Increased intestinal permeability in obese mice: new evidence in the pathogenesis of nonalcoholic steatohepatitis

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Obesity is associated with several chronic disorders such as diabetes, hyperlipidemia, and cardiovascular diseases (6). Although liver disease is not widely appreciated as a complication of obesity, morbidly obese patients display a high prevalence of fatty livers associated with abnormal results of hepatic functional tests (56). Moreover, advanced liver disease related to the fatty liver represents the most common underlying cause of cryptogenic cirrhosis (45). Nevertheless, only 20–30% of pathologically obese patients have histological signs of necroinflammation and fibrosis, suggesting a role for a variety of genetic and environmental cofactors in the progression of obesity-related liver diseases, namely, nonalcoholic fatty liver disease (NAFLD) and nonalcoholic steatohepatitis (NASH) (46, 47).

A growing body of experimental and clinical data suggests that endotoxin and endotoxin-induced proinflammatory cytokines could be among such cofactors (32, 39). Wigg and coworkers (55) reported a higher prevalence of small intestinal bacterial overgrowth (SIBO) and increased circulating TNF-α levels in patients with NASH. In addition, inflammatory-mediated liver damage in various rat models of SIBO is improved by antibiotic treatments (31, 55). Kupffer cells are the major source of inflammatory soluble factors in response to LPS in the liver (52). Moreover, recent evidence has suggested that hepatic stellate cells (HSCs) may also provide a relevant contribution to the hepatic inflammatory network during endotoxemia (9, 43).

Clinical and experimental reports have confirmed that LPS plays an important part in alcoholic liver injury, a disorder histologically indistinguishable from NASH (1, 47). Because the major source of endotoxin is the gut lumen, increased intestinal permeability has been suggested as an important factor in alcohol-induced liver disease. Indeed, several animal studies have supported the view that chronic ethanol abuse disrupts the intestinal epithelium integrity, leading to increased portal endotoxemia and exposure of the liver to high levels of LPS (20). Current data on intestinal dysfunction in NASH patients are, however, contradictory (4, 55). Obesity, which is often associated with NASH, is now considered a low-grade systemic inflammatory condition. Persistent high circulating levels of inflammatory cytokines, which are often observed in obese patients, may cause impairment of intestinal barrier function by altering structure and localization of tight junctions (TJs) (7, 17). The sealing properties of TJs rely on a cluster of junctional proteins that selectively regulate the paracellular transport of ions, solutes, and peptides from the lumen to the intestinal mucosa and bloodstream. Occludin, claudin family members, and junctional adhesion molecule are linked to the actin cytoskeleton by cytoplasmic rafts formed by catenins and zonula occludens (ZO)-1,-2, and -3 (21). The disruption of the TJ complex by several factors, such as bacterial toxins or inflammatory mediators, leads to leakage of water and proteins into the lumen, as described in relapsing diarrhea, and to translocation of intraluminal solutes, such as bacterial endotoxins, into the systemic circulation (25).

In this study, using two models of obese mice [leptin-deficient C57BL/6J ob/ob (ob/ob) and hyperleptinemic C57BL/16 db/db], we assessed the role of increased intestinal permeability in liver injury. New evidence in the pathogenesis of nonalcoholic steatohepatitis.
6 db/db (db/db) mice, which are functionally deficient for the long-form leptin receptor), we showed that metabolic syndrome is associated with an abnormal distribution of junctional proteins within the intestinal mucosa that causes increased intestinal permeability leading to portal endotoxemia. In addition, HSCs isolated from the livers of ob/ob and db/db mice are more sensitive to LPS, developing a stronger inflammatory and fibrogenic phenotype than HSCs from lean control mice.

MATERIALS AND METHODS

Animals. Male 12-wk-old wild-type C57BL/6j mice, mice genetically deficient in leptin (ob/ob mice), and mice functionally deficient for the long-form leptin receptor (db/db mice) were obtained from Harlan (Oderzo, Italy), housed in groups of 2 mice/cage, kept under controlled temperature and humidity conditions, and received standard chow and tap water ad libitum. Animal studies were approved by the Institutional Animal Care and Use Committee of the University of Padua.

Using chamber experiments. Five-centimeter-long segments of the small intestine were collected from age-matched wild-type, ob/ob, and db/db mice, rinsed free of intestinal contents, and opened along the mesenteric border. Mucosal preparations were mounted in Ussing chambers connected to a voltage-clamp apparatus (EVC 4009, World Precision Instruments, Sarasota, FL), as described previously (14). After a 30-min equilibration period, the potential difference (PD; in mV) and short-circuit current (Isc, in μA/cm2) were recorded every 15 min for 60 min. The electrical resistance (in Ω·cm2) was calculated using Ohm’s law from the open-circuit PD and Isc. PD and resistance values were corrected for junctional potentials (<0.1 mV) between luminal and serosal solutions and the buffer resistance, respectively. Epithelial permeability to horseradish peroxidase (HRP) was also determined by a colorimetric assay.

Immunofluorescence analysis of occludin and ZO-1. Ob/ob, db/db, and age-matched wild-type lean mice were killed by cervical dislocation, the abdomen was opened, and a segment of the ileum was immediately removed, longitudinally opened, washed with PBS, mounted in embedding medium (Tissue-Tek, Sakura, The Netherlands), and stored at −80°C until use. Cryosections (8 μm) were fixed in acetone at −20°C for 5 min. Nonspecific background was blocked by an incubation with 2% donkey serum in PBS and 0.3% Triton X-100 (30 min at room temperature). Sections were incubated with mouse anti-occludin or rabbit anti-ZO-1 (1:400, Zymed Laboratories, San Francisco, CA) for 1 h. Sections were washed (3 times for 10 min in PBS) and probed with donkey anti-mouse and anti-rabbit FITC-conjugated antibodies, respectively (ImmunoResearch Laboratories). Slides were washed in PBS (3 times) and mounted in mounting medium (Sigma, Milan, Italy). Sections were visualized on a Leica TCS-NT/SP2 confocal microscope using a ×63 objective, and images were digitally stored with Leica software. As a negative control, slides were incubated with normal rabbit/mouse IgG.

Differential detergent extraction and immunoblot analysis for occludin and ZO-1. Mucosal specimens were scraped off the ileum of ob/ob, db/db, and age-matched wild-type mice. Samples were homogenized and lysed (45 min on ice) in extraction buffer (100 mM KCl, 3 mM NaCl, 0.5 mM MgCl2, and 10 mM HEPES; pH 7.4) containing 1% Triton X-100, 1% Protease Inhibitor Cocktail Set I (Calbiochem, San Diego, CA), and phosphatase inhibitors (25 mM NaF and 10 mM Na3VO4). The particulate material was removed by centrifugation (1,500 g for 5 min at 4°C). The supernatant was collected and designated as the total protein fraction.

At the same time, equivalent mucosal samples were incubated for 30 min at 4°C with 1% Triton X-100 extraction buffer as described above. The Triton X-100-soluble fraction was then subjected to low-speed centrifugation, and the supernatant was used to determine the total protein concentration. The Triton X-100-insoluble fraction was designated as the insoluble protein fraction. The Triton X-100-insoluble residue fraction was passed five times through successive syringes (25, 20, and 18 gauge) in SDS buffer and finally centrifuged at 1,500 g for 5 min at 4°C; this was designated as the insoluble protein fraction (7). The protein concentration was measured by the Bradford method.

Proteins (40 μg/lane) were fractionated on a 7.5% (w/vol) SDS-PAGE gel and transferred to nitrocellulose membranes (Trans-Blot Transfer Medium, Bio-Rad Laboratories, Hercules, CA). Membranes were blocked in PBS (0.05%)-Tween 20 with 5% (w/vol) nonfat dry milk for 1 h at room temperature and then probed with mouse anti-occludin or rabbit anti-ZO-1 (0.5 μg/ml) antibodies overnight at 4°C. After being extensively washed, membranes were incubated for 1 h with HRP-conjugated secondary antibodies (1:2,000, Sigma). Immunocomplexes were visualized using ECL Western blotting detection reagents (Pierce, Milan, Italy). Images of Western blots were acquired using a VersaDoc imaging system (Bio-Rad) and digitally stored with Quantity One (Bio-Rad) software.

Endotoxin assay. Endotoxin levels were assessed in sera collected from the portal veins of ob/ob, db/db, and wild-type mice using the BioWhittaker QCL-1000 chromogenic limulus amoebocytes lysate test kit according to the manufacturer’s instructions (BioWhittaker, Walkersville, MD). Samples were diluted (1:10) and heated for 5 min at 70°C to remove nonspecific inhibitors of endotoxin. Optical densities were measured using an ELISA plate reader (Spectra II Tecan, Graz, Austria) at 405 nm, and the concentrations of endotoxin in samples were calculated from a standard curve of known amounts of Escherichia coli endotoxin. The sensitivity of the assays was 3 pg/ml. All determinations were performed in duplicate.

Isolation and culture of murine HSCs. HSCs were isolated from the livers of wild-type, ob/ob, and db/db mice as previously described (9). HSC purity, confirmed after the first subculture passage by the morphological light microscopic appearance, staining of fat droplets with oil red O, immunofluorescent staining for α-smooth muscle actin (Sigma) and vitamin A-specific ultraviolet fluorescence, was >96%. Any presence of contaminating Kupffer and endothelial cells was ruled out by the absence of nonspecific esterase activity and immunofluorescent staining for factor VIII (Dako, Milan, Italy), respectively.

Subconfluent HSCs were trypsinized, seeded in six-well plates, and grown in complete medium to reach ~80% confluence. The FBS concentration was gradually reduced to 1% (vol/vol), and cell monolayers were incubated for 6 days in medium containing LPS (10 ng/ml) from Salmonella enteritidis (Sigma). Media and stimuli were replaced daily. At least one internal control was performed in each experiment and consisted of HSCs incubated with medium supplemented with 1% (vol/vol) FBS.

RNA extraction and quantitative RT-PCR analysis. Total RNA was isolated from cultured HSCs using OmniZol (Euroclone, Milan, Italy). Contaminating DNA was removed with a DNA-free TM Kit (Ambion, Milan, Italy), and cDNA was synthesized using standard procedures. GAPDH, membrane CD14 (mCD14), IL-6, monocyte chemoattractant protein (MCP-)1, fibronectin, and collagen type 1 steady-state mRNA-specific transcript levels were quantified using real-time PCR technology (ABI Prism 7700 Sequence Detector, Applied Biosystems), SYBR Green PCR Core Reagent kits (Applied Biosystems), and specific sets of primers (see Table 1).

Cytokine ELISA assays. HSCs were cultured in medium containing 1% (vol/vol) FBS alone or supplemented with LPS, as described above. Using commercially available ELISA kits, IL-6 (Bender MedSystems, Milan, Italy) and MCP-1 (BioLegend, San Diego, CA) levels were measured in HSC-conditioned medium, whereas IL-1β, TNF-α, INF-γ (Endogen, Woburn, MA), and IL-6 levels were assessed in serum samples collected from ob/ob, db/db, and lean mice. Optical densities were measured using an ELISA plate reader (Spectra I Tecan) at 450 nm. Cytokine levels were expressed as nanograms per milliliter. Sensitivities of the assays ranged from 3 to 12 pg/ml.
Table 1. Oligonucleotides used in this study

<table>
<thead>
<tr>
<th>Fragment Size, bp</th>
<th>Forward Primer</th>
<th>Reverse Primer</th>
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<tbody>
<tr>
<td>Mouse GAPDH 177</td>
<td>5′-ACTCCACCTCAAGCATAATCC-3′</td>
<td>5′-TCTCCCATGTGTTGAGGAGCA-3′</td>
</tr>
<tr>
<td>Mouse CD14 264</td>
<td>5′-GATCTGTGACTGGCAGTGC-3′</td>
<td>5′-GCCAAGCCAGACTTCAGAC-3′</td>
</tr>
<tr>
<td>Mouse IL-6 105</td>
<td>5′-CCGAGGAGGAGTCTCAC-3′</td>
<td>5′-TCCGACGGTTCGACAGGAG-3′</td>
</tr>
<tr>
<td>Mouse MCP-1 170</td>
<td>5′-CAGTCGAGCTGCAATTTGAAGGC-3′</td>
<td>5′-TATGGAACTCTTAAACCGCTCTGTC-3′</td>
</tr>
<tr>
<td>Mouse fibronectin 120</td>
<td>5′-GGAGAACAGAGGCGAAAGAATATC-3′</td>
<td>5′-TGGTGTACGTGTTGGATGTCG-3′</td>
</tr>
<tr>
<td>Mouse collagen type I 180</td>
<td>5′-AGAAACATCATCACCATTACGCGAGA-3′</td>
<td>5′-GTGGTTTTGTATTCCGATGCTGT-3′</td>
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MCP-1, monocyte chemotactic protein-1.

Statistical analysis. Data are expressed as means ± SE. Comparisons were drawn between groups for parametric data using Student’s t-test. Results were considered statistically significant when P < 0.05.

RESULTS

Lower intestinal resistance and higher portal endotoxia and systemic proinflammatory cytokine levels in obese mice. As shown in Fig. 1, intestinal specimens collected from either ob/ob and db/db mice revealed disrupted mucosal barrier function. Indeed, a significant decrease in small intestinal transepithelial resistance (Fig. 1A) and higher epithelial permeability to HRP (Fig. 1B) were observed in ob/ob and db/db mice compared with lean controls. No differences in electrophysiological parameters were reported in intestinal specimens collected from ob/ob and db/db mice. We then investigated the effect of the increased intestinal permeability on portal blood endotoxia. As shown in Fig. 2A, we found higher endotoxin levels in the portal blood of both strains of obese mice than in age-matched wild-type lean animals. LPS levels in the portal blood of ob/ob and db/db mice were 95 ± 16 and 184.6 ± 14.7 pg/ml, respectively, significantly higher than in lean controls (51 ± 9 pg/ml). Greater intestinal permeability is commonly reported in metabolic disorders, but it has been also described in systemic inflammatory conditions (7). As shown in Fig. 2B, circulating levels of IL-1β, IL-6, INF-γ, and TNF-α were significantly higher in obese than in lean mice. As expected, obese mice also had significantly higher blood glucose levels than lean controls (15.82 ± 1.2 mmol/l in ob/ob mice and 16.4 ± 2.6 mmol/l in db/db mice compared with 10.88 ± 0.8 mmol/l in lean controls, P < 0.05).

Intestinal TJ protein delocalization in obese mice strains. Since the altered paracellular permeability involves a disrupted intestinal barrier, we examined the organization and distribution of TJ proteins by immunohistochemistry and Western blot analysis. As shown in Fig. 3, the immunofluorescence assay performed on intestinal sections of wild-type C57BL/6J mice demonstrated an intact network of occludin and ZO-1 with TJ proteins predominantly localized along the apical cellular border. Instead, immunocytochemistry performed on intestinal cryosections obtained from ob/ob mice revealed a substantial decrease in occludin’s staining and discontinuous signals for ZO-1, suggesting a dramatic redistribution of both proteins in the intestinal epithelium of ob/ob mice (Fig. 3). Similar results were obtained with intestinal sections from db/db mice (data not shown).

Since TJs are structurally characterized as soluble or insoluble proteins by their partition into Triton X-100 buffer (33), we analyzed the expression levels and solubility profiles of occludin and ZO-1 in obese and wild-type lean mice. As shown in Fig. 4A, a broad band between 58 and 71 kDa of junction-associated occludin (65 kDa) was present in both soluble and insoluble protein fractions in lean mice. In ob/ob and db/db mice, however, the protein amount in the fractions was remarkably decreased compared with wild-type lean animals. Moreover, in genetically obese mice, the occludin-associated protein pattern was totally changed, since the lowest-molecular-mass proteins (corresponding to the intramembrane fragment) were barely detectable (21, 22). In specimens collected from C57BL/6J wild-type mice, ZO-1 was exclusively associated with the Triton X-100-insoluble fraction (Fig. 4B), whereas in either ob/ob and db/db mice, ZO-1 clearly partitioned also in the soluble fraction. These findings suggest a shift of intestinal junctional protein from the cytoskeleton, causing a decrease in paracellular sealing.

Enhanced sensitivity of HSCs from obese mice to endotoxin. Because Yang and coworkers (57) reported greater susceptibility of obese mice to LPS-mediated liver injury, we evaluated whether persistent portal endotoxia might increase the sen-
sitivity of HSCs to bacterial cell-wall products, thus favoring the development of an activated phenotype. For this purpose, HSCs were isolated from leptin-deficient ob/ob mice and db/db long-isofrom leptin receptor-defective mice. As shown in Fig. 5, after 6 days of exposure to low LPS concentrations (10 ng/ml), HSCs from genetically obese mice developed a more evident proinflammatory and profibrogenic phenotype than HSCs isolated from lean controls. Indeed, LPS exposure significantly increased IL-6 and MCP-1 steady-state mRNA-specific transcript levels by 4.6- and 3.1-fold in ob/ob mice and 4.3- and 9.8-fold in db/db mice, respectively. Similarly, fibronectin and collagen type I mRNA upregulation was significantly more pronounced in ob/ob- and db/db-derived HSCs than in cells from lean control mice (Fig. 5A).

In addition, LPS exposure induced the release of higher levels of IL-6 (12.2 ± 0.87 ng/ml for ob/ob-derived HSCs and 7.98 ± 0.88 ng/ml for db/db-derived HSCs; Fig. 5B) and MCP-1 (53.1 ± 3.4 ng/ml for ob/ob-derived HSCs and 54.9 ± 5.3 ng/ml for db/db-derived HSCs; Fig. 5C) in HSCs isolated from obese mice compared with HSCs isolated from lean mice.

Fig. 2. Portal endotoxemia and systemic proinflammatory cytokine levels in w/t, ob/ob, and db/db mice. A: endotoxin levels were determined in portal sera by the QCL-1000 chromogenic limulus amoebocyte lysate test kit. Samples were diluted (1:10) in nonpyrogenic water and heated at 70°C to inactivate nonspecific inhibitors of endotoxin. The endotoxin concentration was determined spectrophotometrically at 405 nm and calculated from the standard curve. *P < 0.05 and §P < 0.02 vs. w/t mice; §P < 0.02 vs. ob/ob mice. B: circulating IL-1β, IL-6, TNF-α, and INF-γ levels were measured by ELISA in serum samples. Data are reported as means ± SE of samples collected from at least 6 mice/group. Samples were assayed in duplicate. *P < 0.05 vs. w/t mice; §P < 0.02 vs. ob/ob mice.

Fig. 3. Altered organization of tight junction (TJ) proteins in small intestine specimens of ob/ob mice. Immunofluorescence analysis was performed on frozen sections of small intestines collected from w/t and ob/ob mice. Sections were fixed in cold acetone and incubated with anti-occludin or anti-zonula occludens (ZO)-1 monoclonal antibodies. Specific immunocomplexes were visualized with a Leica TCS-NT/SP2 confocal microscope using a x63 objective. Images are representative of 4 separate experiments. Arrows indicate positive staining.
detection reagents. Results are representative of at least 3 independent experiments. Immunocomplexes were visualized by ECL Western blotting. Fractionation of the total protein fraction (total f.), Triton X-100-insoluble fraction (insol. f.), and Triton X-100-soluble fraction (sol. f.) were performed to quantify IL-6, monocyte chemoattractant protein (MCP)-1, fibronectin, collagen type I, and membrane (m)CD14 mRNA transcript levels. Data are given as ratios of stimulated to respective control, nonstimulated cells. Each experiment was performed at least 3 times with triplicate determinations for each condition; samples were then assayed in duplicate. *P < 0.02 and **P < 0.05 vs. HSCs isolated from w/t mice. A: total RNA was isolated from HSCs, and quantitative RT-PCR analysis was performed to quantify IL-6, monocyte chemoattractant protein (MCP)-1, fibronectin, collagen type I, and membrane (m)CD14 mRNA transcript levels. Data are given as ratios of stimulated to respective control, nonstimulated cells. Each experiment was performed at least 3 times with triplicate determinations for each condition; samples were then assayed in duplicate. *P < 0.02 and **P < 0.05 vs. HSCs isolated from w/t mice. B and C. A: total RNA was isolated from HSCs, and quantitative RT-PCR analysis was performed to quantify IL-6, monocyte chemoattractant protein (MCP)-1, fibronectin, collagen type I, and membrane (m)CD14 mRNA transcript levels. Data are given as ratios of stimulated to respective control, nonstimulated cells. Each experiment was performed at least 3 times with triplicate determinations for each condition; samples were then assayed in duplicate. *P < 0.02 and **P < 0.05 vs. HSCs isolated from w/t mice. B and C. A: total RNA was isolated from HSCs, and quantitative RT-PCR analysis was performed to quantify IL-6, monocyte chemoattractant protein (MCP)-1, fibronectin, collagen type I, and membrane (m)CD14 mRNA transcript levels. Data are given as ratios of stimulated to respective control, nonstimulated cells. Each experiment was performed at least 3 times with triplicate determinations for each condition; samples were then assayed in duplicate. *P < 0.02 and **P < 0.05 vs. HSCs isolated from w/t mice. B and C. A: total RNA was isolated from HSCs, and quantitative RT-PCR analysis was performed to quantify IL-6, monocyte chemoattractant protein (MCP)-1, fibronectin, collagen type I, and membrane (m)CD14 mRNA transcript levels. Data are given as ratios of stimulated to respective control, nonstimulated cells. Each experiment was performed at least 3 times with triplicate determinations for each condition; samples were then assayed in duplicate. *P < 0.02 and **P < 0.05 vs. HSCs isolated from w/t mice. B and C. A: total RNA was isolated from HSCs, and quantitative RT-PCR analysis was performed to quantify IL-6, monocyte chemoattractant protein (MCP)-1, fibronectin, collagen type I, and membrane (m)CD14 mRNA transcript levels. Data are given as ratios of stimulated to respective control, nonstimulated cells. Each experiment was performed at least 3 times with triplicate determinations for each condition; samples were then assayed in duplicate. *P < 0.02 and **P < 0.05 vs. HSCs isolated from w/t mice. B and C. A: total RNA was isolated from HSCs, and quantitative RT-PCR analysis was performed to quantify IL-6, monocyte chemoattractant protein (MCP)-1, fibronectin, collagen type I, and membrane (m)CD14 mRNA transcript levels. Data are given as ratios of stimulated to respective control, nonstimulated cells. Each experiment was performed at least 3 times with triplicate determinations for each condition; samples were then assayed in duplicate. *P < 0.02 and **P < 0.05 vs. HSCs isolated from w/t mice. B and C.
exposure to a proper stimulus through a short-receptor isoform present in peripheral tissues (48). Nevertheless, we observed that circulating proinflammatory cytokine levels and changes in intestinal mucosa resistance were comparable between ob/ob and db/db mice regardless of the associated metabolic syndrome. In this respect, in ob/ob and db/db mice, the intestinal abnormalities seemed to correlate to the obese phenotype rather than to the loss of leptin function or its circulating level. Indeed, adipocytes spontaneously produce and release into the circulation inflammatory cytokines, and obesity is now recognized as a mild systemic inflammatory condition (18, 23).

The sealing properties of the intestinal mucosa require an efficient and anatomically intact epithelium as well as efficient apical cell junctional complexes (37). TJ function is strictly related to the expression, localization, and integrity of a variety of proteins in the lateral membrane; thus, cyto skeletons and bacterial toxins can modify intestinal mucosal barrier function, affecting the expression and/or distribution of specific proteins (19, 26). Therefore, in patients with inflammatory bowel diseases, increased TNF-α affects TJ functionality and alters adhesion molecule expression, influencing mucosal barrier efficacy (50). In obese subjects, soluble factors arising directly from fat tissue or produced as a consequence of the associated metabolic syndrome, like hyperinsulinemia, might directly affect TJ function (17, 36, 49, 54). Thus, both obese mice strains, ob/ob and db/db, show increased circulating levels of inflammatory cytokines such as INF-γ and TNF-α, which are able to induce a redistribution of several functional proteins (2), and IL-1β, which is capable of decreasing TJ ion selectivity in epithelial and endothelial cell monolayers (16, 40). The leakage of intestinal-derived endotoxins into the portal blood, due to the direct effect of ethanol on the intestinal mucosa (after oral ethanol feeding), is a well-established mechanism of alcohol-induced liver damage (1, 20). In the absence of ethanol-mediated mucosal damage, portal endotoxemia in leptin-deficient ob/ob mice as well as in functionally leptin-resistant db/db mice reached abnormally high values, supporting the existence of impaired mucosal barrier function in the presence of obesity. Indeed, when we performed Ussing chamber experiments, we found significantly decreased electrophysiological parameters and a concomitant increase in HRP fluxes, suggesting that altered paracellular permeability is involved in the disruption of intestinal barrier function in genetically obese mice (Figs. 1 and 2). We observed, by confocal microscopy and Western blot analysis, a striking reorganization of occludin and ZO-1 in the ileum of ob/ob and db/db mice, suggesting the rupture of TJ links with the cytoskeleton, a condition known to compromise the sealing properties of TJs (33). Therefore, the substantial changes in expression/distribution of two key TJ proteins in obese mice may explain the enhanced paracellular permeability observed in the intestinal mucosa that can lead to an abnormal leakage of bacterial endotoxins into the portal blood and LPS exposure of hepatic cellular populations.

HSC activation is generally secondary to liver damage and due to the disruption of the normal extracellular matrix and to the release of proinflammatory cytokines from Kupffer cells, hepatocytes, and infiltrating inflammatory cells. Recent evidence, however, has shown that HSCs can directly respond to LPS via a specific receptor complex and contribute to establish and/or enhance endotoxin-mediated liver injury (9, 43). Indeed, our data demonstrated an increase in liver susceptibility to LPS-mediated damage in obese mice that might depend to some degree on enhanced HSC reactivity to LPS (57). Obese mice-derived HSCs seemed to lack the LPS tolerance that develops in a variety of cell types after LPS stimulation to inhibit inflammatory cytokine production to prevent autotoxic effects by inflammatory mediator overproduction (43). On the other hand, HSCs from ob/ob and db/db mice showed enhanced responsiveness to inflammatory mediators similar to what is observed in myofibroblasts, macrophages, and endothelial cells purified from tissues affected by chronic inflammatory disorders and soaked in a milieu rich in inflammatory cytokines (5, 34, 35). Thus, both ob/ob- and db/db-derived HSCs exposed to endotoxin developed an inflammatory and fibrogenic phenotype, whereas this response was observed in the livers of db/db mice but not in ob/ob mice following CCl4 treatment, supporting a role for leptin as a proinflammatory factor required to amplify inflammatory reactions in vivo (28). Thus, proinflammatory cytokines increase fibronectin mRNA levels and protein deposition through a NF-κB-dependent pathway in HSCs isolated from leptin-deficient mice (29). Indeed, in a variety of murine knockout models lacking a proinflammatory factor, such as cytokines, the overall inflammation in vivo is strongly reduced, whereas immune cells are still able to respond to inflammatory stimuli in vitro (35, 58).

In conclusion, we demonstrated disrupted intestinal barrier function in two strains of genetically obese mice leading to a consistent leakage of bacterial endotoxins into the portal blood circulation. Several factors may contribute to the enhanced intestinal mucosal permeability in obese subjects, such as hyperinsulinemia and high circulating levels of inflammatory cytokines, exposing the fatty liver (already predisposed to free radical-mediated damage), to a high load of gut-derived bacterial endotoxins (42, 57). The persistent exposure to LPS and LPS-induced soluble proinflammatory mediators may activate HSCs, which develop to a fibroinflammatory phenotype, amplifying the liver damage. These effects could be further enhanced in patients carrying specific polymorphisms in genes coding for inflammatory cytokines and/or receptors for bacteria-derived endotoxins (8, 13, 51, 41, 53).

REFERENCES


