Integrin signalling regulates YAP and TAZ to control skin homeostasis

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ABSTRACT
The skin is a squamous epithelium that is continuously renewed by a population of basal layer stem/progenitor cells and can heal wounds. Here, we show that the transcription regulators YAP and TAZ localise to the nucleus in the basal layer of skin and are elevated upon wound healing. Skin-specific deletion of both YAP and TAZ in adult mice slows proliferation of basal layer cells, leads to hair loss and impairs regeneration after wounding. Contact with the basal extracellular matrix and consequent integrin-Src signalling is a key determinant of the nuclear localisation of YAP/TAZ in basal layer cells and in skin tumours. Contact with the basement membrane is lost in differentiating daughter cells, where YAP and TAZ become mostly cytoplasmic. In other types of squamous epithelia and squamous cell carcinomas, a similar control mechanism is present. By contrast, columnar epithelia differentiate an apical domain that recruits CRB3, Merlin (also known as NF2), KIBRA (also known as WWC1) and SAV1 to induce Hippo signalling and retain YAP/TAZ in the cytoplasm despite contact with the basal extracellular matrix. When columnar epithelial tumours lose their apical domain and become invasive, YAP/TAZ becomes nuclear and tumour growth becomes sensitive to the Src inhibitor Dasatinib.

KEY WORDS: Hippo pathway, Integrin, Yes-associated protein, TAZ, Stratified squamous epithelium

INTRODUCTION
The Yes-associated protein (YAP) family of transcriptional co-activators are emerging as potent oncogenes that strongly drive cell proliferation in many types of stem/progenitor cells and cancers (Harvey et al., 2013; Irvine and Harvey, 2015; Pan, 2010, 2015; Piccolo et al., 2013). The function of YAP family co-activators was first discovered by Drosophila genetics, where the sole YAP homologue Yorkie (Yki) was found to be necessary and sufficient to promote cell proliferation and tissue overgrowth in epithelia (Huang et al., 2005). Subsequent genetic experiments in mice showed that ectopic expression of YAP (also known as YAP1) was sufficient to drive cell proliferation in liver, intestine, bronchus and skin (Cai et al., 2010; Camargo et al., 2007; Dong et al., 2007; Schlegelmilch et al., 2011; Zhang et al., 2011a; Zhao et al., 2014). Surprisingly, YAP knockout mice have mild phenotypes, although they are deficient in proliferative repair of the intestine and resistant to intestinal tumour formation (Azzolin et al., 2014; Cai et al., 2010), as well as showing reduced bronchial stem cells (Zhao et al., 2014) and kidney defects (Reginensi et al., 2015). An important and widespread physiological role for YAP in mice might be obscured by the possibility of redundancy between YAP and TAZ (also known as WWTR1) a second mammalian family member that is highly similar in both sequence and function.

At the molecular level, Yki and YAP were shown to function by associating with the DNA-binding transcription factor Scalloped (Sd; or TEAD in humans) to drive transcription of anti-apoptotic and pro-proliferative target genes (Koontz et al., 2013; Liuchittenden et al., 2012; Vassilev et al., 2001; Wu et al., 2008). Other co-factors of Yki/YAP that promote transcription include WTS2 (Zhang et al., 2011b), MASK1/2 (Sansores-Garcia et al., 2013; Sider et al., 2013) and the SWI/SNF complex (Jin et al., 2013; Oh et al., 2013). The activity of Yki was found to be regulated by the Drosophila Hippo-Warts (Hpo-Wts) kinase signalling pathway, in which Wts directly phosphorylates Yki to promote its relocation from the nucleus to the cytoplasm (Dong et al., 2007; Huang et al., 2005; Oh and Irvine, 2008). In human cells in culture, YAP nuclear localisation is similarly inhibited upon LATS1/2 kinase phosphorylation, because phosphorylated YAP is retained the cytoplasm by binding to 14-3-3 family proteins (Dong et al., 2007; Zhao et al., 2007). This entire molecular system is now referred to as the Hippo signalling pathway.

Much recent work has aimed to identify upstream regulators of Hippo signalling. A group of apically localised proteins including crumbs (Crb, Crb1/2/3 in humans), Merlin (Mer, NF2 in humans), Expanded (Ex, similar to Willin and AMOT in humans) and Kibra (Kib, KIBRA or WWC1 in humans) were found to activate Hippo signalling (repressing Yki activity) in Drosophila epithelia (Baumgartner et al., 2010; Chen et al., 2010; Genevet et al., 2010; Hamaratoglu et al., 2006; Ling et al., 2010; Varelas et al., 2010; Yu et al., 2010) and in mice (Szymaniak et al., 2015). In addition, a group of adherens junction-localised proteins including Ajuba (Jub), Zyxin (Zyx), Dachs, Mib and Riquiqui (Riq), were shown to inhibit Hippo signalling (activating Yki) in Drosophila epithelia (Cho et al., 2006; Das Thakur et al., 2010; Degoutin et al., 2013; Gaspar et al., 2015; Mao et al., 2006; Rauskolb et al., 2011). Finally, manipulation of the level of F-actin in Drosophila can also affect Hippo signalling, possibly via signalling through the Src kinase, which can promote Yki activation (Enomoto and Igaki, 2013; Fernandez et al., 2011, 2014; Sansores-Garcia et al., 2011). Human YAP and TAZ were subsequently found to act as F-actin responsive mechanosensors in cell culture (Aragona et al., 2013; Benham-Pyle et al., 2015; Dupont et al., 2011; Zhao et al., 2007),...
but how their subcellular localisation is physiologically regulated in human epithelial tissues and cancers in vivo remains a fundamental unsolved problem.

Here, we examine the physiological function and regulation of YAP and TAZ in mammalian epithelial tissues. We focus on stratified squamous epithelia, particularly the skin, and compare our findings with columnar epithelia, such as the intestine and bronchus. We propose that YAP and TAZ act as sensors of both apical and basal signals in vivo, and that this regulatory logic explains why these proteins localise to the nucleus in basal stem/progenitor cells to promote cell proliferation and tissue renewal. Elevation of YAP and TAZ can then drive increased cell proliferation during wound healing or tumour formation.

RESULTS
YAP and TAZ are expressed in both mouse and human skin, and regulate gene expression in basal layer stem/progenitor cells

We began by characterising the expression and subcellular localisation of YAP and TAZ in both mouse and human skin. Both proteins were found to be expressed and nuclear localised in a subset of cells in the skin of the mouse embryo, neonate and adult. Nuclear localisation of YAP and TAZ was particularly prominent in basal layer cells of both interfollicular epidermis and the hair follicle (Fig. 1A). Some nuclear localisation was also detected in the highly flattened squamous cells, consistent with results in cell culture where cell flattening induces nuclear accumulation of YAP and TAZ (Dupont et al., 2011) (Fig. 1A). Human YAP and TAZ show a similar pattern of subcellular localisation in sections of adult human skin (Fig. 1B). Basal layer cells feature nuclear YAP and TAZ, whereas differentiating daughters feature cytoplasmic YAP and TAZ (Fig. 1B). Again, some nuclear localisation is also detectable in highly flattened squamous cells that have terminally differentiated (Fig. 1B).

To confirm that YAP and TAZ are transcriptionally active in the skin, we sought to identify YAP-regulated genes by an RNA-sequencing (RNA-seq) approach in human keratinocytes. mRNA was isolated from cells expressing activated mutant YAP5SA or siRNAs against YAP and subjected to RNA-seq and gene-set enrichment analysis (Fig. 1C, Fig. S1). We found that the YAP-regulated gene sets included: the previously identified Hippo/YAP reactomes; cell cycle reactomes (such as E2F targets or cyclin E-associated genes); cell growth reactomes (such as Myc, global translation regulators or regulation of ornithine...
decarboxylase); cancer signalling reactomes (such as EGFR-Ras signalling targets); and cancer microenvironment/metastasis reactomes (including regulators of cellular interactions with the extracellular matrix) (Fig. S1). We therefore analysed the expression of the corresponding cell cycle [CycE1 (CCNE2), PCNA, E2F1], cell growth [RPTOR, ODC1, ADC (AZIN2)] and EGFR and integrin signalling (CYR61, CTGF, AREG, integrins α3, α6, β1, β2, β4) regulators (Fig. 1D). We found a striking restriction of these YAP targets to the basal layer of the skin, indicating that YAP/TAZ transcriptional regulation is active exclusively in the basal stem/progenitor cell population (Fig. 1D).

**YAP and TAZ are required for skin homeostasis**

To examine the physiological role of YAP and TAZ, we generated double conditional knockout (dKO) mice with the skin-specific Keratin5-CreERT recombinase. Compared with control animals, the YAP/TAZ dKO mice showed a dramatic loss of hair in patches beginning 2 weeks after tamoxifen injection in adult mice, or causing complete blockade of hair growth in neonates treated with tamoxifen (Fig. 2A,B). Histological sections of the skin revealed expression and nuclear localisation of YAP and TAZ in control skin, which was lost in the dKO tissue. Proliferation of basal layer cells, as marked by Ki67 staining, was clearly reduced in YAP/TAZ dKO skin (Fig. 2A,B), as was YAP target gene expression (Fig. S2). These phenotypes are reminiscent of skin-specific conditional knockouts of integrin β1 (ITGB1) (Brakebusch et al., 2000; Grose et al., 2002; Piwko-Czuchra et al., 2009; Raghavan et al., 2000; Singh et al., 2009).

We next tested whether YAP and TAZ contribute to skin repair after wounding. We found that levels of both YAP and TAZ were elevated after wounding, particularly in the basal cell layer of the epidermis where strong nuclear staining is visible (Fig. 2C,D). We next recorded the time taken to repair small (4 mm) wounds in the back skin of control versus YAP/TAZ dKO mice. We found that control wounds normally healed completely by 10 days, whereas dKO wounds failed to heal within 10 days and instead required an additional 2 days to heal (Fig. 2E,F). This delay in healing was not observed when YAP or TAZ were deleted individually. To investigate the cause of the delay in wound healing, we examined...
cell proliferation in wounds of control versus dKO mice. We found that the number of Ki67+ cells was reduced in dKO wounds versus controls (Fig. 2G). These findings demonstrate a crucial, physiological requirement for YAP and TAZ in basal layer stem/progenitor cells to promote cell proliferation.

In the skin of the ITGB1 conditional knockout mice, cells that escape Cre-mediated recombination are able to repopulate the mutant skin in a short time frame (Piwko-Czuchra et al., 2009). We found that the same phenomenon occurs in YAP/TAZ dKO skin, where after Cre activation and YAP/TAZ deletion, either YAP+ or TAZ+ residual cells expanded their territory, consistent with the notion that YAP and TAZ promote proliferation of basal layer cells (Fig. S3). This phenomenon was also evident during wound healing, where YAP or TAZ positive cells were able to populate the wound and allow proliferation and healing in dKO animals (Fig. S3). These findings underscore the importance of YAP and TAZ in epidermal progenitor cell proliferation and skin homeostasis and suggest a close relationship between integrin signalling and YAP/TAZ function.

**Mechanisms controlling nuclear localisation of YAP in basal layer cells**

We next sought to understand how YAP and TAZ become nuclear localised in basal layer cells. Since YAP and TAZ are similar proteins that localise identically in skin, we henceforth focus on the regulation of YAP localisation. Recent work in cultured MCF10A breast cancer cells indicate a role for integrin-Src signalling and EGFR-PI3K signalling in promoting the nuclear localisation of YAP (Fan et al., 2013; Kim and Gumbiner, 2015). To test whether these pathways are active in skin, we examined their expression and subcellular localisation. By mining the Human Protein Atlas dataset, we found that ITGB1, SRC, EGFR and AKT2 (a marker of PI3K activation) are all expressed strongly in basal layer cells, with AKT2 recruited to the interface between basal layer epidermal cells and the underlying basement membrane extracellular matrix (Fig. 3A-E). This pattern is also evident in other squamous epithelia such as cervix or oesophagus and is retained in squamous cell carcinomas (Fig. 3A-E). These data suggest that nuclear YAP localisation might be stimulated by integrin-Src and/or PI3K signalling in basal layer skin keratinocytes (Fig. 3F).

To confirm that integrin-Src and PI3K signalling pathways are required for YAP nuclear localisation in keratinocytes, we systematically manipulated these pathways with siRNA knockdown or treatment with specific inhibitor compounds in human keratinocytes in culture. We found that inhibition of ITGB1 with blocking antibodies or siRNA, inhibition of the downstream effectors SRC or FAK, or inhibition of PI3K profoundly impairs

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**Fig. 3. Integrin-Src and EGFR-PI3K localisation in human stratified squamous epithelia and squamous cell carcinomas (SSCs).** The Human Protein Atlas dataset was mined to compare the expression and localisation of potential YAP regulators in human skin sections. YAP staining reveals basal layer nuclear localisation (A), ITGB1, SRC and EGFR staining reveals basal layer expression (B-D) and AKT2 staining reveals basal subcellular localisation (E) across squamous tissue types and cancers. (F) Model for YAP regulation in stratified squamous epithelia.
YAP nuclear localisation (Fig. 4A,B). Interestingly, inhibition of the PI3K effectors AKT and TORC1 had no effect on YAP localisation, whereas inhibition of PDK1 did partially impair YAP nuclear localisation (Fig. 4C). Notably, drugs inhibiting F-actin, myosin II or Rho kinase had only a moderate effect on YAP localisation in keratinocytes (Fig. 4D). Quantification of these phenotypes highlights the strong effect of inhibition of integrin-Src and PI3K (Fig. 4E). Both Src inhibitors and PI3K inhibitors led to a clear increase in phosphorylated YAP (p-YAP), indicating that Hippo signalling (MST-LATS signalling) is elevated by these treatments (Fig. 4F). We confirmed these findings in a classic ‘scratch-wound’ assay, where Src inhibition completely reversed the nuclear localisation of YAP at the leading edge (Fig. 4G). These findings indicate that integrin-Src and EGFR-PI3K signalling are essential for YAP nuclear localisation in keratinocytes (Fig. 4H).

To extend these findings in vivo, we examined the role of integrin-Src signalling in mouse skin. We compared YAP localisation in untreated and TPA-treated (inflamed) skin samples from control animals and knockouts for FAK or Src (Fig. 5A-C). We found that loss of FAK or Src results in decreased YAP levels and nuclear localisation in both normal and inflamed skin (Fig. 5A-C). Some nuclear YAP remained in flattened cells (Fig. 5A-C, asterisks). Similar results were obtained by treatment of mice with the topical Src inhibitor (Dasatinib), which was able to drastically reduce YAP levels and nuclear localisation in untreated or TPA-treated skin, as well as in skin papillomas induced by a TPA+DMBA treatment regimen (Fig. 5D-I). These findings show that integrin-Src signalling is crucial to promote YAP stabilisation and nuclear localisation in basal layer stem/progenitor cells. Accordingly, recent work indicates that skin papillomas induced by DMBA+TPA in mice can be strongly reduced in size and frequency by homozygous deletion of YAP along with one copy of TAZ or by treatment with Dasatinib (Creedon and Brunton, 2012; Serrels et al., 2009; Zanconato et al., 2015).
Mechanisms controlling YAP cytoplasmic localisation in differentiating daughter cells of squamous versus columnar epithelia

The above analysis suggests that daughter cells differentiate in the skin simply by loss of contact with the basement membrane extracellular matrix and consequent loss of integrin-Src signalling, EGFR-Pi3K signalling and YAP nuclear localisation. This model is plausible in all stratified squamous epithelia, but cannot explain the self-renewal versus differentiation decision in columnar epithelia because differentiated columnar epithelial cells retain contact with the basement membrane. Thus, columnar cells must employ an additional mechanism to promote YAP localisation to the cytoplasm. An obvious candidate is the expression of a differentiated apical plasma membrane domain in columnar epithelial cells, because apical proteins associated with Crumbs (CRB3) are well known to induce Hippo signalling (MST-LATS signalling) to drive YAP to the cytoplasm (Chen et al., 2010; Fletcher et al., 2015; Ling et al., 2010; Szymaniak et al., 2015; Varelas et al., 2010).

To test this notion in vivo, we compared the subcellular localisation of YAP with that of CRB3 in columnar epithelia in the gallbladder, endometrium, lung bronchus, breast duct, urinary bladder, small intestine, colon and salivary gland. In all cases, apical localisation of CRB3 in differentiated daughter cells correlated with cytoplasmic localisation of YAP (Fig. 6A-H). Accordingly, basal layer stem/progenitor cells of the lung, breast or intestine retained nuclear YAP but lack apical CRB3. Notably, CRB3 is not expressed in squamous epithelia so cannot mediate the regulation of YAP in these tissues (Fig. 6I-L). The key Hippo pathway components Merlin, SAV1 and KIBRA colocalised with CRB3 (Figs S4 and S5) (Chen et al., 2010; Genevet et al., 2010; Hamaratoglu et al., 2006; Ling et al., 2010; Yin et al., 2013; Yu et al., 2010; Zhang et al., 2010). These results indicate that a universal regulatory logic exists...
in which YAP nuclear localisation requires contact with the basement membrane but is inhibited by expression of an apical domain (Fig. 6M).

We next sought to confirm that apical and basal signals act antagonistically in columnar epithelial cells. We examined human intestinal epithelial cells in culture that are capable of forming 3D cysts or 2D monolayers in which YAP becomes cytoplasmic. We found that siRNA knockdown of the apical determinant CDC42 or LATS1/2 has similar effects, driving YAP to the nucleus (Fig. 7A,B). Strong YAP nuclear localisation can also be achieved simply by plating these cells at low density, so that they are unable to differentiate an apical domain and also retain a flat morphology with an extensive basal surface area (Fig. 7C). This basal contact appears to invoke the same integrin-Src signals identified in keratinocytes, because blocking of integrins with low Ca\(^{2+}\), anti-ITGB1 antibodies or ITGB1 siRNAs relocalised YAP to the cytoplasm (Fig. 7C). Inhibition of Src, FAK, PI3K or PDK1 also impaired YAP nuclear localisation (Fig. 7D,E). These effects are once again as strong as inhibition of F-actin, myosin II or Rho kinase (Fig. 7F,G). Examination of p-YAP levels indicated that integrin-Src signalling acts via regulation of MST-LATS phosphorylation of YAP (Fig. 7H). These results suggest that apical domain formation activates LATS kinases to retain YAP in the cytoplasm, whereas basal integrin-Src and PI3K signalling inhibits LATS kinases to promote nuclear YAP localisation (Fig. 7I).

To further explore these findings in vivo, we examined how YAP behaves in columnar epithelial tumours that progress to invasive adenocarcinomas. We found that YAP remains cytoplasmic whereas tumours of the colon, stomach, lung, endometrium, urothelium or ovary retained their columnar epithelial form (Fig. 8A-F). By contrast, invasive adenocarcinomas of the same
tissue origin all featured a loss of columnar form and a dramatic localisation of YAP to the nucleus (Fig. 8A-F). These results suggest that loss of the apical domain during tumour progression allows YAP to become nuclear. We therefore tested whether nuclear YAP in invasive adenocarcinomas would be sensitive to inhibition of integrin-Src signalling with Dasatinib. We examined Apc<sup>Δ716−718</sup> p53<sup>Trp53<sup>+/−</sup></sup> mutant intestinal organoids that had been implanted subcutaneously into nude mice. On transplantation, these organoids rapidly produce highly invasive adenocarcinomas, entering the surrounding stromal tissue. We found that YAP localisation became strongly nuclear, specifically in the invasive tumour cells (Fig. 8G). We next treated mice carrying such invasive tumours with the Src inhibitor Dasatinib, which strongly suppressed nuclear YAP localisation and reduced tumour growth and invasion (Fig. 8H).

These findings indicate that Src activity promotes YAP nuclear localisation <em>in vivo</em> and suggest a potential therapy for invasive adenocarcinomas and carcinomas.

**DISCUSSION**

Our results identify a physiological role for YAP and TAZ in skin homeostasis, promoting cell proliferation in basal layer stem/progenitor cells (Figs 1, 2). YAP and TAZ localise to the nucleus of basal layer cells to drive transcription of a set of genes associated with cell cycle progression, cell growth, EGFR signalling and cell-matrix adhesion via integrins. In the absence of YAP and TAZ, proliferation is reduced and dramatic hair loss occurs, indicating that YAP and TAZ are crucial players in the stem/progenitor cell biology of the skin. Importantly, loss of either YAP or TAZ individually had
no visible phenotype, confirming that the two proteins act in a redundant fashion in this tissue.

Both YAP and TAZ localise to the nucleus in the basal layer cells of the skin and we focused on YAP to characterize the molecular mechanisms responsible for this nuclear localisation (Figs 3–5). We examined the model that integrin-Src and EGFR-PI3K signalling promotes YAP nuclear localisation, which was first proposed based on experiments in MCF10A breast cells in culture (Fan et al., 2013; Kim and Gumbiner, 2015), and found that these signalling molecules are indeed strongly expressed in basal layer skin cells and are essential to promote YAP nuclear localisation in keratinocytes in culture and in mouse basal layer skin cells in vivo. Since YAP appears to induce expression of integrins, integrin ligands (CYR61, CTGF) and EGFR ligands (AREG), we propose that a positive feedback loop drives basal layer stem/progenitor cell identity and that this loop is broken when daughter cells lose contact with the basement membrane and differentiate – forming a bistable system of cell fate determination. Our findings provide an explanation for how these signalling pathways integrate to control skin stem/progenitor cell biology.

The notion that nuclear localisation of YAP occurs upon contact with basement membrane extracellular matrix applies equally to other squamous epithelia. By contrast, columnar epithelia differentiate an apical domain that induces YAP relocalisation to the cytoplasm via apical CRB3-MER-KIBRA-SAV signals, which are known to activate the MST and LATS kinases to promote YAP phosphorylation and cytoplasmic retention despite contact with the basement membrane (Figs 6, 7, Figs S4–S6) (Baumgartner et al., 2010; Chen et al., 2010; Fletcher et al., 2015; Genevet et al., 2010; Hamaratoglu et al., 2006; Ling et al., 2010; Sun et al., 2015; Szymaniak et al., 2015; Varelas et al., 2010; Yin et al., 2013; Yu et al., 2010). The CRB3-MER-KIBRA-SAV complex appears to be
absent in squamous epithelia, which never differentiate a true apical domain, leaving basement membrane contact as the sole regulatory mechanism (Fig. 6). Thus, our results show that antagonistic apical and basal polarity signals serve as the primary control mechanism that determines YAP subcellular localisation in vivo. In a striking parallel, the same apical and basal polarity determinants act antagonistically in epithelial membrane polarisation, with integrin and PI3K signalling localising PtdIns(3,4,5)P3 basally, and helping to restrict and/or orient PtdIns(4,5)P2, CDC42 and the CRB3 complex apically (Akhtar and Streuli, 2013; Bryant et al., 2014; Fletcher et al., 2012; Martin-Belmonte et al., 2007; Thompson, 2013). Further work will be necessary to fully elaborate the molecular interactions that mediate the antagonistic relationship between apical and basal signals in cell polarisation and nuclear signalling via YAP.

This fundamental control mechanism appears to be conserved across the animal kingdom. For example, Drosophila simple columnar epithelia such as imaginal discs rely primarily on apical Crb-Mer/Ex-Kibra-Sav signalling to retain Yki in the cytoplasm and restrict tissue growth (Baumgartner et al., 2010; Chen et al., 2010; Genevet et al., 2010; Homanatoglu et al., 2006; Ling et al., 2010; Yu et al., 2010). By contrast, Drosophila stratified columnar epithelia such as the intestine require integrins, Src, EGFR and Yki to promote proliferation of basal layer stem/progenitor cells, suggesting that the regulatory connection between them described here is also conserved (Cordero et al., 2014; Jiang et al., 2011; Kohlmaier et al., 2015; Lin et al., 2013; Shaw et al., 2010; Staley and Irvine, 2010; Xu et al., 2011). Furthermore, ectopic activation of Src, EGFR, PI3K or Yki in simple columnar imaginal discs is sufficient to induce overproliferation of cells, whereas loss of PI3K or Yki strongly impairs imaginal disc tumour formation (Doggett et al., 2011; Enomoto and Igaki, 2013; Fernandez et al., 2014; Herranz et al., 2012, 2014; Strassburger et al., 2012; Willecke et al., 2011).

Our model raises interesting questions about the possible physiological roles of other YAP regulators identified in cell culture, namely that YAP is controlled by Wnt signalling (Azzolin et al., 2014; Cai et al., 2015; Park et al., 2015), GPCR signalling (Yu et al., 2012), PKA signalling (Yu et al., 2013), LKB1-MARK signalling (Mohseni et al., 2014), protease-activated receptors (Mo et al., 2012) or the Mevalonate pathway (Sorrentino et al., 2012). Further work is necessary to understand in which tissues and under what conditions these diverse signals are utilised and integrated in vivo.

Importantly, our model is easily reconciled with a possible role of YAP as a mechanosensor in epithelial tissues in vivo (Dupont et al., 2011). Mechanical force has been proposed to modulate signalling by both the apical Crb-Mer/Ex-Kibra-Sav system in Drosophila (Fletcher et al., 2015; Rauskolb et al., 2014) as well as the basal integrin-Src system in mammalian cell culture (reviewed in Humphrey et al., 2014; Lawson and Burridge, 2014). In the early mouse pre-implantation embryo, cortical tension is as the basal integrin-Src system in mammalian cell culture (reviewed in Humphrey et al., 2014; Lawson and Burridge, 2014). In the early mouse pre-implantation embryo, cortical tension is
were performed using Lipofectamine RNAiMax transfection reagent (Invitrogen). Briefly, cells were seeded in 6-well plates and treated with the siRNA/transfection mix 2 h post seeding. A final concentration of 50-100 nM siRNA was used for transfections. The following day, another transfection was performed before the cells were trypsinised 4 h later and reseeded either for 2D or 3D culture. 2D siRNA treatments were left for a total of 72 h and 3D treatments were left for a total of 120 h. 3D cultures were prepared as previously stated (Elbedwyi et al., 2012). siRNAs were used as siGenome pools (Dharmacon).

**Treatment with inhibitor, blocking antibody and low-calcium medium**

2D mammalian inhibitor treatments were for 4 h. They were as follows: 5 µM PFK52228 (FAK); 5 µM Saracatinib (Src); 5 µM Dasatinib (Src/Abl); 5 µM BX795 (PD1K); 5 µM MM2206 (AKT); 2 µM GDC0941 (PI3K); 100 µM Blebbistatin (myosin); 100 µM Y27632 (ROCK); 2 µM Latrunculin A (actin) and 3 µM Everolimus (mTOR); reagents were supplied by Sigma-Aldrich and Stratech Scientific Ltd. Integrin B1 blocking antibody or control IgG antibody (gifts from Nancy Hogg, Francis Crick Institute) was incubated with the cells for 1 h at a concentration of 10 µg/ml before the cells were replated. Low-calcium conditions were as previously reported (Elbedwyi et al., 2012). 2D wound healing involving plating the cells at high density, causing a scratch and subsequent addition of Dasatinib for 4 h.

**Antibodies, image acquisition and quantification**

Primary antibodies used were: rabbit YAP (H-125, Santa Cruz, sc-15407; 1:200IF, 1:1000 IB), mouse YAP (63.7; Santa Cruz, sc-101199; 1:200 IF, 1:1000 IB), rabbit p-YAP (Cell Signaling Technology, 4911; 1:1000 IB). Samples were imaged with a Leica SP5 confocal microscope using a 63× oil immersion objective and processed using Adobe Photoshop. Fixation and cell culture quantification was carried out as previously described (Fletcher et al., 2015).

**YAP/TAZ conditional deletion**

Tamoxifen (Sigma, 20 mg/ml in peanut oil) was injected intraperitoneally (IP) (5 µl/g body weight) for 5 consecutive days into 8 to 16-week-old controls or transgenic animals carrying K5-CreER T Yapfl/fl Tazfl/fl to induce Yap/Taz knockdown and analysed for Yap/Taz deficiency by immunohistochemistry 7 days thereafter. K5-CreER T Yapfl/fl Tazfl/fl mice used for long-term analysis were subsequently IP injected with tamoxifen every month for 3 consecutive days and analysed 8 weeks after the start of tamoxifen treatment.

**Wound healing**

Following the 5-day tamoxifen treatment, 4 hydroxy-tamoxifen (4OHT, Sigma) was topically applied to shaved back skin for 5 consecutive days at a dosage of 10 mg/ml in ethanol and 100 µl was applied per mouse. Mice were anaesthetised with IsoFlo (Isoflurane, Abbott Animal Health) and treated with the analgesics Vetergesic (Alstoe Animal Health) and Rimadyl (Pfizer) intraperitoneally. Mice were anaesthetised with IsoFlo (Isoflurane, Abbott Animal Health) and treated with the analgesics Vetergesic (Alstoe Animal Health) and Rimadyl (Pfizer) intraperitoneally. 3 µl of p-SRC (1:1000 IB), rabbit p-SRC and 3 µM Everolimus (mTOR) were applied to the shaved back skin for 10 weeks then weekly for a further 4 weeks before the samples were harvested.

**Intestinal experiments**

Mice carrying the AhCre recombinase were induced by three intraperitoneal (i.p.) injections of 80 mg/kg β-Napthoflavone for 1 day. Intestinal phenotypes were analysed 4 or 7 days after transgene induction to assess homeostasis or regeneration, respectively. Intestinal regeneration was induced by irradiating mice with 14Gy gamma-irradiation 4 days after recombinase induction. Mice were sacrificed 72 h post irradiation and the small intestine isolated and flushed with tap water. Ten 1 cm portions of small intestine were bound together with surgical tape and fixed in 4% neutral buffered formalin.

**Organoid transplantation experiments**

Intestinal crypts from VillinCreER Apcfl/fl p53fl/fl mice were removed 4 days following Cre induction with Tamoxifen (2 mg). This causes full recombination at both the Apc and p53 loci and organoids now grow as spheres in an R-Spondin-independent manner (Sato et al., 2009). For transplantation of organoids, 50 organoids were transplanted subcutaneously into nude mice (see Valeri et al., 2014). A dose of 10 mg/kg Dasatinib daily gavage was chosen as we have previously shown to cause a reduction in p-SRC in vivo without toxicity (Morton et al., 2010). Mice were treated continuously from 10 days post injection of spheres.

**Immunohistochemistry**

Mouse back skin samples were harvested and fixed in neutral-buffered formaldehyde 10% v/v and then embedded in paraffin blocks. 4-µm-thick sections were cut, deparaffinised and rehydrated using standard methods. After an antigen retrieval step, sections were stained with Hematoxylin and Eosin (H&E) solution or with primary antibody. Additional images of human samples were obtained by datamining the www.proteinatlas.org database (Berglund et al., 2008; Lundberg and Uhlen, 2010; Pontén et al., 2008; Uhlen et al., 2005, 2015, 2010).

**RNA-seq analysis**

A431 or HaCAT cell lysates transfected with empty vector, YAP1 S5A, control siRNA or YAP1 siRNAs were used. Sequencing was performed on biological triplicates on the Illumina HiSeq 2500 platform and generated ~69 million 100 bp paired end reads per sample (data deposited in GEO under accession number GSE80082). Sequenced reads were trimmed to 75 base pairs and mapped to the Refseq genome model, using RSEM (v.1.2.21). RSEM uses the bowtie2 alignment tool. Gene counts were filtered to remove genes with 10 or fewer mapped reads per sample. TMM (treated mean of M-values) normalisation and differential expression analysis using the negative binomial model was carried out with the R-Biocoductor package ‘edgeR’. Genes with logCPM>1 and FDR<0.05 were judged to be differentially expressed. Enrichments of pathway, category and motif gene sets were assessed using GSEA with logFC pre-ranked gene lists. Gene sets with an enrichment false discovery rate (FDR) value of less than 0.05 were judged to be strongly statistically significant and values of less than 0.25 significant.

**qPCR**

Total RNA was extracted from homogenised mouse skin using an RNaseq Mini Kit (Qiagen). CDNA synthesis for WT or dKO mice was performed using Superscript II (Invitrogen). Primers were purchased as Quantitect Primers (Qiagen). Gene samples were run in triplicate on a Quantstudio 12 Flex Thermocycler. Expression values were calculated using the ∆∆CT method relative to the housekeeping gene β-2-microglobulin (B2M). All error bars indicate s.e.m.
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Competing interests

The authors declare no competing or financial interests.

Author contributions

A.E., Z.I.V.-M. and B.J.T. designed research, planned experiments and analysed the data; A.E. performed mammalian cell culture experiments and RT-PCR. Z.V.M performed the mouse experiments. A.E. and Z.I.V.-M. stained and prepared the data. B.S.-D and R.K.S stained and performed the mouse experiments. A.E. and Z.I.V.-M. performed the RNA-seq. S.B. provided data; A.E. performed mammalian cell culture experiments and RT-PCR. Z.V.M, A.E., Z.I.V.-M. and B.J.T. designed research, planned experiments and analysed the data; A.E., Z.I.V.-M. and B.J.T. planned experiments. B.J.T. performed experiments. A.E., Z.I.V.-M. and B.J.T. wrote the manuscript. Z.V.M and B.J.T. contributed to the acquisition of funding.

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Data availability

RNA-seq data has been deposited in Gene Expression Omnibus ( GEO) under accession number GSE80082 and is available at http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE80082.

Supplementary information

Supplementary information available online at http://dev.biologists.org/lookup/suppl/doi:10.1242/dev.133728/-/DC1

References


Regenerative signaling in the intestine is tightly regulated by the Hippo pathway. In a mouse model of pancreatic cancer, Yap is activated by Wnts and Src, leading to the development of metastases. Recent studies have identified PARs as potential therapeutic targets for regulating the Hippo pathway and cancer progression. In summary, the Hippo pathway represents a promising target for the treatment of cancer and other diseases.