

REVIEW

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Regulation of the blood–biliary barrier: interaction between gap and tight junctions in hepatocytes

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Abstract Hepatocytes tightly connect with each other by intercellular junctions to form liver cell plates. The junctions composed of gap, tight, and adherens junctions and desmosomes concentrate around bile canaliculi. In particular, tight junctions serve as a barrier to keep bile in bile canaliculi away from the blood circulation. Thus, it is very reasonable to call tight junctions of hepatocytes the blood–biliary barrier. On the other hand, gap junctions of hepatocytes are considered to enable ordered contraction of bile canaliculi from centrilobular to periportal hepatocytes by their function of intercellular communication. Gap and tight junctions may thus play a crucial role in bile secretion, one of the most differentiated functions of the liver. In intrahepatic cholestasis, a common pathological condition of the liver, downregulation of gap and tight junctional functions is seen, which results in impaired intercellular communication and in leaky tight junctions. Although the changes in gap and tight junctions had been considered to be independent of each other, recent findings that the tight junction-associated proteins ZO-1 and occludin bind to connexins indicate the possibility of either coordinate or reciprocal regulation of macromolecular complexes containing gap- and tight-junction proteins. In this review, we introduce the interaction and regulation between gap and tight junctions of hepatocytes *in vitro* and discuss the regulatory mechanisms of the “blood–biliary barrier” to study the molecular pathogenesis of cholestasis.

Key words Gap junctions · Tight junctions · Blood–biliary barrier · Actin filament · Hepatocytes · Cholestasis

Introduction

Bile secretion, one of the most differentiated functions of the liver, essentially requires gap and tight junctions. Because gap junctions regulate direct intercellular communication and tight junctions strictly seal the bile canaliculi, bile flow is ensured without leakage of bile from the centrilobular to the periportal zone and then to bile ducts in a highly ordered manner. In humans and animals, most cholestatic liver diseases are associated with profound changes in the pericanalicular region (Fig. 1). Cholestatic hepatocytes show downregulation of gap and tight junctional functions, resulting in impaired intercellular communication of gap junctions^{1,2} and in deteriorated barrier function of tight junctions.^{3–5} Depolymerization of actin-myosin bundles also results in the loss of canalicular membrane tone and failure to contract.^{6,7} Finally, dilated bile canaliculi are observed in cholestatic hepatocytes (Fig. 1D).

In this article, we summarize the recent findings on gap junctions and tight junctions, particularly from the point of view of linkage of these junctions with actin filaments in hepatocytes *in vivo* and *in vitro*, to elucidate the detailed molecular pathogenesis of cholestasis.

Structure of gap and tight junctions in the liver

Thin sections and freeze-fracture images of the junctions between dissociated hepatocytes reveal structures that are similar to those seen *in vivo* (Fig. 2). In vertebrates, tight junctions play a central role in regulating the movement of solutes, ions, and water through the extracellular space in epithelial or endothelial sheets. Tight junctions between hepatocytes are found surrounding the bile canaliculi, where they seal the paracellular spaces between hepatocytes and maintain cellular polarity. By contrast, gap junctions control cell-to-cell movement of solutes, ions, and water, providing an intercellular pathway not accessible to dilution by extracellular fluid. In the hepatic

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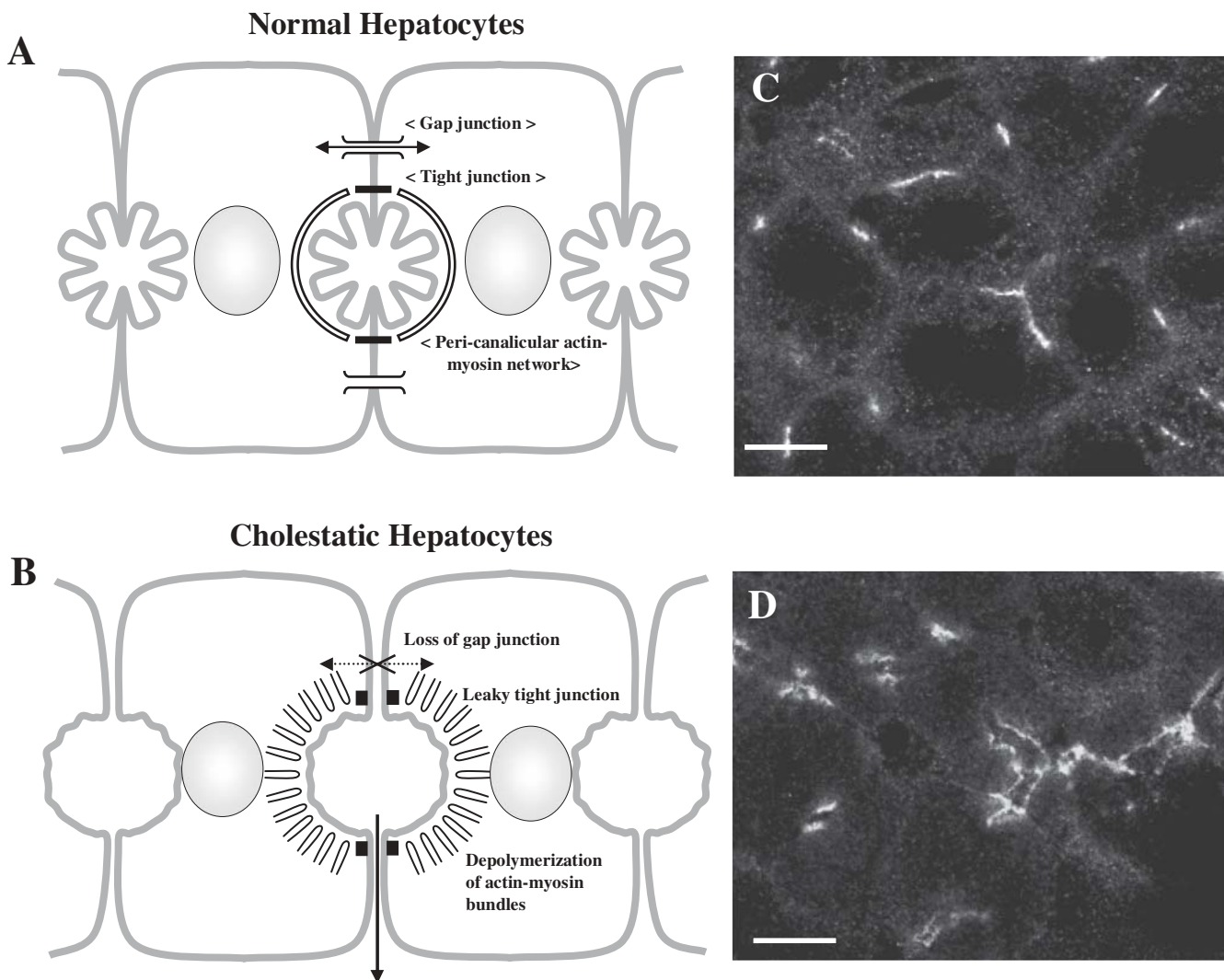


Fig. 1. Changes of gap and tight junctions and cytoskeleton in cholestatic hepatocytes. Normal hepatocytes (**A**) have gap junctions, which facilitate intercellular communication, tight junctions, which seal the canalicular lumen, and a pericanalicular actin-myosin network that facilitates the flow of bile from pericentral to periportal lobular re-

gions. Cholestatic hepatocytes (**B**) show loss of gap junctions, leaky tight junctions, and depolymerization of actin-myosin bundles. **C,D** Fluorescent immunostaining for ZO-1 in normal rat liver (**C**) and common bile duct-ligated rat liver (**D**). At 48 h after common bile duct ligation, dilated bile canaliculi are observed. Bars 10 μ m

acinus, bile flow in hepatocyte canaliculi is thought to require the organized and periodic contraction of bile canaliculi, where cell-to-cell spread of contraction occurs through signaling via gap-junction channels.⁸ In the perfused rat liver, bile secretion induced by glucagon or vasopressin has been shown to be modulated by gap-junction communication.⁹

Gap junctions occupy a large fraction, as much as 3%, of the total surface area of hepatocytes.^{10,11} In freeze-fracture images, gap junctions of liver and hepatocyte cell pairs are recognizable as arrays or plaques of approximately 8- to 9-nm intramembranous particles present in the P-fracture face in vertebrate tissues; complementary pits appear on the E-fracture face. These plaques are generally round or oval and can be quite large in hepatocytes (Fig. 2C), commonly exceeding 1 μ m in diameter and containing more than 10000 particles.

The ultrastructure of tight junctions is quite different from that of gap junctions. In freeze fractures, tight junctions appear as a set of continuous, anastomosing strands in the P-fracture face (Fig. 2B), with complementary grooves in the E-face; in thin section, they appear as very close membrane appositions.^{12,13} The role of tight junctions is to provide a high-resistance barrier to leakage of water and solutes into and from the bile canaliculus (the resistance to current flow has been measured as approximately 50 Kohms by insertion of a microelectrode into the canalicular space¹⁴). The number of tight junctional strands encircling the bile canaliculus is normally high, indicating a tight permeability barrier.¹⁵ As a consequence, the composition of the canalicular fluid can be quite different from that of the other pericellular fluid, allowing the accumulation of high concentrations of preferentially secreted organic anions within this intercellular compartment.^{14,16}

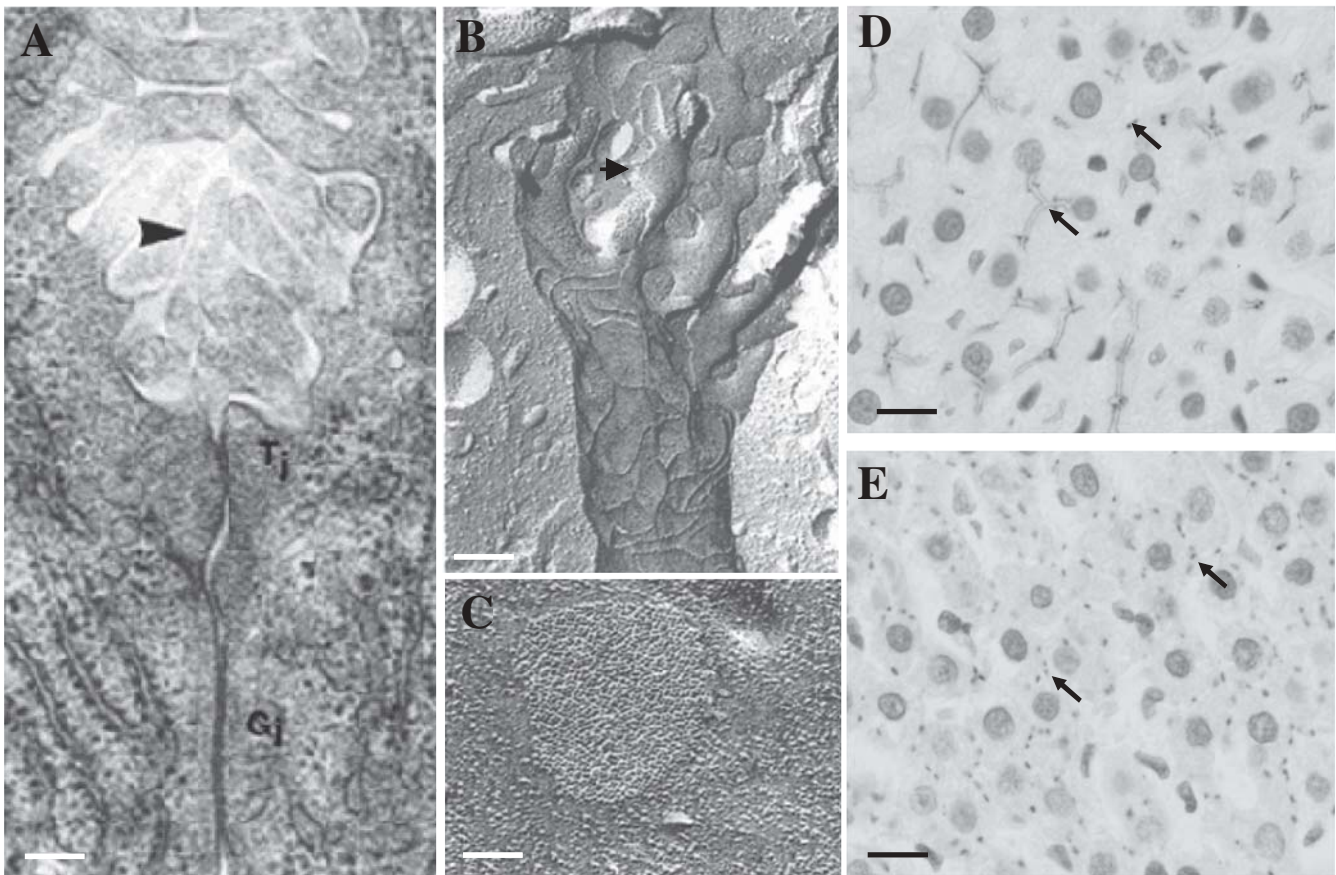


Fig. 2. Fine structure of appositional membranes between rat hepatocytes (**A**, thin section; **B,C**, freeze-fracture; **D,E**, immunostaining of claudin-1 and Cx32 using paraffin sections). **A** Thin-section micrograph illustrates tight junctions (*Tj*) sealing the canaliculus (*arrowhead*) and a large gap junction (*Gj*) below it. **B** Below the bile canaliculi (*arrow-*

head), tight-junction webs seen in this freeze-fracture electron micrograph seal off the canalicular surfaces from the rest of the appositional membrane. **C** Freeze-fracture views show larger gap junctions below and in isolation from tight junctional strands. (From ref. 1, with permission) *Bars A–C* 0.1 nm; *D,E* 20 μ m

Molecular components and regulation of gap and tight junctions

Hepatic gap junctions

Cx32 and Cx26, the components of hepatocyte gap junctions (Fig. 2E), are also found in a variety of other cell types (for review, see ref. 17); moreover, another gap junction protein, Cx43 (or $\alpha 1$), is prominent between other liver cell types, including Ito cells and endothelium. The connexin gene family now comprises at least 20 proteins in vertebrates;¹⁸ connexins are apparently absent in invertebrates, where gap junction channels are formed by a separate gene family encoding innexin proteins.¹⁹

Most cells express more than one type of connexin, leading to the possibility that both homomeric and heteromeric connexons may exist *in vivo*. The existence of heteromeric connexons in the liver has been supported by biochemical experiments that have fractionated detergent-solubilized gap junctions²⁰ and the electrophysiological properties of hepatocytes isolated from Cx32-deficient and wild-type mice.²¹ Experiments examining the movement of ions and

dyes between cells coupled by different connexins have revealed that there are connexin-dependent differences in the permeation of intercellular channels.^{22–24} One striking example of the possible importance to hepatocytes is that homomeric connexons made of Cx32 are permeable to both cAMP and cGMP, whereas heteromeric connexons composed of Cx32 and Cx26 lose permeability to cAMP but not to cGMP.²⁵

Characterization of the genomic sequence corresponding to Cx32 defined a gene structure²⁶ that is now appreciated as being common to almost all other members of the connexin gene family. The Cx32 coding sequence is included within one open reading frame on a single exon, which is separated from a tiny upstream exon (~100 bp) by about 6 kb of an intervening intronic sequence. Promoter mapping in human liver-derived cell line HUH-7 localized a minimal basal promoter within a 70-bp region immediately upstream of the mRNA start sites and DNAase hypersensitive sites 1.2 kb downstream of the Cx32 open reading frame.^{27,28} More recent experiments have identified positive and negative regulatory domains of the Cx32 promoter and nuclear proteins (hepatocyte nuclear factor, HNF-1) that bind to them from experiments performed on MH1C1 rat

hepatoma cells and WB-F344 rat liver epithelial cells.^{29,30} Cx32 expression was significantly decreased in the HNF-1 α -deficient mouse liver.³⁰

Cx26 has the shortest carboxyl tail of all the connexins thus far sequenced and is not phosphorylated.²¹ On the basis of experiments performed in cellfree systems, it has been proposed that Cx26 can insert into membranes post-translationally, whereas Cx32 is believed to insert cotranslationally.³¹ Rapid specific appearance of Cx26 in the plasma membrane after perfusion of the female rat liver without an increase in total protein or mRNA levels was reported.³² Furthermore, brefeldin A, a drug that disrupts the Golgi apparatus, had minimal effects on trafficking of Cx26 to the plasma membrane, in contrast to its disruption of Cx32 trafficking.³³ These findings suggest that the formation of Cx26 homotypic channels on the membranes may follow an alternative nonclassical trafficking pathway bypassing the Golgi system, in contrast to the classical trafficking pathway (ER–IC–Golgi–plasma membrane) followed by Cx32. Cx26 has been proposed to be a tumor suppressor gene, on the basis of subtractive hybridization using normal and malignant human mammary epithelial cells.³⁴ Cx26 expression in human mammary epithelial cells induced by TPA treatment is controlled at the level of transcriptional modification.³⁵ Kiang et al. have cloned and sequenced the 5'-portion of the human Cx26 gene, revealing that the promoter region contains six GC boxes, two GT boxes, a TTAAA box, and a TPA-induced DNase I hypersensitivity region,^{36,37} providing a site by which TPA may exert transcriptional control over Cx26. Nevertheless, induction of exogenous Cx26 in neuroblastoma cells by TPA treatment appears to be controlled by posttranslational mechanisms.³⁸

Hepatic tight junctions

Tight junctions have a complex molecular composition that has only recently begun to be clarified in detail.³⁹ The integral membrane components of tight junctions include occludin, the claudin family, and JAM.

The claudin family at present consists of 20 members and two or more distinct claudins are generally coexpressed in single cells of various tissues;³⁹ for example, claudin-1, -2, and -3 are expressed in the bile canaliculus region of mature hepatocytes (Fig. 2D), while claudin-14 mRNA was detected in the liver.⁴⁰ In the rat liver, claudin-2 shows a lobular gradient increasing from periportal to pericentral hepatocytes, whereas claudin 3 is uniformly expressed.⁴¹ Recent detailed analyses of the manner of interaction of heterogeneous claudin species within and between tight-junction strands suggest that distinct species of claudins are copolymerized linearly to form tight-junction strands as homopolymers or heteropolymers and that the claudins interact between each of the paired strands in a homophilic or heterophilic manner, including both other claudins and/or occludin.⁴² By contrast, only a single occludin transcript has been described, although an alternatively spliced form of occludin (termed occludin 1B) was reported recently.⁴³ As

with the connexins, the major tight-junction components occludin and the claudins are tetraspan proteins with intracellular amino and carboxyl termini. Several cytoplasmic proteins, including ZO-1, ZO-2, ZO-3, 7H6 antigen, cingulin, symplekin, Rab3B, Ras target AF-6, and ASIP, an atypical protein kinase C interacting protein, have been reported to be associated with tight junctions, and some of these are believed to play roles in signal transduction.³⁹ The cytoplasmic domains of occludin and claudins are reported to bind to ZO-1, ZO-2, and ZO-3, forming a macromolecular complex at cell membranes.³⁹ ZO-1, ZO-2, and ZO-3 are members of the membrane-associated guanylate kinase (MAGUK) family of proteins displaying a characteristic multidomain structure composed of SH3, guanylate kinase-like (GUK), and multiple PDZ (PSD95-Dlg-ZO1) domains.³⁹ Although direct involvement of tight junction-associated proteins in the regulation of gene expression has not been still demonstrated, researchers have recently investigated this possibility.^{44–46}

Interaction between gap junctions and tight junctions linked with actin filaments in hepatocytes

Other proteins have been reported to interact with connexin (Table 1). Recently, it has become established that Cx43 interacts with ZO-1 in Cx43 transfectants, in normal fibroblasts, and in cardiac myocytes.^{47,48} This interaction is direct, through binding of the extreme carboxyl terminus of Cx43 and the second PDZ domain of ZO-1.^{47,48} Furthermore, it is well known that small gap-junction plaques are associated with tight-junction strands in some cell types, including hepatocytes (Fig. 3C). In primary cultured rat hepatocytes, Cx32 is partly colocalized with occludin and claudin-1, in which form tight-junction structures (Fig. 3A). To examine the roles of gap junctions in regulating expression and structure of tight junctions, we transfected human Cx32 cDNA into two immortalized mouse hepatocyte lines (CHST8 cells, which lack endogenous Cx32 and Cx26, and Cx32KOH, derived from Cx32-deficient mouse hepatocytes).^{49,50} In Cx32 transfectants, induction of tight-junction strands and the integral tight-junction proteins occludin and claudins were observed, and small gap-junction plaques appeared within the induced tight junction strands. The induced endogenous occludin protein in the transfectants was found to bind to the exogenously expressed Cx32 protein. Furthermore, tight junctional functions, fence, and barrier functions, were increased in Cx32 transfectants.

These results indicate that gap-junction and tight-junction expression are closely correlated in hepatocytes,

Table 1. Other proteins that have been reported to interact with connexins

v-Src and c-Src; Cx43 ^{76–78}
Tubulin; Cx43 ⁷⁹
Caveolin-1; Cx43 ⁸⁰
Zona occludens protein-1 (ZO-1); Cx43, Cx45, Cx31.9 ^{47,48,81–83}
Occludin; Cx26, Cx32 ^{49,50,63,84}

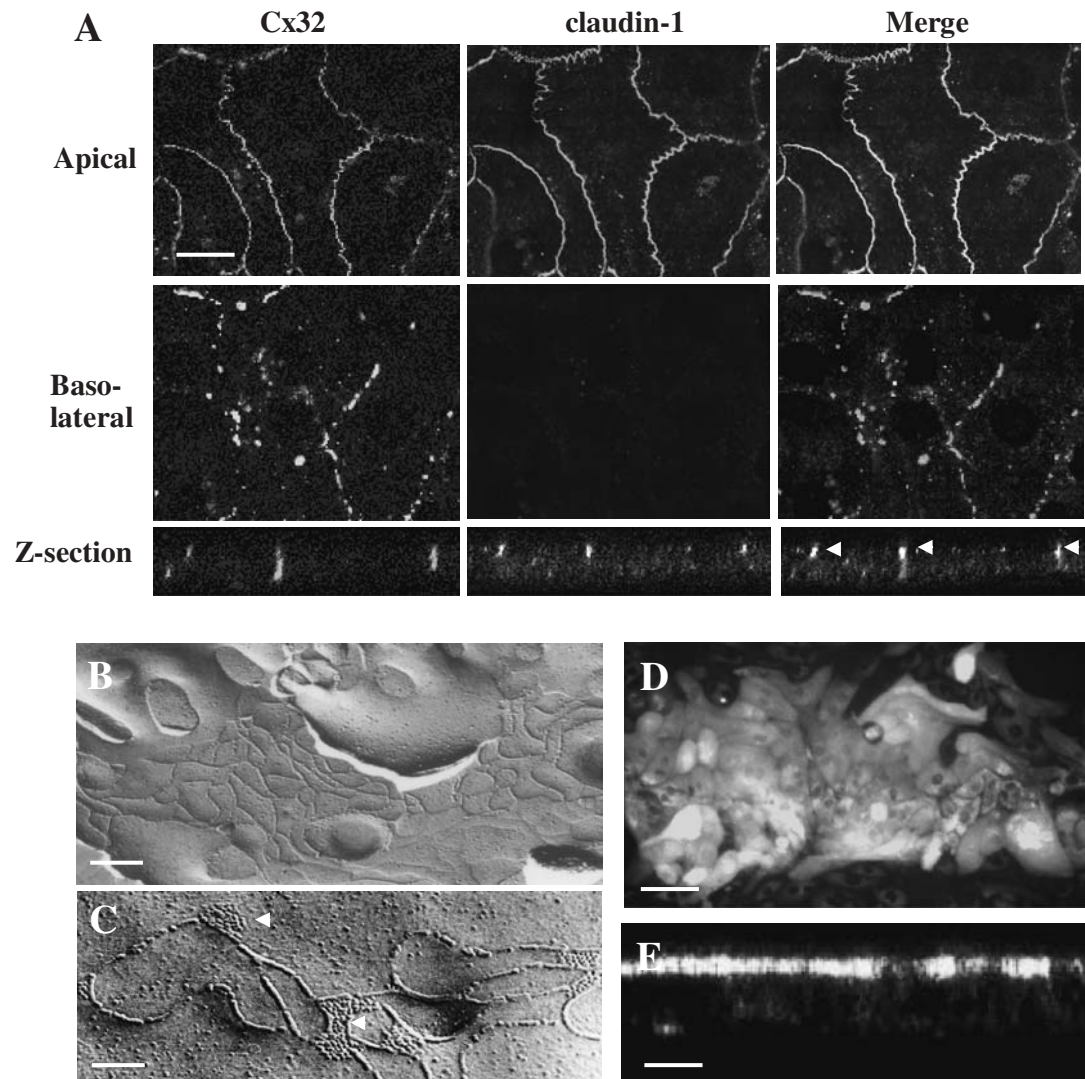


Fig. 3. Interaction between gap junctions and tight junctions in primary cultured rat hepatocytes. **A** Double staining of Cx32 and claudin-1. Cx32-immunoreactive lines are observed on the most subapical plasma membrane at cell borders whereas Cx32-positive spots can be observed on the basolateral membrane. Claudin-1-immunoreactive lines are observed on the most subapical plasma membrane of the cell borders and are colocalized with Cx32-immunoreactive lines (*arrows* in **A**). **B,C** Freeze-fracture. In freeze-fracture analysis of the adluminal

plasma membrane, tight-junction strands form well-developed networks (**B**), and many small gap-junction plaques are observed peripherally or within the tight junction network (*arrowheads* in **C**). **D** Gap junctional intracellular communication (GJIC) using scrape-loading/dye transfer by lucifer yellow. **E** Fence function images of tight junctions. The hepatocytes are labeled with BODIPY-sphingomyelin. The fluorescent probe is effectively retained in the apical domain (**D**). *Bars* **A,E** 10 μm ; **B** 200 nm; **C** 50 nm; **D** 80 μm

and we speculate that through this association gap-junction expression may play a crucial role in the establishment of cell polarity via regulation of tight-junction proteins. This finding supports previous studies in which gap junctions have been associated with other intercellular junctional components. More importantly, however, the present demonstration of a direct linkage between occludin and Cx32 and previous studies showing high-affinity interactions between ZO-1 and Cx43^{47,48} indicate that connexins may form selective associations with specific components of adherens or tight junctions. We have proposed that, through binding of these proteins to cytoskeletal, adhesion, and signaling proteins, different connexins may promote the aggregation of connexin-specific scaffolds at junctional regions, provid-

ing not only intercellular signaling but also sites where intracellular signaling is transduced.⁵¹ Interestingly, in the liver in HNF-1 α -deficient mice, not only a decrease of Cx32 expression but also lack of expression of claudin-2 mRNA and protein was observed, whereas claudin-1 mRNA expression was unaffected.⁴⁵

Using electron microscopy, actin filaments have been localized near the cytoplasmic side of tight junctions, and some integral or peripheral tight-junction proteins that bind to actin filaments have been seen.^{39,52,53} ZO-1 and ZO-2 also bind to actin filaments,⁵³ suggesting a role of tight junctions in the organization of the actin cytoskeleton. Gap junctions are also associated with actin filaments. More recently, forced expression of connexins was found to be accompa-

nied by a profound reorganization of the actin and myosin cytoskeleton in Cx32-transfected C6 glioma cells.⁵⁴ Gap junctions assemble in the presence of cytoskeletal inhibitors, but enhanced assembly requires microtubules.⁵⁵ Primary cultured hepatocytes from Cx32-deficient mice showed the intensity of actin stress fibers.⁵⁶ In the Cx32 transfectants in which the human Cx32 gene was transfected to a mouse hepatocytic cell line derived from Cx32-deficient primary mouse hepatocytes, circumferential actin filaments were increased without a change of actin protein.⁵⁰ These results suggest that a novel linkage may exist between gap junctions and cellular morphology via organization of the actin cytoskeleton in hepatocytes.

Gap and tight junctions in primary cultures of rat hepatocytes

Cx32 reexpression in primary cultured rat hepatocytes is dramatically enhanced in medium containing epidermal growth factor (EGF) and 2% dimethylsulfoxide (DMSO),⁵⁷ and Cx26 can also be induced when glucagon is added together with 2% DMSO.^{58,59} Primary rat hepatocytes cultured with DMSO/glucagon have extensive gap junctional intercellular communication (GJIC), as measured using scrape-loading/dye transfer by lucifer yellow (Fig. 3D), and Cx32- but not Cx26-immunoreactive lines are observed on the most subapical plasma membrane at cell borders (Fig. 3A), while on the basolateral membrane both Cx32- and Cx26-positive spots are colocalized. These latter studies suggest that expression of gap junctions in hepatocytes may be closely related to oxidative stress and that oxygen radical scavengers such as DMSO or melatonin might be important inducing substances.^{60,61} During stimulation and reinhibition of DNA synthesis, differential changes of expression and function of Cx32 and Cx26 were observed.⁶²

In freeze-fracture analysis of primary rat hepatocytes cultured with DMSO/glucagon, tight-junction strands formed well-developed networks, and many gap-junction plaques were observed within the strand network (Fig. 3B,C). Occludin, claudin-1-, ZO-1-, and ZO-2-immunoreactive lines were strongly observed on the most subapical plasma membrane of the cell borders and were colocalized with Cx32-immunoreactive lines (Fig. 3A). Cx32 protein in hepatocytes may bind to tight-junction proteins, occludin, claudin-1, and ZO-1.⁶³ The fence function of tight junctions in the cells, as examined by diffusion of labeled sphingomyelin, was well maintained (Fig. 3E). In a more recent study, treatment with GJIC blockers, 18 β GA and oleamide, inhibited expression of occludin mRNA and protein in hepatocytes. Furthermore, changes of tight-junction strands and occludin expression are observed during DNA synthesis in cultured hepatocytes.^{62,64} Because tight junctions in these differentiated cultured hepatocytes assume the distribution seen in simple polarized epithelial cells, this culture system may provide a useful model in which to study hepatocyte tight junctions.

In primary rat hepatocytes cultured with DMSO/glucagon, circumferential actin filaments were also observed near the tight-junction regions.^{59,65} Treatment of the cells with the actin depolymerizing drug mycalolide B caused the disappearance of both the circumferential actin filaments and occludin, whereas tight-junction strands remained virtually intact, leading to the hypothesis that occludin, but not other transmembrane proteins, plays a role in the linkage between the actin cytoskeleton and tight junctions in hepatocytes.⁶⁶

Perspectives

The signal transduction pathways, activation of mitogen-activated protein (MAP)-kinase and the phosphoinositol 3-kinase (PI3-kinase) signaling cascade, regulate a variety of cellular processes including proliferation, differentiation, and transformation.⁶⁷ A role of gap and tight junctions in inter- or intracellular signaling has been proposed. To elucidate the mechanisms of signal transmission required for the regulation of the gap and tight junctions, researchers have recently examined the effects of signaling pathways such as MAP kinase and PI3 kinase on the regulation of gap and tight junctions.⁶⁸⁻⁷⁴ Our recent experiments indicated that treatment with growth factors [EGF and transforming growth factor-beta (TGF- β)] or proinflammatory cytokine (IL-1 β) may induce downregulation of Cx32 and claudin-1 or upregulation of claudin-2 in primary rat hepatocytes via signaling pathways such as MAP kinase, p38 MAP kinase, and PI3 kinase. It is possible that loss of gap junctions and leaky tight junctions in cholestatic hepatocytes may be caused by various growth factors and proinflammatory cytokines through the signaling pathways.

Although gap and tight junctions perform very different functions, there are numerous points at which functions overlap. Indeed, the findings that the traditionally tight junction-associated protein ZO-1 also binds to a connexin, and that occludin is colocalized with Cx32 in transfectants, indicate the possibility for either coordinate or reciprocal regulation of macromolecular complexes containing gap- and tight-junction proteins. Studies of protein-protein interactions and of coordinate and subordinate regulation of gene families are expected to soon disclose the intricacies of inter- and intracellular signaling and growth control at gap junctions and the regulatory mechanisms of the blood-biliary barrier formed by tight junctions.⁷⁵

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