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A NEW MODEL OF OCCLUDIN REGULATION OF TIGHT-JUNCTIONAL RESISTANCE IN LOW-RESISTANCE EPITHELIA

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ABSTRACT. OCCLUDIN IS A TRANSMEMBRANE tight junctional protein whose importance in gating the intercellular space was recently documented in the low-resistance cultured human vaginal and cervical epithelia. Decreases in tight-junctional resistance (R_{TJ}) were associated with occludin degradation, compatible with disassembly of the tight junctions. However, acute and reversible changes in R_{TJ} could also be induced through modulation of assembled tight junctions. Thus, lowering extracellular Ca^{2+} (Ca_0) induced an acute and reversible decrease in R_{TJ} . The present paper presents a novel hypothesis to explain Ca_0 modulation of the R_{TJ} . Accordingly, the functional components of occludin that gate the intercellular space are occludin extracellular loops. The amino acid sequence of human occludin predicts a unique composition of the extracellular loops. Tethered within the proximal parts of the loops are sequences resembling EF-hand – like Ca^{2+} -binding sites. In contrast the distal parts of the loops are protein stretches enriched with hydrophobic amino acids including glycine-rich sequences that are typical to proteins that can readily fold. Also, occludin first and third transmembrane domains from which the loops stem predict α -helices that could anchor the EF-hands into the plasma membrane, and orient the Ca^{2+} -binding domains outwards into the extracellular space. The hypothesis predicts that binding of Ca^{2+} to the EF-hand – like domains will induce inward folding of the EF-hands, along with envelopment of the Ca^{2+} -pockets by the hydrophobic distal parts of the loops. Exteriorization of hydrophobic domains of occludin extracellular loops will lead to formation of hydrophobic bridges between neighboring cells that effectively occlude the intercellular space.

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1. INTRODUCTION

Tight junctions are specialized type of intercellular connections whose main biological role is to restrict the free movement (transport) of water and solutes through the epithelial intercellular (paracellular) route. In addition to controlling transepithelial transport, tight junctions also control lateral migration and sorting of plasma membrane proteins [1], and play a role in regulation of development [2-4] and aging [5,6], water and solutes metabolism [7], and control of inflammation [8-12] infections [13-15] vascular disease [16] organ failure [17,18] and cancer development [19]. Despite their important biological roles, relatively little is known about the mechanisms of operation and regulation of tight junctions. The present paper presents a novel model of tight-junction regulation, based in part on recent discoveries of hormone regulation of tight junctional resistance and expression of tight junctional proteins, and on structure analysis of extracellular loops of the tight junctional protein occludin.

2. BACKGROUND

Tight junctions are part of the apical junctional complex [20] and are composed of tight junction proteins that encircle the epithelial cells in a belt-like manner. Tight junction proteins are composed of cytoplasmic and transmembrane proteins [21]. Cytoplasmic tight-junction proteins couple the transmembrane tight-junctional proteins to the cortical actin and mediate signal-dependent modifications of tight junctional resistance (R_{TJ}) [21]. Transmembrane tight-junctional proteins, including the junctional-adherence molecules (JAMs, present mainly in endothelial cells, see ref. [22,23]), claudins [24-29], and occludins [30,31], are thought to represent linear polymers of transmembrane proteins with extracellular stretches. These associate laterally with tight-junction strands in the apposing membrane of adjacent cells to "seal" the intercellular space.

An important contribution to the understanding of tight junction function were studies using cultures of normal human ectocervical-vaginal

epithelial cells (hEVEC) on filters. hEVEC is an established experimental system that models the human female lower reproductive tract epithelia [32]. The latter control secretion of fluid into the lumen, which is important for woman's health and human reproduction. The hEVEC system was used by the author [33-75] and by others [76-85] for studies related to the regulation of the R_{TJ} , and to fit experimental results into mathematical models [42,44-46]. hEVEC form a relatively leaky epithelium where the tight junctional resistance (R_{TJ}) contributes only 75-95% to the total paracellular resistance [45], compared to >99% in other, tighter epithelia [86]. This allows to probe the R_{TJ} and to determine accurately even small changes in the resistance. An added advantage of the hEVEC system for studies of R_{TJ} regulation is the fact that hEVEC cells are estrogen responsive, and estrogen status can affect significantly the R_{TJ} [54-62,65]. The results in hEVEC (described below) were confirmed in other types of low-resistance, "leaky" types of epithelia, including CaSki and HT3 [38].

3. ACUTE MODULATION OF THE R_{TJ}

In hEVEC CaSki and HT3 cells, ATP, added at micromolar concentrations (EC_{50} of 3-7 μ M) triggers activation of $P2X_4$ receptors and stimulates calcium influx, followed by release of diacylglycerol (DAG) and activation of protein kinase-C (PKC) [37,38,40-42,44-47,50-53,63,64]. One of the consequences of DAG-dependent activation of PKC in those cells is acute threonine dephosphorylation of the 65 kDa (full-length) isoform of occludin [74]. Since hEVEC and CaSki cells (like other epithelial cells) do not express the JAMs, and since DAG-dependent activation of PKC had no significant effect on claudins [74], it was suggested that the ATP-induced acute increase in R_{TJ} was mediated by $P2X_4$ -related PKC-dependent threonine dephosphorylation of occludin followed by acute conformational changes of occludin that increased gating of the intercellular space [74]. These results refute the previously held opinion that once assembled, the tight junctions form a solid unmodifiable fence-like structure. Instead, the

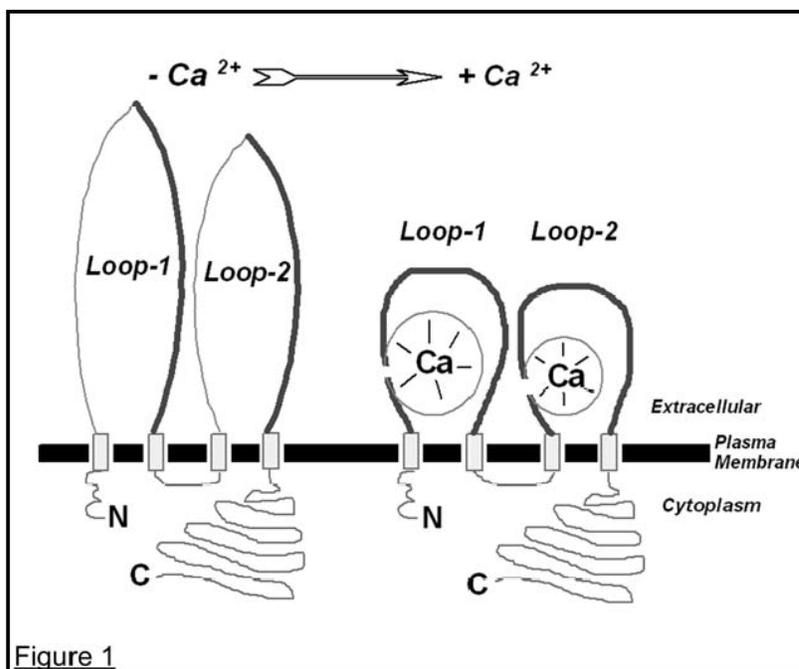


FIGURE 1. PREDICTED STRUCTURE OF OCCLUDIN, AND SCHEMATIC REPRESENTATION OF THE NEW MODEL OF OCCLUDIN REGULATION OF TIGHT-JUNCTION FUNCTION. Occludin is a tetraspan transmembrane protein composed of a short cytoplasmic N-terminus, two extracellular loops (designated Loop 1 and Loop 2), four transmembrane stretches, a short cytoplasmic interconnecting segment, and a long cytoplasmic C-terminus. Each of the two extracellular loops can be described in terms of a proximal EF-hand Ca^{2+} -binding domain (narrow lines) and a distal hydrophobic α -helix and “residual-loop segment” (thick lines). In the absence of Ca^{2+} the extracellular loops are maintained in a relaxed state. In the presence of Ca^{2+} , the Ca^{2+} -binding domains transform into calcium-pockets that pack as a core, and cause the hydrophobic distal α -helices and “residual-loop segments” to swing outwardly and face the extracellular space. Therefore, each of the occludin extracellular loops can flicker between a hydrophilic surface (no- Ca^{2+}), and a hydrophobic surface (Ca^{2+} -bound). In the Ca^{2+} -bound state, hydrophobic surfaces of extracellular loops of neighboring molecules attach and gate the intercellular space to the free movement of hydrophilic molecules.

results indicate signaling-mediated acute and reversible increase in R_{TJ} of assembled tight junctions.

4. OCCLUDIN AND THE R_{TJ}

Studies in hVEC and CaSki cells also highlighted the role of occludin in controlling the R_{TJ} . Human occludin type-I is a 65 kDa protein with an apparent 65 amino acid cytosolic N terminus, two extracellular loops of 56 and 48 amino acids separated by an 11 amino acid cytosolic loop; four transmembrane stretches of 11–24 amino acids; and a C-terminal tail of 256 amino acids that interacts with the cytoplasmic tight-junction proteins (FIG. 1) [25,31]. Both the N- and C-terminus domains have phosphorylation sites

and the functionally active form of the protein localizing to the tight junction is phosphorylated at serine and threonine residues [21,31] (FIG. 1).

The previously held role of occludin as tight junctional protein became unclear following publications that in some types of cells occludin is not sufficient to form an effective barrier, and other proteins, notably the claudins, are required for optimal occlusion of the paracellular space. For instance, embryonic stem cells lacking occludin maintain a partial permeability barrier [87]; and transfection experiments in mouse fibroblasts have shown that occludin alone forms only partial junctional fibrils [88]. However, many other studies indicated that occludin is a necessary component of the junctional fibrils, and that occludin plays an important role in the gating of tight junctions

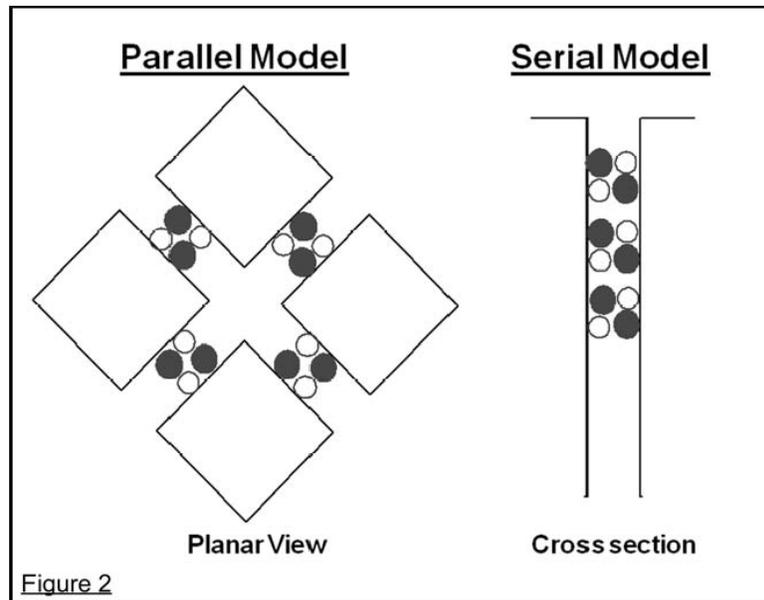


FIGURE 2. SCHEMATIC REPRESENTATION OF THE COOPERATIVE PARALLEL (LEFT) AND SERIAL (RIGHT) MODELS OF TIGHT-JUNCTION ELEMENTS BASED ON Ca^{2+} -DEPENDENT CHANGES IN R_{TJ} IN hEVEC AND CaSKI CELLS. Squares are cells; circles are ocludin extracellular loops (loop-1 depicted as filled circle, loop-2 as empty circle). The parallel model shows a planar view of four cells sectioned at the level of the tight junctions where each cell attaches to its neighbor via the Ca^{2+} -activated ocludin extracellular loops 1 and 2. The parallel model predicts low density of resistive elements that reside at one planar level. Since low density of strands is associated with low R_{TJ} , the cooperative parallel model describes best low resistance epithelia, such as the hEVEC and CaSki. The serial model shows a cross section through two neighboring cells, where the tight junctions are composed of multiple rows of resistive elements that reside serially within the intercellular space. The cooperative serial model describes best high resistance epithelia.

(reviewed in ref. [21]). Thus, depletion of ocludin, or transfections of cells with truncated or mutated forms of ocludin resulted in aberrant formation of tight junctions, with marked decrease in the number of tight-junction strands and abrogation of the paracellular resistance [89,90]. Other studies showed that transfection of ocludin into fibroblasts, which lack endogenous expression of the protein, induces cell-cell adhesiveness [91,92]. Overexpression of ocludin in Madin-Darby canine kidney cells resulted in hyperaggregation of globular, hydrophobic, electronmicroscopy-dense particles in regions of the tight junctions, and increased the paracellular resistance [93-95]. Furthermore, treatment of cells with peptides to ocludin's extracellular loop 2, but not loop 1, decreased paracellular resistance [95,96] by a mechanism that involved reducing the amount of ocludin at the tight junction [96].

In hEVEC and CaSki epithelia, ocludin was found to play a significant role in gating the tight junctions. In hEVEC and CaSki cells ocludin is present in two main forms: the full-length 65 kDa isoform, and a truncated 50 kDa form [66,74]. Treatment with physiological concentrations of the natural estrogen 17β -estradiol modulated expression of both ocludin isoforms: at low concentrations estrogen enhanced synthesis of the 65 kDa isoform, while at higher concentrations, still within the physiological range for the woman, estrogen augmented turnover of the 65 kDa isoform and up-regulation of the 50 kDa isoform. Since estrogen also decreased the R_{TJ} , and because the decreases in R_{TJ} correlated in time with the increase in the 50 kDa ocludin form and both effects could be blocked with tamoxifen, it was suggested that estrogen-abrogation of the R_{TJ} involves ocludin modulation into the 50 kDa isoform [66].

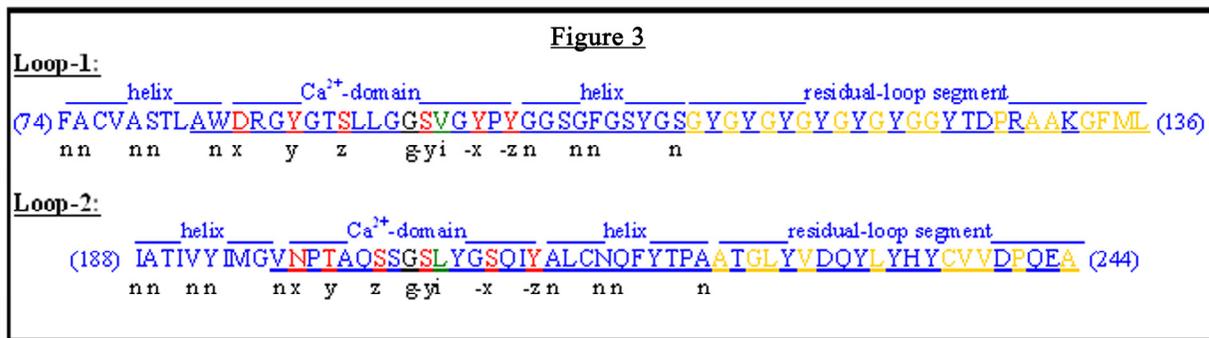


FIGURE 3. PROTEIN STRUCTURE OF HUMAN OCCLUDIN TYPE-1 EXTRACELLULAR LOOPS 1 AND 2 (UNDERLINED) BASED ON THE PREDICTED AMINO ACIDS SEQUENCE OF THE PROTEIN. "n" denotes a hydrophobic amino acid in the α -helix loops, proximal (left) and distal (right) to the Ca²⁺-binding domains. The amino acids that coordinate binding of the Ca²⁺ ion are designated x, y, z, -y, -x, and -z, and are shown in red. The glycine (G, shown in black) and the valine (V) and leucine (L) shown in green in the middle of the Ca²⁺-domain are the "signature" residues (G-x-I/L/V) present in most identified EF-hands.

Moreover, based on the comparative analysis of estrogen effects versus effects of extracellular proteases on occludin expression vis-à-vis changes in R_{TJ} [66] it was recently suggested that the effect of estrogen involves cleavage of occludin near the middle of the extracellular loop 2 [66,74]. This would result in the expression of a defective 50 kDa occludin isoform, and would lead to abrogation of the R_{TJ} by decreasing the availability of intact extracellular loops (FIG. 1). These data can be interpreted in terms of abrogation of the R_{TJ} secondary to disassembly of the tight junctions. Accordingly, estrogen modulation of occludin's extracellular loop 2 leads to abrogation of intercellular occludin-occludin or occludin-claudin connections and results in a decrease in R_{TJ} .

5. EXTRACELLULAR CALCIUM AND THE R_{TJ}

Experiments in hVEEC and CaSki cells also highlighted the role of extracellular calcium (Ca_0) in regulation of the R_{TJ} . We [44,46,51] and others [97-108] have described the dependence of R_{TJ} on Ca^{2+} . Other investigators looked at the effects of calcium on paracellular resistance within hours after lowering extracellular calcium, or after shifting cells back to normal calcium. Studies by others described the "calciumswitch", whereby lowering extracellular calcium abrogates the paracellular resistance, and shifting cells back to

normal calcium restores the resistance [97-108]. The studies provided important information about modulation of paracellular resistance secondary to changes in cytosolic calcium, modulation of the cytoskeleton and adherence junctions, affecting the paracellular resistance secondary to changes in cell configuration and intercellular adherence, and metabolic effects of calcium that affect synthesis, folding and insertion of tight-junctional proteins into the plasma membrane [100,102,103,109-111]. However, the results of these studies cannot be explained in terms of direct modulation of tight junctional proteins by calcium, at extracellular domains.

In contrast to studies by others, our published data can be interpreted as direct regulation by calcium of tight-junctional resistance [44,46,51]:

- a. Lowering Ca_0 decreased R_{TJ} acutely ($t_{1/2}$ of 2.5 and τ of 4.9 min), and reversibly;
- b. The effect was dose-dependent and saturable, with EC_{50} - Ca_0 of 0.3 mM;
- c. The effects of Ca_0 on R_{TJ} were not associated with changes in intracellular calcium;
- d. Lowering Ca_0 had no effect on occludin mRNA or protein levels, or on cellular distribution of occludin;
- e. Within the time-frame of calcium effects on R_{TJ} , lowering Ca_0 had no effect on the tight-junction proteins claudin 4 and ZO-1, or on the

adherence protein E-Cadherin [44,46,51];

f. Among tested bi-tri-valent cations (Ba^{2+} , Cd^{2+} , Co^{2+} , La^{3+} , Mg^{2+} , Mn^{2+} , Sr^{2+} , Zn^{2+}), only Mn^{2+} was found to have partial agonist characteristics of Ca_0 , and it could restore R_{TJ} to near baseline levels [51]. The short time-course of the effects of Ca_0 on R_{TJ} and the reversibility of the effects ruled out modulation of protein synthesis or assembly of tight-junctional proteins as candidates for calcium action [100]. The likely interpretation of our results is that Ca^{2+} interacts with tight-junctional protein(s) directly, at extracellular sites, and induces conformational change that increases gating of the junction.

6. TIGHT-JUNCTION ELEMENTS (UNITS)

Earlier electronmicroscopy freeze-fracture studies showed that the regions of the tight junction which occlude the intercellular space are areas where plasma membranes of neighboring cells come into direct contact. At those sites the tight junctions appear as continuous anastomosing intramembranous strands on the P face, with complementary grooves on the E face [112-120]. The intramembranous particles extend to the extracellular space and form long branching fibrils circumscribing the cell. These areas were functionally interpreted as tight-junction elements (or units). Based on the information presented above, the tight-junction elements are thought to represent linear polymers of transmembrane proteins with extracellular stretches, e.g., occludins and claudins that associate laterally with tight-junction strands in the apposing membrane of adjacent cells to form 'paired' tight-junction strands, and to "seal" the intercellular space. The prevailing theory of gating of the intercellular space is that of homotypic contact across the intercellular spaces between extracellular loops of one type of protein from neighboring adjacent cells, or of heterotypic contact between occludin-claudin extracellular loops [21]. It was suggested that the extracellular loops either form hydrophobic intercellular bridges [21] or isoelectrical domains [121] that gate the intercellular space and effectively block the free movement of water and

ions. The specific role of occludin in such a model was supported by studies showing that the addition in the extracellular fluid of peptides analogous to occludin extracellular loops decreased paracellular resistance [96,122,123]. However the role of occludin vis-à-vis the claudins remains unclear.

Tight-junction elements are modeled as pores that flicker between open and closed states [86], such that each small segment can be at one of two states, sealed (rclosed) or open (ropen). According to this model, the net junctional permeability depends on the density of the pores, and on the probability of the open state of the pore. This model predicted that it may be possible to regulate the junctional permeability by modulating the number of the pores, or by modulating the probability of the open state of the pore [46]. The former mode of regulation will most often require protein synthesis and a longer time for expression, while the latter mode of regulation may involve conformational change of existing tight junction proteins, and require seconds to minutes for expression.

The experimental results in the low-resistance hVEEC and CaSki cells have been previously analyzed in terms of functional calcium-regulation of tight-junctional resistance [46]. Accordingly, each tight-junctional element with a microscopic resistance r_i contributes to the macroscopic transepithelial resistance such that $R_{\text{Total}} \approx \sum r_i$ [46]. This functional model is shown in FIG. 2 and it predicts two Ca^{2+} -binding sites per tight-junction element, where binding of Ca^{2+} in one site is independent of the other. Our previous analyses did not support a non-cooperative bimodal model, which predicts that calcium interacts with junctional elements by binding to single sites, and changes the open/closed probabilities of the junctional elements [46]. Our analyses also did not support a cooperative serial model (FIG. 2, RIGHT PANEL) where the resistive elements reside serially within the intercellular space, and which best describes high resistive epithelia [86]. In contrast, the Ca^{2+} -dependent changes in R_{TJ} in hVEEC and CaSki cells could be best described in terms of a cooperative parallel model (FIG. 2, LEFT PANEL). Accordingly, the macroscopic permeability of the

epithelium is determined by the cooperative opening or closing of the complete set of cell-associated resistive elements where these sets are arranged in parallel. FIG. 2 (LEFT PANEL) describes such a model: it shows a planar view of 4 cells sectioned at the level of the tight junctions, where each cell attaches to its neighbor via two Ca^{2+} -activated occludin extracellular loops. The parallel model predicts low density of resistive elements that reside at one planar level. Since low density of strands is associated with low R_{TJ} [86], the cooperative parallel model describes best low-resistance epithelia, such as hEVEC and CaSki.

At present it is generally accepted that the tight-junction “elements”, identified morphologically as “strands” and functionally as intercellular resistive elements, are extracellular loops of transmembrane tight junctional proteins [21,121]. Therefore, one mechanism of R_{TJ} control could be the regulation of assembly/disassembly of the junctions, by determining changes in the density of the tight-junction elements (pores). This mechanism has been well described [21,121]. An additional, previously less well understood mechanism of R_{TJ} control was recently suggested by our results [44,46,47,51,66], whereby extracellular loops of assembled transmembrane tight junctional proteins undergo conformational change and flicker between an open, low resistance high permeability state, and a closed, high resistance low permeability state. This mechanism predicts R_{TJ} regulation of assembled tight junctions unrelated to changes in the density of extracellular loops of transmembrane tight junctional proteins between neighboring cells.

At present, little is known about the molecular mechanism by which extracellular loops of transmembrane tight junctional proteins of assembled tight junctions “seal” the intercellular space. The model below presents our novel hypothesis that combines the functional morphologic and biochemical data into a composite mechanism of action. The model focuses on the role of occludins, which based on our previous studies appear to be involved with regulation of the R_{TJ} of assembled tight junctions. This is in contrast to claudins which appear to be involved with

regulation of the R_{TJ} through the assembly of tight junctions. Ca_0 effects in low-resistance and high-resistance epithelia

The $\text{EC}_{50}\text{-Ca}_0$ levels for changes in R_{TJ} in the low-resistance hEVEC and CaSki cells were about 300 μM [46] compared to 50–100 μM in high-resistance epithelia [100,103]. Three main explanations were offered for this discrepancy:

a. In high-resistance epithelia Ca_0 modulation of R_{TJ} is mediated through changes in cytosolic calcium, which are sensitive to even small changes in Ca_0 ;

b. The direct calcium-related effects on the open/closed probability of the tight-junctional elements may depend on the density of the junctional elements (n) and/or the number of calcium binding sites (m). Epithelia with a higher density (higher n) have a higher resistance than epithelia with fewer tight-junctional elements [86]. The experimental data in hEVEC and CaSki cells yielded Hill coefficient m of about 2. These data suggest that calcium binds to 2 sites at each functional unit of the tight junctions, and that binding at one site affects binding of calcium at the other site. The analysis also predicts that in a given epithelium the magnitude of m should correlate with the degree of transepithelial resistance, and that the concentration of calcium required to modulate junctional resistance will correlate reciprocally with m , due to the cooperativity of the effect. The latter prediction is supported by the low m (~ 2) and low RTE ($10\text{--}50 \Omega \times \text{cm}^2$) across hEVEC and CaSki cultures [46], versus a high m (4–10), and a high RTE ($6,000 \Omega \times \text{cm}^2$) in high-resistance epithelia such as cultured A6 cells [103];

c. According to the cooperative model [46], increasing n and/or m may decrease the experimental (macro) $\text{EC}_{50}\text{-Ca}_0$ even if the binding affinity of calcium at the molecular level is high. Lowering Ca_0 may not be an effective means to alter the intercellular calcium milieu in tight epithelia. It is therefore possible that the low extracellular calcium required to cause changes in electrical resistance across tight epithelia [100,103] does not reflect the actual calcium concentration in the intercellular space.

7. NEW MODEL: OCCLUDIN REGULATION OF TIGHT-JUNCTION FUNCTION

The author's new hypothesis of occludin regulation of tight-junction function builds on findings in hEVEC and CaSki cells that extracellular loops of the full-length 65 kDa occludin are required for maximal gating of the intercellular space [66,74], and that in these epithelia Cao directly controls the R_{TJ} [44,46,51].

Calcium-binding proteins are composed of one to four repeats of homologous segments, termed "EF hands" (for the Ca^{2+} -binding site between the E and F helices of parvalbumin, [124]). Each EF-hand consists of a α -helix, a Ca^{2+} -binding loop, and a second α -helix [125,126]. Upon activation by Ca^{2+} , the Ca^{2+} -bound – Ca^{2+} -binding protein attaches to target proteins and modulates their activity. The binding affinity of Ca^{2+} to the Ca^{2+} -binding protein is about 10 μ M [127]. The binding affinities of activated Ca^{2+} -binding proteins to target proteins varies between 1 nM to 500 μ M [128], depending on the structural properties of the interaction, and on the surface shared between the two proteins. Binding of calcium may require a full complement of four EF-hands per Ca^{2+} -binding protein [125], but it can also be effectively accomplished with one or two EF-hands [124,126,128-131]. When not bound to Ca^{2+} , EF-hands form structures with a hydrophobic core and a hydrophilic surface [Rev. in 126,128]. Binding of Ca^{2+} induces conformational change [132] so that the hydrophobic residues swing out to form globular structures with a core containing the Ca^{2+} -pocket, and a hydrophobic shell [126]. The direct approximation of the hydrophobic surface of the Ca^{2+} -binding protein with the hydrophobic surface of the target protein leads to binding and/or activation of the target protein (reviewed in ref. [126,128]). In the Ca^{2+} -binding loop one calcium cation binds to six negatively charged amino acids containing either carbonyl oxygen (aspartate, asparagine, glutamate or glutamine), or negatively charged hydroxyl (serine, threonine or tyrosine). The negatively charged amino acids are spaced by 1 to 3 amino acids, and binding of calcium draws radially the amino acids to form a "calciumpocket"

[125,126,128].

The author proposes that extracellular loops of occludin form EF-hand – like Ca^{2+} -binding sites. Based on the published predicted amino acids sequence of human occludin [31], the author has identified amino acid sequences tethered in occludin extracellular loops-1 and -2, that resemble typical EF-hands similar to those previously described in other Ca^{2+} -binding proteins [125,126,128] (FIG. 3). The underlined amino acids in FIG. 3 show the sequences of occludin extracellular loops 1 and 2. Amino-acids numbers in the cartoon are based on published sequence of type-I Human Occludin [31]. The consensus EF-hands are identified by the Tufty-Kretsinger scoring method [133] as indicated below the alignment, where "n" denotes a hydrophobic amino acid in the α -helix loops, proximal (left) and distal (right) to the Ca^{2+} -binding domains. The amino acids that coordinate binding of the Ca^{2+} ion are designated x, y, z, -y, -x, and -z, and are shown in red. The glycine (G, shown in black) and the valine (V) and leucine (L) shown in green in the middle of the Ca^{2+} -domain are the "signature" residues (G-x-I/L/V) present in >95% of identified EF-hands [134,135]. The proposed Ca^{2+} -binding domains in occludin extracellular loops fulfill the criteria of a core of G-x-I/L/V flanked by six negatively charged amino acids containing carbonyl oxygens or negatively charged hydroxyl groups that can bind calcium [125]. Members of the EF-hand superfamily of proteins can display significant variability in their molecular structure [128,136-138], but the core of G-x-I/L/V flanked by six negatively charged amino acids, as predicted in occludin extracellular loops (FIG. 3), is required for binding of Ca^{2+} [128]. The six negatively charged amino acids are spaced by 1 to 3 amino acids, and therefore can form "calcium-pockets" [125]. The proposed α -helix loops fulfill the criteria of amino acids composition, length (8–12 amino acids), proximity, and hydrophobicity [128]. The EF-hand can be flanked proximally by glutamate (E), or any hydrophobic amino acid [126,128].

Based on the analysis in FIG. 3, the author proposes that occludin is a Ca^{2+} -binding protein containing an EF-hand in each of the extracellular

loops. In the absence of Ca^{2+} the loops are maintained in a relaxed (dormant) state (FIG. 1, LEFT PANEL). In the presence of Ca^{2+} , the Ca^{2+} -binding domains transform into calcium-pockets that pack as a core (FIG. 1, right panel), and cause the dormant hydrophobic distal α -helices and “residual-loop segments” to swing outwardly and face the extracellular space (FIG. 1). This allows extracellular loops of occludin projecting off adjacent neighboring cells to interact and form hydrophobic intercellular bridges that effectively seal the intercellular space to the free movement of water and solutes. Consequently, each of occludin extracellular loops can flicker between a hydrophilic surface (no- Ca^{2+}), and a hydrophobic surface (Ca^{2+} -bound).

The above novel hypothesis is supported by the finding that overexpression of occludin results in the formation of hydrophobic fibro-globular structures at extracellular regions of the tight junctions [93-95]. This formation will allow approximation of occludin extracellular loops of adjacent cells [139], and an increase in cell-cell adhesiveness [140,141]. It will subsequently impede the free movement of water, water-soluble molecules and ions in the intercellular space, and thereby result in an increase in the R_{TJ} .

The data in FIG. 3 show a striking similarity in the predicted structure of the EF-hands in the first and second extracellular loops of occludin: occludin first and third transmembrane domains from which the loops stem can be described in terms of α -helices, thereby anchoring the more distal EF-hands into the plasma membrane, and orienting the Ca^{2+} -binding domains outwards into the extracellular space. The Ca^{2+} -binding domains in both loops are of similar lengths (17 and 16 amino acids, respectively), and are continuous with distal α -helices and “residual-loop segments”. FIG. 3 also shows that the “residual-loop segments” of the distal halves of the loops are protein stretches enriched with hydrophobic amino acids. Moreover, the “residual-loop segment” of loop-1 contains the unusual glycine-rich sequence (GY) $_n$ that is typical to proteins that can readily fold. This predicted structure supports the proposed model of conformational change of the loop following

binding of Ca^{2+} .

In summary, based on the above considerations the author proposes that in low-resistance epithelia occludin extracellular loops are the functional domain of the tight junctions that controls gating of the intercellular space. The molecular mechanism of occludin action involves binding of Ca^{2+} to an EF-hand – like domain composing the proximal part of the loops; this induces inward folding of the EF-hand along with envelopment of the Ca^{2+} -pocket by a hydrophobic distal part of the loop. Exteriorization of hydrophobic domains of occludin extracellular loops will lead to formation of hydrophobic bridges between neighboring cells that effectively occlude the intercellular space. Discussion and Conclusions

The new occludin hypothesis raises three questions that need further discussion. The first relates to Ca_0 and its physiological role as regulator of occludin function. The data in low-resistance epithelia showed relatively high $\text{EC}_{50}\text{-Ca}_0$ levels for changes in R_{TJ} , 300 μM [46]. This can be explained by correlating the binding affinity of [Ca^{2+} -binding proteins to target proteins] with the [EF-hands conformation status]: a low number of Ca^{2+} -binding sites indicates a small surface shared between the Ca^{2+} -binding protein and the target protein, and would require higher Ca^{2+} concentrations to activate the target protein [128]. Since only two Ca^{2+} -binding sites per occludin are predicted in those cells, calcium-affinity for modulation of R_{TJ} is expected to be low.

This argument raises a second question, whether Ca_0 can reach the mid-micromolar range in view of the tight regulation of extracellular Ca^{2+} at the 1.2–1.5 millimolar range. The explanation is that while plasma mean Ca_{2+} levels are relatively stable, extracellular Ca^{2+} levels at the cell surface can vary due to the presence of cell surface or cell secreted Ca^{2+} -binding proteins [142,143]. Therefore, the experimental $\text{EC}_{50}\text{-Ca}_0$ levels for changes in R_{TJ} in hVEEC and CaSki cells are in the predicted physiological Ca_0 levels at the cell surface.

The third and most intriguing question relates to the role of occludin *in vivo*. As discussed above,

the specific role of occludin is debated among different investigators mainly because transfection assays and experiments in occludin-deficient transgenic mice showed that occludin, in contrast to the claudins, is not necessary for gating the intercellular space [121]. Our data in the low-resistance hVEEC and CaSki epithelia and the above described novel model of occludin function suggest a specific role for occludin. Changes in occludin phosphorylation status and expression correlated with changes in R_{TJ} [66,74]. Occludin extracellular loops, in contrast to those of the claudins, contain EF-hands – like domains and may function as Ca^{2+} -binding sites and undergo conformational change in response to changes in Ca_0 . In contrast, the structure of claudins extracellular loops predicts a rigid structure that is not compatible with Ca^{2+} -binding characteristics, and claudins gating of the extracellular space appears to depend more on electrostatic forces generated by extracellular loops of neighboring cells than be influenced by Ca_0 . Moreover, claudins first extracellular loop is three times longer than the second [24], in contrast to similar lengths of occludin extracellular loops (FIG. 3).

Based on these data, it appears that occludin and the claudins have different biological roles. Claudins are the main building units of the tight junction, and confer the baseline gating properties of the intercellular space. Claudins regulation of the R_{TJ} depends mainly on the density of the proteins: Cells expressing greater density of claudins will tend to form serial-like tight-junctional structures (FIG. 2) and to generate high-resistance epithelia. Since claudins extracellular loops do not tether Ca^{2+} -sensitive mechanisms, R_{TJ} in epithelia containing tight junctions composed of claudins (*i.e.*, high-resistance epithelia) would be less sensitive to Ca_0 regulation. In those cells Ca_0 changes in assembly/disassembly of the tight junctions will depend mainly on Ca_0 -modulation of cytosolic Ca^{2+} . Similar to the claudins, occludin regulation of the R_{TJ} may also depend on its cellular density and expression. Thus, in estrogen-responsive cells estrogen-induced transformation of the full-length 65 kDa form to the truncated 50 kDa form decreases the R_{TJ} [66,74]. However, in

contrast to the claudins, occludin gating of the intercellular space can be acutely and reversibly regulated irrespective of its density and expression by at least two known mechanisms, threonine dephosphorylation of occludin intracellular domains (*N*- or *C*-termini) [74], and Ca^{2+} binding to occludin extracellular loops (ref. [46], FIG. 3). Therefore, the combined expression of claudins and occludin provides tight junctions with stability (claudins and occludin) and regulability (occludin). The importance of occludin is apparent in low-resistance epithelia while in high-resistance epithelia the role of occludin is probably masked by the predominance of claudins.

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