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Role of ICAP-1 in integrins' dynamic regulation, mechanosensing and contractility of osteoblast cells

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THESIS

To obtain the degree of

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Speciality: Cell biology

Ministerial order: 25 may 2016

Defended by

Alexander KYUMURKOV

The PhD thesis is supervised by **Dr. Corinne ALBIGES-RIZO, CNRS** and

co-supervised by **Dr. Emmanuelle PLANUS, UGA,**

Prepared in **Institute for Advanced Biosciences,**

in **École Doctorale Chimie et Sciences du Vivant**

Role of ICAP-1 in integrins' dynamic regulation, mechanosensing and contractility of osteoblast cells.

Public PhD defense: **24 November 2017,**
in front of jury, composed of:

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THÈSE

Pour obtenir le grade de

DOCTEUR DE L'UNIVERSITÉ GRENOBLE ALPES

Spécialité : Biologie cellulaire

Arrêté ministériel : 25 mai 2016

Présentée par

Alexander KYUMURKOV

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codirigée par **Dr. Emmanuelle PLANUS**, UGA

préparée au sein du **Laboratoire CRI IAB - Centre de
Recherche Oncologie/Développement - Institutse for
Advanced Biosciences**
dans l'**École Doctorale Chimie et Sciences du Vivant**

Rôle d'ICAP-1 dans la régulation de la mécanosensibilité et de la contractilité des cellules ostéoblastiques via la dynamique des intégrins

Thèse soutenue publiquement le **24 novembre 2017**,
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'Brave are they who know everything
yet fear nothing!'

'Knowledge is power. Guard it well!'

'Heresy grows from idleness!'

-Imperial proverbs-





To my mother
À ma mère
На майка ми



= iv =



Acknowledgements

As all paths come to an end my last adventure – my PhD has reached its inevitable end. Considerable amount of people have been by my side – some during the whole endeavor and some for a transient amount of time. I developed a particular relationship with all the people I have worked with in IAB (Institute for Advanced Bioscience), LIPhy (Laboratoire Interdisciplinaire de Physique) in Grenoble and the Institute for Interdisciplinary Neuroscience (IINS) in Bordeaux.

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Thank you for agreeing to revise my work and come to Grenoble to hear my talk. I am sure that your scientific input will enrich my work and my culture. I hope you had good time reading and grading my work as I had good time working on it and writing it. I hope I can indulge you during the question time!

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Special thanks I owe to **Dr. Myriam Régent**, whom I have never met, but whose work I continued and build upon.

I cannot withhold my farewells to the two postdocs staying after me - **Dr. Sanela Vellino** and **Dr. Laure Forel**. Sanela, keep your energy high and your plans for the future even wilder. I know you will make it! Laure, keep being wild and never settle for mediocracy. You have the power in you!

Vacating my desk and my bench, I was feeling confident that I leave the lab to some dynamic and promising PhD students – the ambitious and spirited (!) **Adèle Kerjouan**, bright and lively **Mathilde Proponnet**, the strong and shy **Daphné Vannier** and always smiley and positive **Amaris Guevara**. I will miss you all.

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Abstract

Signal transduction from extracellular matrix originates at the membrane, where the clustering of adhesive receptors is a key step in adapting cellular force and transmitting a message. Both integrin classes $\beta 1$ and $\beta 3$ serve as a scaffold for numerous intracellular proteins and signaling pathway at the focal adhesions on fibronectin environment. In this molecular environment ICAP-1 has been identified as a specific partner of $\beta 1$ integrin. First, I contributed to reveal how the monoubiquitylated form of ICAP-1 was involved in an elaborate signaling network responsible for maintaining cell tensional homeostasis, going from the dynamics of cell adhesion to the adaptation of contractile actomyosin machinery. We have then proposed that ICAP-1 monoubiquitylation by Smurf1 is a key event leading to a switch from ROCK2-mediated to MRCKa-mediated cell contractility. Moreover, ICAP-1 may function in $\beta 1$ integrin dependent and -independent pathways to orchestrate both the chemo and mechanical regulation of cell migration on fibronectin environment. Therefore, we speculated on a more general role of ICAP-1 in cell adhesion and focal adhesion dynamics and the specific objectives of my thesis was to investigate whether ICAP-1 can influence the behavior of integrins and consequently may affect cell function through regulation of cell contractility and force generation. For this purpose, I have worked with cellular environment where $\beta 1$ integrin and/or ICAP-1 were absent by using four cell lines: WT osteoblast cells, $\beta 1$ integrin KO osteoblast cells, ICAP-1 KO osteoblast cells and double KO $\beta 1$ integrin/ICAP-1 osteoblast cells in order to monitor $\beta 3$ integrin behavior. As expected, depletion of $\beta 1$ integrin was associated with the loss of cell spreading and force generation according to traction force microscopy measurements. Surprisingly, the supplementary deletion of ICAP-1 leads to restoration of cell spreading and force generation which were dependent on enlarged $\beta 3$ integrin FAs. $\beta 3$ integrin-mediated forces were correlated with slow diffusion of $\beta 3$ integrin within adhesion sites and slow turnover of $\beta 3$ integrin containing focal adhesion. I addressed the question whether ICAP-1 might regulate $\beta 3$ integrin endocytosis since ICAP-1 interacts with Nm23-H2, a nucleoside diphosphate kinase involved in dynamin-mediated endocytosis. I show that the deletion of either Nm23 or dynamin or clathrin in cells depleted in $\beta 1$ integrin was able to mimic the combined loss of $\beta 1$ integrin and ICAP-1 by restoring cell spreading, force generation and $\beta 3$ integrin dynamics. My results propose that ICAP-1 might be involved in integrin dynamics and force generation by controlling integrin endocytosis through Nm23-dependent scission of endocytic clathrin coated pits.



Table of abbreviations

ABP	Actin binding protein(s)
AFM	Atomic force microscopy
AP2	Adaptor protein complex 2
CamKII	Ca ²⁺ /calmodulin-dependent protein kinase II
CCP	Clathrin coated pits
Cdc42	Cell division control protein
CLIC	Clathrin-independent carriers
ECM	Extracellular matrix
ERK	Extracellular signal-regulated protein kinase
FA	Focal adhesions
FAK	Focal adhesion kinase
FbN	Fibronectin
FRAP	Fluorescence recovery after photobleaching
HSPG	Heparan sulphates
IAC	Integrin adhesion complex
ICAP-1	Integrin cytoplasmic domain associated protein-1
IF	Immunofluorescence
Krit-1	Krev interaction trapped-1
MLC	Myosin light chain (aka RLC)
MLCK	Myosin light chain kinase
MLCP	Myosin light chain phosphatase
MRCK	Myotonic dystrophy kinase-related CDC42-binding kinase
MMPs	Matrix metalloprotease(s)
MT	Microtubules
MYPT-1	Myosin phosphatase targeting protein, subunit of MLCP
PKC	Protein kinase C
PM	Plasma membrane



- PTB** Phosphotyrosine-binding domain
- Rac1** Ras-related C3 botulinum toxin substrate 1
- RLC** Regulatory myosin chain (aka MLC)
- ROCK** Rho-associated kinase aka Rho kinase
- SF(s)** Stress fiber(s)
- TF** Traction forces
- TFM** Traction force microscopy
- TIRF** Total internal reflection fluorescence
- VASP** Vasodilator stimulated phosphoprotein
- WB** Western blot



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I.

Introduction





Chapter 1. Cell shape dictates cell function

How tissues and organs are formed and modified is still open question in the field of cell biology. Since the cell is the functional and structural unit of all the living tissues, changes and reorganizations at the cellular level impact the general tissue morphogenesis. The three main processes – cell division, cell growth and cell death, combined with the individual cell decisions (response to physical or chemical extracellular stimuli) put the basis of the tissue and organ morphogenesis.

1.1. Cell behavior and fate are result of coordination between physical and biological inputs

Cellular shape is the result of mechanical equilibrium between the forces exerted on the cell membrane by intracellular organelles (mainly cytoskeletal networks) and the outside environment (Ingber, 1993; Bereiter-Hahn, 2005).

Being so the physical reality of the cells is controlled by a number of biochemical processes. For better understanding of how the cell shape is controlled, a deeper understanding of the coordination between biochemical signals and cellular mechanical properties is required.

Cells in suspension present mostly round, oval shape, which is energetically favorable, without any visible polarization or special form. For example, non-activated platelets float in the blood stream as discoid particles and their shape is maintained by microtubules organized in ring structure (Diagouraga et al., 2014). Some cells or cell fragments as non-activated platelets retain that form for most of their existence. Majority of cell types though do organize their internal skeleton (cytoskeleton) in variety of modes in order to acquire desired shape and therefore regulate vital physiological processes like transport, replication, formation and maintaining of extracellular matrix and integrating the cells in the overall tissue.



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Moreover different cell processes like cell division (cytokinesis), cell migration or contraction of a muscle fiber also require emerging of front-back polarity and generating anisotropic stress on the extracellular matrix (ECM) (Murrell et al., 2015). The summary balance of the external and internal forces is very closely regulated to ensure controlled cell shape changes, guaranteed by constant feedback between the cell mechanics and gene expression or protein activation.

1.2. How does the cell mechanics drive the cell shape

Cell shape and in general, the shape of objects is product of the mechanical forces forming them so the balance of the mechanical forces on the cell surface will be crucial in determining it. The internal forces on the cellular membrane are mainly due to the direct reorganization of three cytoskeletal networks – the microtubules, intermediate filaments and actin network. For example during the cytokinesis (Eggert et al., 2006), cell migration (Paluch et al., 2006; Lämmermann et al., 2008; Vicente-Manzanares et al., 2007), or apical contraction (Martin et al., 2009) the cell cytoskeletal networks do contract and therefore apply negative pressure on the cell membrane. On the other hand, the polymerization of actin drives membrane extension and formation of protrusions – lamellipodia and filopodia (Borisy and Svitkina, 2000). In addition, intracellular pressure can have osmotic origin or can be built via the contraction of the actin network (Figure 1.1) (Bereiter-Hahn, 2005; Mitchison et al., 2008; Sheetz et al., 2006).

The external forces applied on the cells are mainly from the cell adhesion on the cell microenvironment being cell – cell contacts or cell - extracellular matrix adhesion.

Forces applied on the cell surface can be categorized into three categories:

✎ actively generated within the cell – polymerization of actin or the contraction of actin network; opening of water or ion channels and ergo regulating the osmotic pressure inside the cell (De Vries et al., 2004);



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✎ forces applied on the cell from outside – either by pressure from the other cells, either from the ECM fibers (Yusko and Asbury, 2014);

✎ forces generated at the plasma membrane (PM) itself – lipid segregation or recruitment of curvature inducing proteins, phospholipids or sugars (Lieber et al., 2013; Paszek et al., 2014).

Globally cells do have awareness about their shape and are able to control it directly. Examples of this mechanosensing feedback can be found in the organization of adhesion sites (focal adhesions) and cytoskeletal remodeling in

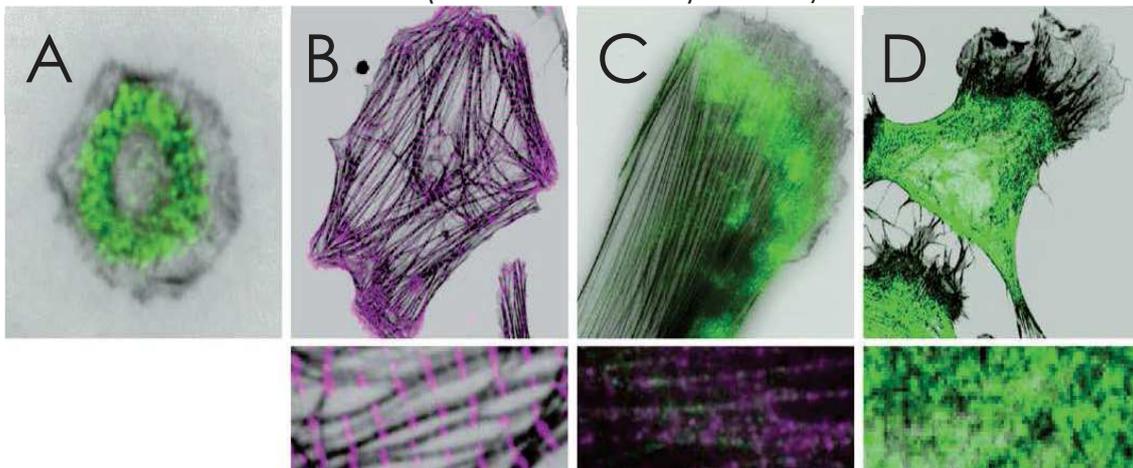


Figure 1.1. Different physical behaviors of the actomyosin cytoskeleton in non-muscle and smooth muscle cells.

The molecular partnership between F-actin and non-muscle myosin II drive the generation of mechanical forces across various length scales in order to modulate cell shape, division and migration.

Several adherent cell types stained for actin, myosin II and α -actinin:

- A. human platelets,
- B. striated muscle from a rat heart,
- C. smooth muscle from a human airway
- D. mouse NIH 3T3 fibroblasts.

Different organization of the contractile cytoskeleton was shown in the magnified boxes.

Adapted from Murrell et al., 2015.

cultured cells. During mitosis eukaryotic cells actively respond to the deformations by recruiting heavily myosin II to counteract the change of the shape (Efler et al., 2006). Interphase fibroblasts also do reinforce their focal adhesions upon pulling (Riveline et al., 2001).



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Multiple single factors do change according to the mechanical fate of the cell – the adhesion, the viscoelastic properties and cortical tension and they are tightly connected between them. Not surprising these mechanical properties are regulated by overlapping biochemical pathways forming self-regulating regulatory networks. As example, the proteins responsible for the actin turnover likely influence the cortical tension and also the viscoelastic properties in general (Janmey and McCulloch, 2007; Tabdanov et al., 2009).

1.3. Functional properties of ECM (Not just pretty fibrils!)

The ECM is more than just a passive network of ligands to support cell attachment: it contains different types of mechanical signals and it provides dimensionality. Here we are focusing on the contribution of the physical properties of the ECM environment on cellular mechanosensing (Hynes, 2009).

The extracellular matrix is present in all tissues and organs. It plays an essential role for the physical maintenance of the cellular components, enabling, in particular, the delimitation of the tissues and the individualization of the organs. Its role is not only structural; it intervenes in biochemical and biomechanical communication between cells, thus participating in differentiation, morphogenesis, homeostasis, etc. The extracellular matrix is essentially composed of water, fibrillar proteins and polysaccharides. However, its detailed composition and structure make it unique for each tissue. It is constantly developing: synthesized and remodeled by cells that are themselves influenced by the matrix. There is therefore a dialogue between the cells and their matrix. It has been presented a general view (Frantz et al., 2010) of the extracellular matrix in physiological condition and in pathological condition, as in the case of ovarian tumor (Figure 1.2) (Frantz et al.,



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2010; Cho et al., 2015). The structure, composition, biological and mechanical properties as well as the balance of intrinsic and extrinsic forces are modified by tumorigenesis (Tilghman et al., 2010).

A large scale project, called “matrizome” has been recently introduced (Naba et al., 2012) where the in vivo and in silico ECM composition of normal and tumorous tissues have been catalogued to address various biological problems about ECM physiology and pathology.

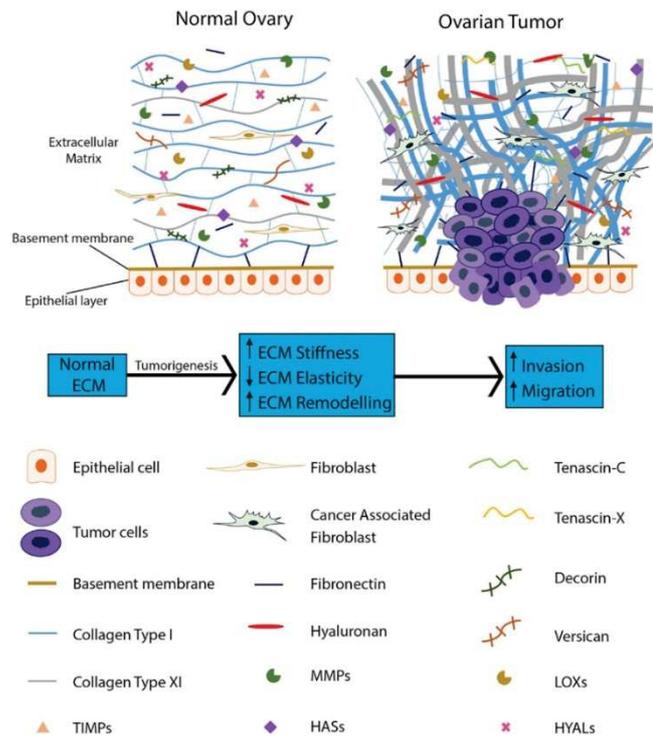


Figure 1.2. The ECM deregulation leads to ovarian tumorigenesis enhanced tumor progression

Normal ovarian ECM is composed mainly of highly organized clusters of collagen fibers with hyaluronic acid inserted between therefore regulating the dispersion of the collagen in the ECM (Cho et al., 2015). Some proteoglycans like decorin and versican are also present to secure pressure in the tissue. In epithelial ovarian cancer, the stromal fibroblasts are activated and the collagen is quickly remodeled into short, thick fibrils, randomly oriented into tracks and angles, tending toward perpendicular than parallel to the epithelial. Adapted from Cho et al., 2015.

1.4. Physical characteristics of the ECM

Another component of the cellular environment has long been ignored - the physical environment, which encompasses all the physical properties of the cellular and matrix environment, including the tissue rigidity. It seems clear, that the skin does not have the same rigidity or elasticity as the bone or the blood and lymphatic system. The rigidity of a number of tissues was measured (Cox and Eler,



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2011) (Figure 1.3). There are 8 orders of magnitude between the softest solid tissue - the brain (10^2 Pa) and the stiffer tissue - the bone (10^9 Pa). Some variations in rigidity have long been used in clinical diagnostics to detect palpation of

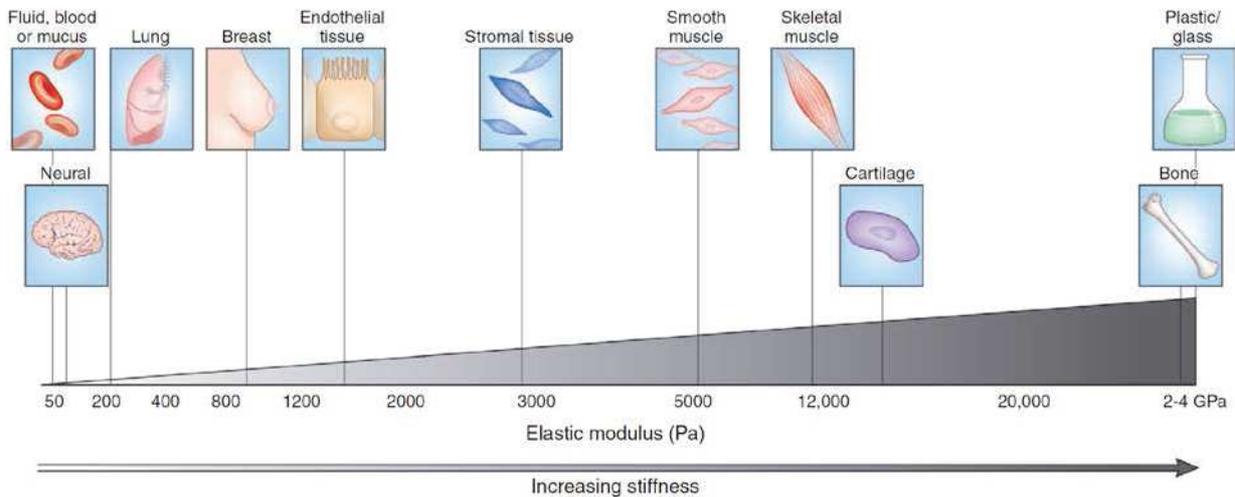


Figure 1.3. Variations in tissue stiffness. The biomechanical characteristics of different tissues in term of stiffness, measured in Pascals (Pa). It is evident that mechanically static tissues like brain or compliant like lungs exhibit low stiffness, while tissues, subjected to strong mechanical pressure like bone or skeletal muscles display stiffness several magnitudes higher. Adapted from Cox et al., 2011.

pathologies such as tumors. Other pathologies are associated with changes in the elastic properties of the tissues such as atherosclerosis, arthritis, osteoporosis, or fibrosis (sclerosis) of the heart, lungs, kidneys and liver (Ingber, 2003a). Finally, it has long been known that most cells from healthy tissue do not survive in suspension and require a solid support to grow in vitro. The lack of interaction between cells and the extracellular matrix causes apoptotic cell death called anoikis (Frisch and Francis, 1994). However, the engagement of integrins with matrix components in solution is not sufficient to inhibit this cell death. The survival signaling therefore depends on the physical properties of the matrix. Cellular growth independent of the support is one of the criteria for determining whether the cells are cancerous or not. Thus, the physics of the environment that influences the survival of the cells has to be considered.



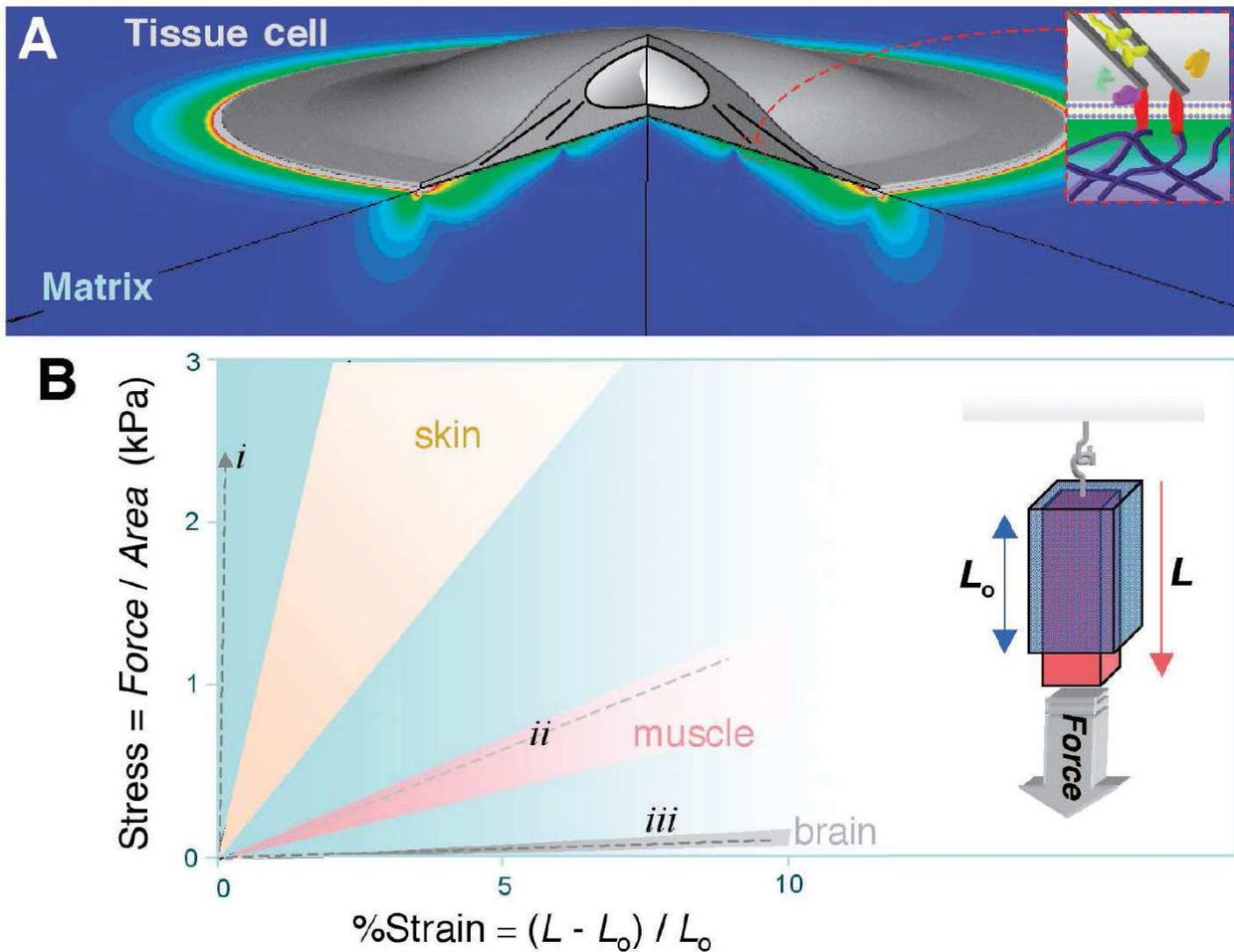


Figure 1.4. Substrate strain and tissue stiffness.

A. A *in silico* model of cell spread on soft matrix. The cell is modeled to be circular and to apply constant and sustained pulling pressure on the substrate from the edges to the nucleus (light grey).

B. Stress versus strain diagram for several soft tissues.

The range of slopes for these tissues is subjected to a small strain and gives the range of Young's elastic modulus, (E), for each tissue. Measurements are made on time scales of seconds to minutes and are in Pascal (Pa). The dashed lines (- - -) are those for (i) PLA, a common tissue-engineering polymer; (ii) artery-derived decellularized matrix; and (iii) matrigel. Adapted from Discher et al., 2005.

The physical environment of the cells is characterized not only by its mechanical properties. Topography and geometry also influence the cell behavior. The geometry of the environment matches the dimensional (2D vs 3D), the spatial organization of the components of the matrix, the orientation of protein fibers such as collagen, the tissue organization. It can be modeled by cell cultures in 3D or



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pseudo-3D method using the method of the sandwich (Deroanne et al., 2001) or well (Ochsner et al., 2010), by the use of matrices organized by micropatterning (They and Bornens, 2006; Destaing et al., 2010) or structured matrices (Gardiner et al., 2015). The topography of the environment can be compared to the surface roughness that can be measured by atomic force microscopy by directly scanning the surface. Experiments done on the micro-pillars (Saez et al., 2005; Buguin et al., 2005) can address simultaneously the geometry (by spacing the pillars) or the topography of the surface (by regulating the height of the pillars and therefore their rigidity). The drawback of working on micro-pillars is that the adhesion surface is restricted and spaced artificially.

Stiffness is a measurement of the relationship between a force applied to a material and its deformation. Important parameters when measuring the stiffness are the Young's modulus (E) (also called modulus of longitudinal elasticity or traction) and Coulomb modulus (G) (also known as shear modulus or slipping) by the mode of application of force the material. For the Young's modulus, the force is applied perpendicularly to the surface of the material, whereas for the Coulomb module the force is applied parallel to this surface (Figure 1.4). These two modules are homogeneous on a constraint expressed in Pascals (Pa) corresponding to a force applied per unit area ($\text{N}/\mu\text{m}^2$); they are connected by the following equation: $E = 2G(1 + \nu)$ where ν is the Poisson coefficient. For a material whose volume does not change under stress, this coefficient is a constant and is equal to 0.5. There is a simple relationship between E and G and measure the leads to measuring the other (Moore et al., 2010). The forces undergone by the cells may be due to flows of shearing fluids such as the blood circulating on the endothelial cells or the compression or tension of the tissues on the cells. They respond to their environment by applying opposing forces (Butcher et al., 2009). To study the effect of the rigidity due to extracellular matrix compression/tension forces on cell behavior, many natural or synthetic matrices have been developed (Ruprecht et al., 2017; Monge et al., 2015).



1.5. Some key components of the extracellular matrix

There are two major classes of macromolecules consisting of extracellular matrix: proteoglycans and fibrous proteins (Mouw et al., 2014) (Figure 1.5). Many growth factors do bind to matrix proteins and play a role in controlling cell proliferation and differentiation, sometimes synergistically with the matrix components (Hynes, 2009).

1.5.1. Proteoglycans

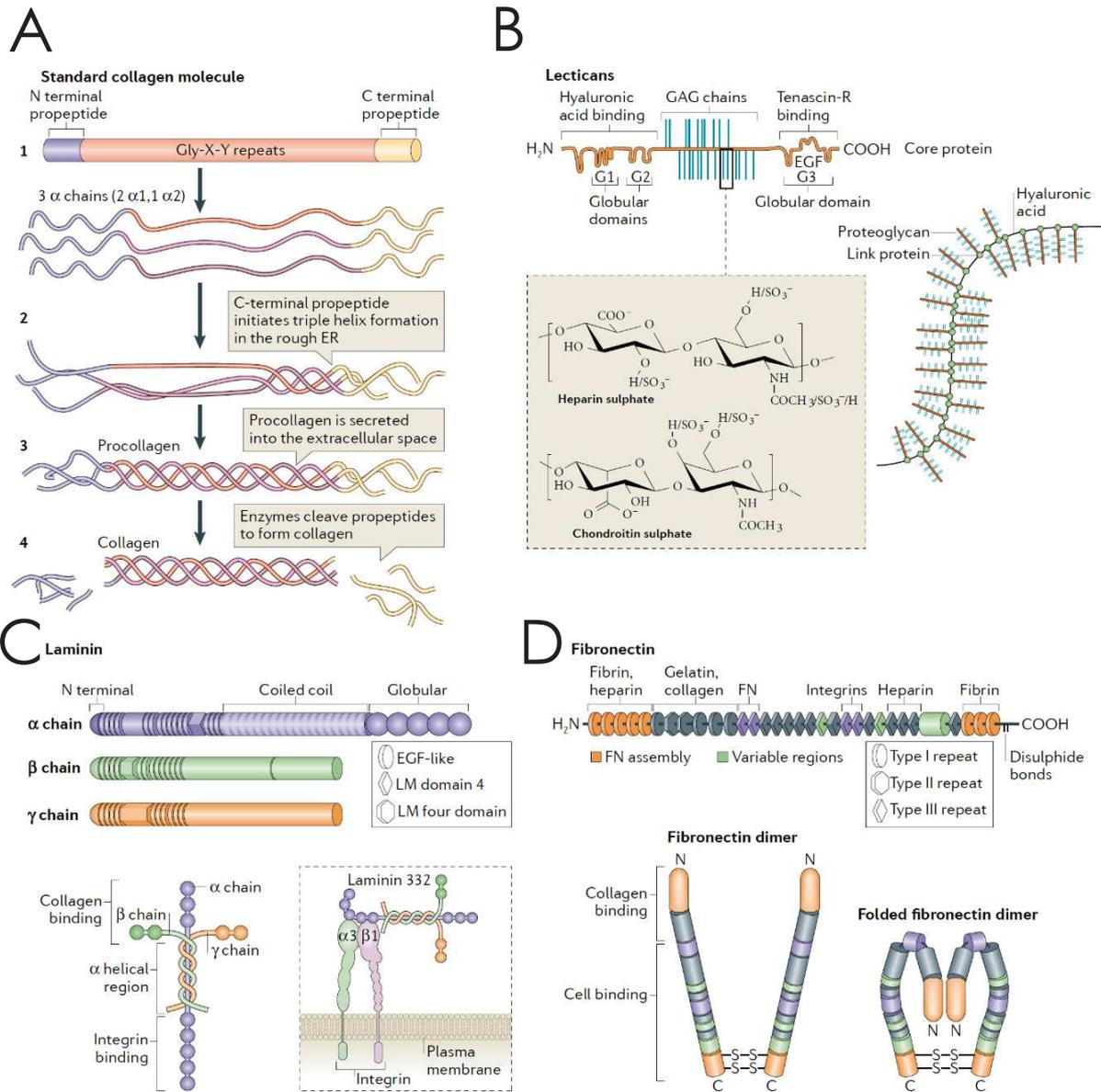
Proteoglycans are abundant components of the cell surface and the extracellular matrix; they regulate the distribution of extracellular signaling factors and modulate the signaling related to cell adhesion and motility. The proteoglycans consist of a protein core carrying long chains of linear disaccharides. Proteoglycans with heparan sulphates (HSPG) are grouped into three classes: transmembrane receptors, glypicons (membrane receptors) and secreted HSPGs (components of the extracellular matrix), including perlecan (Kirkpatrick and Selleck, 2007).

1.5.2. Laminins

Laminins are major components of the basal lamina, particular extracellular matrix defining epithelia and endothelia. They interact with numerous components of the matrix (collagens, glycoproteins like perlecan, etc.) They also form the mesh-like polymer by self-assembly of the basal lamina, much like collagen IV-shaped network. Laminins are hetero-trimeric glycoprotein formed by the combination of a chain α , a chain β and a chain γ . In mammals, there are 12 different heterodimers. The main laminin receptor are integrins $\beta 1$ and $\beta 4$, the dystroglycans and heparan sulphates (Colognato and Yurchenco, 2000).



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1.5.3. Fibronectin

Fibronectin is produced by many cell types, and plays an important role in development, in angiogenesis, wound healing and bone physiology (Tang et al., 2004); its gene inactivation is lethal at the embryonic stage. It is a generally dimeric fibrillar protein whose subunits are covalently linked at their C-terminus by di-sulfide bridges. Each monomer is constituted by the repetition of three types of subdomains (Figure 1.6) which can be modified post-translationally in particular by glycosylations. There are at least 20 variants of human fibronectin, due to alternative splicing, particularly at the V domain (Figure 1.6). The solubility

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properties of fibronectin and its interaction properties with its receptors depend on the presence or absence of the spliced domains. Fibronectin is abundantly present in a soluble form in the blood and in insoluble form in the extracellular matrix. The main roles of fibronectin have been attributed to the matrix and non-blood form. It is a ligand of many integrins. Among the sites of interaction between fibronectin and integrins include RGD (Arginine-Glycine-Aspartic acid) present in domain III 10 which is part of the cell binding domain (CBD): the FN fragment 8 - 10, and the V domain. The FN fragment 12-14 is the main heparin binding domain (HBD or Hep II) which serves Fibronectin also interacts with many other components of the extracellular matrix. Finally, fibronectin is organized by fibrils by the cells: it has self-assembly sites, but some of them will become available only following a conformational change induced by the traction of the cells (Zhong et al., 1998). This process is known as fibrillogenesis. These conformational changes of fibronectin can also lead to exhibition of cryptic sites that could link integrin under the influence of external force (Régent et al., 2011). This is why

Figure 1.5. The main macromolecular components of the extracellular matrix.

A. The standard fibrillar collagen molecule is characterized by amino- and carboxy-terminal propeptide sequences, which flank a series of Gly-X-Y repeats (where X and Y represent any amino acids but are frequently proline and hydroxyproline).

B. Lecticans have a main protein with binding domains for glycosaminoglycan (GAG) chains that has globular domains around it that interact with hyaluronic acid (at the N terminus) and tenascin R (at the carboxy terminus). Common GAGs are chondroitin sulphate and heparan sulphate, the chemical structures of which are shown.

C. Laminins are formed by the incorporation of α , β and γ chains into a cruciform, Y-shaped or rod-like structure.

D. The fibronectin molecule forms a dimer through disulphide bonds on its C terminus. The folded fibronectin molecule forms via ionic interactions between type III domains of neighboring molecules and is deformed by mechanical force to reveal cryptic binding sites for other fibronectin molecules and cell surface receptors when interacting with cells. Adapted from Mouw et al., 2014.



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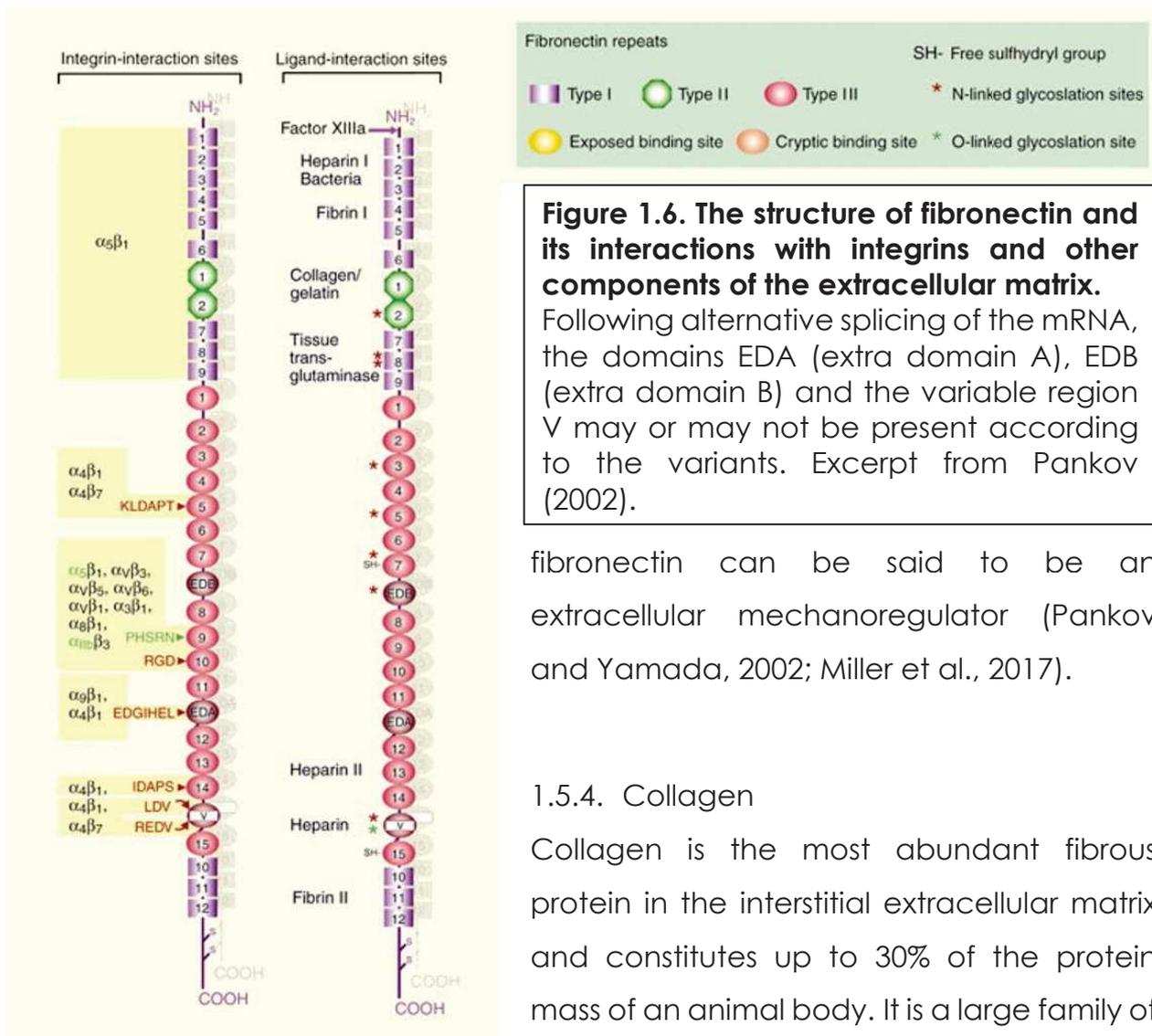


Figure 1.6. The structure of fibronectin and its interactions with integrins and other components of the extracellular matrix. Following alternative splicing of the mRNA, the domains EDA (extra domain A), EDB (extra domain B) and the variable region V may or may not be present according to the variants. Excerpt from Pankov (2002).

fibronectin can be said to be an extracellular mechanoregulator (Pankov and Yamada, 2002; Miller et al., 2017).

1.5.4. Collagen

Collagen is the most abundant fibrous protein in the interstitial extracellular matrix and constitutes up to 30% of the protein mass of an animal body. It is a large family of

proteins possessing very different physical properties, conferring on each tissue its functional specificity. They play a very important role in resistance to tension in the tendons, cartilage and bones. With elastin, they ensure elasticity and cohesion of the skin. They also constitute the transparent matrix of the crystalline lens. A summary of the main classical knowledge about collagens has been published recently (Brinckmann, 2005). Collagens are trimeric proteins forming a straight super-helix. They can be organized in a sheet or cable by the cells, in particular by the fibroblasts (Mouw et al., 2014). Each polypeptide chain consists of a repeat of the tri-peptide Gxy (Glycine-xy) where x and y are frequently prolines and 4-hydroxyprolines. There are at least 28 kinds of collagen. The most common is



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collagen type I. It forms fibrils and is present in tendons, ligaments, cornea, bones or skin. Type IV collagen forms a network and is specific to the basal lamina. Certain collagens possess an RGD (Arginine-Glycine-Aspartic Acid) or GFOGR (Glycine-Phenylalanine-Hydroxyproline-Glycine-Arginine) motif recognized by the integrins. Numerous post-translational modifications have been described. These influence the chemical properties of the collagens, participating in the bridging between themselves or with the other components of the extracellular matrix, which modulates the elastic properties of the collagens and consequently the physical properties of the matrix and the tissues.

1.5.5. Vitronectin

Vitronectin is a glycoprotein present in blood in monomeric form and in the extracellular matrix in multimeric form. Vitronectin is present in the connective tissues of many organs, the wall of blood vessels and lymph nodes. It is involved in many physiological and pathological processes such as homeostasis, angiogenesis, rheumatism and tumor invasion. The main function of vitronectin is to bind the inhibitor of plasminogen activator 1 (PAI-1) and to keep it in active conformation. Vitronectin is a ligand of the receptor uPAR (urokinase-like plasminogen activator receptor) and a ligand of integrins at its RGD motif (Madsen and Sidenius, 2008).

1.6. The extracellular matrix is a critical component of the metastatic niche

Cancer development and metastasis needs not only a localized niche to nourish the main tumor but also a metastatic niche to enable dissemination survival and colonization of distant tissues (Psaila and Lyden, 2009; Malanchi et al., 2012).

Tumor overgrowth naturally generates mechanical pressure on the adjacent tissues and therefore tumor compresses itself. These forces were speculated to



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regulate the tumor growth. This mechanical pressure have been suggested to slow down the tumor evolution, but to trigger cell invasion and metastasis (Alessandri et al., 2013). That specific spot is composed of diverse ECM and sets of enzymes that reorganize it (matrix metalloproteases (MMPs), for example). The cancer cells in those niches cooperate with other local cell types such as bone marrow-derived cells, endothelial cells and fibroblasts. In Lewis lung carcinoma for example the production of fibronectin is increased in the places of future metastasis, which attracts BMDS cells through engagement of their $\alpha 4 \beta 1$ integrin (Kaplan et al., 2005). These cells also employ MMP9 to digest the basal membrane and like that, the ECM reorganizing happens in the early stages of metastasis to enable the circulating tumorigenic cells in the blood stream to colonize distant organs. Fibronectin is not the only ECM component to be engaged in building the metastatic niche. Another component, more predominant in stem cell niches is Tenascin C is secreted from breast cancer cells initially and sequentially by the stromal fibroblasts to ensure the survival and development of the lung metastasis (Oskarsson et al., 2011). Periostin (Malanchi et al., 2012), which plays important role in bone and teeth formation promotes the metastasis by recruiting WNT ligands and boosting the WNT pathways in cancer stem cells (Malanchi et al., 2012). Periostin secretion by fibro blasts is induced by invading tumor cells through TGF β signaling and is needed to maintaining the stemness of the cancer stem cells. Curiously the endothelial tip cells forming the vascular sprouts secrete both TGF β and periostin that induce the angiogenesis and micrometastatic formations (Ghajar et al., 2013). Considering the proteoglycanic ECM components LLC-conditioned growth medium contains versican – large chondroitin sulphate proteoglycan found to be upregulated in vast variety of human cancers. It activates macrophages via the Toll-like receptor 2 (TLR2) and induce the production of interleukin-6 (IL-6) and tumor necrosis factor (TNF) facilitating the formation of pro-inflammatory microenvironment that is conducive for metastatic growth (Kim et al., 2009).



Osteopontin, found in gliomas also preserve the stem cell properties and radioresistance through CD44 signaling (Pietras et al., 2014). More broad and systematic approach to point out the responses to ECM has also contributed to filling the library of the ECM molecules that promote metastatic behavior (Reticker-Flynn et al., 2012).

Taken together, these studies illustrate how the ECM modulates metastasis and implies that inhibiting the ECM niche may be therapeutically crucial in cancer treatment.

1.7. Cell can sense the physical environment and adapt its response (mechanoresponse)

The first technique was published in 1998 (Pelham and Wang, 1998) where biocompatible gel with controlled rigidity was used to show that fibroblasts and epithelial cells can sense different rigidities of the substrate. Profound changes were found at several different levels in cell physiology - the morphology, lamellipodia's activity and migration were affected; the distribution of vinculin and the phosphorylation of tyrosines of several proteins are dependent on rigidity. Other teams were able to show that this sensitivity to the rigidity is for many cell types of different embryonic origins as endothelial cells (Deroanne et al., 2001; Yeung et al., 2005), neutrophils (Yeung et al., 2005) and smooth muscle cells (Engler et al., 2004), but this response is defected in transformed cancerous cells (Wang et al., 2013).

1.7.1. Cell growth and death

The cell cycle is controlled by the rigidity of the cellular microenvironment. The increase in the expression and function of cyclin D1 via FAK (Focal Adhesion Kinase)/Rac1 (Ras-related C3 botulinum toxin substrate 1) but not by ERK (Extracellular signal -regulated protein Kinase) (Klein et al., 2009) is increased



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when the extracellular matrix rigidity is increased. Whereas the rate of cell death by apoptosis is decreased. This cellular sensitivity is lost with the transformation the cells into cancer (Wang et al., 2013). Within a monolayer of epithelial cells, regions where high physical stress is observed, correspond to regions where cell proliferation is increased. Inhibition of the physical tension induced by myosin (with blebistatin) or rupture of intercellular contacts release constraints and inhibit cell proliferation (Nelson et al., 2005).

1.7.2. Cell spreading through the organization of the actin cytoskeleton

Cell spreading is dependent on the stiffness of the extracellular environment and seems to be valid for most of the cell types. Study done on glioma cell lines (Tilghman et al., 2010) show that cancer cells also follow that general rule and the mechanoreponse is preserved even after transformation. The spreading area increases with stiffness as well as the number and size of adhesion structures such as focal adhesions. Actin filaments also adapt by forming thicker cables which are highly decorated with phosphor-myosin when the ECM stiffness is augmented. Figure 1.7 shows the type of response observed for fibroblasts or myoblasts, but also controls the organization of the actin cytoskeleton(Ochsner et al., 2010).

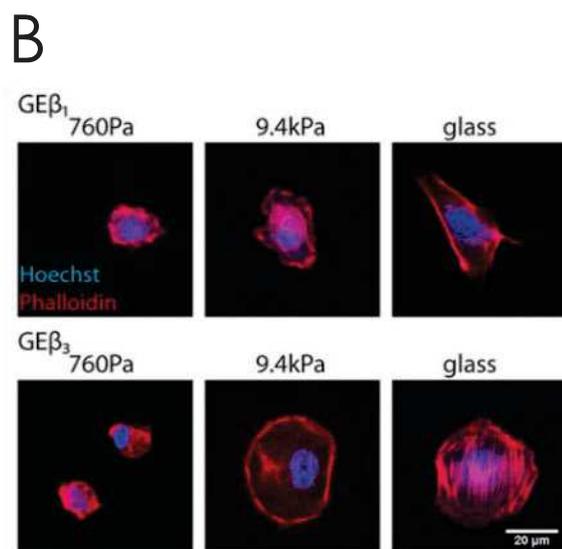
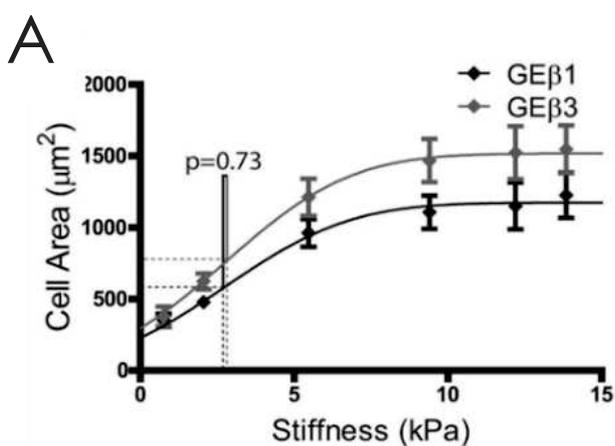


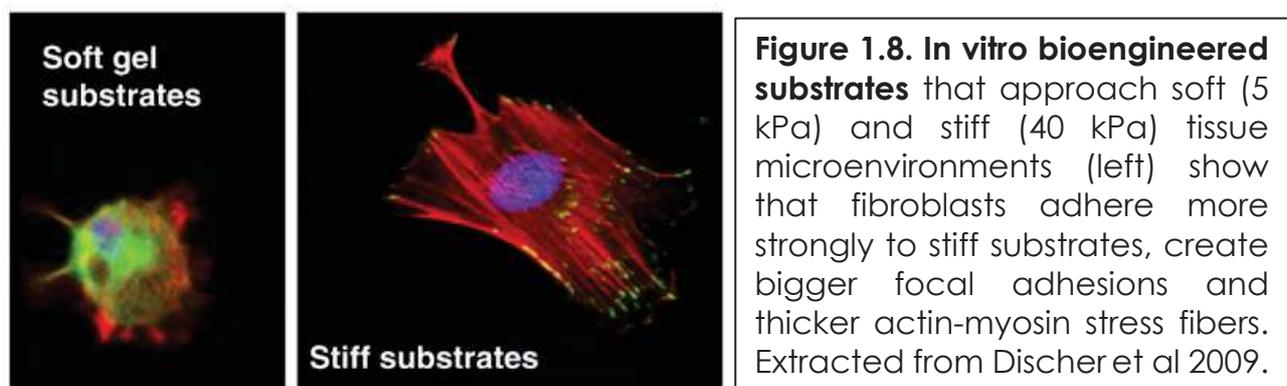
Figure 1.7. Cells respond to increased substrate stiffness by increased spreading.

A. Cellular spread area of mouse embryonic cells expressing $\beta 1$ integrin (GE β 1) and or $\beta 3$ integrin (GE β 3) cells over indicated rigidities. You can appreciate the increased surface area with the increased matrix stiffness.

B. Representative images of cells described in A. Notice the difference in actin organization and nuclear surface. Adapted from Balcioglu et al., 2015.

1.7.3. Cell migration

Cell migration is dependent on the physical environment. Indeed, the rigidity of the extracellular matrix modulates the speed of cell migration (Pelham and Wang,



1998; Peyton and Putnam, 2005; Oakes et al., 2009; Ulrich et al., 2009; Stroka and Aranda-Espinoza, 2009). When plated on rigidity gradients, the cells migrate towards the stiffest substrates. In addition, cells do tend to have larger spreading area, more focal adhesions and thicker actomyosin filaments on rigid substrates. (Figure 1.8). The phenomenon of directed cellular migration towards the harder substrate is called "durotaxis" in reference to the migration headed by a chemical factor gradient, called chemotaxis (Lo et al., 2000; Zaari et al., 2004). Cell migration also depends on the dimensionality of the environment: the migration in 1D fibroblasts (Doyle et al., 2009) resembles more the cellular migration observed in 3D fibrillar matrices than on 2D matrices. Unlike 2D migration, migration along 1D or 3D matrix fibers is independent of the density of the extracellular matrix and is faster.



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1.7.4. Gene expression

Genes regulated by the mechanical properties of the environment are called mechanosensitive or mechanoresponsive genes. During development of the *Drosophila* for example the expression pattern of certain embryonic genes such as *twist* depends on the mechanical deformation of the epidermis (Desprat et al., 2008). When cancer cells – lung carcinoma and squamous cell carcinoma are cultured conventionally and in 3D pseudo-physiological conditions, several gene expression differences were established. In brief, cellular processes like cell-cell and cell-matrix adhesion immune cell response, tissue development is under the differential regulation of the physical 2D or 3D matrix based microenvironment. (Figure 1.9) (Zschenker et al., 2012; Le Beyec et al., 2007). Protein expression of differentiation factors like neurogenic p-NFH, myoblastic Myosin D and osteogenic BF a1 has different optimum depending on the rigidity of the environment in mesenchymal stem cells(Engler et al., 2006; Smith et al., 2017; Discher et al., 2017). Finally, the expression of many proteins of the extracellular matrix, signaling and cytoskeleton is regulated by extracellular mechanical forces and the forces generated by intracellular cells (Chiquet et al., 2009; Chan et al., 2010).



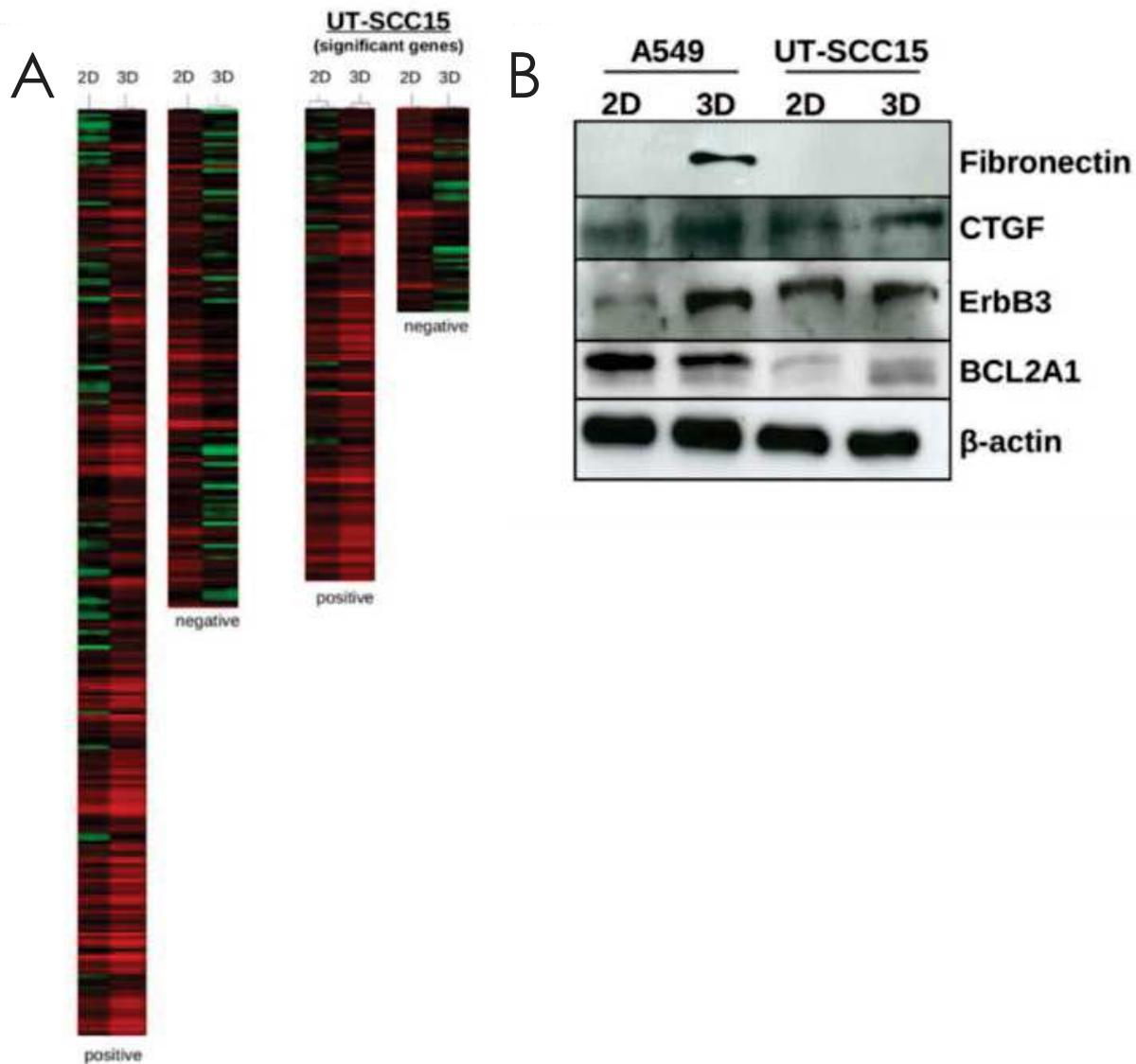


Figure 1.9. RNA ratios of differentially expressed genes and protein evidence of in 3D and 2D cell cultures of A549 and UT-SCC15 cells. (A) Hierarchical clusters of genes of 2D and 3D cell cultures at day 4 after plating. Red indicates overexpression, green - underexpression and black indicates average expression after Significance Analysis of Microarrays (SAM). "Positive" indicates genes upregulated in 3D versus 2D. "Negative" indicates genes downregulated in 3D versus 2D. (B) Western blot confirmation of several of the proteins identified in the microarray gene expression data. Fibronectin (240 kDa), CTGF (38 kDa), ErbB3 (180 kDa) and BCL2A1 (20 kDa) show important differences. β -actin served as loading control. Adapted from Zschenker et al., 2012.



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1.7.5. Cell differentiation

Differentiation of stem cells is probably associated with the integrin-cytoskeletal-based feedback loop between mechanical and biochemical cues in a signaling network that determine their fates. Different mechanisms of matrix stiffness mechanotransduction may exist in three-dimensional environments, which are more physiologically relevant but still poorly studied (Lv et al., 2015) (Figure 1.10). The physical properties of the environment can be modeled by synthetic matrices or by cultures on monolayers of inactivated cells. It is possible to differentiate mesenchymal stem cells into neuronal, myoblastic or osteoblastic cells (Engler et al., 2006) by modulating the stiffness of the adhesion support without the addition of biochemical factors stimulating differentiation. The production of neuronal cells from mesenchymal stem cells is particularly unexpected since these cell types normally come from two different embryonic layers whose specification takes place at the time of gastrulation. The differentiation of mesenchymal stem cells is not only sensitive to the rigidity itself but also to the stiffness gradients of the extracellular medium (Tse and Engler, 2010). This regulation of differentiation by the physical properties of the cellular environment opens up perspectives in the field of biomaterials and regenerative medicine. Differentiation of CDC cells (cardiosphere-derived cell) into mature cardiac cells can be controlled by the physical properties of a hydrogel. In addition, this gel is thermosensitive, biodegradable and compatible to myocardial injections (Li et al., 2011) and could be an important candidate for the contribution and the differentiation of cells to CDC after cardiac infarction. YAP (Yes-associated protein) and its partner TAZ are transcriptional activators that activate proliferation and are oscillating between the nucleus and the cytoplasm (Furukawa et al., 2017). YAP/TAZ were also identified as nuclear relays of mechanical cues from the ECM. Importantly YAP/TAZ are involved in the mechanical differentiation of mesenchymal stem cells. It can be concluded that



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YAP/TAZ are sensors and mediators of mechanical cues instructed by the cellular microenvironment (Dupont et al., 2011).

The existence of a dependent signaling mechanical links between the muscle and the skin in the nematode *Caenorhabditis elegans* has been also published (Zhang et al., 2011). This mechanotransduction is necessary also for the morphogenesis of the epithelium.

Thus, the physical environment of cells modulates many cellular processes. However, the molecular mechanisms that allow cells to sense physical

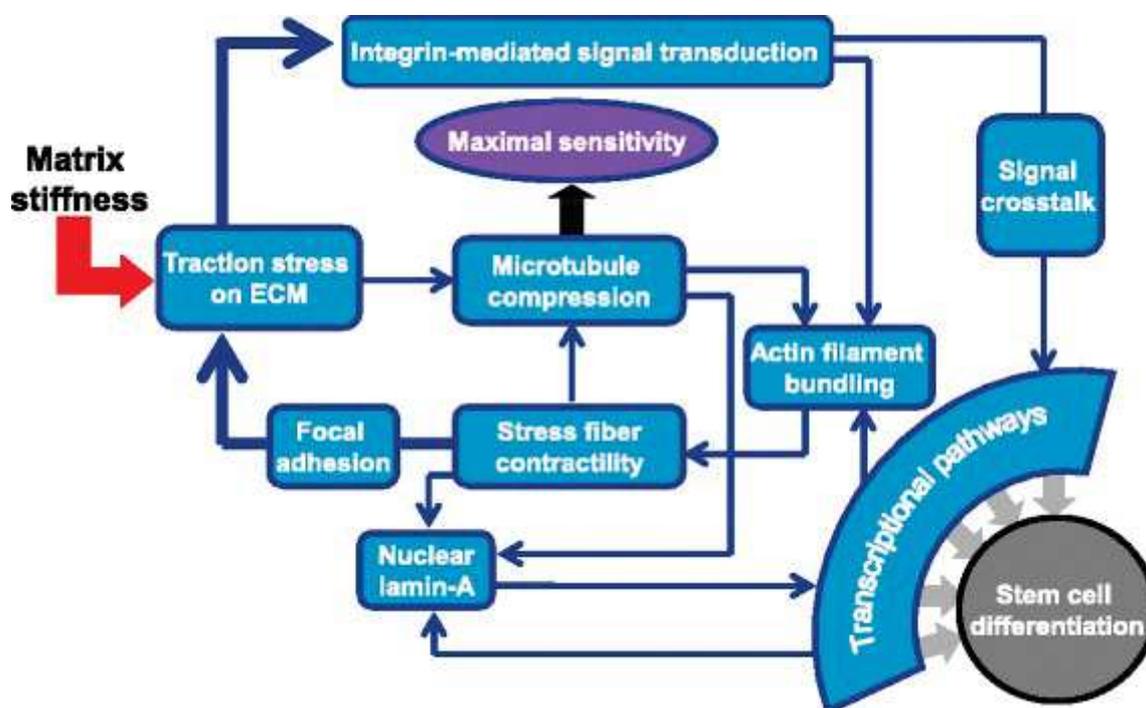


Figure 1.10. Mechanotransduction steps activated by matrix stiffness in stem cell differentiation

The original tension due to stress fiber contraction on their attachment spots on the ECM - FA is counteracted by the microtubules resistance. The cell balances the resultant force from the traction stress with activating integrin dependent signaling pathways that modulate actin polymerization and influences cell contractility. The initial stress is transmitted via the microtubules to the nucleus and is applied on lamin-A (form the family of the intermediate filaments) which activates transcriptional pathways that induces actin filament building. The cell is able to regulate its maximal mechanoreponse via cytoskeletal feedback loops. Adapted from Lv et al., 2015.



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properties and respond to variations in this environment are not really known to this day. The molecular players in cell adhesion are a priori mechanical sensors as possible to form a link between the cell and its environment. It is therefore important to know the molecular actors of adhesion, their interactions and their involvement in adhesion, mechanosensitivity and cell migration. These topics will be discussed in details in the following introduction.



Chapter 2. Actin cytoskeleton as an internal mechanical element of the cell

2.1. Structure of actin microfibrils

Actin is a globular protein of about 44 kDa capable of self-assembly into double polarized helical filament (showing distinguished barbed end (+) and pointed (-) tip).

Figure 2.1 summarizes the dynamics of the actin filament. The equilibrium coefficients are different between the barbed end and the tip end, which explains the treadmilling motion of actin units within the filament in dynamic equilibrium. At the cellular level, the actin filaments can form very diverse intracellular structures such as a network of parallel filaments within filopodia or microvilli, a gel (highly branched and dynamic network) in the lamellipodia and the cell cortex or a cable antiparallel network, giving rise to different kind of stress fibers (SF). At the cellular level, all those structures are involved in the shape of the cell in the functioning of the internal machinery (including intracellular trafficking) and the regulation of cellular processes like migration.

To be so neatly organized, the dynamics of the F-actin are controlled by factors intrinsic to actin itself as the hydrolysis of ATP or arginylation of certain amino residues (Karakozova, 2006) or by extrinsic factors: regulatory actin binding proteins (ABP). These are grouped in two wide classes: proteins regulating the dynamics of actin filaments and proteins that regulate the organization of networks of filaments (Pollard, 2016; Blanchoin et al., 2014). All these proteins are themselves under the control of many diverse signaling pathways.



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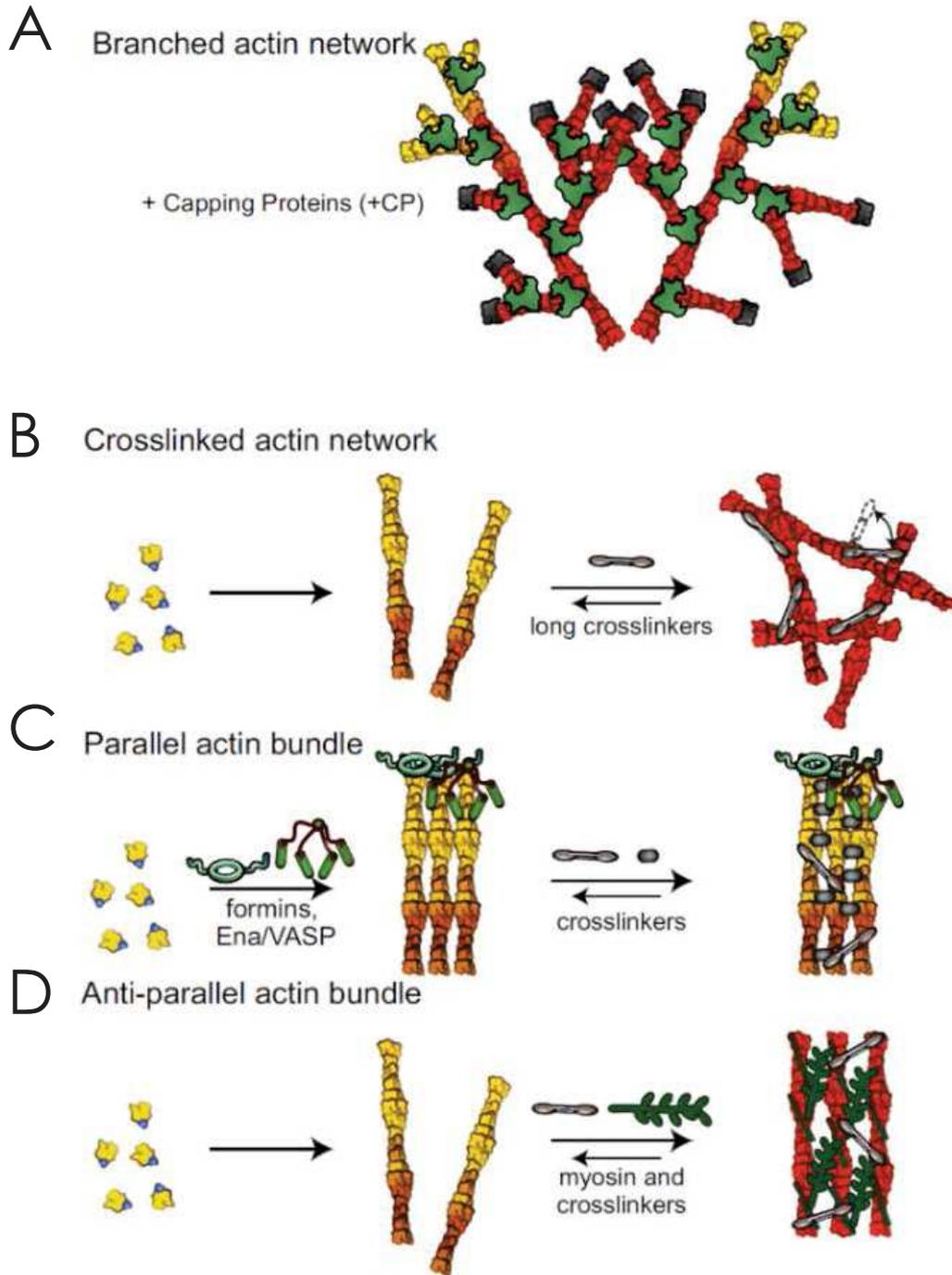


Figure 2.1. Dynamics of the different actin filaments

A. Branched actin network results from the activity of the Arp2/3 complex. Activated by nucleation promoting factors, the Arp2/3 complex forms a branch of actin from primer – already existing chain. In the presence of capping proteins, branches are shorter. This results in dense and rigid nets that can turn into a meshwork.

B. the long crosslinking proteins organize the linear actin filaments into nets. These connections act as rigid links and drive the global elasticity of the actin network according to their binding kinetics and concentration.

C. the short crosslinkers pack actin filaments more tightly into rigid fibers. They are controlled by formins or VASP systems and give rise actin fibers with parallel organization

D. molecular motors like myosin serve as dynamic connections between antiparallel filaments, that makes them effective contractile and spring units. Adapted from Blanchoin, et al., 2014.

2.2. Dynamics of actin microfilaments under the control of ABPs

Some proteins like the Arp2/3 complex promote the nucleation step of the filaments, which is highly energetically unfavorable. It facilitates formation of a branch on an already pre-existing filament. Other proteins regulate the actual growth of the filaments, their stability and/or disassembly. Examples are cap proteins that stabilize the ends of the filaments but also block their growth (tensin or gelsolin). Gelsolin is also able to cut the filaments. Members of the ADF/cofilin family bind the filaments of ADP-actin and promote dissociation of the actin units at the pointed end. Tropomyosins bind along the filaments and stabilize them by disadvantaging their spontaneous depolymerization and the cutting action of gelsolin or ADF / cofilin. They also regulate with troponins, interactions between F-actin and myosin in striated muscles. The dynamics of actin filaments of actin depends on the pool of unbounded G-actin, which is controlled by numerous proteins capable of binding to the monomers actin like profilin which promotes the exchange of nucleotide ADP by ATP and issue of ATP-actin monomers to the



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barbed ends. Figure 2.2 summarizes nicely the complexity of the regulation of the actin cytoskeleton with the example of growing lamellipodium (Blanchoin et al., 2014; Pollard and Borisy, 2003; Pollard, 2016).

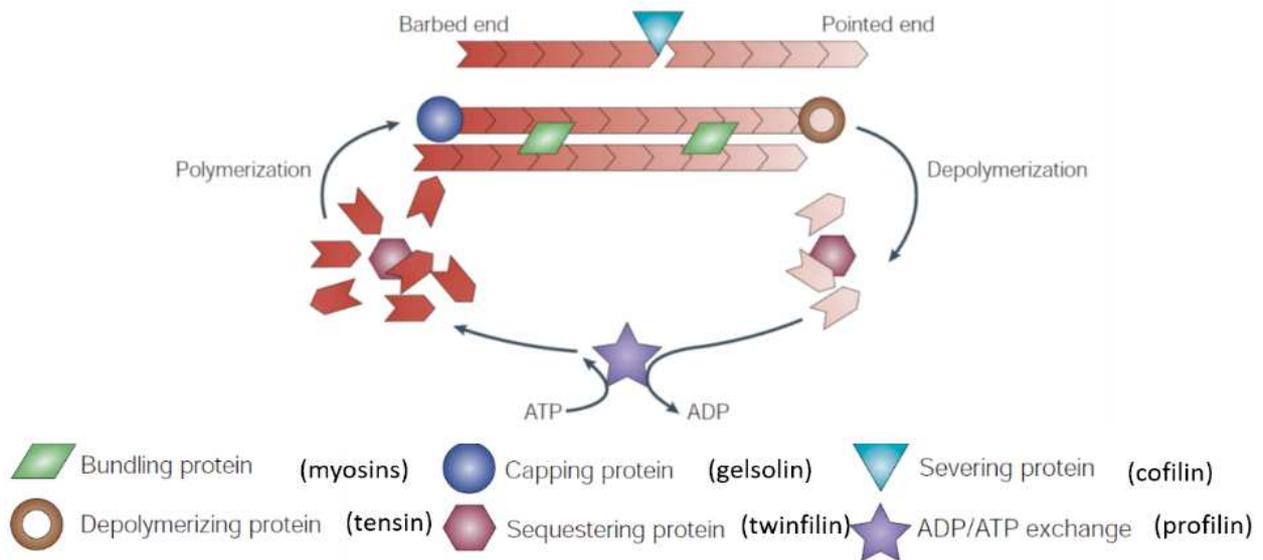


Figure 2.2. The F-actin filaments are formed by G-actin monomers until it reaches equilibrium. Filamentous (F)-actin is, asymmetric and the two extremities have different kinetics. Actin monomers assemble much more rapidly at the 'barbed end' compared to the 'pointed end'. When F-actin and G-actin are at equilibrium, the global critical concentration is intermediate between those of the two ends separately, therefore at this stage, there is a net loss of molecules at the pointed end and a net addition at the barbed end. The fiber seems in balance, which leads to treadmilling — an equal flow of actin subunits through the filament. G-actin binds either ATP or ADP. ATP monomers assemble faster than the ones, bound with ADP. After assembly on a treadmilling filament, ATP is hydrolysed to ADP this changes the filament conformation, forming less stable form at the pointed end, which depolymerizes. So, a treadmilling filament contains ATP-bound subunits at the barbed end, but the actin monomers at the pointed end are ADP-bound. Many proteins bind to actin and influence its dynamics or activity. They are referred to as actin-binding proteins (ABPs). Among ABPs, some link actin filaments in a loose network (crosslinking proteins) or in a tight bundle (bundling proteins), or anchor filaments to the plasma membrane. Others bind to the barbed end of the filament and prevent further elongation (capping proteins), whereas some cause fragmentation of filaments (severing proteins) or might favor the depolymerization of pointed ends. ABPs also regulate the addition of monomers by sequestering them or favoring ADP/ATP exchange. Adapted from Revenu, et al., 2004.



2.3. Regulation of actin network by small GTPases

The small RhoGTPases (RhoA and Rac1) are central regulators of actin dynamics. They are capable to activate the Arp2/3 complex, ROCK family kinases and formins (mDia) (Mullins et al., 1998; Riento and Ridley, 2003). Traditionally Rac1 is described to operate in the leading edge of the migrating cell, where it acts on Arp2/3 complex for lamellipodia formation and RhoA is depicted in the cell rear, where it modulates actomyosin contractility via ROCK kinase family to retract the cell body (Ridley et al., 2003). This black and white view of Rho family proteins seems to be significantly challenged in 3D environment (Tomar and Schlaepfer, 2009; Yamazaki et al., 2009; Kim et al., 2015). Signaling from RhoA and Rac1 seems to occur in pseudo-oscillating fashion. Even more precisely it has been shown (Machacek et al., 2009) that RhoA activity is required in front of the Rac1 in the lamellipodium. In fibronectin rich environment cells presenting dominant RhoA activity at the leading edge tends to be more fast

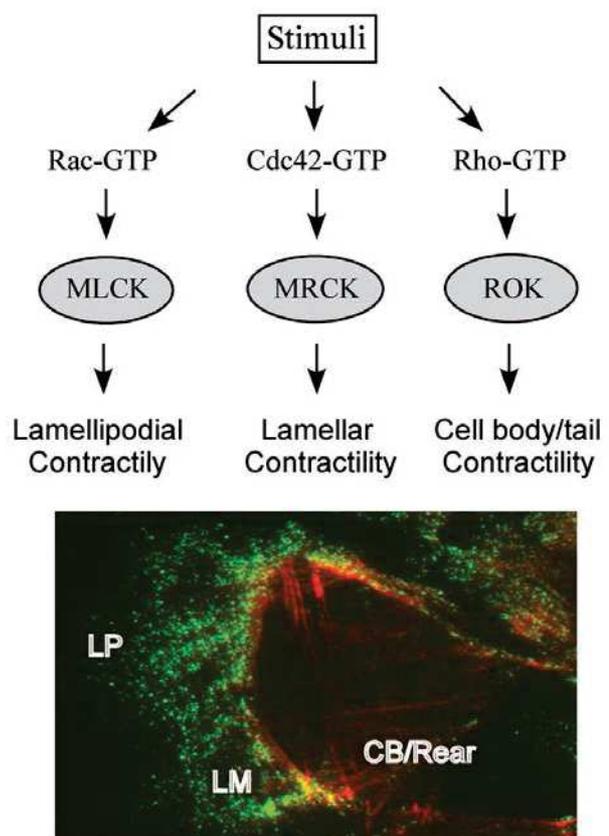


Figure 2.3. RhoGTPases display differential subcellular locations. Upper panel depicts a model for the specific activation of the different kinases, responsible for the phosphorylation of the MLC at various locations in the cell. In response to upstream signals, several kinases are activated and localized to different regions. The coordination of these signaling events is crucial for directional cell migration. Lower panel shows a typical front-rear location for Myosin 2A and 2B (in green) in a migrating U2OS cell. Actin is shown in red. LP – Lamellipodium, LM – lamella, CB.rear – cell body/rear part of the cell. Adapted from Tan et al., 2009.



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in random 2D migration and to have increased invading capabilities in 3D tissue like microenvironment (Caswell et al., 2008; Muller et al., 2009; White et al., 2007; Jacquemet et al., 2013; Paul et al., 2015) (Figure 2.3).

2.4. Regulation of actin network by ABPs

There are clear distinguish between class of proteins allowing the alignment of filaments of actin cables in parallel or antiparallel fashion and that of the proteins allowing orthogonal (intersecting) bonds between filaments. All these proteins possess either multiple actin-binding domains or a single domain and then form multimers (Pollard, 2016). This is the case of α -actinin, which associates with an antiparallel dimer. It is involved in the formation of stress fibers. The spectral tetrameric complex is involved in the formation of the cortical actin gel network, particularly in the red blood cells.

2.5. Contractile actin cytoskeleton: actomyosin network

The growth in actin filaments is capable of generating forces, which can deform the semiliquid plasma membrane. In lamellipodia and filopodia, the development of membrane protrusions is due to the balance of forces on the membrane: the membrane resistance (which is constant) and the pushing forces from the growing of the cortical actin. That protrusion force is the balance between the polymerization of actin at the barbed ends, and the retrograde flow due to the action of myosins and treadmill movement of the actin. The actin filaments can push the membrane so that the actin network growth counteracts retrograde flow including through the network to the anchor extracellular matrix *through* integrins (the transmembrane receptors, that link the cell with the ECM fibers, see Chapter 1.5) and their cytoplasmic partners (Figure 2.4). This anchoring is called *clutch* and



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involves talin (important component of the adhesion site) (Jiang et al., 2003; Giannone et al., 2009) (Chapter 3.5). Dendritic cells (Renkawitz et al., 2009) can migrate dependently or not on the integrins are able to compensate the increases in the retrograde flow and slip due to disengagement of integrins by an increase in the polymerization rate, keeping a speed of protrusion and a constant shape. That is not the case for fibroblasts migrating via integrin-dependent mechanism only.

The actin cytoskeleton builds the cell architecture, organization and cell neurites but the actin fibers are not alone in this network.

2.5.1. Cortical actin

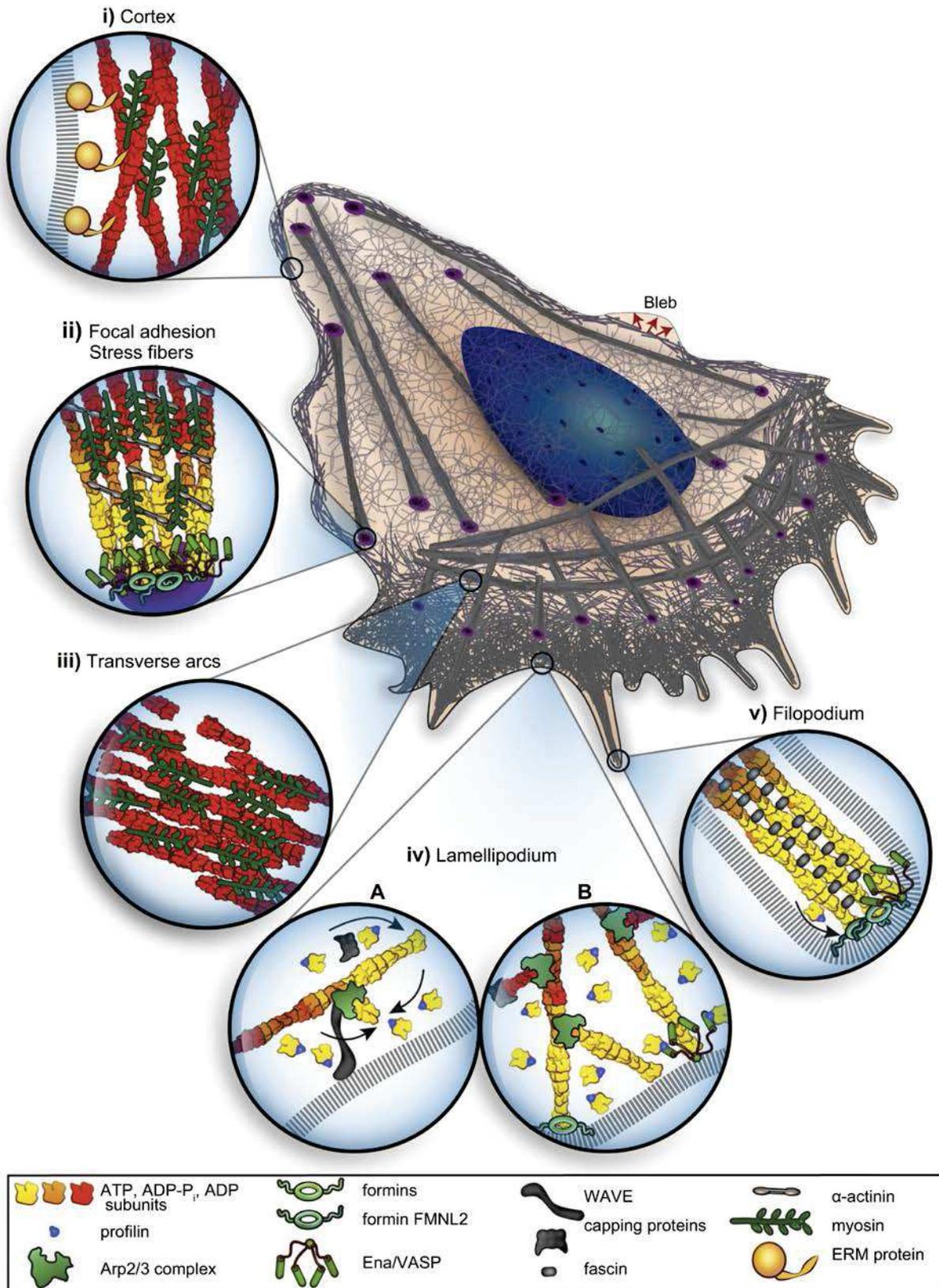
The plasma membrane is closely related to the cellular cortex composed of an actin network, myosins superfamily proteins and membrane associated proteins. The myosin keeps the cortical actin under tension and applies hydrostatic pressure on the cytoplasm. Sometimes the plasma membrane detaches from the cortex and the cytoplasmic pressure causes a bulging of the membrane, forming a hemispherical bubble-like protrusion, called bleb. The assembly of a new actin cortex in the bubble and the activation of actin by myosin allows the retraction of this bubble. In cells that use amoeboid migration, there is a polarized formation of such bubbles in the direction of cellular movement, but the molecular mechanisms involved are still poorly understood (Charras and Paluch, 2008; Mulay et al., 2016).

2.5.2. Stress fibers – ventral (classical) SF, transverse fibers, and dorsal fibers

Stress fibers are contractile structures of actomyosin found in many non-muscular cell types. Numerous antiparallel actin filaments, cross-linked by bridges of α -actinin and by non-muscular myosins II, constitute them. The latter contract the filaments relative to one another continuously (and not discontinuously and induced like the muscular myosins) but not uniformly over the entire fiber.



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There are three categories of stress fibers (Lee and Kumar, 2016) (Figure 2.4): the ventral fibers, connected at each end to focal adhesion, the dorsal fibers connected at one end to a focal adhesion and on the other to the transverse fibers or arcs, which constitute the third category of fibers. Ventral fibers are responsible for changes in cell shape due to an increase in internal tension, such as the formation of the retraction tail in mesenchymal cell migration. During this cell migration, the transverse arcs are derived from the front edge towards the center of the cell, and the retrograde flow of actin is due in part to their contraction. This contractile force is transmitted to the substrate via the dorsal fibers (Hotulainen et al., 2006; Naumanen et al., 2008).

The formation of stress fibers increases with the rigidity of the extracellular matrix and the contractile state of the stress fibers is in equilibrium with the adhesion forces and the resistance to deformation of the cellular environment.

Figure 2.4. Actin organization in vivo.

Migrating cells have specific differentiated organization of the actin filaments in the different subcellular regions, responsible for distinct functions. The actin cortex is attached to the plasma membrane via ERM proteins and contracts via myosin motors.

One category of contractile fibers – the ventral stress fibers are parallel to the ventral PM and normally are organized along the direction of the movement. They connect with the PM via focal adhesions. They are also crosslinked and contracted by myosin motors. Transverse arcs are also antiparallel and are found in the front part of the cell, just after the lamellipodium. They are also contractile, but are not connected to the focal adhesions. In the cell front the lamellipodium consists of quickly reorganized huge branched actin network; initiation of the branched network comes from activated Arp2/3 complex, attaching to an already existing filament and with the help of the proteins of WAVE family. Extension of the network comes through addition of profilin/actin complex (black arrows). Ena/VASP complex, the formin FMNL2 and capping proteins are antagonizing to control the elongation of the actin network by modulating the growing of the filament's barbed end (right zoom). While Ena/VASP and FMNL2 promotes the elongation of the network, the capping proteins stall it.

The sensory organelles – filopods are packed with parallel actin filaments, also elongated by Ena/VASP and FMNL2 and crosslinked with fascin. Adapted from Blanchoin, et al., 2014.



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2.5.3. Contractile actomyosin network

Myosins constitute a large family of molecular motor ATPases, capable of interacting with the actin filaments and generating tension between these filaments. Most of the myosins have three structural domains: a head that interacts with actin and hydrolyzes ATP to move along the filaments, an arm (or neck) on which light regulatory chains can attach, and a tail that allows interaction with other myosins to form filaments or with cargo molecules.

Based on phylogenetic criteria, 28 classes of myosin have been described in the animal kingdom (Hodge and Cope, 2000). The most ubiquitous class in non-muscular myosin class II.

Myosin II is composed of three pairs of peptides: two heavy chains of 230 kDa, two 20 kDa light chains regulating myosin activity (RLC or MLC) and two essential 17 kDa light chains that stabilize the structure of heavy chains (Figure 2.5A). The assembly of the myosins between them by the helical domain of the heavy chains allows the formation of the bipolar filaments of myosins. The non-muscular myosin II is evolutionary older and more diverse than the muscular myosins. The structures that these myosins form are more diverse, much less specialized than the sarcomeric repeats that are characteristic for the striated muscles. For NM decorated stress fibers is characteristic very variable frequency and amplitude of contraction which might stem from different affinity for actin crosslinker and other ABPs that can modulate the dynamics and restructuring of the actin network leading to increased turnover.



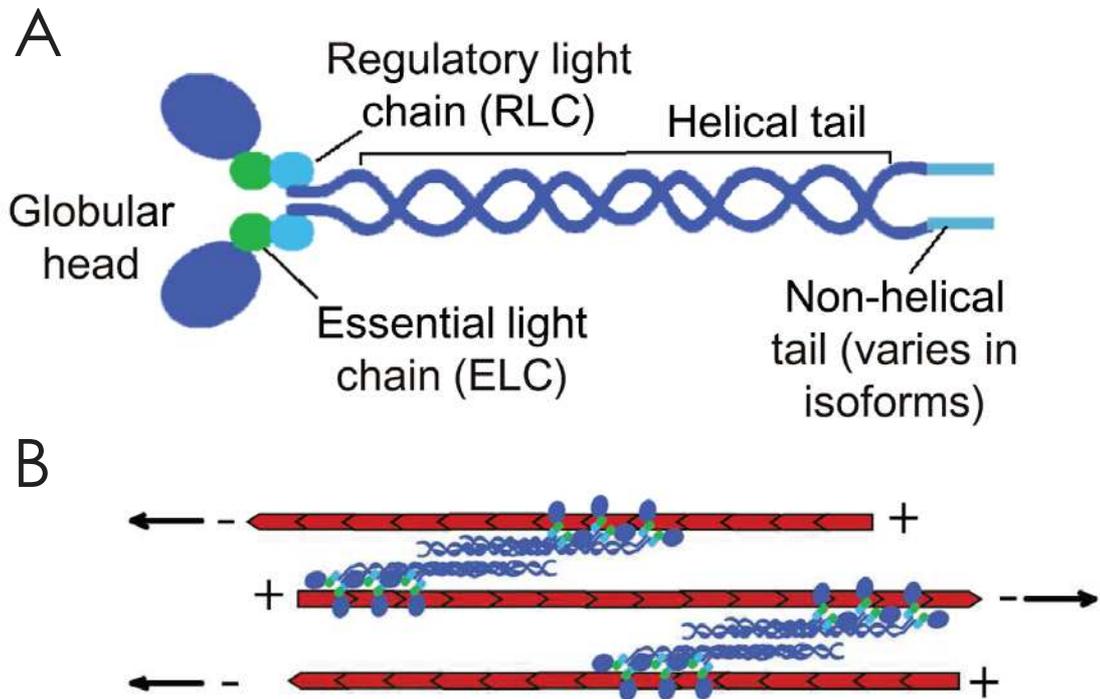


Figure 2.5. Myosin filament structure. Myosin is composed of two heavy chains, each consisting of a globular head and a tail, two essential light chains, and two regulatory light chains. The non-helical tail region varies in the three isoforms.
 A. Schematic representation of the main components of the myosin complex.
 B. Model of the contraction of acto-myosin fiber. Adopted from Lee et al., 2016.

2.5.4. Regulation by phosphorylation of MLC or MHC

The regulation of the formation of the myosin filaments and their ATPase activity depend on the phosphorylation of certain amine residues of the regulatory light chains and the heavy chains.

✪ The regulation by phosphorylation of the light chains (MLC)

The phosphorylation of serine 19 increases the ATPase activity of myosin in the presence of actin by controlling the conformation of the myosin heads, but this phosphorylation does not affect myosin affinity for actin. Following phosphorylation of threonine 18 further enhances myosin's enzymatic activity.



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Finally, it has been shown in vitro that phosphorylation of the light chain inhibits the intramolecular interaction of myosin and promotes both the formation of myosin bipolar filaments comprising between 14 and 20 molecules and the interaction of these filaments with the actin filaments. There are several kinases capable of phosphorylating the regulatory light chain (Figure 2.5B). The most well-known are MLCK (myosin light chain kinase) and ROCK (Rho-associated, coiled-coil containing protein kinase) which act on serine 19 and threonine 18. MLCK is activated by calmodulin-Ca²⁺ and is rather localized in the cellular periphery. ROCK is activated by the small RhoA GTPase protein; It can act not only on MLC but also on other substrates such as the myosin phosphatase (MLCP) subunit MYPT-1 (myosin phosphatase targeting protein); Finally, ROCK is located more centrally than active MLCK in cellular periphery (Totsukawa et al., 2000, 2004). MLC may also be phosphorylated by PKC (protein kinase C) at serine 1, 2 and threonine 9, which decreases the affinity of MLCK for MLC and thus decreases myosin activity.



The regulation by phosphorylation of the heavy chain

The phosphorylation of heavy chains favors the dissociation of myosin filaments or inhibits their formation in vitro. There are several C-terminal phosphorylation sites recognized by different kinases such as PKC or Casein kinase II (CK II) (Dulyaninova et al., 2005; Even-Faitelson and Ravid, 2006). These sites are different according to the isoform of the heavy chain. Phosphorylation can affect the subcellular localization of myosin IIA or the binding of the protein S100A4 (or MTS1), a protein known for its involvement in the metastatic invasion of cancer cells (Dulyaninova et al., 2005; Li and Bresnick, 2006).



The regulation of the activity of myosin by drugs

The ATPase activity of myosin can be artificially blocked by blebbistatin. Its activity can also be indirectly controlled via inhibition of regulatory light chain



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phosphorylation (MLC) either by inhibiting ROCK by Y27632 or by inhibiting MLCK by ML7.



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Chapter 3. Cellular adhesions as actomyosin -dependent anchorages

Cellular adhesive machinery is responsible for cells to sense biochemical and physical properties of the microenvironment and to adapt cellular response through force transmission. It is therefore important to identify molecular actors to elucidate the organization and regulation of the macromolecular structures involved in cell adhesive machinery. Recent proteomic studies have shown that the adhesome consists of 232 molecules, including integrins, various actin regulators, adaptor proteins that link cytoskeletal structures to the cytoplasmic tails of integrins and multiple signaling molecules (Riveline et al., 2001; Zamir et al., 2000a; Byron et al., 2010; Danen et al., 2002; Schiller et al., 2013).

3.1. Integrins marshal cell adhesion and the subsequent signaling

Integrins are major receptors of cell adhesion to the extracellular matrix. They were discovered in the 1980s and the term "integrin" comes from the fact that this family of receptors plays a major role in the integration between the cytoskeleton inside the living cell and the extracellular matrix (Hynes, 2002).

The first gene of the integrin family was cloned in 1986 – the chicken $\beta 1$ integrin (Tamkun et al., 1986). In three decades, more than 49,000 papers on the subject of the integrins have been published and they remain a vast subject of study.

Integrins form heterodimers composed of one of the 18 α - and one of 8 β subunits, that associate non-covalently with one another. Of the theoretically possible 144 associations, only 24 heterodimers are detected. The integrins can be grouped into subfamilies according to their composition: the subfamily of $\beta 1$ integrin (11



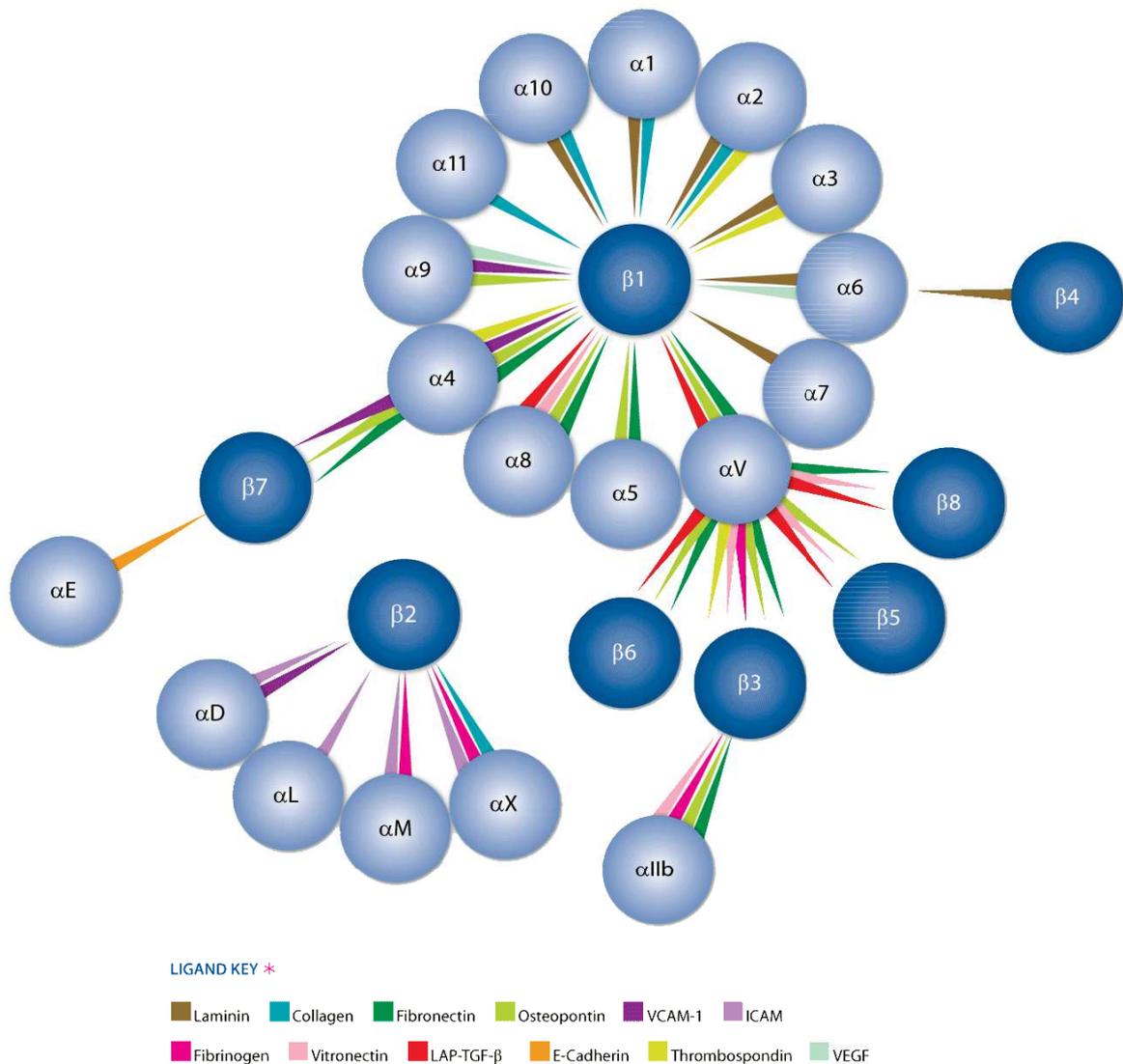


Figure 3.1. The integrin family contains 24 heterodimers in vertebrates. The principal matrix ligands with an RGD motif are fibronectin and vitronectin. The arrows, connecting α and β integrins represent the ECM ligand that this heterodimer will bind. Ref – R&D systems – a bio techie brand.

members), the subfamily of $\beta 2$ integrins (4), of αV integrins (5), etc., or according to the nature of their matrix ligand (Figure 3.1): ligands with the RGD sequence are recognized by 8 integrins, mainly $\beta 1$ and $\beta 3$ integrins. These can also recognize the collagen RGD sequence and certain laminins when this sequence is exposed following denaturation or proteolytic cleavages of these ligands. Native collagen



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is recognized via the GFOGER sequence by four integrin receptors, containing integrins $\beta 1$. Their ability to interact depends also of the multi-molecular organization of collagen into fibrils. Some integrins can have several isoforms due to an alternative splicing, so this further increases the diversity of the integrin family. Not all subunits are expressed in all cells (Barczyk et al., 2010). The integrin repertoire of expression is dynamic, it changes during development and is highly modified in response to micro-environment conditions. Sometimes, the expression of a particular isoform is specific to a cell type or a state of differentiation. This integrins repertoire of attributes the cells both with a specificity of binding to the matrix and a signature of differentiation.

For examples, the cells expressing integrins $\beta 2$ or $\beta 7$ are part of the leukocyte lineage; integrin $\beta 1$ isoform D is cell-specific to the skeletal muscle tissue. The expression of certain integrins may also depend on of the physical properties of the cellular environment (Elosegui-Artola et al., 2014). The integrin expression of $\beta 1$ increases transiently when applying mechanical stress to chondrocyte progenitor cells and remains higher in stressed cells than in the control cells – where the pressure is applied. Contrarily the expression of integrin $\alpha 5$ is not modulated by the mechanical tension (Takahashi et al., 2003).

3.2. Physiological role

Integrins are involved in many processes from embryogenesis and during adult life and their deregulation or mutation may cause more or less severe pathologies. Although there is a redundancy between integrins for recognition of extracellular ligands, (Figure 3.2), they do not have the same affinity for a particular ligand, they are not all expressed in the same cells and they induce different signaling pathways, depending on their specific cytoplasmic partners.

The physiological importance can be underlined by the associated pathologies and by the effect of their gene inactivation in the mouse animal model. The 26



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integrin genes have been inactivated separately, some of these inactivations are lethal at the embryonic and perinatal stages. For some genes, double inactivation was also achieved. So mice $\alpha 5^{-/-}; \alpha V^{-/-}$ die 8 days after fertilization (E8), which corresponds to the gastrulation stage: the absence of the major fibronectin receptors blocks the formation of the anterior mesoderm, while the single inactivation are lethal later (E10, E12 - birth respectively). This shows that the compensation between integrins is partly possible. To better understand the importance of integrins whose gene inactivation is lethal in the embryonic stages,



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Adaptor protein	Integrin to which adaptor binds	Reference
Structural adaptors		
α -actinin	$\beta 1, \beta 2, \beta 3$	(Otey et al., 1993; Pavalko and LaRoche, 1993)
BP180	$\beta 4$	(Koster et al., 2003; Schaapveld et al., 1998)
Filamin	$\beta 1, \beta 2, \beta 3, \beta 7$	(Calderwood et al., 2001; Kiema et al., 2006; Loo et al., 1998; Pfaff et al. 1998; Sharma et al., 1995; Travis et al., 2004; Zent et al., 2000)
Myosin	$\beta 1, \beta 3, \beta 5$	(Jenkins et al., 1998; Sajid et al., 2000; Zhang et al., 2004)
Plectin	$\beta 4$	(Geerts et al., 1999)
Skelemin	$\beta 1, \beta 3$	(Reddy et al., 1998)
Talin	$\beta 1, \beta 2, \beta 3, \beta 5, \beta 7$	(Calderwood et al., 2003; Calderwood et al., 1999; Patil et al., 1999; Pfaff et al., 1998; Sampath et al., 1998)
Tensin	$\beta 1, \beta 3, \beta 5, \beta 7$	(Calderwood et al., 2003; McCleverty et al., 2007)
Scaffolding adaptors		
14-3-3	$\beta 1, \beta 2, \beta 3$	(Fagerholm et al., 2005; Han et al., 2001)
$\beta 3$ endonexin	$\beta 3$	(Eigenthaler et al., 1997; Shattil et al., 1995)
CD98	$\beta 1, \beta 3$	(Zent et al., 2000)
Dab1	$\beta 1, \beta 2, \beta 3, \beta 5, \beta 7$	(Calderwood et al., 2003)
Dab2	$\beta 3, \beta 5$	(Calderwood et al., 2003)
Dok1	$\beta 2, \beta 3, \beta 5, \beta 7$	(Calderwood et al., 2003)
Fhl2	$\beta 1, \beta 2, \beta 3, \beta 6$	(Wixler et al., 2000)
Fhl3	$\beta 1$	(Samson et al., 2004)
Grb2	$\beta 3$	(Blystone et al., 1996; Law et al., 1996)
IAP	$\beta 3$	(Brown et al., 1990)
JAB1	$\beta 2$	(Bianchi et al., 2000)
Kindlin 2	$\beta 1, \beta 3$	(Ma et al., 2008; Montanez et al., 2008)
Kindlin 3	$\beta 1, \beta 3$	(Moser et al., 2008)
Melusin	$\beta 1$	(Brancaccio et al., 1999)
Numb	$\beta 3, \beta 5$	(Calderwood et al., 2003)
Paxillin	$\beta 1, \beta 3$	(Chen et al., 2000; Schaller et al., 1995)
Rack1	$\beta 1, \beta 2, \beta 5$	(Liliental and Chang, 1998)
Shc	$\beta 3, \beta 4$	(Dans et al., 2001; Law et al., 1996)
TAP20	$\beta 5$	(Tang et al., 1999)
WAVE1	$\beta 7$	(Rietzler et al., 1998)
Catalytic adaptors		
Src	$\beta 3$	(Arias-Salgado et al., 2003; Arias-Salgado et al., 2005)
Yes	$\beta 1, \beta 2, \beta 3$	(Arias-Salgado et al., 2005)
Cytohesin 1	$\beta 2$	(Kolanus et al., 1996)
Eps8	$\beta 1, \beta 3, \beta 5$	(Calderwood et al., 2003)
ERK2	$\beta 6$	(Ahmed et al., 2002)
FAK	$\beta 1, \beta 2, \beta 3, \beta 5$	(Chen et al., 2000; Eliceiri et al., 2002; Schaller et al., 1995)
Fyn	$\beta 3$	(Arias-Salgado et al., 2005)
ILK	$\beta 1, \beta 3$	(Hannigan et al., 1996; Pasquet et al., 2002)
Lyn	$\beta 1, \beta 2, \beta 3$	(Arias-Salgado et al., 2005)
PKD1	$\beta 1, \beta 3$	(Medeiros et al., 2005; Woods et al., 2004)
PP2A	$\beta 1$	(Kim et al., 2004)
Shp2	$\beta 4$	(Bertotti et al., 2006)
Other adaptors		
ICAP1 α	$\beta 1$	(Chang et al., 1997; Zhang and Hemler, 1999)
MIBP	$\beta 1$	(Li et al., 1999)

Table 1. Adapter proteins that bind β -integrin cytoplasmic tail.



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organogenesis or adult physiology, conditional inactivation has sometimes been achieved. All these genetically modified animals are models for a number of human diseases such as *epidermolysis bullosa* ($\beta 4$ or $\alpha 6$), muscular dystrophies ($\alpha 2$, $\alpha 5$, $\alpha 7$), osteoporosis ($\beta 3$), leukocyte adhesion disability type I (LAD-I) ($\beta 2$, $\beta 7$ or αL), healing defects ($\alpha 3$, $\alpha 9$, αM or $\beta 3$), cancers. Tumor progression is associated with overexpression or deregulation of certain integrins (Keely et al., 1998; Guo and Giancotti, 2004; Desgrosellier and Cheresh, 2010). As an example, integrin $\alpha V\beta 3$ is associated with the formation of metastasis (Albelda et al., 1990); mutated integrin $\beta 1$ causes squamous cell carcinomas of the tongue (SCC4) (Evans et al., 2003); integrins $\beta 1$ seem important for metastasis and the loss of integrins $\beta 1$ encourages spread of cancer cells in the lymph nodes (Kren et al., 2007); tumor angiogenesis is controlled by integrin $\alpha 1$ and $\alpha 2$; over-expression of integrin $\alpha 5\beta 1$ increases the invasiveness of cells by increasing their internal contractility (Mierke et al., 2011).

3.3. The structure of the integrins

Integrins are transmembrane heterodimeric proteins. Each subunit has only one transmembrane domain. Integrin function depends on its activation state based on their conformational changes and state. The structure of several extracellular domains has been published. Most studied dimers are $\alpha V\beta 3$ integrin with or without interaction with their ligand (Xiong, 2001; Xiong et al., 2002; Takagi et al., 2002), $\alpha IIb\beta 3$ (Takagi et al., 2002) and $\alpha 5\beta 1$ complexed to fibronectin (Takagi et al., 2003) or $\alpha x\beta 2$ (Xie et al., 2010).

The extracellular domains of integrins have several conformations: a closed state where the interaction sites of integrins with their ligand is masked, an opened state where they are exposed and certainly many intermediate states (Xiong, 2001; Xiong et al., 2002; Hynes, 2002; Kinashi, 2005; Anthis and Campbell, 2011) (Figure 3.3).



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At least three domains have been described to be involved in the interaction with the extracellular matrix ligands. Two of these sites are present on the α subunit whose site I/A which is present only on 9 of the 18 α subunits. The structure of the site I/A has been crystalized - it is involved in the coordination of bivalent cations (Mg^{2+} , Mn^{2+}) through its MIDAS motif (metal ion-dependent adhesion site) and is vital for binding certain ligands (Lee et al., 1995; Emsley et al., 2000). The last site is on the β chains. They contain a MIDAS site and an adjacent site (ADMIDAS) involved in inhibitory binding of Ca^{2+} . The exchange between Ca^{2+} ion with Mg^{2+} ion at this site causes a change in conformation of the integrin and activates it. Finally, integrin heterodimer binding to the extracellular matrix is due to the combination of two subunits, but the specificity of interaction between the integrin and the ligand is mainly due to the subunit α . The transmembrane domains are connected by a saline bridge which is broken after binding of certain intracellular proteins (talin) on the cytoplasmic domain of the β integrin, allowing the conformational change of the extracellular part to the open, active form and the intramembrane dissociation of the two subunits (Ye et al., 2010) (Figure 3.2). Except $\beta 4$ integrin, the cytoplasmic tail of integrins is short (around fifty residues) and does not possess catalytic activity. They serve as platforms for numerous interactions, especially the β integrin, which have one or two NPxY (Asparagine-Proline-x-Tyrosine) interaction motifs to interact with PTB (phosphotyrosine binding) domains, contained in many proteins, which regulate the activation state of the integrins and the signaling pathways associated with them (Table 1).

3.4. Integrin associated complex

3.5.1. Extracellular ligands of integrins

A great diversity of ligands for integrin receptors and the greater or lesser specificity of α and β subunits have been largely documented including (Figure 3.3) matrix proteins (fibronectin, collagen, laminin, vitronectin ...), soluble ligands



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(angiostatin, fibrinogen, prothrombin ...) (Humphries et al., 2006) and other membrane receptors presented by the neighboring cells (A disintegrin and metalloprotease molecule - ADAM, intercellular adhesion – ICAM, etc.). The specificity of ligand-integrin interaction and the stabilization of the interaction are based on the two integrin subunits that generally recognize short peptides of which one of the key residues is an acidic amino acid.

The binding of many integrins to fibronectin occurs at the level of the RGD motif carried by the domain III 10 of the fibronectin (Pankov and Yamada, 2002). There is an axillary site called PHSRN site (proline-histidine-serine-arginine-asparagine) at the domain III9 that is called synergistic site, since it promotes a better fixation of the integrin $\alpha 5\beta 1$ to fibronectin (García et al., 2002; Friedland et al., 2009). This binding with the extracellular ligand causes a change in conformation and actually involves the integrins in the cellular signaling. This is called the outside-in signaling. Several proteomic and phosphoproteomic studies have been done in the recent years (Schiller et al., 2013; Robertson et al., 2015; Humphries et al., 2009a) which shed more light on the integrin interactome and provided data for more comprehensive modeling of the FA.

3.5.2. The associated cytoplasmic proteins of integrins

Many proteins interact with the cytoplasmic tails of the integrins (Anthis and Campbell, 2011).



Integrins engaged with ECM recruit a large number of proteins that modulate the link to the actin cytoskeleton. An initial compilation based on published literature identified 156 components of the “adhesome”, with 690 links (i.e. binding, activation, and inhibitory interactions) between the different components (Zaidel-Bar et al., 2007), though many more components within the adhesome have now been identified (Schiller et al., 2011a, 2013; Kuo et al., 2011; Ng et al., 2014). A more recent study combined the several proteomics datasets to create a “consensus-adhesome”, which identified 60 components that represents the core components of IACs, present

on all integrin ligand surfaces (Horton et al., 2015). Proteomic studies have given us insights into the complexities of IACs as signaling hubs. From the many FA proteins, nearly half of these are phosphorylated at adhesions (Robertson et al., 2015). On Figure 3.4 are presented typical MS analysis for isolated FA depending on their integrin content – only $\beta 1$ integrin, only $\beta 3$ integrin or both. There has been

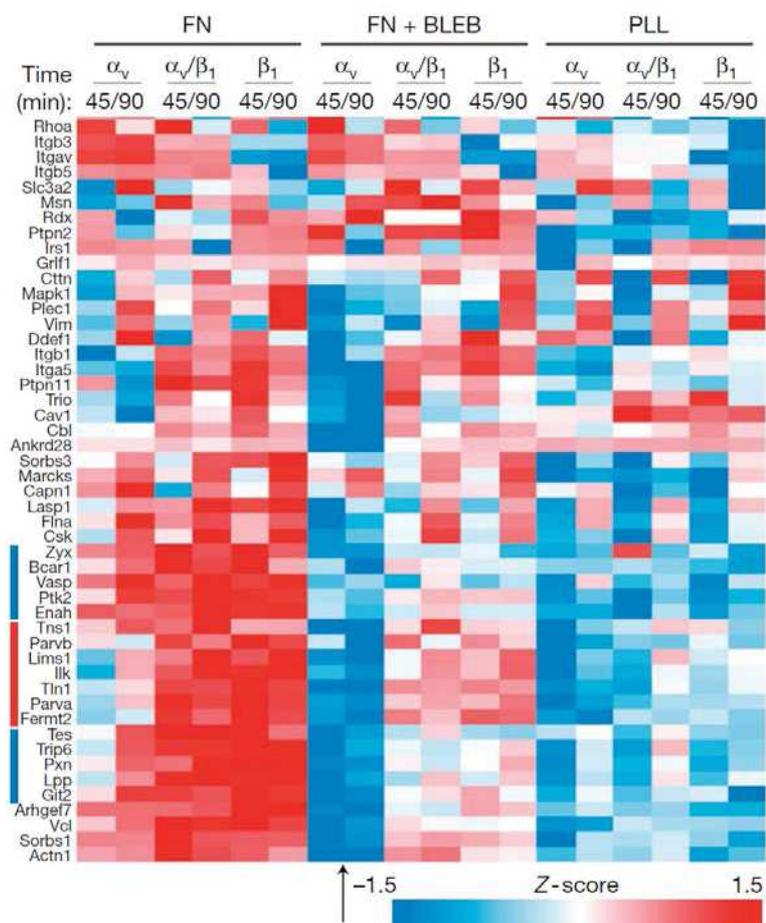


Figure 3.4. Focal-adhesion-enriched isolates analysed by MS before and after adding a contractile inhibitor blebbistatin. The Z -scores of median MS intensities are color coded to indicate the relative protein abundance. A blebbistatin-non responsive cluster is marked with a red line and blebbistatin-sensitive clusters are marked with blue lines (on the left of the protein names). FN – Fibronectin, PLL – poly-L-lysine. Adapted from Schiller et al., 2012.



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identified two subsets of phospho-proteins within IACs: some that are phosphorylated specifically

in response to integrin-ECM engagement, and others that are constitutively phosphorylated which are then recruited to IACs upon integrin-ECM engagement. Clearly, IACs are complex structures with a high degree of plasticity concerning their components. However, rather than being randomly organized, these proteins have a hierarchical structure.

Some proteins bind specifically to one or the other subunit (BP230, plectin, ICAP-1, etc.) while others bind to several subunits (α -actinin, talin, paxillin, etc.) (Figure 3.4). Some have a structural linking role between integrins and actin cytoskeleton or the cytoskeleton of the intermediate filaments while others have an intracellular signaling role with or without catalytic activity. Many studies have focused on the ability of some cytoplasmic partners to activate or inactivate integrins (inside-out) (Shattil et al., 2010). For example, talin is an important cytoplasmic adapter that activates integrin allowing its interaction with its extracellular ligand and with the actin cytoskeleton. ICAP-1, another cytoplasmic adapter, specifically maintains β 1 integrin in its inactivated form by competing with kindlin, a co-activator of talin. The filamin A is another negative regulator, its action is in competition with migfiline. The phosphorylation of the cytoplasmic part of integrins modifies their interactions with their partners. For example, phosphorylation of integrins on certain serines and threonines by protein kinase C inhibits interaction with filamin but does not alter the interaction with the talin, whereas the phosphorylation of the tyrosine of the NPXY by Src inhibits the attachment of talin but promotes that of filamin and angiotensin (Kiema et al., 2006; McCleverty et al., 2007; Oxley et al., 2008; Takala et al., 2008) (Figure 3.5).



Finally, integrin signaling requires coordinated spatial and temporal assembly and disassembly of multiprotein complex that stems from the cytoplasmic tails of mainly $\beta 1$ and $\beta 3$ integrins.

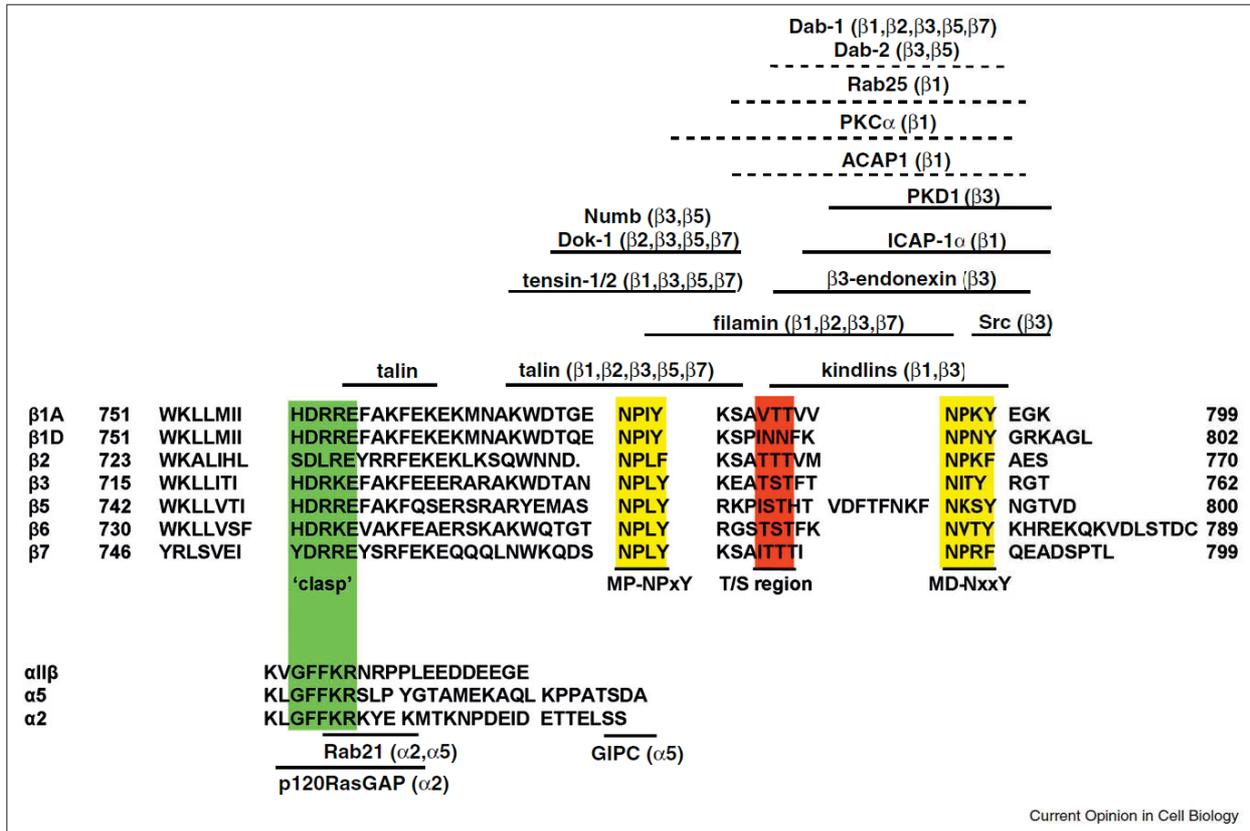


Figure 3.5. Direct integrin cytoplasmic tail partners. Interactions between integrin cytoplasmic tails and intracellular regulators modulates integrin activity and downstream signaling. This is a short summary of the direct integrin interactors, their sites of interaction on α - or β -tails, and their functional role by color. Conserved tail residues are displayed in uppercase; highly conserved residues are bolded. Extracted from Margadant et al., 2011.

3.5. Focal adhesion architecture

3.5.1. Nanoscale organization

The flawless distribution of the FA components is crucial for its proper function. Considering that the FA are relatively densely packed any change of the players inside or their ratio can lead to different cellular response. Using elegant multicolor



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super-resolution microscopy, that question have been addressed (Shroff et al., 2007). This study revealed that even though some adhesion protein might appear co-localizing via conventional fluorescence microscopy they are indeed specially differentiated as distinct nanoclusters. Recently similar data were obtained for integrins $\beta 1$ and $\beta 3$ – both residing in the FA, but forming separate homoclusters at nanoscale with their own separate dynamics (Rossier et al., 2012). 3D iPALM super-resolution study showed that vertical organization of FA is also highly regulated and structured (Kanchanawong et al., 2010). The authors describe a layer of 40 nm between the short integrin tails and the actin filaments. That layer contains number of signaling proteins like FAK and paxillin, intermediate layer containing talin and vinculin and the upper, closer to the F-actin layer, accommodating zyxin and α -actinin.

That spatial segregation of protein interaction can mean that their activity is also temporarily regulated due to dynamic nature of the FA and depending on its maturity. This unorthodox spatial segregation of particular proteins and therefore protein interactions into distinct nano-clusters can prove to be efficient way to regulate spatially but also temporally protein activity. With the maturation of the FA can be expected that these interaction will also evolve since FA maturation is associated for instance with increased interactions of α -actinin in competition with talin for β -integrin tails (Roca-Cusachs et al., 2013). Importantly the mechanical cues transmitted via the adhesion structures could also regulate the in time and space the probability of specific protein interaction as force can distort some mechano-responsive proteins and expose cryptic binding sites as is the case for talin (Liu et al., 2015) (Figure 3.6).



3.5.2. Dynamics at nanoscale

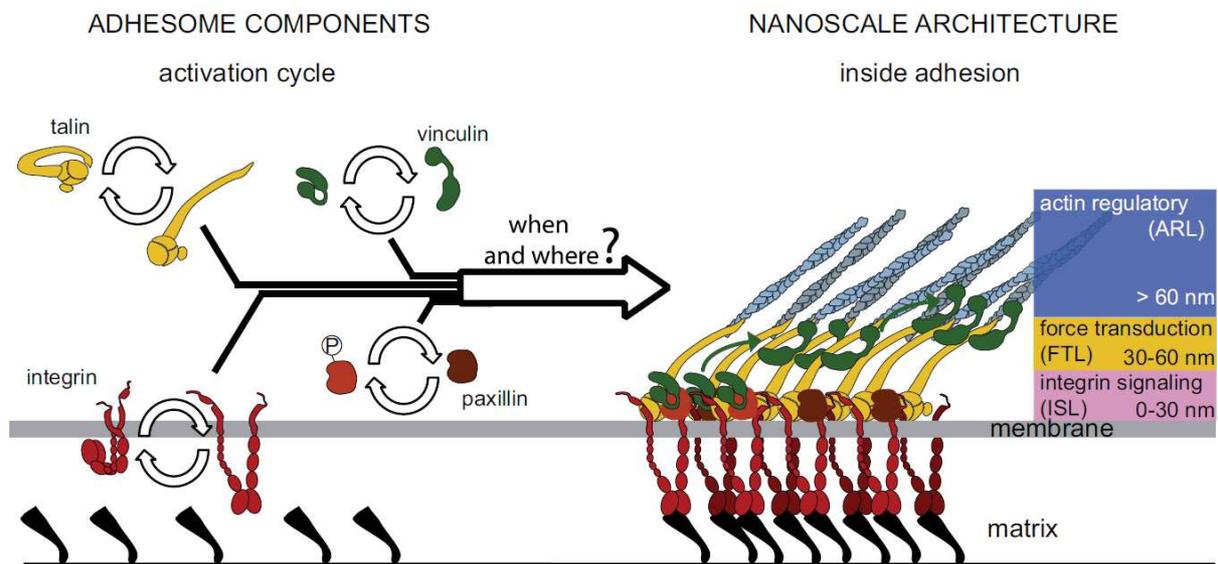


Figure 3.6. Nanoscale organization of FA. FA structure have been exposed by recent high-resolution microscopy techniques as 3D layers, containing specific proteins with specialized functions. The first layer – the integrin signaling layer (in pink) holds the integrin cytoplasmic tails and their immediate partners – FAK and paxillin. The intermediate force transduction layer (yellow) contains the mechanosensitive proteins talin and vinculin, and the upper actin regulatory level (in blue) is composed from α -actinin and zyxin. In addition, the proteins of the adhesome undergo cycles of activation and inactivation via different manners (conformation, phosphorylation, mechanical stretching, etc.) that can be responsible for their location or the recruitment inside FA. Adapted from Rossier et al., 2016.

Crystallographic data indicates that integrins can adopt different conformation (Zhu et al., 2008b) (Chapter 3.1). The shift between different states regulates the binding (and detachment) of different integrin partners. Low resolution dynamics of FA and more specifically integrins have been performed using FRAP (Ballestrem et al., 2001a), but it stays only dynamical measurements on large ensemble of molecules with low spatial resolution. FRAP data reveal the so-called immobile fraction – proteins that do not recover their fluorescence in time. Inside that pool is hidden the real dynamics of single molecules interacting inside the borders of FA. Using single particle tracking (SPT) (Wiseman et al., 2004; Brown et al., 2006;



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Bachir et al., 2014). This is special kind of fluorescent microscopy that detects macromolecular assemblies inside FA that form fluorophores clusters – speckles. The mobility of these spots can be measured in various conditions. In the case of membranous receptor like integrins several studies have been carried out monitoring their interaction with ECM ligands (Rossier et al., 2012; Cairo et al., 2006; Rossier and Giannone, 2016). The ability to follow single (or very few) integrins allows for registering the transition between their activation states. It has been reported (Shibata et al., 2012; Leduc et al., 2013; Rossier et al., 2012) that integrins are capable to enter freely FA by diffusion and perform several cycles of activation (immobilization) and deactivation (free diffusion) before exiting FA. These studies show that most integrins inside FA are not always attached to actin cytoskeleton.



Chapter 4. Cell adhesion dynamics

Cell adhesion of a single cell is a very dynamic process resulting from the coordination between adhesion sites (focal adhesions) and cytoskeleton as illustrated by cell spreading and cell migration. Cell migration and cell spreading are driven by integrin-mediated focal adhesions (FAs), protein assemblies that couple contractile actomyosin bundles to the plasma membrane, transmit force generated by the cytoskeleton to the ECM, and convert the mechanical properties of the microenvironment into biochemical signals, a process called mechanotransduction. The establishment, maintenance and dynamics of these structures during the steps of cell spreading or cell migration are highly regulated (Cavalcanti-Adam et al., 2007). There are three basic components contributing to force on the ECM at an FA: (1) myosin II, which produces force on (2) actin filaments, which act as a conduit of the force to (3) FA proteins and integrins, which comprise the linkage between actin and the ECM through the plasma membrane. Dynamic changes in assembly/disassembly, activity, or protein-protein interactions within any of these three components could be responsible for mediating the fluctuations in force transmission seen in FA (Plotnikov et al., 2012).

4.1. The stages of cell spreading

The spreading of cells on hard substrate is a complex model for understanding the mechanisms associated with cell adhesion dynamics, which are crucial for cell migration and force balance. The spreading of cultured fibroblasts on rigid surfaces proceeds in two distinct stages: radial spreading followed by cell polarization important for cell migration. Cells drastically reorganize their cytoskeleton during this extremely dynamic process. The main visible feature is the increased surface area of contact between the cells and the extracellular matrix



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that is accompanied by a significant flattening of the cell body and an increase of the total surface of the plasma membrane by exocytosis(Gauthier et al., 2009). There are two modes of cell spreading: an isotropic and anisotropic way(Dubin-Thaler et al., 2004). The anisotropic mode shows greater fluctuations in the transient and stochastic membrane edges and an increase in the contact

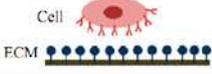
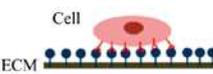
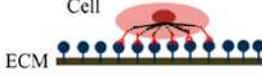
Cell Adhesion Phases	Phase I	Phase II	Phase III
Schematic diagram of cell adhesion			
Schematic diagram of the transformation of cell shape			
Cell adhesion intervention	Electrostatic interaction	Integrin bonding	Focal adhesion
Adhesion stages	Sedimentation	Cell attachment	Cell spreading and stable adhesion

Figure 4.1. Characterizing of the adhesion stages. The spreading surface increases (Phase I) following the inhibition of the internal contractility (Phase II) allowing the protrusions to grow (Phase III), then the cell stabilizes its shape by strengthening the contacts and the tensile forces with the substrate. While the talin do not seem to be necessary for the first two phases of spreading, it is essential for the tensioning of the cells. Adapted from Khalil et al., 2015.

area, which is less rapid than in the isotropic mode. For the isotropic mode, the analysis of the spreading surface over time helped to identify three phases(Doebereiner et al., 2004) (Figure 4.1).

4.1.1. Initial phase

During the initial phase, the cell comes into contact with the matrix. Binding of integrins to the active matrix activates Rac1 pathway and decreases the cortical contractility *via* a decrease in the ROCK pathway. This promotes cell spread that allows new interactions between the matrix and other integrin molecules.



4.1.2. The intermediate phase

The intermediate phase of rapid expansion is linked to the formation of large lamellipodes where the polymerization of the actin filaments is important and allows the protrusion of the plasma membrane.

4.1.3. During the stabilization phase

During the stabilization phase, the cell develops specific adhesion with the matrix and testing the rigidity of the microenvironment via cytoskeletal contraction cycles at the maturing adhesions (Giannone et al., 2004, 2007). The establishment of cellular polarity depends on the spatial coordination between the microtubule organization and the contractility of the actomyosin network.

4.2. Cell migration

Cell migration is a phenomenon involved in many physiological processes (embryogenesis, inflammatory response, wound healing) and pathological (cancer, arthritis, atherosclerosis, osteoporosis). Cell migration is the dynamic and complex result of interactions between the organization and the contractile state of the cytoskeleton, the dynamics of adhesions between cells and the extracellular matrix, vesicular traffic and cellular polarity. This requires integration and temporal and spatial coordination of many subcellular processes. In the case of collective migration, the dynamics of the intercellular junctions are added to this complexity. In this introduction only the migration of isolated cells will be addressed.

In the wide range of the observed cellular forms, two main types of isolated migration have been described: mesenchymal migration of keratocytes and fibroblasts and amiboid migration of neutrophils with reference to the cellular movements of amoebae, the unicellular protozoa.



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4.2.1. Mesenchymal migration

Mesenchymal migration was mainly described on observations of cells evolving in a 2D environment but is now also much studied in 3D matrices, due to the involvement of fibroblasts as lead cells in the collective migration of metastatic cells. The migratory cycle was divided into four stages: protrusion, adhesion, traction and retraction. Initially, the polymerization of the dense actin network pushes the plasma membrane forward, thus forming a thin lamellipode oriented in the direction of migration. In a second step, the protrusion adheres to the extracellular matrix by forming nascent adhesions at the front of the lamellipod. Some of them will mature in focal adhesions and will be translocated to the rear base of the cell. Stress fibers are organized from these focal adhesions and connect them to the focal adhesions of the back of the cell. Thirdly, the contraction of these stress fibers reinforces the adhesions at the front, weakens those at the back and causes the cell body to move forward. Finally, the adhesions at the back are detached allowing the back membrane to retract (Figure 4.2 and 4.3) (Gupton and Waterman-Storer, 2006; Mogilner and Keren, 2009; Friedl and Wolf, 2003; Parri and Chiarugi, 2010; Parsons et al., 2010; Scales and Parsons, 2011). At the lamellipodia located at the front of the cell, protrusion-retraction cycles are observed. During these cycles, myosin pulls the lamellipodial actin network backwards, causing a retraction of the leading edge and initiation of new adhesion sites. The network of actin, condensed by myosin, is detached from the front. The polymerization of a new actin network pushes the membrane forward creating a new protrusion. The introduction of a new myosin cluster at the migration front initiates a new retraction-protrusion cycle (Giannone et al., 2007). This migration is slow (0.1 to 1 $\mu\text{m}/\text{min}$) and is characterized both by significant



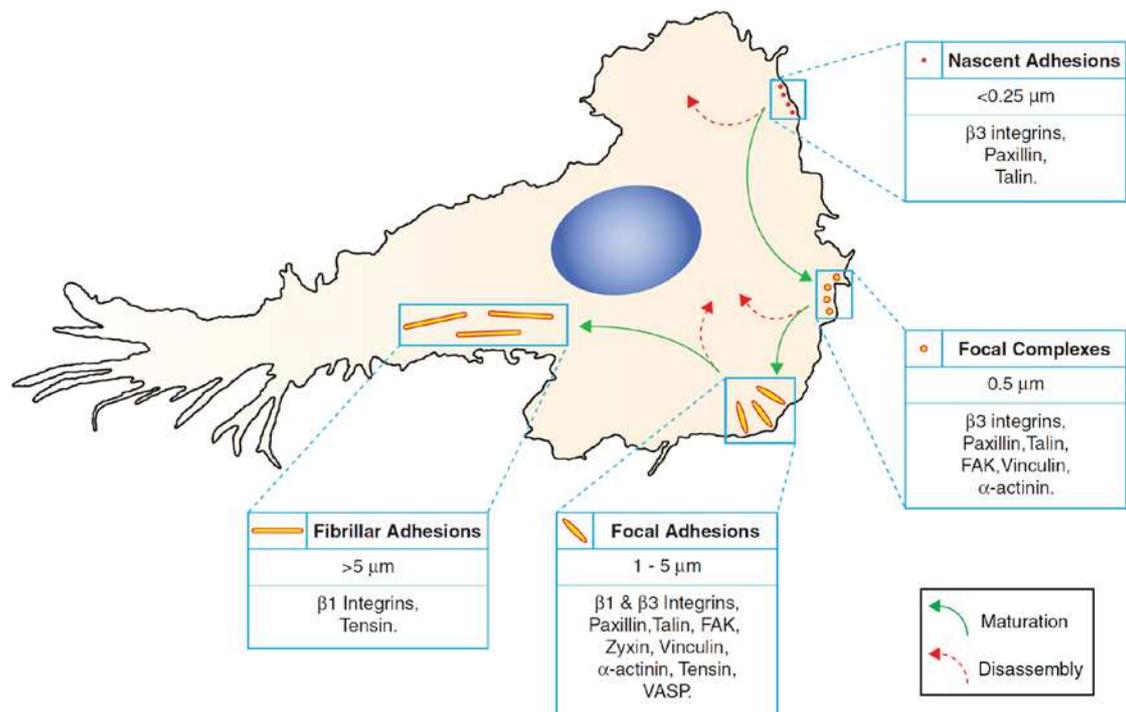


Figure 4.2. Typical representation of cell-matrix adhesions during mesenchymal cell migration. Outlined are the nascent adhesions, the focal complexes, focal adhesions and the fibrillary adhesions and their evolution – assembly in green arrows and disassembly in red arrows. Also, size and known partners are represented. Adapted from Scales and Parsons, 2011.

antero-posterior cell polarization and by a strong dependence on the dynamics of cell-extracellular matrix adhesions, in particular the family of focal adhesions required for the development of traction forces (Friedl and Wolf, 2003). The adhesion dynamics are controlled by the balance between the Rho-GTPase RhoA - of the lamellum at the back of the cell that promotes the maturation of focal adhesions and stress fibers - and Rho-GTPase Rac1 - in the lamellipodia, which promotes the dynamics of nascent adhesions and the polymerization of actin in a dense lattice (Figure 4.2). Moreover, a recent more detailed study of the spatio-temporal localization of the activity of RhoA, Rac1 and Cdc42 proteins at the front edge of the cell allowed us to show another spatial-temporal coordination between these small GTPase proteins, Initiation or stabilization of



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protrusions (Machacek et al., 2009). There is therefore a spatial control of the activation of RhoA and Rac1 to allow directional migration (Parri and Chiarugi, 2010).

4.2.2. Amoeboid migration

Amoeboid migration is mainly studied in 3D. It is less dependent on cell adhesions-extracellular matrix involving integrins than mesenchymal migration and is independent of matrix metalloproteases. Amoeboid migration is poorly directional, but can reach high displacement rates (0.1-20 $\mu\text{m} / \text{min}$) (Friedl and Wolf, 2003). On the other hand, it is highly dependent on the ROCK contractility pathway (Figure 4.3) and is characterized by propulsion movements. Two modes of amoeboid migrations are distinguished: the pseudopodial protrusive mode and the so-called blebby contractile mode due to the presence of membrane

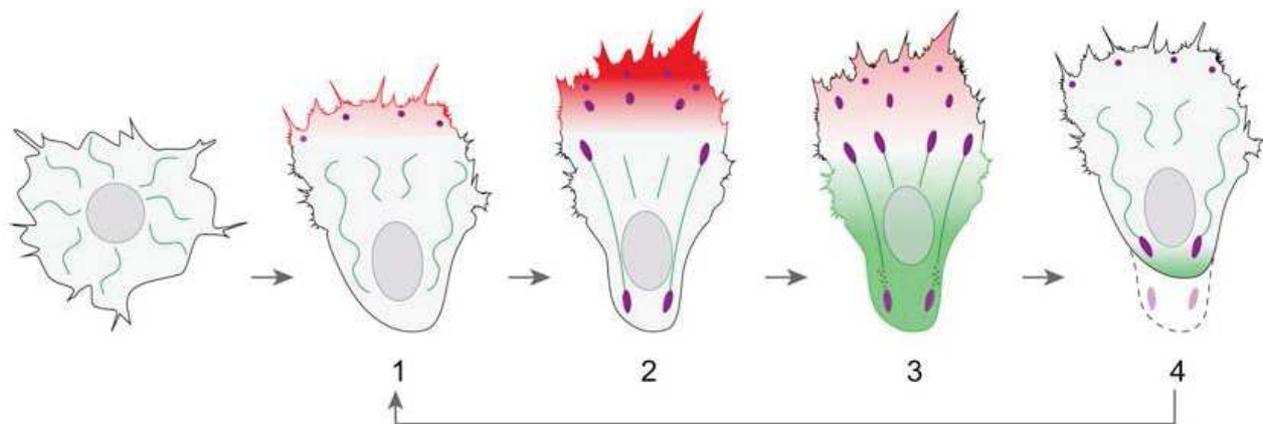


Figure 4.3. Acto-adhesive events during cell migration in culture. Obvious are actin polymerizing events (red), substrate adhesive events (focal adhesions in purple) and the myosin II dependent events (contraction of the cytoskeleton in green). Cells moving on 2D surfaces undergo repeated steps of: (1) extension of the leading edge and formation of immature cell-substrate adhesions; (2) maturation of cell-substrate adhesions; (3) forward translocation of the cell body; and (4) disassembly of focal adhesions coupled to retraction of the rear edge. Adapted from Reig et al., 2014.

bubbles (bleb). There are also models of amoeboid migration in two-dimensional cell environments (Renkawitz et al., 2009). There is a balance between the



adhesive forces due to the interaction between the cell and its support, protrusive forces due to actin polymerization, and internal contractile forces due to actomyosic activity (Lämmermann et al., 2008). Depending on the balance between these types of forces, amoeboid migration will be more or less protrusive or contractile (Renkawitz et al., 2009).

4.3. Growth and maturation of cell adhesion: membership structures

Focal adhesions are mainly observed *in vitro* on cells grown in 2D media. Their existence *in vivo* or 3D *in vitro* is debated, but recent papers (Kubow E. Kristopher et al., 2011; Fraley et al., 2010) show that that these adhesions do exist and can be visualized in cells in 3D matrices. All focal type adhesions have a connection to the actin cytoskeleton, which is, oriented parallel to the membrane in contact with the substrate. The earliest adhesions are called nascent adhesions (sometimes referred as focal complexes). They will dissociate or mature into focal complexes. During cell spreading, some of these complexes will fuse and mature into larger sized adhesions called focal adhesions that can develop into fibrillar adhesions (Figure 4.4).

In migrating (mesenchymal) cells, nascent adhesions form at the front of the lamellipodia-like protrusions. They can either disassemble or elongate at the



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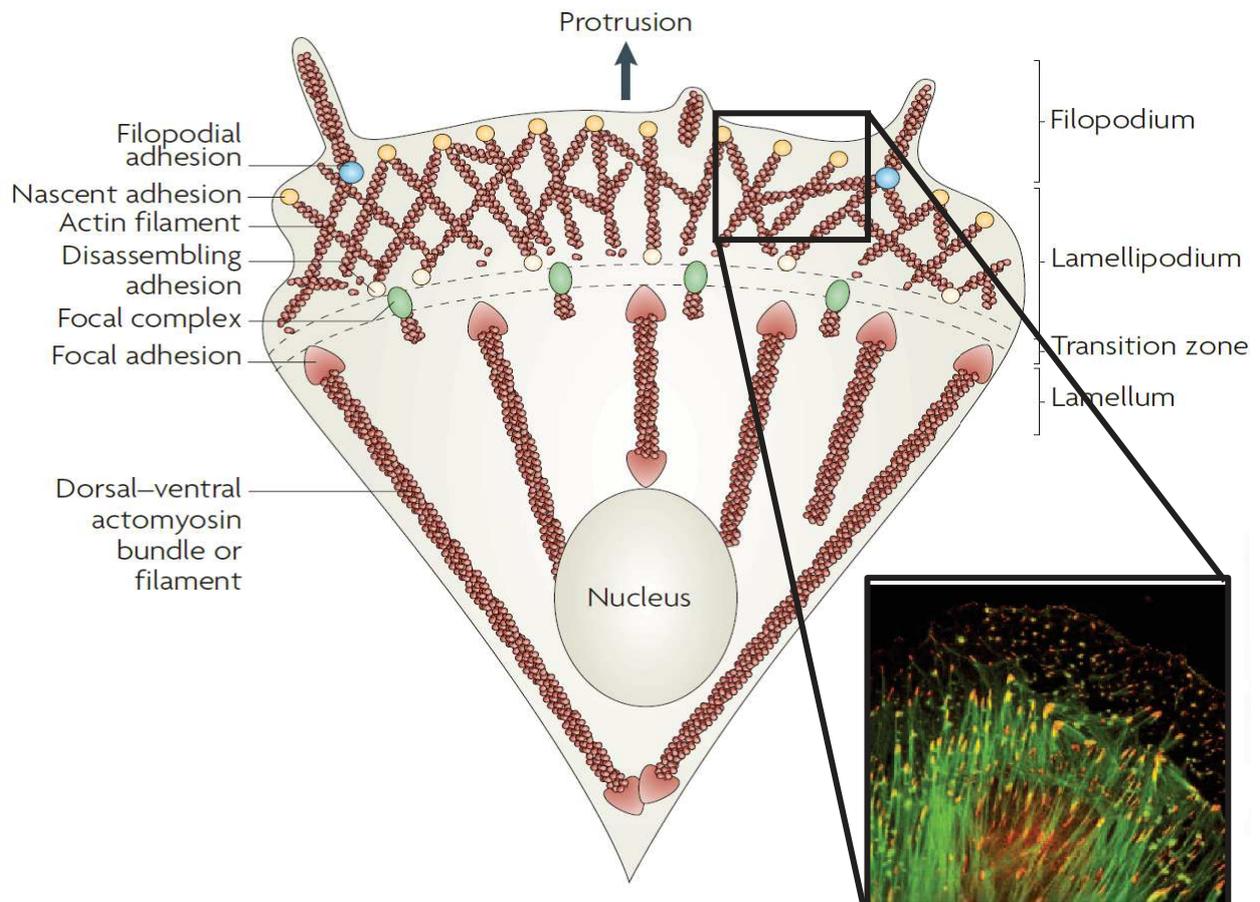


Figure 4.4. Structural elements of the adhesion of a migrating cell.

Adhesion is closely related with the protrusions of the leading edge - filopodia and lamellipodia. The nascent adhesions initially form in the lamellipodia (although some adhesions may also be associated with filopodia) and the rate of nascent adhesion assembly correlates with the rate of cell protrusion. Nascent adhesions either disassemble or stabilize and elongate at the convergence of the lamellipodia and lamella. The maturation to focal complexes and focal adhesions is accompanied by the bundling and cross-bridging of actin filaments, and actomyosin-induced contractility reinforces and stabilizes adhesion formation and increases adhesion size. Adapted from Parsons et al., 2010 and Gimona et al., 2005.

transition between the posterior border of the lamellipodia and the lamella, giving rise to the focal complexes and then subsequently the fibrillar adhesions. This maturation of the adhesions is associated with a modification of the organization of the actin network in fibers. The introduction of myosin II on the actin fibers



induces a local increase in contractility, which stabilizes the adhesions and promotes their growth (Figure 4.4).

4.3.1. Nascent adhesions

Nascent adhesions are complex emerging on the edge of lamellipodia are mainly visible by TIRF microscopy. They are small ($<1 \mu\text{m}$) and dynamic (life span of about 60 seconds) and are formed independently of the activity of myosin II, but in combination with actomyosin fibers. A portion of them can mature in focal complexes (Choi et al., 2008) which are slightly larger ($1\text{-}2 \mu\text{m}$), less dynamic (few minutes) and present at the interface between the lamellipodia and lamella. Their formation is stimulated by Rho-GTPases Rac1 and Cdc42. Their molecular

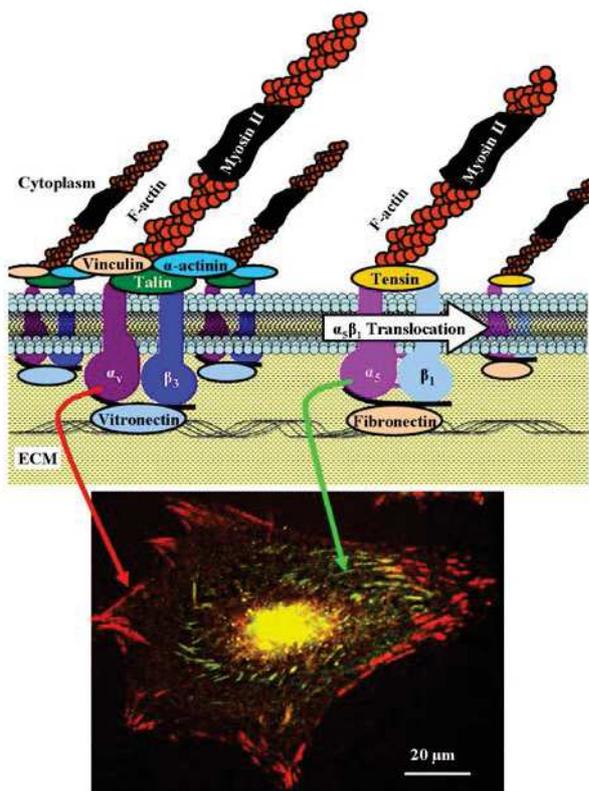


Figure 4.5. Organization of focal and fibrillar adhesions.

Focal adhesions are elongated spindle-like structures located at the periphery of the cell that connect bundles of actin stress fibers (F-actin) via many proteins, including $\alpha_5\beta_3$ integrins and structural proteins like α -actinin, vinculin and talin. Fibrillar adhesions are more centrally located and contain extracellular fibronectin, $\alpha_5\beta_1$ integrins and tensin. The translocation of fibrillar adhesions is highly directional, starting centripetally from the cell periphery towards the center. Double immunostaining for α_5 (red) and α_5 (green) in cells attached to fibronectin revealed the segregation between focal and fibrillar adhesion. Adapted from Marquis et al., 2009.

composition is not very well characterized, especially because the distinction between nascent adhesion, focal complex and focal adhesion is not always obvious: the notion of continuum is increasingly preferable to the existence of



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distinct classes of adhesions (Parsons et al., 2010). These adhesions contain, in addition to integrins, a number of structural proteins: talin, paxillin, vinculin and probably kindlins (Figure 4.5). FAK and Src signaling proteins are also present, they occur in particular in the regulation of assembly and disassembly of these adhesions *via* activity of adapter proteins such as paxillin, ERK or MLCK (Webb et al., 2004). The VASP proteins (vasodilatator stimulated phosphoprotein) and Arp2/3, promoting actin polymerization, are recruited by vinculin and FAK. Arp2/3 also promotes the branching of actin therefore aiding the propagation of the lamellipodia. Local stimulation of the polymerization and the branching of actin promotes the assembly of nascent adhesions (Choi et al., 2008) and indirectly promote the formation of complex by grouping probably focal integrins located in the vicinity of newly formed adhesions (Geiger and Bershadsky, 2001). The nascent adhesions are not sensitive to agents depolymerizing actin, which is why they are supposed to be independent of mechanical forces. For focal complexes, this insensitivity to tension forces is questioning due to the presence of mechanosensitive proteins such as vinculin, and RPTPa (Receptor Protein-Tyrosine Phosphatase a), p130CAS, etc.

4.3.2. Focal adhesions

Focal adhesions are best characterized as incipient adhesions or focal complexes. Discovered by electron microscopy (Abercrombie et al., 1971) on adherent cells cuts *in vitro*, these adhesions have also been observed *in vivo* (Lo et al., 1997). Focal adhesions are elongated structures about 2 μm wide and 3 to 10 μm long, extended by the stress fibers of actomyosin and have a long life (between 30 and 90 minutes). Their recruitment is stimulated by the Rho-GTPase RhoA *via* its action on ROCK and mDia. ROCK activates the light chain of myosin II both by direct phosphorylation and indirectly by inhibiting its MLCP phosphatase *via* phosphorylation the MYPT-1 subunit. This allows the formation of bipolar antiparallel filaments of myosin II and their interaction with the actin



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filaments to assemble into contractile stress fibers. All this increases the internal tension. That mechanical tension will promote the clustering of the integrins, the formation of the focal adhesions and their maturation. Many proteins take part in scaffolding the focal adhesions others are transiently associated. More than 180 proteins and 690 interactions have been described. All these adhesions associated proteins is called "adhesome" (Zaidel-Bar et al., 2007; Zaidel-Bar and Geiger, 2010; Schiller et al., 2011a). These proteins have been grouped into 17 classes according to their biological activity. There are structural proteins (talin, paxillin, vinculin, the α -actinin, zyxin, etc.), Tyrosine kinase signaling proteins - FAK, Src, PYK2 (*Proline-rich tyrosine kinase 2*), serin-treonin kinases - ILK (Integrin like kinase), PKC), regulators of small GTPases - p190RhoGAP, p190RhoGEF, tyrosine phosphatase, regulators of actin polymerization. Most important proteins are shown in Figure 4.5. The composition of adhesions depends on the type of integrins involved in connection with the matrix (Worth et al., 2010), but also the contractile state of the cell (Kuo et al., 2011; Schiller et al., 2011a). A recent proteomic study identified 905 proteins in adhesions (Humphries et al., 2009b). For 459 of them, their abundance in adhesions varies with the inhibition of myosin II. 73% of these proteins are depleted in adhesions when myosin is inhibited, among them are regulators of RhoA activity, proteins activating the formation of stress fibers and proteins involved in disassembling adhesions. In contrast, other proteins (27%) are enriched in adhesions when myosin is inhibited; they are essentially the proteins of the nascent adhesions such as the regulators of the activity of Rac1. It is unlikely that all these proteins are directly dependent on the activity of myosin, these changes in the proteome of the adhesions should rather be the result of a molecular cascade initiated by mechanosensitive proteins. The transmembrane proteoglycans, containing extracellular heparan sulfates, are co-receptors of cell adhesion. They participate in the regulation of focal adhesions and sometimes act in synergy with the integrins. Similar is the case for some growth receptors that work in cooperation with integrins (Fourel et al., 2016). Specifically



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$\beta 3$ integrin is required to interact with BMP receptors in order to control Smad signaling and mechanical stress homeostasis (Fourel et al., 2016).

Disassembly of focal adhesions resulting from both FAK signaling, Src via phosphorylation of paxillin, ERK and MLCK (Webb et al., 2004), the proteolytic cleavage induced by calpain, the targeting microtubules and endocytosis (Dubash et al., 2009). Inhibition of contractility in stress fibers results in rapid disassembly of focal adhesions (Chrzanowska-Wodnicka and Burridge, 1996), whereas disassembly of microtubules induces their formation (Enomoto, 1996).

4.3.3. Fibrillar adhesions

Fibrillar adhesions are observed only on fibronectin ECM. They are thinner and longer than the focal adhesions, they are also more central position in the cell and not perform like focal adhesions. They are dragged by centripetal translocation of integrin $\alpha 5\beta 1$ along contractile stress fibers (Zamir et al., 1999, 2000b; Pankov et al., 2000). This translocation is highly dependent on the intracellular contractility generated by myosin II and ROCK signaling. Meanwhile, fibronectin molecules bound to integrins are stretched, revealing cryptic sites allowing their assembly into fibrils parallel to fibronectin stress fibers and fibrillar adhesions (Pankov et al., 2000). This process is called fibrillogenesis. Fibrillar adhesions are depleted of talin and paxillin, but enriched in α -actinin or tensin (Figure 4.5).

4.4. Integrin endocytosis

Integrins (both α and β chains) are internalized by different ways like by macropinocytosis, clathrin-dependent endocytosis and clathrin-independent endocytosis, which includes endocytosis mediated by caveolae and clathrin-independent carriers (CLICs) (Bridgewater et al., 2012). The integrin heterodimers can be endocytosed independently on their attachment to the ligand. There is



clear data that the internalization and the turnover of the integrin dimers is important step for regulation the cell migration in both 2D and 3D matrices (Caswell and Norman, 2008; Valdembrri and Serini, 2012; Webb et al., 2002).

4.4.1. Clathrin dependent endocytosis

A classical pathway for clathrin dependent integrin endocytosis is presented at Figure 4.6A. The inactive heterodimer links with adapter proteins like Dab2, forms clathrin coated pit and is internalized. Interestingly if cells do not sense enough physical resistance from the ECM β 3 integrin clusters quickly recruit Dab2 and attract the endocytic machinery (Yu et al., 2015).

FA turnover can be facilitated by the microtubules (and more specifically kinesin 15). Figure 4.6B illustrates the delivery of the necessary MMP to cut the ECM links and free the bonded integrins and the molecular players that carry out the integrin endocytosis, including dynamin 2 (Dyn2) (Ezratty et al., 2005; Stehbens et al., 2014). Dyn2 polymerize around the budding vesicle and cut it from the PM (McMahon and Boucrot, 2011). Several adaptors like Dab2, Eps8 and Numb are



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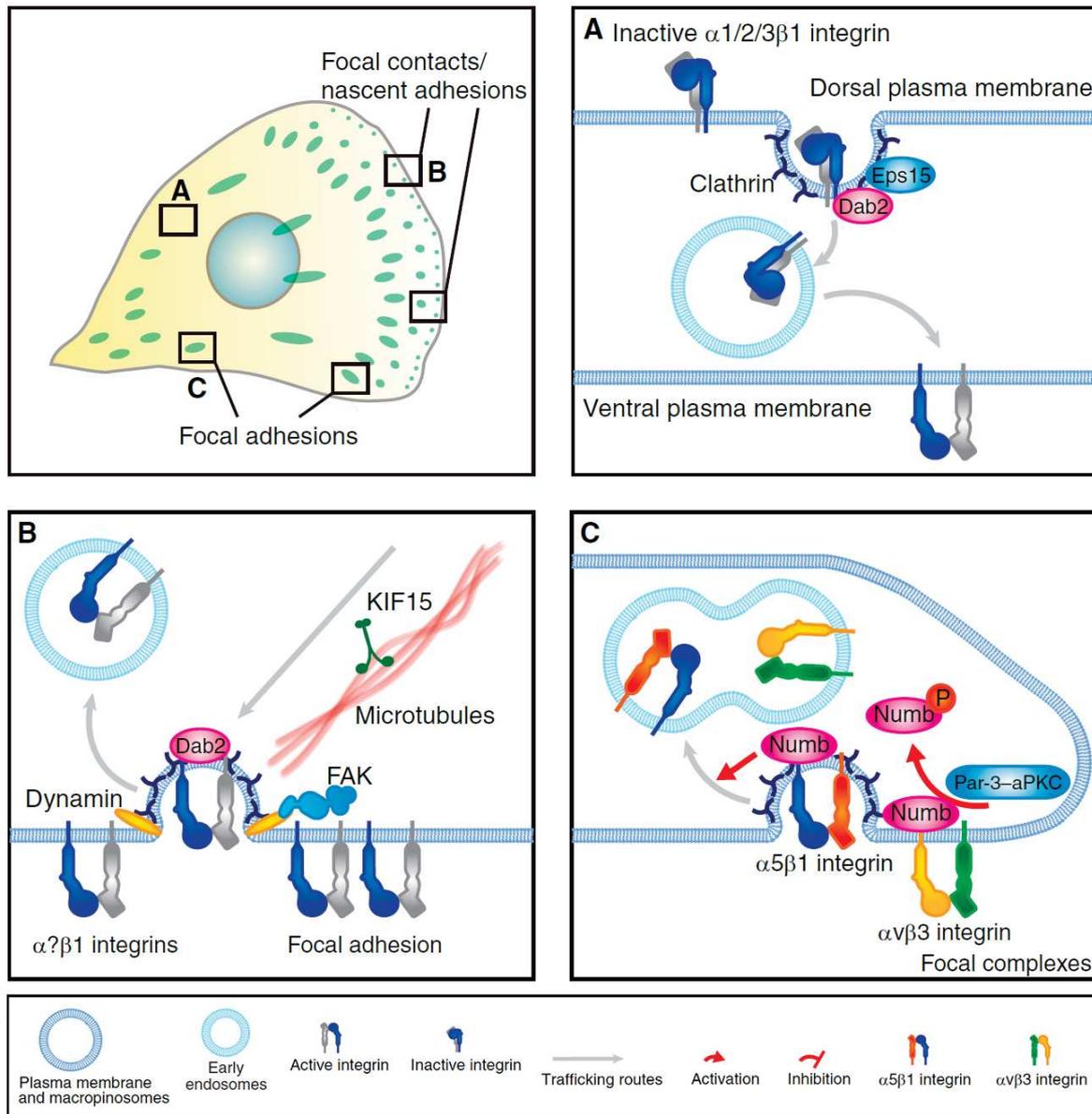


Figure 4.6. Clatrin dependent endocytosis and adhesion turnover.

A. Clatrin dependent endocytosis of $\beta1$ integrin via the adapter protein Dab2.
 B. Microtubule dependent adhesion disassembly leads to deliver of Dab2 at the vicinity of the FA.

C. The cycle of phosphorylation of the adapter protein Numb regulates endocytosis of $\beta1$ and $\beta3$ integrins at the leading edge of the cell. Adapted from Paul et al., 2015.

involved in the regulation of clathrin dependent endocytosis that interact directly via their phosphotyrosine-binding (PTB) domains with conserved NPXY/NxxY motifs



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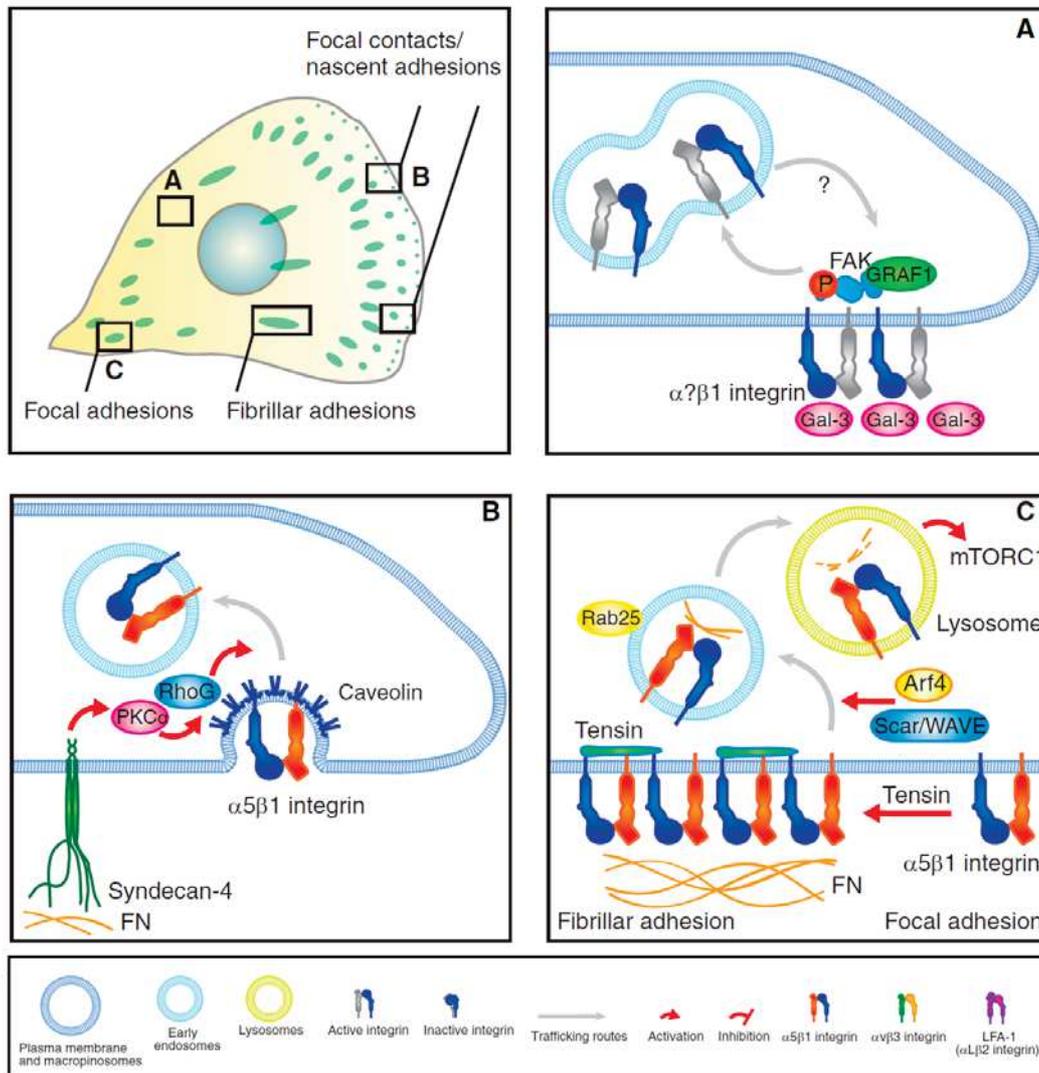
within β -subunit cytoplasmic tails (Calderwood et al., 2003) Figure 4.6C. Numb is of particular interest since it binds $\beta 1$ and $\beta 3$ integrin at the PM. Together with the adapter protein Ap2 regulate the turnover of $\beta 1$ and $\beta 3$ integrin at the leading edge to facilitate the cell migration (Nishimura and Kaibuchi, 2007). Even more the clathrin-dependent endocytosis relies on ARF GTPases: the Arf6 GAP ARAP2 (ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2) is necessary for $\beta 1$ integrin internalization and disassembly of the FA (Chen et al., 2014).

4.4.2. Clathrin-independent ways of integrin endocytosis

The biogenesis of clathrin-independent carriers (CLICs) at the PM requires s glycosphingolipids, the N-glycan-binding protein galectin-3 and GRAF1 (GTPase regulator associated with FAK 1) (Lakshminarayan et al., 2014; Doherty et al., 2011). Figure 4.7A shows that GARF1 binds phosphorylated form of FAK and is reported to localizes to podosome-like adhesions in HeLa and is necessary for cell migration (Doherty et al., 2011). Caveolae are specific membrane domains, rich in cholesterol and sphingolipids that are important both for clathrin-independent and clathrin-dependent transport of integrins (Figure 4.7B). Integrin endocytosis via caveolae has been demonstrated (Upla et al., 2004; Shi and Sotfile, 2008a; Du et al., 2011).



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Chapter 5. Mechanosensing

Cells feel many chemical and physical parameters of the environment and they respond. They adapt their adhesive structures to external constraints such as rigidity or density of the extracellular matrix (Albiges-Rizo et al., 2009). The forces exerted on the cells by outside factors (external or internal) are felt at adhesion structures regardless of their origin (Riveline et al., 2001). The stretching of adherent cells on elastic substrates while as the activation of myosin causes an increase in the size of focal adhesions and activation of FAK (Hamasaki et al., 1995). The focal adhesions are mechano-sensitive (Riveline et al., 2001; Collin et al., 2008). Maturation and growth of focal adhesions require strengthening of the cell/matrix bond in response to the forces exerted by the extracellular microenvironment. This capacity depends on the integrin $\beta 1$ (Friedland et al., 2009), talin (Zhang et al., 2008) and also involves ROCK, who activates myosin, and mDia (formin) that promotes the nucleation of actin and elongation of a parallel network of actin filaments (Chrzanowska-Wodnicka and Burridge, 1996; Rottner et al., 1999). Myosin exerts a force of $5,2 \text{ nN}/\mu\text{m}^2$ on focal adhesions (Schwarz et al., 2002) which exerts a force of $5,5 \text{ nN}/\mu\text{m}^2$ on the substrate (Schwarz et al., 2002). The activation of myosin and the increased cellular contractility changes the protein composition of adhesions (Kuo et al., 2011).

Cellular sensitivity to extracellular stiffness depends on at least two important parameters: the dynamics of adhesion sites and cytoskeletal tension (Fereol et al., 2009), which themselves depend on the components of the physical link between the extracellular matrix and intracellular cytoskeleton (Schwartz, 2010).

Cellular Adaptation to the biophysical properties of the microenvironment requires at adhesion sites the presence of molecular factors capable of adhering, applying pressure and transforming a mechanical signal into an intracellular biochemical signal: this phenomenon is called mechanotransduction.



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Although cells possess several force sensing devices (such as force sensitive channels (Kobayashi and Sokabe, 2010), and cell–cell adhesions (Huvencuers and de Rooij, 2013), due to space constraints we focus here on mechanotransduction events at integrin-associated complexes. These directly connect the ECM with the actin cytoskeleton and are one of the major contributors to mechanotransduction. We will discuss protein dynamics of integrin associated complex in relation to their function in mechanosensing and –signaling.

Four key parameters determine the range of rigidity that the cell can sense via the integrins: the binding force between the integrins and the matrix, the traction force of the cells, the speed of this retraction and the sensitivity of the mechanosensors (Moore et al., 2010). In addition, five types of successive noncovalent interactions are required for the development of forces at the level of the cellular binding with the extracellular matrix: the interaction between myosin and actin, the polymerization of monomeric actin into filaments, the interaction of these filaments with actin binding proteins, the interaction of these proteins with integrins, and finally the interaction of integrins with the extracellular matrix (Moore et al., 2010). The forces of interactions between the actin binding proteins or the integrins are still poorly known.

5.1. Integrins as mechanoreceptors

Complex conformational changes of the integrins control both their affinity for ECM proteins and their association with cytoskeletal partners. In the formation of adhesive contacts, integrins follow a mechanical cycle (Puklin-Faucher and Sheetz, 2009): they bind ECM and cytoskeletal filaments, transforming mechanical forces into intracellular biochemical signal, cluster together and form growing adhesion where the strength of resistance increases and in time, they detach and are being subsequently recycled. Experimental data suggest that the conformation of integrins $\alpha 5\beta 1$ can be modulated by external forces.



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The conformation of fibronectin-related integrin $\alpha 5\beta 1$ is initially loose; it corresponds to the pre-activated state of the integrin and is force independent. The exertion of mechanical forces modifies this conformation to an extended and fully active form where integrin binding to fibronectin is enhanced by the presence of an additional interaction between integrin and fibronectin at the synergistic site (Friedland et al., 2009). This bond, reinforced and stabilized by the force, is called “catch bond” (Dembo et al., 1988) and is characteristic for $\alpha 5\beta 1$. The bindings destabilized by mechanical tension are called “slip bonds” and are employed by integrins $\alpha V\beta 3$. However, functional differences exist between the different bindings: the slip bond is less resistant to forces than that catch bond, but it does initiate signal transduction (Roca-Cusachs et al., 2009).

5.2. Mechanosensors associated with integrins

There are five mechanisms (Moore et al., 2010) that are responsible for cellular mechanosensitivity via integrins: the formation of physical attachment bonds between integrins and their ligands and between actin and myosin, the opening of transmembrane mechanosensitive channels, regulation of the exposure of phosphorylation sites and exposure of binding sites of certain enzymes. Among these mechanisms, several are due to changes in protein conformation that are mechanosensitive, which positively or negatively regulate the activity of proteins.



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The mechanosensitive channels are transmembrane ion channels capable of converting a mechanical force into an electrochemical signal. They are mostly described in sensory mechanisms as hearing (Chalfie, 2009). However, mechanical stress generated by integrin-bound beads on the surface of endothelial cells causes calcium to enter in a few seconds (Matthews et al., 2006), so there are mechanosensitive ion channels coupled to integrins or activated by the mechanical strain on the integrins.

The activity of several kinases depends on the extracellular rigidity (Table 2) (Paszek et al., 2005).

The most well-known is FAK (Focal Adhesion Kinase) protein kinase, whose activity increases with mechanical forces (Wang et al., 2001; Michael et al., 2009). The kinases of the Src kinase family are quickly (300 ms) activated by the RPTP protein in response to the application of extracellular forces by fibronectin beads (von Wichert et al., 2003). However, RPTPa is not directly activated by mechanical forces (Moore et al., 2010). Some proteins change their conformation in response to their mechanical stretching. These changes allow the

Adhesion parameter	Soft matrix	Stiff matrix
Adhesion	+++	+++
Adhesion strength	+++	+++
Adhesion size	++	++++++
$\beta 1$ integrin	+++	+++
Activated $\beta 1$ integrin	+++	+++
Talin	+++	+/-
Lck & Lck ^{pY505}	+++++	+/-
Lyn & Lyn ^{pY507}	+++++	-
Src ^{pY416}	+++++	+
Src	+	+++
FAK ^{pY861}	+++	+++
FAK ^{pY397}	-	+++
Vinculin	-	+++
Actin stress fibers	+	+++
ERK activation	+	+++

Table 2. The extracellular stiffness influences the behavior of epithelial cells (Paszek et al., 2005).

exposure of so-called cryptic sites which may be phosphorylation sites, as is the case for the Cas protein family (Sawada et al., 2006), or sites of interactions. The interaction of paxillin, FAK protein, p130Cas with the cytoskeleton increases with tension (Sawada and Sheetz, 2002). The binding of vinculin to talin is dependent



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on stretching of the latter (del Rio et al., 2009). This stretching leads to the exposure of specific binding sites for vinculin.

Recently the binding between talin and vinculin was clarified using an innovative approach (Hu et al., 2016) - monitoring the *in situ* dynamics of the talin dimer stretch it was shown that that optimal vinculin and vinculin head binding occurred when talin was stretched to 180 nm. Also, multiple vinculins bound within a single second in narrowly localized regions of the talin rod during stretching. As a conclusion, talin stretches as an antiparallel dimer and that activates vinculin

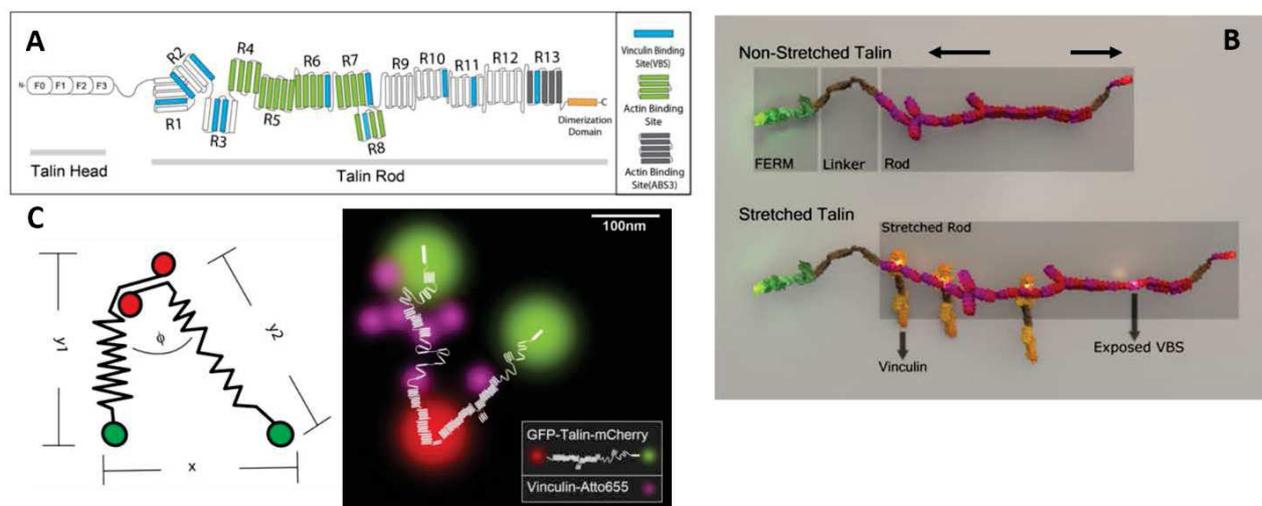


Figure 5.1. Interaction between talin and vinculin is facilitated if talin is stretched mechanically.

A. Talin head domain contains a FERM domain (50 kDa), followed by a flexible “neck” (10 kDa), which is followed by the head domain to its C-terminal rod domain (220 kDa). In blue are presented the vinculin binding parts (see legend).

B. Under the action of force in the direction of the black arrows, the tail of the talin begins to stretch. When the vinculin binding sites (VBS) are exposed to the vinculin, the latter binds to the talin.

C. Hu et al., 2016 proposed that talin do forms antiparallel dimers that activate the cooperative recruitment of vinculin. Extracted from Hu et al., 2016

binding in a cooperative manner, consistent with the stabilization of folded talin by other binding proteins (Figure 5.1).



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Several years ago (Grashoff et al., 2010) it has been created a biosensor of the mechanical tension applied in the adhesions: it is built on the base of vinculin, where a stretchable protein motif was surrounded by two fluorescent proteins and it has been inserted between the head and the tail of the vinculin (Figure 5.2). Vinculin binds talin and thus indirectly integrins and the extracellular matrix with its head and the contractile actin cytoskeleton with its tail. In this position the sensor is able to feel the changes in tension between the inside and the outside of the cell. These force variations are measurable via the level of energy transfer between the two fluorescent proteins (FRET) (Doyle and Yamada, 2010).

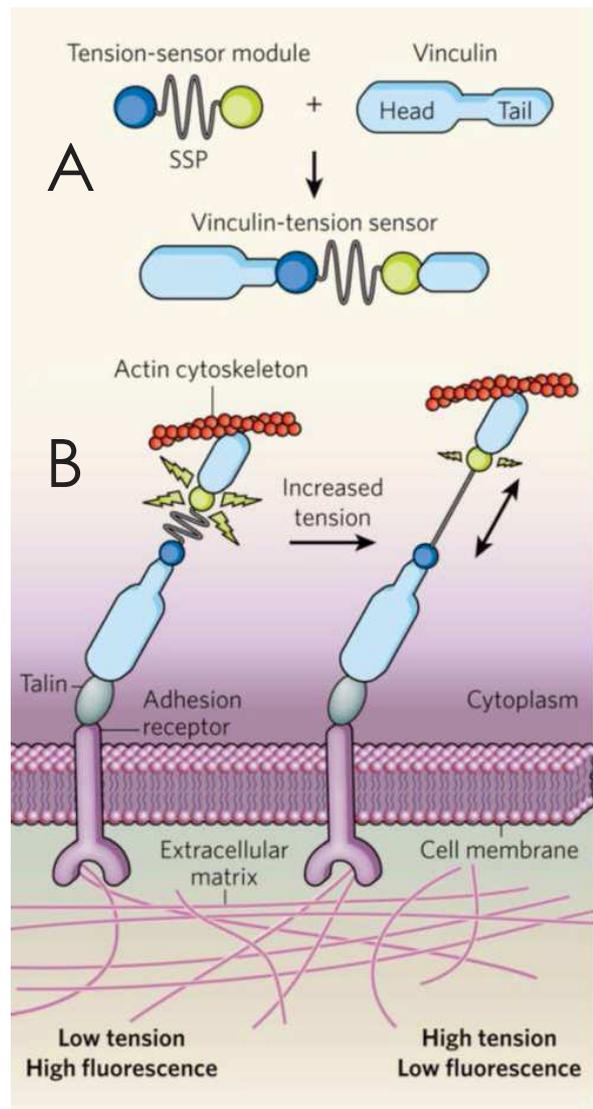


Figure 5.2. Force biosensor.

A. An elastic fragment of an SSP spider silk protein surrounded by two fluorescent proteins was introduced into the vinculin.

B. An increase in the tension in the biosensor causes a stretching of the SSP module and therefore a remoteness of the fluorescent proteins and a reduction of the energy transfer (FRET). Adopted from Doyle and Yamada, 2010.

5.3. Mechanotransduction at a distance

Within the focal adhesions, the integrins are linked to the actin cytoskeleton. Actin network is also connected to nuclear structural molecules (lamines), chromatin and the DNA. Mechanical forces applied to the cell surface at the integrins not



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only activate signaling pathways from the membrane but also cause structural rearrangements in the cytoplasm and nucleus (Maniotis et al., 1997). Mechanical forces applied to the cell surface can act at a distance and can be converted into a chemical-mechanical signal directly into the nucleus in addition to the cytoplasmic mechanotransduction initiated at the plasma membrane by the integrin-associated mechanosensors. This structural connection linked to the possibility of propagating forces over long distances (at the cell scale) is called tensegrity (Ingber, 2003b; a). Mechanical linkage allows mechanical propagation of the signal faster than the propagation of a chemical signal (Figure 5.3A). Numerous proteins are involved in the continuity of the physical bond between the extracellular matrix and the nucleus, in particular the focal adhesion components, the actin cytoskeleton and the nesprine/SUN/lamin network present at the nuclear envelope (figure 5.3B). The deformation of the nuclear envelope induced by a force applied to the surface of the cell stimulates an entry of calcium through nuclear ion channels, which induces the expression of certain genes. The identity of these mechanosensitive nuclear channels is still unknown, but these are certainly related to the mechanosensitive cytoskeleton and to the structural proteins of the nucleus (Wang et al., 2009). Different mechanisms for converting the mechanical signal received by the nucleus into a biochemical signal are possible. The opening of tension-sensitive nuclear pores can modify the transcriptional state of the nucleus. The deformation of the nuclear envelope can reflect on the chromatin and make it more or less accessible to the transcription factors; this deformation can also cause the double helix of DNA to be opened via attachment to the nuclear matrix; the deformation of intra-nuclear structural



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molecules allows the recruitment of factors involved in transcriptional regulation or chromatin modification (Wang et al., 2009).

Finally, the mechanosensitivity of the cells is a global phenomenon, at the level of the adhesions and at the whole cell level. This sensitivity relies on the intracellular mechanical integrity due to the cytoskeletons and the mechanical continuity with the ECM thanks to the connection of the actin cytoskeleton to the extracellular matrix via integrins and their cytoplasmic partners.

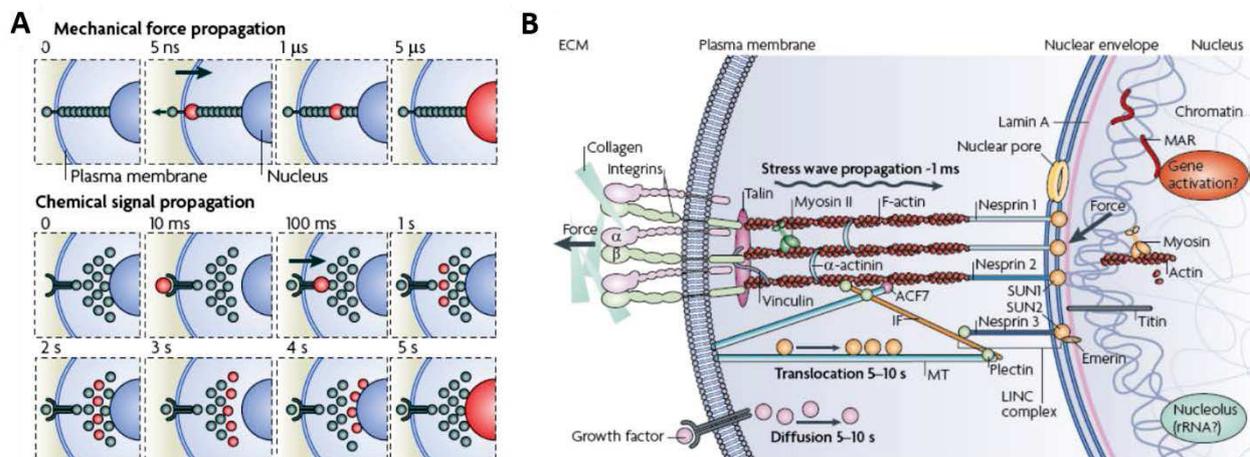


Figure 5.3. Mechanical transduction at a distance.

A. Comparison of the propagation of a mechanical or chemical signal. A force applied to the integrin-bound cytoskeleton reaches the nucleus in less than 5 μ s (top). The mechanical signal transmitted to the cytoskeleton is symbolized by the red dot to the nucleus. A growth factor-type chemical signal is received by tyrosine kinase receptors and propagates into the cytoplasm by a secondary (lower) messenger activation cascade. The signal reaches the nucleus in 5 s. The arrows indicate the direction of the applied force (top) or direction of the propagation signal through the membrane (bottom).

B. The molecular connection between the extracellular matrix and the nucleus involves on the one hand the integrins and the focal adhesions and on the other hand the nesprins linked to the SUN proteins inserted in the internal nuclear membrane themselves connected to chromatin and laminins responsible for the structure of the nucleus and finally the actin cytoskeleton which physically connect the two previous macromolecular structures. MT: microtubules, IF intermediate filaments. Adapted from Wang et al. (2009).



Chapter 6. ICAP-1 as a regulator of the cellular mechanoresponse

The ICAP-1 protein (integrin cytoplasmic domain associated protein-1) has been identified by screening of the cytoplasmic partners of the integrin subunit $\beta 1A$ by the two-hybrid technique (Chang et al., 1997). This interaction was confirmed by several other labs (Zhang and Hemler, 1999a; Degani et al., 2002; Ng et al., 2014; Morse et al., 2014). It is a small protein of 200 amino acids (21 kDa). It is formed by two protein domains: a serine and threonine rich domain and a phosphotyrosine binding domain (PTB), which is able to interact with $\beta 1$ integrin (Figure 6.1).

ICAP-1 is a phosphoprotein within eukaryotic cells (Zhang and Hemler, 1999a). The phosphorylation sites include, PKA, PKC, and CamKII consensus phosphorylation motifs, all located in the N-terminal half of the protein. The T38D mutant of ICAP-1 that mimics the phosphorylated form of the protein strongly increases its

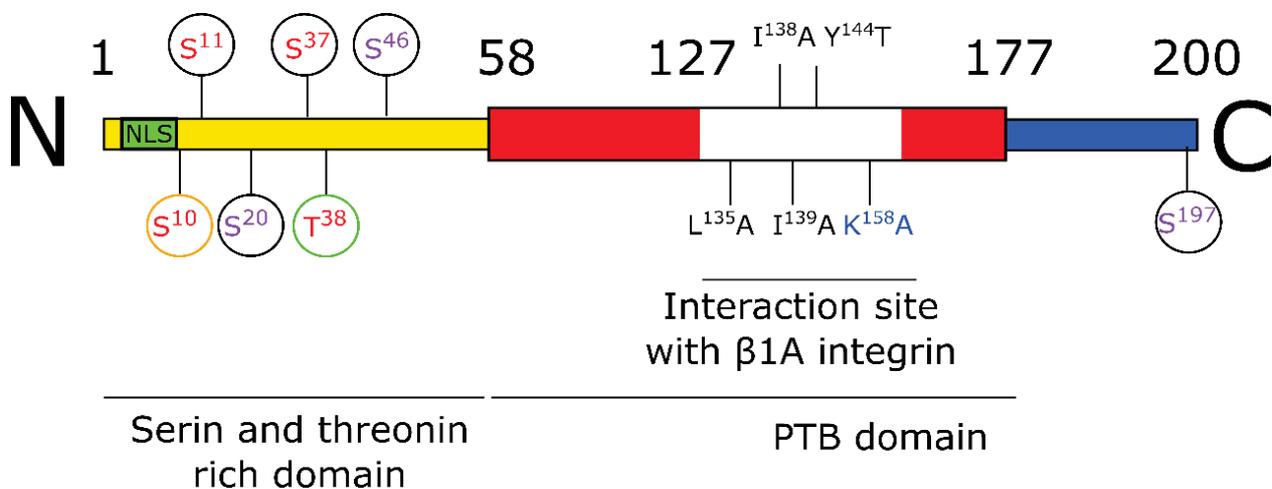


Figure 6.1 ICAP-1. The serine and threonine rich domain form a nuclear localization signal (NLS) and numerous consensus phosphorylation sites (circled): in red the sites recognized by ROCK (RxxS/T or RxS/T), in violet the protein Kinase C (S/TxK/R), orange protein kinase A (RxS/T or RR/KxS/T), green CamKII (I/LxRxxS/T). The mutations indicated in the binding domain with the cytoplasmic part of integrin $\beta 1$ are known to block this protein interaction.

interaction with $\beta 1$ integrin (Morse et al., 2014) and impairs CHO cell spreading on



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fibronectin, suggesting that ICAP-1 behaves as a negative regulator of $\beta 1$ integrin-mediated cell adhesion under the control of protein phosphorylation (Bouvard and Block, 1998). ICAP-1 interacts specifically with the C-terminal NPXY motif of the $\beta 1$ integrin cytoplasmic domain. Alanine scanning mutagenesis of the cytoplasmic tail of $\beta 1$ integrin reveals that Val(787), Val(790), and (792)NPKY(795) are critical for ICAP-1 binding. The NPXY motif is a known binding site for phosphotyrosine binding (PTB) domain proteins and, computational modeling reveals that amino acids 58–200 can fold into a PTB motif (Domain et al., 2002). The specificity of interaction with the various integrin subunits was analyzed in double yeast hybrids and by in vitro interaction assays (Chang et al., 1997; Zhang and Hemler, 1999a; Degani et al., 2002). ICAP-1 does not bind to the subunits $\beta 1B$, $1D$, 2 , 3 nor to the $\alpha 2$, 3 , 4 , 5 , 6 , V , L subunits. Mutagenesis implicated the integrin $\beta 1$ tail NPKY motif and a preceding VTTV sequence as important for ICAP1 binding, and molecular modeling suggested the interaction happens via a classical PTB-domain ligand interaction (Domain et al., 2002). Consistent with published mutagenic analyses (Domain et al., 2002), more recent structural studies (Liu et al., 2013) show that the interaction is mediated by integrin $\beta 1$ residues S783I to N792I (SAVTTVVN). This interaction interface is highly conserved and broadly hydrophobic, with V787I and V790I packing against hydrophobic patches. Surprisingly, although the $\beta 1$ integrin N792PxY motif binds ICAP1 and mutagenesis confirms the importance of Y795I (Domain et al., 2002), Y795I binding to the ICAP1 PTB domain is not observed in the crystal structure.

The binding of ICAP-1 to subunit $\beta 1$ is specific of the isoform A at the second site NPxY⁷⁹⁵. Valines at position -5 and -8 by tyrosine are essential for interaction (Domain et al., 2002). From 8 β integrin chains, only $\beta 1A$ contains the pattern VxxVxNPxY which explains its molecular specificity. However this specificity was questioned (Degani et al., 2002) by showing a two hybrid interaction between ICAP-1 and the $\beta 5$ integrin tail, contrary to the preceding groups. This interaction does not seem to have been confirmed to date.



6.1. ICAP-1: a cell adhesion regulator via the $\beta 1$ integrin

The ICAP-1 protein is a negative regulator of the cellular spreading that engages $\beta 1$ integrin. This has been shown by overexpression (Bouvard et al., 2003; Degani et al., 2002) and by depletion (Bouvard et al., 2007) of the ICAP-1 protein on ECM which can be recognized by $\beta 1$ integrin such as fibronectin, laminin or collagen. The interaction of ICAP-1 with $\beta 1$ integrin negatively affects the integrin's affinity for its ligand (Bouvard et al., 2007; Millon-Frémillon et al., 2008). During the initial stages of spreading, ICAP-1 is localized at the cellular periphery at the level of the lamellipodia with integrins $\beta 1$ (Fournier et al., 2002a). Despite the direct interaction between ICAP-1 and integrins $\beta 1A$, ICAP-1 has never been visualized in focal adhesions (Bouvard et al., 2003) even though the deletion of ICAP-1 leads to the redistribution of focal adhesion all over the ventral face of the osteoblastic, fibroblastic and endothelial cells. The increase of $\beta 1$ integrin- dependent cell motility on fibronectin upon ICAP-1 overexpression (Chang et al., 1997; Domain et al., 2002; Zhang and Hemler, 1999a), the increase of collective migration (Zhang and Hemler, 1999a; Alvarez et al., 2008) and cell rounding up after overexpression of a phosphomimetic mutant of ICAP-1 at the CaMKII site (Brunner et al., 2011b; Millon-Frémillon et al., 2013) suggest that ICAP-1 might regulate $\beta 1$ -integrin function. Biochemical studies and FRAP analysis have highlighted the impact of ICAP-1 on cell adhesion dynamics through its ability to slow down focal adhesion assembly by competing with the co-activator of talin called kindlin (Bouvard et al., 2003; Millon-Frémillon et al., 2008; Brunner et al., 2011b). Unexpectedly, the ICAP-1-dependent decrease in integrin affinity allows cell sensing of matrix surface density suggesting that ICAP-1 might be involved in mechanotransduction process. Later on, the lab has demonstrated the importance of ICAP-1 in inhibiting ROCK1-mediated cell contractility via the regulation of $\beta 1$ integrin affinity (Faurobert and Albiges-Rizo, 2010). Altogether, these results clearly demonstrated



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that a switch between high and low affinity integrin states is required to control cell contractility and to drive an integrated cell response that is appropriate for the ECM environment.

6.2. ICAP-1: a regulator of cell proliferation through regulation of β 1 integrin.

Over-expression of ICAP-1 stimulates cell proliferation whereas its depletion slows down the cell growth (Henri-Noel Fournier, Sandra Dupe-Manet, Daniel Bouvard et al., 2005; Bouvard et al., 2007). The protein ICAP-1 has a functional nuclear localization signal (KKNH⁹) and is targeted to the nucleus after the first steps of the adhesion. The double substitution of lysines in alanines abolishes its nuclear localizing signal. This nuclear location depends on the adhesion engagement of the β 1 integrins and stimulates proliferation via activation of the c-myc gene (Henri-Noel Fournier, Sandra Dupe-Manet, Daniel Bouvard et al., 2005). It has been shown that activation is related to the interaction between ICAP-1 and the protein Nm23-H2 (Henri-Noel Fournier, Sandra Dupe-Manet, Daniel Bouvard et al., 2005).

6.3. ICAP-1: a regulator of cell homeostasis and tissue integrity

The PTB domain allows ICAP-1 to interact with the NPxY motifs. However, these are present in many proteins. Thus, proteins with PTB domains can have several partners with NPxY motifs as well as proteins with NPxY motifs may have multiple partners with PTB domains. These motifs are, of course, present in the cytoplasmic domains of integrins (Brunner et al., 2011b; Faurobert and Albiges-Rizo, 2010; Ren et al., 1999) (Figure 3.3). At present, about ten proteins have been described as partners for ICAP-1 (Table 3).



Partner	Method of identification	Recognized motif	Reference
ECM receptor			
Integrin β1A	Two hybrid technique, pull down, co-immunoprecipitation	NPxY	Chang et al. (1997); Zhang et Hemler (1999); Degani et al. (2002)
Integrin β5	Two hybrid technique	NPxY	Zhang et al. (2002)
LDL receptors			
LRP-1	Two hybrid technique, pull down	NPxY?	Gotthardt et al. (2000)
ApoER2	Two hybrid technique	NPxY?	Gotthardt et al. (2000)
Megaline	Two hybrid technique, pull down	NPxY?	Gotthardt et al. (2000)
Signaling proteins			
Rac1	Pull down	?	Degani et al. (2002)
Cdc42	Pull down	?	Degani et al. (2002)
ROCK	Two hybrid technique, co-immunoprecipitation, FRET	?	Stroeken et al. (2006)
Others			
Krit-1/CCM1	Two hybrid technique, pull down, co-immunoprecipitation	NPxY	Zhang et al. (2001) ; Zawistowski et al. (2002)
Nm23-H2	Two hybrid technique, pull down, ELISA	?	Fournier et al. (2002)

Table 3. Proteins, reported to interact with ICAP-1.

6.3.1. ICAP-1 regulates cell adhesion independently on β 1 integrins

Nm23 proteins are protein kinases that catalyze the phosphorylation of nucleotide diphosphates (NDP) from nucleotide triphosphates (NTP), allowing a transfer of energy from the ATP to the GTP, that are involved in many cellular processes. The interaction between ICAP-1 and Nm23-H2 was shown by our laboratory and later confirmed (Miyamoto et al., 2009). The complex ICAP-1-Nm23-H2 co-localizes with β 1 integrins in early stages of cell spreading. This localization of Nm23-H2 by ICAP-1 at the integrins suggests that Nm23-H2 might modulate signaling induced by Rho-GTPases activated by integrin engagement during cell adhesion (Fournier et al., 2003). It has been reported that ICAP-1 interacts with Rac1 and Cdc42 but not with RhoA (Degani et al., 2002). ICAP-1 inhibits the activation of these Rho-GTPases in the early stages of cell spread, but



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expression of a constitutively active mutant of Cdc42 lifts the inhibition of ICAP-1-mediated spreading, indicating that ICAP-1 works upstream of the small protein G. The dissociation of the GDP with Cdc42 is reduced in the presence of ICAP-1 while dissociation of Cdc42 with the plasma membrane is increased by ICAP-1. This indicates that ICAP-1 would be a GDI (Guanine nucleotide Dissociation Inhibitor) for Cdc42. This function could not be shown for Rac1, indicating that regulation of Rac1 by ICAP-1 would be indirect. However, these results are surprising because the structure of ICAP-1 does not resemble the immunoglobulin domain of the conventional Rho-GDIs; these results also remain to be confirmed. ROCK is a kinase involved in cellular contractility. It interacts with ICAP-1 (Stroeken et al., 2006) and the complex locates at the membrane edges with β 1 integrins. ICAP-1 might recruit ROCK near β 1 integrins, thus locating the activity of ROCK to the membrane. Inhibition of ROCK or depletion of ICAP-1 diminishes the collective cell migration (Alvarez et al., 2008). However, the biological function of ROCK-ICAP-1 complex remains little understood. This interaction suggests though that ICAP-1 could intervene in the control of intracellular contractility. As Nm23 proteins are also involved in endocytosis of receptors, it could not be excluded the involvement of ICAP-1 in integrin trafficking.

6.3.2. ICAP-1 takes part in osteoblast differentiation and angiogenesis

Krit-1 (Krev interaction trapped-1) / CCM1 is a protein with a FERM domain (band 4.1, ezrin, radixin, moesin) initially described as a partner of GTPase Rap1, also called Krev1 (Serebriiskii et al., 1997). Krit-1 maintains cell-cell junction integrity in the endothelium of cerebral vessels (Béraud-Dufour et al., 2007; Glading et al., 2007) and is associated with Congenital cerebrovascular disease CCM (Cerebral cavernous malformation) causing epilepsy and cerebral hemorrhages due to fragility of the endothelia of these vessels. Two other genes called CCM2 and CCM3 are associated with this disease and it has been shown in vitro that the three CCM proteins can associate to form a ternary complex (Hilder et al., 2007).



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The interaction between Krit-1 and ICAP-1 was shown multiple times (Zhang et al., 2001; Zawistowski et al., 2002). Krit-1 has an NPxY motif and the interaction with ICAP-1 is carried out at the level of the PTB, Krit-1 is therefore in competition of the β 1 integrins for ICAP-1 binding (Zhang et al., 2001). The binding of ICAP-1 to Krit-1 activates the latter by breaking of intramolecular interactions and unveils the FERM domain, an interactive platform with other proteins and allowing its localization to the cytoplasmic membrane (Béraud-Dufour et al., 2007). Loss of interaction between Krit-1 and ICAP-1 leads to the degradation by the Krit-1 as well as ICAP-1 by proteosomal degradation (Béraud-Dufour et al., 2007). The binding of CCM2 to the Krit-1-ICAP-1 complex inhibits translocation of the complex in the nucleus. Finally ICAP-1/CCM complex is at the crossroad between integrin-mediated FAs and cadherin mediated adhesion junctions (Faurobert and Albiges-Rizo, 2010).

6.4. The physiological Importance of ICAP-1

The ICAP-1 protein is expressed in all organs except the liver but its level of expression varies according to the tissues and cell types (Zhang and Hemler, 1999a). Although, to date, no genetic disease is associated with its loss or its increase in function due to mutations or genetic deletion of the *icap-1* gene, the physiological importance of ICAP-1 can be emphasized and analyzed by the effect of its gene inactivation in mice (Bouvard et al., 2007). Unlike inactivation of its main partner, β 1 integrin, inactivation of *icap-1* is not lethal at the embryonic stage. At birth and in adulthood, ICAP-1-deficient mice are smaller than wild mice and have several phenotypes: neurological disorders, bone defects (Bouvard et al., 2007), fertility defects and vascular defects (Faurobert et al., 2013). The severity of this the last phenotype depends on the genetic background.

Bone defects are best described in the literature: deficient mice in ICAP-1 show growth retardation and retardation of bone mineralization, a craniofacial



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malformation and a lack of ossification of the calvaria due to decreased proliferation and abnormal cell differentiation (Bouvard et al., 2007). In vitro, the ICAP-1^{-/-} osteoblasts show defects in adhesion, cell migration, compaction and organization of fibronectin matrix (Bouin et al., 2017b) required for bone mineralization, explaining in part the bone phenotype observed in vivo (Bouvard et al., 2007; Millon-Frémillon et al., 2008; Brunner et al., 2011b). Osteoblasts expressing a mutated β 1 integrin, that no longer interacting with ICAP-1 have the same defects as ICAP-1^{-/-} osteoblasts^{6,9}. This suggests that bone defects observed in vivo are due to the interaction between ICAP-1 and the β 1 integrin.



II.

**Scientific context
and general aim of
the study**





II. Scientific context and general aim of the study

Scientific context and general aim of the study

Cells perceive their environment by sensing the chemical and physical properties of the extracellular matrix as a result of the organization on its surface of adhesive machinery which is a proper molecular platform organized around the mechanoreceptors called Integrins. Cells are thus both able to adapt to the topography, the chemical composition and the elasticity of its environment, but they are also able to modify it (degradation, fibrillogenesis).

Usually cells held in place by direct bonding with a complex network of extracellular macromolecules secreted by the cell and also with neighboring cells. Cell adhesion assumes the existence of a physical interface consisting of a hierarchical multi-protein complex. Through this molecular complex, the cell may develop a mechanical action on the environment (the fibrillogenesis is exemplary) and in return, receive information from the environment in the form of stresses and strains transmitted until the nucleus. Adhesion is thus a key to controlling cell proliferation, but also cell migration and cell differentiation. These interactions between the cell and its environment are due to specific transmembrane proteins (first **integrins**) playing the role of **adhesion molecules** and who are known to be also sensitive to the environment, as mechanoreceptors. Integrins are described as biphasic transmembrane receptors that connect the intracellular polymers (actin filaments) to the extracellular polymers (the fibrillar extracellular matrix components). Depending on the mechanical properties of the substrate, and in particular its rigidity, adhesive interfaces are established with specific protein architecture, allowing a cell behavior adapted to this environment. On a substrate such as stiffness exceeds tens of kPa, cells establish stable adhesions with significant size (several μm^2) called



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focal adhesions. This cellular adaptation is thinly regulated thanks to the molecular dynamics of the adhesion structures.

Integrin **$\beta 1$** and **$\beta 3$** are observed and co-localized in focal adhesions. Integrin $\beta 1$ and $\beta 3$ have specific mechanical roles and are associated with different signaling pathways. If $\beta 1$ is widely associated with traction forces generated at the cell/substrate interface, $\beta 3$ is associated with the transmission and traduction of the mechanical signal into a biochemical signal: the mechanotransduction (Roca-Cusachs et al., 2009). These distinct mechanical roles could explain their co-localization and/or their segregation in focal adhesion sites (Zamir et al., 2000a), but today a little is known about their regulation.

The comprehension of this regulation participates to the general understanding of the mechanism at the origin of the cell sensitivity to the mechanical properties of their environment. This field is the subject of intense multidisciplinary research in which Corinne Albigès-Rizo team participates actively. These searches require both the knowledge and skills for the molecular manipulation of tools for cell engineering, measurement techniques of local forces across the cell and measurements of molecular complex dynamic. A unique property of integrins is their tuneable conformation since they can switch from close to open conformation leading respectively to integrins activation or inactivation (Shattil et al., 2010). Some adapters control the activation of integrin which corresponds to a conformational switch from a low to high affinity state for extracellular ligand. For example, whereas talin is important to activate integrin and to connect actin filaments, **ICAP-1 specifically maintains $\beta 1$ integrin in its inactivated form.** The laboratory has shown that ICAP-1 enables the cell to sense



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extracellular ligand density and adapt its adhesive and migratory responses (Millon-Frémillon et al., 2008).

It has been also demonstrated considerable differences in the organization and dynamics of $\beta 3$ and $\beta 1$ integrins within focal adhesions. While $\beta 3$ integrin was stationary within focal adhesions, a significant proportion of immobilized $\beta 1$ integrins displayed retrograde translocation similar to that of F-actin. Such differences would allow the spatial compartmentalization of specific integrins and differential transduction of mechanical force from the actin cytoskeleton to the extracellular matrix, and *vice versa*. Overall, the data were consistent with the notion that, within focal adhesions, $\beta 3$ and $\beta 1$ integrins exhibit distinct biomechanical and mechanoresponsive properties. Indeed, if a potential crosstalk between $\beta 1$ and $\beta 3$ integrin in term of spatial organization exists then the dynamics of one integrin should be influenced by modulation in activity of the other one. Here we chose to characterize the cell/substrate interface from a structural and rheological point of view through the regulation of adhesive interfaces involving $\beta 1$ and $\beta 3$ integrins and ICAP-1 as a particular partner. To determine $\beta 3$ integrins' behavior in focal adhesion according to $\beta 1$ integrin incidence, we have generated ICAP-1^{-/-} osteoblasts mutants to achieve up-regulated conformation of $\beta 1$ integrins, $\beta 1$ ^{-/-} osteoblasts mutants to delete $\beta 1$ completely and osteoblasts deficient in both $\beta 1$ integrin and ICAP-1 (displaying in that case only $\beta 3$ integrins). The specific objectives of my thesis were to investigate whether $\beta 1$ integrin can influence the behavior of $\beta 3$ integrin and consequently may affect cell function through regulation of cell contractility and force generation in regards to ICAP-1 context.



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III.

**Article and
results**





Chapter 7. Article: ICAP-1
monoubiquitylation coordinates matrix
density and rigidity sensing for cell migration
through ROCK2–MRCKa balance

7.1. Specific scientific context:

The cellular conversion from a non-tumorigenic state to a metastatic one is of critical interest in cancer cell biology, as most deaths from cancer occur due to metastasis (Pollard and Borisy, 2003). This metastatic conversion is one of the hallmarks of cancer (Hanahan and Weinberg, 2011). It is highly regulated and defined as a multistep process including cell plasticity, a dysregulation of cell adhesion, degradation of the extracellular matrix (ECM), acquirement of a motile phenotype, vascular infiltration, exit and colonization to a new organ site, dormancy, and re-activation. In addition to genetic factors, environmental factors control this conversion. Indeed cell sample in space and time the heterogeneity in the composition, topography and stiffness of their extracellular matrix (ECM) through integrin-mediated adhesive machinery to adapt their migratory behavior and to invade surrounding tissues (Wirtz et al., 2011) (Pollard and Borisy, 2003). As physical links between ECM and cellular actin cytoskeleton, integrins are membrane mechanoreceptors crucial for force transmission and signal transduction to adapt cell behavior. Actin cytoskeleton generates appropriated traction forces under the control of kinases which activate the motor myosin (Bustelo et al., 2007). In response to different micro-environmental stimuli, cells build diverse contractile networks of actin filaments and myosin motors to orchestrate cell shape changes and optimize cell migration. Cell contractility of the actomyosin has to be tightly regulated in space and time by different biochemical pathways involving the activities of several kinases (ROCK1,



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ROCK2, MRCK, DMPK, CRIK.) responsible for myosin phosphorylation. Furthermore, actomyosin networks display complex dynamics, such as flows and pulses, which participate in spatial and temporal distribution of myosin and evolution of forces during cell adaptation to the microenvironment for cell migration optimization. Whether cell contractility relies on the balance between different kinase activities to control the spatiotemporal activity of myosin or elongation and organization of actin filament need to be investigated. How activities of different kinases are controlled by ECM properties and whether some molecular switches allow interconnection between two types of contractility to adapt the mechanical behavior of motile cells are not understood.

7.2. Specific objectives of the study

ICAP-1, a negative regulator of $\beta 1$ integrin enables the cell to sense ECM density to adapt its adhesive and migratory responses (Millon-Frémillon et al., 2008) and to control fibronectin (FbN) remodeling (Brunner et al., 2011a; Faurobert et al., 2013). ICAP-1 specifically binds to the cytoplasmic tail of $\beta 1$ integrin maintaining the integrin in its inactivated form by competing with the two activators named Kindlin and talin (Montanez et al., 2008; Ye et al., 2014; Brunner et al., 2011a; Millon-Frémillon et al., 2008). ICAP-1 also binds to ROCK1 (Stroeken et al., 2006). Thanks to these interactions, ICAP-1 may be a good candidate for regulating myosin-based contractility and cellular response to ECM stiffness. Tunable post-translational modifications may control ICAP-1 functions enabling the cell to adapt its migratory response. Our laboratory has already shown that the N terminal domain of ICAP-1 contains multiple phosphorylation consensus sites. The calcium and calmodulin-dependent serine/threonine protein kinase of type II (CaMKII) is an important regulator of ICAP-1 for controlling focal adhesion dynamics (Millon-Frémillon et al., 2013, 2008). As ubiquitination is emerging as



important for cell migration dynamics and cell contractility (Sahai et al., 2007; Su et al., 2013; Wang et al., 2003; Schaefer et al., 2012; Carvallo et al., 2010), we addressed whether ubiquitination may control ICAP-1 functions enabling the cell to adapt its migratory response.

7.3. Conclusion

Our results show that ICAP-1 is monoubiquitinated by SMAD ubiquitin regulatory factor 1 (Smurf1) and that Smurf1 is a node to control focal adhesion dynamics and cell contractility. This monoubiquitination impairs ICAP-1 binding to $\beta 1$ integrin and is involved in ECM density and rigidity sensing as well as in coordination of the dynamics of adhesion sites and contractile machinery. ICAP-1 monoubiquitination plays an important role in the responses of migrating cells to mechanical inputs in a $\beta 1$ integrin independent manner by promoting the switch from a ROCK-mediated to a MRCK-mediated contractility pathway.

7.4. Contributions to the article

-cellular culture, SiRNA experiments, TFM, Western blot of P-Myosin, statistical analysis, Critical assistance in the preparation of the manuscript.



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CORRECTION

Correction: ICAP-1 monoubiquitylation coordinates matrix density and rigidity sensing for cell migration through ROCK2–MRCK α balance

Anne-Pascale Bouin, Alexander Kyumurkov, Myriam Régent-Kloeckner, Anne-Sophie Ribba, Eva Faurobert, Henri-Noël Fournier, Ingrid Bourrin-Reynard, Sandra Manet-Dupé, Christiane Oddou, Martial Balland, Emmanuelle Planus and Corinne Albiges-Rizo

There was an error published in *J. Cell Sci.* **130**, 626-636.

The name of the author Alexander Kyumurkov was incorrect in the original author list. The correct spelling is given above.

The authors apologise to the readers for any confusion that this error might have caused.

RESEARCH ARTICLE

ICAP-1 monoubiquitylation coordinates matrix density and rigidity sensing for cell migration through ROCK2–MRCK α balance

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ABSTRACT

Cell migration is a complex process requiring density and rigidity sensing of the microenvironment to adapt cell migratory speed through focal adhesion and actin cytoskeleton regulation. ICAP-1 (also known as ITGB1BP1), a β 1 integrin partner, is essential for ensuring integrin activation cycle and focal adhesion formation. We show that ICAP-1 is monoubiquitylated by Smurf1, preventing ICAP-1 binding to β 1 integrin. The non-ubiquitylatable form of ICAP-1 modifies β 1 integrin focal adhesion organization and interferes with fibronectin density sensing. ICAP-1 is also required for adapting cell migration in response to substrate stiffness in a β 1-integrin-independent manner. ICAP-1 monoubiquitylation regulates rigidity sensing by increasing MRCK α (also known as CDC42BPA)-dependent cell contractility through myosin phosphorylation independently of substrate rigidity. We provide evidence that ICAP-1 monoubiquitylation helps in switching from ROCK2-mediated to MRCK α -mediated cell contractility. ICAP-1 monoubiquitylation serves as a molecular switch to coordinate extracellular matrix density and rigidity sensing thus acting as a crucial modulator of cell migration and mechanosensing.

KEY WORDS: Cell migration, Rigidity sensing, ICAP-1, Integrin, Monoubiquitylation, Cell contractility

INTRODUCTION

Motile cells continuously sample in space and time the heterogeneity in the composition and stiffness of their extracellular matrix (ECM) through integrin-mediated focal adhesions (FAs) (Moore et al., 2010). As a mechanical link between ECM and actin stress fibers, integrins are crucial for force transmission and signal transduction (Moore et al., 2010). FA assembly, growth and maintenance depend on actomyosin traction forces, which adapt to the substrate elasticity (BurrIDGE and Wittchen, 2013). In spite of alternative pathways involving MRCK (which has two isoforms, MRCK α and MRCK β , also known as CDC42BPA and CDC42BPB, respectively), MLCK (also known as MYLK) or mDia (BurrIDGE and Wittchen, 2013; Chen et al., 2014; Jégou et al., 2013; Totsukawa et al., 2004), a key event is the modulation of cellular contractility through myosin-based contractility and ROCK (which has two isoforms, ROCK1 and

ROCK2) activity. However, signaling pathways underlying FA-mediated rigidity sensing and the mechano-response are not fully understood.

ICAP-1 (also known as ITGB1BP1), a negative regulator of β 1 integrin, enables the cell to sense ECM density to adapt its adhesive and migratory responses (Millon-Frémillon et al., 2008) and to control fibronectin (FN) remodeling (Brunner et al., 2011; Faurobert et al., 2013). ICAP-1 specifically binds to the cytoplasmic tail of β 1 integrin, maintaining the integrin in its inactivated form by competing with the two activators named Kindlin and talin (Brunner et al., 2011; Millon-Frémillon et al., 2008; Montanez et al., 2008; Ye et al., 2014). ICAP-1 also binds to ROCK1 (Peter et al., 2006). Thanks to these interactions, ICAP-1 may be a good candidate for regulating myosin-based contractility and cellular response to ECM stiffness. Tunable post-translational modifications may control ICAP-1 functions enabling the cell to adapt its migratory response. As ubiquitylation is emerging as important for cell migration dynamics and cell contractility (Carvallo et al., 2010; Sahai et al., 2007; Schaefer et al., 2012; Su et al., 2013; Wang et al., 2003), we addressed whether ubiquitylation may control ICAP-1 functions, enabling the cell to adapt its migratory response. Here, we show that ICAP-1 is monoubiquitylated by SMAD ubiquityl regulatory factor 1 (Smurf1). This monoubiquitylation impairs ICAP-1 binding to β 1 integrin and is involved in ECM density and rigidity sensing as well as in coordination of the dynamics of adhesion sites and contractile machinery. ICAP-1 monoubiquitylation plays an important role in the responses of migrating cells to mechanical inputs in a β 1 integrin-independent manner by promoting the switch from a ROCK2-mediated to an MRCK α -mediated contractility pathway.

RESULTS**ICAP-1 is monoubiquitylated by Smurf1 at the β 1 integrin-binding site**

To investigate ICAP-1 ubiquitylation, we performed nickel-bead pulldown experiments on Chinese Hamster Ovary (CHO) cells transfected with ICAP-1 either in the presence or absence of co-transfection with His-tagged ubiquitin. The proteasome inhibitor MG132 was added to prevent proteasomal degradation of any ubiquitylated ICAP-1. When expressed alone, ICAP-1 appeared on a western blot an apparent molecular mass that was slightly greater than 20 kDa, whereas co-transfection with His-tagged ubiquitin and pulldown on nickel beads resulted in isolation of ICAP-1 with higher molecular mass forms, with a band above 35 kDa (Fig. 1A), showing that ICAP-1 is indeed ubiquitylated. This band above 35 kDa most likely corresponds to ICAP-1 monoubiquitylation. HA-tagged ubiquitin (HA-Ubi) was also coexpressed with ICAP-1 fused to Flag and our results show that ICAP-1–Flag can be recognized by both anti-Flag and anti-HA antibodies after immunoprecipitation with anti-Flag antibodies (Fig. 1B),

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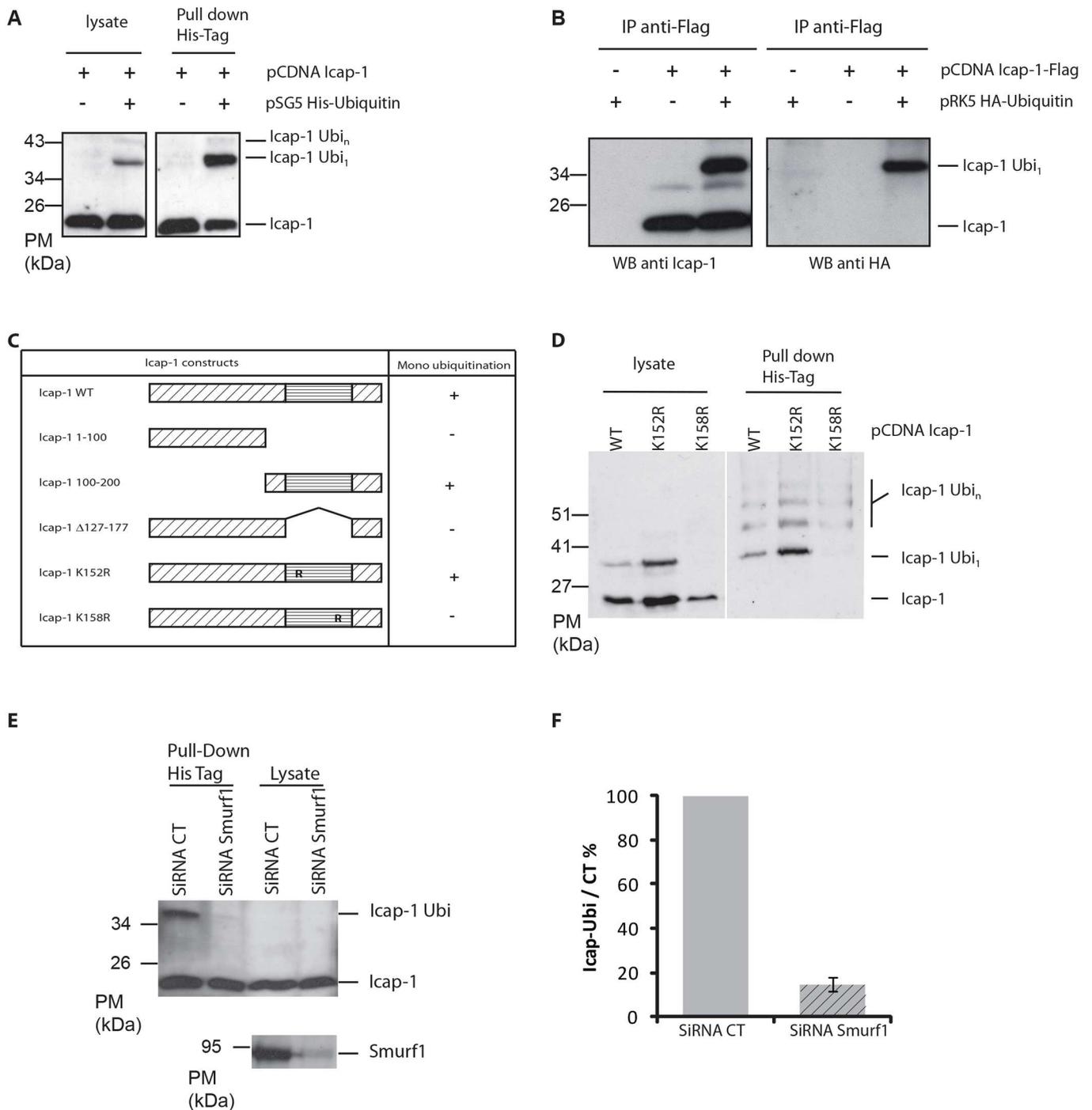


Fig. 1. The Smurf1 ubiquitin ligase is responsible for ICAP-1 monoubiquitylation. (A) ICAP-1 was overexpressed in CHO cells with or without His-tagged ubiquitin. After pulldown on TALON resin, the ubiquitylated proteins were analyzed by western blotting with the anti-ICAP-1 antibody. ICAP-1 was monoubiquitylated (Icap-1 Ub₁) and weakly polyubiquitylated (Icap-1 Ub_n). (B) ICAP-1-Flag immunoprecipitated by anti-Flag antibody can be recognized by anti-HA antibodies (as assessed by western blotting) after co-transfection with HA-Ubi and ICAP-1-Flag in CHO cells. The results are representative of more than three independent experiments. (C) Different ICAP-1 constructs were used to identify the ubiquitylated lysine residue. The horizontal-striped box corresponds to the β 1 integrin-binding site. (D) ICAP-1 WT, ICAP-1 K152R or ICAP-1 K158R were overexpressed in CHO cells with His-tagged ubiquitin. His-tagged pulldown assays show that only the ICAP-1 K158R mutant was not monoubiquitylated. The results are representative of three independent experiments. (E) HeLa cells with or without Smurf1 knockdown were co-transfected with ICAP-1 and His-tagged ubiquitin. After pulldown on TALON resin, the ubiquitylated proteins were analyzed by western blotting with the anti-ICAP-1 antibody. Non-ubiquitylated ICAP-1 was used to ensure equivalent ICAP-1 levels in both lysates. CT, control. (F) Quantification of the level of ubiquitylated ICAP-1 in Smurf1-silenced HeLa cells. Error bars represent s.e.m. ($n=3$). PM, position of molecular mass makers.

confirming that ICAP-1 can be ubiquitylated. Furthermore, to identify which lysine residue is monoubiquitylated, we analyzed whether truncated forms of ICAP-1 could be monoubiquitylated (Fig. 1C). We determined that the monoubiquitylation site was

located in the binding domain for β 1 integrin. The point mutation of either one of the two lysine residues present in this domain identified lysine K158 as the site of monoubiquitylation, as its replacement with arginine led to the absence of the 35 kDa band

(Fig. 1D) without changing the ICAP-1 polyubiquitylation states (Fig. 1D). The non-ubiquitylatable K158R mutant was even less stable than wild-type (WT) ICAP-1, suggesting that the monoubiquitylated form of ICAP-1 is not targeted for proteasomal degradation but rather may have a signaling function (Fig. S1A,B). Because Smurf1 catalyzes the ubiquitylation of the integrin activator talin (Huang et al., 2009), we hypothesized that Smurf1 could be responsible for ICAP-1 monoubiquitylation. To test this hypothesis, Smurf1 was silenced by small interfering RNA (siRNA); there was a high efficiency in reducing Smurf1 transcript and protein levels without affecting ICAP-1 expression (Fig. 1E). ICAP1 monoubiquitylation was blocked when Smurf1 was knocked down, suggesting that Smurf1 is necessary for promoting ICAP-1 monoubiquitylation (Fig. 1E,F). A pull-down assay shows that purified recombinant Smurf1–GST is able to bind to exogenously expressed ICAP-1 in CHO cells, in contrast to the null interaction with GST alone (50-fold less) or with the weak binding to GST fused to Smurf2 (10-fold less) (Fig. S1C). Smurf2 had been chosen as a control because overlapping but distinct substrate and regulator specificity has been observed between Smurf1 and Smurf2 (Lu et al., 2008, 2011). The co-immunoprecipitation between Smurf1–Myc and ICAP-1–Flag expressed in CHO cells confirms that Smurf1 and ICAP-1 belong to the same complex (Fig. S1D). A direct interaction between Smurf1 and ICAP-1 was demonstrated by an ELISA assay using purified recombinant GST–Smurf1 and purified recombinant ICAP-1–His (Fig. S1E). Taken together, our results indicate that Smurf1 is responsible for ICAP-1 monoubiquitylation.

The monoubiquitylation of ICAP-1 prevents binding to $\beta 1$ integrin and regulates $\beta 1$ integrin-dependent adhesion

According to structure predictions and crystallographic data (Chang et al., 2002; Liu et al., 2013), the monoubiquitylation site is located in the $\beta 1$ integrin-binding domain of ICAP-1 facing the isoleucine residue important for the binding to $\beta 1$ integrin (Fig. 2A). As this monoubiquitylation could interfere with the interaction between ICAP-1 and $\beta 1$ integrin, we used two classical methods to produce an ubiquitylated form of a protein (Torrino et al., 2011; Visvikis et al., 2008), first by co-transfecting ICAP-1 with His-tagged ubiquitin and second by creating a chimera made of ubiquitin fused to the C-terminal tail of ICAP-1 (ICAP-1–Ubi) (Fig. 2B). We tested the ability of WT, non-ubiquitylatable (K158R) and monoubiquitylated ICAP-1 (endogenous ubiquitylation or chimera) to interact with the cytoplasmic domain of either $\beta 1$ integrin or $\beta 3$ integrin fused with GST or with GST alone by pull-down assay (Fig. S2A) or by ELISA assay (Fig. 2C). As previously reported (Millon-Frémillon et al., 2008), we confirmed that ICAP-1 specifically interacts with the cytoplasmic domain of $\beta 1$ integrin (Fig. 2C; Fig. S2A). Furthermore, the non-ubiquitylated K158R mutant retained the ability to interact with the cytoplasmic domain of $\beta 1$ integrin, whereas both ubiquitylated forms of ICAP-1 (His-tagged and chimeric) lost the capacity to interact with the cytoplasmic domain of $\beta 1$ integrin (Fig. 2C; Fig. S2A). These results show that ICAP-1 monoubiquitylation prevents the interaction of ICAP-1 with $\beta 1$ integrin.

Next, we investigated whether the monoubiquitylation of ICAP-1 could affect FA organization by rescuing ICAP-1-deficient osteoblast cells with a similar stable expression of WT ICAP-1, non-ubiquitylatable ICAP-1 K158R and of the chimeric ubiquitylated form. All osteoblast cell lines were able to spread onto FN and develop FAs containing $\beta 1$ integrins, as revealed by 9EG7 antibody staining for activated $\beta 1$ integrin (Fig. 2D). Like ICAP-1-deficient

cells, cells expressing the ubiquitylated form of ICAP-1 displayed more numerous $\beta 1$ integrin-containing FAs compared with cells expressing the WT form (Fig. 2D–F) because of the inability of the monoubiquitylated ICAP-1 to inhibit $\beta 1$ integrin. Conversely, cells expressing the non-ubiquitylatable ICAP-1 K158R mutant displayed fewer, smaller and more-punctate adhesion sites (Fig. 2D–F) compared with those of WT ICAP-1, likely due to its ability to interact with $\beta 1$ integrin and thus inhibit the assembly of larger FAs (Bouvard et al., 2007; Millon-Frémillon et al., 2008).

As Smurf1 is responsible for ICAP-1 monoubiquitylation, we investigated whether the formation of $\beta 1$ integrin-containing FAs was dependent on Smurf1 activity. As expected, the deletion of Smurf1 led to a decrease in the number and area of $\beta 1$ integrin-containing FA (Fig. S2B,C,D) phenocopying the non-ubiquitylatable ICAP-1 K158R phenotype (Fig. 2D–F). Conversely, the ubiquitylated ICAP-1 was able to bypass the destructive effect of Smurf1 deletion on $\beta 1$ integrin-containing FAs (Fig. S2B,C,D). Thus, Smurf1-mediated ICAP-1 monoubiquitylation plays a crucial role in the organization of $\beta 1$ integrin-containing FA by preventing or disrupting the ICAP-1– $\beta 1$ -integrin interaction.

ICAP-1 monoubiquitylation is a signal coordinating FN density sensing with rigidity sensing

We wondered whether ICAP-1 monoubiquitylation was involved in FN density and rigidity sensing. To test an effect on FN density sensing, single-cell tracking of sparse cells was performed to monitor the migration speed of ICAP-1-deficient osteoblast or mouse embryonic fibroblast (MEF) cells expressing WT ICAP-1, K158R ICAP-1 or ICAP-1–Ubi in the presence of increasing concentrations of FN. As expected (Discher et al., 2005; Engler et al., 2006; Raab et al., 2012), WT ICAP-1-expressing osteoblasts (Fig. 3A; Movies 1,2) or MEFs (Fig. S3A) displayed faster migration rates with increasing FN density. While the migratory speed of the cells expressing the ubiquitylated ICAP-1 form depended on ECM density, like ICAP-1 null cells, the cells expressing the non-ubiquitylatable K158R mutant maintained the same migration speed whatever the density of FN coating (Fig. 3A; Fig. S3A, Movies 3,4). Moreover, the ability to adapt their migration response to ECM density was lost in cells treated with siRNA against Smurf1 but was rescued in cells co-expressing the monoubiquitylated ICAP-1 showing that the Smurf1-dependent monoubiquitylation of ICAP-1 is necessary for cells to sense and respond to FN density (Fig. S3B).

To explore the possibility that the inability of the K158R mutant to adapt its migration speed to FN density could be due to a greater capacity to lock $\beta 1$ integrin in its inactivated form than with WT ICAP-1, we analyzed the response of cells treated with $\beta 1$ integrin-blocking antibodies to increasing FN density. We showed that these cells were unable to sense the density of FN or adapt their migratory behavior (Fig. 3B), confirming the requirement for $\beta 1$ integrin activation for the adaptation of the cell migration rate to the FN density. Additionally, cells co-expressing a $\beta 1$ integrin mutant that lacks ICAP-1 binding ($\beta 1$ V787T) with the ICAP-1 K158R mutant or in the context of silenced Smurf1 were still able to adapt their migration speed to the FN density (Fig. 3B; Fig. S3C). Therefore, the unresponsiveness of cells to the FN density is most likely due to the inhibitory interaction between the non-ubiquitylatable ICAP-1 and $\beta 1$ integrin. Overall, ICAP-1 monoubiquitylation by Smurf1 is required to release ICAP-1 inhibitory effect on $\beta 1$ integrin in order to permit the adaptation of cell migration to ECM density.

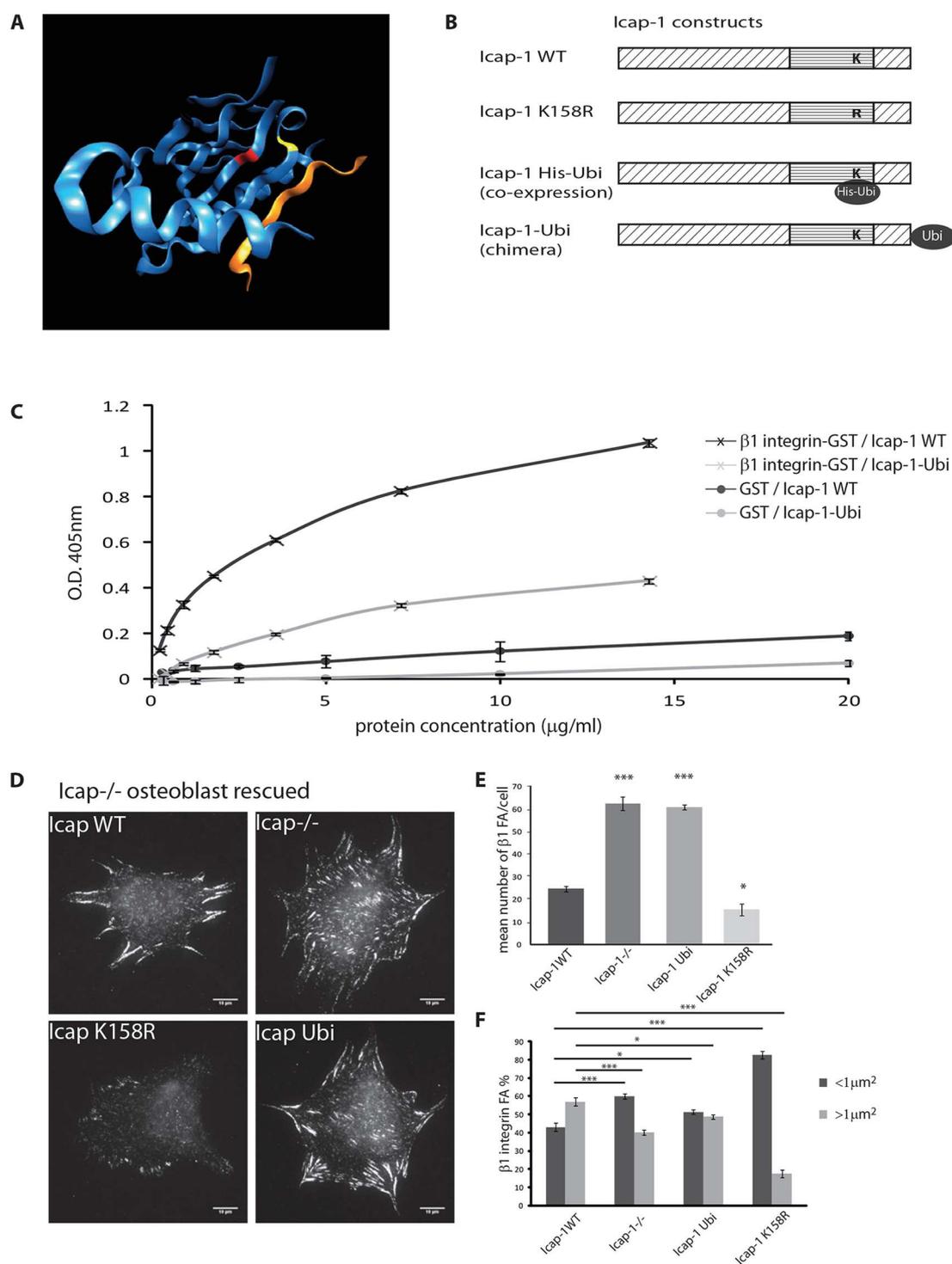


Fig. 2. Ubiquitylated ICAP-1 does not interact with the $\beta 1$ integrin cytoplasmic tail and disorganizes FA distribution. (A) Recently published structure of ICAP-1 interacting with the $\beta 1$ integrin cytoplasmic tail (PDB 4DX9) (Liu et al., 2013). Blue, ICAP-1 protein with I139 represented in yellow and K158 represented in red. Orange, $\beta 1$ integrin cytoplasmic tail. This image was made with VMD, NAMD, BioCoRE, JMV and other software support (these software packages are developed with NIH support by the Theoretical and Computational Biophysics group at the Beckman Institute, University of Illinois at Urbana-Champaign). (B) ICAP-1 constructs used for the study. K158R is the non-ubiquitylatable form. ICAP-1-His-Ubi results from the overexpression of ICAP-1 and His-tagged ubiquitin proteins in CHO cells. ICAP-1-Ubi is a chimeric form with ubiquitin fused at the C-terminus of ICAP-1 to mimic constitutive monoubiquitylation. (C) Interaction between recombinant ICAP-1-His or ICAP-1-Ubi-His and recombinant GST or the GST- $\beta 1$ integrin cytoplasmic domain as determined by an ELISA assay. The results are representatives of three independent experiments. (D) $\beta 1$ integrin staining in ICAP-1-null osteoblasts or ICAP-1-null cells rescued with ICAP-1 WT, non-ubiquitylatable ICAP-1 or the ICAP-1 ubiquitin chimera spread on FN for 2.5 h. The cells expressing the non-ubiquitylatable form (K158R) display smaller $\beta 1$ integrin FAs compared with the cells expressing ICAP-1 WT. Scale bars: 10 μm . (E) Quantification of the $\beta 1$ integrin focal adhesion number and (F) distribution of the $\beta 1$ integrin focal adhesion areas. Analyses were performed on 30–40 cells from two independent experiments. Error bars indicate s.e.m. * $P < 0.05$, *** $P < 0.0005$ (one-way ANOVA and Tukey's HSD test).

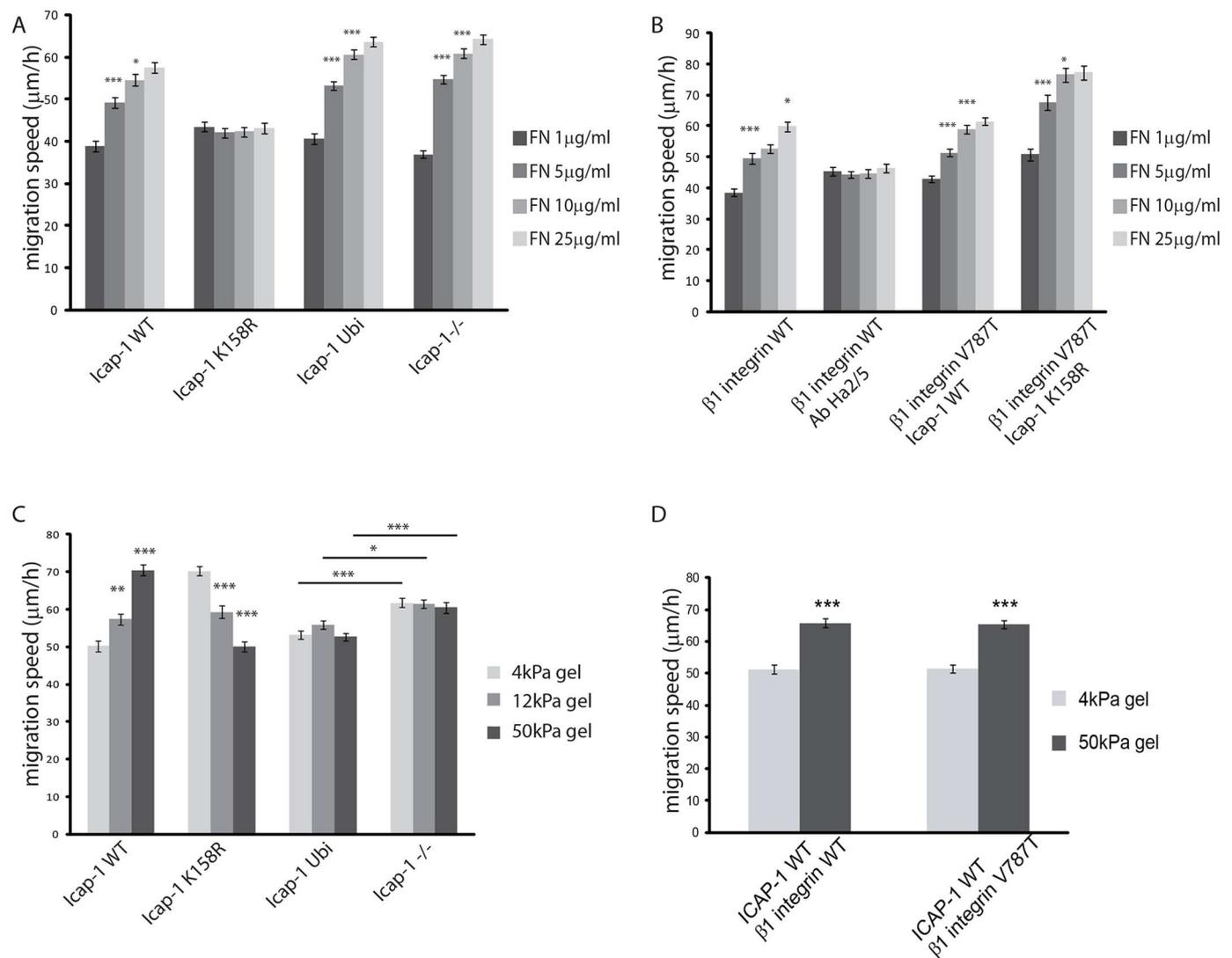


Fig. 3. ICAP-1 ubiquitylation controls FN density and rigidity sensing. Osteoblasts were spread on increasing concentrations of FN and migration was monitored for 5 h using time-lapse microscopy. Cell velocity was determined by individually tracking 150–200 cells from three independent experiments. (A) Cells expressing ICAP-1-WT, the ICAP-1 ubiquitin chimera or cells deficient in ICAP-1 adapted their migratory speed according to the FN density, whereas the cells expressing the ICAP-1 K158R mutant maintained the same speed regardless of the FN density. (B) Similar to the cells expressing ICAP-1 K158R, cells treated with a blocking anti-β1 integrin antibody (Ab Ha2/5) were unable to adapt their migration speed to the FN density. β1 integrin-null cells expressing the β1 integrin mutant that lacks ICAP-1 binding (V787T) were not affected by K158R ICAP-1 expression. (C,D) Osteoblast cells were spread on FN-coated PAA gels of different rigidities. Cell migration was monitored for 5 h using time-lapse microscopy. The cell velocity was determined by individually tracking 150–300 cells in three independent experiments. Similar to in ICAP-1-deficient cells, ICAP-1-Ubi cells did not change their velocity according to gel rigidity whereas WT cells moved more quickly in stiffer gels (C). β1 integrin-null cells expressing the β1 integrin mutant that lacks ICAP-1 binding (V787T) responded to gel rigidity similarly to control cells (D) indicating that the interaction between β1 integrin and ICAP-1 is not necessary to adapt cell migration to substrate stiffness. Error bars indicate the mean±s.e.m. * $P < 0.05$, ** $P < 0.005$, *** $P < 0.0005$ (one-way ANOVA and Tukey's HSD test).

We next evaluated the effects of ICAP-1 monoubiquitylation on the ECM rigidity sensitivity. Osteoblast cells (Fig. 3C) or MEF cells (Fig. S3D) infected with ICAP-1 WT, ICAP-1 K158R and ICAP-1-Ubi were plated onto FN-conjugated elastomeric polyacrylamide (PAA) gels with increasing Young's modulus (E) and monitored for cell migration. As expected, the WT ICAP-1 cells moved more quickly on stiffer gels than they did on softer gels (40% increase on the stiffer substrate) (Fig. 3C; Fig. S3D, Movies 5,6). Cells expressing ICAP-1 K158R still responded to the increase in matrix rigidity, whereas cells expressing the monoubiquitylated ICAP-1 displayed a constant migration velocity that was independent of the stiffness of the substrate, like ICAP-1-deficient cells (Fig. 3C; Fig. S3D, Movies 7,8). However, the migration speed of ICAP-1^{-/-}

cells was slightly but significantly higher as compared to that of ICAP-1-Ubi cells. This suggests that ICAP-1 monoubiquitylation also controlled the capacity of cells to adapt their velocity to ECM rigidity. As monoubiquitylation prevents ICAP-1 and β1 integrin interaction, we then investigated whether rigidity sensing was dependent on ICAP-1 and β1 integrin interaction. Cells expressing the β1 integrin V787T mutant that are unable to interact with ICAP-1 still adapt their velocity in response to the external rigidity (Fig. 3D) whereas ICAP-1 deficiency led to insensitiveness to substrate stiffness (Fig. 3C). Thus, the presence of ICAP-1 is required even though ICAP-1 interaction with β1 integrin is dispensable for rigidity sensing. Monoubiquitylation of ICAP-1 is a signal that allows the sensing of matrix density and rigidity by

decoupling the inhibitory role of ICAP-1 on $\beta 1$ integrin from an unexpected role that is independent of its interaction with $\beta 1$ integrin.

The monoubiquitylation of ICAP-1 increases cell contractility

As rigidity sensing is associated with cell contractility, we sought to determine whether the monoubiquitylated form of ICAP-1 might interfere with cell contractility. First, as a contractility marker, we analyzed the phosphorylation state of myosin light chain (pMLC) by western blotting lysates from WT, and ICAP-1-Ubi and ICAP-1-deficient cells plated onto FN-coated plastic or elastomeric PAA gels with a Young's modulus (E) of 4 or 50 kPa (Fig. S4A). As expected, the level of pMLC in total cell lysates of cells expressing ICAP-1 WT increased with the substrate rigidity. ICAP-1-deficient cells displayed the same behavior as ICAP-1 WT cells. In contrast, cells expressing the monoubiquitylated ICAP-1 showed a constant level of pMLC independently of the rigidity of the substrate. This loss of pMLC regulation is correlated with the inability of ICAP-1-Ubi cells to adapt their velocity to ECM rigidity (Fig. 3C). In addition, an increase of pMLC staining along the stress fibers in ICAP-1-Ubi cells was noted (Fig. 4A). To investigate whether the monoubiquitylated ICAP-1 is involved in the genesis and modulation of forces applied to the substratum, traction force microscopy (TFM) was used. Traction forces generated by the cells were twice as high in ICAP-1-Ubi cells as compared to the WT cells and ICAP-1-deficient cells (Fig. 4B). Therefore, the monoubiquitylation of ICAP-1 increases cell contractility by forcing the phosphorylation of myosin independently of the substrate rigidity.

The monoubiquitylation of ICAP-1 drives MRCK α -mediated cell contractility

Cell contractility relies on the balance between ROCK, MLCK and mDia activities to control elongation and organization of actin filament (Burrige and Wittchen, 2013). To explore the contractility pathways potentially affected by ICAP-1-Ubi, a pharmacological approach was used by testing ROCK, MLCK and mDia inhibitors (Y27632, ML7 and SmifH2, respectively) on the migration of osteoblasts adhered to 4 kPa gels coated with 5 $\mu\text{g}/\text{ml}$ of FN. Like WT cells, ICAP-1-Ubi cells migrated slower upon MLCK and mDia inhibition (Fig. S4B). As previously described (Totsukawa et al., 2000), WT cells migrate faster upon ROCK inhibition. In contrast, ICAP-1-Ubi cells were insensitive to Y27632 treatment since no change in migratory speed response was observed as compared with the WT cells (Fig. S4B). This insensitivity to ROCK inhibition in ICAP-1 Ubi cells is not due to the loss of the interaction between ICAP-1-Ubi and $\beta 1$ integrin since cells expressing the V787T mutant of $\beta 1$ integrin, which is unable to interact with ICAP-1, are still sensitive to ROCK inhibition (Fig. S4C). Thus, ICAP-1-Ubi cell migration is independent of ROCK-controlled contractility, suggesting an alternative contractile pathway for ICAP-1-Ubi cells.

Besides regulating ROCK1 (Peter et al., 2006), ICAP-1 has been shown to inhibit Cdc42 and Rac1 (Degani et al., 2002), which are involved in the regulation of MRCK. Therefore, we sought to assess whether ICAP-1 could regulate MRCK-dependent cell contractility (Leung et al., 1998). To test this hypothesis, we used a siRNA strategy to knockdown ROCK1, ROCK2, MRCK α and MRCK β (Fig. 4C,D). The WT ICAP-1 cells moved more quickly on stiffer gels than they did on softer gels whatever the siRNA used except in conditions of ROCK2 deletion suggesting that WT cells adapt their migratory behavior through a ROCK2-dependent contractility and

this behavior is independent of ROCK1, MRCK α and MRCK β (Fig. 4C). In contrast, only MRCK α silencing in ICAP-1-Ubi cells led to an increase in the cell migration speed when rigidity of the substrate was increased (Fig. 4D). Thus, the cell contractility mode imposed by ICAP-1 monoubiquitylation is dependent on MRCK α and is independent of ROCK1, ROCK2 and MRCK β . To confirm the involvement of MRCK α in the monoubiquitylated ICAP-1-dependent phosphorylation of myosin, we tested the effect of siRNA against MRCK α or ROCK2 on the decoration of stress fibers by T18/S19 phosphorylated MLC (ppMLC) (Fig. 4E). Whereas the siRNA against ROCK2 decreased the level of ppMLC in WT cells, the depletion of MRCK α significantly reduced the level of ppMLC in cells infected with ICAP-1-Ubi. Thus, ICAP-1 monoubiquitylation favors the phosphorylation of myosin II that is dependent on the activity of MRCK α whereas ROCK2 activity is responsible for the phosphorylation of myosin II in WT cells. Taken together, these results show that ICAP-1 monoubiquitylation allows the switch from ROCK2-mediated to MRCK α -mediated cell contractility.

DISCUSSION

Our data show that monoubiquitylation of ICAP-1, a protein that associates with integrin cytoplasmic domains, by Smurf1 is involved in regulating the balance between adhesion and contractility. ICAP-1 monoubiquitylation inhibits its binding to $\beta 1$ integrin, subsequently regulating the number and organization of $\beta 1$ integrin-containing FAs. ICAP-1 and its monoubiquitylated form may be crucial mediators involved in the balance between ROCK2 and MRCK α activities in order to adapt cell contractility to the variability of ECM stiffness. Our results show that these two functions of ICAP-1 are integrated by the cell to sense both matrix density and rigidity.

Smurf1 as a node to control focal adhesion dynamics and cell contractility

In addition to its ability to ubiquitylate talin (Huang et al., 2009), Smurf1 was a good candidate for ICAP-1 monoubiquitylation because Smurf1 associates with the cerebral cavernous malformations (CCM) complex (Croze et al., 2009), which interacts with ICAP-1 (Hilder et al., 2007). Smurf1 also possesses an NPxY motif that might be able to interact with ICAP-1 phosphotyrosine-binding (PTB) domain. Smurf1 is also involved in cell polarity and cell migration (Sahai et al., 2007; Wang et al., 2003). We demonstrated that the monoubiquitylation of ICAP-1 by Smurf1 is not involved in ICAP-1 degradation via the proteasome, but rather, regulates the assembly and organization of FAs by modulating the ICAP-1- $\beta 1$ -integrin interaction. The ICAP-1- $\beta 1$ -integrin interface is likely disrupted upon ICAP-1 monoubiquitylation since K158 is in close vicinity to the I138 residue known to be important for the $\beta 1$ integrin interaction (Chang et al., 2002; Liu et al., 2013).

In addition to their canonical roles in cell growth and differentiation mediated through TGF signaling (Zhu et al., 1999), accumulating evidence indicates that Smurfs play key roles in regulating cell adhesion and migration. Smurf1 is localized in lamellipodia and filopodia, with a fraction of Smurf1 in FAs (Huang et al., 2009; Wang et al., 2003). Smurf1 ubiquitylates molecules involved in both cell adhesion and contractility. Smurf1 controls talin head degradation, and subsequently adhesion stability and cell migration (Huang et al., 2009). RhoA ubiquitylation by Smurf1 causes its degradation at the leading edge of migrating cells and promotes lamellipodium formation (Sahai et al., 2007; Wang et al.,

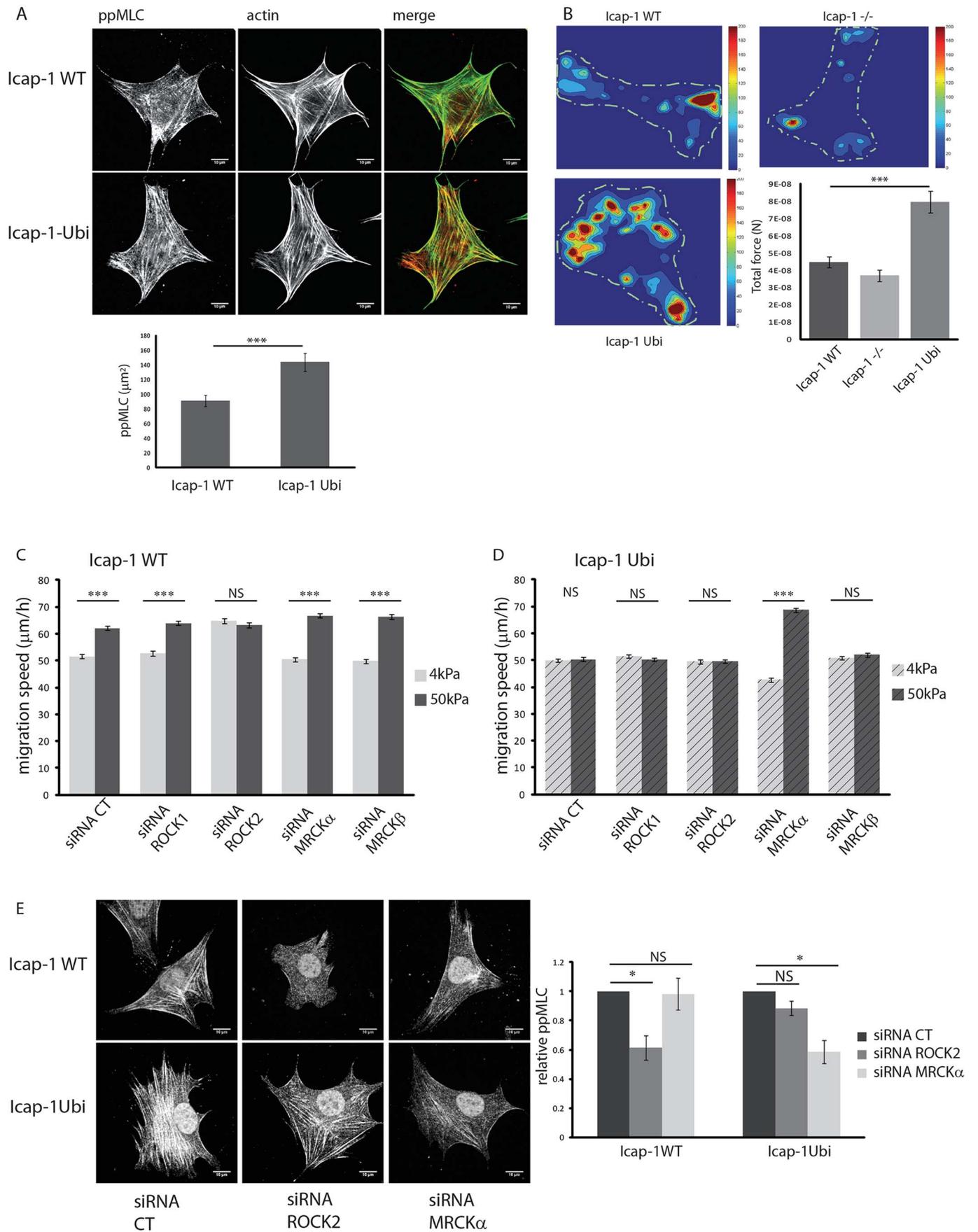


Fig. 4. See next page for legend.

Fig. 4. The monoubiquitylation of ICAP-1 drives an MRCK α -mediated cell contractility. (A) Immunostaining of ppMLC and actin (phalloidin) in WT cells and ICAP-1–Ubi osteoblast cells. Note the increase of ppMLC along the stress fibers as seen from the quantification of 80 cells from three independent experiments. (B) Representative traction force maps obtained by TFM in ICAP-1 WT, ICAP-1-deficient and ICAP-1–Ubi osteoblast cells (images). TFM experiments showed an increase of the force applied on the substrate in ICAP-1–Ubi cells as compared to ICAP-1 WT and ICAP-1-deficient cells ($n=78$ from three independent experiments) (graph). Error bars indicate the mean \pm s.e.m. $***P<0.0005$ (one-way ANOVA and Tukey's HSD test). (C) Osteoblasts were spread on FN-coated PAA gels of different rigidities. Cell migration was monitored for 5 h using time-lapse microscopy. Cell velocity was determined by individually tracking 200–300 cells in three independent experiments. Monitoring of WT cells migration after treatment with scrambled siRNA (siRNA CT) or siRNA against ROCK1, ROCK2, MRCK α or MRCK β on 4 or 50 kPa gels. Note that WT cells are sensitive to ROCK2 siRNA treatment. (D) Monitoring of ICAP-1–Ubi osteoblast cells migration after treatment with scrambled siRNA (siRNA CT) or with siRNA against ROCK1, ROCK2, MRCK α or MRCK β on 4 or 50 kPa gels. Note that ICAP-1–Ubi cells are sensitive to MRCK α siRNA treatment. (E) Immunostaining of ppMLC in WT osteoblast cells and ICAP-1–Ubi osteoblast cells after treatment with siRNA against ROCK2 or MRCK α (left panel). The right-hand panel shows a quantification of ppMLC staining. Note the decrease of ppMLC staining along the stress fibers after siRNA against ROCK2 for the WT cells whereas the decrease of ppMLC is observed after treatment with siRNA against MRCK α for ICAP-1–Ubi cells ($n>80$). Error bars indicate the mean \pm s.e.m. $*P<0.05$; $***P<0.0005$; NS, not significant (one-way ANOVA and Tukey's HSD test). Scale bars: 10 μ m.

2003). Our data demonstrate that Smurf1 is a node controlling both FA dynamics and cell contractility through a common target, ICAP-1. ICAP-1 monoubiquitylation not only regulates the number and organization of β 1 integrin-containing FAs but also inhibits ROCK signaling and promotes the MRCK signaling pathway. Therefore, we add another piece of evidence showing that the RhoA–ROCK pathway is inhibited by Smurf1, and we demonstrate for the first time that Smurf1 controls a switch from a ROCK-dependent to a MRCK-dependent cell contractility.

The monoubiquitylation of ICAP-1 as a switch from ROCK2-mediated to MRCK α -mediated contractility

In addition to its role in the β 1 integrin activation cycle (Millon-Frémillon et al., 2008), ICAP-1 interferes with small GTPase signaling and cell contractility by putting a cap on RhoA activation (Faurobert et al., 2013) and inhibiting Rac1 and Cdc42 (Degani et al., 2002). So far, how ICAP-1 can regulate both RhoA–ROCK signaling and the Cdc42 and Rac1 pathway was unclear. It has been described that a cooperation between RhoA–ROCK and Cdc42 or Rac1–MRCK signaling can control cell contractility cell polarity, morphology and morphogenesis (Gally et al., 2009; Unbekandt and Olson, 2014; Wilkinson et al., 2005). Their respective contribution might depend on ECM rigidity. ICAP-1, independently of its

interaction with β 1 integrin, could act as a sensor of ECM rigidity differently modulating the activity of each enzyme depending on the substrate stiffness. It could act by playing on the level of activation of RhoA, Rac1 or Cdc42 and by directly modulating the activity of ROCK2 and MRCK α . Thus, we propose that ICAP-1 monoubiquitylation by Smurf1 is a key event leading to a switch from ROCK2-mediated to MRCK α -mediated cell contractility. ICAP-1 and its monoubiquitylated form regulate ROCK2- and MRCK α -dependent MLC phosphorylation independently of interaction with β 1 integrin. This is in line with previous studies, which do not attribute a major role of β 1 integrin to ECM rigidity sensing (Jiang et al., 2006). Taken together, our results show that ICAP-1 contributes to an elaborate signaling network responsible for maintaining cell tensional homeostasis, going from the dynamics of cell adhesion to the adaptation of contractile actomyosin machinery. ICAP-1 may function in β 1 integrin-dependent and -independent pathways to orchestrate both the chemo and mechanical regulation of cell migration. These two pathways might regulate distinct signaling cascades through a switch operated by Smurf1 to adapt the cellular migratory response (Fig. 5). ICAP-1 is essential in rigidity sensing and its monoubiquitylation might be crucial for the adaptation of cells to a local variation of ECM stiffness in tissues or a change of ECM composition during development or in pathological situations. ICAP-1 monoubiquitylation would allow the cell to adapt its the contractility depending on substrate stiffness by controlling the balance between ROCK2- and MRCK α -mediated cell contractility. In future studies, it will be important to identify the factors that are regulated by ICAP-1 independently of its interaction with β 1 integrin in order to develop a more complete understanding of the functions of ICAP-1 in mechanosensing.

MATERIALS AND METHODS

Plasmid construction

The plasmids pCMVFlag-Smurf1 WT, pGEX4T1-Smurf1 WT, pGEX4T1-Smurf2 WT, pRK5-Myc-Smurf1 and pRK5-HA-Ubiquitin-WT were obtained from Addgene (Cambridge, MA; numbers 11752, 13502, 13504, 13676 and 17608). pGEX4T1 plasmids containing the β 1 or β 3 integrin cytoplasmic domain, as well as pCLMFG retroviral vectors containing WT β 1 integrin or the V787T mutant, have been previously described (Brunner et al., 2011). The pSG5-ubiquitin-His vector was a kind gift from Saadi Khochbin (U823 INSERM-UJF, Grenoble, France). The full-length cDNA of WT human ICAP-1 was subcloned into the *Eco*RI and *Bam*HI sites of the pBabe-puro retroviral vector (pBabe-ICAP-1 WT). The K158R substitution was introduced into the ICAP-1 cDNA via site-directed mutagenesis (pBabe-ICAP-1 K158R). The Myc tag was inserted at the 3' end of the ICAP-1 or ubiquitin cDNA using PCR. The Myc-tagged ICAP-1 cDNA was subcloned between the *Bam*HI and *Eco*RI sites of the pcDNA3.1 expression vector and mutated to generate the K158R mutant.

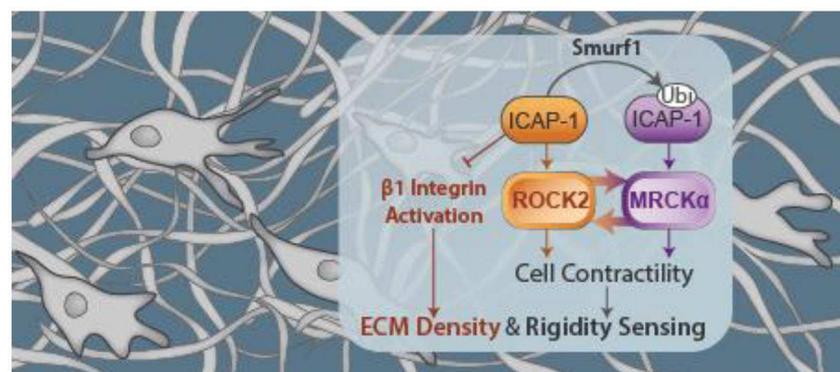


Fig. 5. A ROCK2–MRCK α switch operated through the monoubiquitylation of ICAP-1 by Smurf1 to adapt the cellular migratory response. Smurf1 is able to monoubiquitylate ICAP-1. The monoubiquitylation of ICAP-1 by Smurf1 is required to release inhibitory effect of ICAP-1 on β 1 integrin, thereby facilitating the activation–deactivation cycle of β 1 integrin important for ECM density sensing and adaptive cell migration responses. The monoubiquitylation of ICAP-1 allows the switch from ROCK2-mediated to MRCK α -mediated cell contractility to control ECM rigidity sensing.

The cDNA of Myc-tagged ubiquitin was amplified and inserted at the 3' end of the ICAP-1 cDNA, between the *EcoRI* and *XhoI* sites of the pcDNA3.1 vector (pcDNA3.1-ICAP-1-myc, pcDNA3.1-ICAP-1 K158R-myc and pcDNA3.1-ICAP-1-Ubi-myc). The ICAP-1-Ubi-myc cDNA was subcloned into the pBabe-puro, between the *BamHI* and *SalI* sites (pBabe-ICAP-1-Ubi-myc).

Cell culture, transfection and antibodies

Immortalized osteoblasts were cultured in Dulbecco's modified Eagle's medium (DMEM; Invitrogen, Life Technologies, Cergy Pontoise, France), CHO cells and HeLa cells were grown in α MEM (PAA) at 37°C in a humidified, 5% CO₂ chamber. All media are supplemented with 10% fetal calf serum (FCS; Invitrogen), 100 U/ml penicillin and 100 μ g/ml streptomycin. Immortalized osteoblasts from *icap-1^{-/-}; Itgb1^{flox/flox}* mice were generated as previously described (Bouvard et al., 2007). These cells were treated with or without adenoCre viruses obtained from the gene transfer vector core (University of Iowa) to generate β 1 integrin-null cells. The ICAP-1-null cells were incubated with or without retroviral particles to obtain rescued cells expressing ICAP-1 WT, ICAP-1 K158R or the ICAP-1-Ubi chimera. The cells were selected with 1 mg/ml puromycin to produce cell populations with heterogeneous ICAP-1 expression levels. β 1 integrin-null cells that had already been rescued with ICAP-1 were again infected with retrovirus to obtain double-rescued cells expressing ICAP-1 (WT or mutant) and WT β 1 integrin or the V787T mutant. For all experiments, cells were trypsinized and washed in PBS before plating in DMEM containing 4% FN-free FCS for 3 h. Osteoblasts (90×10^4 cells) were transfected with 25 pmol siRNA and 6 μ l Lipofectamine RNAiMAX reagent (Invitrogen) according to the manufacturer's instructions. The cells were used 2 days after transfection. SMARTpool siRNA (Dharmacon Research Inc., Lafayette, LA) was used against appropriate proteins, along with the control siRNA sequence 5'-AGGUAGUGUAAUCGCCUUG-3'. HeLa cells were transfected with control or Smurf1 siRNA SMARTpool siRNA (Dharmacon Research Inc.) using Lipofectamine RNAiMAX (Invitrogen) according to the manufacturer's instructions; two rounds of transfection were performed. ICAP-1 and His-tagged ubiquitin were overexpressed using Fugene (BD Biosciences, Le Pont de Claix, France) according to the manufacturer's instructions. CHO cells were transfected with ExGen (EUROMEDEX, Souffelweysheim, France) following the manufacturer's instructions using pcDNA3.1-ICAP-1-myc, pcDNA3.1-ICAP-1K158R-myc or pcDNA3.1-ICAP-1-Ubi-myc. CHO cells were cotransfected with pcDNA3.1-ICAP-1-myc or pcDNA3.1-ICAP-1 K158R-myc and pSG5-ubiquitin-His. After 24 h, the transfected cells were incubated with the proteasome inhibitor MG132 (20 μ M) for 4 h. The antibodies used in this study were the following: rat anti- β 1 integrin 9EG7 (1:100; BD Biosciences, 553715), donkey anti-rabbit-IgG conjugated to HRP (1:12,000; Jackson ImmunoResearch, UK, 711-036-152), goat anti-rat-IgG conjugated to Alexa Fluor 488 (1:1000; Invitrogen, A-11006), mouse anti-actin (1:1000; Sigma-Aldrich, Saint Quentin Fallavier, France, A2066), mouse anti-Smurf1 (1:1000; Santa Cruz Biotechnology, Heidelberg, Germany, Sc-100616) rabbit anti-T18/S19 MLC [1:1000 (western blotting) or 1:100 (immunofluorescence); Cell Signaling Technology, Leiden, The Netherlands], and rabbit anti-ICAP-1 (1:1000; Millon-Frémillon et al., 2008).

Purification of His-tagged ubiquitylated proteins

Transfected CHO cells were lysed in phosphate-buffered saline (PBS) containing 10% glycerol, 0.3% NP40, 5 mM NEM, 10 mM NaF, phosphatase inhibitor cocktails 2 and 3 (Sigma-Aldrich), and a protease inhibitor cocktail (cOmplete, EDTA-free, Roche, Meylan, France). After centrifugation (15,000 g for 20 min), the supernatants were incubated with Talon Metal Affinity resin (Clontech, Saint Germain en Laye, France) for 2 h. After three washes, the proteins were eluted in Laemmli buffer and analyzed by western blotting (3% of the total lysate is used for the input track).

Pulldown assays

GST-Smurf1 and GST-Smurf2 were expressed in *E. coli* (BL21 DE3 RIL) as previously described (Wang et al., 2006). Transfected CHO cells were lysed in buffer containing 50 mM Tris-HCl pH 7.7, 150 MG132, protease

inhibitor cocktail and phosphatase inhibitor cocktails 2 and 3. The supernatants were incubated for 3 h with GST-Smurf1-, GST-Smurf2- or GST-coupled glutathione-Sepharose beads. After five washes in lysis buffer, the samples were eluted in Laemmli buffer and analyzed by western blotting (3% of the total lysate is used for the input track). GST- β 1-integrin and GST- β 3-integrin were expressed in *E. coli* (BL21 DE3 RIL), and pulldown experiments with supernatants from transfected CHO cells were performed as previously described (Brunner et al., 2011).

ICAP-1 protein lifetime measurement

Transfected CHO cells were incubated with 100 μ g/ml cycloheximide (Sigma-Aldrich) with or without 20 μ M MG132. Cells were lysed in RIPA buffer at the indicated times, and the protein concentration was measured using the BCA assay. Total proteins (20 μ g) were separated by SDS-PAGE and immunoblotted as below.

Flag immunoprecipitation

Transfected CHO cells were lysed in lysis buffer (50 mM NaCl, 10 mM Pipes, 150 mM sucrose, 50 mM NaF, 40 mM Na₄P₂O₇·10H₂O, 1 mM Na₃VO₄, pH 6.8, 0.5% Triton X-100, 0.1% sodium deoxycholate, and protease inhibitor cocktail). The supernatants were incubated for 1 h with anti-Flag M2 magnetic beads (Sigma-Aldrich). After four washes with lysis buffer, the samples were eluted in lysis buffer containing 100 μ g/ml Flag peptide (Sigma-Aldrich) and analyzed by western blotting (3% of the total lysate is used for the input track).

ELISA assay

The interaction between recombinant ICAP-1 and ICAP-1-Ubi was analyzed using a solid-phase assay. Briefly, a 96-well tray (MaxiSorp, Nunc) was coated with either ICAP-1-His or ICAP-1-Ubi-His (40 μ g/ml) for 16 h at 4°C and blocked with 3% BSA in PBS for 1 h at room temperature. Increasing concentrations of GST, the GST- β 1-integrin cytoplasmic domain or GST-Smurf1 were added for 1 h. After three washes in PBS with 0.1% Tween20, detection of bound proteins was performed by using the antibodies directed against β 1 integrin cytoplasmic domain or Smurf1. Nonspecific binding to BSA-coated wells was subtracted from the results as background.

pMLC western blot analysis

Cells were plated on plastic or on PAA gels with controlled rigidities of 50 kPa or 4 kPa (Cell Guidance System, Cambridge, UK) coated with 1 μ g/cm² (5 μ g/ml) of FN. The next day cells were lysed in Laemmli buffer and analyzed by western blotting. Immunoblots were visualized using the ECL system (Biorad) and Chemidoc imaging system (Biorad).

Traction force microscopy

The PAA substrates were prepared on two-well LabTek slides (Thermo Fischer Scientific, Ulm, Germany) using 8% acrylamide mixed with appropriate percentage of bis-acrylamide and 10 mM HEPES (pH 8.5) gels. After two Sulfo-SANPAH (Thermo Fischer Scientific, Ulm, Germany) activations, the gels were coated with 5 μ g/ml FN (1 μ g/cm²) at 4°C overnight. We used a concentration of 0.15% of bis-acrylamide to create gels with controlled rigidities of 5 kPa. Cells were plated at an approximate density of 2×10^4 cells per cm² for 3–4 h and images were acquired on an iMIC Andromeda (FEI, Gräfelfing, Germany) microscope at 40x magnification. Force calculations were performed as previously described (Tseng et al., 2011).

Random migration analysis

Cells were plated on a 12-well plate containing a PAA substrate (Cell Guidance System) or on an 8-well LabTek slide coated with various FN concentrations at an approximate density of 1.2×10^5 per cm² for 3 h in CO₂-independent DMEM containing 4% FN-free FCS. The cells were maintained at 37°C and imaged on an inverted microscope (Zeiss Axiovert 200) equipped with a motorized stage, cooled CCD camera (CoolSnap HQ2, Roper Scientific) and a 10 \times objective (EC Plan-Neofluar) for live-cell imaging for 5 h at a frequency of 1 image every 4 min. Inhibitors were added as indicated to the medium 10 min prior to the initiation of image acquisition and maintained throughout the migration assay at a final

concentration of 10 μM for Y27632 (Calbiochem), 5 μM for ML7 (Calbiochem) and 2 μM for SmifH2 (Calbiochem). Cell velocity was obtained using the manual tracking plug-in in ImageJ software. A total of 150–300 cells were analyzed from at least five different locations in each experiment, and results were collected from three independent experiments.

Immunofluorescence

Cells were plated at an approximate density of 2×10^4 cells per cm^2 for 2.5 h in 24-well plates on slides coated with 0.6 $\mu\text{g}/\text{cm}^2$ (2 $\mu\text{g}/\text{ml}$) or 1.5 $\mu\text{g}/\text{cm}^2$ (5 $\mu\text{g}/\text{ml}$) of FN in DMEM containing 5% FN-depleted serum; the cells were then fixed and immunostained as previously described (Millon-Frémillon et al., 2008). For the focal adhesion analysis, images were acquired on an Axio Imager (Zeiss) microscope at with a 63 \times objective. We analyzed the $\beta 1$ integrin staining of 30–40 cells from two independent experiments using a thresholding method and the particle analyzer in ImageJ. Particles larger than 0.5 μm^2 were analyzed. Internal focal adhesions are defined as a FA that was more than 3 μm distal to the plasma membrane. For the ppMLC-decorated stress fibers, images were acquired on an iMIC Andromeda (FEI) microscope at with a 40 \times objective. We analyzed the phosphorylation of Thr18 and/or Ser19 on the light myosin chain in 90–100 cells from three independent experiments by using the 'Unsharp mask' and the particle analyzer plug-in in ImageJ software. Objects bigger than 0.5 μm^2 were analyzed.

Statistical tests

All data sets were analyzed with R (<http://www.R-project.org/>). We used an ANOVA-2 analysis and Tukey's HSD post-hoc test when necessary. Results are mean \pm s.e.m. Significance is indicated with asterisks (* $P < 0.05$, ** $P < 0.005$, *** $P < 0.0005$).

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Competing interests

The authors declare no competing or financial interests.

Author contributions

C.A.-R., A.-P.B., and E.P. designed and analyzed the experiments. A.-P.B., M.R.-K., A.-S.R., A.K., E.F., H.-N.F., I.B.-R., S.M.-D., C.O. and M.B. helped with the experimental design and the procedures, performed the experiments, and analyzed the data. C.A.-R., A.P.-B. and E.P. wrote the manuscript. All of the authors provided detailed comments. C.A.-R. initiated the project.

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Supplementary information

Supplementary information available online at <http://jcs.biologists.org/lookup/doi/10.1242/jcs.200139.supplemental>

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Supplemental information:

Supplemental information includes 4 supplemental figures and 8 supplemental movies.

Supplemental figures:

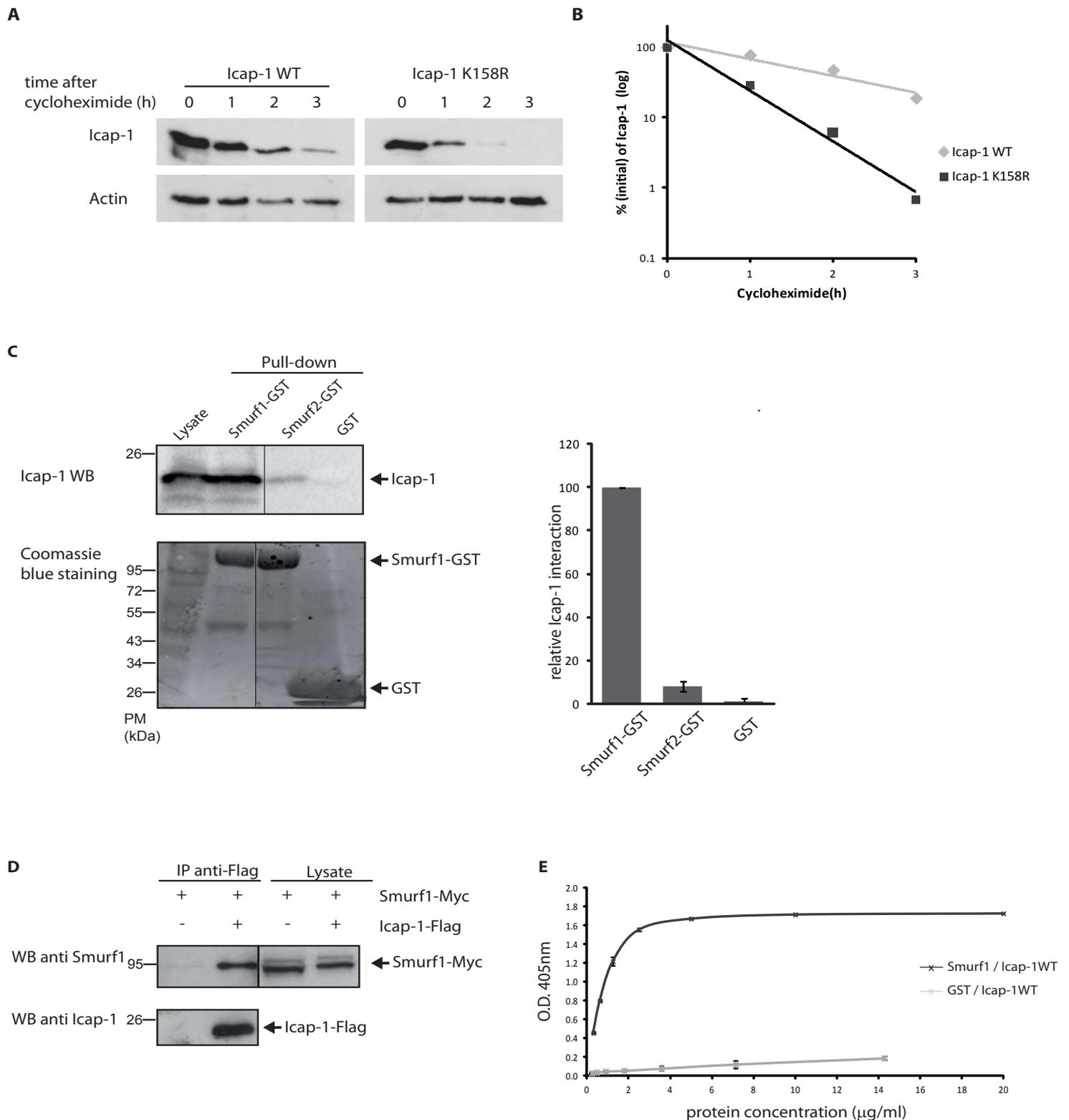
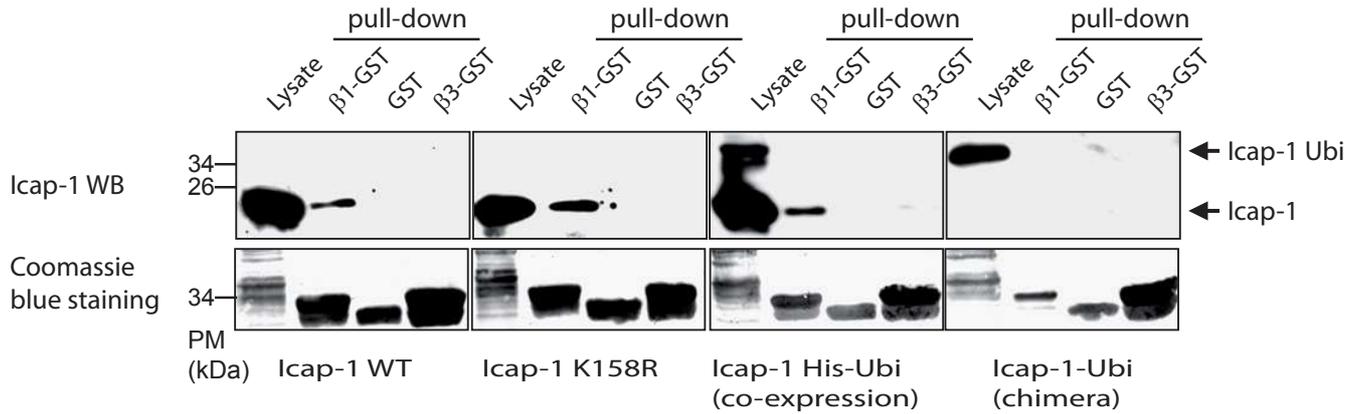


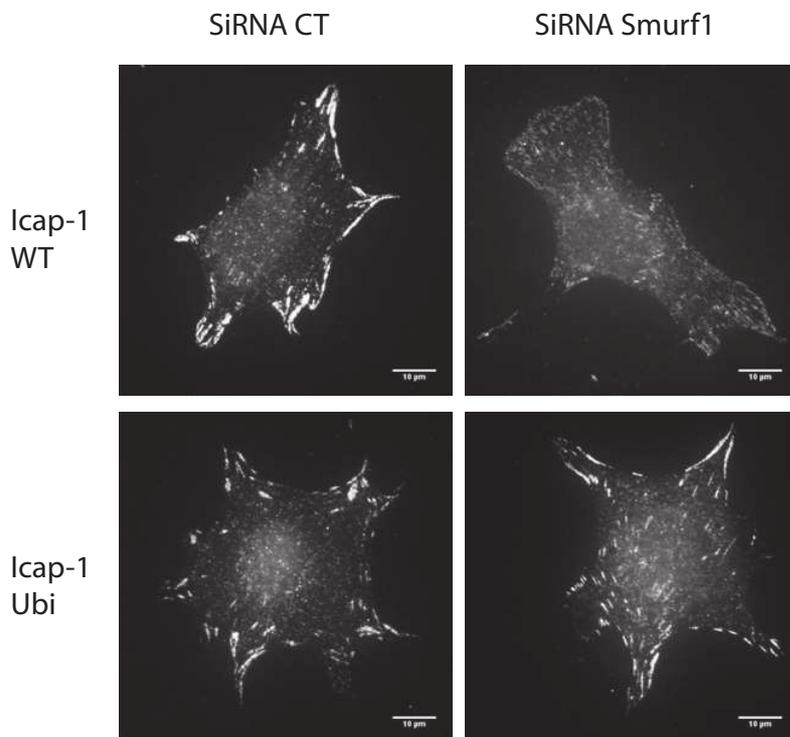
Fig. S1: Monoubiquitination of ICAP-1 by Smurf1 does not lead to ICAP-1 degradation.

A. Cycloheximide was added at t=0 to block protein synthesis. The ICAP-1 protein content in the total lysates was visualized at the indicated times by Western blotting. The results are representative of three independent experiments. B. Quantification of ICAP-1 WT or K158R mutant protein levels over a time-course after the inhibition of protein synthesis. The results are the mean of three independent experiments. C. CHO lysates overexpressing ICAP-1 were incubated with immobilized recombinant Smurf1-GST, Smurf2-GST or GST protein as a control. Interacting protein was analyzed by Western blotting with the anti-ICAP-1 antibody (left panel) and quantified (right panel). The GST protein quantities were controlled using Coomassie blue staining. The results are the mean of two independent experiments. D. Smurf1-myc and ICAP-1-Flag are co-expressed in CHO cells and coimmunoprecipitated with anti-Flag antibodies before blotting against either with anti-Smurf1 or anti-ICAP-1 antibodies. E. Elisa assay showing the direct interaction between Smurf1 and ICAP-1 by using purified recombinant GST-Smurf1 and purified recombinant ICAP-1-His.

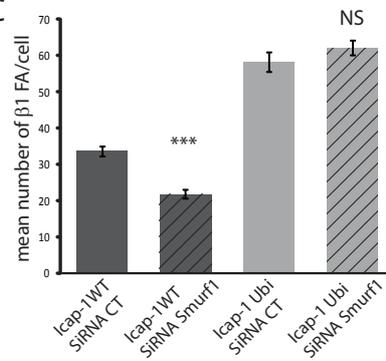
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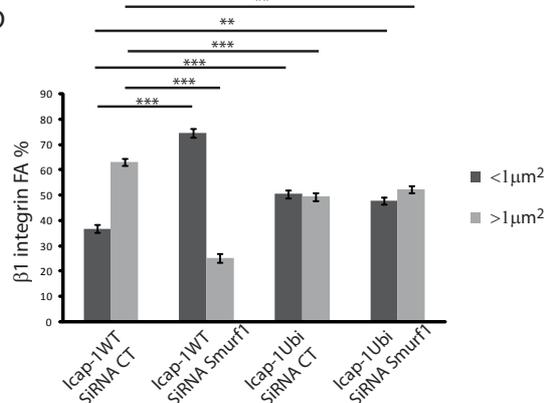
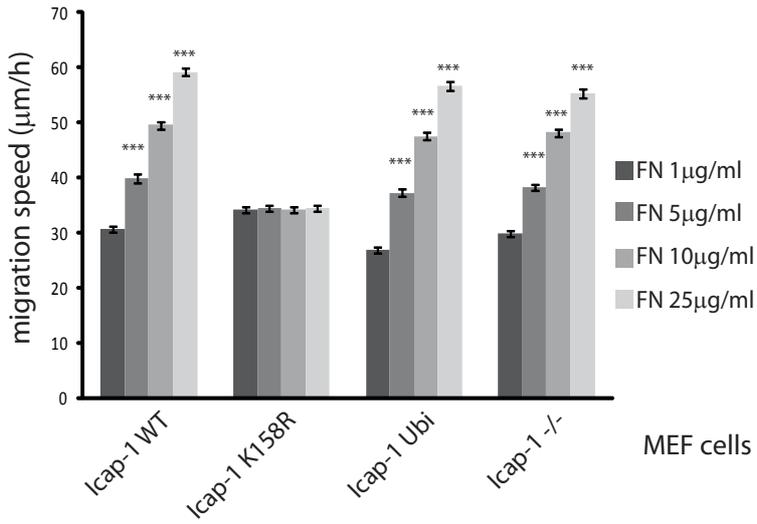


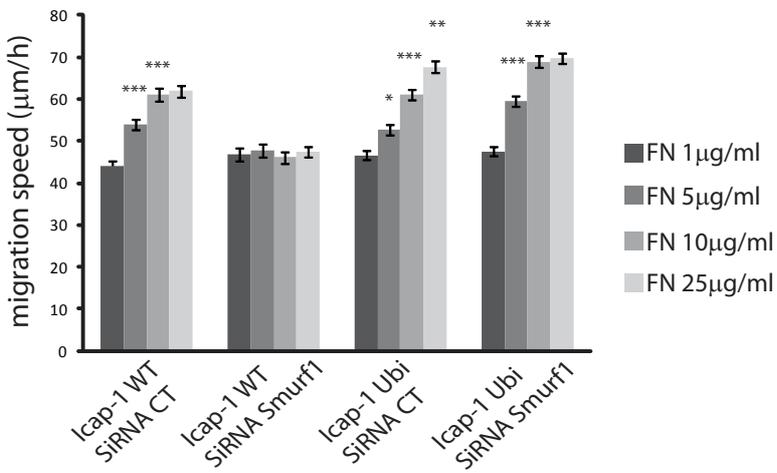
Fig. S2: The deletion of Smurf1 leads to focal adhesion disorganization like ICAP-1 K158R. A. CHO lysates overexpressing the different ICAP-1 constructs were incubated with immobilized recombinant β1-integrin-tail-GST, β3-integrin-tail-GST or GST protein as a control. The interacting proteins were analyzed by Western blotting with the anti-ICAP-1 antibody. The GST protein quantities were controlled using Coomassie blue staining. The results are representatives of three independent experiments. B. β1 integrin staining of ICAP-1-null osteoblasts rescued with ICAP-1 WT or the ICAP-1 ubiquitin chimera treated with

control or Smurf1 siRNA and spread on FN for 2.5 h. Similar to the cells expressing ICAP-1 K158R, the cells expressing ICAP-1 WT that were treated with Smurf1 siRNA displayed fewer and smaller β 1 focal adhesions than the cells treated with control siRNA. C. Quantification of the β 1 integrin focal adhesion number. D. Distribution of the β 1 integrin focal adhesion areas. Analyses were performed on 30–40 cells from two independent experiments. Error bars indicate SEM. * $p < 0.05$, ** $p < 0.005$, *** $p < 0.0005$.

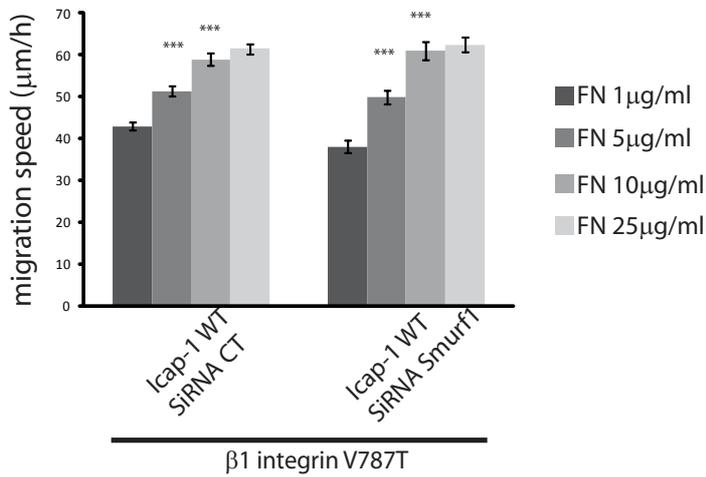
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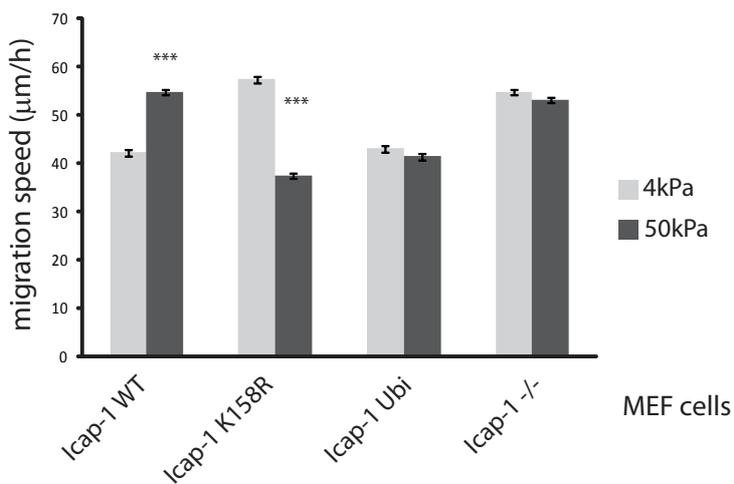


Fig. S3: The deletion of Smurf1 leads to the unresponsiveness of cells to the FN density like ICAP-1 K158R. A. Fibronectin density sensing assay in MEF cells. MEF cells were spread on increasing concentrations of FN and migration was monitored for 5 h using time-lapse microscopy. Cell velocity was determined by individually tracking 150-200 cells from three independent experiments. The cells expressing ICAP-1 WT or the ICAP-1 ubiquitin chimera or cells deficient in ICAP-1 adapted their migratory speed according to the FN density, whereas the cells expressing the ICAP-1 K158R mutant maintained the same speed regardless of the FN density. B. ICAP-1 WT-expressing osteoblast cells that were treated with Smurf1 siRNA were unable to adapt their migratory speed to increasing FN density. This defect was rescued by the ICAP-1 ubiquitin chimera. C. β 1 integrin-null osteoblast cells expressing the β 1 integrin mutant that lacks ICAP-1 binding (V787T) were not affected by Smurf1 siRNA treatment. D. Rigidity sensing assay in MEF cells. Error bars indicate the mean \pm SEM. * $p < 0.05$, ** $p < 0.005$, *** $p < 0.0005$.

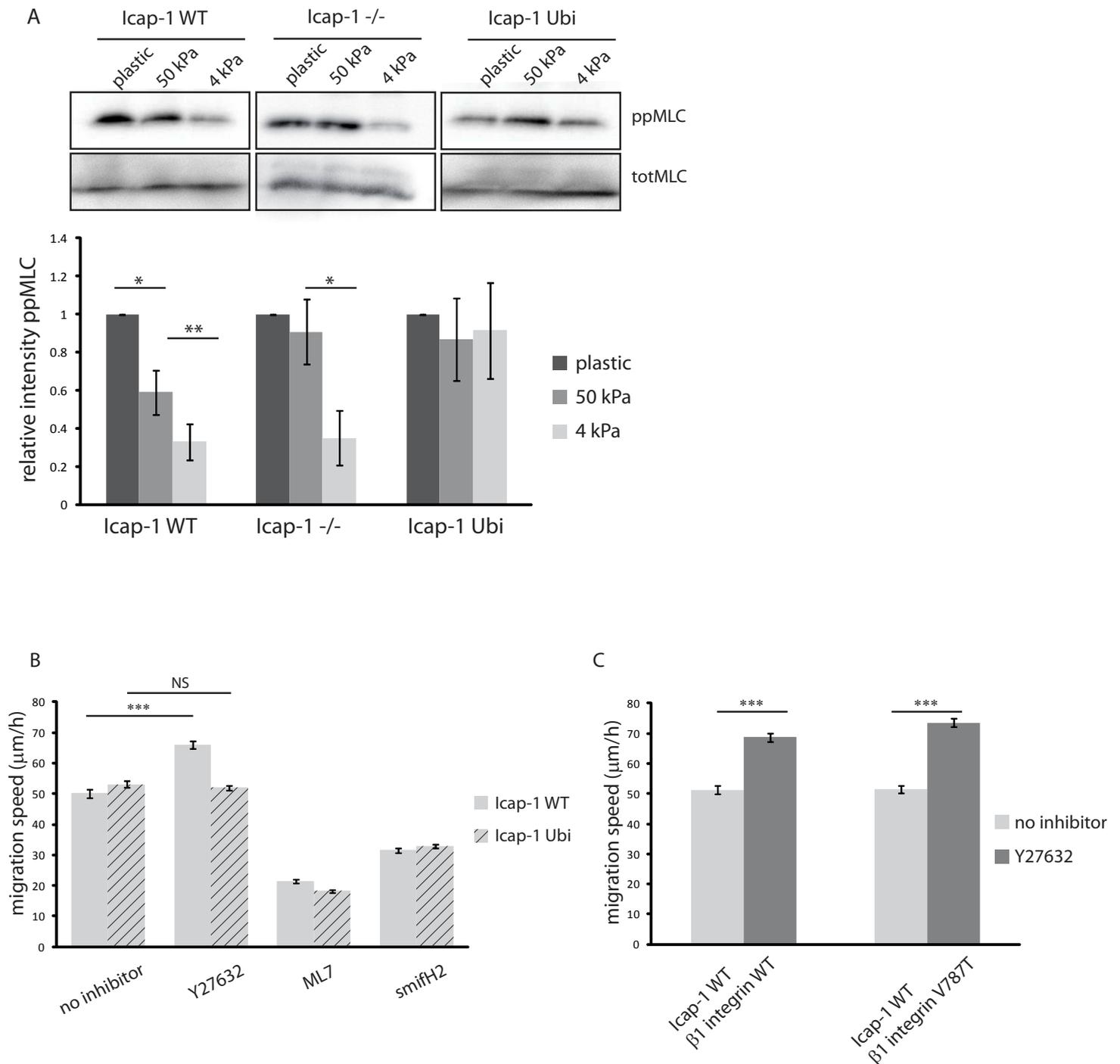


Fig. S4: Identification of contractile pathway in ICAP-1 Ubi osteoblast cells. A. The level of P-myosin is evaluated by western blot in ICAP-1 WT, ICAP-1 deficient and ICAP-1 Ubi cells (upper panel). Note the constant level of P-myosin in ICAP-1 Ubi cells whatever the substrate rigidity after the quantification of the western blot (bottom panel). B. Osteoblasts were spread on FN-coated PAA gels of different rigidities. Cell migration was monitored for 5 h using time-lapse microscopy. Cell velocity was determined by individually tracking of 200-300 cells in three independent experiments to test the effect of inhibitors on WT Osteoblasts cells and osteoblasts transfected with ICAP-1 Ubi cells on 4kPa gels (Y27632: ROCK

inhibitor, 10 μ M, ML7: MLCK inhibitor, 5 μ M, SmifH2: mDia inhibitor 2 μ M). Note that cells expressing ICAP-1 Ubi are insensitive to Y27632. C. β 1 integrin-null cells expressing the β 1 integrin mutant that lacks ICAP-1 binding (V787T) on 4kPa gels responded to Y27632 treatment in a similar manner to that of the control WT osteoblast cells.



Movie S1: Migration of WT osteoblast cells on 1 $\mu\text{g/ml}$ FN



Movie S2: Migration of WT osteoblast cells on 25 $\mu\text{g/ml}$ FN



Movie S3: Migration of ICAP-1 K158R osteoblast cells on 1 $\mu\text{g/ml}$ FN



Movie S4: Migration of ICAP-1 K158R osteoblast cells on 25 $\mu\text{g/ml}$ FN



Movie S5: Migration of WT osteoblast cells on 4 kPa gel coated with 5 $\mu\text{g/ml}$ FN



Movie S6: Migration of WT osteoblast cells on 50 kPa gel coated with 5 μg/ml FN



Movie S7: Migration of ICAP-1 Ubi osteoblast cells on 4 kPa gel coated with 5 $\mu\text{g/ml}$ FN



Movie S8: Migration of ICAP-1 Ubi osteoblast cells on 50 kPa gel coated with 5 $\mu\text{g/ml}$ FN

Chapter 8. ICAP-1 is involved in integrin dynamics and force generation by controlling integrin endocytosis through Nm23-dependent clathrin coated pits.

8.1. Specific scientific context

Signal transduction from extracellular matrix (ECM) originates at the membrane, where the clustering of adhesive receptors is a key step in adapting cellular force and transmitting a message (Cebecauer et al., 2010; Groves and Kuriyan, 2010; Salaita et al., 2010). By following this rule, adhesive receptors, most notably the integrins help cells for perceiving their microenvironment by sensing chemical, physical and mechanical cues of ECM through adhesive machinery and actomyosin-based contractility (Albiges-Rizo et al., 2009; Engler et al., 2006). Actomyosin-mediated contractility is a highly conserved mechanism for generating mechanical stress in animal cells and underlies cell shape, cell migration, cell differentiation and morphogenesis (Murrell et al., 2015). Cell adhesion mediated by fibronectin-binding integrins leads to the formation of nascent adhesions that eventually mature into large focal adhesions connected to actin stress fibers and then eventually convert into central or fibrillar adhesions (Geiger et al., 2001). Most of cells exploring fibronectin-based microenvironments engage $\alpha 5\beta 1$ and $\alpha v\beta 3$ class integrins to orchestrate membrane protrusions, cell contractility and cell migration. The regulation of integrin function can be achieved on several levels, including ligand engagement and binding of intracellular adaptors. These intracellular adaptors are able to control their clustering state and their activation switch crucial for modulating integrin–ligand binding affinity and for serving as nucleation points for the assembly of larger signaling and structural scaffolds (Legate and Fässler, 2009). For example, talin is



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one of the adaptor important for building actin-bound mechanosensitive complexes (Klapholz and Brown, 2017; Shattil et al., 2010). In turn, mechanical force is known to be an important factor in integrin activation and can contribute to both outside-in and inside-out signaling (Alon and Dustin, 2007; Zhu et al., 2008a). Different studies uncovered striking differences in the ability of $\alpha 5\beta 1$ - and $\alpha v\beta 3$ -class integrins to adjust adhesion lifetime and strength to mechanical forces. Whereas $\alpha 5\beta 1$ is known to adhere efficiently to fibronectin and generate cellular traction force, αv -class integrin-mediated adhesion is strongly reinforced by myosin II, and with time the αv -class integrins accumulate in adhesion areas exposed to the highest traction forces (Kuo et al., 2011; Schiller et al., 2013, 2011b). These findings are reminiscent of single protein tracking experiments of $\beta 1$ - and $\beta 3$ -integrins, which showed that $\beta 3$ -integrins are immobilized in large focal adhesions, whilst $\beta 1$ -integrins are more mobile (Rossier et al., 2012). Interestingly, $\alpha v\beta 3$ -integrin has been shown to be needed for cell stiffening on force application, which might be consistent with a role in structural reinforcement of the adhesion (Roca-Cusachs et al., 2009). Reinforcement of focal adhesion and cell contractility is likely coupled with the inhibition of focal-adhesion dissolution process. Focal adhesion disassembly involves microtubule targeting, enhanced integrin endocytosis, calpain-mediated cleavage of talin, and loss of tension following Rho kinase inhibition (Wehrle-Haller, 2012). Together, these observations suggest that $\alpha 5\beta 1$ integrin and $\alpha v\beta 3$ integrin are subjected to functional specifications for adjusting adhesion lifetime and strength to mechanical tension. These studies also predict that the collaborative work between integrin heterodimers is more complex than previously thought. It is still unclear whether and how the two Fibronectin-binding integrin classes signal to each other to orchestrate assembly or disassembly of adhesion sites or to strengthen adhesion or to adapt force to Fibronectin-based environment. The signaling pathways controlling the reciprocity between $\alpha v\beta 3$ and $\alpha 5\beta 1$ need to be explored.



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ICAP-1 was first identified as a specific partner of β 1 integrin (Zhang and Hemler, 1999b; Degani et al., 2002). ICAP-1 encompasses a phosphotyrosine binding domain (PTB domain) which interacts specifically with the cytoplasmic tail of β 1 integrin at the membrane-distal NPXY motif. It was subsequently found to be a partner of Nm23-H2, the human metastatic suppressor (Fournier et al., 2002b). ICAP-1, Nm23-H2 and β 1 integrin are colocalized at the leading edges of cells during the early stages of spreading suggesting a transitory role of this complex in adhesion site dynamics (Fournier et al., 2002b). However, the biological relevance of ICAP-1/Nm23-H2 interaction in cell adhesion field is still unknown. The N terminal domain of ICAP-1 contains multiple phosphorylation consensus sites. The calcium and calmodulin-dependent serine/threonine protein kinase of type II (CaMKII) is an important regulator of ICAP-1 for controlling focal adhesion dynamics (Millon-Frémillon et al., 2013, 2008). Mechanistically, we previously reported that ICAP-1 limits both talin and kindlin interaction with β 1 integrin and thereby restraining focal adhesion assembly. ICAP-1 direct interaction with the β 1 integrin tail and the modulation of β 1 integrin affinity state are required for down regulating focal adhesion assembly. We have also shown that ICAP-1 is involved in cell mechanoresponse and cell differentiation in a β 1 integrin dependent manner (Brunner et al., 2011b; Faurobert et al., 2013; Bouvard et al., 2007; Renz et al., 2015; Millon-Frémillon et al., 2008). However, as ICAP-1 is also able to adapt cell migration in response to substrate stiffness in a β 1-integrin-independent manner (Bouin et al., 2017b), we speculated on a more general role of ICAP-1 in cell adhesion and focal adhesion dynamics. The involvement of ICAP-1 in cell contractility and fibronectin fibrillogenesis makes it an attractive candidate for adapting cell migration (or behavior) by playing a role in force regulation.



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8.2. Specific objectives of this study

To address this question, we have established cellular environment where ICAP-1 and its favorite $\beta 1$ integrin were absent by using four cell lines: WT osteoblast, $\beta 1$ integrin KO osteoblast cells, ICAP-1 KO osteoblast cells and double KO $\beta 1$ /ICAP-1 osteoblast cells in order to monitor $\beta 3$ integrin behavior. Unexpectedly, our data show that $\beta 3$ integrins are able to generate forces in cells depleted in $\beta 1$ integrin and ICAP-1. Our results suggest that ICAP-1 is involved in $\beta 3$ integrin dynamics and force generation by controlling $\beta 3$ integrin endocytosis through Nm23-dependent scission of endocytic clathrin coated pits.



8.3. Results

8.3.1. $\beta 3$ integrin is able to generate traction force in absence of $\beta 1$ integrin and ICAP-1

We addressed the question about $\beta 1$ integrin specificity and the role of its negative regulator called ICAP-1 on $\beta 3$ integrin cell adhesive behaviors by using four osteoblast cell lines: $\beta 1$ integrin^{+/+}-icap-1^{+/+}, $\beta 1$ integrin^{+/+}-icap-1^{-/-}, $\beta 1$ integrin^{-/-}-icap-1^{+/+} and $\beta 1$ integrin^{-/-}-icap-1^{-/-} cells. The deletion of $\beta 1$ integrin or ICAP-1 was confirmed by western blot (Fig. 8.3.1A). Based on western blot analysis (Fig. 8.3.1A), qPCR analysis (Fig. 8.3.1B) and FACS analysis (Fig. 8.3.1C), we checked that the deletion of $\beta 1$ integrin or ICAP-1 do not affect $\beta 3$ integrin expression and its cell surface expression.

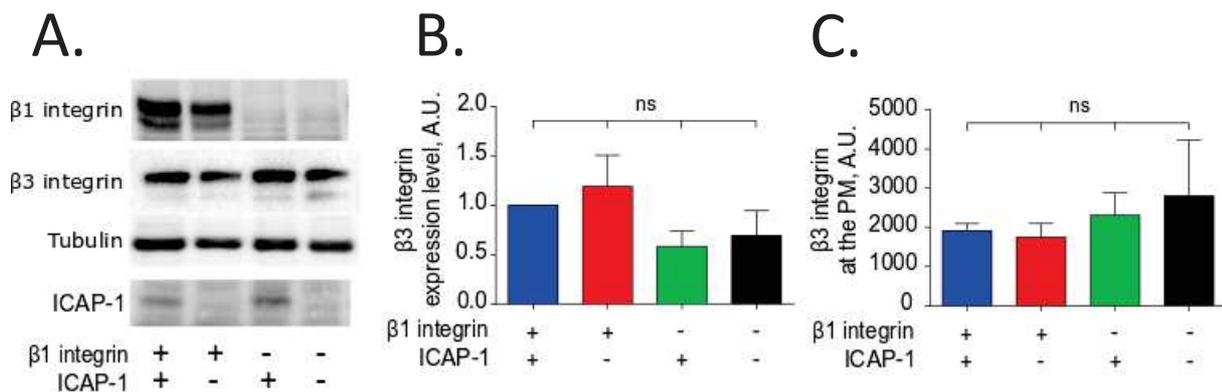


Figure 8.3.1. ICAP-1 KO osteoblasts are able to exert traction force on fibronectin substrate in the absence of $\beta 1$ integrin.

A-C Western blot of total cell lysate confirmed the deletion of $\beta 1$ integrin or ICAP-1 (A). Based on western blot analysis (B), qPCR analysis (C) and FACS analysis (D), we checked that the deletion of $\beta 1$ integrin or ICAP-1 do not affect $\beta 3$ integrin expression and its cell surface expression. Error bars represent standard deviation of at least 20 cells/experiment. ns adjusted p.value > 0.05. Experiment was done three independent times.

To understand to what extent individual integrin classes $\beta 1$ and $\beta 3$ integrins bound to the same ECM ligand use specific pathways to sense and exert force, we designed a quantitative traction force microscopy of osteoblast mutants seeded on fibronectin (FbN) coated hydrogels with a Young's modulus (E) of 5 kPa. First,



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our results reveal that osteoblasts deficient in $\beta 1$ integrin ($\beta 1$ integrin^{-/-}-icap-1^{+/+}) are defective in force generation (Fig. 8.3.1D-E) as it has been already described in the literature (Danen et al., 2002; Schiller et al., 2013). The total cell force measured on $\beta 1$ integrin KO cells decreased by more than 50% as compared to wild-type cells (Fig. 8.3.1E).

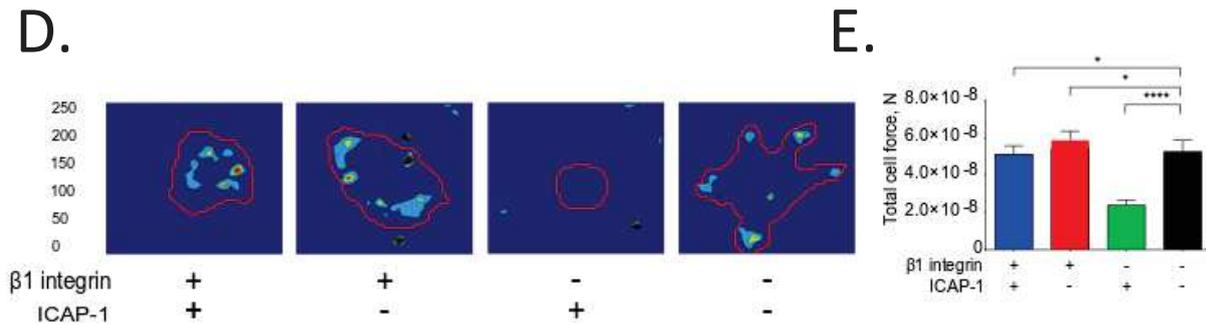


Figure 8.3.1. Osteoblasts are able to exert traction force on fibronectin substrate in the absence of $\beta 1$ integrin.

D-E. Representative traction forces maps and quantification (E) of the total force applied (N) on fibronectin-coated polyacrylamide gel with a defined rigidity of 5 kPa. $\beta 1$ integrin KO cells exert less force than the other osteoblasts mutants. The additional deletion of ICAP-1 led to generation of TFs revealing a novel pathway independent of $\beta 1$ integrins to generate TFs on fibronectin. Error bars represent standard deviation of at least 20 cells/experiment. **** adjusted p.value ≤ 0.0001 , * adjusted p.value ≤ 0.05 .

Secondly and unexpectedly, the additional loss of ICAP-1 in osteoblasts cells deficient for $\beta 1$ integrin was able to rescue the developed contractile energy (Fig. 8.3.1D-E) which is supported by the drastic increase of P-myosin light chain (pp-MLC) as judged by the western blot using double phospho sites specific antibody against myosin light chain (Fig. 8.3.1F).



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The rescue of traction force in $\beta 1$ integrin^{-/-}-icap-1^{-/-} cells was associated with a rescue of cell spreading and restoration of thick stress fibers highly decorated with P-myosin light chain as compared to $\beta 1$ integrin^{-/-} cells which display limited spreading and poorly spread actin cytoskeleton (Fig. 8.3.1G-H). These results indicate that traction strength on deformable FbN substrate is not strictly correlated with the presence of $\beta 1$ integrins and is likely related with another integrin regulated by the presence of ICAP-1.

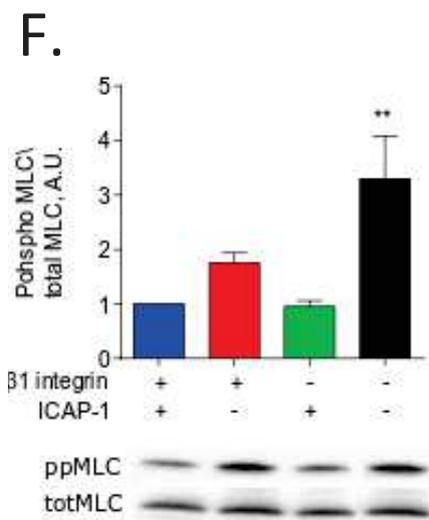


Figure 8.3.1. Osteoblasts are able to exert traction force on fibronectin substrate in the absence of $\beta 1$ integrin.

F. The level of the double phosphorylation (T18/S19) of the MLC was assessed via Western Blot against the total level of MLC of cell lysates of cells spread for 4 hours on fibronectin covered glass. The increased TFs in the $\beta 1$ ^{-/-}/ICAP-1^{-/-} cells correlated with an elevated levels of double phosphorylated myosin light chain (MLC or RLC). Error bars represent standard deviation. ** adjusted p. value ≤ 0.01 . Experiment was done three independent times.

As FbN- coated surface mediates RGD binding to $\alpha 5\beta 1$ and $\alpha v\beta 3$ integrins (Leiss et al., 2008) which exert both specific and redundant functions (Ballestrem et al., 2001b; Danen et al., 2002), we investigated whether the increase of traction forces in $\beta 1$ integrin^{-/-}-icap-1^{-/-} cells was dependent on $\beta 3$ engagement. Silencing the expression of $\beta 3$ integrins via RNA interference lead to a dramatic decrease in cell spreading (Fig. 8.3.1I-J) and ppMLC staining (Fig. 8.3.1I-J). On line with this, siRNA against $\beta 3$ integrin treatment abolished the high traction forces generated by $\beta 1$ integrin^{-/-}-icap-1^{-/-} cells compared to control (Fig. 8.3.1K-L). It is noteworthy that siRNA $\beta 3$ integrin treatment leads to the rounding up of the $\beta 1$ integrin null (Fig. 8.3.1I) suggesting that their modest spreading is dependent on the expression of



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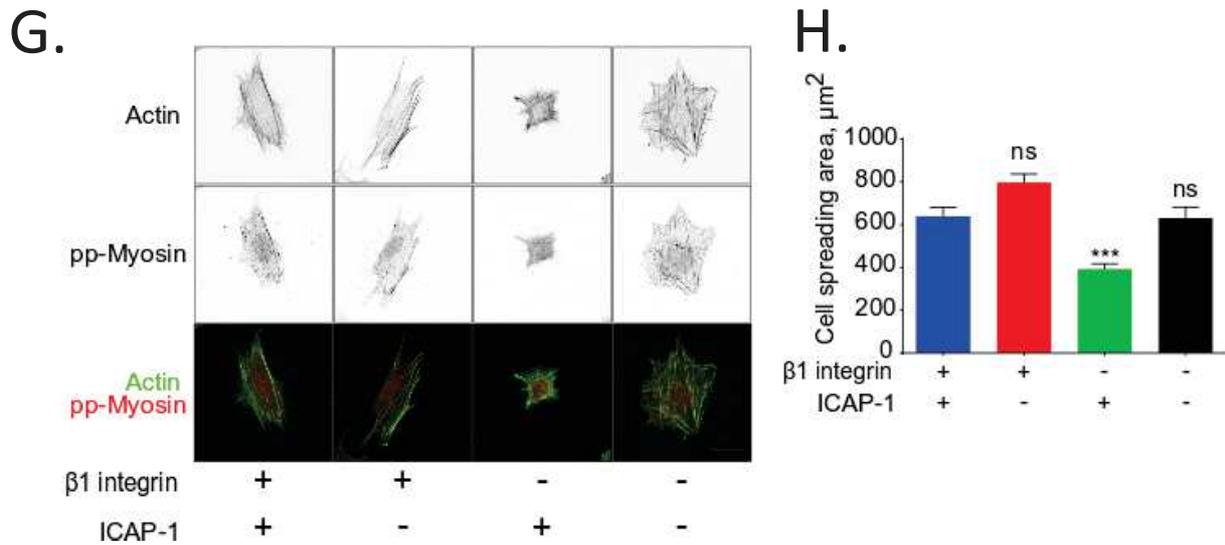
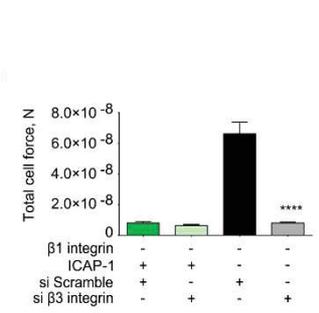
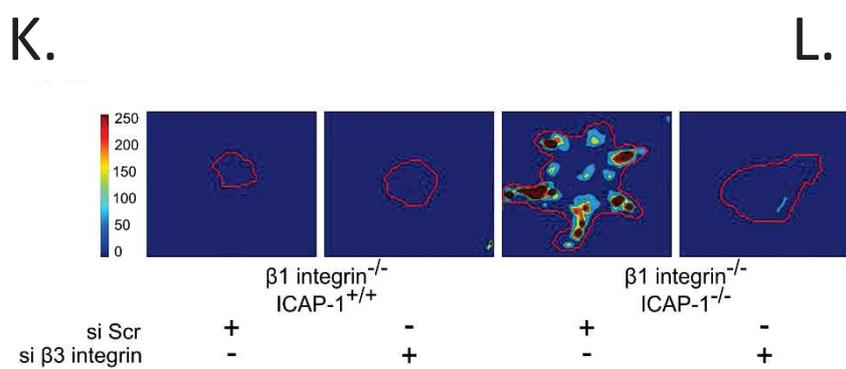
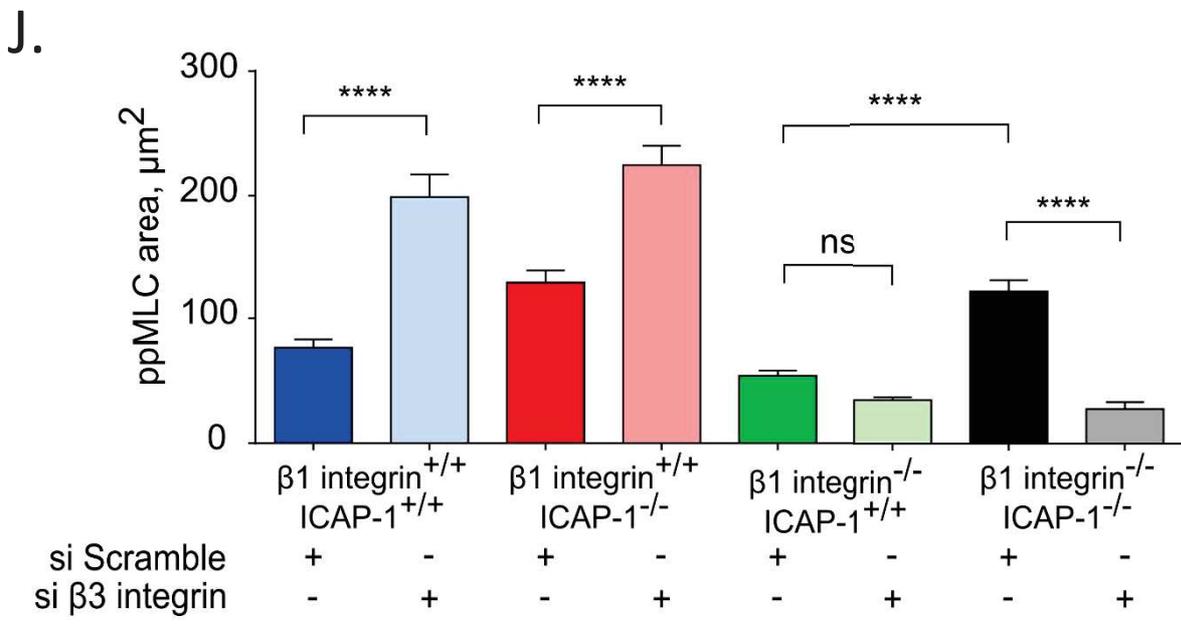
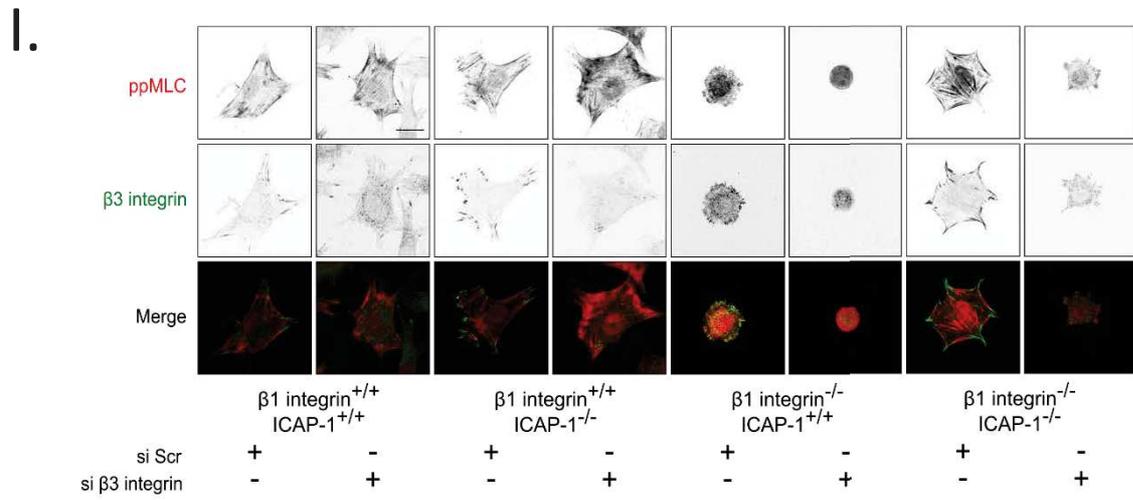


Figure 8.3.1. Osteoblasts are able to exert traction force on fibronectin substrate in the absence of $\beta 1$ integrin.

G-H. Immunofluorescence staining of the ppMLC (red) and actin-F (phalloidin, blue) in the four osteoblasts mutants showed that deletion of ICAP-1 alone does not change the organization of acto-myosin CSK but increases slightly the intensity and the thickness of the fibers (see quantification of the ppMLC area in panel H). Deletion of $\beta 1$ integrin leads to drastic decrease of the cell area and disorganization and decrease of thickness and number of the ppMLC decorated stress fibers. Error bars represent standard deviation of at least 20 cells/experiment. ** adjusted p.value ≤ 0.01 . Experiment was done three independent times.

$\beta 3$ integrins (Fig. 8.3.11-J). Moreover, it is important to notice that $\beta 3$ integrins silencing increases by more than twice the myosin light chain phosphorylation along the actin stress fibers for both $\beta 1$ integrin^{+/+/-}-icap-1^{+/+} cells and $\beta 1$ integrin^{-/-}-icap-1^{-/-} cell lines, suggesting that $\beta 3$ integrins down regulate myosin II reinforcement dependent on $\beta 1$ integrin when cells are spread on FbN stiff environment (Milloud et al., 2017) (Fig. 8.3.11). Altogether these results identify not only the cross talk between $\beta 1$ and $\beta 3$ integrin to regulate cell spreading and force generation but also ICAP-1 as a molecular link to regulate this cross-talk. Finally, our results suggest a new regulatory role for ICAP-1 in the actomyosin contractility loading on $\beta 3$ integrins.





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Figure 8.3.1. Osteoblasts are able to exert traction force on fibronectin substrate in the absence of $\beta 1$ integrin.

I-J. Osteoblasts cells were transfected with $\beta 3$ integrin siRNA for 48h and then let spread in on Fbn coated glass for 24 hours. After PFA fixation, stainings of ppMLC (red) and $\beta 3$ integrin (green) were performed and analysed by fluorescent microscopy. Silencing the expression of $\beta 3$ integrin via siRNA increased the stress fibers even more in the $\beta 1$ positive cells (WT and ICAP-1 KO). In the $\beta 1^{-/-}$ /ICAP-1 $^{-/-}$ cell line removing $\beta 3$ integrin lead complete abolishment of the ppMLC decorated SF (stress fibers) and shrinkage of the cell area. Scale bar represents 20 μm . Quantification of the ppMLC area from the spinning disk images. Customized particle analysis script from ImageJ was used after application of Unsharpen mask and Despeckle filters. The error bars represent standard deviations. **** adjusted p.value ≤ 0.0001 . Experiments were done 3 times with at least 20 cells per condition.

K-L. TFM analysis on beta1 deficient cells shows that the additional silencing of $\beta 3$ integrin in the $\beta 1^{-/-}$ /ICAP-1 $^{-/-}$ cells decimates the TFs, confirming that generation of strong cellular contractility is dependent on $\beta 3$ integrin in absence of $\beta 1$ integrin and ICAP-1. Quantification of the total forces from TFs maps. Error bars represent standard deviation of at least 20 cells/experiment. ** adjusted p.value ≤ 0.01 . Experiment was done three independent times.



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8.3.2. $\beta 3$ integrin dependent traction forces are associated with redistribution, lower membrane mobility and higher life time of large $\beta 3$ integrin focal adhesions.

Next, we investigated whether the loss of $\beta 1$ integrins and ICAP-1 and the associated contractile behavior might be related to a change in $\beta 3$ integrin focal adhesions (FAs) organization and dynamics. All four osteoblast cells lines used here, were able to develop $\beta 3$ integrin FAs on FbN coated surface as revealed by immunostaining or expression of $\beta 3$ integrin-GFP (Fig. 8.3.2A). Nevertheless, the KO of $\beta 1$ integrins reduced noticeably the cell spreading without affecting the adhesion area occupied by $\beta 3$ integrins FAs (Fig. 8.3.2A-B and Fig. 8.3.2G) meaning that $\beta 3$ integrins alone in FbN mediated adhesions fails to support the typical osteoblasts spreading.

Remarkably, the additional depletion of ICAP-1 in $\beta 1$ integrin deficient cells (by gene KO or RNA silencing (Fig. 8.3.3A-B)) promotes significantly and considerably the cell spreading and the size of $\beta 3$ integrins FAs (+/- 80 $\mu\text{m}^2/\text{cell}$: twice as more than the other mutants) (Fig. 8.3.2A-B and Fig. 11.3B).

Our results reveal a crucial role for ICAP-1 in controlling the $\beta 3$ integrin clustering and the distribution of $\beta 3$ integrins containing FAs in absence of $\beta 1$ integrins. We hypothesized then a possible link between $\beta 3$ integrins exchange rates and the presence of ICAP-1. To explore this hypothesis, we compared the dynamic of $\beta 3$ integrins exchange rate in large peripheral focal adhesions link to actin stress fibers. We performed Fluorescent Recovery After Photobleaching (FRAP) using Total Internal Reflection Fluorescent microscopy (TIRF) experiments on the four cell lines transfected with $\beta 3$ integrin- eGFP (Fig. 8.3.2C-F). It appeared that neither the loss of $\beta 1$ integrins nor the one of ICAP-1 alone have any significant effect on the $\beta 3$ integrin-eGFP exchange rate in FAs. However, the oversized $\beta 3$ integrin FAs observed in $\beta 1$ integrin^{-/-}-icap-1^{-/-} cells correlates with a threefold slower $\beta 3$ -EGFP integrin exchange rate (Fig. 8.3.2C) and with an increase of $\beta 3$ - integrin-eGFP FAs life time (Fig. 8.3.2D-E) which correlate with the development of stress fibers highly



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decorated with P-myosin light chain. In the context of $\beta 1$ null cell mutants, these data hint that the loss of ICAP-1 strongly affects the behavior of $\beta 3$ integrins. These findings reveal that $\beta 3$ integrin clustering and dynamics is under the control of ICAP-1 in conditions where $\beta 1$ integrin is absent.

Figure 8.3.2. Size and dynamic of $\beta 3$ integrin FAs are dependent on $\beta 1$ integrins and ICAP-1

A. Indirect immunofluorescence surface staining of $\beta 3$ integrins (Luc.A5 antibody, red) was carried on GFP-osteoblast cells spread for 4 hours cells on fibronectin coated coverslips. $\beta 1$ integrin positive cell lines ($\beta 1^{+/+}/ICAP-1^{+/+}$ and $\beta 1^{+/+}/ICAP-1^{-/-}$) show classical distribution of $\beta 3$ FAs - peripheral and elongated towards the SFs. $\beta 1$ null cell line display small and punctuated FAs around the peripheral rim and multiple punctuated FAs at the ventral cell spread face. The $\beta 1^{-/-}/ICAP-1^{-/-}$ exhibits both peripheral elongated FAs, and ventral elongated FAs, suggesting different activity states of $\beta 3$ integrins. Scale bar represents 20 μm .

B. Quantification of the total focal adhesion area of $\beta 3$ integrin FAs. Loss of $\beta 1$ integrins decreases slightly the total $\beta 3$ integrin adhesive area, while subsequent deletion of ICAP-1 drives massive leap of $\beta 3$ integrin stained adhesive area. **** adjusted p.value ≤ 0.0001 . Experiments were done 3 times with at least 20 cells per condition.

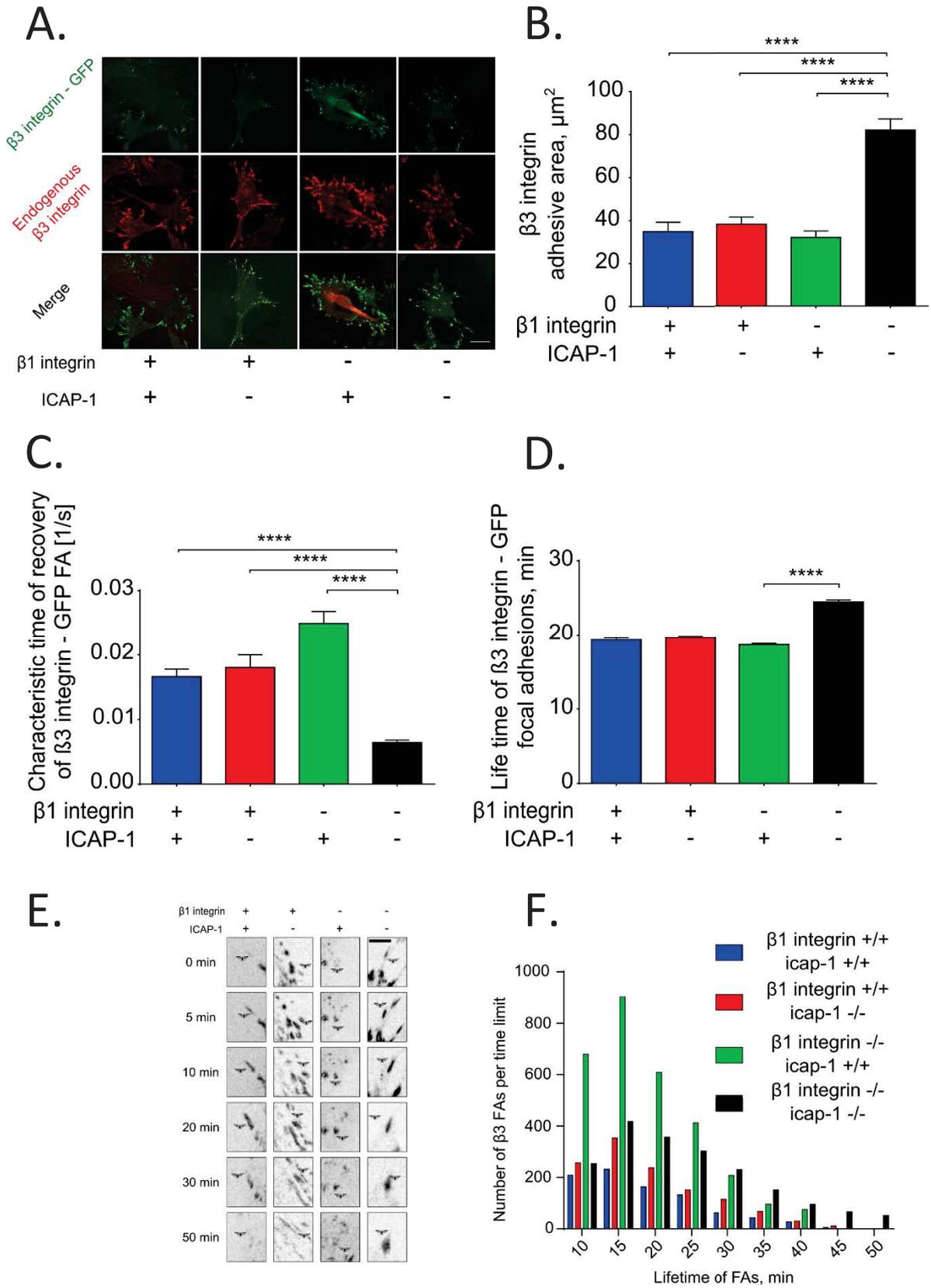
C. FRAP analysis on the GFP- $\beta 3$ integrin FAs reveal that the $\beta 3$ integrin mobility at the plasma membrane is halted in the absence of ICAP-1 and $\beta 1$ KO. 5 FAs per cell were bleached and their recovery were monitored for 5 min. At least 10 cells were analyzed every experiment. Error bars represent standard deviation of at least 20 cells/experiment. **** adjusted p.value ≤ 0.0001 . The experiment was performed in triplicate.

D. TIRF lifetime analysis on the GFP- $\beta 3$ integrin FAs. The lifetime of the GFP- $\beta 3$ integrin containing focal adhesions is increased in $\beta 1$ integrin $^{-/-}/ICAP-1^{-/-}$ cells. Spinning disk videos of GFP- $\beta 3$ integrin were taken for the duration of 2 hours. The adhesion lifetime was analyzed by Focal Adhesion Analysis Server (FAAS) (Berginski and Gomez, 2013) and verified visually. **** adjusted p.value ≤ 0.0001 . The experiment was performed in triplicate.

E. Representative time series of the lifetime of $\beta 3$ integrin – GFP focal adhesions of the four osteoblastic cell lines. Eagles point out FAs in the $\beta 1^{-/-}/ICAP-1^{-/-}$ cells with typical slow down disassembly lifetime. Bar represents 5 μm .

F. Frequency distribution of the FAs lifetimes. The $\beta 1^{-/-}/ICAP-1^{-/-}$ cells shows higher number of FA in the late time points.





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8.3.3. $\beta 3$ integrin dependent traction forces are associated with formation of tensin dependent fibrillar adhesion

We addressed the question whether the increase of $\beta 3$ integrin clustering and force generation in condition where $\beta 1$ integrin and ICAP-1 are depleted, are associated with the ability to form fibrillary adhesions known to be formed under tension. We have already described the ability of $\beta 1$ integrin^{+/+}-icap-1^{-/-} cells to develop more central $\beta 1$ integrin containing focal adhesions as compared to $\beta 1$ integrin^{+/+}-icap-1^{+/+} cells (Millon-Frémillon et al., 2008; Faurobert et al., 2013). At longer times of spreading, *beta1 integrin^{+/+}-icap-1^{+/+}* and *beta1 integrin^{+/+}-icap-1^{-/-}* cells were able to form elongated fibrillar adhesions (Fig. 8.3.3A). Those elongated adhesions were enriched in active $\beta 1$ integrins stained by 9EG7 antibody specific for activated $\beta 1$ integrin chain which co-localized with P-myosin light chain decorating actin stress fibers (Fig. 8.3.3A). As expected, $\beta 1$ integrin^{-/-} cells did not display any elongated fibrillar adhesions whereas the additional loss of ICAP-1 lead to fibrillar adhesions colocalizing with myosin II stress fibers and enriched in $\beta 3$ integrins but devoid of $\beta 1$ integrins (Fig. 8.3.3B). In fibroblast like cells, it is well described that, integrins translocate centripetally from focal adhesions to mature, centrally located, elongated matrix contacts termed fibrillar adhesions, which are enriched in active $\beta 1$ integrins and tensin (Pankov et al., 2000; Zamir et al., 2000b). To explore where tensin resides in cells lacking $\beta 1$ integrins to undergo effective fibrillar adhesions, we investigate tensin co-localization in regard to expression of ICAP-1. Because of antibody limitations, we were unable to study endogenous tensin in mouse osteoblasts, therefore we transiently expressed GFP-tensin-1 in osteoblasts cell lines. Based on TIRF microscopy and analysis by plot profiles of GFP-tensin-1/ $\beta 3$ integrin, tensin-containing $\beta 3$ integrins adhesion were localized at the periphery of *beta1 integrin^{+/+}-icap-1^{+/+}* and *beta1 integrin^{+/+}-icap-1^{-/-}* cells (Fig. 8.3.3C-D). Many elongated adhesions of GFP-tensin were observable in the cell center but were not necessarily associated with $\beta 3$ integrins (Fig. 8.3.3D). The tensin association must be related to $\beta 1$ integrins (data not shown). For $\beta 1$ ^{-/-}



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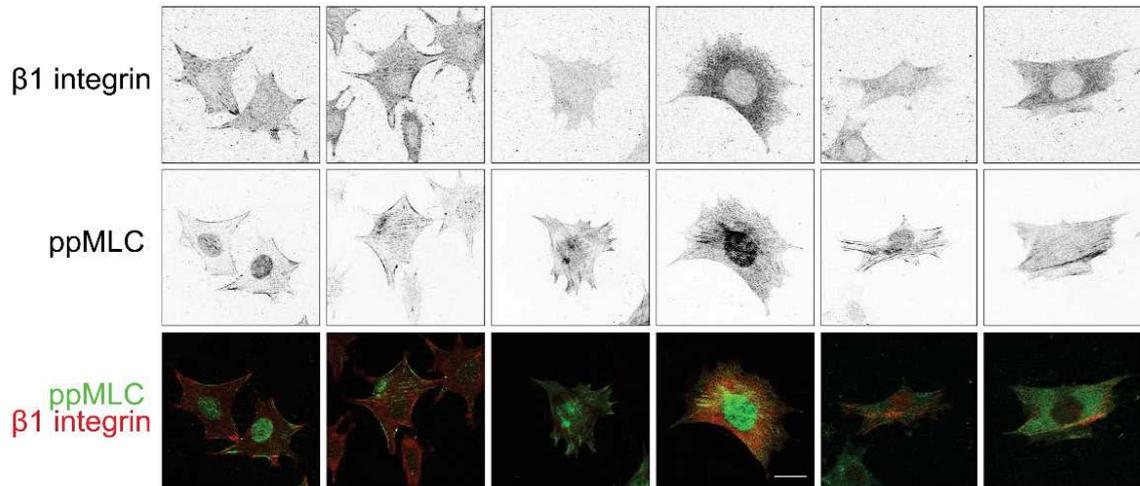
integrin cells ($\beta 1$ integrin^{-/-}-icap-1^{+/+} and $\beta 1$ integrin^{-/-}-icap-1^{-/-} cells), tensin regionalization was dependent on the presence of ICAP-1. Indeed, tensin can be associated with $\beta 3$ integrins at the cell periphery but no co-localization was observed with $\beta 3$ in cell center of $\beta 1$ integrin^{-/-}-icap-1^{+/+} cells. The additional removal of ICAP-1 promotes the co-localization of tensin with $\beta 3$ integrins at the rear of the cell and with elongated tensin fibrillar adhesions centrally positioned on the ventral cell surface (Fig. 8.3.3C-D). Moreover, we noted that the general distribution of $\beta 3$ integrin containing FAs was affected by the lack of $\beta 1$ integrins and not by the lack of ICAP-1. Indeed, in the case of $\beta 1$ integrin^{+/+} cell lines, $\beta 3$ integrins FAs localize at the periphery of spread cells as contrary to $\beta 1$ integrin^{-/-} cell lines where $\beta 3$ integrin FAs were rapidly redistributed between the cell periphery and randomly over the ventral cell face (Fig. 8.3.3E). Together, these results show that the distribution of $\beta 3$ integrin FAs is regulated by the occurrence of $\beta 1$ integrins. However, the additional lack of ICAP-1 promotes the formation of bulky $\beta 3$ integrin FAs and $\beta 3$ enriched fibrillar adhesions associated to tensin.



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A.

$\beta 1$ integrin	+	+	-	-	+	-
ICAP-1	+	-	+	-	-	+
si $\beta 1$ integrin	-	-	-	-	+	-
si ICAP-1	-	-	-	-	-	+



B.

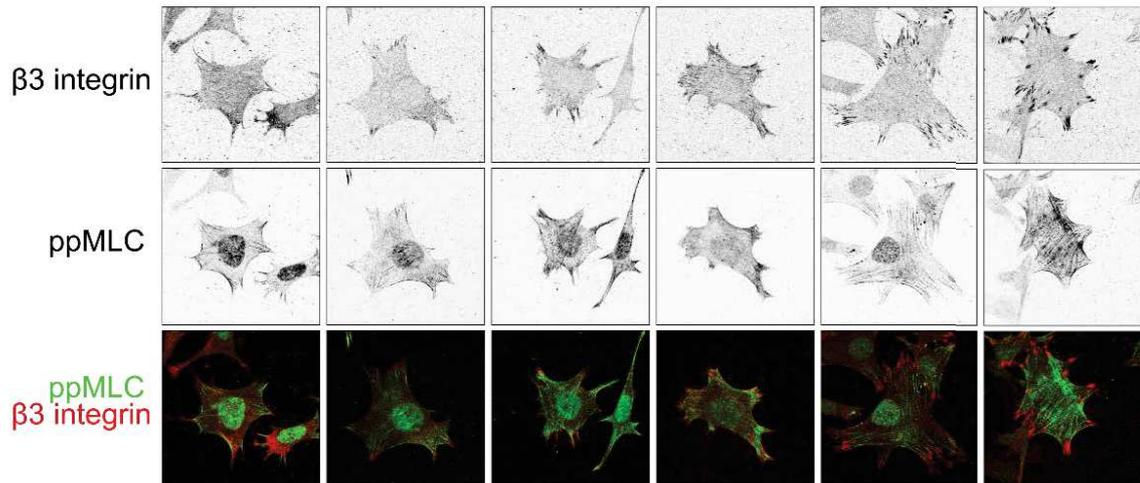


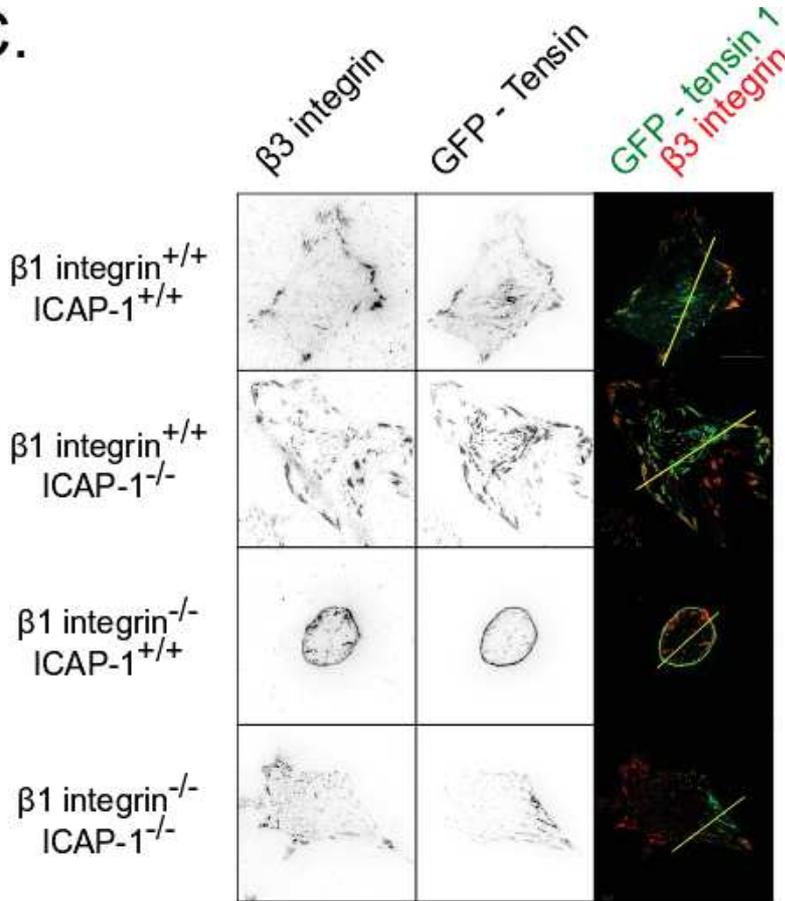
Figure 8.3.3. Restoration of traction forces in the $\beta 1^{-/-}/ICAP-1^{-/-}$ is associated with the recruitment of tensin 1 along the fibrillar $\beta 3$ integrin adhesions.

A-B. Indirect immunofluorescence surface staining of $\beta 1$ integrins (9EG7, red) or $\beta 3$ integrins (Luc.A5, red) and ppMLC (T18/S19, green) of osteoblastes mutants spread on Fbn coated glass. $\beta 1^{+/+}$ mutants express elongated activated $\beta 1$ integrins adhesion from the periphery to the ventral face co-localized with myosin stress fibers and $\beta 3$ FAs to the cell periphery at the end of myosin stress fibers; $\beta 1^{-/-}$ cells express $\beta 3$ FAs to the cell periphery to the ventral face co-localized with slight myosin stress fibers, no $\beta 1$ staining. $\beta 1^{-/-}/ICAP-1^{-/-}$ cells express large $\beta 3$ FAs to the cell periphery at the end of myosin stress fibers and elongated $\beta 3$ integrins adhesion from the periphery to the ventral face co-localized with thick myosin stress fibers, no $\beta 1$ staining. Note that siRNA- $\beta 1$ integrin reverts the phenotype $\beta 1^{+/+}/ICAP-1^{+/+}$ to a $\beta 1^{-/-}/ICAP-1^{+/+}$ phenotype and siRNA-ICAP-1 reverts the phenotype $\beta 1^{-/-}/ICAP-1^{+/+}$ to a $\beta 1^{-/-}/ICAP-1^{-/-}$ phenotype.

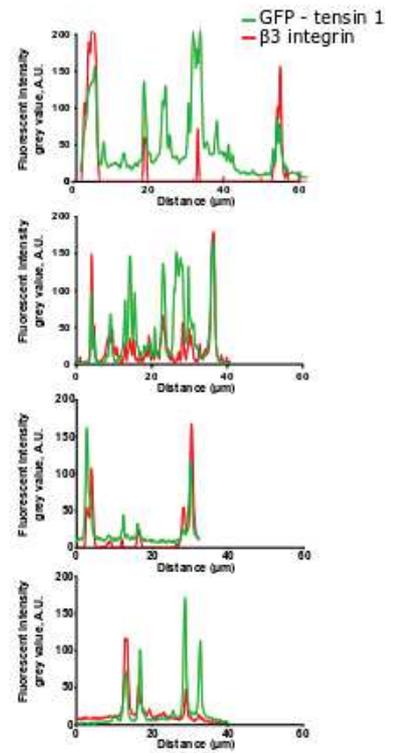


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C.



D.



E.

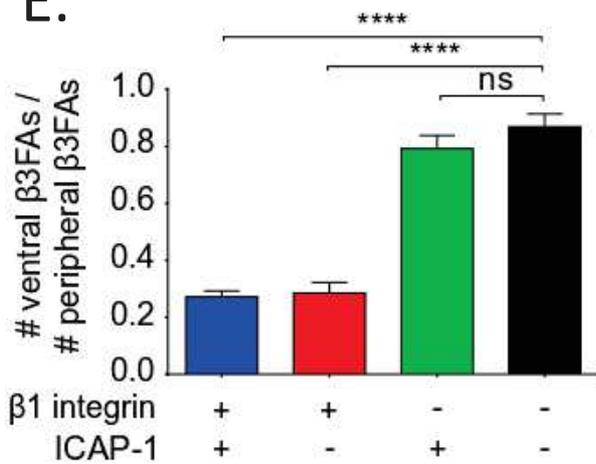


Figure 8.3.3. Restoration of traction forces in the $\beta 1^{-/-}$ /ICAP-1 $^{-/-}$ genotype leads to recruiting tensin 1 along the fibrillar $\beta 3$ integrin adhesions.

C-D. representative TIRF microscopy images and plot profiles of osteoblasts mutants expressing GFP-tensin-1 spread on Fbn and stained for $\beta 3$ integrins (Luc.A5, green). Intensities profiles of the GFP-tensin and $\beta 3$ integrin were obtained across the yellow lines in each corresponding image. localization of GFP-tensin1 shows typical retardation in respect to $\beta 3$ integrin containing focal adhesions in $\beta 1^{+/+}$ cell lines. Plot profiles show that the co-localization of tensin and $\beta 3$ integrins covered a larger cell area. Conversely, in $\beta 1$ deficient cells co-localization of tensin and $\beta 3$ integrins is stuck at the cell periphery, the additional loss of ICAP-1 redistributes the co-localization of tensin and $\beta 3$ integrins all over the ventral cell area. Bar scale represents 20 μm .

E. Quantitative ratio between the unusual ventral $\beta 3$ FAs vs the more classical peripheral. It is obvious that $\beta 1$ KO cells have excess of ventral FAs, but with different morphology and probably function. **** adjusted p.value ≤ 0.0001 . Experiments were done 3 times with at least 20 cells per condition.



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8.3.4. Loss of ICAP-1 promotes $\beta 3$ integrin fibrillar adhesion which are associated with FbN fibrillogenesis.

Our results suggest an unexpected role of ICAP-1 on $\beta 3$ integrins clustering and maturation into fibrillar adhesion associated with an actomyosin contractility. We addressed the question of the cellular functionality of this $\beta 3$ integrin clustering by analyzing the FbN fibrillogenesis process, known to be dependent on the actomyosin contractility (Wu et al., 1995). Indeed, FbN matrix assembly results from the coordinated engagement of $\alpha 5\beta 1$ and $\alpha V\beta 3$. In this process the application of actomyosin-dependent tensile forces and the translocation of $\alpha 5\beta 1$ to form fibrillar adhesions are essential to regulate FbN fibrillogenesis.

To assess the regulation of the actomyosin tensile forces loading on $\beta 1$ and/or $\beta 3$ integrins by ICAP-1, fibrillogenesis assays were performed in the four osteoblast cell lines. Osteoblasts cell lines were cultured on uncoated cover slides in the absence of serum for 12h to 16h hours, to give them time to synthesize and organized their own FbN fibrils. The organization of the FbN fibrils is dependent on the secreted endogenous FbN. In condition where endogenous FbN is reduced, using specific FbN RNAi only few cells were competent to adhere and spread (Fig. 8.3.4F), confirming that the FbN fibrillogenesis process observed *in vitro* over uncoated substrate is largely dependent on secretion of FbN by osteoblasts cells.

In these conditions we observed that the area and the length of the *de novo* FbN fibrils were slightly increased with the deletion of ICAP-1 as compared to $\beta 1$ *integrin*^{+/+}-*icap-1*^{+/+} (Fig. 8.3.4.A-C-D-E). On the other hand, the lack of $\beta 1$ integrins drastically impaired the formation of dense meshwork of FbN fibrils as already described (Brunner et al., 2011b). As assumed, the additional loss of ICAP-1 allowed



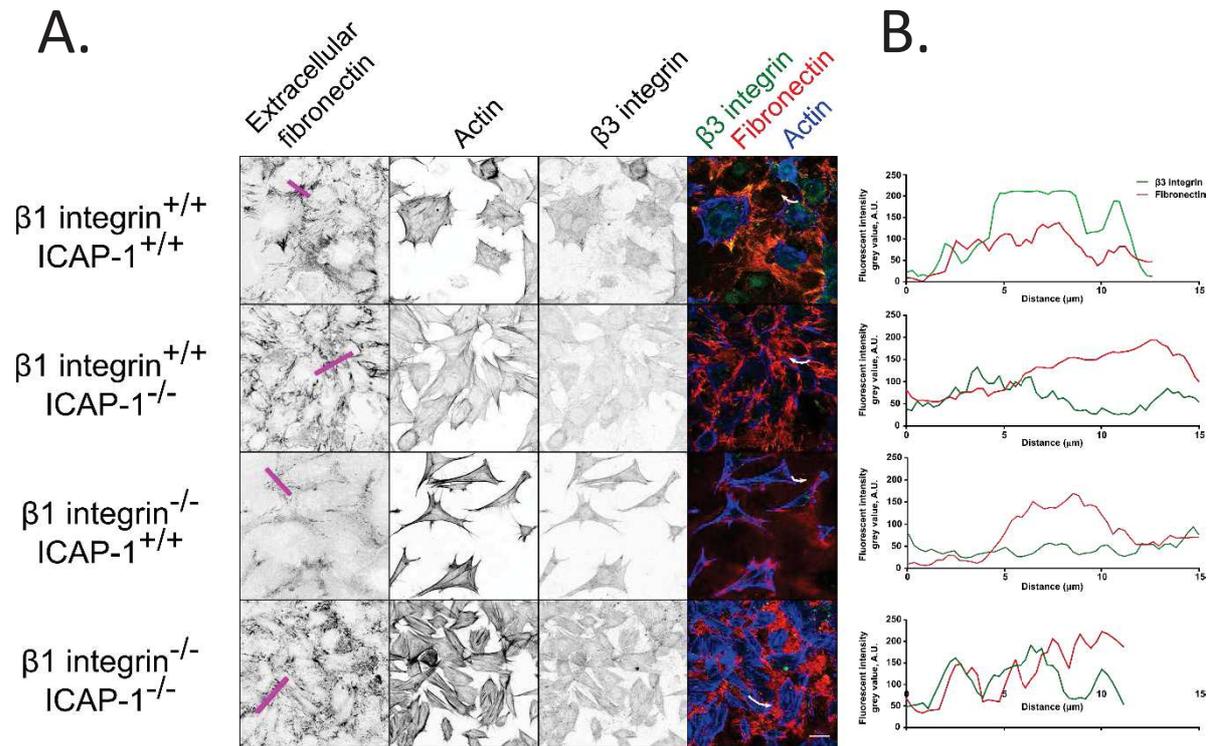


Figure 8.3.4. Loss of ICAP-1 promotes $\beta 3$ integrin fibrillar adhesions which are associated with FbN fibrillogenesis.

A. Osteoblasts cells were spread in serum free medium on glass for 24 hours. Indirect immunofluorescence was performed visualizing the extracellular fibronectin (cellular fibronectin antibody, red), F-actin (phalloidin, blue) and $\beta 3$ integrins (Luc.A5 antibody, green) and cell culture were analyzed by fluorescent microscopy. Not surprisingly, the $\beta 1^{+/+}$ cell lines orchestrate FbN fibrillogenesis events and $\beta 1^{-/-}$ cells demonstrated very poor organization of synthesized fibronectin. $\beta 1$ integrin $^{-/-}$ /ICAP-1 $^{-/-}$ on the other side showed significant amount of FbN fibrillogenesis. Bar scale represents 20 μ m.

B. Representative plot intensities profiles of $\beta 3$ integrin (green) and FbN fibrils (red) were obtained across curves (whit arrow) in each corresponding cell lines. Co-localization of FbN fibrils and $\beta 3$ integrin adhesions covered a long distance in $\beta 1^{+/+}$ cells and in the double KO. Conversely, in $\beta 1$ deficient cells co-localization of FbN fibrils and $\beta 3$ integrins only on a short distance. see text for more explanation.

the formation and organization of short but thick and numerous FbN fibrils (Fig. 8.3.4.A-4C-4D-4E). The plot profiles of fluorescent fibrils intensity confirm thinner and less dense FbN fibrils in $\beta 1$ integrin $^{-/-}$ -icap-1 $^{+/+}$ cells as compared to $\beta 1$ integrin $^{+/+}$ -icap-1 $^{+/+}$ and to the double KO $\beta 1$ integrin $^{-/-}$ -icap-1 $^{-/-}$ (Fig. 8.3.4.D, plot profiles trail the red lines). Despite their better spreading induced by the deficiency of serum



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in the cell culture medium, $\beta 1^{-/-}$ integrin cells were not able to organize well the FbN into fibrils as compared to the double KO cells (Fig. 8.3.4.A). It is important to note that the level of FbN fibrillogenesis is largely dependent on cell culture confluence. Nevertheless, even at high confluence only some short and thin FbN fibrils ($< 5 \mu\text{m}$) could be seen (data not show).

The analysis of intensities profiles of fibronectin/ $\beta 3$ integrin (Fig. 8.3.4.B) of $\beta 1^{+/+}$ cell lines reveal the co-localization of $\beta 3$ integrins and FbN fibrils followed by their mismatch, suggesting that the late elongation of the FbN fibrils is supported by another integrin (Fig. 8.3.4.B). Indeed, the fibrils elongation to the cell center is related to $\beta 1$ integrins in the two cell lines containing $\beta 1^{+/+}$ integrin (Fig. 8.3.4.G). Besides, in the case of the double KO of $\beta 1$ integrin/ICAP-1, the intensities profiles show the co-localization of $\beta 3$ integrin all along FbN fibrils and validate the mechanical involvement of the $\beta 3$ integrins fibrillar adhesions in the assembly of the FbN fibrils (Fig. 8.3.4.B). By following the FbN fibrils and $\beta 1$ integrins all over the cell shape with optical sections of confocal images we confirm the congruence of $\beta 1$ integrins with FbN fibrils from the basal to dorsal face in $\beta 1^{+/+}$ integrin cell lines (Fig. 8.3.4.G). On the other hand, following FbN fibrils and $\beta 3$ integrins reveal that FbN fibrils on dorsal face can also be accompanied by $\beta 3$ integrins but it occurs only in conditions where $\beta 1$ integrin is present. (Fig. 8.3.4.G-H). Thus, even though $\beta 3$ integrins containing FAs are oversized and elongated as fibrillar adhesion in the case of the double KO of $\beta 1$ integrin/ICAP-1, they take the facility to move to the dorsal face. These results suggest that the loss of ICAP-1 confers to $\beta 3$ integrins the capabilities to build up an efficient contractile apparatus to remodel the fibronectin matrix at the basal face of the 2D spread cells but impaired in 3D matrix organization. According to our results, it may exist two distinct types of fibronexus in our osteoblasts cell lines: (i) a ventral substrate-adhesive nexus consisting of fibronectin and $\beta 3$ integrins containing adhesions and (ii) dorsal association matrix fibers consisting of FbN fibrils and $\beta 1$ integrins adhesions with or without $\beta 3$ integrins. In order to observe the dynamic of FbN remodeling process in the four



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osteoblasts cell lines, we took advantage of the biochemical properties of FbN and its high affinity for gelatin (Engvall and Ruoslahti, 1977). We used conjugated gelatin with Fluo Alexa 563 to localize cell surface fibronectin fibrils in live osteoblasts in cultures (Hsieh et al., 1980). To do so, osteoblast cell mutants were seeded in serum free medium on uncoated cover slide chamber for overnight time long then the synthesized endogenous fibronectin hidden on the surface of the cells was probe using fluorescent gelatin and live time imaging records were performed (Fig. 8.3.4.1). As expected, we observed a fibrillogenesis extended and organized in FbN fibrils in $\beta 1$ *integrin*^{+/+} cell lines as well as in $\beta 1$ integrin null cells deficient in ICAP-1. In contrary but as well as expected, the $\beta 1$ integrin 1 KO cells do not exhibit FBN fibrils on their surface. However, it was observed numerous endocytosis vesicles full of fluorescent gelatin revealing in this mutant a strong internalization process of matrix. Thus, $\beta 3$ integrin FAs dependent traction forces promoted by the loss of ICAP-1 are efficient and functional enough to remodel the fibronectin matrix. Furthermore, it would appear that this phenotype is associated with a defect of endocytosis of $\beta 3$ integrins binding FbN at the cell membrane.



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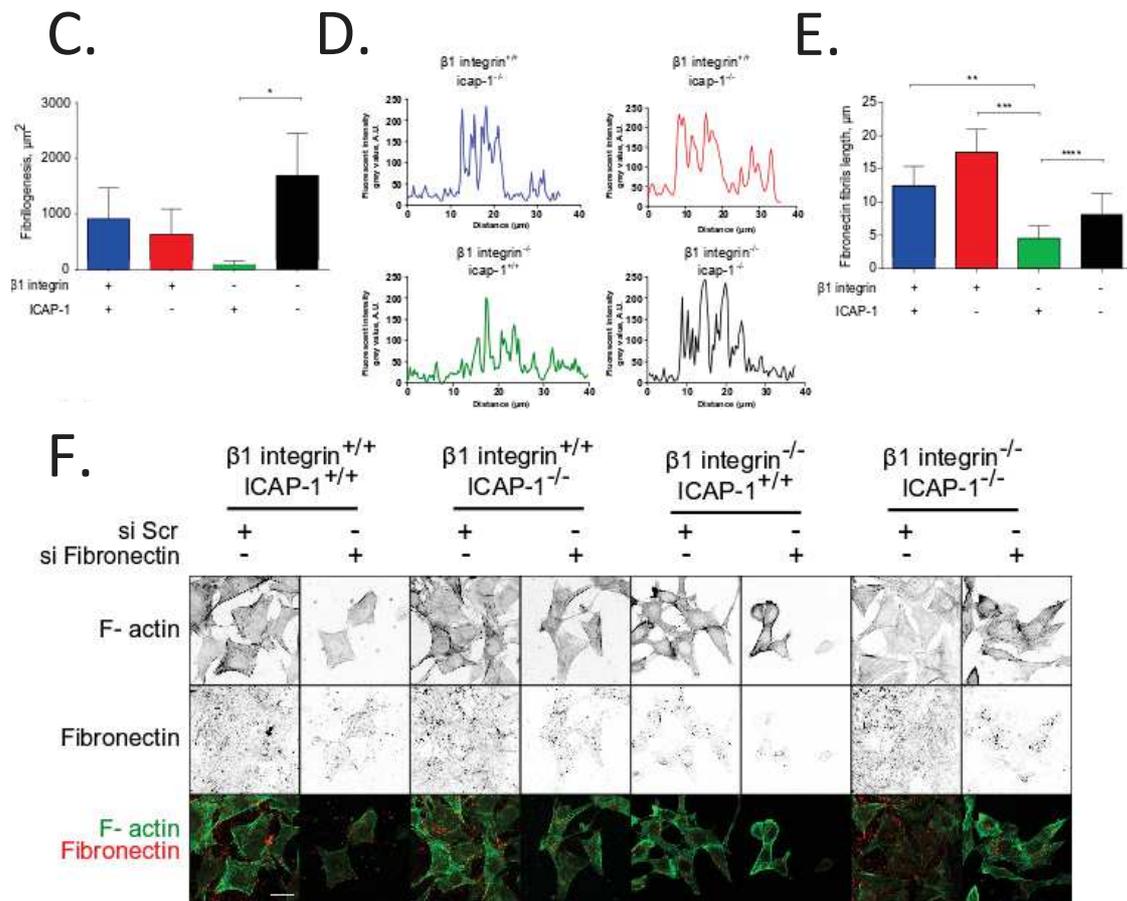


Figure 8.3.4. Loss of ICAP-1 promotes $\beta 3$ integrin fibrillar adhesions which are associated with FbN fibrillogenesis.

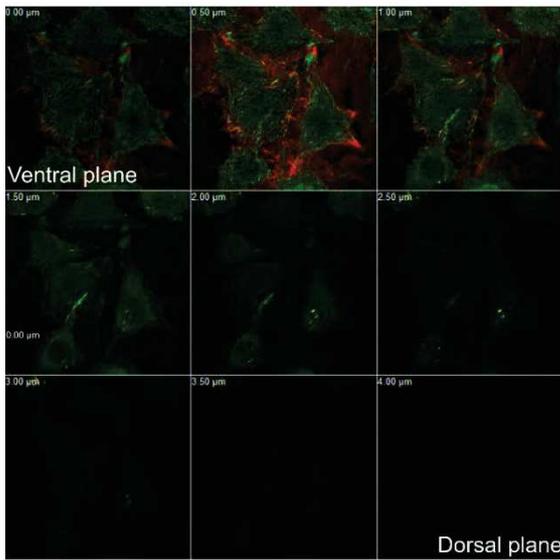
C-E. Thresholded images of deposited and organized in the process of fibrillogenesis were processed and quantified. (C) quantification of FbN fibrils area. (D) Intensity profiles of FbN fibrils were obtained across the red lines in each corresponding cell culture. The intensity of the fluorescence reveals the density of FbN in fibrils and the picks area the thicker of the fibrils. The loss of ICAP-1 in $\beta 1$ -/- cells increases both the density and the thicker of FbN fibrils. (E) The FbN fibrils length quantification reveals that the loss of ICAP-1 increases the length compare to the respective cell lines with or without $\beta 1$ -/- integrin.

F. Osteoblasts cells were transfected with fibronectin or scramble siRNA for 48h and then let spread in serum free medium on uncoated glass for 24 hours. After PFA fixation, staining of F-actin (phalloidin, green) and extracellular fibronectin (gelatin-Alexa 563, red) were performed and analyzed by fluorescent microscopy. Not surprisingly, fibronectin siRNA drastically impairs FbN fibrillogenesis in all osteoblasts mutants. All four osteoblast cell lines require endogenous FbN to spread and organize their actin cytoskeleton since disruption of FbN expression diminishes severely the spreading area. Bar scale represents 20 μm .

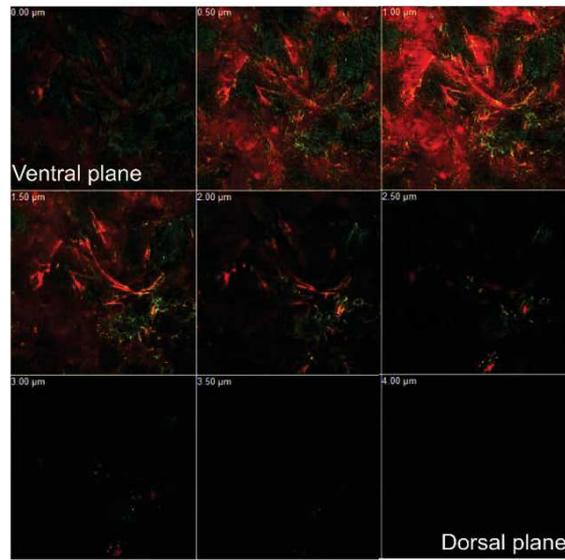


G.

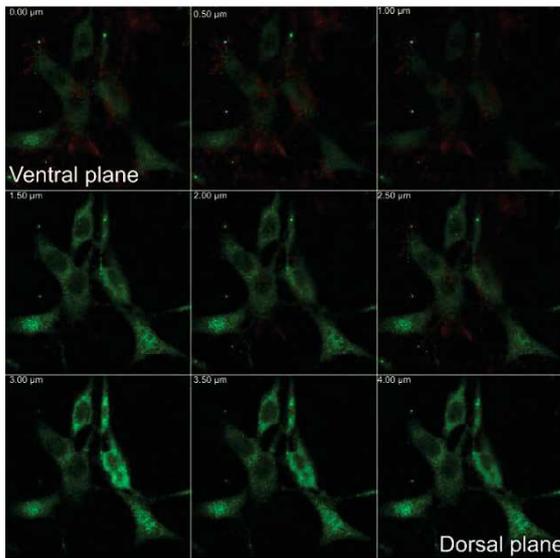
$\beta 1$ integrin^{+/+}
ICAP-1^{+/+}



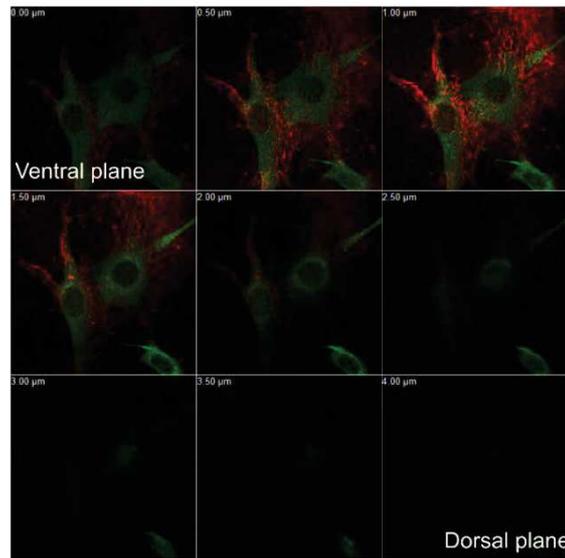
$\beta 1$ integrin^{+/+}
ICAP-1^{-/-}



$\beta 1$ integrin^{-/-}
ICAP-1^{+/+}



$\beta 1$ integrin^{-/-}
ICAP-1^{-/-}

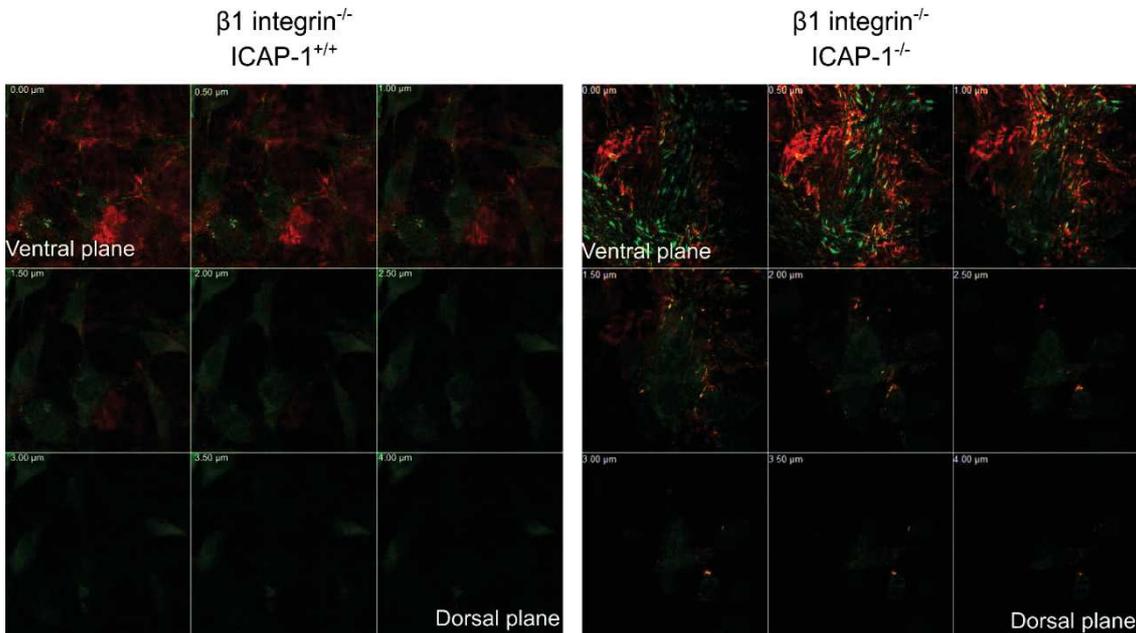
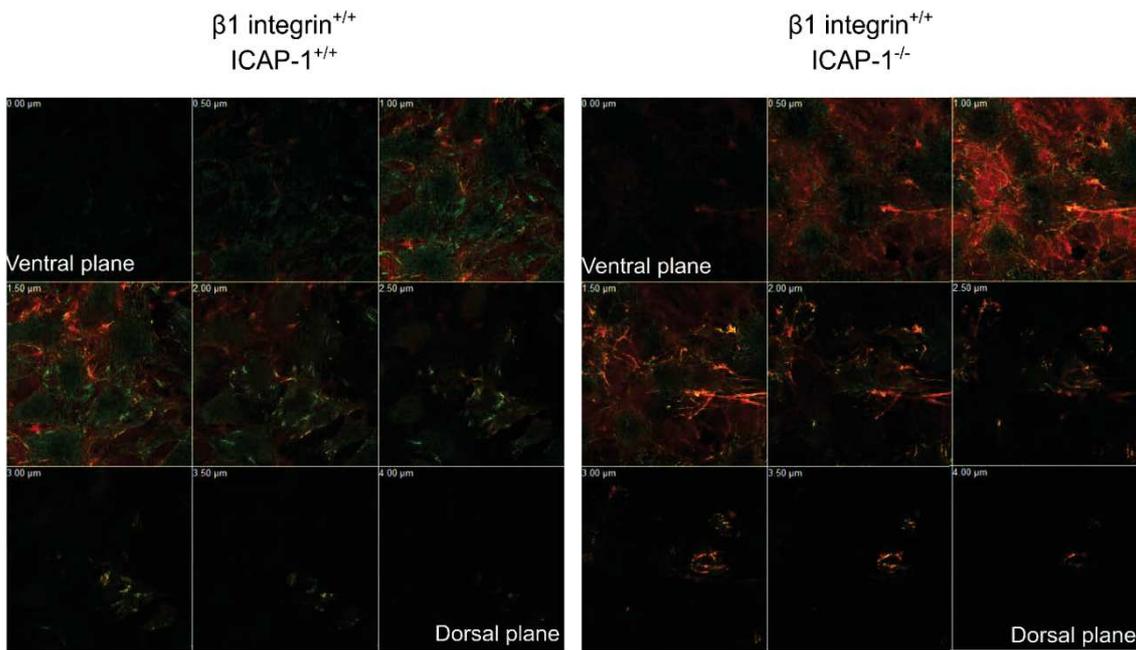


$\beta 1$ integrin
Extracellular
fibronectin



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H.



$\beta 3$ integrin
Extracellular
fibronectin



Figure 8.3.4. Loss of ICAP-1 promotes β 3 integrin fibrillar adhesions which are associated with FbN fibrillogenesis.

G-H. Optical sections of osteoblasts cell cultures undergoing fibrillogenesis process. After PFA fixation and staining, confocal galleries images from the ventral to the dorsal sides were generated every $1\mu\text{m}$, to reveal double fluorescence and co-localization of FbN fibrils (red) with β 1 or β 3 integrin adhesions (green, G and H respectively). Note that for β 1 integrin deficient cells β 3 integrin adhesions associated with FbN fibrils could not move to the cell dorsal side and they are keep on the ventral side. Indeed, β 1 deficient cells were not able to pull FbN fibrils over the cell roofs, even though β 1^{-/-}/ICAP-1^{-/-} has no troubles in organizing ventral FbN fibrils. Bar scale represents $20\mu\text{m}$.



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I.

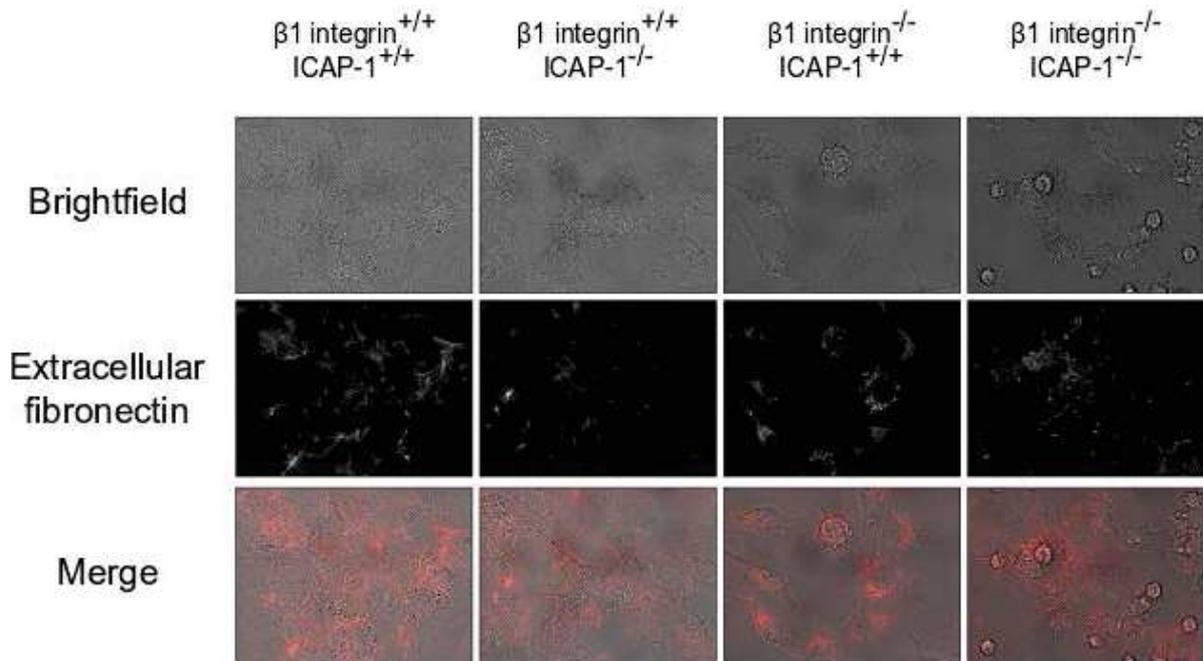


Figure 8.3.4. Loss of ICAP-1 promotes $\beta 3$ integrin fibrillar adhesions which are associated with FbN fibrillogenesis.

I. Representative images of live time imaging records. Osteoblast cell mutants were seeded in serum free medium on uncoated cover slide chamber for overnight. Endogenous fibronectin hidden on the surface of the cells was probe using fluorescent Alexa 563 gelatin and washout after 30 min incubation. Extended and organized FbN fibrils were observed for *beta1 integrin*^{+/+} and for *beta 1 integrin*^{-/-} ICAP-1^{-/-}. In contrary *beta 1* KO cells do not exhibit FbN fibrils on their surface but numerous endocytosis vesicles full of fluorescent. Bar scale represents 20 μ m.



8.3.5. The $\beta 3$ integrin dependent contractility in cells devoid of $\beta 1$ integrin and ICAP-1 is associated with a defect of $\beta 3$ integrin endocytosis

As endocytic membrane traffic regulates bioavailability of cell-surface molecules and therefore the intensity and/or specificity of receptor-initiated signals (Ceresa and Schmid, 2000; Scita and Di Fiore, 2010), we hypothesize that the decrease of $\beta 3$ integrin turnover observed in $\beta 1$ /ICAP-1 double KO might be linked to a defect in $\beta 3$ integrin endocytosis. For this, cells were plated onto glass surfaces coated with fibronectin and confocal microscopy was used to determine the uptake of

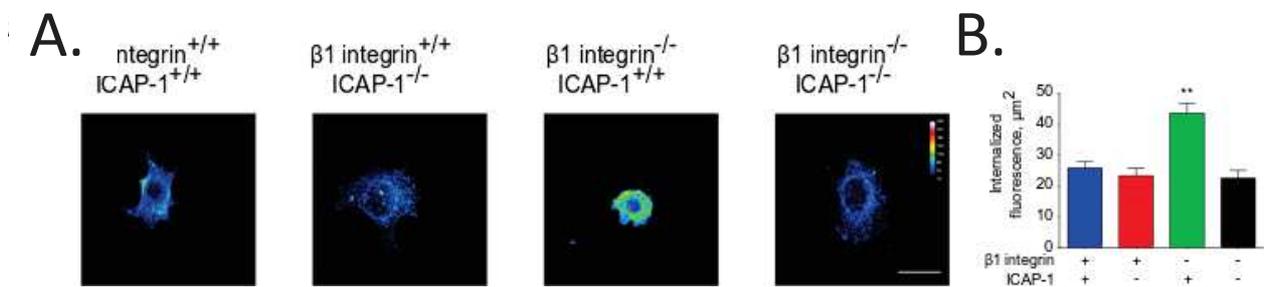


Figure 8.3.5.1. The $\beta 3$ integrin dependent contractility is associated with the defect of $\beta 3$ integrin endocytosis

A. The $\beta 3$ integrin uptake was measured using $\beta 3$ integrin specific antibody (LucA.5). Representative confocal images of osteoblast cells plated on fibronectin coated glass and stained for FITC conjugated $\beta 3$ integrin specific antibody (LucA.5). Shown are x-axis and Z-axis after 3D reconstruction profile. The images were taken after 20 min incubation at 37°C followed by acid wash. Scale bar is $20\ \mu\text{m}$.

B. Quantification of the proportion of endocytosed $\beta 3$ integrin receptors based on antibody staining ($n=20$ cells pooled from three independent experiments, mean \pm SEM) after 3D reconstruction of z-stacks. Note higher $\beta 3$ integrin endocytosis in the case of $\beta 1$ integrin $^{-/-}$ -icap-1 $^{+/+}$ cell line and a rescue of $\beta 3$ integrin endocytosis rate in $\beta 1$ integrin $^{-/-}$ -icap-1 $^{-/-}$ cell line.

** adjusted p.value ≤ 0.01 . Experiment was done three independent times.

anti-integrin $\beta 3$ antibodies (LucA.5 conjugated with FITC). Fluorescent antibodies were transported into cytoplasmic vesicles that were visible above the plane of cell surface in the case of WT osteoblasts (Fig. 8.3.5.1A and 8.3.5.1B).

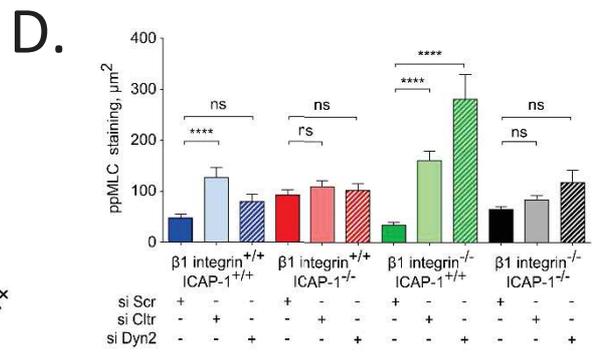
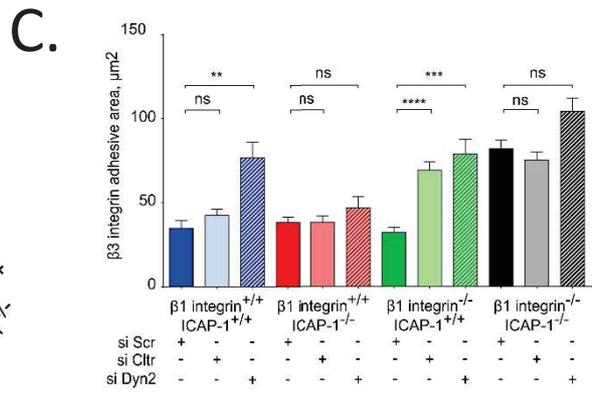
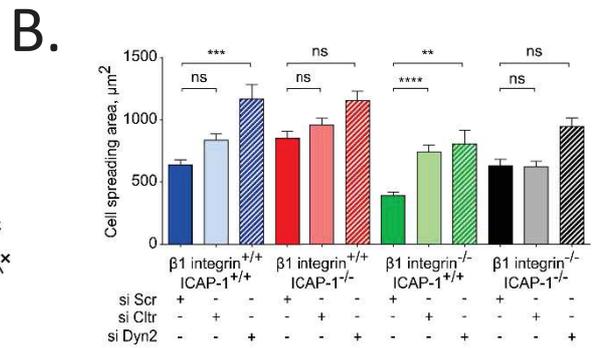
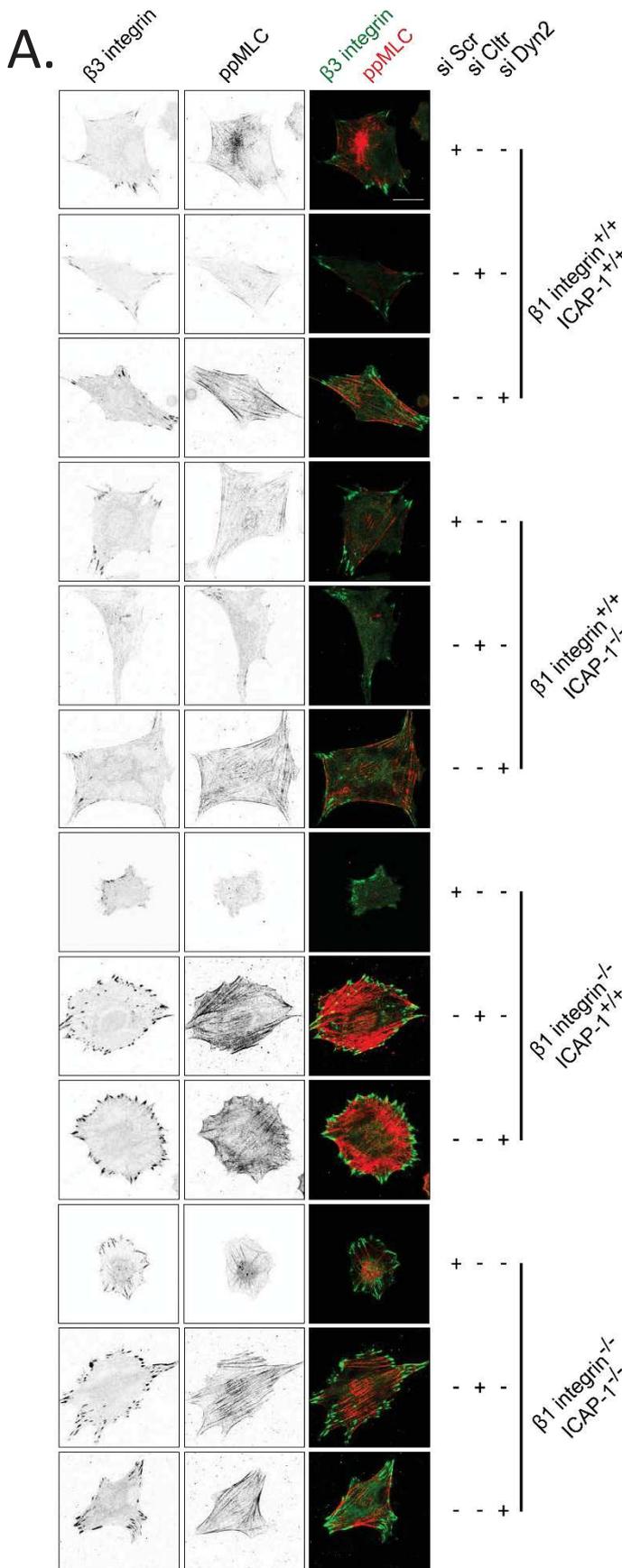
The number of LucA5-positive intracellular vesicles was significantly reduced in the case of the double deletion $\beta 1$ integrin/ICAP-1 compared to $\beta 1$ null cell line, suggesting a defect in $\beta 3$ integrin endocytosis. As surface $\beta 3$ integrins are



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constitutively endocytosed through clathrin-mediated routes (Arjonen et al., 2012; Yu et al., 2015; Ezratty et al., 2009), we addressed the question whether the deletion of clathrin or dynamin might mimic the loss of ICAP-1 in cells depleted in $\beta 1$ integrin. First alterations of clathrin and dynamin expression in WT cells lead to an increase of cellular spreading which is correlated with an increase of $\beta 3$ integrin focal adhesion area and P-myosin light chain intensity (Fig. 8.3.5.2). Whereas $\beta 1$ integrin deficient cells displayed a decrease in their spreading surface (Fig. 8.3.1G) and a reduction in area of $\beta 3$ integrin containing focal adhesion (Fig. 8.3.2B) as compared to the WT cells, the deletion of clathrin (Fig. 8.3.5.2A-D) or dynamin (Fig. 8.3.5.2A-D) in $\beta 1$ integrin deficient cells restore their ability to spread, to form bigger $\beta 3$ integrin focal adhesion and to generate actin stress fibers highly decorated with P-myosin light chain. Importantly, the deletion of either clathrin or dynamin did not change the phenotype of cells depleted in ICAP-1 or in cells devoid of both ICAP-1 and $\beta 1$ integrin in term of cell spreading, size of $\beta 3$ integrin focal adhesions and P-myosin staining. Firstly, our results demonstrate that impairment of endocytosis modifies $\beta 3$ integrin signaling through an increase of $\beta 3$ integrin clustering which is correlated with an increase of cell spreading and reorganization of actomyosin cytoskeleton. Secondly our data show that cells devoid of ICAP-1 are not sensitive to the alteration of clathrin-based traffic machinery suggesting a potential role of ICAP-1 in $\beta 3$ integrin endocytosis.





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Figure 8.3.5.2. Clathrin and dynamin inhibition in $\beta 1$ KO cells restores cellular $\beta 3$ integrin mediated spreading and acto-myosin cytoskeleton mimicking the phenotype of $\beta 1$ integrin^{-/-}-icap-1^{-/-} cells

A. Spinning disk representative micrographs of the four osteoblast cell lines treated or not with clathrin or dynamin siRNAs. Inhibition of clathrin and dynamin in $\beta 1$ integrin^{-/-}-icap-1^{+/+} cell line allows the rescue of cell spreading through $\beta 3$ integrin mediated focal adhesion and development of acto-myosin cytoskeleton (see green bars in quantification graph below). Note the lack of effect of SiRNA in cell lines depleted in ICAP-1 ($\beta 1$ integrin^{+/+}-icap-1^{-/-} in red bars and $\beta 1$ integrin^{-/-}-icap-1^{-/-} in black bars). Scale bar is 20 μ m.

B. Quantification of cell spreading area before and after treatment with clathrin SiRNA and dynamin siRNA.

C. Quantification of area of $\beta 3$ integrin containing adhesion sites area before and after treatment with clathrin SiRNA and dynamin siRNA.

D. Quantification of P-myosin staining area before and after treatment with clathrin SiRNA and dynamin siRNA.

ns adjusted p.value > 0.05; * - p.value \leq 0.05; ** p.value \leq 0.01; *** p.value \leq 0.001; **** p.value \leq 0.0001.



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8.3.6. ICAP-1 partner, Nm23-H1/2, is involved in the β 3 integrin dependent contractility and β 3 integrin dynamics

Next, we investigated the mechanism by which ICAP-1 might affect β 3 integrin endocytosis. We have previously shown the interaction between ICAP-1 and the Nucleoside Diphosphate Kinase called Nm23-H2 (Fournier et al., 2002b). Genetic and functional studies have demonstrated the ability of Nm23-H2 to fuel dynamin to drive clathrin dependent endocytosis (Boissan et al., 2014; Krishnan et al., 2001; Dammai et al., 2003; Nallamotheu et al., 2008). Based on these findings, we addressed the question whether Nm23-H2 might impact on β 3 integrin dynamics and consequently on cell spreading and cell contractility. For this purpose, we analyzed adhesive behavior of cells in conditions where Nm23-H2 was deleted. As Nm23-H2 forms a complex with Nm23-H1 to be recruited to clathrin-coated pits by their physical interaction with dynamin (Boissan et al., 2014), both Nm23-H1 and Nm23-H2 were knocked down using specific RNAi since they form a complex. The deletion of Nm23 rescued the ability of β 1 integrin depleted cells to spread onto fibronectin (Fig. 8.3.6A, B). The restoration of cell spreading is associated with an increase of β 3 integrin clustering as demonstrated by the increase of the area of β 3 integrin containing focal adhesion (Fig. 8.3.6C, E) and reorganization of actomyosin cytoskeleton as confirmed by the increase of P-myosin staining (Fig. 8.3.6D). More importantly, the deletion of Nm23 leads to a decrease of β 3 integrin turnover as judged by FRAP experiments performed onto β 1 integrin depleted cells (Fig. 8.3.6C). The deletion of Nm23 is inefficient in the case of cells already depleted in ICAP-1. The effect of Nm23 down regulation is significantly detected in WT cells as judged by the increase of cell spreading and the reorganization of actomyosin network whereas the turnover of β 3 integrin and the area of β 3 integrin containing focal adhesion are not changed. The presence of β 1 integrin might protect β 3 integrin from the deletion of Nm23. Finally, our results show that ICAP-1 and Nm23 are both implicated in cell spreading and actomyosin



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reorganization likely through a fine tuning of $\beta 3$ integrin endocytosis which impacts on $\beta 3$ integrin turnover and size of associated focal adhesion.





A.

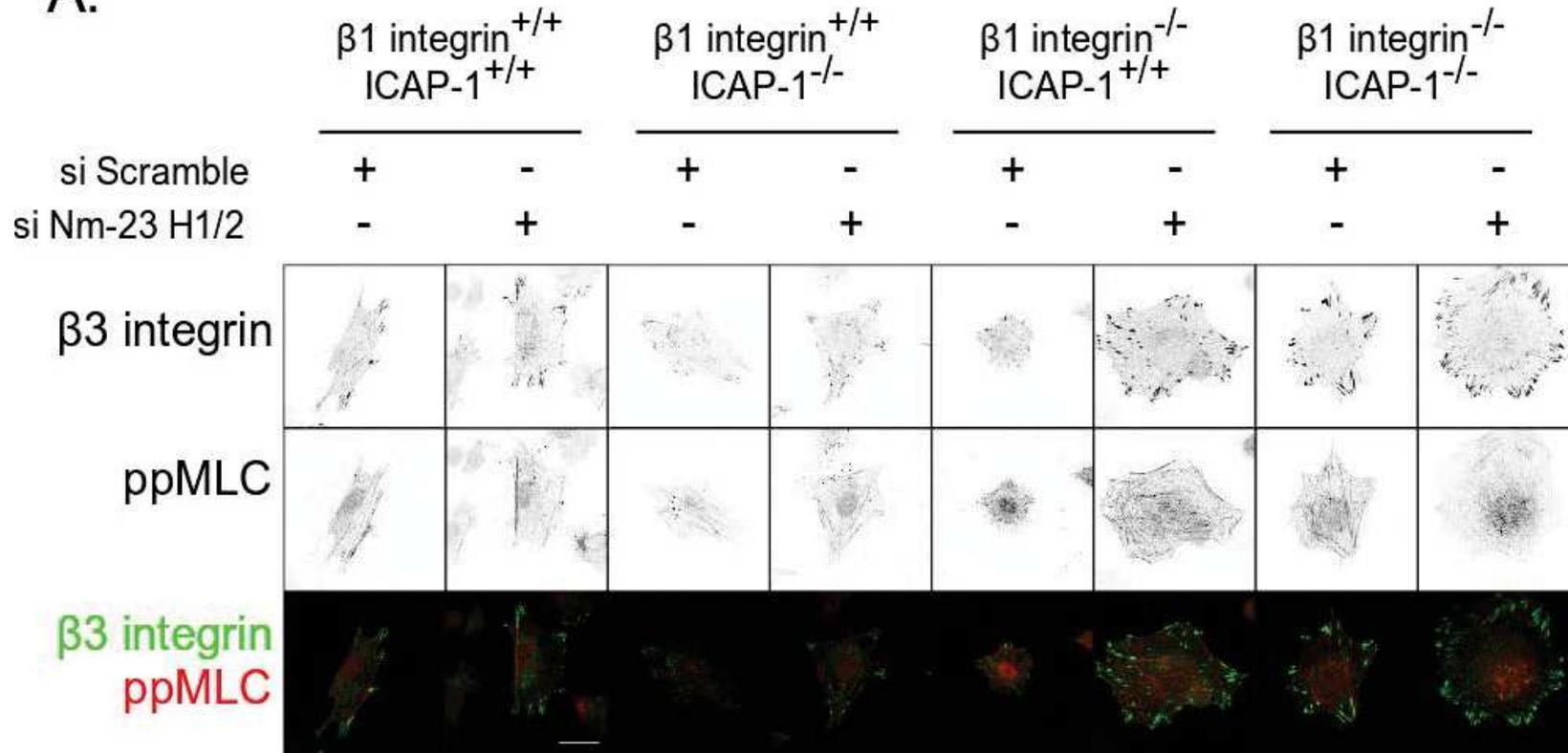


Figure 8.3.6. Nm23-H1/2 (partner of ICAP-1, CCP complex and dynamin) is involved in the $\beta 3$ integrin dependent contractility and dynamics

A. Spinning disk representative micrographs of the four osteoblast cell lines before and after silencing of Nm-23-H1/2. Silencing of Nm-23-H1/2 in $\beta 1$ integrin^{-/-}-icap-1^{+/+} cell line is able to rescue of cell spreading through $\beta 3$ integrin mediated focal adhesion and development of acto-myosin cytoskeleton likely through $\beta 3$ integrin trapping at the cell membrane (see green bars in quantification graph below). No effect of SiRNA Nm-23-H1/2 in cell lines depleted in ICAP-1 ($\beta 1$ integrin^{+/+}-icap-1^{-/-} in red bars and $\beta 1$ integrin^{-/-}-icap-1^{-/-} in black bars). Scale bar is 20 μ m.

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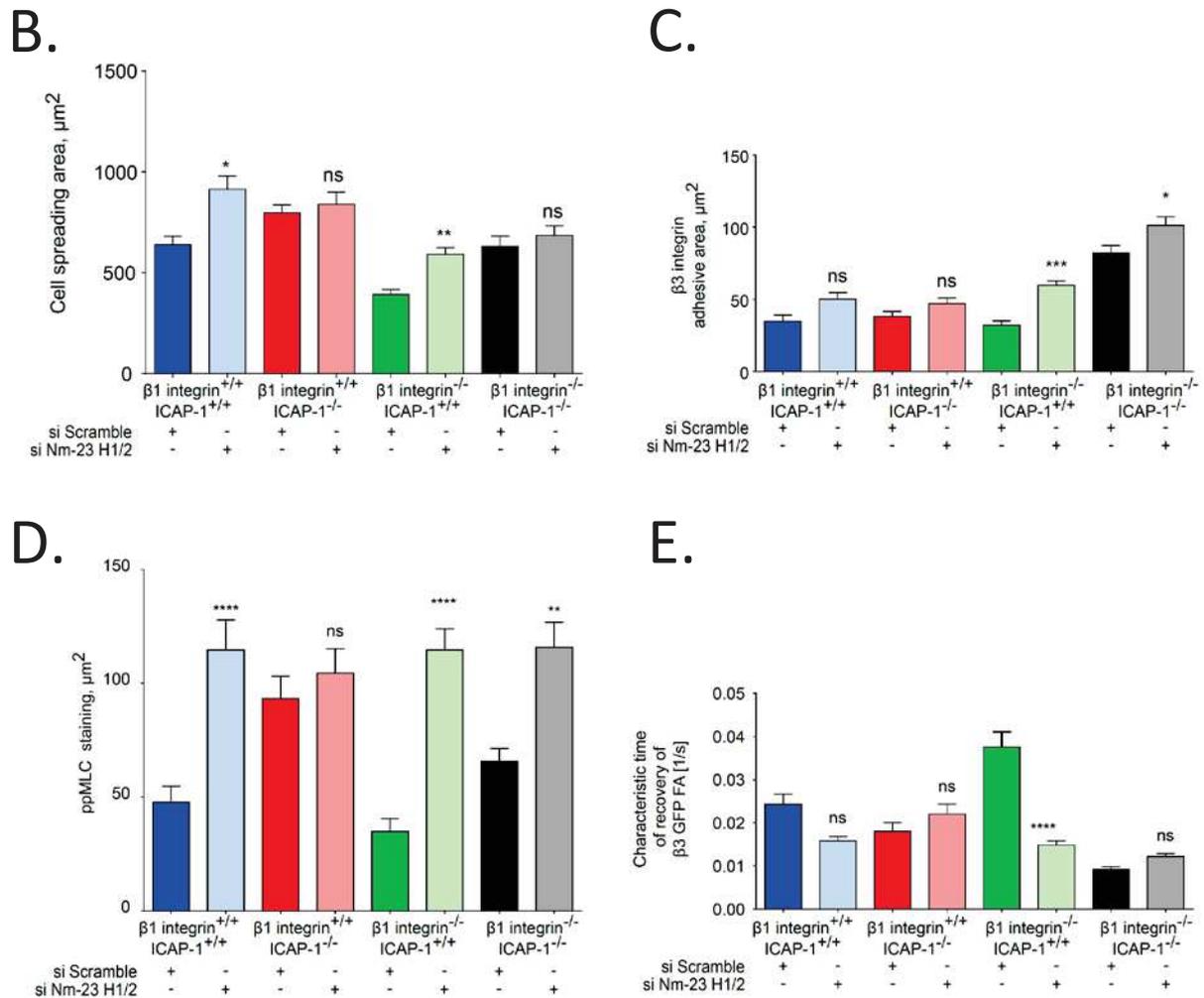


Figure 8.3.6. Nm23-H1/2 (partner of ICAP-1, CCP complex and dynamin) is involved in the $\beta 3$ integrin dependent contractility and dynamics

B. Quantification of cell spreading area before and after silencing of Nm-23-H1/2.

C. Quantification of area of $\beta 3$ integrin containing adhesion sites area before and after silencing of Nm-23-H1/2.

D. Quantification of P-myosin staining area before and after silencing of Nm-23-H1/2.

E. TIRF/FRAP analysis shows that deletion of Nm-23-H1/2 complex impedes the turnover of $\beta 3$ integrin – GFP at the plasma membrane in $\beta 1$ integrin^{-/-}-icap-1^{+/+} cell line. 50 FA (5 FA per cell) were bleached for each experiment and their recovery was monitored for 5 min. Error bars represent standard deviation of at least 10 cells/experiment. **** adjusted p.value ≤ 0.0001 . The experiment was performed in triplicate. ns adjusted p.value > 0.05 ; * - p.value ≤ 0.05 ; ** p.value ≤ 0.01 ; *** p.value ≤ 0.001 ; **** p.value ≤ 0.0001 .



IV.

**Discussion,
conclusion and
perspectives**





IV. Discussion, conclusion and perspectives

8.4. Discussion

8.4.1. Force development and mechanical remodeling of ECM through $\beta 3$ integrins are regulated by ICAP-1

Our results show that the deletion of ICAP-1 restores cellular spreading of $\beta 1$ integrin KO cells which are known to be round and devoid of traction forces. In these conditions, the cellular spreading is due to the increase of $\beta 3$ integrin clustering which is associated with the impressive development of the actomyosin cytoskeleton related to high contractile events on the FbN substrate and the development of FBN fibrils. Our data demonstrate that ICAP-1 modulates the organization of cell matrix adhesion and actomyosin contractility loading on $\beta 3$ integrins independently of $\beta 1$ integrin signaling.

It has been previously proposed that the progression from newly formed nascent adhesions to mature focal adhesions and fibronectin–matrix remodeled fibrillar adhesions can be conceptualized as a myosin II-dependent maturation process from small cell–matrix adhesions with high turnover rate to progressively larger and enduring adhesion sites (focal adhesion and fibrillar adhesion) stabilized by the connection to the cytoskeleton (Schiller et al., 2011b). Here, our data show that the loss of ICAP-1 decreases drastically the turnover of $\beta 3$ integrins in the focal adhesions and one of the major consequence was to increase the actomyosin pattern of the spread cells increasing the associated contractile energy at the adhesions sites with the fibronectin substrate. In the lab, we have previously demonstrated that in endothelial cells the destabilization of ICAP-1 through the loss of its partner CCM1/2 complex resulted in an increase of $\beta 1$ activation and led to increase RhoA-dependent contractility. The resulting abnormal distribution of forces led to aberrant extracellular matrix remodeling around lesions of CCM1- and CCM2-deficient mice (Faurobert et al., 2013). Here, for osteoblasts which spread over fibronectin substrate, the effect of the loss of ICAP-1 is not actually significant on cell contractility and on the associated extracellular remodeling



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even though we can observe a tendency to slightly increase actomyosin contractility with an increase in the associated fibrillogenesis. Effect of the loss of ICAP-1 becomes major when $\beta 3$ integrins are no longer associated with the expression of $\beta 1$ signaling. As focal adhesions always contain combinations of several integrins it is unknown whether to what extent individual integrin classes bound to the same ECM ligand (e.g. $\alpha 5\beta 1$ and $\alpha v\beta 3$ on FbN), use special pathways to sense and exert force. In 2013, Shiller et al (Schiller et al., 2013) identified a functional synergy between $\alpha 5\beta 1$ and αv -class integrins signaling hubs leading to feedback amplification of myosin II activity. In this study, by comparing $\beta 1$ integrin KO cells et $\beta 1$ integrin/ICAP-1 double KO cells, we were authorized to reveal the influence of ICAP-1 over $\beta 3$ integrins by pointing out the restoration of spreading and traction force in $\beta 1$ integrin null cells. One can then ask the question of why the cells in the absence of $\beta 1$ integrins and in the presence of ICAP-1 express a poor spreading and contractile phenotype on FBN substrate. This can be considered by the view that for $\beta 1$ integrin KO cells, ICAP-1 does not anymore interact with $\beta 1A$ integrins cytoplasmic domain and released from this interaction would no longer be titrated by $\beta 1$ integrins. Thus, liberated ICAP-1 could interact and inhibit other partners such as Rac1 or Cdc-42 that could lead to the down regulation of activity of lamellipodia/filopodia motilities and to a poor cell spreading (Degani et al., 2002). As described before, $\alpha 5\beta 1$ and $\alpha v\beta 3$ integrins bind to FBN. However, $\alpha 5\beta 1$ but not $\alpha v\beta 3$ supports high levels of RhoA activity at later stages of cell adhesion, which are associated with recruitment of tensin into fibrillar adhesions and FBN fibrillogenesis (Danen et al., 2002). Expression of an activated mutant of RhoA stimulates $\alpha v\beta 3$ -mediated fibrillogenesis as the loss of ICAP-1 in osteoblasts $\beta 1$ integrin KO mutant does. It would be easy then to formulate the link between the loss of ICAP1 and the activation of RhoA. Unlike Rac1 and Cdc-42, no direct link was established between ICAP-1 and RhoA. However, the plausible global GDI activity of ICAP-1 is controversial and is not supported by solid structural data, with the sequence and conformation of ICAP



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being relatively far-off from those of the classic Rho GDI. On the other hand, ICAP-1 and ROCK (the Rho kinase) were co-immunoprecipitated from C2C12 cells and also identified by using the yeast two-hybrid assay (Stroeken et al., 2006; Alvarez et al., 2008). Thus, ICAP-1 might interact with ROCK and regulate the stiffening of the intracellular environment. We have recently shown that ICAP-1 and its monoubiquitylated form regulate ROCK2- and MRCK α -dependent myosin phosphorylation independently of interaction with β 1 integrins (Bouin et al., 2017b). Indeed, our results propose a novel role of ICAP-1 on β 3 integrins clustering, β 3 dynamics and on the associated actomyosin contractile pathway. In this issue, ICAP-1 might negatively control contractile actomyosin cytoskeleton organization and would no longer allow the maturation of adhesion sites into FAs and then fibrillar adhesions. We cannot rule out the fact that the increase of contractile actomyosin cytoskeleton can be also lead to a defect in membrane tension and consequently in endocytic process. A recent study corroborates with these later findings by demonstrating the sensitivity of β 3 integrins regarding force generation. Indeed the loss of physical forces on ligand-bound integrins can switch β 3 activation from classical focal adhesion formation to a pathway of clathrin-mediated endocytosis of β 3 clusters (Yu et al., 2015). Finally, our results identify ICAP-1 as a novel factor contributing to β 3 integrin regulation through an elaborate signaling network responsible for maintaining cell tensional homeostasis independently of its interaction with β 1 integrins.

8.4.2. ICAP-1 as an adaptor protein in integrin endocytic process to regulate β 1 and β 3 integrin cooperativity

Integrin internalization occurs through clathrin-dependent and clathrin independent mechanisms and many integrins can follow more than one route into the cell to control adhesion turnover, cell migration, morphogenesis and cancer metastasis (Caswell et al., 2009; Shi and Sottile, 2008b; Mellman and Yarden, 2013; Yu et al., 2015). Clathrin-dependent trafficking of integrins has



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proven to be essential for adhesion disassembly and this process is governed by the intracellular domains of both α and β subunits (Margadant et al., 2011; De Franceschi et al., 2016; Ezratty et al., 2009; Arjonen et al., 2012). Nevertheless, the existence of specific regulatory pathways that would trigger preferential internalization of one integrin heterodimer over another is still matter of debate.

Our study demonstrated that β 3 integrin dynamics is affected by the simultaneous loss of β 1 integrin and ICAP-1. This decrease of β 3 integrin dynamic in absence of ICAP-1 and β 1 integrin is correlated with the alteration of β 3 integrin trafficking. Our data show also that the additional loss of clathrin or Nm23-H2 in cells depleted in β 1 integrin mimics the loss of ICAP-1. Moreover, the loss of Nm23-H2 or clathrin does not allow restoration of β 3 integrin mediated cell spreading in cells depleted in ICAP-1. These results suggest that ICAP-1, Nm23-H2 and clathrin might work together to control β 3 integrin endocytosis. On line with this, Clathrin/AP2 mediated endocytosis is associated with adhesion disassembly and clathrin coated pits (CCP) are enriched at adhesive contacts by colocalizing with integrins (Ezratty et al., 2009). However in addition to the essential core components of cargo, AP-2 adaptor and clathrin, many other endocytic accessory proteins or co-adaptors associate with CCP and aid in cargo selection, in the efficiency of cargo enrichment at the CCP, and in execution of subsequent membrane deformation, fission, uncoating and endosomal fusion events (Yap and Winckler, 2015). Some prominent examples are PTB domain proteins named Dab2 and Numb known to associate with conserved NPXY motifs shared by all the cytoplasmic domains of β -integrin subunits and to be involved in integrin trafficking by interacting with endocytic machinery like AP2 and clathrin or endocytic accessory proteins (Eps15). Dab2 and Numb accumulate at or near focal adhesions shortly before their disassembly (Chao and Kunz, 2009; Teckchandani et al., 2009; Nishimura and Kaibuchi, 2007; Ezratty et al., 2009). Like Numb and Dab2, ICAP-1 belongs to the PTB domain protein family. Whereas ICAP-1 interacts with the distal NPXY motif of β 1 integrin, Dab2 binds the same distal



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NPXY motif of $\beta 1$, $\beta 2$, $\beta 3$, $\beta 5$ and $\beta 7$ integrins and Numb associates with the proximal NPXY of $\beta 3$ and $\beta 5$ integrins. The involvement of ICAP-1 in the endocytic machinery is supported by its direct interaction with nm23-H2 (Fournier et al., 2002), which is a nucleoside diphosphate kinases (NDPKs) involved in dynamin-mediated endocytosis (Boissan et al., 2014). Nm23-H2 is complexed with AP2 (Zala and Boissan 2017) and is important for scission of endocytic clathrin coated pits (Boissan et al., 2014). Many proteomic based studies have identified nm23 as partner of both $\beta 1$ and $\beta 3$ integrin associated complexes (Kuo et al., 2011; Schiller et al., 2011b, 2013). It is tempting to think that ICAP-1 might be involved in the membrane localization of nm23-H2 as already described (Fournier et al., 2002b), in the activity of nm23-H2 or in the physical proximity between nm23-H2 and integrin. Whereas we have shown that ICAP-1 is involved in $\beta 3$ integrin endocytosis, we cannot exclude the implication of ICAP-1 in $\beta 1$ integrin endocytosis. Preliminary experiments have confirmed a defect in $\beta 1$ integrin endocytosis in ICAP-1 depleted cell highlighting a general role of ICAP-1 in integrin endocytosis (data not shown). As ICAP-1 is not observed in focal adhesion, we can suppose that ICAP-1 would play its role in integrin endocytosis outside focal adhesions. This hypothesis is supported by high resolution imaging of ICAP-1 showing its ability to localize outside focal adhesion site and to conserve its membrane localization even in cells depleted in $\beta 1$ integrin (Collaboration with Giannone lab).

Despite these advances, it remains unclear how the individual NPXY motifs present in the cytoplasmic domain of integrins regulate trafficking of different integrin and through which PTB domain proteins this is effectuated. The physiological relevance of having many adaptors or co-adaptors like ICAP-1, Numb or Dab2 in the same cell might respond to integrin specificity and physical properties of the microenvironment. The mechanical state of a cell is a master regulator of its endocytic clathrin coat dynamics (Ferguson et al., 2017). Tension on the membrane can hinder this process as it increases the energy cost of curvature formation (Sheetz, 2001). As an illustration, Dab2 is not found at $\beta 3$ integrin-



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mediated focal adhesion sites formed on RGD-glass suggesting different adaptors depending on the stiffness of the microenvironment. Indeed, it has been shown that the development of actomyosin contractility inhibits Dab2 binding to $\beta 3$ integrin, and the loss of cell-matrix force development is one of the key mechanisms activating Dab2 binding to $\beta 3$ integrin clusters resulting in endocytosis of $\beta 3$ integrins in soft conditions (Yu et al., 2015). Assuming a possible interaction between $\beta 3$ integrin and a modified form of ICAP-1, ICAP-1 might take over on Dab2 in stiffer microenvironment as ICAP-1 and Dab2 are sharing the same distal NPXY motif to interact with integrin. As far as $\beta 1$ integrin endocytosis is concerned, Dab2 and clathrin are not found to activated $\beta 1$ integrin clusters (Yu et al., 2015) indicating that the turnover of $\beta 1$ integrin may be regulated by a different pathway involving eventually ICAP-1 in stiffer microenvironment.

8.5. Conclusion and perspectives

Our data demonstrate that ICAP-1 regulates $\beta 3$ integrins and therefore it influences the organization of cell matrix adhesion and actomyosin contractility independently of $\beta 1$ integrin signaling.

Finally, because migratory and adhesive behavior is mediated by $\beta 1$ and $\beta 3$ integrin cooperation (Schiller et al., 2013), the regulation of their respective intracellular trafficking in a coordinated manner is likely essential for rapidly and efficiently adapting the responsiveness of migratory cells to extracellular guidance cues. Originally identified as specific for $\beta 1$ integrin, ICAP-1 might coordinate $\beta 1$ and $\beta 3$ integrin endocytosis to adapt integrin dynamics and force generation in a context dependent manner, supporting the idea that endocytic process is a good way to tune integrin cooperativity.

Several questions still remain unanswered though. Are $\beta 3$ integrins recruiting other partners at the level of FAs as a consequence of their slow turnover? It is not difficult to imagine that the molecular environment of $\beta 3$ integrin will change if its mobility is delayed and it will modulate its signaling at the FA level. A feasible



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approach to identify the different $\beta 3$ integrin partners in different cellular environment is subcloning it in BiOLD2 vector – an engineered biotin ligase that is able to biotinylate neighboring partners and subsequently analyze the biotinylated proteins by quantitative mass spectrometry. Also, results from variation in the length between $\beta 3$ integrin and the biotin ligase (to discriminate between close and more distant partners) could shed more light on the protein content of the $\beta 3$ FAs in an ICAP-1 context of $\beta 1$ integrin null cells. Since FA turnover and microtubule (MT) dynamics has been described (Stehbens and Wittmann, 2012). Even more since the MT are main ways to deliver endocytosis related protein as dynamin (Chao and Kunz, 2009; Engler et al., 2007; Ezratty et al., 2009) and/or are implicated in Rho-ROCK contractility pathway by delivering GEF-H1 (Heck et al., 2012). It seems feasible to hypothesize that the MT dynamics would influence the turnover and the actomyosin contractility loading on $\beta 3$ integrins at the cell membrane. ICAP-1 can influence that process directly at MT level, since as we show, it is important for the proper function of Nm-23 complex and Nm23 is reported to interact with directly with the MT (Ikeda, 2010). The interaction between ICAP-1 and Nm-23-H2 has been published before (Fournier et al., 2002a), but direct interaction between $\beta 3$ integrin and Nm-23-H2 are still not solid despite several proteomic studies (Bharadwaj et al., 2017; Humphries et al., 2009b; Alanko et al., 2015. Integrin Endosomal Signalling Suppresses Anoikis -, 2015). Proximity ligation assays (*in situ* PLA) – is a powerful technology which allows direct detection of endogenous protein interactions and modifications with high specificity and will efficient to establish if indeed $\beta 3$ integrin/Nm-23-H2 form a complex at the plasma membrane and whether ICAP-1 behavior could influence the integrins turn over.

In collaboration with Giannone's laboratory, using super-resolution microscopy and single particle tracking we have recently shown that $\beta 1$ and $\beta 3$ integrins move and function as distinct homotypic nanoclusters within focal adhesion demonstrating the nanoscale dynamics of integrins within focal adhesion (Rossier



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et al., 2012). This nano-organization and clear segregation of β integrins seems to be a universal phenomenon since we have also shown these patterns in other adhesion structures such as invadosome (Destaing et al., 2010). My working hypothesis here, should be based on my current results identifying ICAP-1 as molecular basis of the cross-talk between $\beta 1$ and $\beta 3$ integrins. The attracting hypothesis is that the dynamic of $\beta 3$ integrins within focal adhesion might be regulated by ICAP-1 at the cell membrane nearby to control development of local forces and to drive associated signaling necessary for cell adhesion, migration and invasion.



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Materials and methods





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9.1. Antibodies and chemicals

Human plasma fibronectin was purchased from Sigma-Aldrich. All siRNA (ON-TARGETplus) were obtained from ThermoFisher. Anti $\beta 3$ integrin antibody was purchased from Emfret (Clone LucA.5, #M030-0, for the variant, conjugated with FITC - # M031-1), the double phosphorylated (T18/S19) myosin light chain antibody was obtained from Cell signaling (#3674), the unmodified myosin light chain antibody and tubulin were purchased from Sigma-Aldrich, #M4401 and #T4026 respectively. The fibronectin antibody was bought from Milipore (#AB2033). The transferrin antibody was purchased from Abcam (#ab82411).

The HRP conjugated antibodies were obtained from Jackson ImmunoResearch - F(ab')₂ Anti-Rabbit HRP (#711-036-152) or Anti-Mouse IgG, Light Chain HRP (#115-035-174).

The fluorescent secondary antibodies conjugated with AlexaFluor 488 (#A-11063), AlexaFluor 546 (#A-11003) or AlexaFluor 633 (#A-21053) were obtained from ThermoFisher Scientific. Phalloïdin, coupled with Atto 647 was also purchased from ThermoFisher scientific (#A22287).

9.2. Cell culture

Immortalized osteoblasts from *icap-1^{+/+}*; $\beta 1$ *integrin^{flox/flox}* and *icap-1^{-/-}*; $\beta 1$ *integrin^{flox/flox}* mice were generated as described previously (Bouvard et al., 2007). These cells were infected or not by adenoCre viruses from gene transfer vector core (University of Iowa) in order to obtain $\beta 1$ integrin-null cells. Clonal lineages of cells were maintained in culture in DMEM (Life technologies #31966-021) supplemented with 10 % FBS (Dominique Dutcher, #S1810-500), 100 U/mL penicillin



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and 100 µg/mL streptomycin (PAN Biotech #P06-07100) at 37°C in a 5% CO₂-humidified chamber. For all experiments, cells were washed by PBS (Dominique Dutcher, #L0615-500), detached using trypsin (Dominique Dutcher, #L0615-500) and treated with 1mg/mL trypsin inhibitor (Sigma-Aldrich, #T6522). Cells were then plated in DMEM containing 10 % FBS for 4h and then the appropriate analysis was carried out. Where needed a serum free medium OptiMEM was used (Life Technologies, #51985-026) as substitute.

9.3. Production of β3-GFP expressing osteoblast cell lines

The four osteoblast clones - *icap-1^{+/+}*; *icap-1^{-/-}*; *β1 integrin^{floxed/floxed}*; *β1 integrin^{floxed/floxed}* and *icap-1^{-/-}* were infected using lentiviral infection system from Invitrogen with pLenti – murine β3-GFP vector.

9.4. Western blotting

Cells were plated on 50% confluence and left to spread overnight. The next day, the dishes were washed twice with ice cold PBS and lysed in cold RIPA buffer, supplemented with 1x cOmplete protease inhibitors, 5 mM NaF and 2 mM Na₂orthovanadate. After protein quantification via Pierce™ BCA Protein Assay (ThermoFisher Scientific, #23227), the samplers were mixed with Laemmli sample buffer (0.4% SDS, 20% glycerol, 120 mM Tris-Cl (pH 6.8) and 0.02% (w/v) bromophenol blue) and loaded on electrophoretic PAA gels. Following the standard wet blotting protocol, the nitrocellulose membranes (Amersham, #10600003) the membranes were probed with the appropriate primary antibodies, diluted in 5 % BSA in TTBS and incubated overnight. The membrane was subsequently incubated with the appropriate secondary antibodies, also diluted in 5 % BSA in TTBS for one hour and then developed using Clarity ECL kit



(Biorad, #170-5061) and recorded with ChemiDoc Imaging System and analyzed with ImageLab software.

9.5. Traction force microscopy

The poly-acrylamide hydrogels with defined rigidity of 5 kPa and containing fluorescent microbeads (Life technologies, #F8783) were cast in 2 well LabTeks (ThermoFisher, #154461), coated with BindSilane (Sigma-Aldrich, #GE17-1330-01) and covered with coverslip, coated with Sigmacote (Sigma-Aldrich, #SL2). After the polymerization of the polyacrylamide the wells were flooded with water and the coverslips were detached gently. For the functionalization a protocol from Przybyla et al., 2015 was used. Briefly, solution of tetramethacrylate, N6 and Irgacure was deposited on the gels and baked under UV light (312 nm) for 5 min. Then 5 $\mu\text{g/ml}$ fibronectin was deposited on the gels and incubated at 4°C overnight.

Cells were allowed to adhere and spread 4 hour in DMEM containing 10% FBS and then placed in 4% FBS. Just before the acquisition, the membrane was stained with red fluorescent membrane marker PKH26 (Sigma-Aldrich, # PKH26GL).

Images were taken using spinning disk microscope, equipped with heating chamber, CO₂ installation, using 40x magnification oil objective. A fluorescent image of the beads with the cell spread on and fluorescent image of the cell membrane was obtained. Then the culture medium was replaced with pure solution of trypsin and after verification that cells were completely detached the second image of the fluorescent beads were taken. Isolated cells were randomly chosen for each experimental condition.

Force calculations were performed as previously described (Tseng et al., 2011) Briefly the displacement fields describing the deformation of the PA substrate are determined from the analysis of fluorescent beads images before and after removal of the adhering cells with trypsin treatment. The displacement field is



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obtained by a two-step method consisting of particle image velocimetry followed by individual bead tracking (Butler et al., 2002; Sabass et al., 2008). A special procedure is used to evaluate displacements in the area of the adhesive pattern where gel deformation is expected to be largest. Depending on the pattern shape, traction forces may be strongly localized leading to large displacements in very small areas. In this case, failure to correctly track a few beads in such areas would significantly alter the calculated force magnitude. Therefore, the pattern area is divided into smaller windows that are allowed to overlap, before applying the cross-correlation and tracking analysis. Reducing the size of the windows makes it possible to retrieve larger displacements with cross-correlation and, using overlapped windows, we can avoid missing beads close to the windows boundaries. All image processing and analysis were performed using Matlab (Gao and Kilfoil, 2009).⁵⁴ To calculate cell-induced traction stress from displacement data, we have used the Fourier-transform traction cytometry (FTTC) method (Sabass et al., 2008). We kept the regularization parameter at small values ($\lambda < \sim 10^{-9}$) in order to maintain the best spatial resolution, which is estimated to be about 5 mm in our case.

9.6. Plasmids and DNA constructions

The GFP – tensin 1 construction was cloned in the lab. Briefly, the chicken variant of tensin 1 was subcloned in pEGFP-C2 expression vector.

For the detection of the expression levels of $\beta 3$ integrin, we used the following qPCR primers - 5' – AGC AAC GTC CTC CAG CTC ATT G and 3' – TTG AGG GTG GCA TTG AAG C.



9.7. Focal adhesion lifetime analysis

Cells stably expressing β 3-GFP were spread in 2 well LabTeks and left to spread for 4h. Spinning disk videos were taken for the length of 2h with 1 min frequency. The lifetime analysis was performed with Focal Adhesion Analysis Server (Berginski and Gomez, 2013).

9.8. Immunofluorescence

Cells were plated at an approximate density of 6×10^4 per cm^2 for 4h, fixed with 4% PFA, permeabilized with 0.3% Triton X-100 and blocked with 10% goat-serum in PBS then with appropriate primary antibodies and after rinsing, with appropriate Alexa-Fluor-conjugated secondary antibody and phalloïdin. Finally, the coverslips were mounted in Mowiol/DAPI solution.

9.9. siRNA treatments

Cells were plated in six well plate at low density – 6×10^3 cells per cm^2 and left to spread overnight. The next day they were transfected with the appropriate siRNA using RNAiMAX system (ThermoFisher Scientific). The medium was changed the next day and a second hit with the same siRNA was performed. The transfected cells were used in 24 hours after.

All used siRNA were purchased from Dharmacon as follows: siRNA against β 3 integrin – L-040746-01-0005; siRNA against dynamin 3 - L-044919-02, siRNA against clatrin – L-063954-00, siRNA against caveolin – L-058415-00, siRNA against Nm23-H1 – L-040142-00 and siRNA against Nm23-H2 - L-040143-00; for all experiments we used an non targeting siRNA as control – D-001810-10-20.



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9.10. FRAP analysis

Cells stably expressing β 3-GFP were spread in 2 well LabTeks and left to spread for 4h. FRAP videos were taken using multimodal microscope for photo manipulations equipped with TIRF 63x objective. The analysis was carried out using build in FRAP analysis module in the FEI offline analysis.

9.11. Image analysis and statistical tests

For ppMLC staining or surface analysis, we measured the necessary signal using a thresholding method with manual correction when needed. More than 30 cells were measured in each condition that allowed us to do a non-parametric Kruskal-Wallis test (non-parametric) followed by Wilcoxon test with a Bonferroni correction when KW tests were significant (using GraphPad); experiments were done at least 3 times.

For focal adhesion analysis, we measured the β 3 staining signal of at least 20 cells using a manual threshold and the particle analyser of ImageJ software. Particles over $1 \mu\text{m}^2$ were analysed. The number of focal adhesion per cell and the total adhesive area per cell were analysed by a Kruskal-Wallis test (non-parametric) followed by Wilcoxon test with a Bonferroni correction when KW tests were significant; the mean area of focal adhesions was analyzed by an anova-2 analysis and TukeyHSD post-hoc tests (using GraphPad). Experiments were done 3 times.

9.12. Fibronectin fibrillogenesis

100,000 cells were plated on lab-Tek glass slide 4 chambers and allowed to adhere for 24 h in serum free medium made of OptiMEM. Then cells were fixed with 4% PFA. Cells were stained with anti-fibronectin, anti-beta1 (9EG7), anti-beta3



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(LucA.5), phalloidin or DAPI. The length of individual fibers was determined manually in ImageJ. To assess fibronectin coverage, the images were processed with fast Fourier transform bandpass filters to visualize all fibers, and the amount of fibronectin was measured by thresholding using Fiji (Schindelin et al., 2012).

For live-cell imaging, 70,000 cells were plated on cover glass slide 4 chambers and allowed to adhere for 24 h in serum free medium made of Opti-MEM. Then, Alexa 568 Gelatin (diluted 1/20 in PBS) were added to cell culture for 30 min. Labelling gelatin with Alexa 568 dye was described somewhere else (Sharma et al., 2013). Unbound gelatin was washout and replace by OptiMEM serum free medium, live time imaging records were performed.

9.13. Labeling Gelatin with Alexa 546 Dye

Bio-Gel P-30 powder was diluted in PBS and loaded onto glass column. After the column was drained of the PBS, a mixture of 0.2% gelatin solution and 0.2 M sodium bicarbonate solution was prepared. The Alexa 546 dye was diluted in DMSO and added to the gelatin solution and rotated at RT for 1 h. The dye-gelatin solution was deposited on the top of the column. As the dye-gelatin solution reaches the bottom of the column, the dye labeled gelatin was collected into eppendorf tubes stored at 4 °C for up to 2 months.

9.14. Fluorescent integrin antibody uptake assays

Cells were spread for 4h on FbN coated LabTek slides in DMEM, supplemented with 10% FBS and 1% P/S. When the cells were fully spread the fluorescent antibody (5 µg/ml) was added and the cells were incubated for 20 min at 37°C. At the end of the incubation period the cells were acid washed (0.2 M glycine, 0.15M NaCl, pH 3) for 3 min, fixed in 4% PFA, permeabilized and co-staining for transferrin was



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performed to confirm that intracellular vesicles, marked by fluorescent $\beta 3$ integrin antibody are due to endocytic process.

9.15. Fluorescence-activated cell sorting

Cells were gently detached with trypsin, then treated with trypsin inhibitor (#T0256). Then, they were placed in round-bottom 96 well plate and blocked with 1% BSA in PBS for 30 min at 37°C. Then cells were incubated with the appropriate antibodies and secondary antibodies as control diluted in PBS/1%BSA for 30 min on ice. After subsequent incubation with secondary antibodies cells were fixed in 4% PFA for 10 min and surface staining was detected with BD Accuri C6 flow cytometer and analyzed with the provided software.



VI. References





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