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Structural and Functional Analysis of J Chain-Deficient IgM

Erik J. Wiersma, Cathy Collins, Shafie Fazel, and Marc J. Shulman

Previous studies have discerned two forms of polymeric mouse IgM: moderately cytolytic (complement-activating) pentamer, which contains J chain, and highly cytolytic hexamer, which lacks J chain. To investigate the relationships among polymeric structure, J chain content, and cytolytic activity, we produced IgM in J chain-deficient and J chain-proficient mouse hybridoma cell lines. Both hexamer and pentamer were produced in the absence as well as the presence of J chain. Hexameric IgM activated (guinea pig) complement approximately 100-fold more efficiently than did J chain-deficient pentamer, which, in turn, was more active than J chain-containing pentamer. These results are consistent with the hypothesis that J chain-containing pentamer cannot activate complement. We also analyzed the structure of IgM-S337, in which the μ-chain bears the C337S substitution. Like normal IgM, IgM-S337 was formed as a hexamer and as both J chain deficient- and J chain-containing pentamers. Unlike normal IgM, IgM-S337 dissociated in SDS into various subunits. For IgM-S337 pentamer, the predominant subunits migrated as μ2x2 and μ4x4, and the subunit distribution was unaltered by J chain. However, J chain was found only in the μ2x2 species, suggesting that some arrangement of inter-μ bonds directs incorporation of J chain. IgM-S337 hexamer also dissociated to μ2x2 and μ4x4, but also yielded several species migrating much more slowly in SDS-PAGE than wild-type μ12x2. To account for these forms, we propose that each μ-chain can interact with three other μ-chains and that some hexameric molecules contain two catenated μ6κ6 circles. 


J chain is a 15-kDa glycoprotein covalently associated by disulfide bonds with polymeric forms of IgM and IgA (1, 2). The Ig μ heavy chain has three cysteine residues available for intermolecular disulfide bonds. C337, C414, and C575 lie in the Cμ2, Cμ3, and Cμ4/4tail domains, respectively, and are thought to join μ-chains via homo-pairs (C337-C337, C414-C414, and C575-C575) (3, 4). Each pentameric IgM molecule contains approximately one J chain attached to the penultimate amino acid of the μ-chain, C575 (2, 5–8). J chain is disulfide bonded via its C14 and C68 to no more than two μ-chains (6, 9). Most or all incorporation of J chain into IgM occurs relatively late in the intracellular assembly process, at a stage when IgM polymers have been formed but are not yet fully linked by disulfide bonds (5, 10).

Two functions have been described for Ig-associated J chain. J chain is necessary for binding of IgM and IgA to the poly-Ig receptor, which functions in epithelial transcytosis of IgA (11–13). Also, J chain modifies polymeric assembly of IgM, in that relatively more pentamer and less hexamer are produced in the absence of J chain. The fraction of IgM that was seen as pentamer in the absence of J chain has varied among different studies, ranging from none up to 50% (14–16). Pentameric IgM differs from hexameric IgM in several ways. First, J chain is found in pentameric, but not hexameric, IgM. Second, pentameric IgM is less cytolytic than hexameric IgM (17, 18). Third, analysis of mutant IgM has suggested that more inter-μ-chain C414-C414 bonds are formed in hexameric IgM than in pentameric IgM (19, 20). These correlations could have multiple explanations. For example, incorporation of J chain into pentamer might affect the disulfide bonding of IgM and in this indirect way depress its cytolytic activity. Alternatively, the hexameric C1q complement component might interact better with hexameric than with pentameric IgM. As well, IgM-bound J chain might sterically hinder the binding of C1q and thereby decrease the cytolytic activity of pentameric IgM.

To extend our understanding of the relationships among disulfide bonding, cytolytic activity, and incorporation of J chain, we have examined the structure and function of wild-type IgM produced in cells expressing or not expressing J chain. We have similarly examined IgM in which one or more μ-chain cysteine residues have been replaced by serine. Our results indicate that pentameric IgM is produced in the absence of J chain and that this J chain, like J chain, is much less cytolytic than hexameric IgM. We have not detected any difference in the inter-μ-chain disulfide bonding when comparing J+ and J– pentameric IgM, but incorporation of J chain appears to be restricted in some way by the C414-C414 bond. Our analysis also suggests that each μ-chain in hexameric IgM might be bonded to three other μ-chains rather than to only two μ-chains as is conventionally depicted.
**Protein analysis**

Biosynthetic labeling of cells was performed as described previously (4), except that \(^{35}\)S-methionine (SJ.204, Amersham, Arlington Heights, IL) was used at a concentration of 50 to 100 \(\mu\)Ci/ml for labeling.

\(^{35}\)S-labeled or unlabeled IgM was prepared from supernatants either by affinity purification using DNP-Sepharose (17) or by immunoprecipitation using anti-IgM Abs and protein G-agarose (4).

IgM was fractionated by sucrose density gradient centrifugation at 23,000 rpm for 16.75 h in an SW41 rotor as previously described (17).

To produce IgM bearing normal and mutant \(\mu\)-chains, we sought to isolate a hybridoma mutant cell line that had ceased to produce J chain but which would nevertheless express the transfected \(\mu\) genes. In earlier work we fortuitously isolated a transfectedoma, T/\(\mu\)-S414(0), expressing the mutant protein IgM-S414, but not J chain (19, 20). This cell line produces no detectable J chain protein or mRNA. The cause of this J chain deficiency is not known. To obtain a cell line that had lost the \(\mu\)-S414 pSV2neo vector, the T/\(\mu\)-S414(0) cell line was subjected to 300 to 400 rad from a 137 Cs source and subcloned. Approximately 800 single precursor colonies were tested by ELISA for IgM production. One negative colony was obtained; it was G418 sensitive and lacked both \(\mu\) mRNA (Fig. 1) and \(\mu\) DNA (not shown). We then confirmed that this colony produced the \(\kappa\)-chain and lacked J chain mRNA (Fig. 1). This cell line, denoted G10, was used to express normal and mutant \(\mu\) genes.

**Efficient production of IgM pentamer in the absence of J chain**

To study the role of J chain in IgM structure and function, we transfected the G10 cell line with plasmids encoding either wild-type \(\mu\)-chain or \(\mu\)-S337. From each transfection, two independent transformants were chosen for further study. Their IgM, denoted J\(^-\) IgM-wt and J\(^-\) IgM-S337, was compared with IgM produced by previously established \(J/^+\) transformants expressing J\(^+\) IgM-wt or J\(^+\) IgM-S337 (4). Each transformant produced a level of IgM expression corresponding to 10 to 60% of that of the parental Sp6/HL hybridoma, with overlapping ranges for each pair.

We initially investigated how secreted J\(^+\) IgM-wt was assembled using sucrose density gradient (SDG) centrifugation in combination with nonreducing SDS-PAGE to assess the state of polymerization, as hexamer is expected to sediment more rapidly than pentamer in SDG centrifugation and to migrate more slowly.
than pentamer in SDS-PAGE. For this analysis, J\textsuperscript{1} IgM-wt and J\textsuperscript{2} IgM-wt were metabolically labeled with \( ^{35} \text{S} \)-methionine, and secreted IgM was purified by its affinity to DNP-Sepharose. This IgM was then separated by (nondenaturing) SDG centrifugation into various polymeric and monomeric species. As shown in Figure 2A, J\textsuperscript{2} IgM-wt had a more prominent monomer peak than J\textsuperscript{1} IgM-wt. To obtain a more complete separation of the polymeric species, the faster and slower polymeric fractions of the gradient were separately pooled and resedimented (Fig. 2A). Analysis of selected fractions from the secondary gradients indicated that for both J\textsuperscript{1} IgM-wt and J\textsuperscript{2} IgM-wt, the faster sedimenting material was greatly enriched for species that have lower mobility in SDS-PAGE, and that, conversely, the slowly sedimenting material had a higher mobility in SDS-PAGE (Fig. 2B). Moreover, the slowly sedimenting J\textsuperscript{1} IgM polymers have the same mobility in SDS-PAGE as the slowly sedimenting J\textsuperscript{2} IgM polymers, which have been previously identified as pentamer (17, 18). We conclude from these results that both J\textsuperscript{1} IgM-wt and J\textsuperscript{2} IgM-wt include both pentameric and hexameric species. The sequential gradients yielded pentameric material that contained no detectable hexamer band on SDS-PAGE. The hexameric material usually contained detectable pentamer (see below).

In light of previous studies in which hexameric IgM was the predominant species produced in the absence of J chain (14, 15), we were surprised to find that production of hexamer and pentamer did not change much in the absence of J chain. To confirm that secreted J\textsuperscript{1} IgM-wt protein actually lacked J chain, we compared its J chain content with that of J\textsuperscript{2} IgM-wt. Individual hexamer, pentamer, and monomer species were extracted from the SDS-PAGE gel as shown in Figure 3A. After reduction, alkylation, and acetone precipitation, the samples were analyzed by AU-PAGE for J chain. To compare the different samples for J chain content, several concentrations of J\textsuperscript{1} IgM-wt pentamer were loaded onto the gels. As expected from previous reports, J chain was found in J\textsuperscript{1} IgM-wt pentamer but not in monomer. The preparation of J\textsuperscript{2} IgM-wt hexamer contained about 2% as much J chain as did the preparation of pentamer, but this is probably due to contaminating pentamer (Fig. 3B). By contrast, we detected no J chain in J\textsuperscript{1} IgM-wt pentamer or hexamer (<2% of J\textsuperscript{1} IgM-wt pentamer). This experiment was repeated for IgM-wt and IgM-S337 transformants without prior SDS-PAGE separation of its DNP-purified secreted IgM. In these experiments (not shown), J\textsuperscript{2} IgM-wt and J\textsuperscript{1} IgM-S337 proteins also had no detectable J chain (<3% of the content of their J\textsuperscript{1} counterparts). These experiments indicated that IgM pentamer was efficiently assembled even in the absence of J chain.

Purification of IgM by binding to DNP-Sepharose and elution with DNP-alanine has the potential to enrich preferentially for some species. Therefore, we have also examined the species present in IgM that was prepared by immunoprecipitation, as this procedure was previously found to better measure the composition of the primary SDG separation, pentamer- and hexamer-enriched fractions were separately pooled as indicated and recentrifuged (open and filled symbols, respectively). Two secondary gradients are shown together for each of the J\textsuperscript{1} IgM (middle panel) and J\textsuperscript{2} IgM (bottom panel), where the filled and open symbols represent hexamer and pentamer, respectively. B. SDS-PAGE analysis of fractions from secondary SDG. The indicated fractions from pentamer- and hexamer-enriched polymers prepared in A were analyzed following immunoprecipitation. DNP-purified, but unseparated J\textsuperscript{1} IgM-wt and J\textsuperscript{2} IgM-wt were included to indicate the multiplicity of species. Samples were separated in the upper phase of a two-phase gel containing 3% acrylamide and 0.4% agarose.
of secreted IgM (4). 35 S-labeled IgM-wt was prepared from two
m-wt-J1 and two m-wt-J2 transformants by immunoprecipitation,
and individual SDS-PAGE bands were quantified by PhosphorIm-
ger analysis. For J2 IgM-wt the following distribution of species
was found (mean ± SD): hexamer, 20 ± 9%; pentamer, 49 ±
10%; and monomer, 31 ± 3%. For J1-IgM-wt the corresponding
values were: hexamer, 16 ± 14%; pentamer, 77 ± 14%; and
monomer, 7 ± 3%. This comparison suggests that J chain in-
creases the production of secreted pentamer at the expense of
monomer. There was approximately threefold more covalent dimer
and trimer in J2 IgM-wt than in J1 IgM-wt; each species consti-
tuted ≈4% of the total secreted J2 IgM-wt protein.

J chain-deficient IgM pentamer activates complement poorly

Previous reports have shown that pentameric J1 IgM is much less
cytolytic than hexameric J2 IgM, but it has been unclear whether
this difference is due to the presence of J chain in pentamer or to
some other structural difference between the two types of polymer.
To distinguish these possibilities we compared the cytolytic activity of the pentamic and hexameric species of J1 IgM and J2 IgM
prepared by sequential SDG centrifugation. For J1-IgM-wt the following distribution of species was found (mean ± SD): hexamer, 20 ± 9%; pentamer, 49 ±
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creases the production of secreted pentamer at the expense of monomer. There was approximately threefold more covalent dimer and trimer in J2-IgM-wt than in J1 IgM-wt; each species constituted ≈4% of the total secreted J2 IgM-wt protein.

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To distinguish these possibilities we compared the cytolytic activity of the pentamic and hexameric species of J1 IgM and J2 IgM
prepared by sequential SDG centrifugation. To gauge whether
cytolytic activity was derived from a single species, we assayed
three fractions from different positions in the pentamer and hex-
amer peaks. As described in Materials and Methods, IgM from the
indicated SDG fractions was serially diluted and adsorbed to TNP-
coupled erythrocytes. The IgM-TNP-erythrocytes were then incu-
bated in the presence of guinea pig serum as a complement source,
and lysis was assessed spectrophotometrically (Fig. 4). As a mea-
sure of cytolytic activity we have calculated the amount of IgM that lysed 50% of the erythrocytes (Table I). Pentamer from both J1 IgM-wt and J2 IgM had higher lytic activity than unfractionated IgM-wt, and this activity increased for the faster sedimenting fractions. SDS-PAGE analysis of these fractions indicates that the fractions
denoted hexamer contained some pentameric IgM (Fig. 2B). The
level of contaminating pentamer was less in faster migrating frac-
tions, which had greater hemolytic activity. To estimate the activity of pure hexamer, we assumed that contaminating pentamer did not significantly contribute to the total lytic activity. Pentamer con-
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For simplicity, J chain is not included in these models.

A puzzling feature was that the activity of J\textsuperscript{+} pentamer compared with that of hexamer (~0.8%) was much lower than the 5% value seen in earlier studies from this and another laboratory (17, 18). We have tested whether this difference reflects changes in the method of assay, with variable results. That is, in repeated testing using the method of Davis et al. (17) we found that J\textsuperscript{+} pentamer ranged from 1.4 to 12% of the cytolytic activity of hexamer. We have not identified the source of this variation.

**Analysis of disulfide bonding pattern in J chain-deficient IgM-S337 polymers**

Inter-\(\mu\)-chain disulfide bonding in polymeric IgM-wt is mediated by three cysteines, C337, C414, and C575, which are believed to form homo-pairs, e.g., C337-C337 (Fig. 5A). However, the connectivity of the \(\mu\)-chains, i.e., the series and parallel arrangement of disulfide bonds (see Fig. 5 for definitions), is not known. To

![FIGURE 5. Models of mutant IgM pentamers. A. Ig domains and cysteine residues available for inter-\(\mu\)-chain bonding. B. Possible arrangement of disulfide bonds and subunits of IgM-S337 pentamer. In the \(\mu\)4e4 unit (\(\mu\)-chains 5, 6, and 7), the C414-C414 and C575-C575 bonds are in series. In the \(\mu\)2x2 unit, composed of \(\mu\)-chains 3 and 4, C414-C414 and C575-C575 bonds are in parallel, i.e., the two bonds bridge the same \(\mu\)-chains. C. Model for IgM-S(337, 414) pentamer. In this model the pentamer is maintained by C575-C575 bonds in series with noncovalent interactions between C\(\mu\)2 domains. For simplicity, J chain is not included in these models.](Image)
were run: DNP-purified IgM-wt (1080-kDa hexamer, 900-kDa pentamer, separated samples. As molecular mass standards, the following samples preparations did not align exactly with corresponding bands from SDG-cated. For comparison, affinity-purified IgM-S337, not separated by SDG, hexamer or pentamer, respectively. P1 and P2 indicate SDS-PAGE bands associated specifically with either lyzed by SDS-PAGE following immunoprecipitation. H1 through H4 and A from secondary SDG. Fractions from the secondary SDG in used for secondary SDG, are indicated. These examples illustrate how the size of the subunits (here μ2κ2 and μ4κ4) indicates whether C414-C414 and C575-C575 are in series, but not whether they are parallel. We have tested for differences in the covalent assembly of pen- tameric and hexameric J+IgM-S337 and J−IgM-S337 by examin- ing the species that are produced from these polymers upon dena- turation by SDS. Pentameric and hexameric J+IgM-S337 and J−IgM-S337 were prepared by sequential SDG centrifugations (Fig. 6), as described above for J+IgM-wt and J−IgM-wt. As was seen for IgM-wt, the fraction of IgM-S337 sedimenting as mono- mer in the primary gradients was about threefold higher in prepar- ations of J−IgM-S337 than in the case of J+IgM-S337, further supporting the idea that IgM-S337 assembles like IgM-wt. As in the analysis of IgM-wt (Fig. 3A), pentamer-enriched IgM-S337 sedimented more slowly than did hexamer-enriched polymers in the secondary gradients. The fact that IgM-S337 polymers had similar sedimentations in secondary and primary gradients and did not release a detectable level of monomer indicates that these poly- mers are stable despite their noncovalent structure. In a separate preparation of IgM-S337 (not shown), we found that pentamer was much less cytolytic than hexamer, in agreement with an earlier analysis of IgM-S337 (19); for pentamer from both J+ and J−IgM- S337, >700 ng/ml was required for 50% lysis, while hexamer from J+ and J− transformants gave 50% lysis at 12 and 6.5 ng/ml, respectively. Selected fractions from the secondary gradients of J+IgM-S337 and J−IgM-S337 were analyzed for subunit composition by SDS- PAGE (Fig. 6B). As reported previously (19) monomer (μ2κ2) and dimer (μ4κ4) species were the predominant subunits for all polymeric fractions tested, each accounting for 30 to 50% of the total IgM, as quantified by PhosphorImager. Extended exposure of the SDS-PAGE gel revealed many bands. Nevertheless, we dis- cerned no major differences in band pattern between J+IgM-S337 and J−IgM-S337 pentamers. As will be considered in Discussion, these results suggest that J chain does not greatly alter the extent to which C414-C414 and C575-C575 link μ-chains in series. Like hexameric IgM-wt, hexameric IgM-S337 was highly het- erogeneous, and here also the J+IgM-S337 and J−IgM-S337 gave comparable patterns (Fig. 6B). As in the case of pentameric IgM- S337, the predominant species were μ2κ2 and μ4κ4. Hexamer

![Image](http://www.jimmunol.org/Downloadedfrom)
lacked several of the minor species that were present in pentameric IgM-S337 (designated P1 and P2) and that migrated slower than \( m_4k_4 \). Moreover, unlike pentameric IgM-S337, hexameric IgM-S337 included several bands (H1–H4) that migrated more slowly than either pentameric or hexameric IgM-wt. The identities of these very slowly migrating species are considered further in Discussion.

We were concerned that some of the subunits present in both the pentamer- and hexamer-enriched fractions might truly be associated with only one polymeric species or the other, but may exist in all fractions because SDG centrifugation had yielded incomplete separation. It was not possible to assess the purity of the noncovalent pentamer and hexamer in the same direct manner as we did for IgM-wt. Nevertheless, our data suggest that cross-contamination was not a serious problem. Thus, the fact that pentamer-enriched fractions from IgM-S337 were much less cytolytic than hexamer-enriched fractions indicates that pentamer fractions were not severely contaminated. Also, very pure pentamer was obtained under the same separation conditions used for IgM-wt. IgM-S337 hexamer fractions might have been contaminated to some extent with pentamer, but this also was probably not severe. Thus, IgM-S337 pentamer fractions contained two species with unique SDS-PAGE mobility (P1 and P2 in Fig. 6B). These species could not be detected in the slowly sedimenting hexamer fractions, although other bands that are common to pentamer and hexamer fractions had similar intensities. These observations indicate that hexamer obtained from the faster shoulder of the peak included very little pentamer contamination.

**Disposition of J chain within IgM subunits**

As shown above, IgM-S337 yielded predominantly species with the composition \( \mu_2k_2 \) and \( \mu_4k_4 \). The double mutant, IgM-S(337, 414), also assembles efficiently into polymers, but the polymers dissociate in SDS into \( \mu_2k_2 \) subunits held together by the C575-C575 disulfide bond (4) (Fig. 5C). As indicated in Figure 7, the overall J chain content of secreted IgM-S337 and IgM-S(337, 414) was similar to that of IgM-wt, consistent with earlier findings that C575, but not C414 or C337, is necessary for J chain incorporation (20). To examine how J chain was distributed among the various substructures present in IgM-S337 and IgM-S(337, 414), \(^{35}\)S-labeled polymeric IgM was purified by SDG centrifugation (not shown). IgM from the polymer-containing fractions was immunoprecipitated and then analyzed by SDS-PAGE (Fig. 8A). Some of the minor bands shown in Figure 6B were not detected here, probably because of the shorter exposure time. The various bands were extracted from the gel and analyzed by AU-PAGE (not shown). The significance of the restricted distribution of J chain is considered further in Discussion.
As noted in the introduction, there is direct evidence that an individual \( \mu \)-chain binds via C575 to at most one J chain and that an individual J chain binds via its C14 and/or C68 to at most two \( \mu \)-chains. These observations have left open the possibility that some J chains are bound to \( \mu \) only via C14, while other J chains are bound only via C68. To test whether an individual J chain in fact bridges two \( \mu \)-chains by binding to C575, we have examined the disposition of J chain in IgM-S(337, 414). The major bands migrated approximately as \( \mu \)2\( \kappa \)2 (species D, 21% of the total polymer; species E, 69% of the total polymer) as well as various minor bands of faster mobility. J chain was detected in species D and to a much lesser extent in species E, but not in species F, G, or H. Considering that only C575 was available for intermolecular disulfide bonding in IgM-S(337, 414), the presence of J chain in this \( \mu \)2\( \kappa \)2 unit indicates that J chain bridged the \( \mu \)-chains via a C575-J-C575 linkage.

IgM-S337 and IgM-S(337, 414) polymers yielded \( \mu \)2\( \kappa \)2 subunits (species B, D, and E) that had slightly different mobilities. Nevertheless, under reducing conditions, \( \mu \)-chains from these three species had the same SDS-PAGE mobility, identical with that of \( \mu \)-chain from wild-type polymers (not shown). This suggests that the mobility difference between species D and E seen under nonreducing conditions reflects the presence of J chain, and that differences in intrasubunit disulfide bonding might be responsible for the different mobilities of species B and E.

Discussion

This study has addressed four related issues: the effect of J chain on IgM structure, the arrangement of disulfide bonds between \( \mu \)-chain and J chain, the connectivity of the \( \mu \)-chains within polymeric IgM, and the structural features that determine the cytolytic activity of IgM.

Previous analyses of IgM produced in the absence of J chain have led to different conclusions. Cattaneo et al. (16) concluded from their electron microscopic analysis of IgM produced by transfected glial cells that 50% of the IgM made in the absence of J chain was pentameric. This might be an overestimate, as this study did not distinguish hexamer in which one arm was obscured from their electron microscopic analysis of IgM produced by transfection with a J chain-deficient hybridoma cell line. We do not know the reason for these differences. Of the slowly migrating hexameric subunits, H4 migrated approximately with hexameric IgM-wt in SDS-PAGE, and H3, H2, and H1 migrated successively slower. These bands were not heptamer, octamer, and nonamer, because they comigrated with wild-type hexamer in SDG under native conditions. Figure 9 illustrates models for hexameric IgM-S337 that might account for many of the observed subunits. These models make two assumptions: 1) that in hexameric IgM all \( \mu \)-chains are joined by C414-C414 in series with C337-C337 (or, in the case of IgM-S337, C414-C414 in series with noncovalently interacting \( \mu _{2}\)-\( \mu _{2}\) domains), and 2) that C575-C575 bonds can occur in multiple ways. The first assumption is supported by the observation that IgM-S575 can assemble as covalent hexamer, and in this case the C414-C414 bonds must all be in series with C337-C337 (17). This arrangement might be a hallmark of all hexameric IgM. Figure 9 illustrates the second assumption that there are different modes of C575-C575 bonding. Models A and B are those originally proposed for human IgM by Feinstein and colleagues in which each \( \mu \)-chain interacts with only two other \( \mu \)-chains (30, 31). In the case of IgM-S337, these structures would denature in SDS to yield \( \mu _{2}\)2\( \kappa _{2}\) and \( \mu _{4}\kappa _{4}\) subunits, respectively. In models C through E, each \( \mu \)-chain interacts with three other \( \mu \)-chains; structure C would denature to yield three \( \mu _{4}\kappa _{4}\) subunits, structure D would yield \( \mu _{12}\kappa _{12}\), and structures E and F would yield two \( \mu _{6}\kappa _{6}\) subunits. Structures such as E can occur as four distinct isoforms that differ in their degrees of catenation. In this figure we have illustrated the two extreme cases with zero (E) and three (F) links. By analogy with catenated DNA we would expect that singly, twofold, and threefold catenated \( \mu _{6}\kappa _{6}\) circles would migrate progressively faster in electrophoresis. Thus, the catenated structures might account for the three slowest bands (H1–H3). Species H4 might correspond to model A or D or to a more complex molecule with topologic knots. We suppose that uncatenated \( \mu _{6}\kappa _{6}\) circles would migrate like a trimer, a species that was conspicuous by its absence, but the loose structure of such a molecule might have rendered its mobility anomalous. We suppose that hexameric
IgM-wt might also assemble with these different arrangements of C414-C414 and C575-C575 bonds. However, in this case the C337-C337 bonds would be expected even in SDS to maintain the hexameric IgM-wt as a compact structure, which then migrated as a single band regardless of catenation.

We further investigated the relationship between J chain and inter-\(\mu\)-chain disulfide bonding by examining how J chain is distributed among the subunits in IgM-S337 and IgM-S(337, 414). In IgM-S(337, 414), C575 is the only cysteine available for interchain disulfide bonding, so our finding (Fig. 8) that \(\mu_2\kappa_2\) subunits contained covalently bonded J chain indicates that the C575 residues were used to link both \(\mu\)-chains as well as the J chain, i.e., that J chain bridged two \(\mu\)-chains via C575. Moreover, our results indicate that J chain was present mainly or exclusively in this cross-linked mode. That is, if a significant proportion of J chain were incorporated by a single \(\mu\)-J disulfide bond, the J chain would also have been present in the less abundant species F through H (Fig. 8), where, in fact, it was not detected. In the simplest case the \(\mu\)-J-\(\mu\) disulfide bonds exist in series with \(\mu_2\kappa_2\) interactions. An analogous arrangement has been confirmed for IgA (32). Our data do not show whether the \(\mu\)-chains were linked by a single J chain (\(\mu\)-J-\(\mu\)) or by multiple J chains (\(\mu\)-J-J-\(\mu\)). However, in a study by Frutiger et al. (6), cyanogen bromide digestion of IgM polymer resulted in covalent J chain fragment of 23 kDa, consistent with only one J chain cross-linking \(\mu\)-chains, (\(\mu\)-J-\(\mu\)).

For IgM-S337 polymers, we found that \(\mu_2\kappa_2\) subunits, but not \(\mu_4\kappa_4\) subunits, contained J chain. The failure of \(\mu_4\kappa_4\) subunits to incorporate J chain is intriguing, as these units contained both C575-C575 and C414-C414 bonds. This implies that J-chain incorporation was affected by structural features besides the availability of C575, namely the presence of C414-C414 bonds. Figure 10 illustrates one of many possible models, namely a model in which stereochemical effects prevent J chain from bonding either to \(\mu\)-chains linked by C414-C414 (\(\mu\)-chains 8 and 9) or to their neighboring \(\mu\)-chains (\(\mu\)-chains 7 and 10). That is, the C414-C414 bond might cause tight packing and exclude J chain from both \(\mu_4\kappa_4\) and the adjoining two \(\mu_2\kappa_2\) subunits but allow incorporation into the more distant \(\mu_2\kappa_2\) subunits (\(\mu\)-chains 2 and 5). This hypothesis might also explain why a pentamer does not incorporate more than one J chain, as the typical pentamer might contain either a \(\mu_4\kappa_4\) subunit (bearing C414-C414 in series with C575-C575) or a \(\mu_2\kappa_2\) subunit (in which C414-C414 is parallel with C575-C575). Similarly, the absence of J chain in hexamer might be explained by its numerous C414-C414 bonds. However, many other models are possible, including structures in which J chain links nonneighboring \(\mu\)-chains (20).

This analysis also provides insight into why pentameric IgM activates complement less efficiently than does the hexameric species. We have found that J- pentamer, like J- pentamer, was approximately 100-fold less active than hexameric IgM, indicating that some pentamer-specific feature other than J chain was responsible for the low cytolytic activity of pentamer. One possibility is that the hexameric C1q complement protein is well activated only by a hexameric substrate, although this hypothesis is rendered unlikely by the observation that C1q binds to IgM with only three or four arms (33). Alternatively, the high activity of the hexamer might relate to the arrangement of C414-C414 bonds in hexameric IgM, as the C414S substitution abrogates cytolytic activity (19, 34). As discussed above, the C414-C414 bonds in hexameric IgM...
might uniformly and completely join µ-chains in series with C337-C337, while this series arrangement might occur to a much lesser extent in pentameric IgM. There are several reasons why cytolytic activity might require C337-C337 in series with C414-C414 bonds is required so that movement of the variable regions alters the structure of C


3 domains. Another model, suggested by Feinstein and colleagues, is that IgM undergoes a conformational change when it interacts with multivalent Ag and that the rigidity imparted by C414-C414 bonds is required so that movement of the variable regions alters the structure of Cµ2/Cµ3/Cµ4 (35).

In this study we have found substantially less activity for pentameric IgM, particularly for J+ IgM, than was reported in earlier studies (17, 18). This difference might reflect differences in the degree of hexamer contamination in the pentamer-enriched preparations. We have also not completely ruled out the effects of different assay conditions. It is important to test the generality of our findings. In particular, our cytolytic assays used mouse IgM to activate guinea pig complement, and it will be interesting to assess the results with mouse IgM, particularly for J chain-deficient molecules. Our results are consistent with the hypothesis that J+ pentamer is completely noncytolytic. That is, J+ pentamer appeared to be more active than J- pentamer, raising the possibility that the low activity of the normally J+ pentamer IgM derived wholly from a subpopulation of J-chain-deficient molecules. Our results thus suggest that the most important role for J chain is in the binding of IgM to the poly-Ig receptor for transepithelial transport of IgM. That this J chain-containing IgM has little or no cytolytic activity invites the speculation that there is some physiologic advantage to a system in which only inactive IgM is transcytosed. A related point has been made with regard to IgA, which also contains J chain and is noncytolytic (13). Perhaps it is important to avoid inflammatory reactions in tissues that are heavily exposed to foreign materials, and perhaps simple aggregation of invading microorganisms within an excretory organ such as the gut provides an efficient and effective method of neutralizing infection.

Normal IgM is a highly heterogeneous collection of molecules in which heterogeneity is generated by variations in disulfide bonding. In gross terms, IgM appears predominately as pentamer and hexamer; smaller molecules, monomer, dimer, trimer, and tetramer, are also found (36, 37). There is an additional heterogeneity among the pentameric and hexameric species in which the inter-µ-chain disulfide bonds are formed in multiple ways. There are other proteins that are also assembled into polymers of different sizes, and in which all or most polymer subunits are held together by disulfide bonds: IgA, serum pulmonary surfactant protein (SP-D), and human von Willebrand factor (38–40). Similar to IgM, the intersubunit disulfide bonds of IgA and SP-D have alternative arrangements. By contrast, some proteins assemble into a single polymeric species with a well-defined conformation: human serum amyloid P component, earthworm hemoglobin, yeast proteasome, protective antigen from Bacillus anthracis and bacteriophage Φ capsid proteins (41–45). The subunits of such polymers are held together solely or primarily by noncovalent forces. It is intriguing that in these examples noncovalently assembled molecules occur as unique structures, while those using disulfide bonds occur in multiple arrangements. The reason for these differences might be that intersubunit disulfide bonds can trap polymers in configurations that would not be stable if maintained solely by noncovalent interactions. By contrast, in the absence of disulfide bonding, assembly can reach equilibrium in which the structure of lowest free energy predominates.

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References


