^+$ and $KKAy^-Apoe^{-/-}$ mice had comparable blood pressure (data not shown). There were no differences in blood pressure between $KKAy^+Apoe^{-/-}$ and $KKAy^+Apoe^{-/-}Ccr2^{-/-}$ mice (ESM Fig. 1b).

Systemic inflammation In humans, pro-inflammatory cytokines such as IL-6 and TNF α have been extensively associated with the metabolic syndrome [25]. However,

we did not find any differences in circulating TNF α and IL-6 levels between KK $Ay^+Apoe^{-/-}$ and KK $Ay^-Apoe^{-/-}$ mice (data not shown). We also tested a different source of inflammation such as the amount of circulating adipokines, and we found significantly low adiponectin and high leptin levels in KK $Ay^+Apoe^{-/-}$ mice compared with C57BL/6 controls (data not shown). However, there were no differences in circulating levels of adiponectin, leptin or resistin between KK $Ay^+Apoe^{-/-}$ and KK $Ay^+Apoe^{-/-}$ Ccr2 $^{-/-}$ mice, including KK Ay^- mice as a control (ESM Table 2). Therefore, we tested other potential indicators of inflammation such as the proportion of inflammatory monocytes in blood. We found a significant increase in the proportion of inflammatory monocytes in KK $Ay^+Apoe^{-/-}$ mice compared with KK $Ay^+Apoe^{-/-}$ Ccr2 $^{-/-}$ mice (Table 2).

Complications of the metabolic syndrome in our murine model

Cardiovascular disease The metabolic syndrome is a major risk factor for the development of atherosclerosis with high overall mortality; this risk factor applies independently of diabetes mellitus [26]. We observed that $KKAy^{+}$ mice (with intact Apoe gene) did not develop atherosclerotic plaques even when on a high-fat diet (HFD) or under chronic inflammation induced by weekly lipopolysaccharide (LPS) injections (ESM Fig. 1c). We then asked whether the metabolic syndrome state in KKAy⁺Apoe^{-/-} mice could worsen the atherosclerotic phenotype of Apoe^{-/-} mice. We found that KKAy+Apoe-/- mice developed significantly larger atherosclerotic plaques than KKAy Apoe — mice (Fig. 2a, b). These plaques also contained significantly higher proportion of macrophage infiltration (Fig. 2c, d). Furthermore, the protection against the metabolic syndrome that is afforded by the Ccr2-null state in KKAy⁺Apoe^{-/} mice was associated with a significant reduction in atherosclerotic plaque burden (Fig. 2a, b) and macrophage density (Fig. 2c, d).

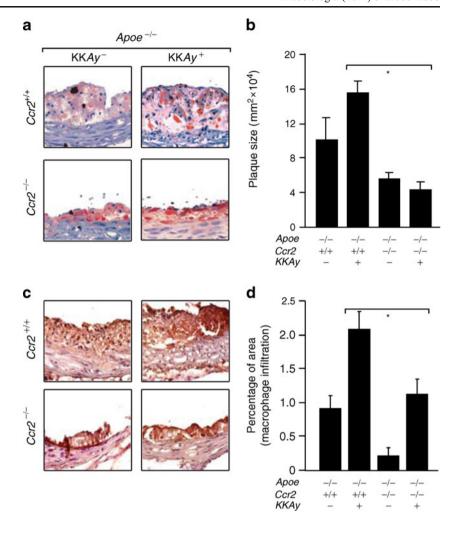
Table 2 Effect of *Ccr2* inactivation on the proportion of inflammatory monocytes in different organs

Organ	KKAy ⁺ Apoe ^{-/-}		Statistics	
	Ccr2 ^{+/+}	Ccr2 ^{-/-}	p value	df
Liver	7.3±0.5	1.6±0.4	0.001	24.2
Epididymal fat pads	4.6 ± 0.9	4.2 ± 0.8	NS	_
Pancreas	3.3 ± 1.1	2.5 ± 1.1	NS	_
Muscle	24.4 ± 3.0	19.3 ± 2.5	0.0001	9.7
Blood	10.7 ± 0.5	1.1±0.3	0.0001	84.7

Values are mean \pm SE; n=9-15; df=4; partial correlation accounting for age, sex and body weight



Fig. 2 Effects of Ccr2-null state on the development of atherosclerosis in the metabolic syndrome. a Representative images of aortic plaque size; tissue was stained with Sudan IV and the findings quantified (b). c Representative images of macrophage infiltration; tissue was stained with ER-HR3 and the findings quantified (d). Results show decreased plaque burden and macrophage infiltration in $KKAy^{+}Apoe^{-/-}Ccr2^{-/-}$ mice compared with KKAy+Apoemice. Experiments were repeated three times; n=3-5. p < 0.05



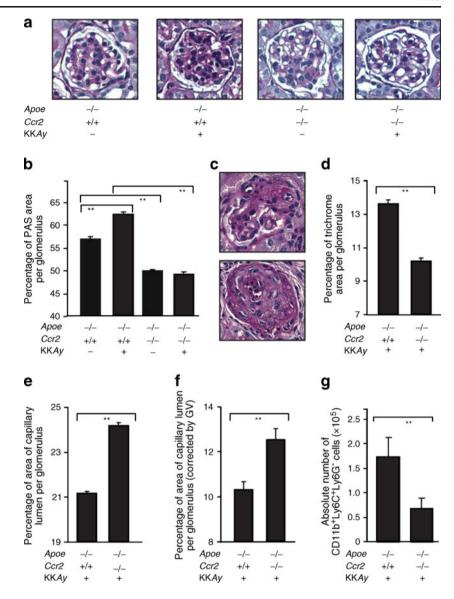
Diabetic nephropathy The metabolic syndrome is a major risk factor for the development of diabetic nephropathy [3]. The pathology of diabetic nephropathy is characterised by mesangial expansion, glomerular basement membrane thickening and nodular sclerosis [27, 28]. Most murine models fail to duplicate the pathological features of diabetic nephropathy (ESM Table 3). In KKAy+Apoe-/- mice, but not in KKAy⁺ or Apoe^{-/-} mice, we observed several histopathological features of diabetic nephropathy (Fig. 3a, b). Inactivation of Ccr2 seems to afford protection against features of diabetic nephropathy. Mesangial expansion, as indicated by glycogen deposition in the glomeruli, was more prominent in kidneys from KKAy+Apoe-/- mice than in those from KKAy-Apoe-/- and KKAy+Apoe-/- Ccr2-/- mice (Fig. 3a, b). Electron microscopy revealed thickened basement membrane in KKAy⁺Apoe^{-/-} mice compared with KKAy Apoe /- mice (ESM Fig. 2). Nodular sclerosis was present in 20 to 30% of KKAy+Apoe-/- mice, while KKAv-Apoe-/- and KKAv+Apoe-/- Ccr2-/- mice had no signs of sclerosis (Fig. 3c). The presence of histopathological features of diabetic nephropathy and the protection afforded by the Ccr2-null state were further substantiated by decreased collagen deposition (Fig. 3d) and open capillary lumen area (Fig. 3e), even when corrected for glomerular volume (Fig. 3f). Clinically, serum creatinine and the urinary albumin:creatinine ratio were not significantly different among all groups (data not shown), suggesting that a longer follow-up is necessary, or that additional factors (e.g. hypertension, bradykinin, angiotensin) are required to influence renal function.

Potential mechanisms accounting for the protective effects of *Ccr2* inactivation

Accumulation of inflammatory monocytes in epididymal fat pads is thought to contribute to local production of inflammatory cytokines and mediators that promote insulin resistance [29]. We found that the protective effects of *Ccr2* inactivation against insulin resistance in KK*Ay*⁺*Apoe*^{-/-} mice were unlikely to be due to changes in the amount of epididymal fat pads (Table 1) or to have occurred via quantitative changes in inflammatory monocyte content of epididymal fat pads, since the proportion



Fig. 3 Ccr2 inactivation and kidney involvement in the metabolic syndrome. Periodic acid-Schiff's reagent (PAS) staining, shown as histopathological images (a) with quantification (b), showed glycogen deposition in all four groups of mice (age 25±5 weeks). c Staining showed nodular sclerosis to be present only in KKAv⁺Apoe^{-/-} mice (two representative stained sections from these mice are shown).d Collagen deposition was assessed by Masson's trichrome staining. e Percentage of capillary lumen area per glomerulus and (f) lumen area corrected by glomerular volume (GV) were calculated as described. In all the cases, 50 to 80 glomeruli were analysed per mouse. g The Ccr2-null state was associated with less macrophage infiltration in the kidneys. Images and data are representative of three experiments; n=3-5 per group. **p<0.01



of these cells was comparable between KK $Ay^+Apoe^{-/-}$ and KK $Ay^+Apoe^{-/-}$ mice, even after controlling for body weight (Table 2 and Fig. 4). Likewise, there were no differences in the proportion of inflammatory monocytes in the pancreas (Fig. 4 and Table 2). In contrast, we found a significant reduction in the proportion of inflammatory monocytes in the liver, muscle, kidney and blood of KK $Ay^+Apoe^{-/-}Ccr2^{-/-}$ mice (Figs 3g and 4 and Table 2).

We surmised that differences in the proportion of inflammatory monocytes in organs other than epididymal fat pads could be closely involved in the regulation of glucose metabolism and also contribute to the development of insulin resistance. Indeed, we found that the proportion of inflammatory monocytes in the liver, pancreas and muscle, but not in the epididymal fat pads and blood, were significantly correlated with peripheral glucose levels

(Table 3 and ESM Fig. 3). Even after accounting for differences such as age and body weight, these differences remained significant (Table 2). Together the data in Tables 2 and 3 suggest that inactivation of *Ccr2* in KK*Ay*⁺*Apoe*^{-/-} mice may ameliorate insulin resistance via modulation of inflammatory monocyte accumulation, mostly in liver and muscle, but not in the epididymal fat pads.

Lastly, we asked whether absence of CCR2 was associated with changes in the phosphorylation of molecules in the insulin-signalling pathway. Based on several studies in humans documenting that early changes in muscle are associated with insulin resistance [30], we focused on this tissue. In the muscle of KK $Ay^+Apoe^{-/-}$ mice, inactivation of Ccr2 was associated with significantly lower levels of glycogen synthase kinase 3β (GSK- 3β) phosphorylation (pGSK- 3β), but not of Akt, IGF-1R and p70S6 kinase (ESM Fig. 4 and data not shown). This difference was also



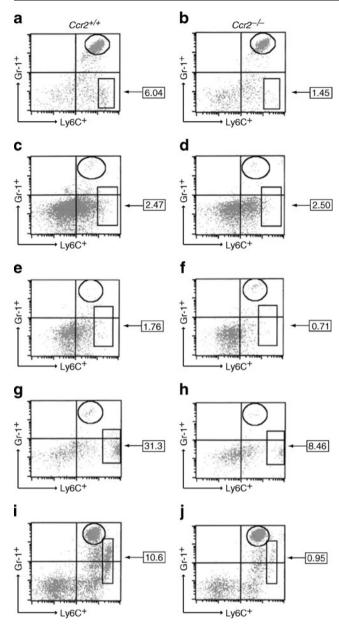
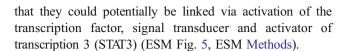


Fig. 4 FACS plots representing the percentage of inflammatory monocytes in different organs of $KKAy^+Apoe^{-/-}$ and $KKAy^+Apoe^{-/-}$ Ccr2 $^{-/-}$ mice. All plots were gated on CD11b $^+$ and specific populations for Gr-1 and Ly6C $^+$ were selected as shown. Infiltration in liver (**a**, **b**), epididymal fat pads (**c**, **d**), pancreas (**e**, **f**), muscle (**g**, **h**) and blood (**i**, **j**) is shown; n=9-15 per group

observed in the liver, but not in the epididymal fat pads. Lower levels of pGSK-3 β in KK $Ay^+Apoe^{-/-}Ccr2^{-/-}$ muscle tissue remained significant even after controlling for body weight (p=0.005). Remarkably, levels of pGSK-3 β in muscle correlated with serum glucose at 120 min postinsulin administration (r=0.85, p=0.014, df=5; partial correlation using body weight and genotype as covariates, n=10). Ingenuity pathways analysis looking for interactions between CCR2 and pGSK-3 β in insulin resistance revealed



Discussion

Here we generated a model system to capture the complex pathogenesis and clinical manifestations of the metabolic syndrome and its complications. We show that inactivation of *Apoe* in KKAy⁺ mice leads to the development of features that define the metabolic syndrome, such as obesity, insulin resistance and dyslipidaemia, and to complications including atherogenesis and diabetic nephropathy. In this model system, *Ccr2* gene inactivation was associated with a reduction in insulin resistance and weight gain, but dyslipidaemia was not affected. We also found a decrease in plaque burden and observed changes in the kidney normally seen in diabetic nephropathy. The data suggest that a potential mechanism for the protective effects of *Ccr2* inactivation is a reduction in the proportion of inflammatory monocytes in the liver and muscle, but not in the epididymal fat pads.

To our knowledge, other murine models do not display the defining features and complications of the metabolic syndrome that we have described in KKAy⁺Apoe^{-/-} mice (ESM Table 1). For example, Gao et al. [31] studied the role of apolipoprotein E in a mouse model of diabetes, for which they backcrossed KKAy⁺ mice with Apoe^{-/-}, Apoe^{-/+} or Apoe^{+/+} mice; unfortunately they did not describe in detail cardiovascular complications, i.e. atherosclerosis.

We chose KKAy⁺ mice because, similarly to humans, the development of the metabolic complications in this system is polygenic [13]. Genetic inactivation of Apoe in these mice was important because C57BL/6J wild-type mice on a HFD [32] only developed a mild form of insulin resistance and dyslipidaemia, with almost undetectable plaques and minimal diabetic nephropathy [33]. Likewise, type 2 diabetes-prone KKAy⁺ mice on a HFD followed by LPS injections as administered here do not develop significant atherosclerosis. Apoe^{-/-} mice, a well-known murine model classically used for the study of dyslipidaemia-induced

Table 3 Correlation between inflammatory monocytes and glucose levels

Organ	Correlation	p value
Liver	0.42	0.041
Epididymal fat pads	_	NS
Pancreas	0.58	0.029
Muscle	0.55	0.006
Blood	-	NS

Analysis includes the use of age, sex and body weight as covariates; n=30



atherosclerosis, do not develop insulin resistance and, even on a HFD, the defining features of the metabolic syndrome tend to be mild [34].

The work shown here provides further support for the notion that CCR2 plays a critical role in the metabolic syndrome, but also reveals potentially new pathogenic effects. It has been postulated that, in the context of obesity, CCR2-CCL2-dependent monocyte recruitment into adipose tissue promotes local inflammation and impairment of adipocyte function [35]. Adipocytes and inflammatory monocyte-derived macrophages in the epididymal fat pads produce pro-inflammatory cytokines such as IL-6 and TNF α , which can induce insulin resistance [10]. Administration of propagermanium for pharmacological blockade of CCR2 in mice reduced adipose tissue inflammation and the related insulin resistance [36]. Our data also support the notion that defective macrophage migration induced by modulation of the Ccr2-Ccl2 axis may play a major role in atherosclerosis and diabetic nephropathy.

Unlike previous reports using less complex diet-based models [9], our work indicates that CCR2 may contribute to the pathogenesis of the metabolic syndrome via its effects on accumulation of inflammatory monocytes in the muscle and liver, but not in the epididymal fat pads. The precise mechanism responsible for CCR2-driven accumulation of inflammatory monocytes in liver and muscle, which might result in insulin resistance, remains to be explored. A reasonable hypothesis is that infiltrating inflammatory monocytes produce inflammatory mediators that affect local responses to insulin in the liver and muscle. In support of this concept, our results showed decreased phosphorylation of GSK-3ß in muscle and liver of Ccr2knockout mice. GSK-3\beta regulates insulin action and glucose metabolism in human skeletal muscle [37]. In the kidney [38], GSK-3β has been shown to regulate glucoseand insulin-induced extracellular matrix production in renal proximal tubular cells. In the arterial wall, GSK-3β modulates the development of atherosclerosis [39]. Pathway analysis (ESM Fig. 5, ESM Methods) suggested that STAT3 could act as a link between CCR2 and GSK-3ß in the development of insulin resistance. Future studies will need to directly explore the mechanisms underlying the effects of tissue-specific inflammatory monocyte infiltration on insulin signalling and glucose uptake, for example by using radioactive tracers and insulin clamp processes.

Our finding that KK $Ay^+Apoe^{-/-}$ and KK $Ay^+Apoe^{-/-}$ Ccr $2^{-/-}$ mice had similar food intake revealed that Ccr2 inactivation does not affect the satiety regulation pathways that are disrupted in mice with the Ay^+ allele (ESM Methods). This finding contrasts with the observation of Weisberg et al. [9] that inactivation of Ccr2 in mice on a HFD reduces

food intake. This discrepancy may be due to the fact that our mice were fed a normal diet and became obese due to hyperphagia.

We characterised two complications of the metabolic syndrome, namely atherosclerosis and diabetic nephropathy. KKAy⁺ mice, even when fed a HFD, develop minimal or no atherosclerotic plaque lesions, and only minor morphological renal abnormalities (data not shown). Apoe^{-/-} mice normally develop hypercholesterolaemia and atherosclerosis [14], but do not have prominent kidney abnormalities (ESM Table 3). In our studies, KKAy⁺Apoe^{-/-} mice were characterised by severe and accelerated atherosclerotic plaque burden (1–2 log increase in plaque size compared with Apoe^{-/-} mice), and by kidney changes indicative of diabetic nephropathy, e.g. marked glycogen and collagen deposition in the glomeruli, as well as glomerulosclerosis (20% of mice), all in the context of macrophage infiltration.

In our studies, we did not find any differences in the albumin:creatinine ratio from 24 h urine samples in KKAy⁺Apoe^{-/-} mice, indicating that, over the time period studied, only the histological changes, but not clinical manifestations of diabetic nephropathy were present. The inability to recreate hypertension in our model system may have prevented the emergence of full-blown diabetic nephropathy. Future experiments will need a longer follow-up in order to determine whether KKAy⁺Apoe^{-/-} mice develop hypertension and proteinuria at later time points. In any case, factors affecting proteinuria or loss of renal function may be different from those affecting mesangial expansion and fibrosis, implying that multiple pathways are involved in the development of diabetic nephropathy [40].

Collectively our findings highlight the usefulness of a novel murine model for dissecting the pathogenesis of the metabolic syndrome. In this model system, we found that CCR2 plays a critical role. This finding suggests that modulation of the chemokines axis could be a relevant approach for therapy of the defining features and complications of the metabolic syndrome.

Acknowledgements We thank Y. Patel (Department of Pathology, UTHSCSA) for help with HPLC measurement of creatinine. This work was supported by grants from Fraternal Order of Eagles, a Veterans' Administration Merit Award, and NIH RO1 AR 052755 to S. S. Ahuja.

Contribution statement All authors were involved in conception and design, analysis and interpretation of data, drafting or revision, and final approval of the article to be published.

Duality of interest The authors declare that there is no duality of interest associated with this manuscript.



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