

# Chapter 5

## Regulation of Cadherin–Catenin Biology by Mechanical Force and Phosphorylation

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**Abstract** In the adherens junction (AJ), cadherin and catenin proteins form a cell–cell adhesion complex that is indispensable for tissue morphogenesis and homeostasis. The complex mechanically couples neighboring cells through intercellular binding by cadherins, and actin binding and regulation by the cytoplasmic catenins. In addition, the cadherin–catenin complex participates in signaling pathways that direct cellular organization, proliferation, and motility. Some of these signaling pathways can be regulated by mechanical stimulation or posttranslational modification of the components of the AJ. In light of these findings, we discuss our current understanding of how AJ signaling and mechanical functions are regulated by phosphorylation and force, and speculate on the mechanisms underlying the coordination between these two types of modifications.

**Keywords** Cadherin • Catenin • Force • Tension • Phosphorylation • Proliferation • Actin • Kinase • Phosphatase

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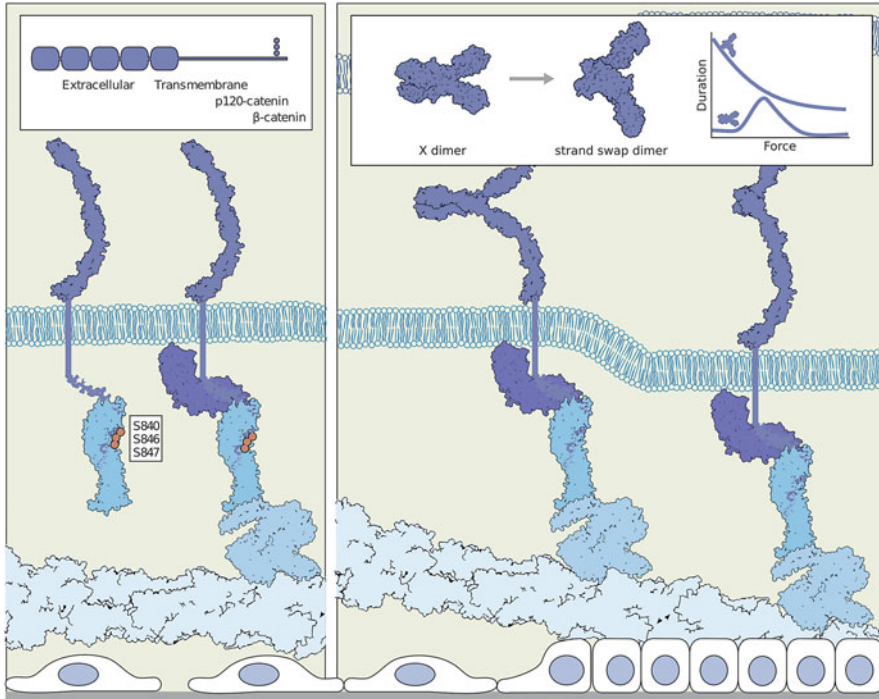
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## 5.1 Cadherin Extracellular Domain Interactions

The adherens junction (AJ) contains classical cadherins, which are single-pass transmembrane proteins with five extracellular cadherin (EC) repeat domains that form a rigid curved structure stabilized by  $\text{Ca}^{++}$  (Shapiro and Weis 2009; Pokutta et al. 1994). Cell–cell adhesion is established through trans binding between the N-terminal EC1 domain of cadherins on opposing cells, and X-ray crystal structures have revealed two kinds of interfaces between these interacting EC1 domains (Manibog et al. 2014; Rakshit et al. 2012; Brasch et al. 2012; Harrison et al. 2010). In the first, the N-terminal  $\beta$ -strands of each domain exchange to form part of a  $\beta$ -sheet in the partner molecule (strand-swap dimer). The second interface involves association of the base of EC1 and the  $\text{Ca}^{++}$ -binding site between it and EC2 to form an X-dimer. Kinetic and equilibrium measurements, as well as atomic force microscopy assays and steered molecular dynamics simulations, indicate that the X-dimer is an intermediate in the formation of the more stable strand-swap dimer (Manibog et al. 2014; Rakshit et al. 2012; Brasch et al. 2012; Harrison et al. 2010). The strand-swap dimer is formed by molecular interactions very similar to those in the unbound monomer, and involves the kinetically unfavorable refolding of the interacting EC1s to accommodate the partner  $\beta$ -strand. Thus, the X-dimer may be a low energy “encounter complex” intermediate that overcomes the kinetic barrier to the strand swap (Fig. 5.1).

The extracellular region of E-cadherins of the same cell can form *cis* interactions, which appear to contribute to the stability of cell–cell contacts. The existence of *cis* clusters has been inferred from crystal structures (Harrison et al. 2011), fusion constructs (Pertz et al. 1999), and chemical cross-linking (Takeda et al. 1999), but the interactions are apparently too weak to be detected in solution or in single-molecule assays, suggesting that rates of association and, thus, binding probabilities are low (Zhang et al. 2009). Combined atomic force microscopy and FRET measurements found that even though two cadherin extracellular domains do not bind in *cis* as single molecules, their proximity increases the probability of establishing a *trans* interaction (Zhang et al. 2009). Mutational disruption of E-cadherin *cis* interactions inferred from crystal structures prevented recruitment of endogenous E-cadherin to cell–cell junctions, indicating that *cis* interactions are required for AJ maturation (Harrison et al. 2011). Moreover, disruption of either *trans* or *cis* E-cadherin interactions by site-specific mutagenesis demonstrated that *trans* interactions in turn stabilize *cis*-mediated clusters of E-cadherin lacking the cytoplasmic domain, and that anchoring E-cadherin to the actin cytoskeleton guides the assembly of these clusters (Hong et al. 2013). Together, these studies indicate that *trans* and *cis* cadherin binding may cooperate during formation of cell–cell contacts.

Mechanical force may also have a role in stabilizing the cadherin adhesive interaction (Fig. 5.1). Notably, the two *trans*-dimer configurations have different unbinding kinetics in response to applied tension (that is, an opposing mechanical force): the X-dimer forms a catch bond, whose lifetime increases with tension,



**Fig. 5.1** Regulation of E-cadherin interactions by phosphorylation and force. Cadherin-mediated adhesion regulates the maturation of initial cell–cell recognition to loosely adherent cell clusters, to compacted groups of cells in colonies. E-cadherin is constitutively phosphorylated at S840, S846, and S847, facilitating binding to  $\beta$ -catenin and shuttling to the plasma membrane. E-cadherin is under constitutive tension after being incorporated into the plasma membrane and association with the actin cytoskeleton. E-cadherin trans X-dimer bonds are stabilized by force and may precede formation of stable strand-swap dimers, E-cadherin cis interactions, and the mature Adherens junction

whereas the strand-swap dimer behaves as a slip bond, whose duration decreases monotonically with respect to applied tension (Rakshit et al. 2012). It is unclear if cadherin catch bonds have a significant role *in vivo*. Formation of E-cadherin strand-swap dimers does not seem to require tension. *In vitro* spectroscopy experiments indicate that most extracellular dimers can form strand-swap slip bonds after an unloaded (no tension) contact time of 3 s (Rakshit et al. 2012). Moreover, mutations that compromise the affinity of the X-dimer slow, but still permit, the formation of the strand-swap dimer (Harrison et al. 2010). The X-dimer bond is most stable at  $\sim 30$  pN, a level that is unlikely to be reached by a single myosin motor (Norstrom et al. 2010) coupled to the cadherin–catenin/actin complex. It is possible that catch bond behavior enables lower levels of tension to extend the lifetime of the X-dimer bond and thereby increase the probability of transition into

the more robust strand-swap dimer conformation during initial cell–cell contact formation.

Cadherins are under tension in mature cell–cell contacts. A Förster resonance energy transfer (FRET)-based tension sensor (Grashoff et al. 2010) introduced into the cytoplasmic domain of E-cadherin indicated that E-cadherin is under constitutive tension of approximately 2 pN in cultured epithelial cells (Borghi et al. 2012). Tension along E-cadherin required catenin-mediated linkage to an intact contractile actomyosin network. In another study, the same E-cadherin sensor was used to observe cadherin-specific tension during collective cell migration of border cells in the *Drosophila* ovary. In this context, the average tension was also  $\sim 2$  pN, and was sensitive to the activity of the small Rho family GTPase Rac. Rac regulates the nucleation of branched actin filaments (Cai et al. 2014), and these may change cadherin tension by protruding into the nearby membrane and changing membrane shape. Another study also found that the morphology and contractility of the cytoskeleton influences force transmission at cadherin–catenin complexes, which experience a decrease in tension when shear force redirects intercellular tension to PECAM-1, an adhesion molecule abundant in endothelial cell–cell junctions (Conway et al. 2013).

Even though the cadherin FRET sensor has been successfully used to detect tension at cell–cell adhesions, it has a narrow dynamic range. The force versus FRET efficiency calibration curve characterized in the original vinculin FRET sensor showed that FRET indices at forces greater than 7.5 pN are indistinguishable from the background signal (Grashoff et al. 2010). Due to this limitation, the cadherin force sensor cannot be used to test if intercellular cadherin bonds in cells are ever subject to 30-pN forces, which stabilize the bonds in the X-dimer conformation. Since the inception of the vinculin tension sensor, several FRET-based genetically encoded and synthetic tension sensors have been developed (Cost et al. 2015). Unfortunately, these sensors are subject to their own unique limitations, and further techniques will need to be developed to chart a comprehensive map of forces at cell–cell junctions.

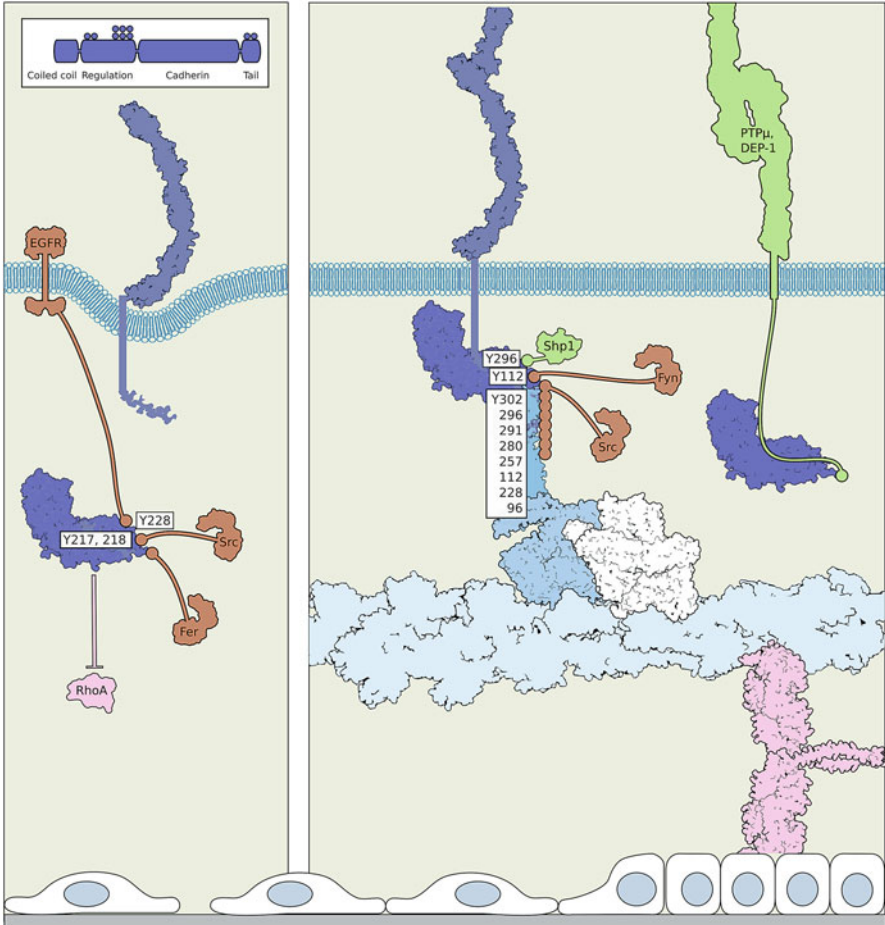
At the cellular scale, forces at cell–cell junctions have been inferred using traction force microscopy based on the principle of mechanical equilibrium (Maruthamuthu et al. 2011; Ng et al. 2014; Sim et al. 2015). In these experiments, cells are plated on a compliant substrate functionalized with extracellular matrix (ECM), whose deformation can be used to calculate stresses at the cell–substrate interface. Cells typically do not move substantially during the timescale of substrate deformation, so the cells are assumed to be under mechanical equilibrium in which cell–cell forces balance cell–ECM forces. Using this strategy, cell–cell junctions were found to be subject to hundreds of nN of tension. However, this tension is not confined to the AJ, as epithelial cells also form intermediate filament-bound desmosomes and an actin filament-bound tight junction. A study combining traction force microscopy and the cadherin FRET tension sensor found that average tension along cadherin molecules was constant in spite of significant changes in

cell–ECM and cell–cell forces (Sim et al. 2015). Moreover, increased forces at cell–cell contacts did not result in changes of total cadherin levels at cell–cell junctions. Instead, cadherin was found to be locally enriched at the edges of the contacts as cell–cell forces increased. These findings suggest that cells may maintain molecular-level mechanical homeostasis at the AJ by modulating the localization of cadherin-based complexes.

## 5.2 Cadherin Intracellular Domain Interactions: p120-Catenin

Interactions between cadherin, catenin proteins, and the actin cytoskeleton are tightly regulated to coordinate AJ assembly and disassembly in response to external or internal cues. In epithelial tissues, the cadherin–catenin complex is composed of E-cadherin and its associated cytoplasmic catenins: p120-catenin,  $\beta$ -catenin, and  $\alpha$ E-catenin.  $\beta$ -Catenin binds the cytoplasmic domain of E-cadherin upon synthesis in the endoplasmic reticulum. After delivery of the heterodimer to the plasma membrane, the complex is stabilized by intercellular trans E-cadherin interactions (see above) and p120-catenin binding to the cadherin juxtamembrane domain. Finally,  $\alpha$ E-catenin mechanically integrates the cytoskeletons of adjacent cells by binding to  $\beta$ -catenin and linking actin filaments to the complex (Ozawa et al. 1990; Hinck et al. 1994).

p120-Catenin regulates the rate of cadherin endocytosis, and the dynamics of the actin cytoskeleton through interactions with Rho family GTPases (Fig. 5.2, left). p120-Catenin was first identified as a Src kinase substrate in a study designed to screen for genes related to transformation (Reynolds et al. 1994), but subsequent studies demonstrated that in nontransformed cells, direct binding between p120-catenin and cadherin stabilizes cadherin at the plasma membrane at the onset of strong cell–cell adhesion (Thoreson et al. 2000; Yap et al. 1998; Davis and Reynolds 2006). Moreover, internalization assays demonstrated that p120-catenin binding prevents cadherin endocytosis by blocking binding of Hakai, an E3 ligase that ubiquitylates the E-cadherin cytoplasmic domain, targeting the complex to the endocytic machinery (Hartsock and Nelson 2012; Xiao et al. 2005). Src phosphorylation of p120-catenin at Y217 and Y228 increases p120-catenin affinity for E-cadherin and RhoA GTPase (Roura et al. 1999). Similarly, Fyn/Fer kinases phosphorylate p120-catenin and increase its affinity for E-cadherin (Rosato et al. 1998). However, Src and Fer/Fyn kinases also phosphorylate  $\beta$ -catenin Y654 and Y142, respectively, leading to dissociation from E-cadherin and  $\alpha$ E-catenin and subsequent deterioration of cell–cell adhesion (Roura et al. 1999; Piedra et al. 2003). Together, these results raise the question: why is the affinity of p120-catenin to cadherin increased by kinases that also destabilize cadherin’s interactions with the other catenins?



**Fig. 5.2** p120-Catenin-mediated regulation of actin dynamics, E-cadherin endocytosis, and phosphatase activity at the AJ. Cytosolic p120-catenin tyrosine-phosphorylated by growth factor cascades and/or Src and Fer kinases (orange) downregulates RhoA GTPase activity. Without p120-catenin binding, E-cadherin is targeted for endocytosis. Upon recruitment to the AJ at high cell densities, p120-catenin and its associated kinases can activate phosphatases (green) that counteract tyrosine-phosphorylation of  $\beta$ -catenin and  $\alpha$ E-catenin, stabilizing the cadherin–catenin complex at the AJ

Phosphorylation-mediated disruption of the cadherin–catenin complex may be opposed by p120-catenin (Fig. 5.2, right). In addition to binding to E-cadherin, p120-catenin associates with several tyrosine phosphatases, including the receptor-type tyrosine phosphatases PTP $\mu$  (Zondag et al. 2000) and DEP-1 (Holsinger et al. 2002), and the cytosolic tyrosine phosphatase SHP-1 (Reynolds et al. 1994). The receptor-type tyrosine phosphatases are upregulated at high cell density (Ostman et al. 1994) and could counteract Src and Fer/Fyn phosphorylation of the cadherin–catenin complex during cell–cell junction maturation. In addition,

p120-catenin recruits Fer to cell–cell adhesions, promoting activation of PTP1B, a cytosolic tyrosine phosphatase that counteracts phosphorylation of  $\beta$ -catenin Y142 and Y654 (El Sayegh et al. 2005; Xu et al. 2004). Thus, p120-catenin may play a critical role in maintaining the balance of kinase and phosphatase activity in the context of cell–cell adhesion.

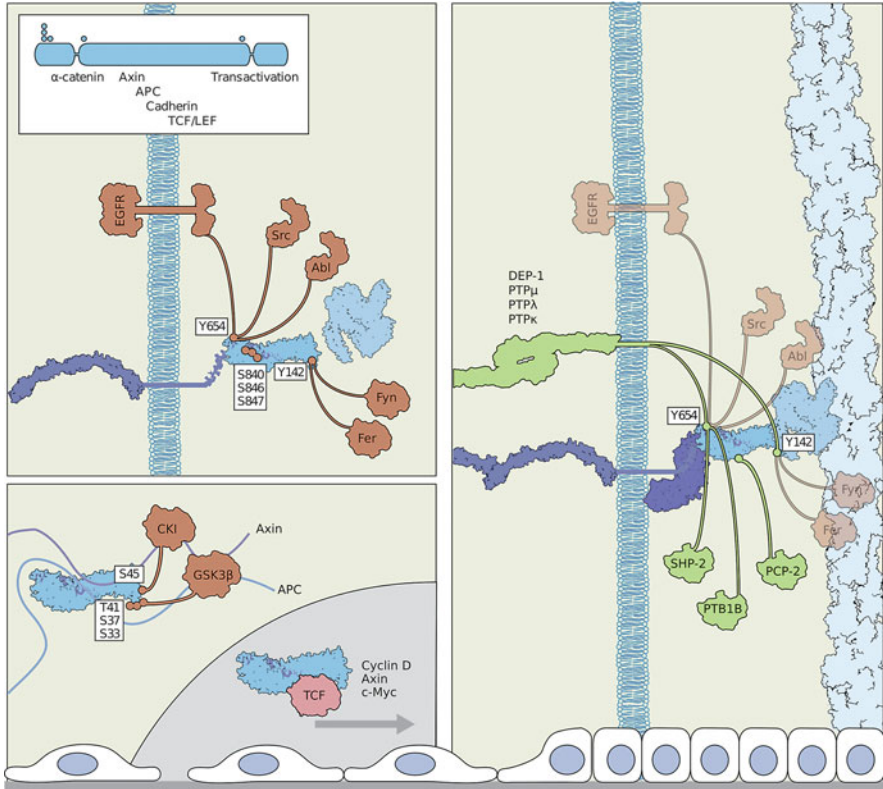
p120-catenin also regulates actin dynamics through its interactions with Rho family GTPases (Grosheva et al. 2001; Noren et al. 2000; Anastasiadis et al. 2000). Actin dynamics regulate the architecture of the cytoskeleton, thus p120-catenin likely affects how the cadherin–catenin complex transmits mechanical stimuli. In one study, for example, overexpression of p120-catenin inhibited RhoA activity, resulting in formation of branch-like actin protrusions and destabilization of stress fibers (Reynolds et al. 1996). These findings indicate that p120-catenin, when dissociated from E-cadherin, induces a more migratory phenotype driven by branch-like actin protrusions (Noren et al. 2000; Reynolds et al. 1996). This phenotype is evident in nascent cell–cell contacts (Toret et al. 2014; Yamada and Nelson 2007), but is suppressed by RhoA activity as cell–cell contacts expand (Yamada and Nelson 2007). In addition, studies show that RhoA activity can be mechanically activated in a variety of cell types (Zhao et al. 2007a; Abiko et al. 2015) and is correlated with local levels of stress (Reffay et al. 2014). Whether p120-catenin plays a role in this pathway remains to be determined. p120-Catenin can modulate GTPase activity by acting as a guanine nucleotide dissociation inhibitor (Anastasiadis et al. 2000) or associating with guanine nucleotide exchange factors such as p190RhoGAP (Wildenberg et al. 2006) and Vav2 (Fukuyama et al. 2006). How these interactions are affected by mechanical perturbation of cell–cell contacts has not been investigated.

### 5.3 Cadherin Intracellular Interactions: $\beta$ -Catenin

$\beta$ -Catenin, an armadillo repeat protein (Huber et al. 1997a), binds to the cytoplasmic domain of E-cadherin distal to the juxtamembrane domain and the p120-catenin binding site. In turn,  $\beta$ -catenin binds the actin binding protein  $\alpha$ E-catenin (Huber et al. 1997b). Binding of  $\beta$ -catenin confers structure to the cytoplasmic domain of E-cadherin, which protects cadherin from proteolysis (Huber et al. 2001) and reduces the turnover rate of the E-cadherin/ $\beta$ -catenin heterodimer at the plasma membrane. Calorimetry and mutagenesis studies indicate that the affinity of E-cadherin/ $\beta$ -catenin is increased when S840, S846, and S847 in the E-cadherin cytoplasmic domain are phosphorylated (Lickert et al. 2000; Serres et al. 2000; Choi et al. 2006; Fig. 5.1). These phosphorylation events occur constitutively (McEwen et al. 2014) and may stabilize the cadherin–catenin complex.

There are many posttranslational modifications that regulate the turnover of  $\beta$ -catenin in the cadherin–catenin complex (Fig. 5.3, top left). Phosphorylation of Y654 by Src or Abl, both cytoplasmic kinases, disrupts a hydrogen bond between the  $\beta$ -catenin Y654 phenolic hydroxyl group and a cadherin aspartate residue





**Fig. 5.3** Regulation of  $\beta$ -catenin localization, stability, and transcriptional activity by cell density and the balance of tyrosine kinase and phosphatase activities. Interactions of  $\beta$ -catenin with E-cadherin and  $\alpha$ E-catenin are negatively regulated by phosphorylation of  $\beta$ -catenin by receptor and cytoplasmic tyrosine kinases EGFR, Src, Abl, Fer, and Fyn (*red/orange components*), which phosphorylate Y654 and Y142 residues in  $\beta$ -catenin. In contrast,  $\beta$ -catenin interactions with E-cadherin and  $\alpha$ E-catenin are positively regulated by serine/threonine phosphorylation of E-cadherin (S840, S846, and S847) and  $\beta$ -catenin dephosphorylation (Y654 and Y142) by protein tyrosine phosphatases that bind p120 and  $\beta$ -catenin (*green components*). Degradation of cytoplasmic  $\beta$ -catenin is driven by phosphorylation by CKI and GSK3 $\beta$  and scaffolding by the tumor suppressors Axin and APC. The localization and phosphorylation state of  $\beta$ -catenin are associated with changes in cell density and affect cell–cell adhesion, cell migration, and the level of transcriptionally active  $\beta$ -catenin

(Huber and Weis 2001), resulting in at least a fifteen-fold reduction in affinity (Roura et al. 1999; Catimel et al. 2006). Another means of perturbing this interaction is via Src-mediated phosphorylation of N-cadherin Y860, as found in endothelial cells (Qi et al. 2005). Although Src disrupts E-cadherin/ $\beta$ -catenin heterodimerization, the p120-catenin-associated cytoplasmic kinases Fer and Fyn (Kim and Wong 1995) disrupt  $\beta$ -catenin/ $\alpha$ E-catenin interactions through tyrosine-phosphorylation of  $\beta$ -catenin (Rosato et al. 1998) Y142 (Piedra et al. 2003), which is located in the  $\beta$ -catenin/ $\alpha$ E-catenin binding interface (Pokutta and Weis 2000).



Fer and Fyn are examples of kinases that regulate cadherin–catenin complex stability downstream of signaling pathways mediated by receptor tyrosine kinases (RTKs). One of the most studied RTKs known to regulate the cadherin–catenin complex is the epidermal growth factor (EGF) receptor. EGF receptor activation induces dissociation of cell aggregates, cell rounding, and membrane ruffling (Fujii et al. 1996). The EGF receptor can bind directly to  $\beta$ -catenin (Hoschuetzky et al. 1994) and phosphorylate Y654 (Hazan and Norton 1998), weakening  $\beta$ -catenin affinity for E-cadherin. Without the cadherin– $\beta$ -catenin interaction,  $\alpha$ E-catenin cannot link the actin cytoskeletons of neighboring cells, resulting in reduced cell–cell adhesion and transition to a migratory phenotype. There is also evidence for the intersection of Src kinase and EGFR activation pathways, as inhibition of Src kinase blocks EGF-stimulated DNA synthesis and subsequent proliferation (Bromann et al. 2004). Activation of MET tyrosine kinase, another RTK, by hepatocyte growth factor (HGF) also results in  $\beta$ -catenin phosphorylation and subsequent nuclear accumulation (Monga et al. 2002).

When not associated with E-cadherin,  $\beta$ -catenin can participate in Wnt-dependent and -independent proliferation pathways (Fig. 5.3, bottom left). These require the translocation of  $\beta$ -catenin to the nucleus (McCrea et al. 1991; Nelson and Nusse 2004), where it associates with TCF/LEF transcription factors and induces specific gene transcription (He et al. 1998; Korinek et al. 1997; Morin et al. 1997). The amount of cytoplasmic  $\beta$ -catenin and thereby its transcriptional function can be regulated by a proteasome-targeted destruction complex (Aberle et al. 1997) comprising the tumor suppressors Adenomatous Polyposis Coli (APC) (Rubinfeld et al. 1993; Su et al. 1993) and axin (Zeng et al. 1997), the serine and threonine kinases GSK-3 (Dominguez et al. 1995; He et al. 1995; Kimelman and Pierce 1996) and CK1 (Liu et al. 2002; Amit et al. 2002), protein phosphatase 2A (Seeling et al. 1999), and the E3-ligase  $\beta$ -TrCP (Winston et al. 1999). Axin scaffolds the phosphorylation of  $\beta$ -catenin S45 by CKI (Amit et al. 2002; Sakanaka 2002), and then T41, S37, and S33 by GSK3 (Liu et al. 2002; Sadot et al. 2002); phosphorylation of S33 and S37 leads to ubiquitylation by  $\beta$ -TrCP and destruction in the proteasome. Canonical Wnt signaling promotes cell proliferation by inhibiting the activity of the  $\beta$ -catenin destruction complex, and these pathways are dysfunctional in many cancers (Fodde and Brabletz 2007).

Mechanical strain activates the transcriptional function of  $\beta$ -catenin independently of the Wnt signaling pathway during gastrulation in *Danio rerio* and *Drosophila melanogaster* (Brunet et al. 2013; Desprat et al. 2008). During gastrulation, the blastula, a spherical sheet of cells, folds inwards to create the gastrula, a structure comprising the three germ layers that give rise to specific organs during embryonic development. Folding of the blastula requires actomyosin contractility and correlates with Src-mediated phosphorylation of  $\beta$ -catenin Y654. In the absence of endogenous actomyosin contractility,  $\beta$ -catenin phosphorylation could be rescued by exogenous compression of the blastula using magnetic beads (Brunet et al. 2013). Mechanical strain across a contact-inhibited epithelial monolayer in vitro also results in increased  $\beta$ -catenin nuclear signaling, and cell-cycle progression (Benham-Pyle et al. 2015). This increase in signaling requires cadherin-

mediated cell–cell adhesion, as expression of a truncated E-cadherin lacking the extracellular domain blocked activation of  $\beta$ -catenin and cell-cycle progression following mechanical strain.

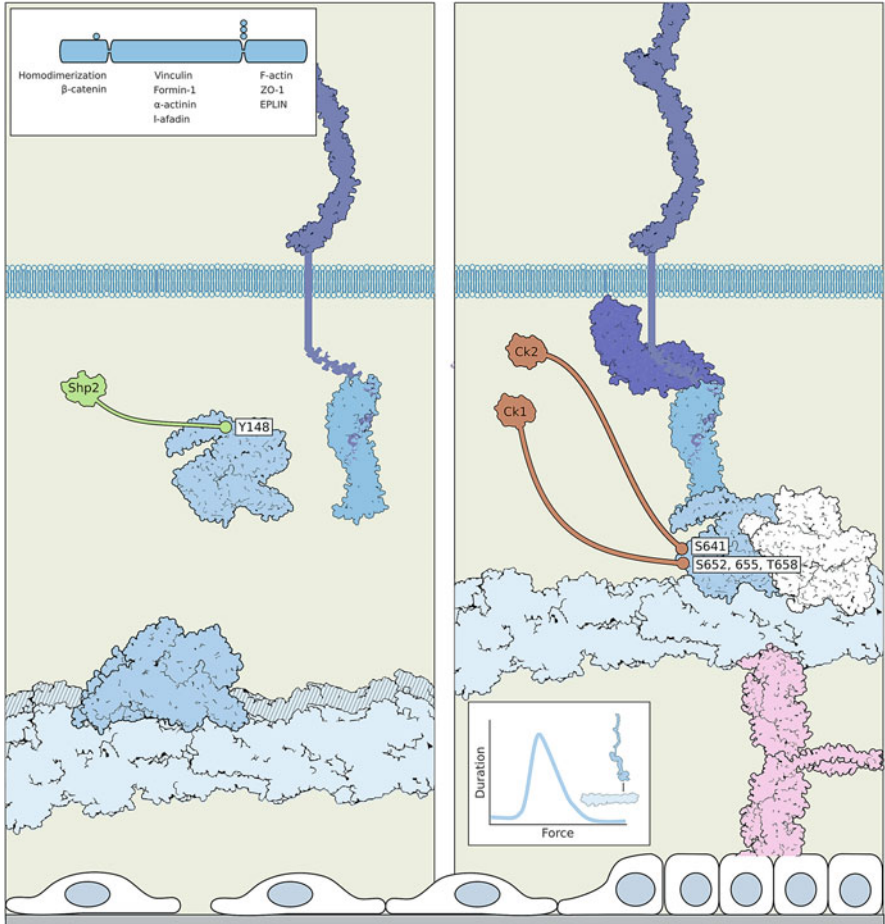
At present, it is unclear how mechanical strain is transduced to Src or  $\beta$ -catenin activation. Because Src phosphorylation was rescued using nonspecific magnetic compression of tissues (Desprat et al. 2008), Src may be subject to mechanical regulation independently of the cadherin–catenin complex at sites of cell–cell adhesion. Abl kinase, which affects cell–cell adhesion similarly to Src, possesses an actin binding domain (Van Etten et al. 1994), and myristoylation anchors the kinase to the plasma membrane (Hantschel et al. 2003). Interestingly, combined actin binding and myristoylation inhibit Abl activity (Hantschel et al. 2003; Woodring et al. 2001), which is lower in stable cell–cell contacts (Bays et al. 2014). These results suggest that mechanical stimuli could activate Abl at cell–cell contacts by dissociating it from the actin cytoskeleton.

Wnt-independent nuclear localization of  $\beta$ -catenin also depends on cell density (Dietrich et al. 2002). As cell density increases,  $\beta$ -catenin shifts from a nuclear pool to a junctional pool, and confluent cells stop proliferating due to contact inhibition. Cell density changes are accompanied by dramatic changes in cell morphology, and these changes may affect force generation and transmission at the AJ. Thus, it is possible that changes in mechanical strain and cell density modulate  $\beta$ -catenin junctional stability and transcriptional activity in similar ways (Brunet et al. 2013; Desprat et al. 2008; Benham-Pyle et al. 2015).

Phosphorylation of  $\beta$ -catenin and hence its transcriptional activity can be inhibited by several protein tyrosine phosphatases (PTPs) at cell–cell junctions (Fig. 5.3, right). PTP $\kappa$  binds  $\beta$ -catenin *in vitro* and dephosphorylates tyrosine-phosphorylated  $\beta$ -catenin from cell lysates (Fuchs et al. 1996), and PTP $\lambda$  similarly associates with  $\beta$ -catenin (Cheng et al. 1997). Several protein tyrosine phosphatases such as the cytosolic PTP-PCP2 also dephosphorylate  $\beta$ -catenin that had been phosphorylated downstream of growth factor signaling pathways (Yan et al. 2002). In high-density cultures, phosphatases localize to cell–cell junctions (Rijksen et al. 1993) and cadherin–catenin complexes may be directly involved in their recruitment (Piedra et al. 2003).

#### 5.4 Cadherin–Catenin Intracellular Interactions: $\alpha$ E-Catenin

$\alpha$ E-catenin, which binds to cadherin through  $\beta$ -catenin, anchors the AJ to the actin cytoskeleton directly or indirectly through different actin-binding partners. The amino terminus of  $\alpha$ E-catenin comprises a  $\beta$ -catenin binding domain and, in the mammalian homologue, an overlapping homodimerization domain (Pokutta and Weis 2000). The N-terminus is followed by a modulation domain that binds several actin-binding proteins including vinculin (Hazan et al. 1997; Choi et al. 2012),



**Fig. 5.4** Regulation of cytosolic and junctional  $\alpha$ E-catenin. Cytosolic  $\alpha$ E-catenin can be dephosphorylated by Shp2 phosphatase (green), and can also form homodimers that have a higher affinity for actin filaments and inhibit Arp2/3-mediated branching. Junctional  $\alpha$ E-catenin is subject to phosphorylation by CKI/II (orange), and acto-myosin generated tension which increases the actin binding affinity of the cadherin–catenin complex by modulating transitions between weakly and strongly bound catch bond states. Under tension,  $\alpha$ E-catenin acquires an open conformational state associated with vinculin recruitment (dark purple), and possibly other actin binding proteins (see domain organization)

I-afadin (Pokutta et al. 2002), formin-1 (KobielaK et al. 2004), and  $\alpha$ -actinin (Knudsen et al. 1995); the C-terminal domain also binds ZO-1 (Itoh et al. 1997) and EPLIN (Abe and Takeichi 2008). Thus, the cadherin–catenin complex can bind the actin cytoskeleton and regulate its nucleation (KobielaK et al. 2004; Tang and Briehner 2012) and morphology (Abe and Takeichi 2008) through multiple actin binding partners. The C-terminal domain of  $\alpha$ E-catenin binds directly to actin filaments (Pokutta et al. 2002; Rimm et al. 1995; Fig. 5.4, left).

$\alpha$ E-Catenin contains a bone fide actin-binding domain and a long-standing hypothesis in the field is that the cadherin–catenin complex binds to actin filaments directly. However, a simple actin pelleting assay was unable to reconstitute this interaction *in vitro* (Yamada et al. 2005) because binding to  $\beta$ -catenin decreases the actin binding affinity of  $\alpha$ E-catenin by >20-fold (Drees et al. 2005; Miller et al. 2013). These findings were puzzling inasmuch as other experiments demonstrated that actin binding is necessary for cell–cell adhesion (Imamura et al. 1999) and that adhesion can be induced by E-cadherin– $\alpha$ E-catenin chimeras (Nagafuchi et al. 1994; Pacquelet and Rørth 2005).

Because E-cadherin is under constitutive tension in cells (see above), an optical trap was used to reconstitute a direct cadherin–catenin/actin interaction by applying tension to the  $\alpha$ E-catenin/F-actin bond (Buckley et al. 2014). This work supported a two-state catch bond model in which increasing tension shifts the cadherin–catenin/actin bond from a weakly bound state to a strongly bound state (Fig. 5.4, right). However, the molecular basis for cadherin–catenin/actin catch bond states is unclear due to a lack of detailed structural information. Crystal structures of nearly full-length dimeric  $\alpha$ E-catenin have been published (Rangarajan and Izard 2012; Rangarajan and Izard 2013), but because  $\beta$ -catenin–bound  $\alpha$ E-catenin behaves differently from the dimer in *in vitro* biochemical assays (Drees et al. 2005; Miller et al. 2013), the available structures may not provide a strong basis for understanding actin binding by the complex. It is also possible that the kinetic states in the two-state cadherin–catenin/actin catch bond model are associated with the conformation of actin filaments, which change upon cooperative binding of  $\alpha$ E-catenin (Hansen et al. 2013).

Mechanical tension may regulate the affinity of  $\alpha$ E-catenin for several of its binding partners. In cell culture models, an antibody that recognizes the vinculin binding domain of  $\alpha$ E-catenin localizes to cell–cell junctions as long as actomyosin is contractile (Yonemura et al. 2010). Although full-length  $\alpha$ E-catenin does not bind full-length vinculin in solution, the vinculin head domain readily binds part of the modulation domain of  $\alpha$ E-catenin, and the affinity decreases as flanking domains of  $\alpha$ E-catenin are included (Choi et al. 2012). Significantly, stretching of  $\alpha$ E-catenin using magnetic tweezers promotes vinculin head domain binding (Yao et al. 2014), but whether this force-mediated structural change is sufficient to recruit full-length vinculin to the cadherin–catenin complex at the AJ is unclear. Pulling on cadherin-coated magnetic beads attached to cells recruits full-length vinculin to cadherin-mediated attachment sites (le Duc et al. 2010), and this recruitment requires Src/Abl phosphorylation of vinculin Y822 in the head domain (Bays et al. 2014). Abl phosphorylates the vinculin head domain *in vitro*, but it may not phosphorylate full-length vinculin due to autoinhibitory interactions between the actin-binding domain and the rest of the molecule. Together, these data indicate that the actin-binding activity of vinculin at cell–cell junctions may be coactivated by force-induced conformational changes of  $\alpha$ E-catenin and phosphorylation by Abl. It is possible that phosphorylation regulates  $\alpha$ E-catenin interactions as well; for example, the linker that connects the  $\alpha$ E-catenin modulation and actin binding domains is constitutively phosphorylated by CKI and CKII (Fig. 5.4, right).

However, these particular modifications do not seem to affect binding of actin (Drees et al. 2005) or vinculin and other actin binding partners (Drees et al. 2005; Escobar et al. 2015).

$\alpha$ E-catenin may also mediate crosstalk between the cadherin–catenin complex and other adhesion complexes at cell–cell junctions. A prominent example is the nectin family of Ig superfamily adhesion proteins (Takai et al. 2008), which can affect the spatial localization of cadherin–catenin complexes during assembly by recruiting them to nascent cell–cell junctions. The recruitment may occur through afadin, an actin-binding protein that can bind directly to nectins (Takai et al. 2008) and the cadherin–catenin complex through  $\alpha$ E-catenin (Pokutta et al. 2002). Ponsin and vinculin may also mediate interactions between afadin and the cadherin–catenin complex (Tachibana et al. 2000; Mandai et al. 1999). However, ponsin does not bind afadin and vinculin simultaneously in vitro (Mandai et al. 1999), but vinculin coimmunoprecipitates with ponsin when  $\alpha$ E-catenin is present (Peng et al. 2012), suggesting it may be necessary to reconstitute a ponsin/afadin/vinculin complex.

Recent work has shown that  $\alpha$ E-catenin also regulates the Hippo pathway protein YAP1, implicating the AJ in another cell proliferation pathway. Initially discovered in *Drosophila*, the Hippo pathway is a serine/threonine kinase cascade comprising Hippo (Harvey et al. 2003), Warts (Xu et al. 1995), Salvador (Pantalacci et al. 2003), and Mats (Lai et al. 2005). To control organ size during development, the Hippo–Salvador complex activates the Warts–Mats complex, which phosphorylates *Drosophila* YAP1, deactivates YAP1 transcriptional activity, and excludes it from the nucleus (Dong et al. 2007; Oh and Irvine 2008; Zhao et al. 2007b). Recent studies indicate that  $\alpha$ E-catenin acts as a suppressor of the transcriptional activity of YAP1 (Schlegelmilch et al. 2011; Silvis et al. 2011). This function of  $\alpha$ E-catenin is cell-density dependent and requires an interaction with the scaffolding protein 14-3-3 to sequester YAP1 at the AJ and in the cytosol. Expression of a truncated E-cadherin lacking the extracellular domain disrupts YAP1 sequestration in the cytoplasm (Benham-Pyle et al. 2015), suggesting that trans interactions between E-cadherin and mechanical coupling between cells may be required for sequestration of YAP1 in the cytoplasm or interaction with the cadherin–catenin complex. As does  $\beta$ -catenin, YAP1 becomes localized to the nucleus and transcriptionally active upon mechanical strain of contact-inhibited epithelial cells, but the molecular mechanism of activation is unknown (Benham-Pyle et al. 2015). Because YAP1 activation is sensitive to the morphology and contractile state of the actin cytoskeleton (Dupont et al. 2011; Wada et al. 2011), it is possible that YAP1 is mechanically activated through interactions with cytosolic  $\alpha$ E-catenin. Cytosolic  $\alpha$ E-catenin forms homodimers that bind and bundle actin filaments in the absence of tension and inhibit Arp2/3-mediated actin polymerization (Drees et al. 2005; Benjamin et al. 2010). Finally, both YAP1 and  $\alpha$ E-catenin have been linked to the  $\beta$ -catenin destruction complex (Brunet et al. 2013), indicating that YAP1 phosphorylation independent of the Hippo pathway may disrupt Yap1 interactions with the 14-3-3 scaffold.

## 5.5 Moving Forward

Several themes emerge from the large body of work seeking to understand how cadherin and catenin proteins are regulated by phosphorylation and mechanical force. Cell biology, biochemistry, and genetic data indicate that a balance of cell density-dependent phosphorylation and dephosphorylation events regulates cadherin-mediated adhesion. At low cell densities, high tyrosine kinase activity, some of which is downstream of growth factor signaling pathways, upregulates the motility and proliferation machinery necessary to develop a dense multicellular organization. As cell density increases, tyrosine phosphatase activity increases, perhaps to the point of counteracting kinase activity, resulting in the stabilization of the cadherin–catenin complex at cell–cell junctions while turning off motility and proliferation signals. Interestingly, many receptor protein tyrosine phosphatases possess extracellular domains similar to those found in cell adhesion molecules (Stoker 2005), and thus these phosphatases may be recruited and activated by cadherin-mediated adhesion via mechanisms similar to those reconstituted on lipid bilayers (Hui and Vale 2014; Greene et al. 2014; Lin et al. 2014).

Recent biophysical and bioengineering methods have uncovered evidence that cadherin and catenin biology is regulated mechanically. A salient finding is that cadherin and  $\alpha$ E-catenin form catch bonds between *trans*-interacting E-cadherin extracellular domains (Manibog et al. 2014) and F-actin (Buckley et al. 2014), respectively. However, additional experiments are needed to determine whether E-cadherin and  $\alpha$ E-catenin catch bonds contribute to signaling in a cellular environment. The rate of tension loaded in force spectroscopy experiments is much faster than that generated by molecular motors associated with the cytoskeleton in the cytoplasm (Finer et al. 1994). If this rate is too low, then bonds dissociate before experiencing levels of tension that slow down unbinding (Dudko et al. 2008). Thus, it is not clear if cadherin and  $\alpha$ E-catenin “feel” sufficient force *in vivo* to display catch bond behavior. To date, the best evidence of a catch bond operating in physiological conditions comes from studies of neutrophils detaching from selectin-binding surfaces under shear flow (Schmidtke and Diamond 2000; Yago et al. 2004). Gathering additional evidence for this type of cadherin/cadherin or  $\alpha$ E-catenin/F-actin bond *in vivo* will likely require a combination of FRET-based force measurements and single-molecule tracking.

It seems increasingly likely that mechanical force not only alters the structure and molecular composition of the AJ, but also contributes to signaling from the AJ to regulate growth, invasion, and cell division. Mechanical strain across contact-inhibited epithelial monolayers induces cell-cycle entry and DNA synthesis, which require *trans* interactions between neighboring cells (Benham-Pyle et al. 2015). Density-dependent mechanical properties regulate the exclusion of transcription factors (YAP1,  $\beta$ -catenin) from the nucleus. Moreover, mechanical perturbations of the AJ can result in numerous phosphorylation events, triggering remodeling and release of previously sequestered signaling molecules (Brunet et al. 2013; Desprat et al. 2008; Benham-Pyle et al. 2015). It remains unknown how mechanical force at



the AJ triggers increased kinase activity or release of sequestered transcription factors, and this will be an important topic for future work.

The morphology of the actin cytoskeleton regulates how force is generated and transmitted at the AJ. Actin networks can adopt distinct architectures: a highly branched network that is nucleated downstream of Rac1 and Cdc42, and an unbranched contractile network downstream of RhoA (Ridley 2006). These types of networks have different mechanical properties. Branched networks can tolerate compressive forces better than linear networks because network-level forces dissipate at the nodes connecting actin branches, and the high spatial density of these nodes generates short branches that buckle at larger compressive forces (Pujol et al. 2012). Thus, a branched network is better suited for generating protrusive forces, such as those found at the leading edge of migrating cells. At the AJ, these protrusive forces may move the plasma membrane locally and associated cadherin–catenin complexes. In addition, these complexes could experience an increase in tension if they are anchored to actin filament bundles that do not move with respect to the branching network. In contrast to branched networks, contractile networks are comprised of actin filaments bundled by myosin motors or other actin bundling proteins such as  $\alpha$ -actinin and cytosolic  $\alpha$ E-catenin. In these networks, motors generate contractile forces, and the bundled filaments transmit tension without undergoing much deformation (strain) given the Young's modulus of individual actin filaments ( $\sim 50$  pN/nm; Kojima et al. 1994). Due to this mechanical resilience, a contractile actin network can efficiently induce mechanical strain on associated protein scaffolds (Claessens et al. 2006). In turn, the strain on these components can manifest as changes in conformation and dissociation rates. This myosin-dependent process drives morphogenetic changes such as planar cell intercalation, where AJs perpendicular to the axis of elongation disassemble to give rise to aligned AJs (Bertet et al. 2004).

The combination of phosphorylation and mechanical studies of the cadherin–catenin complex generate a model in which a stable E-cadherin/ $\beta$ -catenin/ $\alpha$ -catenin complex is buttressed on either end by force-dependent interactions with E-cadherin molecules on neighboring cells and F-actin in the cytoplasm. The stability of E-cadherin/ $\beta$ -catenin/ $\alpha$ -catenin interactions can then be tightly regulated by kinases and phosphatases to quickly dissociate the complex when needed, for example, in response to tissue wounding or other morphogenetic signals. It is likely that the combination of mechanical and biochemical modifications facilitates switches between different functions of cadherin and catenin proteins. As such, it will be important to address how mechanical forces contribute to phosphatase and kinase activities at the AJ, and how these modifications then contribute to the regulation of cell migration and growth.

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