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The J Chain Is Essential for Polymeric Ig Receptor-Mediated Epithelial Transport of IgA

Finn-Eirik Johansen, Ranveig Braathen, and Per Brandtzaeg

Local production of secretory (SIgA) provides adaptive immunologic protection of mucosal surfaces, but SIgA is also protective when administered passively, such as in breast milk. Therefore, SIgA is a potential candidate for therapeutic administration, but its complex structure with four different polypeptide chains produced by two distinct cell types complicates recombinant production. The J chain is critical in the structure of SIgA because it is required for efficient polymerization of IgA and for the affinity of such polymers to the secretory component (SC)/polymeric (p)IgR. To better understand the role of the J chain in SIgA production, we have generated various mutant forms of the human J chain and analyzed the function of these mutants when coexpressed with IgA. We found that the C terminus of the J chain was not required for the formation of IgA polymers, but was essential for the binding of pIgA to SC. Likewise, we found that two of the intrachain disulfide bridges (Cys^{13}, Cys^{101} and Cys^{102}:Cys^{134}) were also required for the binding of pIgA to SC but, interestingly, not for IgA polymerization. Conversely, the last intrachain disulfide bridge (Cys^{72}:Cys^{92}) was not essential for either of these two J chain functions. Finally, we demonstrated that the presence of only Cys^{15} or Cys^{69} was sufficient to support polymerization of IgA, but that these polymers were mostly non-covalently stabilized. Nevertheless, these polymers bound free SC with nearly the same affinity as pIgA containing wild-type J chain, but were transcytosed by pIgR-expressing polarized epithelial cells at a reduced efficiency.

plgR (reviewed in Ref. 19). To better understand these two functions of the J chain, we have used a mutational approach to generate deletion mutants and mutants that abolish J chain intrachain disulfide bonds or disulfide bonds between the J chain and the α-chain of the IgA. In this report, we demonstrate that the C terminus of the J chain is dispensable for plgA formation but nevertheless is required for the affinity of such polymers to SC. We also show that the same holds true for two of the three intrachain disulfide bridges. Finally, we document that either one of the two disulfide bonds normally present between the J chain and the α-chain is sufficient for polymer formation. Although these polymers are mostly noncovalently stabilized, their affinity to SC is nearly the same as that of the recombinant wild-type plgA, but they appear to be inferior ligands in plgR-mediated transport compared with covalently stabilized wild-type J chain-containing plgA.

Materials and Methods
Plasmid construction
The plasmid for episcopal expression of wild-type J chain, pCEP-wt chain, was based on pMEP4 (Invitrogen, De Schelp, The Netherlands) and pCH-J chain (14). A BamHI-BamHI fragment from pCH-J chain that contained the CMV promoter and the human J chain open reading frame was subcloned into BglII- and BamHI-digested pMEP4. C-terminal deletion mutants were constructed by PCR with J chain-forward (14) and different downstream primers that introduced a stop codon followed by a BamHI recognition site immediately after the SC codon in the J chain sequence with pCH-J chain as template. The resulting PCR products were subcloned as above. C134S was made by PCR with forward and J chain-reverse (14) as outer primers and different inner primers that mutated the last cysteine codon. PCR products were subcloned as above. C-terminal deletion mutants (except C134S) were made by PCR splice overlap extension with J chain-forward (14) and different downstream primers that introduced a stop codon followed by a BamHI recognition site immediately after the SC codon in the J chain sequence with pCH-J chain as template. The resulting PCR products were subcloned as above. C134S was made by PCR with J chain-forward and a reverse primer that mutated the last cysteine codon with pCH-J chain as template. The resulting PCR products were subcloned as above. C-terminal deletion mutants (except C134S) were made by PCR splice overlap extension with J chain-forward and J chain-reverse (14) as outer primers and different inner primers. PCR products were subcloned as above. C134S was made by PCR with J chain-forward and a reverse primer that mutated the last cysteine codon to serine and introduced a BamHI recognition site immediately after the stop codon, and subcloned as above. For detailed construction of C153S and C99S, the inserts were subcloned into pCH. Vectors without inserts were used as negative control (mock) in all transfections. Details of all plasmids will be provided upon request. The complete open reading frame of all plasmid expression plasmids was verified by sequencing (Medigenomics, Martinried, Germany).

Cell culture and transfections
The 5-iodo-4-hydroxy-2-nitrophenylacetly (NIP)-specific IgA-producing Chinese hamster ovary (CHO) cell line o4.2 that has been described previously (14) was cultured in Ham’s F-12 supplemented with 10% FCS, 2 mM glutamine, and 50 μg/ml gentamicin. For semistable transfections (episomal expression), cells were seeded at 10–100,000 cells/cm2. The colonies were pooled and seeded into six-well trays for metabolic labeling and SDS-PAGE. Transfected cells were carried over to the J chain and SC affinity measurements. However, the relative values of J chain content and SC affinity measured this way could be compared only within a single experiment.

Purification and fractionation of NIP-specific IgA
NIP-specific IgA was purified from CHO cell supernatants on NIP-Sepharose as described previously (14). For fractionation by fast protein liquid chromatography (FPLC), the eluted IgA was dialyzed against 20 mM Tris-HCl (pH 7.1) and loaded onto a Mono Q column connected to an AKTA-FPLC system (Amersham Pharmacia Biotech, Little Chalfont, Buckinghamshire, U.K.). The IgA was eluted by a linear salt gradient from 2.5 to 500 mM NaCl in 20 mM Tris-HCl (pH 7.1) and collected in 300-μl fractions which were analyzed for IgA concentration by ELISA. Peak fractions were analyzed for molecular size by nonreducing SDS-PAGE followed by immunoblotting, and for SC affinity by ELISA. Several fractions (as indicated in Fig. 4) were pooled before analysis by native PAGE and immunoblotting as well as for transcytosis assays.

Immunoblotting
IgA (30 ng) was resolved by nonreducing SDS-PAGE on a 5% (w/v) acrylamide gel with the Criterion system (Bio-Rad, Hercules, CA) and transferred onto polyvinylidene difluoride membrane (Millipore, Bedford, MA). The membrane was blocked by first air drying and then incubation in 10% skimmed milk in PBS plus 0.05% Tween 20 (PBST). Subsequent incubations were performed in PBST. The blocked membrane was first incubated with a rabbit antisem to human IgA (diluted 1/3000; DAKO) for 90 min, washed three times for 5 min, and then incubated with HRP-conjugated donkey anti-rabbit Ig (diluted 1/3000; Amersham Pharmacia Biotech) for 90 min. After washing three times for 5 min, the membrane was incubated with SuperSignal (Pierce) for 5 min. For detection of the substrate was detected with a light-sensitive camera (Chemidoc; Bio-Rad). For IgA immunoblotting, the membrane was stripped in 0.1% SDS and 100 mM β-mercaptoethanol for 30 min at 37°C, washed in PBST, and incubated with rabbit antisem to human J chain (previously adsorbed against monomeric IgA) diluted 1/6000. Secondary Ab and revealing reaction were as above. For native immunoblot, 60 ng of IgA was resolved on a 5% (w/v) acrylamide gel with the Criterion system (Bio-Rad) and then transferred to polyvinylidene difluoride membrane and processed as above.
Results

Structural analysis of the human J chain

There are no three-dimensional structure data available for the J chain of any species. Therefore, we used computer-assisted secondary structure predictions as a first approach to delineate the structure and hence better understand the function of the J chain. A schematic depiction of human J chain that combines the known pattern of disulfide bonding with the predicted secondary structure is shown in Fig. 1. The Jpred program (http://jura.ebi.ac.uk:8888/submit.html) predicted that the J chain mostly consists of \( \beta \)-strands and extended coils with two short \( \alpha \)-helices (Fig. 1). Intrachain disulfide bonds between Cys\(_{13}^\) and Cys\(_{101}^\), Cys\(_{72}^\) and Cys\(_{92}^\), and Cys\(_{109}^\) and Cys\(_{134}^\) further restrict the possible conformations of the J chain.

Role of the J chain C terminus in IgA polymerization and SC binding

The J chain performs two essential functions for SIgA formation: it enhances dimerization (and some formation of larger polymers) of IgA; and it is required for the affinity of plgA to SC/plgR. To delineate which regions of the J chain are required for these functions, we first made sequential C-terminal deletions in the J chain sequence. We found that deleting the J chain to amino acid position 113, 105, or 96 appeared to reduce the level of J chain incorporation into IgA (Fig. 2A), but this could not be definitely concluded because the level of incorporation was measured with a polyclonal antiserum to the J chain. Deletion of this C-terminal region might therefore also remove epitopes detected by the antiserum. Deletion from amino acid 76 or more appeared to preclude incorporation of J chain into the coexpressed IgA (Fig. 2A), but this could not be definitely concluded once the level of incorporation was measured with an affinity-purified monoclonal antibody to the J chain.

Deleting the last 25 amino acids (including Cys\(_{134}^\)) did not significantly affect the level of IgA polymerization promoted by the J chain (Fig. 2B; \( \Delta 113 \)). Further deletion of eight or 17 more amino acids still allowed polymer formation, although at slightly reduced efficiency and occasionally giving rise to different polymer sizes (Fig. 2B; \( \Delta 105 \) and \( \Delta 96 \), respectively). In agreement with our inability to detect \( \Delta 76 \)- and \( \Delta 73 \)-mutated J chain associated with IgA, these mutants did not contribute to enhanced polymerization of IgA. Although the smallest C-terminal deletion in the J chain (25 aa) did not significantly affect polymerization of coexpressed IgA (Fig. 2A; \( \Delta 113 \)), it was clear that this deletion was sufficient to abrogate all affinity of the produced plgA to SC (Fig. 2C; \( \Delta 113 \)). Further deletions of the J chain also resulted in pIgA without affinity to SC (Fig. 2C; \( \Delta 105 \) and \( \Delta 96 \)).

Role of J chain disulfide bridges for IgA polymerization and SC binding

The human J chain forms three intrachain disulfide bridges as well as two bridges to the tailpieces of two opposing IgA \( \alpha \)-chains. To assess the importance of these bonds, we mutated each cysteine individually as well as Cys\(_{13}^\) and Cys\(_{69}^\) in combination (C15+69S). We found that mutating any one of the J chain cysteines reduced the level of J chain incorporation to between 30 and 70% compared with the level of wild-type J chain incorporated into coexpressed IgA (Fig. 3A). However, mutation of Cys\(_{13}^\) and Cys\(_{69}^\) in conjunction appeared to abolish incorporation of the mutated J chain into IgA (Fig. 3A; C15+69S). Mutation of Cys\(_{13}^\), Cys\(_{101}^\), Cys\(_{109}^\), or Cys\(_{134}^\) did not appear to affect polymer formation (Fig. 3B). Surprisingly, all of these mutations abolished the affinity of

![FIGURE 1](http://www.jimmunol.org/)

Schematic depiction of the human J chain structure showing proposed \( \beta \)-strands (broad arrows) and \( \alpha \)-helices (cylinders). The eight J chain cysteines (Cys\(_{13}^\), Cys\(_{15}^\), Cys\(_{69}^\), Cys\(_{72}^\), Cys\(_{92}^\), Cys\(_{101}^\), Cys\(_{109}^\), and Cys\(_{134}^\)) are indicated. Secondary structure prediction was performed with Jpred (http://jura.ebi.ac.uk:8888/submit.html). The three intrachain disulfide bridges (Cys\(_{13}^\)-Cys\(_{101}^\), Cys\(_{72}^\)-Cys\(_{92}^\), and Cys\(_{109}^\)-Cys\(_{134}^\)) are indicated. Cys\(_{15}^\) and Cys\(_{69}^\) form disulfide bonds with one \( \alpha \)-H chain tailpiece (oTP) of each monomer in the IgA dimer.
the J chain-positive pIgA to SC (Fig. 3C). Mutation of Cys15, Cys72, and Cys92 reduced the level of J chain-mediated pIgA formation, while mutation of Cys69 and the double mutant (C15 + 69S) did not enhance pIgA formation above the level seen without coexpressed J chain (Fig. 3B). Mutation of Cys15, Cys69, Cys72, or Cys92 still resulted in J chain-positive IgA with significant affinity for SC (Fig. 3C), while the C15 + 69S mutant did not affect the property of the coexpressed IgA.

The significant affinity of C15S and C69S J chain-positive IgA to free SC prompted us to test whether these Igs could be transcytosed by plgR-expressing MDCK cells. We found that both mutants of J chain-positive IgA were transported from the basolateral membrane to the apical chamber of polarized plgR-expressing MDCK cells. However, the level of transport was only 17% (C15S) and 9% (C69S) of the level of transport of wild-type J chain (data not shown). Importantly, this low level was significantly above the level of transport or paracellular leakage of monomeric IgA expressed without J chain or of coincubated IgG, which both resulted in ~5% transport compared with pIgA containing wild-type J chain (data not shown).

Single CHO cell clones produce different molecular forms of IgA

Molecular size analysis revealed that each pool of IgA and J chain transfectants produced more than one molecular form of IgA (Figs. 2B and 3B). Furthermore, Western blotting of C15S- and C69S-containing IgA demonstrated that the J chain could be found in both monomers and polymers of IgA (data not shown). To determine whether the discrepancy between the good affinity to SC and the poor ability to be transcytosed by plgR-expressing polarized epithelial cells of C15S- and C69S-containing IgA might be due to a differential contribution of the various molecular forms in the two assays, we decided to purify the different molecular forms of IgA produced by each transfectant. First, we made stable transfectants of C15S, C69S, and wild-type J chain-expressing, IgA-producing CHO cells and purified IgA from supernatants of each cell line by affinity chromatography. To further fractionate each sample of recombinant IgA we chose Mono Q anion exchange chromatography because gel filtration would presumably be inefficient at separating monomeric IgA with J chain from monomers without. For IgA expressed without J chain, Mono Q fractionation revealed three distinct peaks centered around fractions 36, 48, and 65 (Fig. 4A). Surprisingly, fraction 48 showed low but significant affinity for SC (Fig. 4A), while the other two peaks had no affinity for SC. Nonreducing SDS-PAGE followed by Western blotting revealed that only fraction 48 contained covalently stabilized dimers (Fig. 4B).

IgA with wild-type J chain eluted with a larger peak centered at fraction 45 (with a shoulder extending to fraction 54) from the Mono Q column. Fraction 45 was nearly pure J chain-positive dimeric IgA, while fraction 53 was a mixture of dimeric J chain-positive IgA and monomeric IgA (Fig. 4, C and D). Not surprisingly, fraction 45 demonstrated the highest affinity to free SC (Fig. 4C). IgA with C15S-mutated J chain eluted with an additional peak centered at fraction 51, and IgA with C69S-mutated J chain eluted with two additional peaks centered at fractions 46 and 53 (Fig. 4, E and G). The additional peak from C15S-containing IgA and the two additional peaks from C69S-containing IgA all demonstrated significant affinity to SC, i.e., 72–94% of wild-type fraction 45 (Fig. 4, E and G). Nonreducing SDS-PAGE revealed that these fractions contained a mixture of J chain-positive dimeric IgA, IgA monomers, and J chain-positive monomeric IgA migrating slightly above the ordinary monomers (Fig. 4, F and H).

The Mono Q elution profile of each preparation of IgA prompted us to investigate whether there might be noncovalently stabilized pIgA produced by the C15S and C69S transfectants. Therefore, we pooled the fractions that made up the SC-binding peak (indicated in Fig. 4) and analyzed each pool by native gel electrophoresis (Fig. 5). Indeed, the pooled fractions from the C15S and C69S transfectants revealed that the distribution of IgA dimers and larger polymers in these pools was nearly identical with the distribution of polymers in the wild-type J chain pool.

Noncovalently stabilized J chain-positive pIgA shows high affinity for free SC, but is inefficiently transcytosed by plgR-expressing MDCK cells

IgA from supernatants of CHO clones stably expressing C15S- or C69S-mutated J chain was relatively inefficiently transcytosed by human plgR-expressing MDCK cells compared with pIgA from wild-type J chain-expressing clones (data not shown). Because these experiments used crude IgA preparations, this result could be due to a less efficient transcytosis of plgA with mutated Cys15 or Cys69 in the J chain. Alternatively, these mutations could result in less efficient assembly of plgA, but the plgA formed could be an equally good substrate for epithelial transcytosis as plgA with wild-type J chain. To test these possibilities, we pooled the fractions from the Mono Q purification of each IgA variant that contained pIgA and tested each pool in our transcytosis assay. We found that polymers containing C15S- or C69S-mutated J chain
were transcytosed to a level of 19 and 50%, respectively, of wild-type IgA polymers (Fig. 6). The level of transcytosis of each pool correlated well with the level of SC binding of each peak fraction, although reduction in efficiency compared with wild-type IgA caused by the mutations was greater for transcytosis than for SC binding. Finally, we did not find that the fraction of IgA lacking J chain, which contained some pIgA (Fig. 6, mock-B), was transcytosed to a level above that of monomeric IgA (Fig. 6, mock-A) or coincubated IgG (Fig. 6, dotted line), although it demonstrated some binding to SC in the ELISA (Fig. 4A).

**FIGURE 4.** Purification and analysis of different molecular forms of IgA produced by CHO-cell clones cotransfected with empty vector (mock: A and B), wild-type J chain (wt: C and D), Cys\(^{14}\)Ser (C15S: E and F), or Cys\(^{69}\)Ser (C69S: G and H) J chain variants. A, C, E, and G: IgA concentrations of eluted fractions from the Mono Q columns (curve) and their relative binding to free SC of selected fractions (columns). Fractions pooled for native gel electrophoresis and transcytosis assays (Figs. 5 and 6) are indicated by horizontal bars. B, D, F, and H. The indicated fractions were resolved by 5% nonreducing SDS-PAGE and immunoblotted with an antiserum to human IgA (left). The filter was then stripped and probed with an antiserum to human J chain (right). No bands appeared on the blot in B when probed with antiserum to human J chain (not shown).

**Discussion**

We have investigated the role of the J chain in the polymerization of human IgA and its contribution to the affinity of such polymers for free SC as well as their ability to be transcytosed by the plgR. We found that although the J chain C terminus was dispensable for IgA polymerization, it was required to endow the pIgA with affinity to SC. Furthermore, two of three intrachain disulfide bridges (Cys\(^{13}\)-Cys\(^{101}\) and Cys\(^{109}\)-Cys\(^{134}\)) were shown to be dispensable for plgA formation but essential for conferring affinity to SC. We
Role of J chain in IgA polymerization

The J chain is not absolutely required for polymerization of IgA, but its coexpression significantly enhances the production ratio of plgA to monomers (14, 33). The three intrachain disulfide bridges of the human J chain divide the polypeptide into a large loop (Cys135 to Cys101) with a smaller loop within this loop (Cys172 to Cys192) (Fig. 1). Additionally, the C-terminal 29 amino acids form a small loop bridged by Cys210 to Cys234. We found that the C-terminal loop was dispensable for polymerization of IgA. Furthermore, none of the intrachain bridges was absolutely required for plgA formation. These data suggested that the three-dimensional structure of the J chain is not so important for IgA polymerization as long as there are cysteines in the appropriate places that can be linked to the cysteines of the α-chain tailpieces. Alternatively, the J chain could fold into two distinct domains, where the N-terminal domain structure is intact in our mutants and sufficient for polymerization of IgA.

The C15S and the C69S mutants of the J chain are precluded from covalently linking two IgA monomers (25) but may still enhance plgA formation by bringing two monomers together to promote direct covalent bonding between two opposing α-chain tailpieces. In agreement with this possibility, we found a small increase in covalent plgA production when IgA was coexpressed with either of these mutants. Surprisingly, we found that J chain-positive IgA containing either the C15S or the C69S mutant had only slightly reduced affinity to free SC compared with IgA containing the wild-type J chain. This result was probably due to noncovalently stabilized dimers present in these IgA preparations. In fact, the third cysteine (equivalent to human Cys869) is lacking in the J chain from Xenopus laevis (34), suggesting that disulfide bonding between the J chain at this position and IgA or IgM is not required for function in that species. The fact that either Cys15 or Cys869 could be mutated without affecting the formation of noncovalently stabilized polymers suggested that covalent bond formation in J chain-mediated polymerization does not occur in a specific sequence. Rather, a complex between two IgA monomers and the J chain is first formed, and then either Cys15 or Cys869 can form a disulfide bridge with the adjacent IgA monomer. Presence of this complex also increases the likelihood of disulfide bond formation between the two IgA monomers. However, in the absence of such covalent stabilization, a single bond between the J chain and one of the two IgA monomers appears to be sufficient to form stable polymers. Notably, these polymers disintegrate in SDS because one of the IgA monomers interacts only noncovalently with the covalent IgA monomer-J chain complex. We concluded that covalent bonding between one monomeric IgA molecule and the J chain is required for IgA polymerization, because the double mutant (C15+69S) did not increase polymerization of IgA at all, although its intracellular expression level was similar to that of the wild-type J chain (data not shown). Thus, while the J chain may function as a scaffold for IgA polymerization, it also has a more active role as its covalent interaction with IgA greatly enhances the efficiency of plgA formation.

Role of J chain in SC binding and plgR-mediated epithelial transcytosis

Knockout mice deficient in J chain or plgR have demonstrated that both molecules are required for the generation of SIgA in vivo (33, 35–37). Furthermore, rabbit IgG Abs to the J chain and Fab of such Abs could block plgA-SC interaction in vitro and inhibit plgR-mediated transcytosis of IgA, suggesting a direct role of the J chain in the binding of plgA to plgR (38, 39).

We used a mutational approach to address the role of J chain structural elements in creating the plgA docking site for SC/plgR. Interestingly, the requirements of the J chain structure that allowed for binding of plgA to SC was much more stringent than those determining IgA polymerization. The C-terminal structure of the J chain was essential to create a binding site for SC on plgA because even the smallest C-terminal deletion we tested abolished SC interaction. Furthermore, disruption of the Cys101 to Cys134 disulfide bond (either C109S or C134S) abolished binding to SC, indicating that this C-terminal loop was required for SC binding, perhaps via direct interaction with the plgR. Interestingly, the amino acid sequence between Cys101 and Cys109 is very highly conserved among different species, suggesting a particular functional importance of this region of the J chain. Alternatively, the C-terminal...
loop could be critical for a structural feature of the J chain required for pIgA binding to pIgR. Ablation of the disulfide bond between Cys\textsuperscript{13} and Cys\textsuperscript{101} also had a dramatic effect on the affinity of pIgA to SC, although in some experiments we could detect significant, although marginal, binding activity even with these incorporated mutants of the J chain. The last intrachain bond, between Cys\textsuperscript{72} and Cys\textsuperscript{82}, appeared to be less required for binding to SC, perhaps because J chain without this bond is still able to maintain its overall three-dimensional structure. The apparent reduction in IG A dimers formed when this bond was prohibited (Fig. 3B) could be a result of Cys\textsuperscript{69} (or Cys\textsuperscript{15}) being less accessible for disulfide bond formation with the \(\alpha\)-chain. The relative high affinity of these IG A molecules to SC suggested that the supernatants from C72S- and C92S-transfected CHO cells contained noncovalently stabilized IG A dimers in addition to the covalent dimers seen by SDS-PAGE, although we did not attempt to verify this possibility.

When we fractionated CHO cell-produced IG A without J chain by anion exchange chromatography, we found that the IG A eluted in three distinct peaks, indicating three different species of NIP-specific IG. The first peak appeared to be slightly smaller than monomers by SDS-PAGE, perhaps reflecting partially assembled IG A lacking a single L chain. The second peak contained some dimers and larger polymers (seen by native acrylamide gel electrophoresis) and, surprisingly, demonstrated marginal affinity to free SC. This result showed that the J chain is not absolutely required for IG A polymerization or for some binding to free SC. Binding of J chain-negative IG A to SC has also been observed previously, indicating that the \(\alpha\)-chain contains an interaction site for SC (40). The third peak contained only IG A monomers that demonstrated no affinity for free SC. Thus, the \(\alpha\)-chain interaction site for SC apparently requires covalent attachment between two opposing tailpieces to create a novel surface constituting a functional binding site for SC/pIgR. Alternatively, this site is present on monomeric IG A, but polymerization results in higher affinity measurable in our SC binding assays. However, the latter explanation is unlikely, because we failed to detect any affinity between IG A monomers and SC by increasing the concentration of monomers (data not shown). In accord with our findings in this report, J chain-negative myeloma IG A and human hexameric IG M (without J chain) failed to bind SC properly (7). Also, J chain-deficient myeloma IG A and murine IG A isolated from J chain knockout mice were not transcytosed by the pIgR (35, 41).

When we analyzed the chromatography-purified IG A from CHO cells by native gel electrophoresis, we found that mutating Cys\textsuperscript{15} or Cys\textsuperscript{69} in the J chain yielded a fraction of IG A that was indistinguishable from the pIgA fraction produced with wild-type J chain (Fig. 5). Furthermore, the peak pIgA fraction from these two mutants showed \(\sim 72\) (C15S) and 94% (C69S) efficiency of SC binding compared with wild-type pIgA. However, the level of pIgR-mediated transcytosis was reduced to only 19 and 50% of that of wild-type pIgA, respectively. These findings suggested that a binding site for SC/pIgR is not sufficient for efficient transcytosis by the pIgR-expressing epithelium, but that covalent stabilization of pIgA is also required. One possible explanation could be that noncovalently stabilized pIgA is less resistant to the reduced pH in the endosomal compartment of the MDCK cells. Thus, in vivo, there might be an additional level of quality control of pIgA that is to be become luminal SIgA.

In conclusion, we have demonstrated that the integrity of the J chain structure is more important for receptor-mediated epithelial transcytosis of pIgA than for polymerization per se. Thus, the striking J chain expression by mucosal plasma cells seems to have production of SIgA and SIgM as its biological goal. Indeed, no other functional role has been identified for this polypeptide (42). Furthermore, we showed that a single disulfide bond between the J chain and one IG A monomer was sufficient to enhance polymerization of IG A, although the resulting polymers were mostly noncovalently stabilized. Surprisingly, these polymers retained high binding affinity for free SC but were relatively poorly transcytosed.

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