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Activation of the Lectin Pathway by Natural IgM in a Model of Ischemia/Reperfusion Injury


Reperfusion of ischemic tissues elicits an acute inflammatory response involving serum complement, which is activated by circulating natural IgM specific to self-Ags exposed by ischemia. Recent reports demonstrating a role for the lectin pathway raise a question regarding the initial events in complement activation. To dissect the individual roles of natural IgM and lectin in activation of complement, mice bearing genetic deficiency in early complement, IgM, or mannan-binding lectin were characterized in a mesenteric model of ischemia/ reperfusion injury. The results reveal that IgM binds initially to ischemic Ag providing a binding site for mannan-binding lectin which subsequently leads to activation of complement and injury. The Journal of Immunology, 2006, 177: 4727–4734.

A large body of evidence has accumulated over the past two decades implicating a major role for the complement system in ischemia/reperfusion (I/R) injury in humans (13–16) and animals (12, 17–23). Studies (24–26) using mice deficient in complement C4, C3, total Ig (Rag1−/−), or a subset of B-1 lymphocytes (25−/−) found they were protected in the hind limb and intestinal I/R models. Moreover, reconstitution of mice totally deficient in Ab (Rag1−/−) with IgM prepared from wild-type (WT) sera restored injury (26). A single I/R-specific natural IgM clone, CM22, was identified in the intestinal and hind limb models (27, 28). Recently, highly conserved self-Ags, namely, non-muscle myosin H chain type II (NMHC-II) A and C, were identified (2) as the self-targets, confirming a crucial link in the mechanism of complement-mediated induction of I/R injury. NMHC-II is expressed in all eukaryotic cells and three forms (A, B, and C) of NMHC-II have been identified (29, 30). They are highly conserved among mice and humans but the distribution of the three isoforms varies among tissues. Functionally, NMHC-II isoforms bear ATPase activity, form molecular motors within the cell, and are thought to be important in regulating cytokinesis, cell motility, and cell polarity (31).

Although the above evidence suggests a pivotal role of the classical pathway of complement for reperfusion injury, studies of the lectin pathways have suggested it is also involved (32, 33). In vitro studies of endothelium found that both classical and lectin pathways may be activated under hypoxia/reperfusion condition. In addition, MBL was found as a deposit throughout the ischemic area at risk in myocardial (33) and renal (34) I/R models. A study (35) in a stroke model also found that the powerful neuroprotective action of C1 inhibitor (C1-INH) on brain I/R injury does not require C1q, an early component in the classical pathway of complement. Recently, Stahl and colleagues (36, 37) reported that MBL-deficient mice displayed limited injury in the intestinal or myocardial I/R models. They showed that C2-knockout, but not C1q-deficient, mice were protected in the intestinal I/R model (36). Similarly, C1q-deficient mice were not protected in a myocardial model (37). Their studies suggest that C2 and MBL, but not C1q, are necessary for I/R injury. In addition, Moller-Kristensen et al. (38) reported that the MBL-deficient mice were protected in the renal I/R model. Thus, these reports raised a question regarding the initial events following I/R.

The classical pathway can be initiated by Ab-Ag interaction followed by the activation of C1 and downstream components (C4, C2, and C3). Characterization of the lectin pathway is relatively recent. It is triggered by MBL recognizing certain patterns of carbohydrate structures (39–43). MBL naturally exists in a complex with the MBL-associated serine proteases (MASPs) (44–48). The MASPs are activated when MBL binds to a fitting carbohydrate pattern, resulting in cleavage of the polypeptide chains of the...
Materials and Methods

Animals and intestinal model of ischemia reperfusion injury

WT C57BL/6 and Rag1\(^{-/-}\) mice (C57BL/6 genetic background) were purchased from The Jackson Laboratory and bred under specific pathogen-free conditions. MBL-A\(^{-/-}\) knockout mice were generated and maintained as described previously (55). C1q\(^{-/-}\) mice are bred onto the 10th generation of the C57BL/6 background (56).

Surgical protocol for I/R was performed as previously described (2, 26, 27). Briefly, after anesthesia, a laparotomy is performed, and the microclip was removed, and all animals were kept warm during reperfusion. At the end of experiment, the ischemic segment of the jejunum was harvested and the central 4 cm was excised for pathological analysis.

Histopathology and immunohistochemistry analysis

Cryostat sections of intestinal tissues were stained with H&E, blind-coded by a different person, and examined by light microscopy for mucosal damage. The pathology score was assessed based on a procedure modified from Chiu (57, 58), which included a direct inspection of all microvilli over a 4-cm stretch of jejunum as described (27).

Immunoprecipitation and protein identification by tandem mass spectrometry

Immunoprecipitation was performed using a standard protocol (2, 60). Briefly, intestinal tissues were flushed with sterile saline and immediately cryofrozen. Intestines were homogenized and lysates were preclaried with cyanogen bromide-activated Sepharose 4B (Amersham Biosciences) and Sepharose coupled with goat anti-rat IgG (Caltag Laboratories). Postcleared supernatants were incubated with Sepharose conjugated with goat anti-mouse IgM (Caltag Laboratories) to capture IgM-bound immunocomplexes. The bound samples were eluted and subsequently analyzed on SDS-PAGE (6%) under reducing conditions. Protein bands were visualized by staining with GeiCode Blue (Pierce). Individual Coomasie blue-stained bands were excised from SDS gels, destained, and subjected to enzyme digestion as described previously (61). The peptides were separated using a Nanoflow Liquid Coupled Chromatography System (Waters Cap LC), and amino acid sequences were determined by tandem mass spectrometer (Q-TOF micro). Mass spectrometry data were processed and subjected to database searches using Mascot (Matrixscience) against Swissprot, TREMBL/New, or the National Center for Biotechnology Information nonredundant database.

In vitro MBL-binding assay

Purified CM31 and CM22 monoclonal IgMs were coated in polystyrene microtiter wells (Maxisorp; Nunc) in concentrations at 0.1, 1, and 10 \(\mu g/ml\) diluted in 150 mM NaCl/20 mM Tris-HCl (pH 9.4) by incubation overnight at 4°C. Similarly, mannan was coated into wells at a concentration of 10 \(\mu g/ml\). The wells were washed three times in 150 mM NaCl, 15 \(\mu g/ml\) NaNO\(_3\), 10 mM Tris-HCl (pH 7.4; TBS) with 0.05% (v/v) Tween 20 (TBS/Tw) and blocked for 1 h at room temperature with 0.1% (w/v) human serum albumin (State Serum Institute) diluted in TBS. The wells were washed three times either in TBS/Tw or TBS/Tw/Ca\(^{2+}\) or in TBS/Tw with 1 mM CaCl\(_2\) (TBS/Tw/Ca\(^{2+}\)) or in TBS/Tw with 1 mM EDTA (TBS/Tw/EDTA). Mouse serum (M-5905; Sigma-Aldrich) was diluted 10-, 100-, 1,000-, 10,000-, and 100,000-fold in TBS/Tw/Ca\(^{2+}\) or in TBS/Tw/EDTA. Following incubation overnight at 4°C, the wells were washed three times either in TBS/Tw/Ca\(^{2+}\) or TBS/Tw/EDTA. Bound murine MBL-A and MBL-C was detected by time-resolved immunofluoresometry as described elsewhere (62). In brief, biotinylated mAbs, recognizing either murine MBL-A (I3H6) or MBL-C

![FIGURE 1](http://www.jimmunol.org/)  
Correlation of IgM and MBL deposition in the intestine tissues of I/R-treated animals. Representative cryosections of intestinal tissues were harvested following intestinal I/R. WT mice (i and ii), IgM(CM32), reconstituted RAG-1\(^{-/-}\) mice (iii and iv), and IgM(CM31), reconstituted RAG-1\(^{-/-}\) mice (v and vi), i, iii, and v, Stained with anti-IgM-biotin followed by streptavidin-Alexa-568 (red); ii, iv, and vi, Stained with rat anti-mouse MBL followed by goat anti-rat IgG-FITC (green). All sections were counterstained with DAPI (violet). Original magnification, 400.
(I4D12), were applied to wells and diluted in TBS/Tw/Ca²⁺/H11001 to concentrations of 0.4 and 0.25 g/ml, respectively. After three washes, the wells received Eu³⁺/H11001-labeled streptavidin diluted in TBS with 25 μM EDTA and, after three washes, signals were read in a Delphia fluorometer (Delphia).

Results
To study the role of the lectin pathway in the mesenteric model of I/R injury, we examined the deposition of MBL in injured tissues. Jejunum tissues isolated from WT animals treated for 40 min of ischemia and 3 h of reperfusion were analyzed by immunohistochemistry for IgM and MBL deposition. As reported previously (27), IgM deposited within the injured microvilli. Moreover, staining with MBL-specific Ab identified colocalization of MBL and IgM (Fig. 1, i and ii). WT mice and MBL−/− mice (iii and iv). i and iii. Stained with anti-IgM-biotin followed by streptavidin-Alexa-568 (red). ii and iv. Stained with anti-C3-FITC (green). All sections were counterstained with DAPI (violet).

To explore further the role of MBL in this model, mice lacking both MBL-A and MBL-C were characterized (55, 59). Although the mice are totally deficient in MBL, they retain an intact classical pathway of complement (55). Analysis of intestine pathology after 3 h of reperfusion revealed that the deficient mice failed to develop injury compared with MBL-sufficient littermates (injury scores: 13 ± 13% vs 46 ± 28%, respectively; p < 0.05; Fig. 2, a and b), consistent with an earlier report (36). Furthermore, the protection in MBL−/− mice correlated with the absence of IgM and C3 deposition (Fig. 2c). It is also interesting to note that the I/R injury

FIGURE 2. MBL−/− mice are protected from intestinal reperfusion injury. a, Representative sections from I/R-treated WT and MBL−/− mice (both on the 129/B6 genetic background) were stained with H&E. Arrows indicate typical pathology features of injury. Original magnification, ×200. b, Pathology scores were assigned based on the degree of injury. Each symbol represents an individual mouse. The horizontal bars represent the arithmetic means of the injury scores. Asterisks indicate statistical significance (Student’s t test; p < 0.05). c, IgM and complement C3 were absent within the microvilli of MBL−/− mice. Representative cryosections were stained with Ab specific for mouse IgM or C3. Original magnification, ×400. i and ii, WT mice and MBL−/− mice (iii and iv). i and iii. Stained with anti-IgM-biotin followed by streptavidin-Alexa-568 (red). ii and iv. Stained with anti-C3-FITC (green). All sections were counterstained with DAPI (violet).

FIGURE 3. a, Deposition of IgM in microvilli during the early phase of reperfusion in MBL−/− mice. Animals underwent 40 min of ischemia followed by 15 min of reperfusion. Represented intestinal sections were stained with anti-IgM-biotin/streptavidin-Alexa-568 (red) and rat anti-mouse MBL/goat anti-rat IgG-FITC (green). b, Immune precipitation of IgM self-Ags complex at early reperfusion. Intestinal lysates were prepared from MBL−/− mice subjected to 40 min of ischemia/15 min of reperfusion. IgM self-Ags immunocomplexes were isolated as described in Materials and Methods, and separated on 6% polyacrylamide SDS-PAGE (reducing gel) followed by Coomassie brilliant blue staining. Apparent molecular weight (kDa) markers are indicated on the left. The arrow indicates the dominant band at 250 kDa that was cut and used for subsequent protein sequencing by tandem mass spectrometry.
scores of WT mice have a spectrum of variation as observed previously (2). This is likely due to the different pathogenic natural IgM levels in individual WT animals. In other words, those mice with a high level of pathogenic natural IgM may have a more severe reperfusion injury, whereas those with a low level of pathogenic natural IgM may be less injured.

The finding that MBL−/− mice were protected from I/R injury with the absence of IgM deposition 3 h postreperfusion raised the question whether IgM bound initially but was released in the absence of MBL or whether the deficient mice have an altered repertoire of natural Ab, i.e., missing pathogenic IgM. To determine whether IgM-ischemic Ag complexes form in the early phase of reperfusion, MBL−/− mice were subjected to 40 min of ischemia and the tissues were harvested at an early time point of reperfusion (15 min). Immunostaining identified deposits of IgM within the intestinal villi (Fig. 3a). The presence of IgM in the early but not late time points of reperfusion suggests that pathogenic IgM is present and binds transiently but does not lead to injury in the absence of MBL, at least under the conditions of this model.

In a recent report (2), one major target of IgM in the mesenteric model was identified as nonmuscle myosin H chain (NMHC-II-A and -C). To determine whether a similar target was involved in the

![FIGURE 4.](http://www.jimmunol.org/)

**FIGURE 4.** Clq−/− mice are not protected from intestinal reperfusion injury. a, i and ii, Representative sections (stained with H&E) from I/R-treated WT and Clq−/− mice (both on the B6 genetic background). Arrows indicate pathologic features of injury. Original magnification, ×200. b, Scatter plot shows the pathology scores of each treated group. Statistical analysis by Student’s t test found no significance between the Clq−/− vs WT groups. c, IgM colocalize with complement C3 and MBL within the microvilli of Clq−/− mice. i and iii, Stained with anti-IgM-biotin followed by streptavidin-Alexa-568 (red). ii, Stained with anti-C3-FITC (green); was stained with anti-MBL followed by goat anti-rat-FITC (green; iv). All sections were counterstained with DAPI (violet). Original magnification, ×400.

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<tr>
<th>Matched Proteins</th>
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<tr>
<td>NMHC-II-A (gi/20137006)</td>
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*Tandem mass spectrometry result of isolated ischemic tissue. Immunoprecipitations were performed as described in Materials and Methods. Bands obtained from SDS-PAGE were digested and extracted for protein identification by tandem mass spectrometry. Peptides identified from the I/R-specific 250-kDa band were matched to isoform A of NMHC-II. The Mascot score is defined as $-10 \times \log(p)$, where $p$ is the probability that the observed match is a random event. Individual ion score $> 53$ indicates identity or extensive homology ($p < 0.05$).
MBL−/− mice, a biochemical approach was used to analyze IgM-immune complexes. Earlier studies (2) determined that the optimal time point for IgM-NMHC-II complexes was 15 min post-reperfusion. Therefore, intestinal tissues were harvested from MBL−/− mice at 15 min postreperfusion, and preformed IgM-Ag complexes were isolated by incubating the lysates with beads.

FIGURE 5. Murine MBL binding to monoclonal IgMs. a, The binding of mMBL-A or mMBL-C was tested by incubating wells coated at 0.1, 1, or 10 μg/ml with either CM22 or CM31 IgM. Murine serum, diluted in buffer with either 1 mM Ca2+ or 5 mM EDTA, was added to the wells in concentrations from 0.001 to 10% (v/v). The bound MBL was detected by incubation with rat mAbs to mMBL-A or mMBL-C. b, Wells were coated at 10 μg/ml with protein A-purified murine IgG and the binding of murine MBL were tested as in A. c, For comparison the binding of murine MBLs to mannan coated at 10 μg/ml was tested as for the Igs in a and b.
influenced by genetic background (63–66). In contrast to MBL/H11006 animals (pathology scores: 25 vs 21% vs 22% respectively; Fig. 4, a and b). In addition, the variation pattern of injury scores among C1q−/− group is similar to that of the WT group, which indicates both groups have a similar pathogenic natural IgM repertoire. Moreover, immunohistochemistry analysis showed that MBL and C3 codeposited with IgM in the microvilli of I/R-treated mice (Fig. 4c). Thus, mice deficient in C1q are not protected in the mesenteric model because the presence of MBL is sufficient to initiate injury. These results are consistent with the previous report by Hart et al. (36) that injury in the mesenteric model was independent of C1q. Although C1q does not appear to be required for local injury, immunohistochemistry analysis of sections prepared from I/R-treated WT mice identified C1q colocalization with IgM within the microvilli (data not shown).

These in vivo results suggest that MBL functions downstream of IgM-ischemic Ag interaction and possibly through direct binding of MBL to IgM. To test this possibility, we used a time-resolved immunofluorometric assay-based binding assay (62). Monoclonal murine IgMs were immobilized in polystyrene plates followed by the addition of purified murine MBL-C or MBL-A protein. The bound MBL on immobilized IgM were detected by specific Ab against MBL (62). To verify whether the binding depended on Ca2+, 1 mM CaCl2, or 5 mM EDTA, was added to the buffer. Murine IgG was used as a negative control in the binding assays, and directly immobilized mannan was included as a positive control (Fig. 5, b and c). Our results indicate that both MBL-C and MBL-A bind to immobilized natural IgM clones in a dose- and calcium-dependent manner (Fig. 5a).

**Discussion**

Until recently, it was generally held that complement-dependent injury in the mesenteric (and skeletal muscle) models of I/R injury were mediated via IgM activation of the classical pathway. The recent observation that the lectin pathway was also essential raised the question of the order of initiating events. Using mice deficient coated with Ab specific for murine IgM. Analysis of the isolated immune-complexes identified a dominant band at ~250 kDa (Fig. 3b). Protein sequence analysis by mass spectrometry identified NMHC-II A as the major protein (Table I). Thus, as reported earlier, nonmuscle myosin H chain is a major target for natural IgM in the early stage following the reperfusion of ischemic jejunum (2).

The finding that MBL is required for complement activation raises the question whether the C1q-dependent classical pathway functions in this model of reperfusion injury. To address this question, mice genetically deficient in C1q were characterized in the mesenteric I/R model. Because C1q−/− mice were in the C57BL/6 genetic background and MBL−/− mice were in the 129/B6 genetic background, WT mice with a C57BL/6 genetic background were used as controls for C1q−/− mice to prevent a biased conclusion influenced by genetic background (63–66). In contrast to MBL−/− mice, the injury levels in C1q−/− mice were similar to those of WT animals (pathology scores: 25 ± 21% vs 22 ± 17%, respectively; Fig. 4, a and b). In addition, the variation pattern of injury scores among C1q−/− group is similar to that of the WT group, which indicates both groups have a similar pathogenic natural IgM repertoire. Moreover, immunohistochemistry analysis showed that MBL and C3 codeposited with IgM in the microvilli of I/R-treated C1q−/− mice (Fig. 4c). Thus, mice deficient in C1q are not protected in the mesenteric model because the presence of MBL is sufficient to initiate injury. These results are consistent with the previous report by Hart et al. (36) that injury in the mesenteric model was independent of C1q. Although C1q does not appear to be required for local injury, immunohistochemistry analysis of sections prepared from I/R-treated WT mice identified C1q colocalization with IgM within the microvilli (data not shown).

In vitro-binding studies by others (53, 54) and as indicated in Fig. 5 of this study indicate that murine MBL can directly bind to murine IgM. The responsible binding site(s) on murine IgM is unclear, but it is likely that certain carbohydrate patterns exist on IgM, and such glycosylation could take place when natural Abs are produced. Indeed, the observation that the binding is calcium dependent supports that the interaction between IgM and MBL is linked through carbohydrate binding. The central role of the calcium ion in mediating contact to carbohydrate ligands in the MBL C-type carbohydrate recognition domain is structurally well characterized, and all carbohydrate interactions are thus calcium dependent.

In humans, 20% of the total serum IgM can bind to immobilized MBL, and these MBL-binding glycoforms contain 97% more GlcNAc-terminated glycans (54), which are strong ligands for MBL.

Our results do not exclude the possibility that IgM and MBL may work in a synergistic way, in which the interaction between IgM and ischemic Ag leads to the exposure of binding sites for MBL. Such targets could be either ischemic Ags or other candidates on ischemia-assaulted cells. It is known (8, 10) that ischemia causes rapid apoptosis in intestinal mucosa, and MBL can interact with structures exposed on apoptotic cells to initiate activation of complement C4 on the targets (67, 68). Nevertheless, in view of the in vitro data on the binding of MBL to IgM, the inability of CM22 IgM to induce injury in the absence of MBL, and the inability of MBL to induce damage in the absence of IgM, it appears that the most parsimonious account of the complement activation described in our study is that the IgM deposition triggers complement activation through MBL.

The finding that C1q was not essential for local injury but colocalized with IgM deposition suggests that it could have another role such as amplification of remote injury. Indeed, in a skeletal muscle model where remote lung injury is a prominent outcome of I/R, C1q appears to be important in severity of lung inflammation (R. Chan, F. D. Moore, M. Carroll and W. Austen, unpublished observations).

In summary, these results identify a new synergistic interaction between natural IgM and MBL leading to activation of the lectin pathway and acute inflammation in the mesenteric model of I/R injury. It will be important to learn whether these two important recognition proteins of innate immunity participate in other examples of synergy either in host protection or sterile response to self-targets (innate immune reaction in the absence of foreign Ag, i.e., bacteria).
Acknowledgments

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Disclosures

M. C. Carroll, F. D. Moore, and E. M. Alicot have equity in DeImmune Therapeutics.

References


