ABSTRACT
Phosphorylation of a highly conserved serine cluster in the intracellular domain of E-Cadherin is essential for binding to β-Catenin in vitro. In cultured cells, phosphorylation of specific serine residues within the cluster is also required for regulation of adherens junction (AJ) stability and dynamics. However, much less is known about how such phosphorylation of E-Cadherin regulates AJ formation and dynamics in vivo. In this report, we generated an extensive array of Drosophila E-Cadherin (DE-Cad) endogenous knock-in alleles that carry mutations targeting this highly conserved serine cluster. Analyses of these mutations suggest that the overall phosphorylation potential, rather than the potential site-specific phosphorylation, of the serine cluster enhances the recruitment of β-Catenin by DE-Cad in vivo. Moreover, phosphorylation potential of the serine cluster only moderately increases the level of β-Catenin in AJs and is in fact dispensable for AJ formation in vivo. Nonetheless, phosphorylation-dependent recruitment of β-Catenin is essential for development, probably by enhancing the interactions between DE-Cad and α-Catenin. In addition, several phospho-mutations dramatically reduced the biosynthetic turnover rate of DE-Cad during apical-basal polarization, and such biosynthetically stable DE-Cad mutants specifically rescued the polarity defects in embryonic epithelia lacking the polarity proteins Stardust and Crumbs.

KEY WORDS: DE-Cadherin, β-Catenin, Shotgun, Armadillo, α-Catenin, Adherens junctions, Apical-basal polarity, Drosophila, Crb, Sdt

INTRODUCTION
Adherens junction (AJ) complexes are composed of the transmembrane protein E-Cadherin and cytosolic proteins β-Catenin (β-Cat) and α-Catenin (α-Cat) (Harris and Tepass, 2010). Direct binding between β-Catenin and the intracellular tail of E-Cadherin is essential for AJ complex formation and trafficking. Such interaction also recruits α-Catenin, which links the AJ complex to the F-actin network (Buckley et al., 2014). Previous studies have identified a highly conserved serine cluster in the E-Cadherin intracellular tail phosphorylation of which drastically increases the binding affinity of E-Cadherin to β-Catenin by ~800 fold in vitro (Choi et al., 2006; Huber and Weis, 2001; Lickert et al., 2000). In addition, cell culture studies showed that phosphorylation of specific serine residues within the cluster could play distinct roles in regulating AJ formation and stability (Choi et al., 2015; Lickert et al., 2000; McEwen et al., 2014). In Drosophila, we previously reported that the biosynthetic turnover of AJs is differentially regulated during apical-basal polarization in Drosophila embryonic epithelia (Huang et al., 2011). The increased AJ stability in polarized cells coincides with the stronger binding between Drosophila E-Cadherin (DE-Cad, also known as Shotgun or Shg) and β-Catenin (also known as Armadillo or Arm; Peifer and Wleschaus, 1990) (Huang et al., 2011), making DE-Cad phosphorylation an attractive mechanism for modulating the DE-Cad/β-Catenin interaction during cell polarization.

Nonetheless, it remains to be determined whether phosphorylation of the conserved serine cluster in E-Cadherin plays significant roles in AJ formation, development and cell polarity in vivo. Recent studies in Caenorhabditis elegans based on transgenic expression of phospho-mutant E-Cadherins suggest a requirement of site-specific phosphorylation in the serine cluster for development, but it is unknown how β-Catenin binding is affected in vivo in such mutants (Choi et al., 2015). Using our genomic engineering method (Huang et al., 2009), we generated an extensive array of Drosophila DE-cadherin knock-in alleles carrying specific deletions and phospho-mutations in the conserved serine cluster. One unique advantage of these knock-in mutants is that all mutant DE-Cad proteins are expressed from the endogenous locus to allow clean and consistent genetic assays. Using such engineered DE-Cad knock-in alleles exclusively, we first aimed to confirm whether the conserved serine cluster is essential for function of DE-Cad in AJ formation and development. Second, we aimed to determine how the phosphorylation potential of the serine cluster is required for DE-Cad to interact with β-Catenin and α-Catenin in vivo. Finally, we also aimed to identify potential site-specific phosphorylations that might interact with the apical polarity complex Stardust (Sdt)-Crumbs (Crb) to regulate the AJ formation and dynamics during apical-basal polarization.

RESULTS AND DISCUSSION
A short motif containing the conserved serine cluster in the DE-Cad intracellular domain is essential for AJ formation in vivo
The intracellular tail of E-Cadherin contains two functional domains: a juxtamembrane domain that regulates steady-state levels of the AJ complex by interacting with p120-catenin (Adherens junction protein p120, p120ctn), and a C-terminal motif that is required for binding β-Catenin (Fig. 1A,B) (Nagafuchi et al., 1994; Oda et al., 1993; Pacquelet et al., 2003; Stappert and Kemler, 1994). To narrow down further the minimal motif in
DE-Cadherin required for recruiting β-Catenin to AJ in vivo, we generated three DE-Cad knock-in mutants carrying deletions of 83aa (DE-CadΔβ), 60aa (DE-CadΔβS) or an internal 22aa (DE-CadΔS) that remove the conserved serine cluster (Fig. 1A,B). Similar to DE-Cadnull (shg2), all three mutants are embryonic lethal (Table S1) with a severe loss-of-cuticle phenotype (Fig. 1C) that indicates a strong disruption of epithelial polarity and integrity. In larval wing disc epithelia, mutant cells expressing DE-CadΔβS and DE-CadΔS fail to form discernable AJs, which are labeled by junctional β-Catenin staining, and instead show cytosolic GFP+ puncta devoid of β-Catenin (Fig. 1D; Fig. 2A; all DE-Cad mutants generated in this report are tagged with GFP at the C terminus). The mutant clones are also of small and rounded shapes characteristic of DE-Cadnull mutant clones (Tepass et al., 1996). Such phenotypes suggest a complete loss of β-Catenin binding to DE-CadΔβS and DE-CadΔS and are consistent with the requirement of β-Catenin binding for trafficking of E-Cadherin to the plasma membrane (Chen et al., 1999). Loss of β-Catenin recruitment by DE-CadΔS is not simply due to the shortening of the DE-Cad intracellular tail, as a DE-CadΔS+LK knock-in allele with ΔS deletion replaced with a generic 22 aa linker (Varnai et al., 2006) showed phenotypes identical to DE-CadΔS (Fig. 2A). For clarity, we will hereafter refer to this 22 aa motif as ‘S-motif’ (Fig. 1A).

The conserved serine residues are required for DE-Cad functions in development in a quantitative manner
To identify whether any of the conserved serines in the S-motif are specifically required for β-Catenin recruitment, AJ formation and development, we generated an array of DE-Cad phospho-mutants (Table S1; Fig. 1A), which will hereafter be referred to collectively...
as \( \text{DE-Cad}^* \). Most of the \( \text{DE-Cad}^* \) mutants carried various combinations of single or multiple non-phosphorylatable \( S \rightarrow A \) and/or phosphomimetic \( S \rightarrow D \) mutations within the \( ^{1457}\text{SLSSLAS} \) serine cluster, which is nearly 100% conserved among the S-motifs of \text{Drosophila} \) and mammalian E-Cadherins (Fig. 1A). Viability tests (Table S1) suggest that \( \text{DE-Cad}^* \) mutants remain viable as long as two or more serine residues remain in the cluster. In addition, none of the four serine residues appears to be specifically required \( \text{in vivo} \) for \( \text{DE-Cad} \) functions in development (Table S1). Furthermore, \( \text{DE-CadS4D} \), in which all four serine residues are mutated to phosphomimetic Asp, is homozygous viable, suggesting that regulating the phosphorylation of the SLSSLAS cluster is not essential for development. Our data are consistent with a model in which the overall phosphorylation level, rather than phosphorylation of any specific serine residues in S-motif, is crucial for \( \text{DE-Cad} \) function \( \text{in vivo} \).

A recent study showed that phosphorylation of a conserved serine residue upstream of the SLSSLAS cluster directly regulates the stability of vertebrate E-Cadherin (McEwen et al., 2014). We thus generated mutants targeting \( ^{1454}\text{Ser} \), which is the equivalent residue in \( \text{DE-Cad} \) (Fig. 1A). \( \text{DE-Cad} \) knock-in mutants carrying a single mutation of \( ^{1454}\text{Ser} \rightarrow \text{Ala} \) or \( \text{Asp} \) (i.e. \( 'A-SSSS' \) or \( 'D-SSSS' \); Table S1) are viable but such mutations are lethal when combined with \( S4D \) mutations (i.e. \( 'A-DDDD' \) or \( 'D-DDDD' \); Table S1), suggesting that it is only in \( S4D \) mutants that the potential phosphorylation of \( ^{1454}\text{Ser} \) becomes essential for generating sufficient negative charges on the S-motif for recruiting \( \beta\text{-Catenin} \) (see below). Overall, in contrast to the results in cultured cells and in \text{C. elegans}, our data suggest that none of the conserved phosphoserines is specifically required for essential \( \text{DE-Cad} \) functions \( \text{in vivo} \); instead, these serine residues appear to be required in a quantitative manner for viability and development.

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Fig. 2. Phosphorylation potential of the conserved serine cluster in the S-motif regulates AJ formation. (A,B) Immunostaining of larval wing disc epithelial clones of selected \( \text{DE-Cad} \) knock-in mutants. All mutant clones were generated against \( \text{DE-Cad::GFP} \) and are marked by loss of nuclear RFP. Wild-type twin clones are marked by increased RFP expression. (C) Measured GFP (i.e. \( \text{DE-Cad}^*::\text{GFP} \)) and \( \beta\text{-Catenin} \) intensities and GFP/\( \beta\text{-Catenin} \) ratios in AJs in mutant clones. \( \text{DE-Cad}^\text{null} \) (i.e. \( \text{shg2} \)) \( \text{DE-Cad} \) and \( \text{DE-CadS4D} \) mutant cells do not form AJs and are therefore not included. Names of lethal \( \text{DE-Cad}^* \) mutants are in red. (D) \( \beta\text{-Catenin} \) levels in AJ complexes immunoprecipitated from zygotic homozygous embryos of \( \text{DE-Cad::GFP} \) wild type or mutants as specified. (D’) Quantified \( \beta\text{-Catenin}/\text{DE-Cad}^*::\text{GFP} \) ratios from the data shown in D, based on three separate rounds of immunoprecipitation results. * \( P<0.05 \), ** \( P<0.005 \) (two-tailed \( t \)-test). KO, knockout; WT, wild type. Scale bar: 5 \( \mu \text{m} \) (for A and B).
Loss of phosphorylation potential of S-motif moderately reduces β-Catenin levels in AJs in vivo

We further focused on a subset of DE-Cad* mutants to investigate how phospho-mutations in the S-motif affect AJ formation and β-Catenin/DE-Cad interactions in vivo. We used FRT-mediated mitotic recombination to generate simultaneously mitotic clones of both wild-type DE-Cad::GFP and mutant DE-Cad*::GFP in wing disc epidermis. As both wild-type and mutant DE-Cad proteins are tagged with GFP, their levels can be quantified in the same sample by immunostaining with an anti-GFP antibody, and co-immunostaining with an anti-β-Catenin antibody can be used to quantify β-Catenin levels simultaneously. In contrast to mutant clones of DE-CadΔβS, ΔS and ΔS+LK that show complete loss of AJs in larval disc epithelia, clones of all the examined DE-Cad* phospho-mutants form apparently normal AJs in larval wing disc epithelia as judged by GFP and β-Catenin staining (Fig. 2A). Moreover, although in vitro studies showed that phosphorylation of the serine cluster on the S-motif increases β-Catenin binding to the E-Cadherin intracellular tail by several hundred fold (Huber and Weis, 2001), none of the AJs formed by DE-Cad* phospho-mutants shows more than 60% reduction of β-Catenin (Fig. 2A,C; Table S1). Even in AJs formed by non-phosphorylatable DE-CadS4A or DE-CadS5A, β-Catenin levels are only reduced to ~56% and ~46% of wild-type AJs, respectively (Fig. 2A,C). In AJ complex immunoprecipitated from zygotic wild-type AJs, respectively (Fig. 2A,C). In AJ complex immunoprecipitated from zygotic DE-CadS4A mutant embryos, β-Catenin is also only reduced approximately three-fold (Fig. 2D,E).

Why do AJs formed by non-phosphorylatable DE-Cad mutants such as S4A and S5A still contain high levels of β-Catenin? We noticed that the S-motif is also rich in acidic residues such as Asp and Glu (Fig. 1A). In particular, 1451Asp and 1466Asp residues in DE-Cad are in the same locations as 857Ser and 872Ser in human E-Cad and therefore might play phosphomimetic functions. We mutated both to Asn in the DE-Cad2DN mutant and found that the β-Catenin level is also reduced in AJs (Table S1). Taken together, our data suggest that the in vivo recruitment of β-Catenin to AJs depends on the total negative charges on the DE-Cad S-motif, including basal charges from acidic Asp and Glu residues and additional charges from phosphorylation of the conserved serine cluster.

Covalently linking α-Catenin to DE-Cad compensates for the loss of phosphorylation-dependent β-Catenin in AJ formation and development

Although removing potential phosphorylation on the S-motif only moderately reduces β-Catenin in AJs, DE-Cad* mutants that reduce the β-Catenin levels by more than 30% in mutant AJs are consistently lethal (Fig. 2C; Table S1). Live imaging showed that DE-CadS4A maternal mutant embryos develop normally until germband retraction after which the epidermis appears to break down during dorsal closure (Movies 1 and 2), suggesting that AJs formed by DE-CadS4A might not be robust enough to support tissue remodeling in late embryogenesis. A major function of β-Catenin is to recruit α-Catenin, which attaches the AJ complex to F-actin by a tension-dependent mechanism (Buckley et al., 2014), and covalently linking α-Catenin to E-Cadherin can at least partially compensate for the loss of β-Catenin in AJ formation (Bianchini et al., 2015; Desai et al., 2013; Nagafuchi et al., 1994; Pacquelet et al., 2003; Sarpal et al., 2012). Indeed, fusion of α-Catenin completely rescues the developmental lethality of DE-CadS4A (Fig. 2B,C). Importantly, the rescue is not due to DE-CadS4A-αCat recruiting more β-Catenin, as AJs formed by DE-CadS4A-αCat show no obvious increase in β-Catenin compared with AJs of DE-CadS4A. Fusion of α-Catenin also rescued the AJ formation defects of DE-CadΔβS and DE-CadΔS, but both fusion mutants remain lethal (Table S1) with a very low level of β-Catenin recruited to AJs (Fig. 1B,Fig. 2B,C). Our data suggest that the major in vivo function of phosphorylation-dependent recruitment of β-Catenin by DE-Cad could be limited to enhancing the interaction between DE-Cad and α-Catenin, as loss of such β-Catenin can be fully compensated for by fusion of α-Catenin to DE-Cad for AJ formation and development. However, phosphorylation-independent recruitment of β-Catenin by DE-Cad has an essential role in development and cannot be compensated for by covalent fusion of α-Catenin to DE-Cad.

Conserved serine residues regulate the biosynthetic turnover of DE-Cad during apical-basal polarization

To investigate whether phosphorylation of the S-motif could regulate AJ turnover dynamics, we carried out whole-cell fluorescence recovery after photobleaching (FRAP) assays (Huang et al., 2011) to measure specifically the biosynthetic turnover rates of selected DE-Cad* mutants in polarizing and polarized cells (Fig. 3A; Fig. S1A,B; Table S1). Stage 9-11 embryos were selected for assaying polarizing epithelial cells and stage 15 embryos for assaying polarized cells. Whole-cell FRAP assays were performed in lateral epidermis (Huang et al., 2011). Although all DE-Cad* show reduced levels of β-Catenin in AJs in vivo, overall it appears that loss of phosphorylation potential of the SSLLSAS motif in DE-Cad does not significantly increase the biosynthetic instability of DE-Cad in AJs (Fig. 3A; Table S1). In contrast, fusion of α-Catenin to DE-CadS4A dramatically reduced DE-CadS4A turnover by 80%, making DE-CadS4A-αCat the most biosynthetically stable mutants we have characterized so far (Fig. 3A). This stabilizing effect is not due to α-Cat fusion to DE-Cad alone, as wild-type DE-Cad-αCat only showed mildly reduced biosynthetic turnover in polarizing cells (Fig. 3A). In addition, DE-CadASSA has significantly reduced biosynthetic turnover in polarizing cells and increased turnover in polarized cells – essentially a reversed differential regulation pattern of AJ dynamics compared with wild-type DE-Cad during cell polarization (Huang et al., 2011). Consistent with our whole-cell FRAP results, latrunculin treatment also showed that in DE-CadS4A-αCat and DE-CadASSA embryos the AJ-localized DE-Cad, and presumably AJs, are more resistant to the loss of F-actin (Fig. 3B). The viability of DE-CadASSA and DE-CadS4A-αCat mutants demonstrates that Drosophila can tolerate a surprisingly wide range of DE-Cad biosynthetic turnover rates during cell polarization and development.

Biosynthetically stable DE-Cad mutants rescue the polarity defects in sdt and crb embryonic epithelial cells

Sdt and Crb form an apical polarity complex that is essential for establishing apical-basal polarity in early embryonic epithelial cells, and their mutant embryos show identical defects in AJs and apical-basal polarity (Bachmann et al., 2001; Hong et al., 2001; Tepass and Knust, 1993). It has been proposed that the Sdt-Crb complex is specifically required in polarizing or remodeling cells subject to fast turnover of AJs (Campbell et al., 2009). To test this hypothesis directly, we combined sdt or crb with biosynthetically stable DE-CadASSA or DE-CadS4A-αCat mutants. In DE-Cad; crb and DE-Cad::α-Cat; crb mutant embryos, DE-Cad and DE-Cad::α-Cat, as well as the apical polarity marker Baz are all severely disrupted at early stages (Fig. 3C). In contrast, mutant embryos of DE-CadASSA; crb, or sdt; DE-CadASSA or sdt; DE-CadS4A-αCat
showed a dramatic rescue of AJ formation and polarity by restoring the apical localization of mutant DE-Cad and Baz (Fig. 3C). In addition, although Sdt and Crb are mutually dependent on each other for localizing to apical membrane (Hong et al., 2001), Crb apical localization was restored in mutant embryos of sdt; DE-CadASSA and sdt; DE-CadS4A-αCat. As expected, the more stable DE-CadS4A-αCat yielded a much stronger rescue of AJ formation and polarity defects than DE-CadASSA (Fig. 3C). Our data support the hypothesis that the Sdt-Crb complex is specifically required in polarizing cells undergoing fast AJ turnover, whereas in polarized cells biosynthetically stable AJs make Sdt-Cbr dispensable. Interestingly, DE-CadASSA or DE-CadS4A-αCat did not rescue Baz localization in amnioserosa cells in crbKO and sdtKO mutant embryos (data not shown), suggesting that the Sdt-Crb complex acts through mechanisms independent of AJ stability to maintain polarity in these actively constricting cells (David et al., 2010; Flores-Benitez and Knust, 2015; Harden et al., 2002).

In summary, we have shown that the conserved serine cluster motif is structurally required for AJ formation in vivo. Although a lack of proper antibodies meant that it was not possible for us to determine the phosphorylation levels of the serine cluster in wild-type and mutant DE-Cad proteins, the extremely conserved nature of the S-motif and the phenotypes of DE-Cad phospho-mutants support the suggestion that phosphorylation of the S-motif in DE-Cad is highly likely in vivo. However, our in vivo data showed that there is a surprisingly strong phosphorylation-independent recruitment of β-Catenin by DE-Cad that appears to be sufficient for AJ formation. Although phosphorylation-dependent recruitment of β-Catenin in AJs is indeed required for development, its role appears to be limited to enhancing the interaction between α-Catenin and the DE-Cad/β-Catenin complex. In contrast to transgenic rescue assays that showed that the 145Ser-equivalent residue in worm E-Cadherin is essential for development, our Drosophila knock-in mutants showed that none of the conserved serine residues is specifically required for AJ formation and development in vivo. Mechanisms reconciling such differences remain unclear to us, but our data are consistent with a model in which total negative charges on the conserved serine cluster enhance the potential binding between Drosophila DE-Cad and β-Catenin in AJs. However, site-specific phosphorylation of the serine cluster can dramatically regulate the biosynthetic stability of DE-Cad proteins in AJs, and it will be of great interest to identify...
the specific serine residues and kinases that are involved in such regulation.

MATERIALS AND METHODS

Fly genetics

Generation of DE-Cad knock-in alleles was carried out by genomic engineering as described previously (Huang et al., 2009). DE-Cad mutants were recombined with FRT-G13 chromosome for clonal analysis. Mutants of crtl[104] and sad[104] were described previously (Huang et al., 2009). Additional materials and methods For details of generation of larval mitotic recombiant clones and germline clones, and a full list of fly stocks and genotypes of samples presented in figure panels, see supplementary Materials and Methods.

Immunostaining and quantification

Immunostaining of wing discs and embryos were described previously (Huang et al., 2009). For primary and secondary antibodies, see supplementary Materials and Methods. Images were collected on Olympus FV1000 confocal microscopes (Center for Biologic Imaging, University of Pittsburgh Medical School, PA, USA) and processed in Adobe Photoshop for compositions. The images containing z-sections were analyzed using Imaged and custom scripts in Photoshop. Junctional signals of GFP and β-Catenin were quantified using custom software as previously described (Huang et al., 2009).

Whole-cell FRAP assays and live imaging of embryogenesis

Staged embryos were collected and their eggshells were manually removed. Dechorionated embryos were placed in air-permeable chambers filled with halocarbon oil (#95) on custom-made slides to ensure their normal development during the imaging session (Huang et al., 2011). Whole-cell FRAP assays were carried out using a Nikon confocal microscope A1 (Center for Biologic Imaging, University of Pittsburgh, PA, USA). Quantification of the FRAP recording images and data processing were described previously (Huang et al., 2011).

Cuticle preparation

Dechorionated embryos were mounted on slides in a mixture of lactic acid (S25374, Fisher Science Education) and Hoyer’s solution (1:1). The slides were baked at 65°C for 16 h before imaging. Lethal DE-Cad mutants were balanced on CyO, twi-GFP chromosome and zygotic mutant embryos were identified by the absence of GFP expression prior to cuticle preparation.

Immunoprecipitation of DE-Cad/β-Catenin complex from embryos

Embryos were collected for 2 h at 25°C then aged for 4 h at 25°C for collecting early embryos or 10 h at 25°C for late embryos. Immunoprecipitation of the AJ complex and western blotting were carried out as previously described (Huang et al., 2009).

Drug treatments in embryos

Embryos were dechorionated in bleach, washed and then placed in a 1:1 mixture of Schneider’s medium and n-octane (Teodorro and O’Farrell, 2003). Latrunculin (stock solution of 1 mM in DMSO; final concentration of 20 μM; Sigma, L5288) or an equal amount of DMSO were added to Schneider’s medium and embryos were shaken at 400 rpm (on an orbital shaker) for 30 min. Embryos were then quickly rinsed in n-octane, briefly dried in air and immediately mounted in halocarbon oil (#95) in an air-permeable chamber for imaging.

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Competing interests

The authors declare no competing or financial interests.

Author contributions


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Supplementary information

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