

Mechanosensing defects and YAP-signaling in LMNA-related congenital muscular dystrophy

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1. INTRODUCTION

1.1. LAMINOPATHIES

Mutations in the *LMNA* gene cause more than ten different disorders, commonly named laminopathies. Laminopathies are characterized by a great clinical as well as genetical variability. The first *LMNA* mutation associated with a genetic disorder was identified in autosomal dominant Emery-Dreifuss Muscular Dystrophy (EDMD) (Bonne et al. 1999). Since then, it has been shown that laminopathies can affect different tissues including adipose tissue, nervous system and skeletal and/or cardiac muscles but, also cause systemic disease, the premature aging syndromes. However, the most frequent diseases associated with *LMNA* mutations are characterized by skeletal and cardiac muscle involvement. Different phenotypes have been reported with skeletal muscle involvement: limb-girdle muscular dystrophy type 1B (LGMD1B), autosomal dominant Emery-Dreifuss muscular dystrophy (EDMD2) and a form of congenital muscular dystrophy (L-CMD) (Maggi, Carboni, and Bernasconi 2016). These disorders differ in term of age at onset, first symptoms and pattern of affected muscles. More than 200 mutations were identified to cause these disorders, which are spread throughout the whole *LMNA* gene. However, relationships between genotypes and phenotypes remain poorly understood (Bertrand et al, 2011). Mutations in lamin-binding proteins, including emerin and nesprins can also caused striated muscular dystrophies. These diseases are often referred as nuclear envelopathies.

LMNA-RELATED CONGENITAL MUSCULAR DYSTROPHY

LMNA-related congenital muscular dystrophy, or L-CMD, is a rare but especially severe early-onset form of laminopathies. Children, suffering from L-CMD, show a severe weakness and wasting of skeletal muscles with a characteristic development of a “dropped head” syndrome phenotype. This clinical phenotype is further described with selective axial weakness, wasting of the cervicoaxial muscles, proximal involvement of the upper limbs, distal involvement in lower limbs, an early development of talipes feet and a rigid spine with thoracic lordosis. Later, patients develop proximal contractures, sparing elbows and most children require ventilatory support. L-CMD patients frequently develop a cardiac dysfunction and ventricular arrhythmias in their second decade (Quijano-Roy et al. 2008). The onset of this disease is in the first years of life and rare cases

have been reported where children evolved no motor-development and already showed fetal immobility. Histopathological studies on patient biopsies revealed dystrophic changes and an abnormal variability of fiber size (Fig.1).

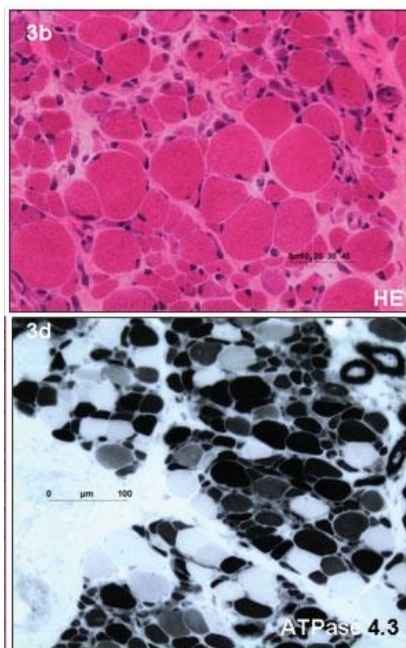


FIGURE 1-1: H/E and ATPase stained muscle sections from L-CMD patients. Modified from Quijano-Roy et al, 2008

L-CMD is caused by autosomal dominant *de novo* heterozygous mutations of the *LMNA* gene. The disease has been first described in 2008, by Quijano-Roy et al. In the 15 reported cases, more than 10 different *LMNA* mutations were identified to cause L-CMD (Quijano-Roy et al. 2008). Two of those patients have been identified to carry the p.delK32 mutation ($\Delta K32$) (Fig. 2). A knock-in mouse model has been generated for this mutation as a model for L-CMD (Azibani et al. 2014). Heterozygous $\Delta K32$ mice die between the ages of 10 and 20 months from dilated cardiomyopathy (CMD), a common late symptom of laminopathies. However, surprisingly, these mice do not show any spontaneous skeletal muscle defects (Cattin et al. 2013). In contrast, homozygous $LMNA^{\Delta K32/\Delta K32}$ mice exhibit

a severe delay in striated muscle maturation and growth retardation. These mice die in their second week of life, most likely from metabolic defects (Bertrand et al 2012). The expression of lamin A/C protein is severely reduced in homozygous $LMNA^{\Delta K32/\Delta K32}$ mice (only 20% of Lamin A/C levels compared to WT). Moreover, mutant A-type lamins are mainly localized in the nucleoplasm rather than the nuclear envelope in $LMNA^{\Delta K32/\Delta K32}$ mice (Bertrand et al. 2012).

However, unlike the $\Delta K32$ mouse model, which requires homozygous expression of the mutant lamin A/C (Bertrand et al., 2011), human cells from L-CMD patients carry only one mutated *LMNA* allele. Recent data show that L-CMD causing *LMNA* mutations impair the ability of muscle cell precursors to sense tissue stiffness and to respond to mechanical challenges (Bertrand et al. 2014). Moreover, *LMNA*-mutated myoblasts show enhanced activity of Yes-Associated protein (YAP)-dependent signaling which is paradoxically reduced after cyclic stretch (Bertrand et al. 2014). Furthermore, L-CMD mutant myoblasts failed to align in 3D soft matrix (Bertrand et al. 2014).

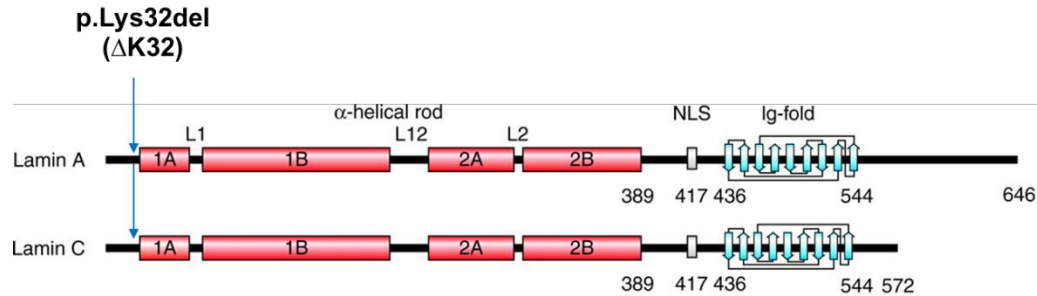


FIGURE 1-2: LaminA/C protein structure. The blue arrow indicated the side of the (Δ K32) mutation site. Modified from (Dechat et al. 2010)

A-TYPE LAMINS

L-CMD causing mutations are found all along the LMNA gene which codes for A-type lamins. A-type lamins contain at least three isoforms; lamin A, lamin C, and lamin A Δ 10, which result from alternative splicing. A fourth isoform, lamin C2, has been found in rodents (Link et al. 2013). The two main isoforms are lamin A and lamin C (Fig. 2). The N-terminal domain of lamin A and C are identical for the first 566 amino acids whereas they differ at the C-terminal end. Lamin A derives out of the full-length transcript containing all 12 exons, whereas the lamin C transcript contains only the first 10 exons. The mature lamin A protein is synthesized through a precursor, prelaminA, which is farnesylated and carboxymethylated at the cysteine residue at the C-terminal CAAX box. The C-terminal residues, including the farnesylated and carboxymethylated cysteine, are then cleaved off by Zmpste24/FACE1 to generate the mature lamin A. Mature lamin A and lamin C proteins share a N-terminal head domain, a central α -helical rod domain, a nuclear localization signal sequence (NLS) and an Ig-fold. Lamin A and Lamin C differ at their C-terminal end, with an 80 amino acids long unique region for lamin A. Lamin C has a unique six amino acids long region in the C terminal domain. (Dechat et al, 2008).

A-type lamins are type V intermediate filaments nuclear envelope. Together with B-type lamins they form the nuclear lamina, which is adjacent to the inner nuclear membrane. B-type lamins are farnesylated and form independent but interconnected networks with A-type lamins (Schermelleh et al. 2008; Goldberg et al. 2008; Shimi et al. 2008; Kolb et al. 2011). B-type lamins form a thin meshwork, which is associated with the inner nuclear membrane (INM) and the nuclear

pore complexes (NPCs), whereas A-type lamins form a thicker network (Davidson and Lammerding 2014)

A and B-type lamins differ in their solubility during cell mitosis as well as in their expression patterns. B-type lamins are expressed throughout development and differentiation, beginning in the unfertilized egg. In contrast, A-type lamins are only expressed at very low levels in early development and their expression increases with cell differentiation (Burke and Stewart 2002; Eckersley-Maslin et al. 2013). LaminA is expressed ubiquitously in vertebrate cells, however, expression levels vary largely between different tissues. LaminA expression levels are very low in the central nervous system whereas they are particularly high in muscle and other tissues derived from mesenchymal cells (Davidson and Lammerding 2014; Hanif et al. 2009; Yang et al. 2011)

To form the two-dimensional supramolecular structure of the nuclear lamina, mature lamin protein first assemble into dimers. These dimers polymerize into a polar head-to-tail polymer. A non-polar protofilaments is formed through lateral assembly of the dimers. This non polar protofilaments in turn assembles in an antiparallel order into intermediate filaments (Dechat et al. 2008). The laminA network is reversibly disassembled during mitosis in early G1 phase (Adam and Goldman 2012). The disassembly of the A-type lamina is regulated by phosphorylation of laminA (Dechat et al. 2000; Moir et al. 2000; Naetar et al. 2008). Two phospho-acceptor sites flank the central rod domain of A-type lamins at serine 22 and serin 392. Their phosphorylation via the mitosis specific kinase Cdk1 drives the disassembly during nuclear envelope breakdown in the early stages of mitosis (Dessev, Iovcheva-Dessev, and Goldman 1990; Kochin et al. 2014).

The LMNA Δ K32 mutation corresponds to a deletion of a lysine on position 32, which is located in the highly-conserved coil 1A region at the N terminus of the first lamin rod domain. The Δ K32 mutation in human corresponds to the Δ K46 in *c.elegans*. The Δ K46 mutation alters the lateral assembly of head to tail assembly polymers, which results in increased mobility and solubility of mutant lamins as well as in the formation of A-type lamins aggregates in the nuclear interior (Bank et al. 2012; Zwerger et al. 2013).

Several functions of A-type lamins have already been proposed. A-type lamins are crucial for the structural stability of the nucleus, the maintenance of nuclear architecture and nuclear

positioning. A-type lamins have further been implicated in the regulation of chromatin organization, epigenetics, gene transcription, cell cycle regulation, cell apoptosis and differentiation (Broers et al. 2006). In particular, A-type lamins have multiple functions through associations with chromatin, nuclear histones and various transcription factors to maintain chromatin structure and regulate gene expression (Meier et al. 1991; Verstraeten et al. 2007; Dechat et al. 2008). A-type lamins also directly bind to promoters both at the nuclear periphery and the nuclear interior (Lund and Collas 2013). According to the so called “gene regulation hypothesis”, A-type mutations alter the regulation of different genes. This in turn may contribute to the clinical variability of laminopathies. The differentially expression of transcription factors in distinct tissues can thereby determine the affected tissue (Azibani et al., 2014)

Another hypothesis explaining LMNA related muscular dystrophies is the “structural hypothesis”. The major functions attributed to nuclear lamins include the regulation of the nuclear size and shape by maintaining the structural integrity of the nuclear scaffold and by defining the mechanical properties of the nucleus (Dechat et al. 2008). Particularly, A-type lamins define the viscosity and stiffness of a nucleus (Davidson et al. 2014; Jevtić and Levy 2014). Nuclear deformability is sensitive to A-type lamin expression and laminopathies are associated with altered nuclear shape (Swift et al. 2013; Lammerding et al. 2006; Sullivan et al. 1999). An increased nuclear fragility in response to physical stress has been demonstrated in LMNA deficient cells (Lammerding et al. 2004; Broers et al. 2005; Nikolova et al. 2004; De Vos et al. 2011).

In contracting tissues, such as skeletal or cardiac muscles, disrupted nuclei may promote tissue damage and apoptosis. EDMD and DCM disease causing mutations led to decreased nuclear stiffness and increased nuclear deformation and ruptures *in vitro* and *in vivo* (Zwerger et al. 2013; De Vos et al. 2011; Gupta et al. 2010).

NUCLEO-CYTOSKELETAL COUPLING AND NUCLEAR MECHANOTRANSDUCTION

A third pathophysiological model has been proposed after the discovery of the nucleo-cytoskeletal coupling by the LINC complex (Linker of Nucleoskeleton to Cytoskeleton Complex). This multiprotein complex is composed of Sun and Nuclear Envelope Spectrin Repeat (NESPRIN) proteins, which span the nuclear envelope. At the inner surface of the inner nuclear membrane, Sun proteins bind to A-type lamin and emerin. In the luminal space, Sun proteins interact with Nesprins (Salpingidou et al. 2007; Östlund et al. 2009; Liang et al. 2011). At the cytoplasmic side, nesprins connect with actin-, microtubule- and intermediate filament networks of the cytoskeleton. Thereby, the LINC complex builds a physical connection between the nucleo- and cytoskeleton (Fig. 3). Although the molecular dynamics of the LINC complex remain largely unknown, critical functions of the LINC complex have been proposed. The positioning of the nucleus inside the cell during cell migration and the localization of synaptic nuclei in muscle fibers dependent on the LINC complex (Lombardi et al. 2011; Roux et al. 2009; Luxton et al. 2010; Lei et al. 2009; Yu et al. 2011).

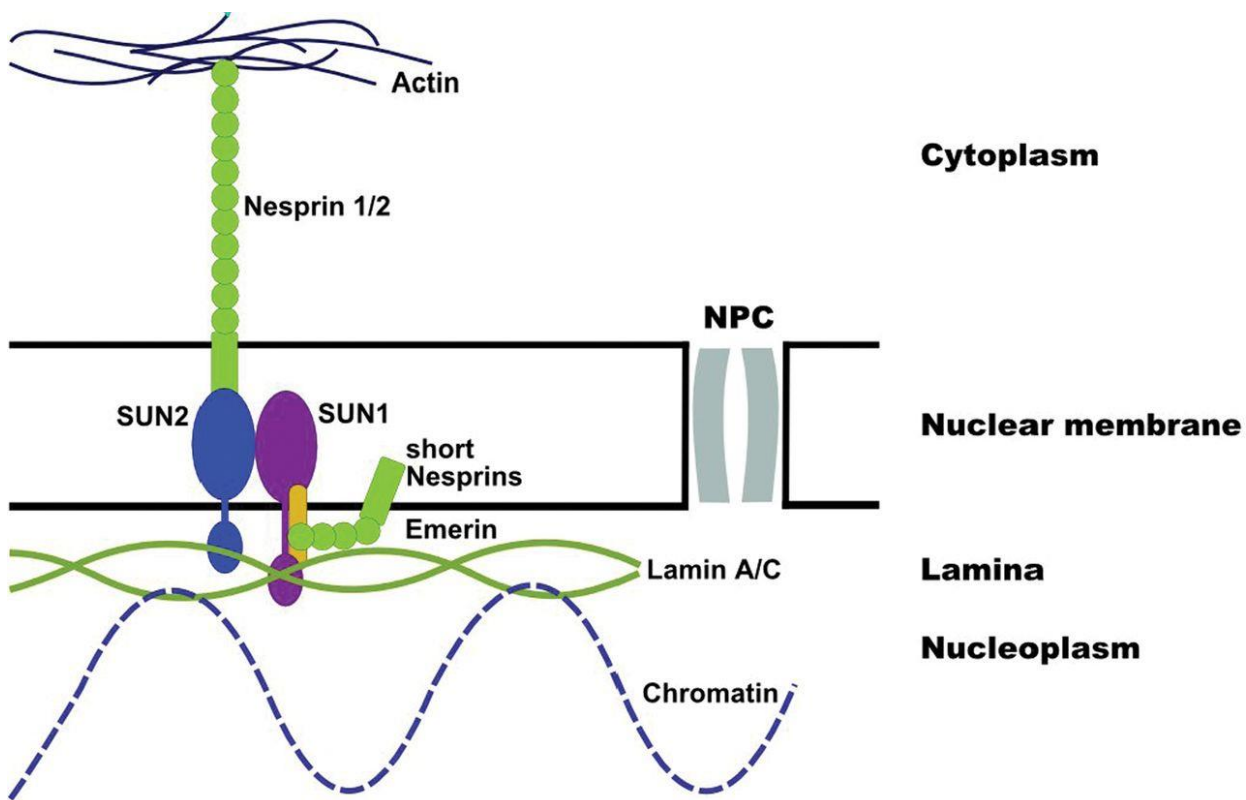


FIGURE 1-3: The LINC complex. Modified from (Meinke, Nguyen, and Wehnert 2011)

Furthermore, the LINC complex transmits mechanical forces between the cytoskeleton and the interior of the nucleus (Lombardi and Lammerding 2011; Zwerger et al. 2013). In a subset of muscular dystrophy causing LMNA mutations, the interaction between A-type lamin and Sun is disrupted (Haque et al. 2010). The force transmission between the nucleus and cytoskeleton is impaired in several myopathic lamin mutations (Zwerger et al. 2013). Furthermore, mutations in nesprin proteins cause muscular dystrophy. Taken as a whole, these studies strongly support the hypothesis that an impaired nucleo-cytoskeletal coupling contributes to the pathophysiology of LMNA related muscular dystrophies (Zhang et al. 2007). A possible mechanism regulating the nuclear resistance against mechanical rupture has recently been proposed. It has been shown that A-type lamin protein levels depend on the stiffness of the ECM and accumulate at the nuclear envelope after strain (Swift et al., 2013)

Lamin mutations also affect the physical properties of the cytoskeleton, most likely due to defects in the nucleo-skeletal coupling. Lamin A/C-deficient cells have a reduced cytoskeletal stiffness and an aberrant organization of cytoskeleton networks. The actin cytoskeleton of LMNA deficient cells shows a severe disorganization in the perinuclear region, as found in cells with disrupted LINC complex (Broers et al. 2005; Lee et al. 2007; Khatau et al. 2009; Lammerding et al. 2004). A subset of actin fibers in the perinuclear region of adherent cells is called the “actin cap”. The actin cap consists of thick, actomyosin filament bundles which cover the top of the nucleus and are mostly aligned with the overall cell orientation (Khatau et al. 2009). These actin fibers are structurally and functionally distinct from dorsal and basal actin fibers, which do not directly connect to the nucleus (Hotulainen and Lappalainen 2006).

Altered actin dynamics have been reported in LMNA deficient and LMNA mutant cells (Chambliss et al. 2013; Ho et al. 2013). Moreover, the microtubule-, vimentin- and desmin network are also disorganized in LMNA deficient cells (Nikolova et al. 2004; Hale et al. 2008). This suggests that lamins do not only define the architecture of the nucleus, but also impact on the architecture of the whole cell through LINC complex mediated coupling between the nucleus and the cytoskeleton.

In addition, mechanical forces imposed on the nucleus modify the stiffness of the nuclear envelope (Guilluy et al., 2014) and modify the organisation of the nuclear lamina (Swift et al., 2013). These mechanical inputs can be the ECM stiffness or an applied strain generated by the cell environment (Guilak 1995; Maniotis, Chen, and Ingber 1997; Lombardi et al. 2011; Anno,

Sakamoto, and Sato 2012). Furthermore, altered signaling of mechanosensitive pathways have been reported in lamin A/C and emerin mutated cells. Expression of an emerin mutant alters serum response factor (SRF) dependent transcription (Guilluy et al. 2014). Consistently, lamin A-C and emerin regulate the nuclear localization of megakaryoblastic leukemia 1 (MKL1) and SRF-dependent transcription (Ho et al. 2013). Moreover, myoblasts carrying L-CMD causing mutations show enhanced YAP signalling activity (Bertrand et al. 2014). These results indicate that the nuclear mechanosensing may impact on regulating mechanosensitive pathways (Guilluy and BurrIDGE 2015).

1.2.SKELETAL MUSCLE

Skeletal muscle is the most abundant tissue in our body and represents 40%-50% of the human body mass. It is a dynamic tissue which is able to adapt to exercise training or disuse. Furthermore, it has one of the best-studied stem cell-dependent regenerative process. After injury, a complex orchestrated regenerative response restores the cytoarchitecture (Cossu and Biressi 2005; Hawke and Garry 2001; Dhawan and Rando 2005). In contrast, skeletal muscle is subject to many degenerative disorders with only a few therapeutic options.

MYOGENESIS

In mice, embryonic myoblasts fuse and form the primary myofibers during primary myogenesis. Later, fetal myoblasts, which develop from distinct but related progenitors (Hutcheson et al. 2009), fuse with each other and form the secondary myofibers (Duxson, Usson, and Harris 1989). During secondary myogenesis, myofibers express different myosin heavy chain isoforms. This differential expression leads to future fast- and slow- muscles of the adult, which ultimately, defines the type, form and location of muscle fibers (Lyons et al. 1990). A third type of muscle precursor cells are the adult satellite cells which function as the precursors during muscle growth and regeneration (Lepper and Fan 2010; Murphy and Courtneidge 2011; Sambasivan et al. 2011). In postnatal muscle growth, activated satellite cells fuse with the ends of existing myofibers and thereby increase the size of the existing fibers (Kitiyakara and Angevine 1963; Williams and Goldspink 1971; Snow 1977; Cusella-De Angelis et al. 1994; Edom-Vovard et al. 1999; Tseng and Levin 2008).

SKELETAL MUSCLE REGENERATION

Regeneration in the skeletal muscle recapitulates some of the processes which occur during embryonic muscle development. In response to muscle injury, satellite cells start to proliferate, migrate, differentiate and fuse (Fig. 4) to regenerate the parent myofiber (Robertson et al. 1990; Schmalbruch 1976; Snow 1977; Papadimitriou et al. 1990; Robertson, Papadimitriou, and Grounds 1993). Newly regenerated myofibers are easily identified by the presence of centrally located nuclei. Part of satellite cells return to their normal position underneath the basal lamina of muscle fibres.

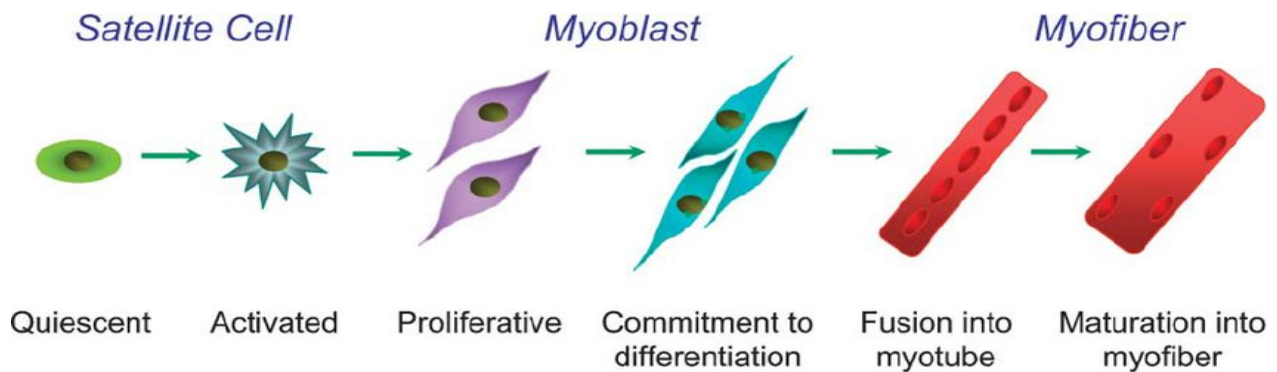


FIGURE 1-4: Satellite cell myogenesis (Zammit, Partridge, and Yablonka-Reuveni 2006).

SATELLITE CELLS

The mononucleated satellite cells gained their name based on their unique satellite position around the polynucleated myofiber (Mauro 1961). Satellite cells have a specialized niche in the adult skeletal muscle, localized between the basal lamina and the sarcolemma. The number of satellite cells is dependent on species, age, and muscle fiber type. Satellite cells are characterized by their small size, high nuclear to cytoplasm ratio, relative absence of cytoplasmic organelles, and increased nuclear heterochromatin. Moreover, these characteristics represent a quiescent state of the cell. Satellite cells are the adult stem cells of skeletal muscle tissue as they are able to rebuild their pool of quiescent satellite cells by asymmetric cell divisions (Moss and Leblond 1971; Schultz and Jaryszak 1985; Bischoff 1994; Kuang et al. 2006). When satellite cells are activated, for example in response to injury, they leave quiescence and proliferate as skeletal myoblasts

(symmetric divisions). Satellite cells are tightly regulated by transcription factors including Pax7, the most frequently used marker of satellite cells (Seale et al. 2000; Zammit et al. 2006). Beyond others, Pax7 controls the activation of satellite cells through induction of specific Myogenic Regulatory Factors (MRFs) (Sassoon 1993; Cornelison and Wold 1997a; Nicolas, Gallien, and Chanoine 1998; McKinnell et al. 2008). MyoD is one of the first transcription factors expressed in myogenic progenitors whereas myogenin expression is induced later (Davis, Weintraub, and Lassar 1987; Hopwood, Pluck, and Gurdon 1989; Kuang et al. 2007; Rhodes and Konieczny 1989; Wright, Sassoon, and Lin 1989; Jennings 1992).

MYOBLAST CELL-CELL-CONTACT SIDES

Cell-contact sites between myoblasts are formed by a macromolecular complex, which includes cadherins and catenins. Cadherins are membrane proteins, which contain two or more extracellular cadherin domains. The extracellular domains form a homotypical Ca^{2+} -dependent binding with cadherins of neighboring cells, forming cell–cell adhesion (Leckband and Prakasam 2006; Pokutta and Weis 2007). Cell-cell junctions of myoblasts are distinct from the general adherence junction present in other cells, because myoblasts can fuse with each other. Two distinct stages are defined in cell-cell contact formation between myoblasts: Adherens Junction1 (AJ1) is a cell-cell contact, which is still in formation, whereas AJ2 corresponds to an already established cell-cell contact (Causeret et al. 2005). AJ2 is further characterised by the presence of actin stress fibers between adjacent cells and the presence of cadherin/catenin complexes which accumulate at the intercellular junction (Fig 5).

The formation of cadherin clusters at intercellular junctions requires a myosin II dependent coupling of actin to cadherins (Shewan et al. 2005). The association between cadherin and actin stabilizes the cadherin clusters, thus preventing rupture. Cadherin cluster formation is a dynamic process, regulated by a dynamic competition between cluster formation, breakup, and endocytosis

CADHERINS

Cadherins provide the mechanical stability of cell-cell contacts. Cadherin regulation in skeletal muscle has mainly been studied during myoblast fusion. M-cadherin is expressed in a

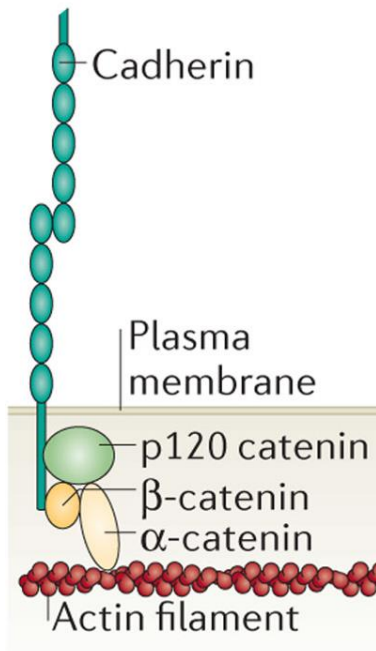


FIGURE 1-5: Cadherin/catenin complex. Modified from (Ratheesh and Yap 2012)

subpopulation of quiescent satellite cells. It is strongly up-regulated in activated satellite cells suggesting a potential function in skeletal muscle regeneration (Donalies et al. 1991; Irintchev et al. 1994; Cornelison and Wold 1997b). In myofibers *in vivo* and after completion of myotube formation *in vitro*, M-cadherin expression is downregulated (Beauchamp et al. 2000; Kuch et al. 1997; Pouliot, Gravel, and Holland 1994). Overexpression of M-cadherin in cadherin-deficient mouse fibroblasts resulted in enhanced calcium-dependent cell adhesion (Kostetskii et al. 2001). The M-cadherin mediated cell-cell interaction is necessary for the fusion of embryonic myoblasts and for the fusion of myoblasts with myofibers (Zeschnigk et al. 1995; Kaufmann et al. 1999; Wernig et al. 2004; Charrasse et al. 2006). Additionally, inhibition of M-cadherin homophilic cell-cell interactions inhibits myoblast fusion in a dose-dependent manner, without affecting the expression of

differentiation markers (Zeschnigk et al. 1995).

However, M-cadherin knockout mice showed a normal muscle development and regeneration. In this animal model, N-cadherin protein levels are increased which suggests that N-cadherin can compensate for the absence of M-cadherin (Hollnagel et al. 2002). In contrast, N-cadherin knockout mice die before E10, with disorganized somites. Therefore, skeletal muscle development cannot be investigated in N-cadherin knockout mice (Radice et al. 1997).

Primary N-cadherin null myoblasts differentiate and fuse normally. This is most likely due to the increased expression of other cadherins including M-cadherin (Charlton et al. 1997). N-cadherin is found at the cell-cell contacts in AJ1 where it accumulates during AJ2. Furthermore, N-cadherin mediated-adhesion has a major role in the induction of skeletal muscle differentiation

(Knudsen, Myers, and McElwee 1990; Mege et al. 1992; George-Weinstein et al. 1997; Redfield, Nieman, and Knudsen 1997; Goichberg and Geiger 1998).

Cadherins are also adhesion-activated signaling receptors. Rho-family GTPases are regulated by cadherins (Wheelock and Johnson 2003). In turn, RhoA activity regulates M-cadherin stability (Charrasse et al. 2006). Rho GTPases are potent regulators of actin dynamics and are involved in the regulation of myoblast fusion and the induction of myogenesis (Luo et al. 1994; Hakeda-Suzuki et al. 2002; Charrasse et al. 2003; Fernandes et al. 2005). The coordinated regulation of RhoA and Rac1 during myogenesis induction has been shown to be orchestrated by N-cadherin (Charrasse et al. 2002). Furthermore, M-cadherin also regulate Rac1 activity during myoblast fusion (Charrasse et al. 2007).

CATENINS

The cytoplasmic domains of cadherins interact with β -catenin, which is a central structural adaptor protein that links cadherins to the actin cytoskeleton (Fig 5). Furthermore, β -catenin is a key transcription co-factor in the Wnt signaling pathway (Gottardi and Gumbiner 2001). β -catenin localizes to myoblast cell-cell contact sites. In muscle cells, the M-cadherin/ β -catenin complex also interacts with microtubules (Vasyutina et al. 2009).

The cadherin/ β -catenin complex is involved in the alignment of myoblasts during fusion (Kaufmann et al. 1999). β -catenin-mediated Wnt signaling is involved in muscle development (Cossu and Borello 1999; Zhang et al. 2012). Moreover, β -catenin is essential for myoblast differentiation (Wróbel, Brzóska, and Moraczewski 2007). In non-proliferating satellite cells, β -catenin is located at the cell membrane. In proliferating cells β -catenin translocates to the nucleus where it acts as transcriptional coactivator in the canonical Wnt signaling pathway (Otto et al. 2008; Zammit 2008). β -catenin/Wnt signaling regulates the expression of myogenic regulatory factors (MRFs) such as MyoD and Inhibitor of Differentiation 3 (ID3) (Zhang et al. 2012). Blocking Wnt/ β -catenin signaling in proliferating cells decreases proliferation and inhibits myoblast fusion (Suzuki, Pelikan, and Iwata 2015). Cadherins can inhibit the activity of β -catenin/canonical Wnt signaling (Simcha et al. 2001; Stockinger et al. 2001; Kuphal and Behrens 2006; Sadot et al. 1998). Specifically, knockdown of M-cadherin in C2C12 myoblasts increases the phosphorylation of β -

catenin at Ser33/37/Thr41 by GSK-3 β . The increased phosphorylation enhances myogenic differentiation induced by canonical Wnt signaling (Wang, Mohamed, and Alway 2013).

1.1. MIGRATION

MYOBLAST MIGRATION

Myoblast migration is crucial for the achievement of cell–cell adhesion and for the formation and growth of myotubes *in vitro* (Kang et al. 2004; Bae et al. 2008; Jansen and Pavlath 2006; Mylona et al. 2006; O'Connor et al. 2007; Griffin et al. 2010b). Myoblast fusion generally occurs between muscle cells that are initially positioned at a distance from each other. *In vivo*, during development in mice, myoblasts often migrate long distances to form muscles in the limbs (Dietrich 1999; Christ and Brand-Saberi 2002; Birchmeier and Brohmann 2000). During muscle regeneration, myoblasts migrate towards a myotube target (Fig.6). *In vivo*, live-cell imaging of satellite cells provides direct evidence for myoblast migration in adult muscles (Ishido and Kasuga 2011). Myoblast migration is guided by attractants secreted by the damage myofiber (Bondesen et al. 2007; Griffin et al. 2010b). Proper cell fusion requires precise regulation and localization of myogenic progenitor cells (Krauss et al. 2005).

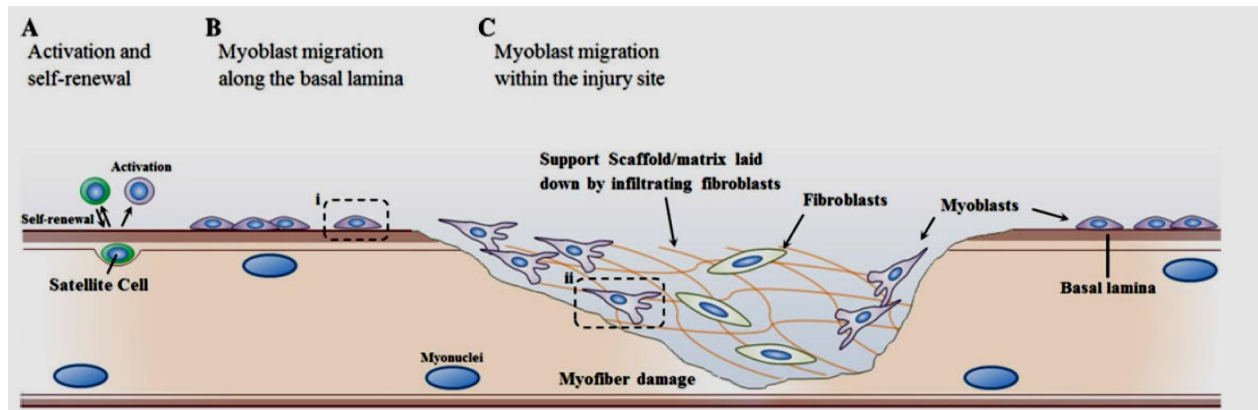


FIGURE1-6: Myoblast migration during muscle repair (Goetsch, Myburgh, and Niesler 2013).

In vitro, satellite cells migrate extensively on their associated myofibers and concurrently express receptors for chemottractants (Siegel et al., 2009). Moreover, myoblasts cultured on artificial substrates are motile and migrate in response to different chemokines and growth factors (Corti et al. 2001; Ödemis et al. 2007; Griffin et al. 2010b; Robertson, Papadimitriou, and Grounds

1993; Bischoff 1997; Lee et al. 1999; Villena and Brandan 2004; Nedachi et al. 2009; Tokura et al. 2011). Thereby, specific chemoattractants have been identified which modulate the velocity or direction of migrating cells (Horsley et al. 2003; Jansen and Pavlath 2006; Lafreniere et al. 2006; Griffin, Kafadar, and Pavlath 2009). Moreover, cell differentiation modulates cell motility. Myocytes are less motile and less sensitive to many inducers of migration than myoblasts (Powell 1973; Nowak et al. 2009; Griffin et al. 2010a).

Collective cell migration is a type of migration in which a group of cells move together without completely losing their cell-cell contacts. To move in a collective manner, individual cells need to align and synchronize their movements relative to that of their neighbouring cells. To date, the role of cell-cell interactions during myoblast migration and the collective character of myoblast migration has rarely been studied. C2C12 cells do not endogenously exhibit a collective cell migration as epithel or endothel cells do (Plutoni et al. 2016). However, live-cell imaging of C2C12 cells revealed that fibronectin promotes a directional collective migratory behavior (Vaz et al. 2012). In addition, transplanted myoblasts *in vivo* migrate as groups of cells (El Fahime et al. 2000).

ROLE OF CADHERINS IN COLLECTIVE MIGRATION

Classic cadherins play a central role in cell–cell contact and adherence junction formation. Therefore they are important factors of collective cell migration (Halbleib and Nelson 2006). It has been shown that collective cell migration depends on both growth factor-mediated regulation and mechanically-stimulated regulation (Theveneau and Mayor 2013; Wang et al. 2010; Reffay et al. 2014; Hidalgo-Carcedo et al. 2011; Das et al. 2015; Bianco et al. 2007). Self-generated chemokine gradients appear to be essential to guide cells through this process (Dona et al. 2013).

Mechanical stress is produced at cell-cell junctions during collective cell migration (Tambe et al., 2011). Moreover, it has been shown that neighbouring cells join forces together to migrate along a minimum of intercellular shear stress. Thus, collective cell migration is guided by intercellular mechanical stress. This intercellular stress has been shown to be cadherin dependent (Tambe et al. 2011). Moreover, it has been proposed that mechanical coupling between migratory cells induce force-dependent signals, which may in turn contribute to the orchestration of collective cell movement (Hirashima et al. 2013; Mertz et al. 2012; Tambe et al. 2011).

However, precise mechanosensitive pathway, which translates cadherin mediated cell–cell adhesion into cell motion, remains to be elucidated. Recent data indicate that cadherin rich protrusions (cadherin fingers) guide cells during collective cell migration from (Hayer et al., 2016). Local actin polymerization and membrane tension regulate the formation of cadherin fingers. Furthermore, P-Cadherin, another cadherin isoform, has been shown to promote collective cell migration (Plutoni et al. 2016). P-Cadherin is not expressed in C2C12 cells or satellite cell-derived myoblasts. However, P-cadherin is expressed in muscle progenitor of mice embryos during early myogenesis which suggests a collective migration of muscle precursor cells during early myogenesis.

As stated before, cadherins are largely regulated by Rho family GTPases. Rho GTPases play a key role in the coordination of collective migration (Weber, Bjerke, and DeSimone 2012; Das et al. 2015). RhoA and RhoE activity seem to be involved in decreasing the contractility at cell–cell contact sites between migrating cells, which guides collective cell migration (Hidalgo-Carcedo et al. 2011; Omelchenko and Hall 2012; Tanbe et al., 2011). Moreover, a correlation between E-cadherins and Rac1 activity has been shown in border cell migration, which hints to a Rac1 dependent formation of cell-cell contacts during migration (Cai et al. 2014). The development of a front-to-rear polarity in the cytoskeletal architecture is crucial for both single and collective cell migration. Polarity is regulated by zone-specific activation of small Rho GTPases (Das and Spatz 2016). Furthermore, expression of P-cadherin in C2C12 cells increases the collective character of migrating C2C12 cells through activation of another Rho GTPase, Cdc42 (Plutoni et al., 2016).

MECHANOBIOLOGY

Mechanobiology is an emerging scientific field which describes how cell and tissues sense and respond to physical forces. Mechanobiology comprises the processes of mechanosensing and mechanotransduction. “Mechanosensing” refers to the sensing of mechanical properties of the environment by the cell, while “mechanotransduction” refers to the conversion of mechanical signals into biochemical signals. Mechanical stimuli obviously regulate skeletal muscle tissue as muscle grows in response to exercise and degrades if not used. Therefore, the importance of “mechanotransduction” in skeletal muscle homeostasis was first described more than 30 years ago

(Goldberg 1968; Vandenburgh and Kaufman 1979). More recent studies reveal that aside from biochemical inputs, all tissues and cells are regulated by the physical properties of their environment. In recent years, mechanotransduction has emerged as a major field in biomedical studies.

Several models have been developed to describe mechanisms involved in mechanotransduction. In one of them, the cell itself is considered as a compartmentalized mechanical body with given physical properties such as its viscosity, elasticity or stiffness. These cellular mechanical properties are primarily defined through the organization and dynamics of the cyto- and nucleoskeleton. The cytoskeleton, in turn, is connected to the extracellular matrix (ECM) and to neighboring cells by cell surface multiprotein complexes such as focal adhesions or cell-cell junctions. Through these connections, cellular mechanics are in a permanent coordination with extracellular constraints. Actin fibers, microtubules and intermediate filaments are components of the cytoskeleton. Thereof, actin dynamics evolved to be the most important modulators of mechanotransduction (Ramaekers and Bosman 2004). Changes in extracellular mechanics are simultaneously translated into various cell processes which are regulated by cytoskeletal dynamics including cell morphology or the activation of signaling pathways (Fischer et al. 2016).

1.2.YAP

The transcriptional co-activator YAP (Yes-Associated Protein) is one of the most prominent signaling proteins involved in mechanobiology. In its unphosphorylated active conformation, YAP, together with its paralog TAZ (Transcriptional co-activator with PDZ-binding motif), localizes to the nucleus and regulates the activity of several transcription factors, the most important being TEAD family transcription factors (Zhao et al. 2008) (Fig.7). Prominent target genes of YAP include CTGF, Cyclin D1, myogenic transcription factor Myf5 and also the expression of contractile proteins like β -myosin heavy chain or skeletal α -actin (Dong et al. 2007; Watt et al. 2010).

YAP controls a wide range of cellular functions. During embryogenesis in mice, YAP is expressed at all stages. Homozygous disruption of the YAP allele in mice results in embryonic lethality at E8.5 (Morin-Kensicki et al. 2006). Nuclear YAP activity typically drives proliferation and survival and inhibits apoptosis (Dong et al. 2007). YAP mediates cell contact inhibition. Therefore, YAP activity regulates organ size *in vivo* (Zhao et al. 2007; Camargo et al. 2007; Dong

et al. 2007). As a regulator of the cell-cycle, aberrant regulation of YAP can lead to tumorigenesis including skeletal muscle cancer (Dong et al. 2007; Tremblay et al. 2014) Furthermore, YAP is involved in cell fate decisions in different progenitor cell pools, including satellite cells of skeletal muscle, in which YAP activity promotes proliferation and blocks differentiation (Camargo et al. 2007; Cao, Pfaff, and Gage 2008; Watt et al. 2010; Schlegelmilch et al. 2011).

YAP also influences cell migration. It was shown that YAP overexpression in MCF10A or HEK293 cells increases migration. Moreover, YAP knockdown abolishes migration in T47D cells and renal carcinoma cell lines (Haskins, Nguyen, and Stern 2014; Schutte et al. 2014; Sorrentino et al. 2014; Moroishi et al. 2015). As regulator of proliferation, apoptosis and migration, YAP is an important player in regenerative processes in different tissues including heart muscle tissue, where YAP knockdown severely impairs the regenerative capacity (Xin et al. 2013; Mateus et al. 2015). In brief, YAP is a regulator of the cell cycle and cell fate decisions and consequently, a regulator of development, organ size and tumorigenesis.

YAP is overexpressed in many human cancers. Different YAP overexpression systems are used to analyze YAP function or regulation. However, the regulation of YAP gene expression itself is nearly completely unknown. YAP is ubiquitously expressed in a wide range of tissues, except in peripheral blood leukocytes (Komuro et al. 2003). Regarding YAP protein level regulation, a few transcription factors or binding sites have been identified in the YAP promoter region (Wu et al. 2013; Danovi et al. 2008). This includes the β -catenin/TCF4 complex which can control YAP gene expression by binding of this complex to a DNA enhancer element within the first intron of the YAP gene (Konsavage et al. 2012). Above that, microRNAs target YAP mRNA and have been shown to suppress YAP mRNA and protein levels (Liu, Poon, and Luk 2010).

UPSTREAM REGULATION

Canonical regulation of YAP activity depends on the Hippo pathway activity. At the core of the mammalian Hippo pathway is a kinase cassette containing Mammalian Ste20-like 1/2 kinase (MST1/2) and large tumor suppressor 1/2 kinase (LATS1/2) (Fig. 7). YAP activity is regulated by phosphorylation at five different phosphorylation sites which are located in HXRXXS consensus motifs for LATS1/2 kinases. The widely studied LATS mediated phosphorylation is at Serine 127. This phosphorylation leads to binding of YAP to the 14-3-3 proteins, and consequently sequestration of YAP in the cytoplasm (Zhao et al. 2007). In addition, phosphorylation at Serine

381 by LATS1/2, primes YAP for further phosphorylation by casein kinases CK1 δ or CK1 ϵ and subsequent ubiquitination via SCF β TRCP E3 ubiquitin ligase and proteasomal degradation (Zhao et al. 2010). LATS1/2 kinases are canonically activated by phosphorylation of activated MST1/2 kinases (Visser and Yang 2010). YAP activity is balanced through a negative feedback loop. YAP dependent TEAD activity induces LATS2 kinase expression and activation which, in turn, leads to phosphorylation and inactivation of YAP (Moroishi et al. 2015).

A specific Hippo receptor, as the primary trigger of the Hippo signaling cascade, has not been identified. Moreover, the dependence of YAP regulation on Hippo signaling in several contexts including mechanotransduction has been questioned (Aragona et al. 2013). However, a great number of other YAP activators and inhibitors are known, although their interplays are not completely uncovered today (Fig. 7).

GPCR RECEPTORS

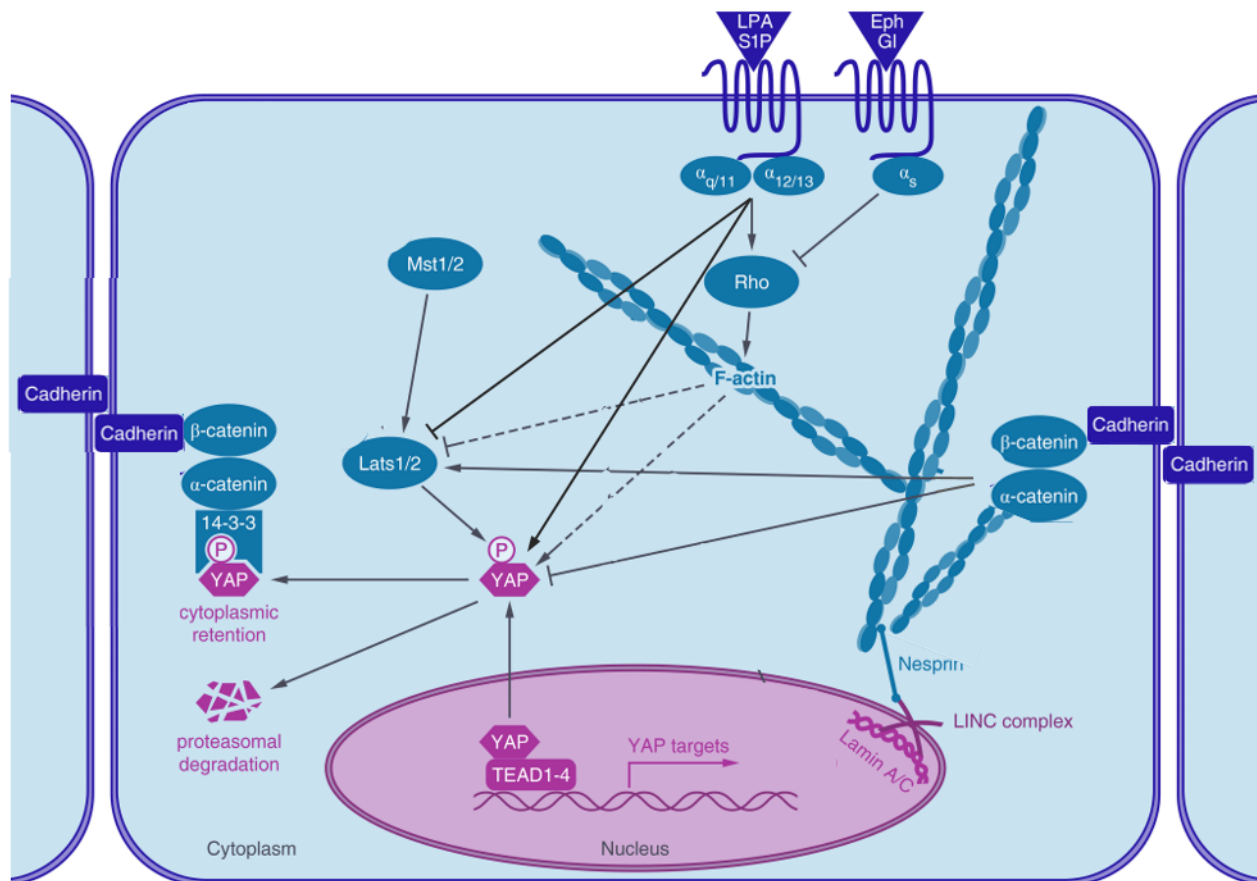


FIGURE 1-7: Regulation of YAP activity. Modified from (Fischer et al. 2016)

YAP can be regulated through G-protein coupled receptors (GPCRs). Lysophosphatidic acid (LPA) or sphingosine-1-phosphate (S1P) are components of fetal calf serum which is a supplement of most culture media. LPA and S1P can activate G12/13-, Gq/11-, and Gi/o-coupled receptors. Hence, fetal calf serum can activate YAP/TAZ so that serum starvation inhibits YAP activity via reduced GPCR signaling (Yu et al. 2012) (Fig. 7).

The exact pathway by which GPCRs act on YAP is still under review. Regulation of YAP by G-proteins has been shown to be either mediated by the Rho family of GTPases, actin dynamics and LATS (Yu et al. 2012) or by the PI3-kinase (PI3K) and phosphoinositide-dependent kinase (PDK1) (Gumbiner and Kim 2014).

CONTACT INHIBITION OF PROLIFERATION (CIP)

Cells grown at low density show a nuclear localization of YAP, whereas, in high cell density, YAP is sequestered in the cytoplasm (Zhao et al. 2011). This has been consistently shown in several cell types including, epithelial and mesenchymal cells (Zhao et al. 2007; Schlegelmilch et al. 2011; Kim et al. 2011). In *drosophila*, overexpression of YAP can overcome contact inhibition of proliferation (CIP), leading confluent cells to over-proliferate. Thereby, overexpression of the wildtype YAP *drosophila* analogue Yki led to an increase in transcriptional activity but only a slight increase in organ size. In contrast, the overexpression of the S127A phosphorylation-deficient mutant of Yki lead to significant increase in organ size (Zhao et al. 2007).

The canonical Hippo signaling in mammals has been first described in the context of CIP. It has been shown that YAP inactivation and cytoplasmic retention is mediated by activation of the Hippo pathway. More precisely, LATS1/2 mediated phosphorylation of YAP at Serine 127 induced its inactivation (Zhao et al. 2007). Consistently, overexpression of LATS1 induces the cytoplasmic translocation of YAP even in sparse cells. Moreover, LATS knockdown induces a nuclear localization of YAP even in dense culture (Kim et al. 2011). However, the involvement of LATS in CIP has been more recently questioned (Silvis et al., 2011; Schlegelmilch et al., 2011, see below).

CADHERIN-CATENIN MEDIATED YAP INACTIVATION

The cadherin-catenin protein complex at cell-cell contact sites has been identified as the key transmitter of cell-cell contact into YAP inactivation during CIP. The cytoplasmic tail of cadherins interacts with catenins, β -catenin, p120-catenin, γ -catenin and α -catenin (Fig 5). Catenins therefore connect cadherins to the actin cytoskeleton (Perez-Moreno and Fuchs 2006; Pokutta and Weis 2007; Nishimura and Takeichi 2009).

Catenins also serve as signaling molecules (Perez-Moreno and Fuchs 2006). β -catenin has a dual role in cell adhesion and transcriptional coactivator of the WNT-signaling pathway (Nelson and Nusse 2004; Bienz 2005). The p120-catenin, β -catenin and γ -catenin are armadillo family proteins, whereas α -catenin differs notably in both sequence and structural organization. The armadillo family catenins bind directly to the cytoplasmic tail of cadherins, whereas, α -catenin connects to the complex via binding to β -catenin or γ -catenin. Only α -catenin binds to actin, thus, providing the link to the actin cytoskeleton (Fig. 5).

Most studies have investigated the effects of E-cadherin, the prototypical epithelial cadherin on YAP (McClatchey and Yap, 2012). However, a similar inhibition of proliferation has been reported for VE-cadherin, suggesting that other members of the cadherin family share the role of E-cadherin in CIP (Caveda et al. 1996; Lampugnani et al. 2006).

Expression of E-cadherins and their association with α - and β -catenin are required for density dependent nuclear exclusion of YAP (St Croix et al. 1998). The absence of E-cadherin in cancer cell lines correlated with decreased inhibition of proliferation. Vice versa, expression of E-cadherin in cadherin-deficient cell lines inhibited cell proliferation (St Croix et al. 1998). *In vivo*, immunostaining of sections of human keratoacanthoma tumors for YAP revealed a significant correlation between low E-catenin abundance and nuclear Yap1 localization (Silvis et al. 2011).

Furthermore, YAP relocates to the nucleus in confluent monolayers *in vitro* when cadherin dependent cell-cell connections are disrupted by removing extracellular calcium (Schlegelmilch et al. 2011). It has been demonstrated that protein levels of E-cadherin tune the efficacy of CIP (Kim et al. 2009). Moreover, expression of a mutant E-cadherin lacking the β -catenin binding domain, is not sufficient to inactivate YAP and a knockdown of β -catenin prevents YAP nuclear exclusion. In addition, β -catenin knockdown decreases YAP phosphorylation at Serine 127 and its nuclear accumulation. Finally, it has been shown YAP inactivation by homophilic ligation of E-Cadherins was shown to further require α -catenin and LATS, but not MST (Kim et al. 2011) (Fig. 7).

Several studies indicate that cell-cell contact-induced inactivation of YAP occurs downstream of LATS, independently of the Hippo pathway. An indirect interaction between α -catenin and YAP has been shown which involves the binding of YAP to the 14-3-3 protein and subsequently, the cytoplasmic retention of YAP (Silvis et al., 2011; Schlegelmilch et al., 2011). Accordingly, α -catenin has been shown to be crucial for nuclear exclusion of YAP in high contact conditions. Knockout of α -catenin increases nuclear localization of YAP and cell proliferation, which can only be abolished by knockdown of YAP but not LATS or MST (Silvis et al., 2011). Moreover, Schlegelmilch et al. do not find a reactivation of YAP after depletion of MST or LATS in keratinocytes (2011). In both studies, increased LATS activity does not correlate with YAP inhibition. These findings lead to the proposal that α -catenin controls YAP activity by modulating the interaction between YAP and the 14-3-3 protein. Thus, cytoplasmic retention of YAP in high contact conditions occurs independent of LATS activity (Schlegelmilch et al., 2011) (Fig. 7). Conflicting data also exist regarding the phosphorylation of YAP at serine 127 during CIP.

After knockdown of α -catenin, decreased levels of phosphorylated YAP are found alongside stable total YAP levels by Schlegelmilch and colleagues. Further investigations revealed a dephosphorylation of YAP after α -catenin knockdown by the protein phosphatase PP2A (Schlegelmilch et al., 2011). In contrast, Silvis et al. find that α -catenin knockout cells have reduced levels of phosphorylated but also total YAP protein. They conclude that the phosphorylation of YAP at serine 127 is not involved in CIP (Silvis et al., 2011). Not only do cell-cell contacts regulate YAP activity but, interestingly, adherence junction formation has been recently shown to be regulated by YAP activity. In detail, YAP overexpression alters the assembly of adherence junction *in vivo*. Moreover, in primary hepatocytes *in vitro*, YAP overexpression was shown to antagonized E-cadherin junction assembly by regulating actin cytoskeleton architecture through myosin light chain expression (Bai et al. 2016).

YAP REGULATION IN MECHANOTRANSDUCTION

Increasing evidence points to YAP as the key regulator of mechanotransduction. Piccolo and colleagues have shown that mechanical forces can serve as inputs for the regulation of YAP. YAP localization and transcriptional response is regulated by ECM stiffness or cell-spreading (Dupont et al. 2011) (Fig.8). It has been proposed that actin dynamics play a critical role of in the regulation

of YAP by mechanical cues. In particular, YAP activity has been correlated with the presence of actin stress fiber. YAP is inactivated after F-actin depolymerization or Rho inhibition but not after disruption of the microtubules network (Dupont et al., 2011; (Halder, Dupont, and Piccolo 2012; Zhao et al. 2012). Similarly, *in vivo*, in *Drosophila*, increased actin stress fiber assembly correlates with YAP nuclear localization and overgrowth of the wing disc (Sansores-Garcia et al. 2011; Fernandez et al. 2011). However, the specificity of this effect and the mechanism linking stress fiber formation to YAP activity is controversial and the focus of ongoing research.

YAP regulation by cell morphology and cell-contact inhibition has been further investigated in epithelial cells. It has been shown that mechanical forces overarch the regulation of YAP by CIP. YAP can be inactivated by a reduced cell spreading area, independent of cell-cell contacts. Using microdomain culture system, in which the cell area is defined whereas the formation of cell-cell contacts are prevented, the group of Sasaki has proposed a model where cell morphology alone modulates YAP activity (Wada et al. 2011). Moreover, the requirement of focal adhesion sites for the regulation of YAP by cell morphology was excluded by seeding epithelial cells on poly-lysine (Zhao et al. 2012).

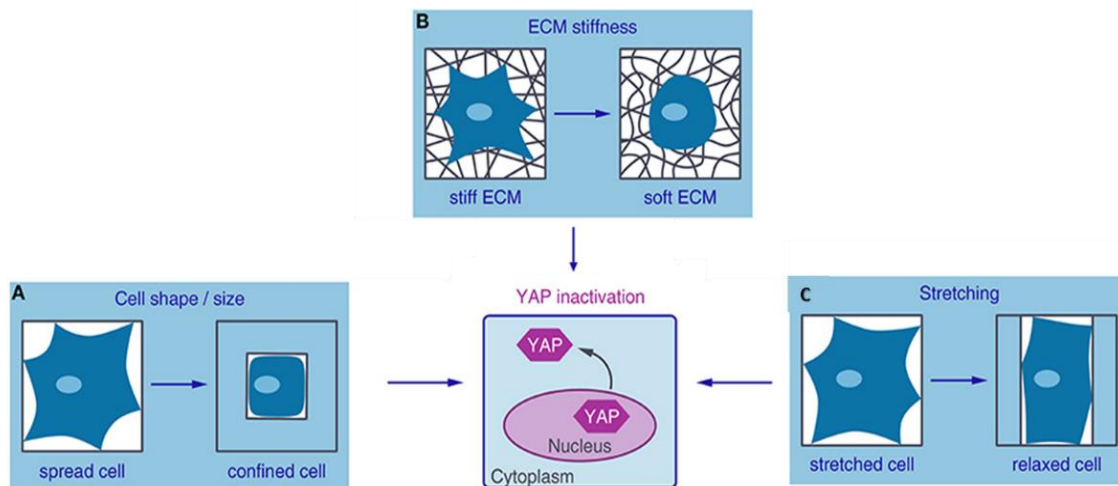


FIGURE 1-8: YAP regulation in mechanotransduction. Modified from (Fischer et al. 2016)

The actin-capping and -severing proteins; Cofilin, GapZ, and Gelsolin have been identified as gatekeepers by limiting YAP activity in cells which experience low mechanical stress. By depleting actin-capping/severing proteins, actin stress fiber formation increases and YAP activity in dense monolayers is restored (Aragona et al. 2013). In addition, YAP activity can be reactivated in postconfluent culture conditions by stretching the cells while preventing cell-cell contact loose

(Aragona et al., 2013). Cyclic stretching can reactivate YAP on soft surfaces and is associated with an increase in cell spreading, stress fiber formation and proliferation (Cui et al. 2015) (fig. 8).

YAP nuclear translocation is further dependent on nuclear mechanotransduction through the LINC-complex. Transfer of the strain to the nucleus is essential for YAP localization and activity. YAP nuclear re-localization after strain can be prevented by knocking down Nesprin, a protein of the LINC-complex (Driscoll et al. 2015). Consistently, satellite cell-derived myoblasts carrying a mutation in A-type lamins were unable to activate YAP after cyclic stretch (Bertrand et al. 2014).

YAP SIGNALING IN SKELETAL MUSCLE MOGENESIS AND HOMEOSTASIS

YAP transcriptional activity is important in myogenesis, muscle homeostasis and muscle disorders. YAP activity in muscle tissue activates the muscle promoter elements MCAT. MCATs are regulated by TEAD family transcription factors and are found in promoters of genes coding for contractile proteins such as β -myosin heavy chain or skeletal α -actin and regulators of myogenic differentiation (Myf5, Mrf4, myogenin) (Mar and Ordahl 1988; Yoshida 2008; Ribas et al. 2011; Benhaddou et al. 2012).

In muscle development, regeneration and homeostasis activated satellite cells expand, migrate, differentiate and fuse with existing myofibers (Zhang and McLennan 1994). A differential regulation of YAP activity during satellite cell maturation has been shown, *in vitro* and *ex vivo*, on murine myoblasts. High YAP activity promotes proliferation of activated muscle progenitor cells whereas, YAP inactivation is needed for myogenic differentiation. YAP localization was primarily nuclear in proliferative culture. After myogenic differentiation YAP localization was cytoplasmic, and differentiated muscle fibers showed decreased Yap mRNA, YAP protein levels and increased YAP phosphorylation (Watt et al. 2010; Judson et al. 2012).

Moreover, YAP knockdown reduced proliferation of satellite cell-derived myoblasts. However, it had no impact on the progression of myoblast differentiation (Nagata et al. 2006). Furthermore, YAP overexpression led to inhibition of MyoD expression (Gee et al. 2011). In skeletal myofibers, YAP levels were reduced during postnatal maturation (Watt et al. 2015). Mechanistically, overexpression of constitutively active YAP *in vitro*, in myoblast precursors, resulted in increased Cyclin D1 and Myf5 expression as well as in decreased expression of

myogenin, which inhibits terminal myogenic differentiation (Ishibashi et al. 2005; De Falco and De Luca 2006; Watt et al. 2010).

Interestingly, standard culture conditions for myoblast differentiation show striking similarities with those for YAP inactivation. Indeed, myoblast differentiation preferentially occurs at high cell density, reduced serum concentration and substrates softer than standard cell culture plastic (Yaffe and Saxel 1977; Kaushik and Engler 2014).

In sections of healthy muscle tissue, YAP staining is weak and predominantly cytoplasmic (Croze et al. 2014). This suggests that YAP activity does not play a transcriptional role in the function of adult muscle. However, conflicting data on the role of YAP in adult muscle homeostasis and muscle mass regulation have been reported (Judson et al. 2013) (Watt et al. 2015) (Goodman et al. 2015). High levels of a constitutively active YAP led to degeneration, atrophy and necrosis of skeletal muscle fibers after use of a skeletal muscle fiber but not satellite cell specific knock-in mouse model. Interestingly, this muscle wasting phenotype is largely reversible. Gene expression profiling of these mice show similarities to muscles from mdx mice, a model for Duchenne muscular dystrophy (Hoffman, Brown, and Kunkel 1987). In contrast, it was found that YAP is a positive regulator of skeletal muscle size through a TEAD-dependent but mTOR-independent regulation of protein synthesis.

In a chronic mechanical overload model in mice, YAP expression and phosphorylation is increased, supporting the hypertrophic role of YAP in muscle. Vice versa, overexpression of YAP in the mouse tibialis anterior lead to hypertrophy. In addition, increasing muscle mass, through the blocking of myostatin and activin signaling in mice *in vivo*, increases total YAP and YAP phosphorylation. Finally, also physical exercises increase YAP phosphorylation in mouse limb muscles (Hulmi et al. 2013). Together, these results suggest that YAP is inactivated in healthy adult skeletal muscle tissue and that YAP is reactivated, most probably in satellite cells, for muscle growth and regeneration.

YAP signaling defects have been implicated in other skeletal muscle diseases. Rhabdomyosarcomas are cancers of skeletal muscle tissue that are divided into different subtypes. These include embryonal rhabdomyosarcoma (eRMS) and alveolar rhabdomyosarcoma (aRMS). Levels of YAP phosphorylation show high variability between different RMS cell lines. However, total YAP protein levels were elevated in RMS cells and histological RMS tumor sections show

increased nuclear YAP stainings (Croze et al. 2014). Overexpression of constitutively active YAP in activated, but not quiescent satellite cells, lead to muscle tumors similar to those found in eRMS. *In vitro* and *in vivo*, YAP knockdown experiments reveal that lowering YAP expression in human eRMS can rescue tumorigenicity (Tremblay et al. 2014). Interestingly, overexpression of constitutive active YAP in skeletal muscle fibers *in vivo* induced muscle atrophy (Judson et al., 2013). Finally, in myoblasts from L-CMD patients, YAP-dependent signaling is increased in soft environment and paradoxically reduced after cyclic stretch (Bertrand et al. 2014).

The regulation of YAP in skeletal muscle remains incompletely characterized. In adult skeletal muscle, major Hippo pathway components including YAP are expressed in fast and slow muscles (Watt et al., 2010). In a neurogenic atrophy model, MST1 expression was found to be upregulated in fast- but not in slow-dominant muscle. Furthermore, knockout of MST1 attenuated fast-dominant skeletal muscle wasting (Wei et al. 2013). In addition, MST1 was found to be activated during myoblast differentiation by caspase3 and active MST1 is needed for proper myoblast differentiation (Fernando et al. 2002). Understanding YAP regulation in skeletal muscle may be a key to understand and possibly treat skeletal muscle disease.

1.3. BMP SIGNALING

Bone morphogenetic proteins (BMPs) are members of the transforming growth factor beta (TGF β) superfamily of cytokines. BMPs compose a group of secreted growth factors which regulate many cellular functions including cell differentiation, proliferation, survival/apoptosis and cell migration (Sieber et al. 2009). Bone morphogenetic protein-2 (BMP-2) stimulates osteoblast differentiation but inhibits myogenic differentiation in C2C12 myoblasts (Katagiri et al., 1994). BMP-2 activates intracellular signaling by binding to a type I and type II receptor complex. Upon ligand binding, the constitutive active type II receptor activates the type I receptor by transphosphorylation. The activated type I receptor then in turn phosphorylates receptor-bound R-Smads (Smad1/5/8) which, leads to a release of activated Smads into the cytoplasm. These activated Smads form a complex with the co-Smad, smad 4. Together, this complex is translocated into the nucleus where it induces transcription via binding to BMP responsive elements or transcriptional coactivators (Chen and Massague 1999; Massague, Seoane, and Wotton 2005; Sieber et al. 2009). BMP-2 induces the transcription of Inhibitor of Differentiation (IDs) proteins. ID proteins are antagonists of the basic

helix–loop–helix family of transcription factors which, positively regulate differentiation of different tissue, including skeletal muscle tissue (Ruzinova and Benezra 2003).

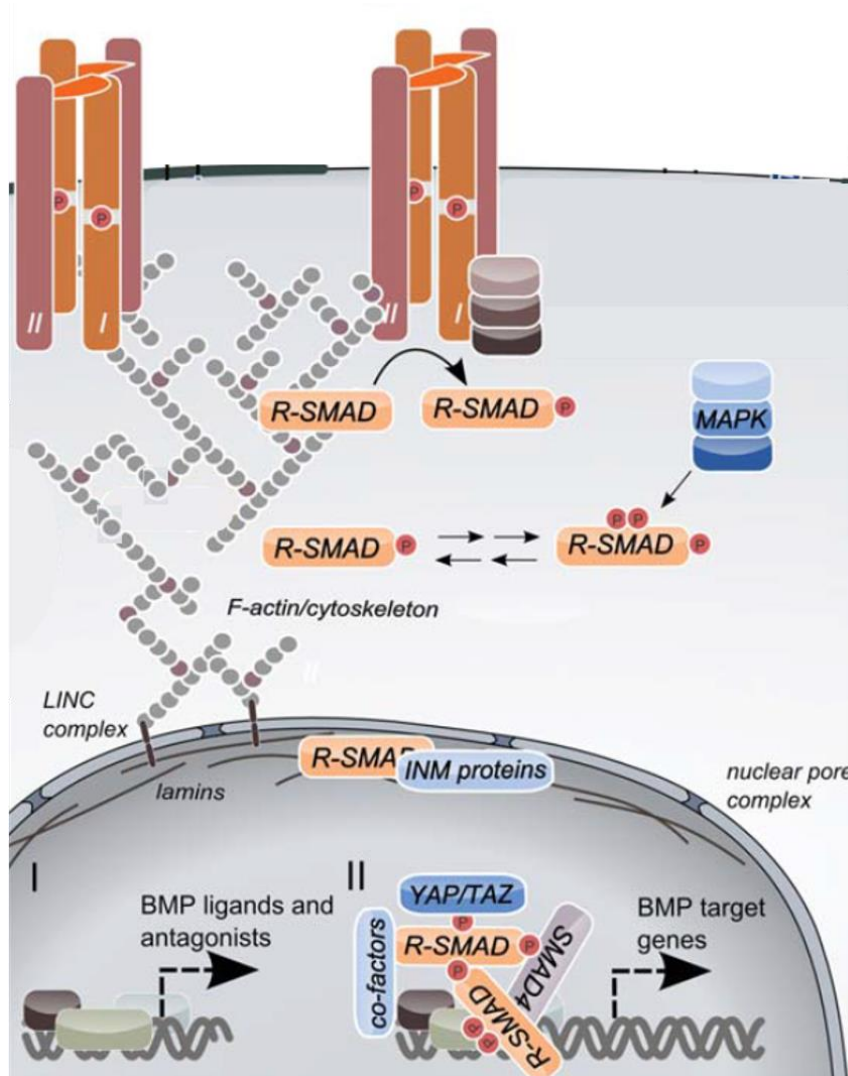


FIGURE 1-9: BMP/smad signalling cascades. Modified from (Kopf et al. 2012).

BMP signaling has been implicated in mechanobiology (Maeda et al. 2011; Kopf et al. 2014). BMP-2 and mechanical force induce bone formation. Experiments which combine BMP-2 and mechanical stimulation of osteoblasts showed that those two factors act synergistically on Smad 1/5/8 activation. The phosphorylation of R-Smads is increased in intensity and duration after BMP2 stimulation and simultaneous mechanical loading (Kopf et al. 2012). The mechanism, which incorporates mechanical signals into Smad signaling, remains to be elucidated. However,

different hypotheses are currently tested which include the regulation of BMP receptor presentation at the plasma membrane or integration of mechanical signals into BMP signaling through crosstalks with other mechanosensitive pathways like Hippo/YAP Signaling (Kopf et al., 2014)

Several crosstalks between YAP and Smad signaling have been identified, including interactions with Smad2/3, Smad7 and Smad 1 (Grannas et al. 2015; Varelas et al. 2010; Narimatsu et al. 2015; Ferrigno et al. 2002). Generally, the stability of R-Smads is regulated by phosphorylation in their linker-region by MAPKs and GSK3- β (fig. 1.9). This phosphorylation

pattern can either prime Smad for degradation or stabilize Smads through additional binding of transcriptional coactivators (Aragon et al. 2011). In particular, YAP interacts with Smad1, as YAP can bind to the linker region of Smad1 and thereby stabilizes the transcriptional active smad complex (Alarcon et al. 2009). Interestingly, also crosstalks between lamins and BMP signaling have been identified. MAN1, a protein of the nuclear envelope which binds to lamins can bind R-Smads and thereby affect BMP signaling activity (Pan et al. 2005). Furthermore, Smad4 binds to Otefin, another protein of the inner-nuclear membrane, and therefore regulates Smad4 transcriptional activity (Jiang et al. 2009).

2. AIMS

L-CMD is characterized by excessive muscle weakness and loss of skeletal muscle mass (Quijano-Roy et al. 2008). L-CMD is a severe and early onset muscular dystrophy caused by mutations in the LMNA gene. The LMNA gene codes for A-type lamins, intermediate filaments of the nucleoskeleton, which contribute to the nuclear structure and stability. As stated previously in this manuscript, mechanosensing defects have already been reported in L-CMD patient cells on soft surfaces (Betrandt et al., 2014). YAP is a key regulator in mechanotransduction (Dupont et al., 2011). Canonically, YAP is regulated by the HIPPO pathway with its core kinase Lats. Active Lats inactivates YAP through phosphorylation at Serine 127. Lats, in turn, is activated by phosphorylation at Threonine 1079 by Mst. Phosphorylated YAP is retained in the cytoplasm through interactions with the 14-3-3 protein (Zaoh et al., 2007).

As transcriptional co-activator non-phosphorylated, active YAP localizes to the nucleus, where it induces transcription, mainly through TEAD family transcription factors (Zhao et al., 2008). In $\Delta K32$ mutant myoblasts, increased YAP activity has been reported on soft surfaces (Betrandt et al., 2014). However, YAP activity in standard culture conditions as well as mechanisms leading to aberrant YAP activity in $\Delta K32$ mutant myoblasts remain to be described. Therefore, I first aimed to analyze the activity of the mechanosensitive signaling pathways Hippo/YAP in $\Delta K32$ mutant myoblasts in standard culture conditions (hard surface, sparsely seeded).

The BMP pathway is another signaling pathway implicated in mechanotransduction (Maeda et al., 2011; Kopf et al., 2014). Mechanical cues have been reported to act synergistically with BMP receptor-mediated signaling on Smad transcriptional activity (Kopf et al., 2012). Canonical BMP signaling acts through a receptor mediated phosphorylation of R-smads. Phosphorylated R-smads associate into a transcriptional active smad complex, enter the nucleus and activate transcription by binding to the BMP responsive element (BRE) in promotor regions. Moreover, YAP can bind Smad1, thereby, stabilizing the transcriptional active smad complex (Alarcón et al., 2009). Therefore, I aimed to analyze if the activity of the mechanosensitive BMP signaling pathways is also impaired in $\Delta K32$ mutant myoblasts.

Although YAP has been widely shown to be involved in mechanotransduction, the mechanism by which YAP senses mechanical cues only begins to be elucidated. Therefore, here I aimed to dissect and describe the regulation of YAP in Δ K32 mutant myoblasts compared to WT myoblasts. Beside canonical Hippo signaling, different routes of YAP regulation have been discovered, involving or not the Hippo core kinase Lats (fig. 7). For example, YAP activity is regulated by growth factor induced GPCR signaling and by cell contact inhibition (Yu et al., 2012; Zhao et al., 2007). Therefore, I aimed to dissect aberrant regulation of YAP in Δ K32 mutant myoblasts by investigating total YAP levels, cellular YAP localization, YAP phosphorylation and the transcriptional activity of YAP in different conditions including serum-starved condition as well as in dense culture conditions.

In dense culture conditions cell-cell contacts are formed, when membrane bound-cadherins of adjacent myoblasts bind to each other. As myoblasts can undergo fusion, cell-cell contact sides in myoblasts differ from those in other cells. Two stages, AJ1 and AJ2, have been identified during the formation of cell-cell contacts (Causeret et al., 2005). In the latter stage, AJ2, the cadherin/catenin protein complexes are located along the tips of actin stress fibers, creating the characteristic, zipper-like staining pattern at cell-cell junctions. Cadherin/catenin complexes at cell-cell junctions are stabilized through α -catenin mediated binding to the actin cytoskeleton. YAP is inactivated in dense culture conditions by 14-3-3 protein mediated sequestration of YAP into the cytoplasm. The inactivation of YAP in dense conditions can be mediated by 1) the formation of cadherin/catenin complexes at cell-cell contact sides or 2) independently of cell-cell contacts, through reduced spreading area and F-actin depolymerisation (Zaoh et al., 2007; Schlegelmilch et al., 2011; Silvis et al., 2011; Dupont et al., 2011; Halder et al., 2012; Zhao et al., 2012; Fernández et al., 2011; Sansores- Garcia et al., 2011).

According to the 1st hypothesis, α -catenin mediates YAP cytoplasmic retention and binding of YAP to the 14-3-3 protein (Schlegelmilch, 2011). β -catenin was also crucial for YAP inactivation by cell-cell contact as knockdown of β -catenin prevented YAP nuclear exclusion (Kim et al., 2011). According to the 2nd hypothesis, a reduced spreading area inactivates YAP, independently of the Hippo core kinases and independently of cell-cell contact formation (Dupont et al., 2011). Therefore, I next aimed to investigate whether defective regulation of YAP in K32

mutant myoblasts was related to a defective organization of the actin cytoskeleton and/or impaired formation of cell-cell contact sites.

Cadherin-dependent mechanotransduction is crucial for cell-migration (Hirashima et al. 2013; Mertz et al. 2012; Tambe et al. 2011). Moreover, YAP and BMP signaling were shown to influence cell migration (Haskins et al., 2014; Schütte et al., 2014; Sorrentino et al., 2014; Moroishi et al., 2015). In addition, myoblast migration is a critical step in skeletal muscle myogenesis and regeneration (Goetsch, Myburgh, and Niesler 2013). Myogenic progenitor cells must be precisely regulated and positioned for proper cell fusion. Thus, migration is crucial to achieve cell–cell adhesion (Kang et al., 2004; Bae et al., 2008; Jansen and Pavlath, 2006; Mylona et al., 2006; O'Connor et al., 2007). Moreover, striated muscle disease causing LMNA mutations have been implicated in migration defects (Folker et al. 2010). Therefore I finally aimed to investigate if the mechanotransduction defects in $\Delta K32$ mutant myoblasts affect the migration pattern of $\Delta K32$ mutant myoblast.

SUMMARY

- i. First, I aimed to analyze the activity of the mechanosensitive signaling pathways Hippo/YAP and BMP/smads in $\Delta K32$ mutant myoblasts in standard culture conditions (hard surface, sparsely seeded).
- ii. Then, I aimed to dissect and briefly describe the aberrations in the regulation of YAP. Therefore, I aimed to investigate total YAP levels, cellular YAP localization, YAP phosphorylation and the transcriptional activity of YAP in standard culture conditions, in serum-starved conditions and dense culture conditions.
- iii. Thereafter, I aimed to investigate the mechanism which lead to a defective regulation of YAP in $\Delta K32$ mutant myoblasts. Hence, I focused on the organization of the actin cytoskeleton and the formation of cell-cell contact sites in $\Delta K32$ mutant myoblasts.
- iv. Finally, I aimed to investigate if the mechanotransduction defects in $\Delta K32$ mutant myoblast affect the migration pattern of $\Delta K32$ mutant myoblast.

3. MATERIALS AND METHODS

HUMAN MYOBLASTS CULTURE

Experiments were performed on immortalized human myoblasts. Human myoblasts were derived from patients carrying a heterozygous p.Lys32del LMNA (Δ K32) mutation (Quijano-Roy et al. 2008). Myoblasts from a male control subject without muscular disorders were used as control (WT). Following muscular biopsy, cells were first expanded and enriched in myoblasts by magnetic cell sorting with the use of anti-CD56/NCAM to reach a purity of at least 95%. Immortalized lines from WT and Δ K32 myoblasts were obtained by transducing cells with pBABE retroviral vectors carrying Cdk4 and hTERT (Mamchaoui et al. 2011). Puromycin and neomycin were used as selection markers.

CELL CULTURE

Immortalized myoblasts were cultured in growth medium consisting of 1 vol 199 Medium to 4 vol DMEM (Life technologies, Carlsbad, CA, USA) supplemented with 20% fetal calf serum (Life technologies, Carlsbad, CA, USA), 5 ng/ml hEGF (Life technologies, Carlsbad, CA, USA), 0.5 ng/ml bFGF, 0,1mg/ml Dexamethasone (Sigma-Aldrich, St. Louis, Missouri, USA), 50 μ g/ml fetuin (Life technologies, Carlsbad, CA, USA), 5 μ g/ml insulin (Life technologies, Carlsbad, CA, USA) and 50mg/ml Gentamycin (GibcoTM, Life technologies, Carlsbad, CA, USA) or DMEM. Cell cultures were performed on 2D conventional rigid substrates or on soft hydrogels (12 kPa, Matrigen, Brea, California, USA). All experiments on soft hydrogels and its controls were performed with fibronectin coated surfaces at a concentration of 10 μ g/ml (Sigma-Aldrich, St. Louis, Missouri, USA). On rigid substrates cells were grown on uncoated cell culture plastic unless stated otherwise. Dense or sparse culture conditions were achieved by seeding 1×10^5 or 1×10^4 cells per cm^2 growth area.

COATINGS

Fibronectin coatings were performed by diluting Fibronectin (Sigma Aldrich, St. Louis, Missouri, USA) in PBS to a final concentration of 1-10 μ g/ml. Cell culture plastic was covered with the fibronectin solution and incubated for 1h at 37°C. Then, the solution was removed and the cell culture plastic was dried for several hours in the sterile bank.

CHEMICALS, RECOMBINANT GROWTH FACTORS AND INHIBITORS

Recombinant human BMP2 was kindly provided by Walter Sebold (University of Würzburg, Würzburg, Germany). All chemicals were purchased from Sigma Aldrich unless stated otherwise. Myosin II inhibitor blebbistatin, ROCK inhibitor Y27632, the microtubule assembly inhibitor nocodazole (Sigma-Aldrich, St. Louis, Missouri, USA), LatrunculinA (Milipor, Billerica, MA, USA) were diluted to final concentrations of 25 μ M; 10 μ M; 1 μ g/ml and 5 μ M in the culture medium. Cells were incubated with each drug for the indicated times. The actin stabilizing drug Jasplakinolide (Santa Cruz, Dallas, Texas, USA) was added at a concentration of 500nM. Controls were performed with the according concentrations of DMSO. Eukaryotic translation inhibitor Cycloheximid (CHX) and proteasome inhibitor MG-132 (both Sigmar Aldrich, St. Louis, Missouri, USA) were diluted in growth Medium to a final concentration of 30 μ g/ml and 25 μ M and added to the adherent myoblasts for 2, 4, 6, and 8h. Proliferation inhibitor Mitomycin C (Sigma-Aldrich, St. Louis, Missouri, USA) was diluted in growth medium to a final concentration of 30 μ g/ml and added to the adherent cells for 1h before the migration experiments.

LUCIFERASE REPORTER ASSAYS

Myoblasts were transfected with Lipofectamin® 2000 or Lipofectamin® 3000 (both Invitrogen, Carlsbad, CA, USA) reagents in growth media without antibiotics in solution at RT for 6h, otherwise according to manufacturer's instructions. TBS (Tead Binding Sequence: 14 times GGAATG)- and BRE (BMP Response Element)- Firefly Luciferase reporter constructs were used at a 1:5 ration to the co-reporter vector for the weak constitutive expression of wild-type Renilla luciferase (pRL-TK, Promega GmbH, Mannheim, Germany). Transfected cells were seeded into 24-,48- or 96-well plates and recovered overnight in growth medium. For the BRE-assay, cells were starved in growth Medium or DMEM with 0,5% FCS for 3h and stimulated with the indicated concentrations of BMP2 for 24h, or as indicated. For the TBE, assay cells were cultivated for 24h after transfection under the stated conditions. The cells were lysed with passive lysis buffer (PJK GmbH, Kleinblittersdorf, Germany). Luciferase activity was measured with a Mithras LB940 (Wildbad, Germany) by addition of firefly Luciferase substrate Beetle Juice (PJK GmbH, Kleinblittersdorf, Germany) and Renilla Juice (PJK GmbH, Kleinblittersdorf, Germany).

IMMUNOCYTOCHEMISTRY

Experiments have been performed on fibronectin coated cell culture plastics (1µg/ml fibronectin in PBS, 1h at 37°C). Myoblasts were fixed for 10 min with 4% formaldehyde, permeabilized for 15 min with 0.5% Triton X100 and blocked with 5% BSA or normal goat serum (St. Louis, Missouri, USA) diluted in PBS. Actin was stained with fluorescent labelled phalloidin (Interchim, Mannheim, Germany or SantaCruz, Dallas, Texas, USA). Primary antibodies were diluted in PBS with 1% BSA and incubated overnight at 4°C and secondary antibodies were incubated for 1h at room temperature. The preparations were mounted with fluorescent mounting medium containing DAPI (Vectashield, Vector Labs, Burlingame, CA, USA) or incubated with 300nM DAPI (Sigma Aldrich, St. Louis, Missouri, USA) solution for five minutes and mounted in Fluorount-G (Southern Biotech, Birmingham, AL, USA). Primary antibodies used are listed in table (Table 1). As secondary antibodies, the Alexa-conjugated secondary antibody system (Invitrogen, Carlsbad, CA, USA) was utilized.

CELL PROLIFERATION ASSAY

Cells were grown on glass coverslips in growth medium at different densities for 24h. Proliferation was measured with the help of the Click-iT® EdU Alexa Fluor® 488 kit (Life Technologies, St. Louis, Missouri, USA). EdU was added to the culture media in concentrations of 1µM for durations of 16h. Cells were permeabilized and fixed with 4% formaldehyde. The fixed cells were stored at 4°C and stained the next day according to manufacturers instruction. The staining mix was prepared fresh each time. After staining, the cells on coverslips were counterstained and mounted with fluorescent mounting medium containing DAPI (Vectashield, Vector Labs, Burlingame, CA, USA) and imaged by fluorescence microscopy.

TABLE 3-1: ANTIBODIES

Target protein	Company	Dilution
GAPDH (cs-2118)	Cell Signaling Technology	WB 1:1000
Lats-1 (cs-3477)	Cell Signaling Technology	WB 1:1000
M-cadherin (ab65157)	Abcam	WB 1:1000
M-cadherin (bd-11100)	BD	WB 1:1000
N-cadherin (ab19348)	Abcam	WB 1:1000
pSmad1(Ser463/465)/pSmad5(Ser463/465)/ pSmad9(Ser465/467) (D5B10)	Cell Signaling Technology	WB 1:1000
pLats 1(Thr1079) (CS-8654)	Cell Signaling Technology	WB 1:1000
pSmad 1/5 (Ser463/465) (cs-9516)	Cell Signaling Technology	WB 1:1000 IF 1:250
pYAP(Ser127) (cs-4911)	Cell Signaling Technology	WB 1:1000
Smad1 XP (cs-D5907)	Cell Signaling Technology	WB 1:1000
YAP/TAZ (sc-10119s)	Santa Cruz Biotechnology	WB 1:1000 IF 1:200
α -Tubulin	Home made (AG Knaus)	WB 1:1000
β -Catenin (cs-9581)	Cell Signaling Technology	WB 1:1000 IF 1:200
Syntaxin-6 (C34B2)	Cell Signaling Technology	IF 1:50
Pan-cadherin (ab6529)	Abcam	IF 1:100

WOUND HEALING ASSAY

The scratch wound healing assay was performed using cell culture inserts (ibidi GmbH, Martinsried, Germany) according to the manufacturer's instructions on fibronectin coated (5 μ g/ml, 1h at 37°C) tissue culture plastic, if not indicated differently. 25x10⁵ Myoblasts were seeded into every insert 24h before insert removal. 1 hour prior to insert removal, cells were incubated with 30 μ g/ml mitomycin C to block cell proliferation. After insert removal, cells were washed with PBS and further cultivated in growth media. For live cell imaging, the wound closure was permitted to proceed in the live cell imaging, heating and CO₂ chamber (ibidi GmbH, Martinsried, Germany). Cells were imaged every 5 minutes for the indicated periods by fluorescence and/or phase-contrast

microscopy using the AxioVision 4.9 software. Cell movements and contacts were tracked by analyzing time-lapse images. For Immunocytochemistry, the wound healing assay, as described above, was performed in Chamber slides (Nunc™ Lab-Tek™, Thermo Fischer, Waltham, MA, USA). Closure was permitted to proceed under standard incubation conditions for the indicated periods. Cells were then fixed and immuno-stained as described above.

CELL TRACKING

Cell tracking was performed by Marc Osterland at the Zuse Institute Berlin. The image analyses were performed using Python 2.7.12, OpenCV 3.0, and scikit-image 0.12.3. In the interest of a clear differentiation between background and foreground, the optical flow was computed. The foreground is defined as the area with non-zero optical flow. The relatively darker cell bodies, which are surrounded by a bright halo in phase contrast microscopy, were segmented by an inverse adaptive threshold. Based on this cell body mask a distance map was computed. On these distance maps Watershed segmentation was applied to approximate the whole cell area. Therefore, the connected components from the cell body mask were used as seeds and the foreground mask as a restrictive mask. The neighborhood was then determined by counting adjacent cell areas. To calculate the cell speed, an overlap heuristic was applied on the cell areas. For each cell in a time step the cell of the preceding time step with the largest overlapping area was determined and added to a trajectory. In a post-processing step, tracking gaps due to segmentation failures in single time steps were closed using extrapolation of that track. The resulting tracks then formed the basis for the velocity analysis.

CELL ORIENTATION ANALYSIS

Cell orientation analysis were performed by Marc Osterland at the Zuse Institute Berlin. The images were taken in a 9 by 8 grid with approx. 10% overlap. Using the ImageJ plugin by Preibisch et al (2009), these images were stitched to a single, large image. The nuclei were segmented using adaptive thresholding on the DAPI channel. Clustered nuclei were separated using Watershed segmentation on the inner distance map of the nuclei with distance peaks as seeds. The Syntaxin 6 channel was smoothed using a Gaussian kernel after high intensity outliers were filtered. Then, centers of the nuclei were connected to an orientation vector with the closest intensity peak on the Syntaxin 6 channel. All connections were manually checked and corrected, where necessary. Based

on the orientation vectors, the orientation angle for each cell was calculated. The Local Orientation Variance (LOV) was computed with a sliding circular window on the image area, computing the variance with Von Mises distance of the angles of all cells within this window, resulting in the LOV map. The LOV was omitted if less than three cells were in the window. Given almost equal image dimensions for each experiment, the LOV map were scaled to the mean image size. The average LOV map for each condition was determined by computing the mean over all experiments for each position.

MICROSCOPY

Fluorescent signals were visualized using a Leica SP2 (Leica Microsystems, Wetzlar, Germany) microscope and an inverted fluorescence Axiovert 200 microscope (Carl Zeiss, Oberkochen, Germany). Life-cell imaging was performed with the Axiovert 200 equipped with a live cell imaging heating and CO₂ chamber mounted to a CoolSnapHQ CCD camera (Roper Scientific, Trenton, NJ, USA). Mosaic pictures have been generated with the help of the AxioVision 4 Module Mark & Find software. Confocal images were taken with an Olympus FV 1000 (Olympus, Hamilton, Bermuda).

IMAGE ANALYSIS

Standard image analyses and quantitative immunofluorescent analysis were performed using ImageJ software. Cell spreading area was measured by quantifying the area of Phalloidin -positive areas from > 50 cells per cell line.

ACTIN FIBER ORIENTATION ANALYSIS

Actin fiber orientation analysis was performed on z-stacks of confocal images. Therefore, a maximum projection of the z-layers of each image was generated with imageJ. Direction analysis with the ImageJ plugin OrientationJ were then applied every projected image.

TABLE 3-2: SEQUENCES OF PRIMERS USED IN RT-QPCR

Name	Abbreviation	Fw/rev	Sequence
human Inhibitor of Differentiation1	hID-1	fw	GCTGCTCTACGACATGAACG
		rev	CCAAGTGAAGGTCCCTGATG
human Inhibitor of Differentiation2	hID-2	fw	GTGGCTGAATAAGCGGTGTT
		rev	TGTCCTCCTTGTGAAATGGTT
human Inhibitor of Differentiation3	hID3	fw	CTCCGGCAGGAGAGGTT
		rev	AAAGGAGCTTTTGCCACTGA
human Myogenin	hMyoG	fw	CAGGGGTGCCAGCGAATGC
		rev	ATCTGTAGGGTCAGCCGTGA
human Myogenic differentiation	hMyoD	fw	CCGACGGCATGATGGACTAC
		rev	GCGACTCAGAAGGCACGTC
human Myosin heavy chain IIa	hMHC_IIa	fw	GCAACTCACTTACCAAAGT
		rev	GACCTGGGACTCAGCAATGT
human Myosin heavy chain IIb	hMHC_IIb	fw	GCTGAAGAGGCTGAGGAACA
		rev	TTTGTGTGAACCTCCCGACT
human Glycerinaldehyd- 3-phosphat- Dehydrogenase	hGAPDH	fw	GAAGGTGAAGGTCGGAGTC
		rev	GAAGATGGTGATGGGATTTTC
human Yess-associated protein 1	hYAP1	fw	GCTACAGTGTCCCTCGAACC
		rew	CCGGTGCATGTGTCTCCTTA
human connective tissue growth factor	h-CTGF	fw	ACCGACTGGAAGACACGTTTG
		rew	CCAGGTCAGCTTCGCAAGG
human connective tissue growth factor	h-RPLPO	fw	CTCCAAGCAGATGCAGCAGA
		rew	ATAGCCTTGCGCATCATGGT
human Glycerinaldehyd- 3-phosphat- Dehydrogenase	h-GAPDH	fw	TGC-CAT-GTA-GAC-CCC-TTG-AA
		rew	TGG-TTG-AGC-ACA-GGG-TAG-TT
human myosin light chain 9	h-Myl9	fw	CGA-ATA-CCT-GGA-GGG-CAT-GAT
		rew	AAA-CCT-GAG-GCT-TCC-TCG-TC

SDS-PAGE AND PROTEIN ANALYSIS

Cells were lysed in total protein extraction buffer (50 mM Tris-HCl, pH 7.5, 2% SDS, 250 mM sucrose, 75 mM urea, 1 mM DTT) with protease inhibitor (25 µg/ml Aprotinin, 10 µg/ml Leupeptin, 1 mM 4-[2-aminoethyl]-benzene sulfonylfluoride hydrochloride and 2mM Na₃VO₄) or directly in 2x Lämmli buffer. Nuclear-/cytosolic fractioning was performed with the help of NE-PER™ Nuclear and Cytoplasmic Extraction Reagents (Thermo Fisher, Waltham, MA, USA) and according to manufacturers instructions. Protein lysates were subjected to SDS-PAGE and transferred to PVDF or nitrocellulose membranes by Western blotting. Membranes were blocked for 1 h in 0.1% TBS-T containing 5% BSA, washed three times in 0.1% TBS-T and incubated with indicated primary antibodies overnight at 4°C (see table 1). For HRP-based detection, goat anti-mouse, goat anti-rat or donkey anti-goat HRP conjugates were used. Detection of adsorbed HRP-coupled secondary antibodies was performed by ECL reaction with Immobilon Western Chemiluminescent HRP Substrate (Millipore, Billerica, Massachusetts, USA). HRP signals were detected using a CCD-based detection system (Vilber Lourmat). Membranes subjected to a second round of immunoblotting were stripped with stripping buffer (62.5mM Tris-HCL pH 6.8, 2%SDS, 100mM β-mercaptoethanol) and incubated at 55°C for 30 minutes with mild shaking before excessive washing with tap water and re-blocking. Quantification was performed using ImageJ.

STATISTICAL ANALYSIS

SPSS (IBM Corporation, Armonk, New York, USA) was used to calculate means and standard error of the mean (SEM) of measured quantities. Statistical significances were assessed by two-tailed unpaired t-tests when comparing means of two groups. Differences between conditions were considered significant at $p < 0.05$.

QUANTIFICATION OF GENE EXPRESSION

The mRNA was isolated from cell lysates using the RNeasy mini kit (Qiagen, Hilden, Germany) with the Proteinase K step, according to the manufacturer instruction for YAP response genes, or using the NucleoSpin RNA II Kit (Machery Nagel, Düren, Germany) for BMP receptor and IDs expression analysis. The complementary DNA (cDNA) was transcribed by SuperscriptIII (Life Technologies, Carlsbad, CA, USAEuro) or qScript™cDNA SuperMix (Quanta Biosciences, Gaithersburg, MD, USA).

Gene expression was quantified by using PerfeCTa®SYBR®Green SuperMix (Quanta, Biosciences, Gaithersburg, USA) with the help of LightCycler 480 II (Roche Diagnostics GmbH, Mannheim, Germany). The primers were designed by Primer-BLAST (NCBI) and synthesized by Eurogentec (Liège, Belgium) or TIB Molbiol (Berlin, Germany). Expression of all target genes was normalized to the expression of house-keeping genes hypoxanthine-guanine phosphoribosyltransferase (HPRT), GAPDH or RPLP0 as indicated which accounts for potential changes in cell numbers. Primer sequences are listed in Table 2.

4. RESULTS

INCREASED YAP ACTIVITY IN $\Delta K32$ MUTANT MYOBLASTS

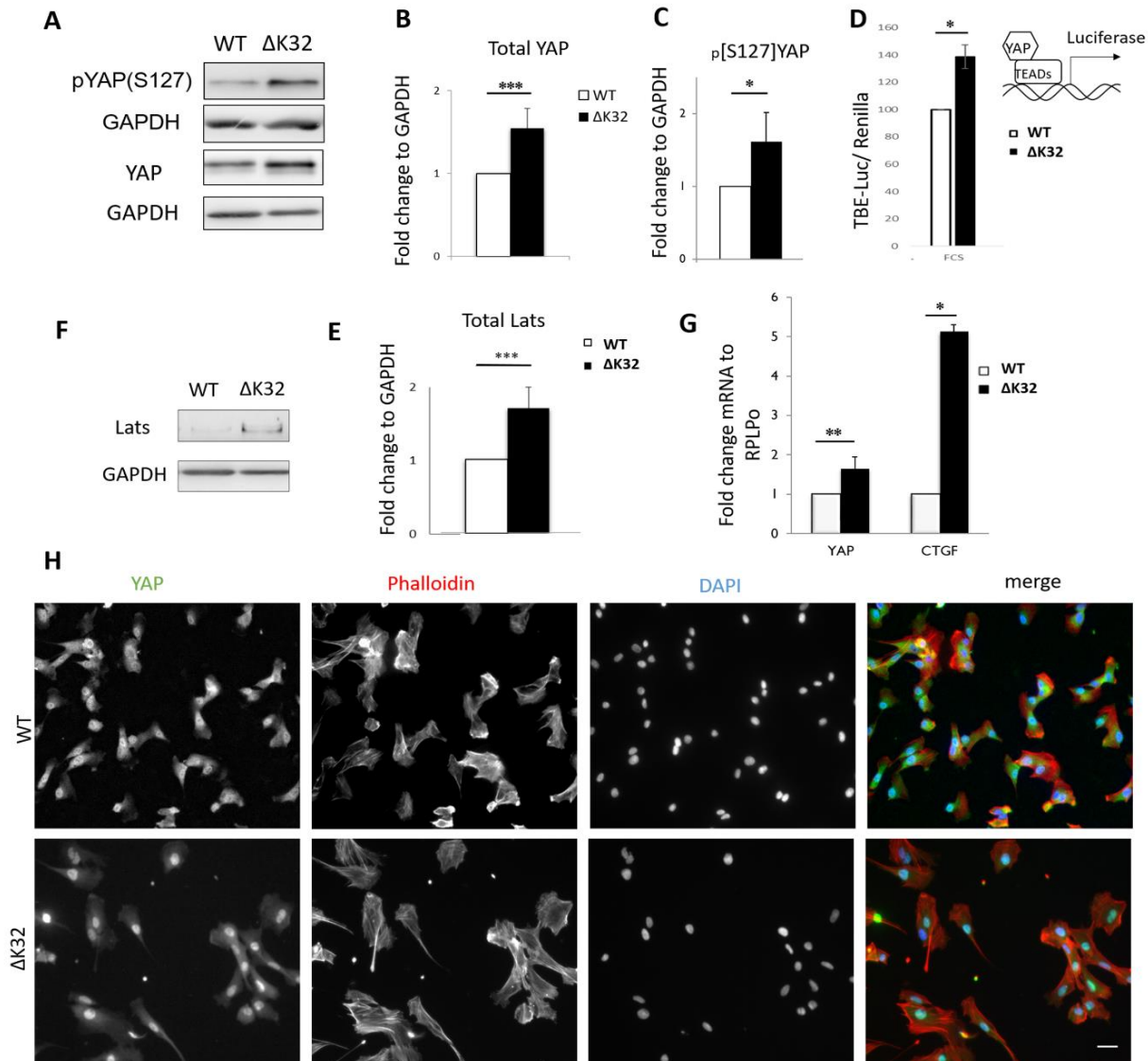


Figure 4-1: Increased YAP signaling in $\Delta K32$ mutant myoblast. Significantly increased protein levels of YAP, p-YAP(S127) and Lats in $\Delta K32$ mutant myoblast compared to WT myoblasts (A, B, C, E, F). Tead-dependent dual luciferase reporter assay shows a significantly increased transcriptional activity of YAP in $\Delta K32$ mutant myoblast compared to WT (D). Significantly increased mRNA levels of YAP and the YAP response gene *ctgf* (G). YAP (green) cellular localization is nuclear in WT and $\Delta K32$ mutant myoblasts. Cells were counterstained with dapi (blue) and phalloidin (red) (H). Representative western blots are shown. Quantifications represent means \pm SEM of ≥ 3 independent experiments. Values are foldchanges, normalized to WT. (*) p -value ≤ 0.05 ; (**) p -value ≤ 0.005 , (***) p -value ≤ 0.0005 . scale bar = $30\mu\text{m}$.

To analyze the activity of mechanosensitive YAP signaling in LMNA mutant myoblasts, YAP activity was first analyzed in WT and $\Delta K32$ mutant myoblasts cultured on conventional hard

surface and plated in sparse conditions. YAP protein and mRNA levels were significantly higher in Δ K32 compared to WT myoblasts (fig. 4-1 A, B, G). Also, protein levels of the hippo core kinase Lats were significantly increased in Δ K32 mutant myoblast compared to WT (fig. 4-1F, E). In addition, the phosphorylation of YAP at Serine 127 was significantly increased in Δ K32 compared with WT myoblasts (fig. 4-1 A, C). YAP cellular localization was mainly nuclear in both WT and Δ K32 mutant myoblasts (fig. 4-1 E). However, the transcriptional activity of YAP was increased in Δ K32 myoblasts compared to WT myoblasts, as attested by the TEAD Luciferase reporter gene assay and the increased expression of the YAP response gene *ctgf* (fig. 4-1 D, G).

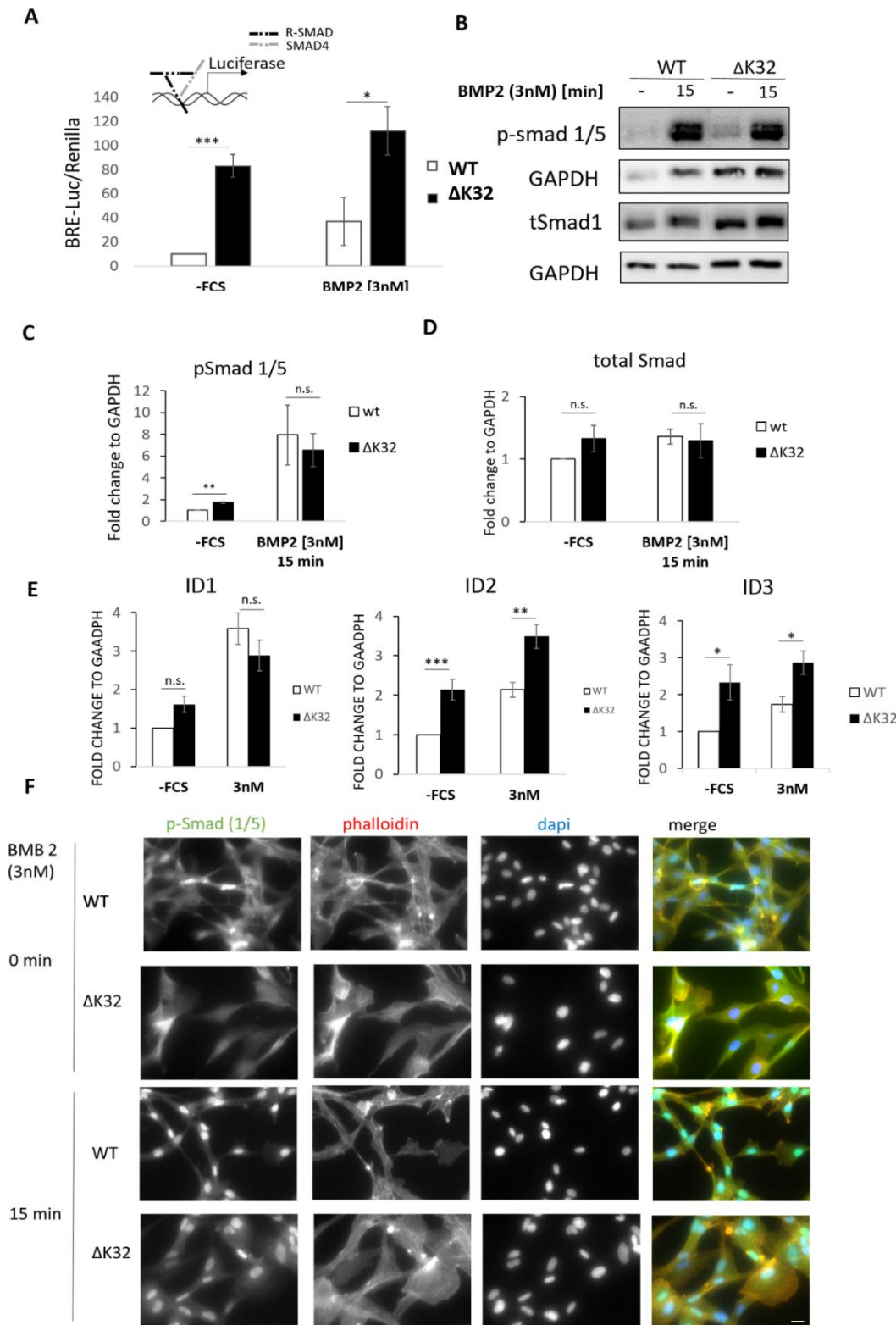
INCREASED SMAD TRANSCRIPTIONAL ACTIVITY IN Δ K32 MYOBLASTS

To determine whether the activity of another mechanosensitive pathway, the BMP pathway, was also impaired in Δ K32 myoblasts, Smad 1/5/8 transcriptional activity in Δ K32 myoblasts was analyzed using a dual luciferase reporter assay on the BMP-responsive-element. In sparse conditions, there was a strong and significant increase of Smad transcriptional activity in Δ K32 compared to WT myoblasts in starved condition (fig. 4-2A). After stimulation with BMP2, Smad transcriptional activity was enhanced in both cell types, while there was still a significant higher transcriptional activity of Smads in Δ K32 mutant myoblasts compared to WT (fig. 4-2A). Moreover, mRNA levels of Smad response genes *id2* and *id3* were significantly increased in Δ K32 compared to WT myoblasts in starved condition and after stimulation with BMP2 [3nM] for 6h (fig. 4-2C). Total Smad 1 and pSmad 1/5 protein levels were analyzed by western blot in starved condition and after stimulation with BMP2 for 15 min (fig. 4-22D). The phosphorylation of Smad 1/5 was slightly but significantly increased in Δ K32 compared to WT myoblasts in starved condition but, not after stimulation with BMP2 (fig. 4-2E). There was no significant difference in total Smad1 protein levels between WT and Δ K32 myoblasts, in starved condition or after stimulation (fig. 4-2F).

The cellular localization of pSmad1/5 was analyzed by immunofluorescence in starved condition and after stimulation with BMP2 for 15 min. The cellular localization of pSmad1/5 was equally distributed in the cytoplasm and the nucleus in starved conditions in WT and Δ K32 myoblasts. The localization of pSmad1/5 was mainly nuclear after stimulation with BMP2 (fig. 4-2B). Taken together, these results showed an increased transcriptional activity of the BMP pathway

in $\Delta K32$ compared to WT myoblasts. If this increased activity is caused by mechanosensing defects of $\Delta K32$ mutant myoblasts, remains to be investigated.

Figure 4-2: Increased smad transcriptional activity. $\Delta K32$ mutant myoblasts showed an increased Smad transcriptional activity in starved condition and after stimulation with BMP2 [3nM] (A). $\Delta K32$ mutant myoblasts also showed significantly increased mRNA levels of Smad response genes *ID2* and *ID3* in starved condition and after stimulation with 3nM BMP2 for 6h compared to WT myoblasts. *ID1* mRNA expression was not significantly increased (E). pSmad 1/5 protein levels were significantly increased in $\Delta K32$ mutant compared to WT myoblasts in starved but not stimulated condition, while total Smad1 levels remained stable (B, C, D). A representative western blot is shown. Myoblasts were stained for pSmad (green) and counterstained with phalloidin (red) and DAPI (blue) to visualize cellular localization. In $\Delta K32$ and WT myoblasts, pSmad 1/5 localization was cytoplasmic and nuclear in starved condition and became mainly nuclear after stimulation with 3nM BMP2 (F). Quantifications represent mean values +/- SEM from ≥ 3 independent experiments. Values are fold changes, normalized to WT-FCS. (*) p-value ≤ 0.05 ; (**) p-value ≤ 0.005 , (***) p-value ≤ 0.0005 ; (n.s) not significant. Scale bar= 10 μ m



YAP OVER-ACTIVITY IS INHIBITED BY GROWTH FACTOR STARVATION

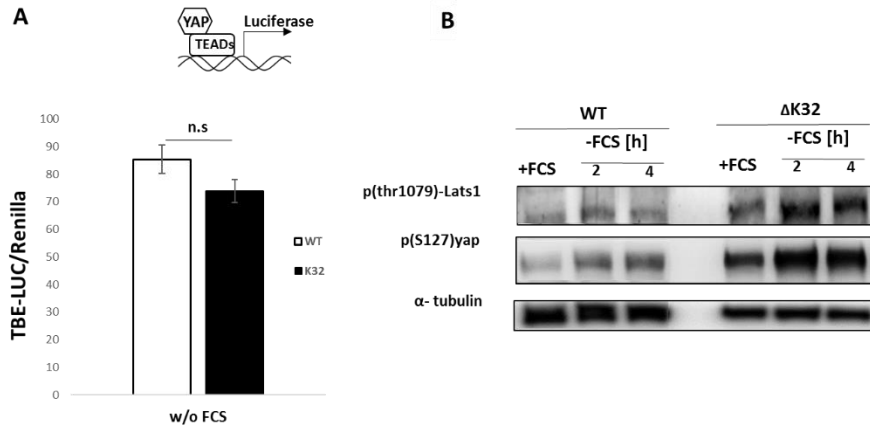


Figure 4-3: Regulation of YAP in $\Delta K32$ mutant myoblast. No significant difference in the transcriptional activity between WT and $\Delta K32$ mutant myoblasts, after starvation with 0% FCS (A). After starvation with 0% FCS for the indicated time, p(S127) YAP and p(Thr1079) levels increased in WT and $\Delta K32$ mutant myoblasts compared to unstarved condition, while total YAP levels remained stable (B). A representative western blot is shown (B). Tead-dependent luciferase assay was quantified as mean \pm SEM ≥ 3 independent experiments. Values are fold changes to renilla luciferase activity. (n.s) not significant.

To dissect the regulation of YAP signaling in $\Delta K32$ mutant myoblasts, YAP transcriptional activity and phosphorylation were analyzed after starvation of cells with 0 % FCS. Interestingly, there was no significant difference in the tead-dependent transcriptional activity of YAP in $\Delta K32$ and WT myoblasts in starved

conditions (fig. 4-3A). Starvation induced an increase in the phosphorylation of Lats (thr1079) and YAP (S127) in both WT and $\Delta K32$ mutant myoblasts compared to full-medium condition (fig. 4-3B). However, protein levels of pYAP remained significantly increased in $\Delta K32$ compared to WT myoblasts after starvation. These results showed that the increased transcriptional activity of YAP, but not the increased protein levels, can be abolished by growth factor mediated phosphorylation of YAP.

INCREASED NUCLEAR LOCALIZATION OF YAP IN $\Delta K32$ MUTANT MYOBLASTS IN DENSE CONDITION

YAP is normally retained in the cytoplasm in dense culture conditions (Zhao et al.,2007). To further dissect the regulation of YAP in $\Delta K32$ myoblasts, immunofluorescence studies of YAP cellular localization in dense culture conditions were performed. In dense condition, YAP was excluded from the nucleus in WT myoblasts (90 %) whereas, YAP remained predominantly nuclear in $\Delta K32$ mutant myoblasts (fig. 4-4A, B). Increased nuclear localization of YAP in mutant cells correlated with a slight but significant increase of YAP transcriptional activity, as indicated by increased

TEAD-dependent Luciferase reporter assay activity and increased expression of the YAP response genes *ctgf* and *myl9* (fig. 4-4C, D).

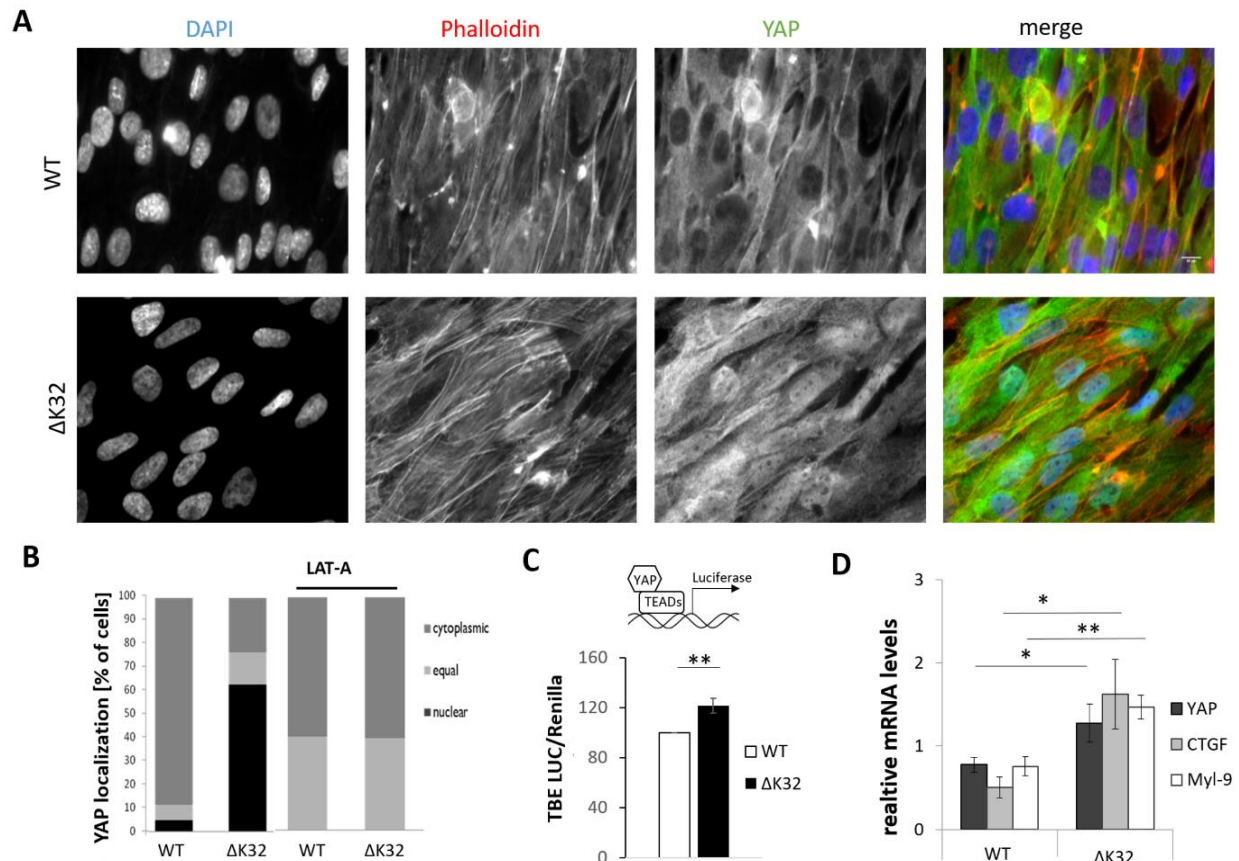


Figure 4-4: Increased nuclear localization of YAP in dense condition. YAP (green) cellular localization was analyzed in dense culture conditions 24h after plating and counterstained with phalloidin (red) and DAPI (blue) (A). In WT myoblasts, YAP is mainly cytoplasmic, while in $\Delta K32$ mutant myoblasts, YAP remains predominantly nuclear. Quantifications show the number of cells (%) with a nuclear (black), equally distributed (light-grey) or only cytoplasmic (dark grey) YAP staining (B). A dual reporter assay on TEAD-dependent Luciferase expression shows an increased YAP transcriptional activity for $\Delta K32$ mutant myoblasts (D). mRNA levels of YAP response genes *Myl-9* and *ctgf*, as well as YAP were increased (E). Quantifications represent means \pm SEM of ≥ 3 independent experiments. Values are fold changes. C is normalized to WT. (*) p-value ≤ 0.05 ; (**) p-value ≤ 0.005 ; (***) p-value ≤ 0.0005 ; (n.s) not significant. Scale bar= 10 μ m.

These results show a defect in the inactivation of YAP in $\Delta K32$ mutant myoblasts in dense conditions. However, cell starvation abolished the increased transcriptional activity of YAP in

Δ K32 mutant myoblasts plated in dense conditions. There was no significant difference in YAP activity between WT and Δ K32 mutant after removal of FCS (fig. 4-5).

REGULATION OF YAP AT INCREASING CELL DENSITY

YAP cytoplasmic retention in dense conditions was shown to be either regulated through contact inhibition of proliferation (CIP) or through a reduced cell size and decreased F-actin formation, independent of cell-cell contacts (Zaoh et al., 2007; Schlegelmilchetal., 2011; Silvisetal., 2011; Dupont et al, 2011). To investigate if YAP nuclear localization in Δ K32 mutant myoblasts remains

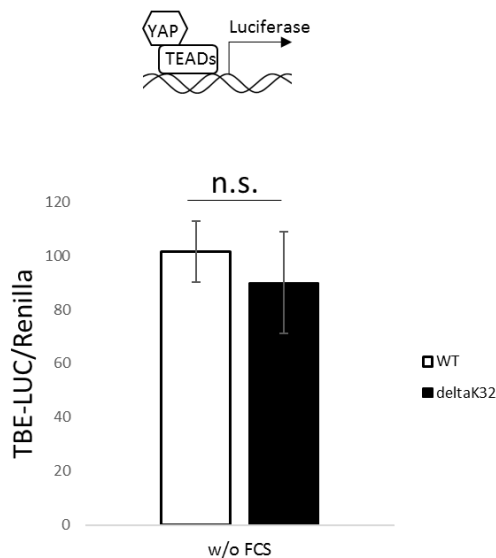


Figure 4-5 No significant difference of YAP activity between Δ K32 and WT cells after starvation. Tead-dependent luciferase assay in dense condition after starvation with 0% FCS. Quantifications are means \pm SEM of ≥ 3 independent experiments. Values are foldchanges to renilla luciferase activity. (n.s) not significant.

dependent on F-actin polymerization in dense culture conditions, WT and Δ K32 mutant myoblasts were treated with the F-actin polymerization inhibitor Latrunculin A. Inhibition of actin polymerization in dense condition caused an exclusion of YAP from the nucleus in Δ K32 mutant myoblasts (fig. 4-4B). In WT myoblasts, treatment with Latrunculin A led to a further increase of YAP nuclear exclusion. This demonstrates that Δ K32 mutant myoblasts preserved the general ability to exclude YAP from the nucleus.

During cell contact inhibition, YAP cytoplasmic retention was reported to be regulated by increased phosphorylation of YAP at Serine 127 (Zaoh et al., 2007). To analyze the effects of cell-cell contact on YAP phosphorylation, the p(S127) phosphorylation of YAP was determined with growing cell density (fig. 4-6A, B). p(S127) YAP protein levels decreased with increased density in both WT and Δ K32 mutant myoblasts (fig. 4-6 B). In addition, total YAP levels decreased from sparse to dense culture conditions in both WT and Δ K32 mutant myoblasts (fig. 4-6B). Interestingly, in dense culture conditions, total YAP and p(S127) YAP protein levels did not differ in Δ K32 mutant compared to WT myoblasts (fig. 4-6C,D). YAP transcriptional inactivation through cell-contact is associated with a decrease in cell proliferation (Zaoh et al, 2007). To determine if the increased YAP activity

in $\Delta K32$ mutant myoblast led to an increased cell proliferation, WT and $\Delta K32$ mutant myoblasts proliferation.

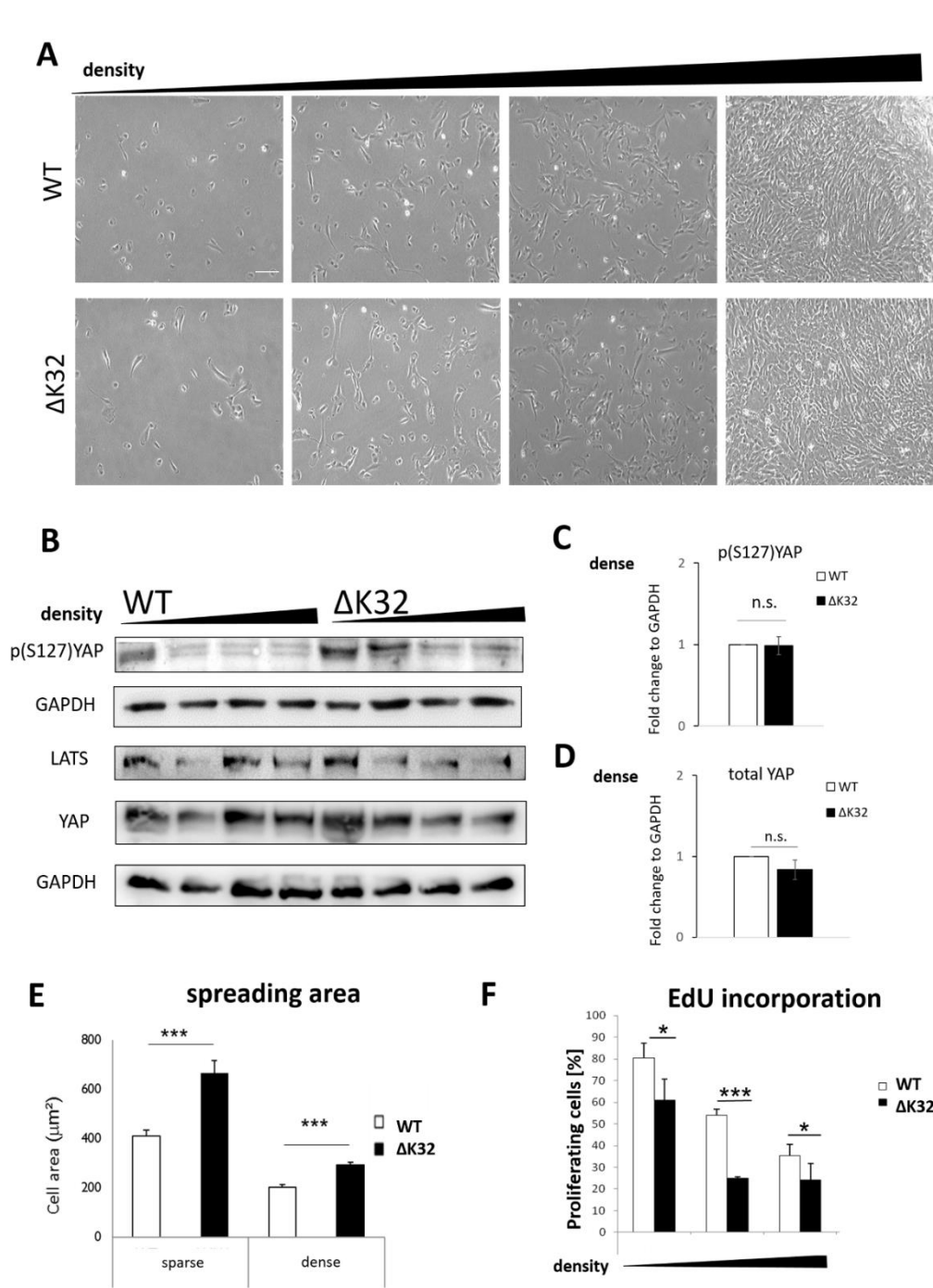


Figure 4-6: Regulation of YAP with increasing density. To analyze YAP phosphorylation kinetics, $\Delta K32$ and WT myoblasts were seeded with increasing density (A). Representative western blot and quantification of total YAP and p(S127) YAP with increasing density (B). Total YAP and p(S127) YAP levels decreased with increasing density. The increased YAP and p(S127) YAP levels of $\Delta K32$ mutant myoblasts were abolished in dense condition compared to WT myoblasts (C, D). $\Delta K32$ mutant myoblasts have an increased spreading area in sparse and dense conditions compared to WT myoblasts (E). $\Delta K32$ mutant myoblasts had a reduced proliferation in all densities compared to WT cells (F). (D, E, F) Quantifications represent means \pm SEM of ≥ 3 independent experiments. D and E are shown as foldchanges, normalized to WT. (*) p-value ≤ 0.05 ; (**) p-value ≤ 0.005 ; (***) p-value ≤ 0.0005 ; (n.s.) not significant. Scale bar = 100 μm

Altogether, these results indicated that YAP transcriptional activity was increased in $\Delta K32$ mutant myoblasts in both, sparse and dense condition, but increased total YAP and p (S127) YAP protein levels were only observed in $\Delta K32$ myoblasts plated in sparse conditions. Increased YAP activity was not associated with an increased proliferation of $\Delta K32$ compared to WT myoblasts. Finally, YAP over-activity in $\Delta K32$ mutant could be abolished by growth factor starvation.

To determine if the increased YAP activity of $\Delta K32$ mutant myoblasts in sparse and dense conditions could be related to an increased cell size, the spreading area of $\Delta K32$ mutant myoblasts was measured. Compared to WT myoblasts, the spreading area of $\Delta K32$ mutant was significantly higher in both sparse and dense culture conditions (fig. 4-6E).

DISORGANIZED ACTIN FIBER NETWORK IN $\Delta K32$ MYOBLASTS

Actin organization plays a crucial role in YAP regulation (Dupont et al., 2011; Halder et al., 2012; Zhao et al., 2012). Moreover, disorganized perinuclear actin stress fibers (actin cap) have been reported in A-type lamin deficient (Lee et al., 2007; Chambliss et al., 2013; Khatau et al 2009) and A-type lamin mutant cells (Schwartz et al., submitted). We investigated the organization of actin fibers in $\Delta K32$ mutant myoblasts in sparse and dense culture conditions (fig. 4-7 and 4-8).

Supranuclear actin of WT myoblasts was composed of parallel aligned actin fibers, which cover the nucleus (top) in sparse and dense conditions. The number of actin bundles on the top of the nucleus was lower in $\Delta K32$ mutant myoblasts in sparse and dense conditions (fig. 4-7A left). In sparse conditions, the basal actin cytoskeleton (bottom) of WT myoblasts was characterized by the presence of actin bundles as well as several dots, suggestive of actin depolymerization. The presence of these dots apparently increased in dense condition in WT myoblasts. In contrast, $\Delta K32$ mutant myoblasts did not show this dotted phalloidin staining pattern in sparse or dense conditions. Instead, $\Delta K32$ mutant myoblasts had polymerized actin fibers beneath the nucleus in sparse and dense conditions (fig. 4-7A right). These results strongly suggest a depolymerization of actin fibers from sparse to dense conditions beneath the nucleus in WT, but not in $\Delta K32$ mutant myoblasts.

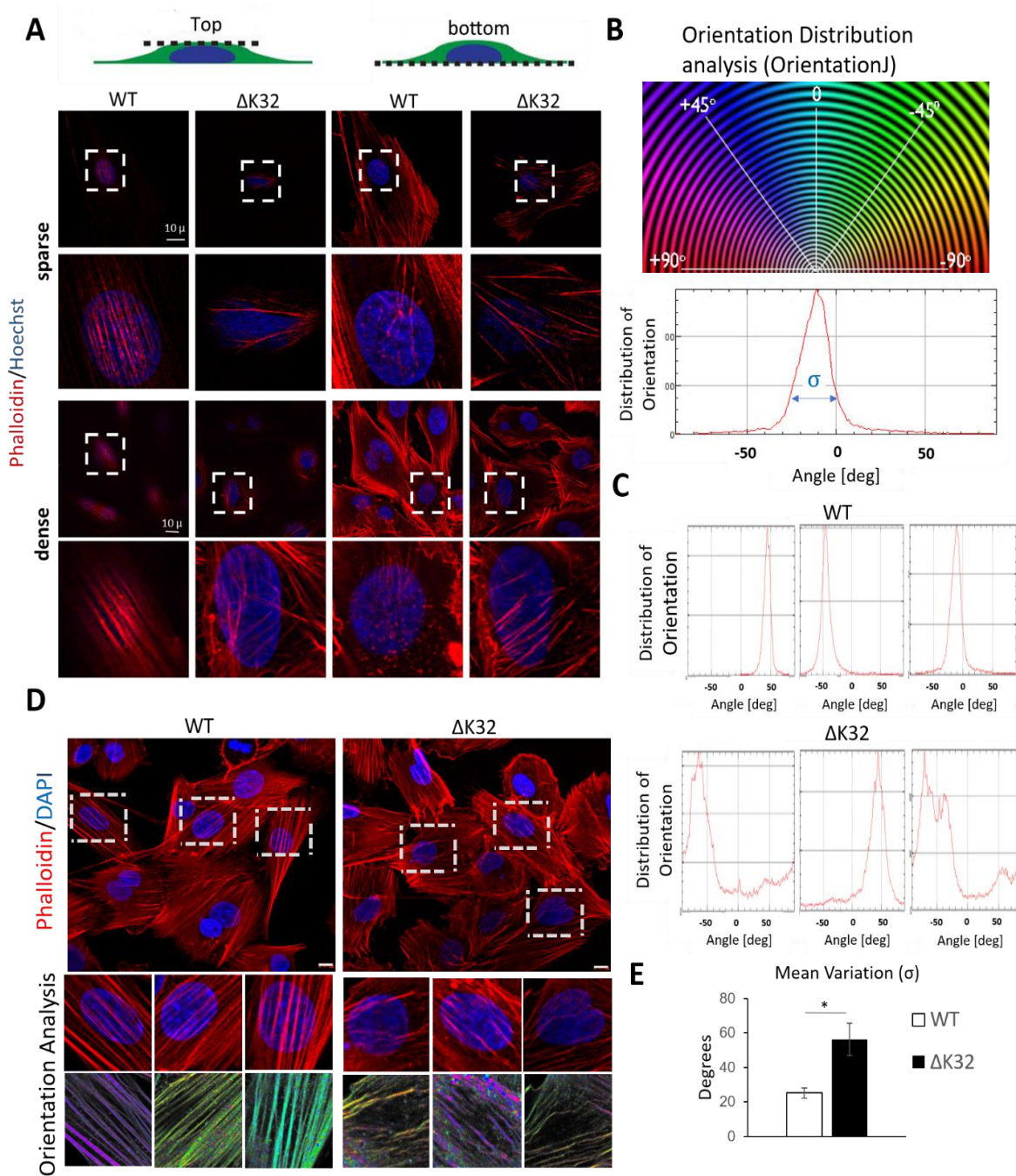


FIGURE 4-7: Defective organization of perinuclear actin in Δ K32 mutant myoblasts. WT and Δ K32 mutant myoblasts were stained with phalloidin (red) and Hoechst or dapi (blue). Confocal images of the top and the bottom of perinuclear actin show an abnormal organization of the perinuclear actin in Δ K32 mutant myoblasts(A). Perinuclear F-actin was analyzed for Orientation Distribution with OrientationJ (ImageJ)(B-E). Actin fibers were colored dependent on their orientation angle (D) and histograms represent the number of pixels for each orientation angle (C). The mean variation of the distribution of the orientation of perinuclear f-actin fibers is significantly increased in Δ K32 mutant myoblasts (E). Quantifications represent means of ≥ 3 independent analysis, \pm SEM(*) p -value ≤ 0.05 ; (**) p -value ≤ 0.005 , (***) p -value ≤ 0.0005 ; (n.s) not significant. Scale bar = $10\mu\text{m}$

To further characterize the organization of actin fibers, we analyzed their orientation using maximum projections of z-stacks. The orientation angle of each actin fiber was determined and each fiber was colored, so that similar angles will have similar colors. In addition, the distribution of the orientation angles was quantified and depicted as histogram. The mean variation of the distribution of the orientation is defined as sigma (σ) (fig. 4-7B).

WT myoblast had a parallel organization of actin stress fibers in the perinuclear region, which is reflected in a monotonous coloration of actin fibers. In contrast, Δ K32 myoblasts showed multicolored actin fibers in the perinuclear region (fig. 4-7D). Histograms of WT actin fibers showed narrow shaped peaks whereas distribution peaks of Δ K32 myoblasts were more wide (fig. 4-7C). The mean variation (Ω) of the distribution was significantly increased in Δ K32 mutant myoblasts (fig. 4-7E). Taken together, these results suggested quantitative and qualitative defects of perinuclear actin fibers in Δ K32 mutant myoblasts.

Actin fibers reorganized in confluent WT myoblasts, forming parallel actin fibers, which span the whole cell body and connect to cell-cell junctions. In contrast, the actin cytoskeleton of Δ K32 mutant myoblasts was less frequently organized in parallel bundles and mostly did not span the whole cell body (fig. 4-8A, B). Orientation analysis of actin fibers revealed that the orientation of actin fibers was lower in Δ K32 compared to WT myoblasts. The orientation of actin fibers in WT myoblasts was parallel, as reflected in mainly monotonous colored fibers of one cell. In contrast, orientation analysis of Δ K32 myoblasts actin revealed multicolored fibers in each cell (fig. 4-8B), attested by a wider shaped distribution peak of the actin cytoskeleton in Δ K32 than in WT myoblasts (fig. 4-8D). Together these results indicate a defective orientation of perinuclear and whole cell actin fibers in Δ K32 myoblasts compared to WT myoblasts.

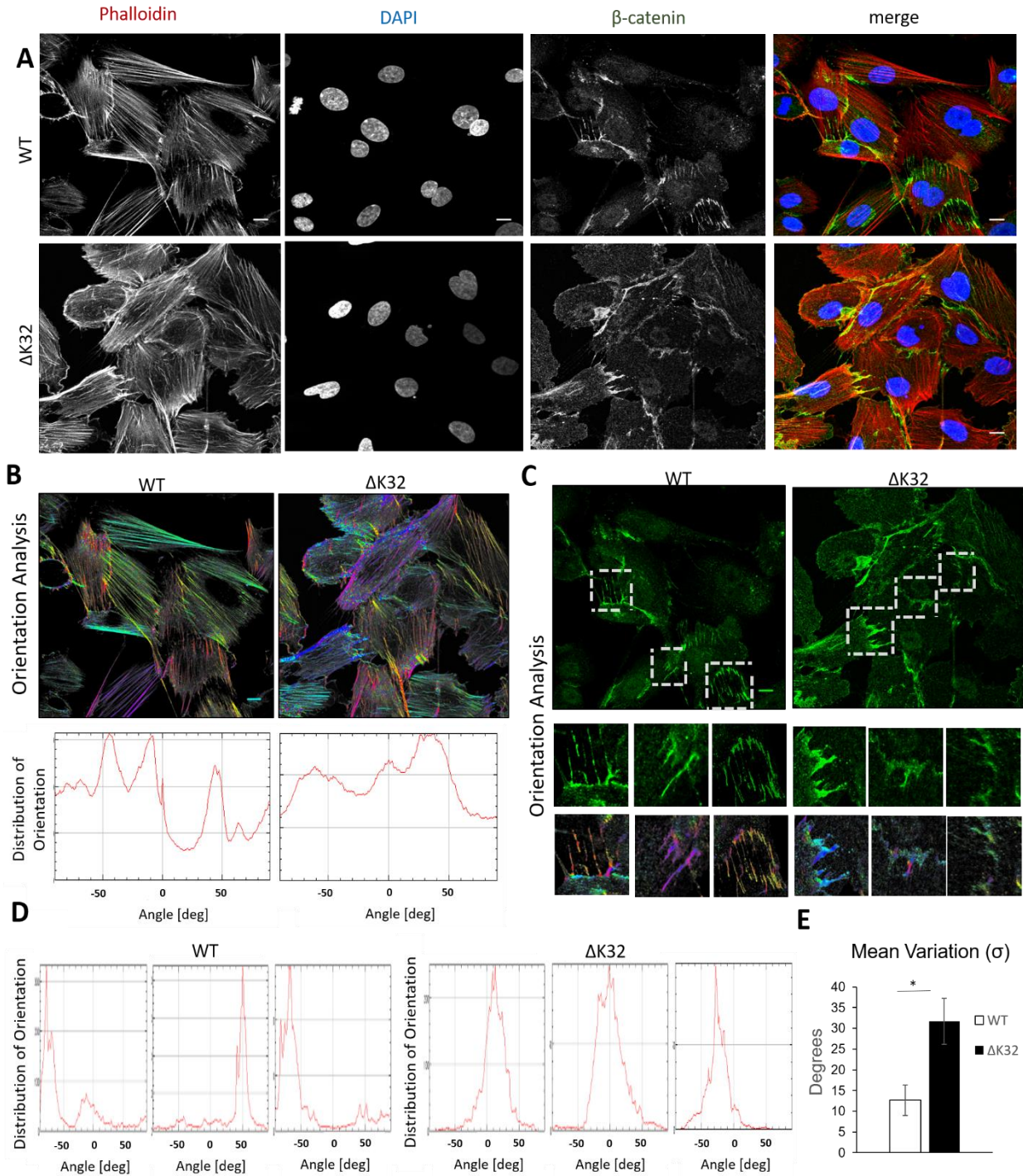


Figure 4-8: Disorganization of actin stress fibers in $\Delta K32$ mutant myoblasts affects the organization of adherence junctions. WT and $\Delta K32$ mutant myoblasts were stained for F-actin (Phalloidin, red), β -catenin (green) and dapi (blue) (A,C). Whole cell F-actin (B) and β -catenin stainings (C) were analyzed for Orientation Distribution with OrientationJ (ImageJ). Actin fibers were colored dependent on their orientation angle (B,C) and histograms represent the number of pixels for each orientation angle (B,D). The mean variation of the distribution of the orientation of the zipper-like β -catenin staining is significantly increased in $\Delta K32$ mutant myoblasts (E). Scale bar = 10 μ m. Quantifications represent means of ≥ 3 independent image analysis, \pm SEM. (*) p -value ≤ 0.05 ; (**) p -value ≤ 0.005 , (***) p -value ≤ 0.0005 ; (n.s.) not significant. Scale bar = 10 μ m

DISORGANIZED CELL-CELL CONTACT SIDES IN $\Delta K32$ MYOBLASTS

As the organization of actin fibers in $\Delta K32$ myoblasts may affect the organization of cell-cell contact sites, cell-cell contact formation was analyzed (fig. 4-8A,C). In stage AJ2, cell-cell junctions between myoblasts show a zipper-like structure at the tip of actin fibers. In WT myoblasts, the β -catenin staining pattern was zipper-like and parallel organized. In contrast, the β -catenin staining pattern in $\Delta K32$ myoblasts was more diffuse, indicating a reduced formation of AJ2 stage cell-cell junctions in $\Delta K32$ myoblasts. Orientation analysis of β -catenin stainings are depicted in figure (fig. 4-8C,D). The mean variation (σ) of β -catenin stained cell-cell contacts was significantly increased in $\Delta K32$ myoblasts compared to WT myoblasts (fig. 4-8E). These results supported our hypothesis that disorganization of actin fibers in $\Delta K32$ myoblasts contribute to the disorganization of cell-cell contact sites.

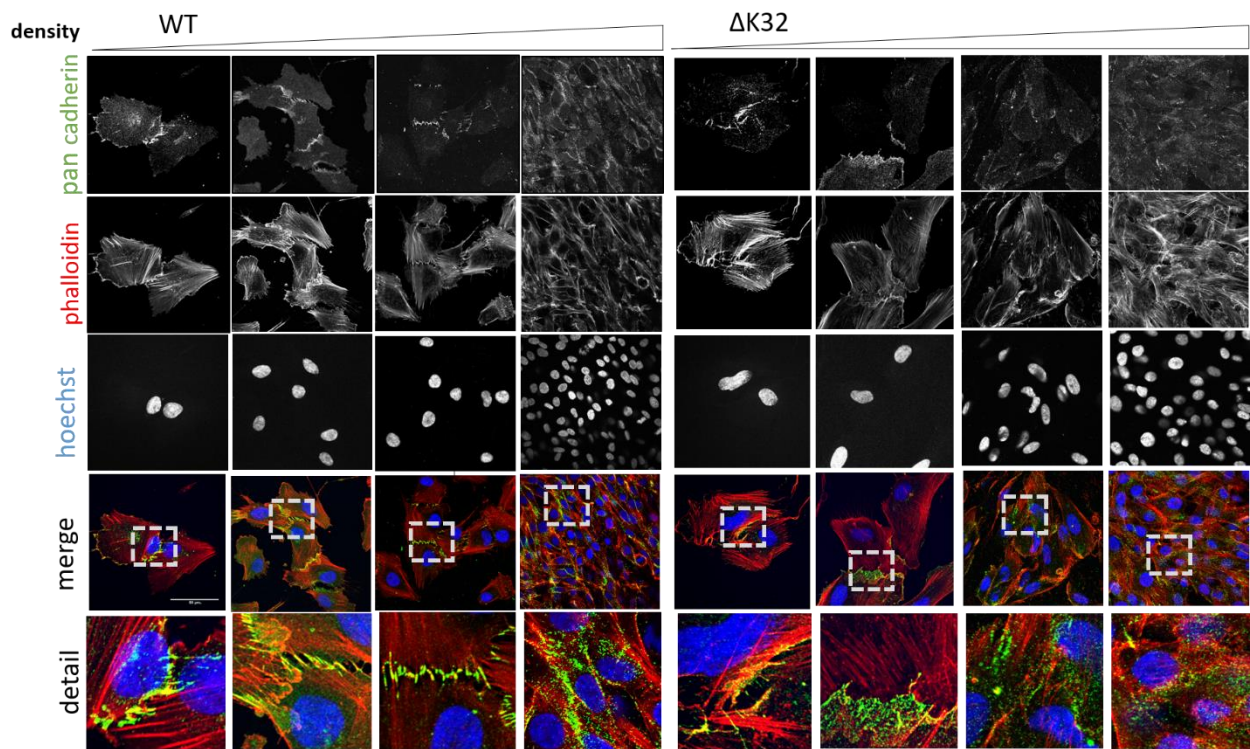


Figure 4-9: Defective recruitment of cadherins to cell-cell junctions in $\Delta K32$ myoblasts. WT and $\Delta K32$ mutant myoblasts were stained with an anti-pan-cadherin antibody (green) at different densities and counterstained with Phalloidin (red) and DAPI (blue)(A). WT myoblasts showed the typical zipper-like cadherin staining pattern, while $\Delta K32$ mutant myoblasts showed no or a diffuse cadherin staining pattern at cell-cell junctions. Scale bar = 50 μ m

DEFECTIVE FORMATION OF CELL-CELL CONTACT SITES

We hypothesized that the increased YAP activity affects the expression and localization of M- and N-cadherin, which are the predominantly expressed cadherins in myoblasts. In human myoblasts, we were unable to obtain a specific immunostaining of M-cadherin. Immunofluorescence labelling was obtained using a pan-cadherin antibody. Whereas WT myoblasts showed the characteristic zipper-like cadherin pattern at cell-cell junctions, $\Delta K32$ mutant myoblasts showed no or only a weak and diffuse staining (fig. 4-9).

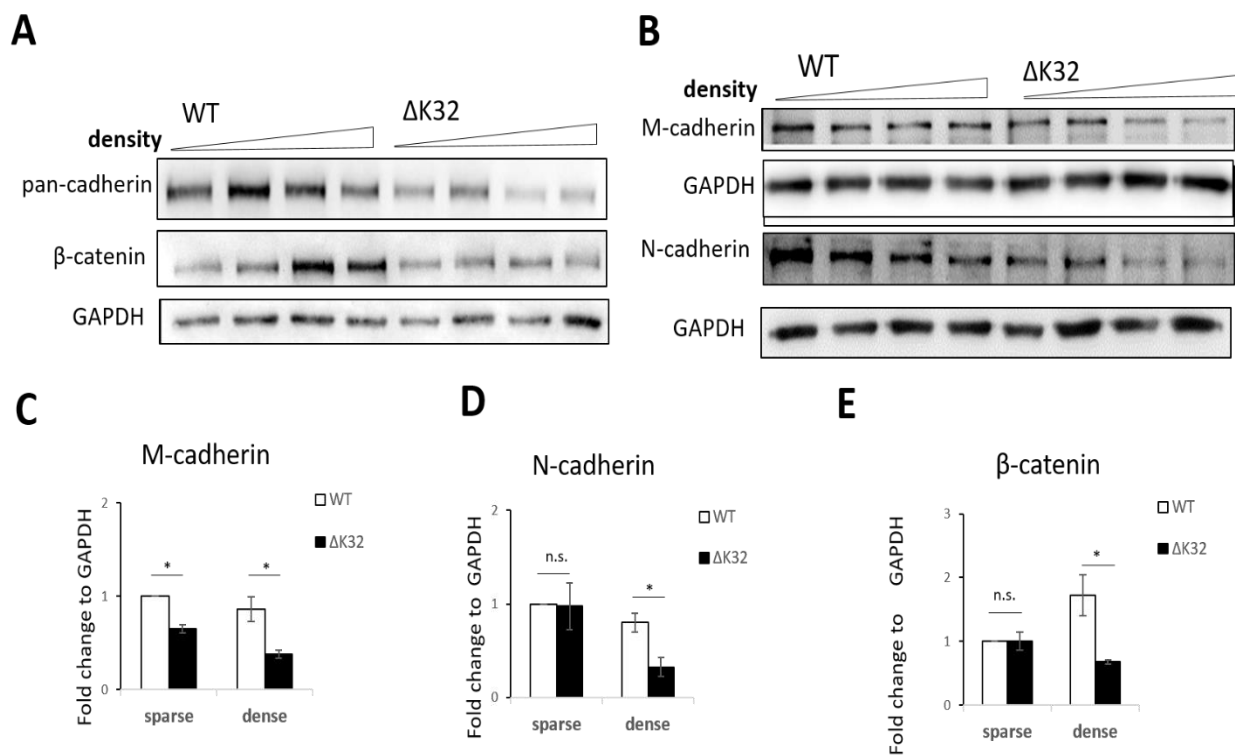


Figure 4-10: Decreased cadherin protein levels in $\Delta K32$ myoblasts. Protein levels of different members of the cell junction were analyzed at different cell densities (A,B). In sparse condition M-cadherin but, not N-cadherin protein levels were significantly lower in $\Delta K32$ mutant compared to WT myoblasts (C,D). $\Delta K32$ mutant myoblasts had significantly reduced M- and N-cadherin levels in dense condition (C,D). While β -catenin protein level increased in WT myoblasts with growing density, it decreased in $\Delta K32$ mutant myoblasts (E). Quantifications represent means of ≥ 3 independent experiments, \pm SEM, shown as fold changes, normalized to WT sparse. (*) p -value ≤ 0.05 ; () p -value ≤ 0.005 , (***) p -value ≤ 0.0005 ; (n.s) not significant.**

We then analyzed cadherin protein levels at various cell densities (fig. 4-10A,B). $\Delta K32$ myoblasts had significantly lower M-cadherin protein levels in sparse and dense conditions compared to WT myoblasts (fig. 4-10C). In addition, N-cadherin protein levels were significantly lower in $\Delta K32$ mutant compared to WT myoblasts in dense condition (fig. 4-10D).

The α - and β -catenin protein complexes regulate the connection between actin fibers and cadherins at cell-cell contact sides. In sparse condition, β -catenin protein levels did not differ in WT and Δ K32 myoblasts. With increasing cell density, β -catenin protein levels increased in WT myoblasts but did not change in Δ K32 myoblasts (fig. 4-10A). As a result, the protein level of β -catenin was significantly higher in WT compared to Δ K32 myoblasts in dense condition (fig. 4-10D). These results point to a reduced expression of cadherins in leading to a reduced recruitment of cadherins to form cell-cell contacts. Additional experiments are on-going to determine the role of YAP in cell-cell contact defects of Δ K32 myoblasts.

LOSS OF CELL-CELL CONTACT IN Δ K32 MUTANT MYOBLASTS MIGRATION

We next sought to determine whether the defective cell-cell contact formation of Δ K32 mutant myoblasts affected the migration pattern in Δ K32 mutant myoblasts. Migrating myoblasts were recorded by life-cell imaging in a wound healing assay and analyzed in regard to cell-cell interactions (fig. 4-11A). The histogram in figure 4-11B depicts the percentage of migrating cells without interaction partner as a function of time. Compared to WT, the number of Δ K32 mutant myoblasts which lost cell-cell contact and migrated without interaction partner was significantly increased (fig. 4-11C). After 12h, Δ K32 mutant myoblasts were spread throughout the whole migration area, whereas WT myoblasts remained in groups (fig. 4-11D). These results suggest that defects in cell-cell contact formation in Δ K32 mutant myoblasts modified the migration pattern from a sheet like to a single cell migration pattern.

Conflicting results regarding the migration speed of LMNA-deficient cells have been reported (Lee et al., 2007; Davidson et al., 2014). Here, migration speed was measured as the migrated distance per time for each tracked cell. Additionally, the number of neighbor cells was determined for each migrating cell at every timepoint. We found that the mean migration speed of WT and Δ K32 mutant myoblasts depended on the number of neighbors migrating together. In both, WT and Δ K32 mutant myoblasts, migration speed increased with an increasing number of neighbors. However, with the same number of neighbors, preliminary data suggest, that the mean migration speed of Δ K32 mutant myoblasts was reduced compared to WT myoblasts (fig. 4-11E).

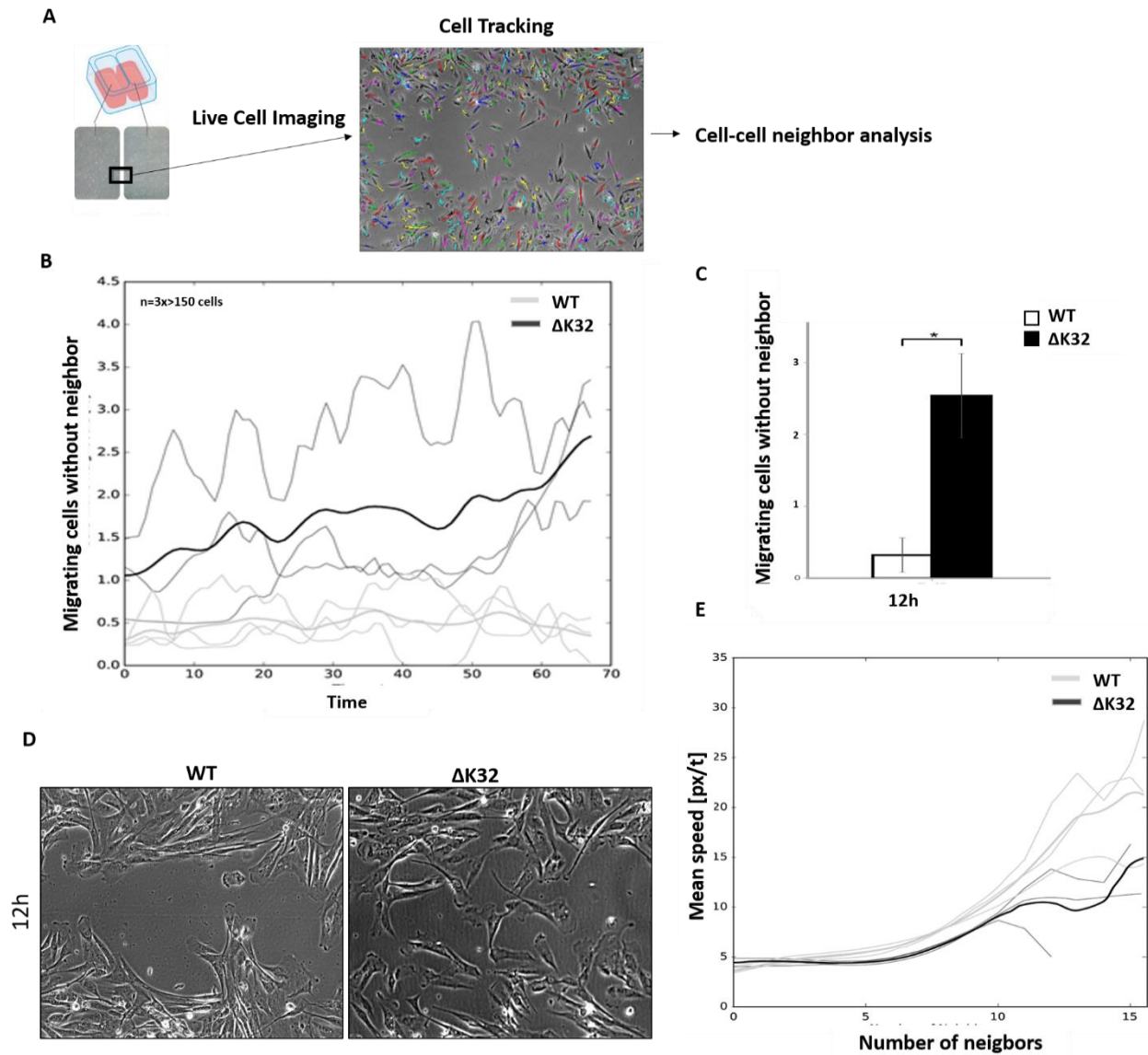


Figure 4-11: Loss of cell-cell contact during migration in $\Delta K32$ mutant myoblasts. Time-lapse videos of WT and $\Delta K32$ mutant myoblasts migrating in a wound healing assay were recorded for 12h. Videos were analyzed with a software written by Marc Osterland (A). Cell-cell interaction analysis revealed that a significant higher percentage of $\Delta K32$ mutant myoblasts lose cell-cell contact during migration and migrate as a single cell. In contrast, WT myoblasts migrated in groups of cells (B-D). (B) shows the percentage of each cell type, which migrate without interaction partner for every timepoint. After 12h the number of $\Delta K32$ mutant myoblasts migrating without interaction partner is significantly increased (C). In the endpoint image, after 12h migration, $\Delta K32$ mutant myoblasts are more spread in the original gap space than WT myoblasts (D). Migration speed was quantified as migrated distance per time for each tracked cell. The histogram shows the migration speed depending on the number of neighbors. With similar quantities of neighbors, WT myoblasts migrate faster than $\Delta K32$ mutant myoblasts. Quantifications represent means of ≥ 3 independent experiments, \pm SEM, shown as fold changes, normalized to WT sparse. (*) p -value ≤ 0.05 ; (**) p -value ≤ 0.005 , (***) p -value ≤ 0.0005 ; (n.s) not significant.

ΔK32 MUTANT MYOBLASTS FAILED TO SYNCHRONIZE THEIR ORIENTATION TO EACH OTHER

Previous studies report that the ability of lamin deficient cells to polarize at the wound edge is defective (Lee et al, 2007; Houben et al., 2009). I analyzed nuclear repositioning in migrating myoblasts but did not find significant defects in migrating ΔK32 myoblasts. To extend this analysis, the relative orientation of ΔK32 mutant myoblasts to each other during migration was determined. ΔK32 and WT myoblasts were stained with a trans-golgi marker (Syntaxin-6) following 12h migration in the wound healing assay. Cell-orientation vectors were generated starting at the nuclear center and ending at the trans-golgi (fig. 4-12A).

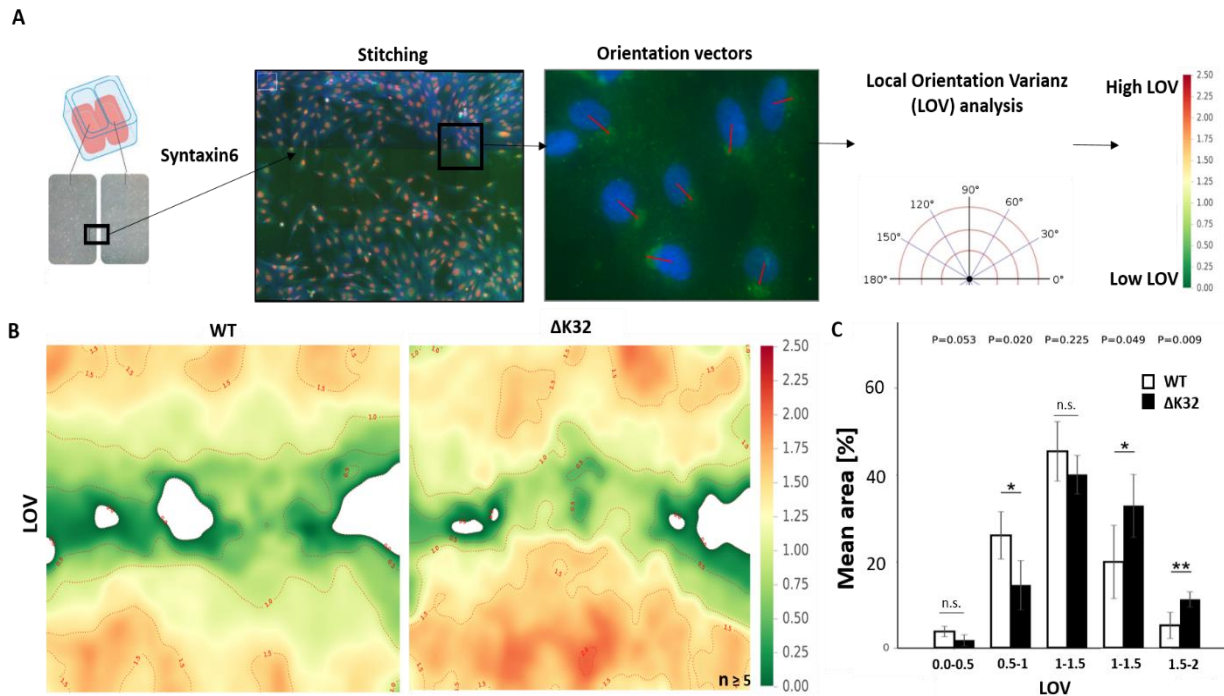


Figure 4-12: Defective synchronization of cell-orientation in ΔK32 mutant myoblasts. WT and ΔK32 mutant myoblasts were stained with syntaxin6 after migrating in a wound healing assay for 12h (E). Orientation vectors were generated and used to calculate the local orientation variance (LOV). F shows mean LOVs quantified from ≥ 5 independent experiments and color-coded as indicated. ΔK32 mutant myoblasts show another distribution of the LOV than WT myoblasts (F). LOVs were grouped in 0.,5 steps and the covered area for each LOV group was quantified for each cell type (G). In wound healing assays of ΔK32 mutant myoblasts larger areas have high LOVs (1 - 2,5). Quantification represent means of ≥ 5 independent experiments. (*) p-value ≤ 0.05; (**) p-value ≤ 0.005, (***) p-value ≤ 0.0005; (n.s) not significant.

The Local Orientation Variance (LOV) was then calculated, based on the orientation vectors of neighboring cells. The LOV index quantifies if cells in proximity to each other are orientated in a similar direction. Figure 10F depicts the mean LOVs (≥ 5 experiments) in WT and

Δ K32 mutant myoblasts. The LOV is coded as color gradient from green to red for low to high LOVs.

WT myoblasts showed a large area with a very low LOV (green) around the original scratch area. Further away from the original scratch area, the LOV increases into a light green and orange area, which code for intermediate LOVs. Only a small area, far from the original scratch area, showed a high LOV (red). As a consequence, WT myoblasts only had a high LOV in the middle of the cell-layer, where cells did not migrate yet. In areas where WT cells migrated, neighboring WT cells had a similar orientation. In contrast, Δ K32 mutant myoblasts showed an area of high LOV (red) close to the original scratch area. This showed, that neighboring, migrating Δ K32 mutant myoblasts did not have a similar orientation (fig. 4-12B).

Finally, the covered area for each LOV was quantified for WT and Δ K32 mutant myoblasts (fig. 4.12C). The mean area covered with low LOVs (LOV= 0 - 1,5) was increased in WT myoblasts, while mean areas of high LOVs (LOV = 1,5 - 2,5) were significantly increased in Δ K32 mutant myoblasts (fig. 4.12C). Altogether, these results suggest that neighboring Δ K32 mutant myoblasts fail to synchronize their orientation to each other during migration, which leads to a more single than sheet-like migration pattern.

5. DISCUSSION

This PhD project aims to analyze the role of YAP deregulation and mechanosensing defects in the pathophysiology of LMNA-related congenital muscular dystrophy. Using immortalized human myoblasts carrying the LMNA p.Lys32del (Δ K32) mutation, we showed, that defective inactivation of YAP in confluent K32 mutant myoblasts was associated with a defect in the maturation of cell-cell contacts and a defect in collective migration. Increased YAP activity in Δ K32 mutant myoblasts was not associated with impaired inactivation of YAP by canonical Hippo pathway signaling. Overall, the data strongly suggested that YAP deregulation in Δ K32 mutant myoblasts impairs mechanosensing at cell-cell junctions through a Hippo independent mechanisms and contributes to a defective migration pattern.

Mutations of the LMNA gene, which codes for A-type lamins, cause laminopathies, a highly heterogeneous group of disorders, including muscular dystrophies and cardiomyopathies (Worman and Bonne 2007; Bertrand et al. 2011). While the disease mechanisms underlying LMNA-related muscular dystrophy remains somewhat elusive, recent discoveries point to key interactions between A-type lamins and stress response pathways. There is growing evidence that the integrity of the nucleus and mechanotransduction signaling may be impaired in diseases caused by mutations in A-type lamins and lamin-associated proteins (Lammerding et al. 2004; Hale et al. 2008; Lammerding et al., 2005; Emerson et al. 2009). The mechanosensibility of myoblasts from L-CMD patients has recently been determined in 3D soft microenvironment as well as on 2D substrates of various stiffness (Bertrand et al, 2014; Schwartz et al., in revision). Severe defects in the capacity of lamin A/C mutated cells to sense their environment stiffness and to respond to mechanical stress have been reported and related to a deregulation of YAP (Bertrand et al 2014). However, the molecular mechanisms responsible for the increased YAP activity remains unknown.

INCREASED YAP ACTIVITY IN Δ K32 MUTANT MYOBLASTS: ROLE OF THE HIPPO PATHWAY

We found that the transcriptional activity of YAP was significantly increased in Δ K32 mutant compared to WT myoblasts plated on conventional hard surface. Therefore, YAP overactivity in lamin A/C mutated cells was not restricted to cultivation in a soft environment as previously

reported (Bertrand et al, 2014), but rather appeared as a constitutive abnormality of myoblasts with a L-CMD causing mutation.

Because YAP is canonically regulated by the Hippo pathway with its core kinase LATS, my 1st aim was to determine whether impaired Hippo pathway activity caused the increased YAP activity. With an active Hippo pathway, activated MST activates LATS, which in turn phosphorylates YAP. Phosphorylated YAP is sequestered in the cytoplasm and degraded (Zhao et al., 2007; Zhao et al., 2010). Therefore, activation of Hippo signaling prevents YAP transcriptional activity.

In standard human myoblast medium, which contains 20% of fetal calf serum, total and active LATS (phospho(thr1079)LATS) as well as phosphorylated YAP(S127) protein levels were significantly increased in Δ K32 compared to WT myoblasts. This indicates that the Hippo pathway is active in Δ K32 mutant myoblasts. We concluded that the overactivation of YAP in Δ K32 mutant myoblasts was not due to a decreased Hippo pathway activity.

A recent report shows that YAP transcriptional activity induces the expression of LATS which, in turn, phosphorylates YAP (Moroishi et al., 2015). This intrinsic negative feedback mechanism may contribute to explain the increased levels of phosphorylated YAP in Δ K32 myoblasts.

YAP can be inactivated by growth factor starvation, through a LATS-mediated phosphorylation of YAP at serine 127 (Yu et al., 2012). Our results showed that growth factor starvation increased the activity of LATS, the phosphorylation of YAP (S127) and consequently decreased the transcriptional activity of YAP in both Δ K32 mutant and WT myoblasts. We concluded, that the inactivation of YAP through growth factor mediated HIPPO activation was not impaired in Δ K32 mutant myoblasts.

Taken together, we concluded that the overactivation of YAP in Δ K32 mutant myoblasts was not due to impaired Hippo signaling pathway but, that the increased activity of YAP in Δ K32 mutant myoblasts occurred through Hippo-independent regulation of YAP. Consistently, the regulation of YAP by the Hippo pathway in the context of mechanotransduction has been questioned (Aragona et al., 2013). Analyzing YAP phosphorylation at Serine127 is widely used as an indicator for Hippo pathway activity. However, it has been shown that LATS can be activated

through non canonical Hippo pathway signaling (fig. 1.7). Therefore, it is possible that YAP phosphorylation at Ser127 occurs through non canonical Hippo pathway signaling.

INCREASED YAP ACTIVITY IN Δ K32 MUTANT MYOBLASTS: ROLE OF CELL SPREADING AREA

The cell spreading area and cell shape regulate YAP activity (Wada et al., 2011). Δ K32 mutant myoblasts have increased total YAP protein levels as well as an increased spreading area compared to WT myoblasts. Total YAP levels decreased together with the spreading area from sparse to dense conditions in both cell lines. Interestingly, protein levels of phosphorylated YAP increased by growth factor mediated YAP inactivation, whereas they decreased through density mediated inactivation of YAP. However, in dense culture conditions, the spreading area and YAP transcriptional activity remained higher in Δ K32 mutant compared to WT myoblasts. These results suggest that total YAP levels may depend on the cell spreading area and therefore, may tune the sensitivity to YAP activation. To validate this hypothesis, we propose to analyze YAP protein levels in cells plated in restricted areas, using micropatterning techniques.

REGULATION OF YAP BY CELL CONTACT INHIBITION IS DEFECTIVE IN Δ K32

In dense culture conditions, YAP was excluded from the nucleus in WT but not Δ K32 mutant myoblasts. This in turn may contribute to the increased transcriptional activity of YAP in Δ K32 myoblasts at high density. In non-cancer cells, cell-cell contact and high cell density activate the Hippo pathway to inhibit YAP activity (Zaoh et al., 2007). Further studies revealed that the formation of cadherin/catenin complexes at cell-cell junctions modulate YAP inhibition in high cell density (Zaoh et al., 2007; Kim et al., 2011; Schlegelmilch et al., 2011, Zaoh et al., 2012).

Expression of E-cadherins, as well as their association with α - and β -catenin, are required for density dependent nuclear exclusion of YAP (Kim et al., 2009). Furthermore, YAP relocates to the nucleus in confluent monolayers when cadherin dependent cell-cell connections are disrupted (Schlegelmilch et al., 2011). It has been demonstrated that protein levels of E-cadherin can even tune the efficacy of contact mediated inhibition of proliferation (Kim, Kushiro et al. 2009). Furthermore, knockdown of β -catenin prevents YAP nuclear exclusion (Kim, Koh et al. 2011).

Δ K32 mutant myoblasts showed a defective formation of cell-cell contacts in dense conditions. M-, N-cadherin and β -catenin protein levels were significantly reduced in confluent Δ K32 mutant compared to WT myoblasts. Also, the characteristic zipper-like staining pattern of cell-cell junctions was only found in WT myoblasts. Taken as a whole, our data strongly suggested a link between reduced M-cadherin, N-cadherin and β -catenin protein levels and the increased YAP nuclear localization and YAP activity in Δ K32 mutant myoblasts at high cell density. To unveil the link between YAP over activity and the reduced cadherin/catenin protein levels in Δ K32 mutant myoblasts, cadherin/catenin levels after YAP overexpression and siRNA mediated YAP silencing should be investigated. Additional experiments are on-going to dissect potential mechanisms.

IMPAIRED INTEGRITY OF THE ACTIN CYTOSKELETON IN Δ K32 MUTANT MYOBLASTS

The actin cytoskeleton is coupled to A-type lamins of the nucleoskeleton via the LINC-complex (Salpingidou. et al., 2007). To date, all LMNA mutations that cause striated muscle disease compromise the Nesprin/Sun/lamin interactions, resulting in dysfunctional nucleo-cytoskeletal linkages (Haque et al. 2010; Folker et al., 2010, Chang et al., 2013, Chang et al., 2015). Accordingly, the Δ K32 lamin mutation most likely impairs the integrity of the nucleo-cytoskeletal linkages. A Co-Immunoprecipitation with the Sun proteins of the LINC-complex and the Δ K32 mutant A-type Lamins remain to be performed in order to support this hypothesis.

Although the detailed mechanism remains to be determined, there is growing evidence that a dysfunctional LINC complex may impair the dynamics and organization of the actin cytoskeleton (Lammerding et al., 2004; Hale et al., 2008; Khatau et al. 2009; Luxton et al., 2010). Functional loss of A-type lamins alters actin structures around the nucleus in cells cultured on rigid substrates (Khatau et al, 2009; Chambliss et al 2013; Kim et al 2012), In addition, cells from LMNA^{-/-} mice exhibit abnormal actin fiber localization and polymerization (Broers at al., 2005; Lee at al., 2007; Khatau et al.,2009; Lammerding et al., 2004). The cytoplasm of LMNA deficient MEFs is softer, less elastic, and more compliant than the cytoplasm of WT cells (Lee et al., 2006).

Consistently, we reported alteration in the orientation of perinuclear actin fibers in Δ K32 mutant myoblasts. Furthermore, only WT myoblasts reorganized their actin fibers into parallel aligned fibers in dense culture conditions, while the orientation of actin fibers of Δ K32 mutant myoblasts was less parallel. Δ K32 mutant myoblasts have already been reported to fail to adapt

their cytoskeletal organization to a mechanical challenge (Betrandt et al., 2014). Here, we can extend this observation and report that $\Delta K32$ mutant myoblasts fail to adapt their actin cytoskeleton to high cell-cell contact condition.

Mechanotransduction depends on actin dynamics (Dupont et al., 2011). We found an increased variation of the orientation of actin fibers in the perinuclear region and in basal actin fibers of $\Delta K32$ mutant myoblasts. In addition, the expression of a myosin light chain protein (myl9), which regulates the formation of actin stress fibers, was increased in $\Delta K32$ mutant myoblasts. Furthermore, force transmission between the nucleus and the cytoskeleton is impaired in several myopathic lamin mutations (Zwerger et al., 2013; Bertrand et al.; 2014). Therefore, the defective orientation of actin fibers in $\Delta K32$ mutant myoblasts may impair the transmission of forces from the cell periphery. This, in turn, may lead to the aberrant mechanosensitive signaling activity. Additional studies are required to precise the molecular mechanisms which regulates the interplay between YAP activity and actin-mediated intercellular stress in $\Delta K32$ myoblasts given that a reduced actin contractility was expected to reduce YAP activity. Furthermore, fluorescence microscopy can not provide information about the mechanical forces which are generated by actin fibers. To study mechanical forces generated by $\Delta K32$ mutant myoblasts another method like traction force microscopy need to be performend.

DEFECTIVE FORMATION OF CELL-CELL CONTACTS

YAP overexpression was recently found to antagonize E-cadherin junction assembly by regulating actin cytoskeleton architecture through increased expression of myosin light chain 9 (myl) (Bai et al., 2016). Consistently, $\Delta K32$ mutant myoblasts had an increased expression of YAP and myl9 in dense condition, which may cause the defective formation of cell-cell junctions.

Alternatively, actin disorganization may directly affect the formation of cell-cell contacts in $\Delta K32$ mutant myoblasts. The characteristic zipper-like staining pattern of cell-cell junctions was only found in WT myoblasts. Mature cell-cell junctions are formed by cadherin/catenin complexes at the tips of actin fibers, to which they connect via α -catenin mediated binding (Causeret et al. 2005). Cadherin clusters have been shown to be stabilized at cell-cell junctions by binding to actin fibers (Truong et al., 2013). Therefore, the defective formation of cell-cell junctions in $\Delta K32$ mutant myoblasts may be caused by the impaired orientation of actin fibers in $\Delta K32$ mutant myoblasts.

To further investigate if the decreased formation of cell-cell contacts in $\Delta K32$ mutant myoblasts is caused by the impaired actin cytoskeleton or by the increased YAP activity, cell-cell contact formation in $\Delta K32$ mutant myoblasts after knockdown and overexpression of YAP needs to be analyzed. Alternatively, the formation of cell-cell contacts after actin destabilization in WT myoblasts can be analyzed.

ABERRANT MIGRATION BEHAVIOUR OF $\Delta K32$ MUTANT MYOBLASTS

Our data showed an increased loss of cell-cell contacts during migration of $\Delta K32$ mutant myoblasts compared to WT myoblasts. As a result, an increased number of $\Delta K32$ mutant myoblasts migrated alone whereas a sheet like migration was observed in WT myoblasts. Further we reported an increased variance in the polarization between neighboring $\Delta K32$ mutant myoblasts compared to WT myoblasts.

Cell-cell contacts are critical for the coordination of cell movements during collective migration (Arboleda-Estudillo et al., 2010; Murrell et al., 2011; Tambe et al., 2011). Cadherin-dependent adhesion contributes to the regulation of cell polarization and directionality during collective cell migration (Cai et al., 2014). Moreover, cadherin-dependent propagation of mechanical stresses at cell-cell junctions orchestrates collective cell migration. Thereby, neighbouring cells join their forces together to then migrate along a minimum of intercellular shear stress. Hence, collective migration is guided by mechanical stress (Tambe et al. 2011; Trepap et al., 2011).

Knockdown of P-cadherin or overexpression of dominant negative E-cadherin reduces the coordination of cells orientation (Ng et al., 2012). Recent data indicate that formation of cadherin rich protrusions (cadherin fingers) guides cells during collective cell migration (Hayer et al., 2016). Therefore, the reduced collective migration pattern of $\Delta K32$ mutant myoblasts is most likely caused by a defective cadherin-dependent transmission of forces between cells. Therefore, we provided, herein, the first evidence that a LMNA mutation causes a defective mechanotransduction at cell-cell contact sides, which, causes a defect in the coordination of collective cell migration.

Further data are needed to confirm this hypothesis. For instance, expression of M-cadherin with a tension sensor module could be used to determine intercellular force transmission, as already developed for VE-cadherin (Conway et al., 2013). Alternatively, intercellular stress maps of

migrating myoblasts could be used to assess a disturbed transmission of forces between migrating $\Delta K32$ mutant myoblasts (Tambe et al., 2011).

Notably, defects in the polarization of LMNA deficient cells have already been reported at early time points after initiation of migration; i.e., 30min, 1h and 3h after the onset of migration. (Lee et al., 2007; Houben et al., 2009; Chang et al., 2015; Folker et al., 2010). Polarization defects have been attributed to a defect of nuclear repositioning in LMNA deficient cells. Nuclear repositioning is achieved by retrograde flow of 'transmembrane actin associated nuclear (TAN) lines, which are defective in lamin A/C deficient cells (Folker et al., 2010).

Interestingly, at later time points, the orientation of LMNA mutant cells towards the wound edge is nearly similar to WT cells, (Houben et al., 2009). We analyzed nuclear repositioning in $\Delta K32$ mutant myoblasts during random cell migration. No significant difference in nuclear repositioning was observed between $\Delta K32$ and WT myoblasts. However, to finally exclude a defect in nuclear repositioning in $\Delta K32$ mutant myoblasts, a computer based time-lapse video analysis needs to be performed.

In L-CMD patients, a strong variation of muscle fiber size has been reported (Quijano-Roy et al., 2008). Myoblast migration is a critical step in myogenesis and skeletal muscle regeneration. Sub-optimal migration can reduce the number of myoblasts which enter fusion or reduce myoblast alignment and consequently impair adaptation or repair of skeletal muscle tissue. Thus, the reported collective cell polarization and migration defects may contribute to the pathophysiology of L-CMD. Further experiments need to be performed to understand the consequences of migration defects in the pathophysiology of L-CMD. Although the collective character of migrating myoblasts *in vivo* has not been shown so far, cell density is known to be a critical factor of myoblast fusion *in vitro*. In the classical fusion assay myoblasts need to be cultivated in dense condition. The presented results provide some evidence, that $\Delta K32$ mutant myoblasts may fail to achieve high cell confluence *in vivo*, as they increasingly lose cell-cell contact during migration. To test if the migration defect of $\Delta K32$ mutant myoblasts affects myoblast fusion, an alternative fusion assay, which includes myoblast migration, would need to be developed.

ΔK32 MUTANT MYOBLASTS PROLIFERATION

YAP is a positive regulator of the cell cycle (Dong et al. 2007; Zhao et al., 2007). Surprisingly, ΔK32 mutant myoblasts did not have an increased proliferation capacity, although, YAP transcriptional activity was increased in sparse and dense conditions. On the contrary, ΔK32 mutant myoblasts proliferation was slightly but significantly reduced compared to WT, at all tested densities. This apparent contradiction may be due to the fact that A-type lamins play important role in cell proliferation. Therefore, the ΔK32 LMNA mutation may cause a disturbance during mitosis which overrules the YAP-mediated cell-cycle regulation.

INCREASED TRANSCRIPTIONAL SMAD ACTIVITY IN ΔK32 MUTANT MYOBLASTS

Lastly, our results pointed to potential defects in BMP signaling. Here, we reported a strong increase in the transcriptional activity of Smads in ΔK32 mutant compared to WT myoblasts in starved condition as well as after stimulation with BMP2. Consistently, BMP stimulation has been shown to act synergistically with mechanical signals on Smad activity (Kopf et al., 2012). However, we only found a slight increase in the phosphorylation of Smad1/5 in ΔK32 mutant compared to WT myoblasts in starved condition. Moreover, after stimulation with BMP2 there was no difference in the level of phosphorylation of Smads between ΔK32 mutant and WT myoblasts. If the. These results point to an enhanced transcriptional activity of Smads which, may be independent of Smad phosphorylation.

Nuclear YAP can bind and stabilize the Smad complex, leading to an increased transcriptional activity (Alarcón et al., 2009). Therefore, the increased transcriptional activity of Smads, in ΔK32 mutant myoblasts, may be caused by the increased pool of nuclear YAP. Hence, YAP has been proposed as a mechanically activated transcriptional co-regulation which, may integrate mechanical stimulations into BMP signaling (Kopf et al., 2014). Further investigations are needed to determine whether the increased Smad transcriptional activity of Smads is caused by mechanosensing defects of ΔK32 mutant myoblasts and if these mechanosensing defects are integrated in the BMP pathway by YAP. For example, an increased activation of the BMP pathway by increased expression of BMPs by ΔK32 mutant myoblasts needs to be excluded. Furthermore, Smad transcriptional activity after knockdown of YAP in ΔK32 mutant myoblasts should be investigated. More direct evidence could be achieved through a quantitative co-

immunoprecipitation of YAP and Smad or a FRET based visualization of the YAP/Smad interaction.

In addition, further studies are needed to determine the role of YAP and BMP signaling defects in lamin mutant myoblasts. BMP signaling has been shown to affect planar cell polarity and cortical actin organization during the migration of mesenchymal progenitor cells (Hiepen et al., 2014). Furthermore, BMP signaling was recently shown to regulate the presentation of cadherins on the cell surface (Benn et al., 2016). Additionally, also YAP has been implicated in the regulation of cell migration (Haskins et al., 2014; Schutte et al. 2014; Sorrentino et al. 2014; Moroishi et al. 2015). Moreover, Merlin, an upstream regulator of the Hippo pathway, is critical for cortical actin dynamics, which have been shown to contribute to the orchestration of collective migration (Zhou and Hanemann 2012; Cooper and Giancotti 2014; Das et al., 2015). To further investigate the role of YAP and Smad over-activity in the defective coordination of migration in $\Delta K32$ mutant myoblasts, cell-cell interaction and cell orientation analysis during migration of $\Delta K32$ mutant myoblasts should be analyzed after inhibition of YAP and Smad activity via siRNA or small molecule inhibitors.

CONCLUSION

In conclusion, this PhD thesis shows that YAP deregulation impairs mechanosensing at cell-cell junctions and contributes to a defective migration pattern in $\Delta K32$ mutant myoblasts through a Hippo independent mechanisms. Although additional experiments are needed, we propose the following mechanisms to explain the pathogenic feature in $\Delta K32$ mutant myoblasts.

LMNA mutation causes a defective anchorage of actin fibers to the nucleus which in turn impairs the integrity of the actin cytoskeleton and alters the force transmission of mechanical cues from the cell periphery, including cell-cell contacts.

Mechanosensing defects of $\Delta K32$ mutant myoblasts increased the activity of mechanosensitive YAP and Smad signaling. In dense culture conditions, $\Delta K32$ mutant myoblasts failed to inactivate YAP. Interestingly, the growth factor mediated inactivation of YAP through phosphorylation by LATS was not impaired in $\Delta K32$ mutant myoblasts. Thus, the translation of cell-cell contacts into YAP regulation but, not the translation of growth factor stimulation into YAP regulation is severely impaired in $\Delta K32$ mutant myoblasts. Furthermore, we provided some

evidence that the regulation of YAP by mechanical cues includes a regulation of total YAP protein levels, which, may tune the sensitivity to YAP activation.

Impaired force transmission by the actin cytoskeleton and decreased formation of stable, actin-associated cell-cell contacts impacted on migration, from a sheet like to a single cell like migration pattern. $\Delta K32$ mutant myoblasts lost cell-cell contact during migration and showed a reduced synchronization of their polarization. Because myoblast migration is a critical step in myogenesis and skeletal muscle regeneration, these defects may contribute to the pathophysiology of L-CMD.

6. ABSTRACTS

ENGLISH

Mechanotransduction is critical for tissue development, homeostasis and diseases. YAP (Yes-Associated Protein) signaling has emerged as a particularly important regulator of the mechano-response. A defective mechanosensing response, including aberrant YAP signaling, has been recently reported in human myoblasts from patients suffering from LMNA related congenital dystrophy (L-CMD) (Bertrand et al., 2014). L-CMD is a severe early-onset form of muscular dystrophies caused by mutations in A-type lamins. My PhD project aims to further dissect mechanosensing defects of immortalized muscle precursor cells which carry the L-CMD causing $\Delta K32$ mutation.

My results showed that $\Delta K32$ mutant myoblasts had a defective translation of mechanical forces at cell-cell contact sides. $\Delta K32$ mutant myoblasts failed to inactivate YAP in high cell-cell contact conditions, as attested by an increased transcriptional activity of YAP and a persistent nuclear localization. YAP overactivity in $\Delta K32$ mutant myoblasts was not related to an impaired activation of the Hippo signaling pathway. Defective YAP signaling was associated with a disorganization of different subsets of the actin cytoskeleton, including the supranuclear actin, the basal actin and the actin fibers at cell-cell junction. The formation of mature cell-cell contacts in $\Delta K32$ myoblasts was defective, and the protein expressions of both M- and N-cadherins were significantly reduced in high cell-cell contact conditions. Moreover, $\Delta K32$ mutant myoblasts showed an increased loss of cell-cell contact during migration, which caused a shift from a sheet-like to a single cell migration pattern. Finally, we reported an increased transcriptional activity of mechanosensitive Smad 1/5/8 signaling in $\Delta K32$ mutant myoblasts. Taken together, these results suggest that mechanosensing defects in $\Delta K32$ mutant myoblasts affect the ability of myoblast to form cell-cell contacts and to migrate collectively. These mechanosensing defects may contribute to the pathophysiology of L-CMD.

DEUTSCH

Mechanotransduktion ist kritisch für die Entwicklung von Geweben, Homöostase und in der Entstehung von Krankheiten. YAP (Yes-Associated Protein) hat sich als besonders wichtiger Regulator der Mechanotransduktion herausgestellt. Eine fehlerhafte Mechanotransduktion, einschließlich abweichender YAP-Signaltransduktion, wurde kürzlich in menschlichen Myoblasten von Patienten mit Kongenitaler Muskeldystrophie mit LMNA-Mutation (L-CMD) (Bertrand et al., 2014) beschrieben. L-CMD ist eine schwere, früh einsetzende Form der Kongenitalen Muskeldystrophien, die durch Mutationen in A-Typ-Laminen verursacht wird. Mein PhD-Projekt zielt darauf ab, Mechanotransduktionsdefekte in immortalisierten Muskelvorläuferzellen, die die L-CMD verursachende $\Delta K32$ Mutation tragen, weiter zu analysieren.

Meine Ergebnisse zeigten, dass $\Delta K32$ mutierte Myoblasten eine defekte Übertragung von mechanischen Kräften an Zell-Zell-Kontakten aufwiesen. In $\Delta K32$ mutierten Myoblasten konnte YAP unter hohen Zell-Zell-Kontaktbedingungen nicht inaktiviert werden. Dies wurde durch eine nukleare Lokalisation und eine erhöhte transkriptionelle Aktivität von YAP gezeigt. Die erhöhte Aktivität von YAP in $\Delta K32$ mutierten Myoblasten war nicht mit einer beeinträchtigten Aktivierung des Hippo-Signalwegs verbunden. Die aberrante YAP-Signaltransduktion war hingegen mit einer veränderten Organisation von verschiedenen Teilen des Aktin-Zytoskeletts, einschließlich des supranuklearen Aktins, des basalen Aktins und der Aktinfasern am Zell-Zell-Übergang, verbunden. Die Ausbildung von reifen Zell-Zell-Kontakten in $\Delta K32$ -Myoblasten war gestört und die Proteinlevel von M- und N-Cadherin waren signifikant reduziert in hoher Zell-Zell-Kontaktbedingung. Darüber hinaus zeigten $\Delta K32$ mutierte Myoblasten einen verstärkten Verlust von Zell-Zell-Kontakten während der Migration, was eine Verschiebung von einem „sheet-like“ zu einem „single-like“ Zellmigrationsmuster verursachte. Abschließend zeigten wir eine erhöhte transkriptionelle Aktivität der mechano-sensitiven Smad1/5/8 in $\Delta K32$ mutierten Myoblasten. Zusammengefasst deuten diese Ergebnisse darauf hin, dass Defekte in der Mechanotransduktion in $\Delta K32$ mutierten Myoblasten die Fähigkeit dieser Zellen beeinträchtigt Zell-Zell-Kontakte auszubilden und kollektiv zu migrieren. Diese Defekte in der Mechanotransduktion können zur Pathophysiologie von L-CMD beitragen.

FRANÇAIS

La mécanotransduction est une propriété essentielle au développement des tissus, leur homéostasie et leur physiopathologie. La voie de signalisation YAP (Yes-Associated Protein) est apparue comme un régulateur particulièrement important de la mécano-réponse. Un défaut de mécanosensibilité défectueuse, associant une signalisation aberrante de la voie YAP, a récemment été rapportée dans des myoblastes humains de patients souffrant de dystrophie musculaire congénitale liée à des mutations du gène de la lamine (L-CMD) (Bertrand et al., 2014). La L-CMD est une forme grave de dystrophie musculaire à début précoce. Mon projet de doctorat visait à disséquer les défauts de la mécanosensibilité de cellules précurseurs du muscle présentant la mutation $\Delta K32$.

Mes résultats ont montré que les myoblastes mutants $\Delta K32$ présentaient des un défaut de contact cellule-cellule, attestant d'anomalies de transmission des forces mécaniques entre cellules. Contrairement à ce que l'on observe dans les cellules contrôles à confluence, la voie YAP reste activée dans les myoblastes mutants $\Delta K32$. Cela s'est traduit par une activité transcriptionnelle accrue de YAP et une localisation nucléaire persistante de YAP dans les myoblastes $\Delta K32$. La suractivité de YAP dans les myoblastes mutants $\Delta K32$ n'était pas liée à une altération de la voie Hippo, voie de signalisation canonique qui régule YAP. La signalisation YAP défectueuse a été associée à une désorganisation de différents sous-ensembles du cytosquelette d'actine, incluant l'actine supranucléaire, l'actine basale et les fibres d'actine de la jonction cellule-cellule. La formation et la maturation de jonctions cellule-cellule était défectueuse dans les myoblastes $\Delta K32$, et les expressions protéiques des deux principales cadhérines, M et N-cadhérins, étaient significativement réduites à confluence. De plus, les myoblastes mutants $\Delta K32$ présentaient une perte accrue de contact cellule-cellule pendant la migration, responsable d'une perte de la migration collective dans les cellules mutantes. Enfin, nous avons rapporté une augmentation de l'activité transcriptionnelle de la signalisation Smad 1/5/8 dans les myoblastes mutants $\Delta K32$. En conclusion, ces résultats de thèse suggèrent que les défauts de mécanosensibilité dans les myoblastes mutants $\Delta K32$ affectent la capacité des myoblastes à former des contacts cellule-cellule et à migrer collectivement. Ces défauts de mécanosensibilité peuvent contribuer à la physiopathologie de la L-CMD.

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8. PUBLICATIONS

Technau C and Fischer M, Mamchaoui K, Bigot A, Lok T, Verdier C, Duperray A, Michel R, Holt I, Voit T, Quijano-Roy S, Bonne G, Coirault C (in press). Nuclear-cytoskeletal linkages mediate inside-out mechanical coupling in muscle cell precursors through FHOD1. Scientific Reports.

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