

Chapter 3

GTPases Rac1 and Ras Signaling from Endosomes



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Abstract The endocytic compartment is not only the functional continuity of the plasma membrane but consists of a diverse collection of intracellular heterogeneous complex structures that transport, amplify, sustain, and/or sort signaling molecules. Over the years, it has become evident that early, late, and recycling endosomes represent an interconnected vesicular-tubular network able to form signaling platforms that dynamically and efficiently translate extracellular signals into biological outcome. Cell activation, differentiation, migration, death, and survival are some of the endpoints of endosomal signaling. Hence, to understand the role of the endosomal system in signal transduction in space and time, it is therefore necessary to dissect and identify the plethora of decoders that are operational in the different steps along the endocytic pathway. In this chapter, we focus on the regulation of spatiotemporal signaling in cells, considering endosomes as central platforms, in which several small GTPases proteins of the Ras superfamily, in particular Ras and Rac1, actively participate to control cellular processes like proliferation and cell mobility.

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3.1 Introduction

3.1.1 *An Overview of the Endosomal System*

Endocytosis describes the internalization of nutrients, receptor–ligand complexes, fluids, lipids, extracellular proteins and viruses, and many other biomolecules. Once inside cells, endosomes are responsible for the fine-tuning of multiple pathways that enable the degradation, recycling, storage, activation, or signaling of incoming molecules. Since their discovery in the late 70s, using biochemical analysis and cellular fractionation techniques on extracts from rat liver (Bergeron et al. 1978; Posner et al. 1980; Marsh et al. 1983; Debanne et al. 1982), the knowledge on the complexity of the endosomal compartment has vastly increased. Over the years, a huge number of publications revealed an astonishing complex system of vacuolar-tubular endosomal structures with distinct characteristics that are dynamically interconnected, communicating with the plasma membrane and other cellular compartments like the trans-Golgi network (TGN). The proper functioning of this endocytic system guarantees balanced cellular homeostasis and essential cellular processes like proliferation, migration, invasion, division, polarity among many others (Scita and Di Fiore 2010; Huotari and Helenius 2011; Gould and Lippincott-Schwartz 2009).

The endosomal membrane system consists of several different compartments. Early endosomes (EEs) are the first and main sorting station in the endocytic pathway where endocytosed molecules that enter the cell via clathrin-dependent (CDE) or clathrin-independent (CIE) pathways are routed to different cellular destinations. From EEs, most internalized molecules are recycled back to the plasma membrane directly by transport vesicles or indirectly through passage via recycling endosomes (REs). Molecules in EE that are neither segregated for recycling nor directed to the TGN, where it can be delivered to the cell surface via the secretory pathway, are destined for degradation along the lysosomal pathway. For this to occur, EEs mature to late endosomes (LEs)/multivesicular bodies (MVBs) and thereafter fusion with lysosomes (Scita and Di Fiore 2010; Huotari and Helenius 2011; Mayor and Pagano 2007). There is also a continuous exchange between the TGN and the EEs in order to direct acid hydrolases from the Golgi apparatus to lysosomes. The structure, identity, and functionality of each endosomal compartment is characterized by a specific luminal pH regulated by the vacuolar proton pump V-ATPase and most relevant to this review, a specific combination of proteins, lipids, and signaling complexes attached to its cytosolic membrane surface. In particular, the family of Rab GTPases is critical for the organization of microenvironments that determine endosomal functions. Rab proteins define the identity of endosomal subdomains by recruiting effectors and facilitate membrane flux along the endocytic pathway (Jovic et al. 2010; Zerial and McBride 2001). In the following, we will briefly outline the characteristics of the various endosomal compartments, their respective Rab proteins and the Rab effectors that define their identity. Intriguingly, some of these proteins and lipids listed below and required to determine uniqueness and guiding of vesicle transport within the endosomal compartment are intimately linked to the trafficking and signaling of rat

sarcoma (Ras) and Ras-related C3 botulinum toxin substrate 1 (Rac1) proteins from EEs, REs, and LEs (see Sect. 3.1.2 onwards).

EEs represent a weakly acidic (pH 6.8–6.1) compartment that is mainly located in the periphery of the cell. This compartment is principally characterized by a tubulo-vesicular morphology and the presence of Rab5 and its effector Vps34, a phosphatidylinositol 3-kinase type III that generates the phosphoinositide (PI) PtdIns(3)P. The presence of active Rab5 (Rab5-GTP), which is generated in a guanine exchange factor (GEF) [rabaptin 5-associated exchange factor for RAB5 (Rabex5)] and PtdIns(3)P-dependent manner, allows the recruitment of the effector early endosome antigen 1 (EEA1), which together with SNAREs (syntaxin 6 and 13) enables endosome fusion. Rab5-GTP and PtdIns(3)P also recruit rabenosin-5, which interacts with EH domain-containing protein 1 (EHD1) and regulates recycling from EEs. In addition, EEs contain distinctive membrane microdomains enriched in specific proteins [including Rab4, Rab11, ADP ribosylation factor 1 (Arf1), complex protein I (COPI), retromer, Rab9, or Rab7] that together with the cytoskeleton, actin, and microtubules, regulate the subcellular trafficking of certain cargoes through slow and fast recycling routes to the plasma membrane, the degradative pathway to lysosomes or retrograde transport to the TGN (Huotari and Helenius 2011; Vonderheit and Helenius 2005; Rojas et al. 2008; Bonifacino and Rojas 2006; Hayer et al. 2010; Bonifacino and Hurley 2008; Pfeiffer 2009; Zerial and McBride 2001; Sigismund et al. 2012; Johannes and Popoff 2008). There is also a subpopulation of EEs that instead of EEA1 contain the Rab5 effector Adaptor protein containing PH domain, PTB domain, and Leucine zipper motif 1/2 (APPL1/2). As outlined below, the presence of APPL1/2 on EE might be responsible to create specific endosomal subpopulations that can trigger signaling events related to cell growth (see Sect. 3.1.2) (Miaczynska et al. 2004; Schenck et al. 2008; Zoncu et al. 2009).

Rab5 also promotes the transformation of EEs to LEs by ensuing conversion from a Rab5-positive to a Rab7-positive (LE) compartment. This Rab conversion is achieved when the Mon1-complex binds to PtdIns(3)P and facilitates the exchange of the Rab5-GEF Rabex5 for the Rab7-GEF that is associated with the homotypic fusion and protein sorting (HOPS) complex (Poteryaev et al. 2010; Rink et al. 2005). In this LE maturation, intraluminal vesicles (ILVs) are acquired through the participation of the endosomal sorting complex required for Transport (ESCRT) complexes by a regulated posttranslational ubiquitination and de-ubiquitination modification. Although a simple maturation that confers the conversion of EE to LE compartment is possible, it seems that a fission of domains within EE that acquired LE features participates in the formation of the LE compartment. The resulting endosomal carrier vesicles (ECVs) from this fission process move to the center of the cell via microtubules and fuse with the LE compartment. The vacuolar LEs, arranged in a perinuclear location, are more acidic (pH: 6.0–5.0), contain Rab7 and the PtdIns(3,5)P₂, which is synthesized by the PtdIns(3)P 5-kinase FAB1/PIKfyve. Finally, LEs will mature or fuse

with lysosomes containing acidic hydrolases (proteases and lipases among others). This compartment has a pH around 5.0–4.5, and its membrane is protected by the presence of lysosome-associated membrane proteins (LAMP) proteins (Huotari and Helenius 2011; Poteryaev et al. 2010; Jovic et al. 2010; Scott et al. 2014; Platta and Stenmark 2011).

3.1.2 Endocytosis and Signaling from Endosomal Compartments

Over the last decades, it has become apparent that signaling within the endosomal system contributes to an enormous variety of events that participate in a range of cellular processes. This has led to the widely accepted concept of the “signaling endosome.”

This concept recognizes endocytosis to play a key role attenuating signals generated by activated receptors at the plasma membrane, directing them into the degradative-lysosomal pathway. On the other hand, on route to lysosomes, these active receptors can continue to signal in EEs and LEs/MVBs. Therefore, endosomes act as signaling platforms to maintain or prolong signals generated at the plasma membrane. Sustained stimulation can be also enhanced by increased recycling of receptors to the plasma membrane, which is often observed in tumor cells in order to intensify proliferative signals. In addition, endosomes also seem to promote localized and selective recruitment of scaffold and effectors proteins, thereby assembling specific modules. These signaling building blocks can also be transported and directed, through endocytosis-mediated recycling, to specific places in the cell or to specific domains at the plasma membrane to achieve functionality (Sigismund et al. 2012; Lobert and Stenmark 2011; Jones et al. 2006; Frittoli et al. 2011; Taub et al. 2007; Teis and Huber 2003; Palamidessi et al. 2008; White et al. 2006; Sorkin and von Zastrow 2009; Platta and Stenmark 2011; Ohashi et al. 2011; Puthenveedu et al. 2010; Dobrowolski and De Robertis 2011; Schiefermeier et al. 2014; Villasenor et al. 2016).

A substantial number of publications, using biochemical cellular fractionation techniques as well as new live cell imaging techniques such as fluorescence resonance energy transfer (FRET), fluorescence-lifetime imaging microscopy (FLIM), photoactivatable fluorescent proteins (PAFPs), or Ras and interacting protein chimeric unit (Raichu) biosensors (Gonnord et al. 2012; Miaczynska and Bar-Sagi 2010; Murphy et al. 2009), have highlighted the role of the endocytic system to attenuate or sustain signaling, to participate in specific outcomes and to direct modules or complexes to specific subcellular sites or microdomains. The potential relevance of the endocytic system is highlighted in cancer, where altered dynamics of the endocytic pathway are often associated with an inability to properly internalize, recycle, or degrade key cancer drivers such as receptor tyrosine kinases, leading to aberrant proliferation

and metastasis of tumor cells (Stasyk and Huber 2016; Lanzetti and Di Fiore 2008; Porthor and Barbieri 2015).

Before embarking on the focus of this chapter, the signaling of the small GTPases Ras and Rac on endosomes (Sect. 3.2), it is essential to outline the overarching role of cell surface receptors in signal transduction. Hence, in the following, we will first illustrate in more detail the endosome signaling outputs for some receptors.

Specific endosomal signaling has been demonstrated for several families of cell surface receptors, in particular, receptor tyrosine kinases (RTKs) such as the epidermal growth factor receptor (EGFR), platelet-derived growth factor receptor (PDGFR), hepatocyte growth factor receptor (HGF-R or Met), tropomyosin receptor kinase A (TrkA), and insulin receptor (Ins-R). In addition, serine/threonine kinases such as transforming growth factor beta (TGF β) receptors, G-protein coupled receptors (GPCRs), or Wnt and Notch receptors have also been reported to signal from endosomes (Stasyk and Huber 2016; Joffre et al. 2011; Wang et al. 2002; Sorkin and von Zastrow 2009; Dobrowolski and De Robertis 2011; Kermorgant and Parker 2008; Murphy et al. 2009; Flinn et al. 2010; Gould and Lippincott-Schwartz 2009; Lanzetti and Di Fiore 2008; Le Roy and Wrana 2005; Tomas et al. 2014; Mellman and Yarden 2013; Barrow-McGee and Kermorgant 2014).

To reach the endosomal compartment, the above-mentioned receptors appear to employ different internalization routes, either via CDE or CIE. Interestingly, depending on ligand concentration, some receptors can be internalized by both entry routes, which then differentially impacts on their signaling output. For instance, while CIE for TGF β -R and EGFR directs ligand-receptor complexes to lysosomes for degradation, the CDE routes these receptors to signaling competent endosomal vesicles distinct from the lysosomal pathway (Sigismund et al. 2008, 2012). Moreover, signaling of these TGF β - and EGF receptors, that remain ligand-bound and active after internalization, are principal examples for the creation of a very localized and specific signal transduction elicited from EE microdomains exclusively located within a population of Smad anchor for receptor activation (SARA)- and APPL-positive endosomes, respectively. SARA, which binds PtdIns(3)P on EEs, is a scaffold protein that interacts with TGF β -R and Mothers against decapentaplegic (SMAD) family member 2 enabling the phosphorylation of the former by TGF β and its translocation to the nucleus to regulate gene transcription (Hayes et al. 2002; Tsukazaki et al. 1998; Di Guglielmo et al. 2003). On the other hand, APPL, which recruits protein kinase B (PKB or AKT) and its substrate glycogen synthase kinase 3 (GSK3), is activated and translocated to the nucleus by the endocytosed EGFR (Miaczynska et al. 2004).

Other examples for the relevance of endosomal signaling establishing discrete cellular functions include the sustained signaling of GPCRs on endosomes, which is important to ensure continuous cyclic AMP production and mitogen-activated protein kinase (MEK)—extracellular signal-regulated kinases (ERK) signaling beyond its initial activation at the cell surface (Villardaga et al. 2014; Shenoy and Lefkowitz 2011; Sorkin and von Zastrow 2002). Internalization of nerve growth factor (NGF) bound to its TrkA receptor has also been proven necessary to prolong activation of Rap1 GTPase and to promote neuronal survival via ERK5 activation and cAMP response element binding protein (CREB)-dependent transcription (Wu et al. 2001;

Watson et al. 2001). In addition, the NGF-TrkA receptor–ligand complex can also activate the Ras/mitogen-activated protein kinase (MAPK) pathway from endosomes in neuronal cells (Howe et al. 2001).

EGFR exemplifies a classical example of specific and sustained signaling on endosomes. EGF induces the accumulation of EGFR and downstream signaling molecules such as SH2-containing collagen related (Shc), growth factor receptor-bound protein 2 (Grb2), son of sevenless (Sos), Ras, as well as the serine/threonine kinases rapidly growing fibrosarcoma protein 1 (Raf-1), Mek, and Erk1/2 in endosome compartments (Balbis et al. 2007; Lu et al. 2009; Moreto et al. 2008; Pol et al. 1998; Sorkin and von Zastrow 2009; Teis et al. 2006; Di Guglielmo et al. 1994; Nada et al. 2009; Teis et al. 2002; Wang et al. 2002). In fact, early pioneering work from Vieira et al. elegantly demonstrated the importance of CDE for the control of the EGFR signaling cascade (Vieira et al. 1996). In these studies, inhibition of EGFR internalization, through over-expression of a dominant-negative mutant of the vesicular fission protein dynamin (Dynk44A), drastically interfered with activation of Raf-1 kinase downstream Ras and consequently MAPK signal output, indicating a crucial role of endosomes in the EGFR/Ras/Raf-1/MAPK signaling cascade (Vieira et al. 1996; Moreto et al. 2008). Furthermore, in elegant experiments from Wang et al., the EGFR tyrosine kinase inhibitor AG1478 was used to inhibit EGFR signaling at the cell surface, leading to the internalization of nonactive EGF-EGFR complexes into endosomes. Subsequent removal of AG1478 then enabled activation of endosome-associated EGFR followed by Ras, ERK1/2, and Akt signaling to promote cell proliferation and survival (Wang et al. 2002).

Under certain conditions, EGFR signaling likely occurs in the LE compartment, as the late endosomal adaptors p14 and Mek partner-1 (MP1) can recruit Mek1 to participate in EGFR-induced MAPK activation (Teis et al. 2002, 2006). Indeed, in primary hepatocytes late endosomal EGFR signaling has recently been demonstrated to participate in cell cycle progression (Luo et al. 2011). The p14/MP1 complex also serves as a scaffold to recruit Rag GTPases, which sense amino acid levels and together with Ras homolog enriched in brain (Rheb) and hVps34, activate mammalian target of rapamycin complex 1 (mTORC1) in the endo-lysosomal (LE/Lys) compartment to promote cell growth via protein synthesis (Sancak et al. 2010; Zoncu et al. 2011; Duan et al. 2015).

In addition, p14/MP1 in the LE/Lys compartment is also critical for cell migration, as the adaptor complex is directed to the cell periphery, in a Rab7-regulated manner, in order to promote focal adhesion (FA) turnover for cell motility and tumor invasion (Schiefermeier et al. 2014). Furthermore, in the context of cell migration, EEs, and LE/Lys have also been identified to facilitate receptor-mediated signaling events that activate and transport Rac1 GTPase to the leading edge (Palamidessi et al. 2008; Menard et al. 2014; Joffre et al. 2011). Specific guanine exchange factors (GEFs) of the small GTPase Rac1 are known to activate Rac1 in EEs and LEs. This is followed by vesicular transport to the plasma membrane, where active Rac1 then regulates the actin cytoskeleton to promote the formation of lamellipodia in the leading edge, altogether creating forward movement. In the rear of migratory cells, EE and LE control the delivery of the pro-migratory Endo180 receptor to promote adhesion

disassembly by the Rho kinase-derived contractile signals (Gould and Lippincott-Schwartz 2009; Sturge et al. 2006).

Further to the trafficking routes of Rac1 and Endo180 receptor to the front and rear of moving cells, respectively, several recent publications have highlighted the importance of recycling for the delivery of integrins from endosomes to specific plasma membrane domains, which in combination with the export of membrane type-1 matrix metalloproteinase 1 (MT1-MMP) also regulates motility and invasiveness (De Franceschi et al. 2015; Alanko and Ivaska 2016). Along these lines, impaired cholesterol export from LEs in Niemann–Pick type C1 (NPC1) mutant cells or upon overexpression of annexin A6 interfered with the task of the RE compartment to deliver cargo to the cell surface. This imbalanced distribution of intracellular cholesterol strongly reduced integrin recycling from RE to plasma membrane, and consequently, inhibited cell migration (Garcia-Melero et al. 2016; Reverter et al. 2014). Integrins are transmembrane adhesion proteins that by forming FAs connect the F-actin cytoskeleton to the extracellular matrix (ECM), thus attaching cells to their surroundings. In migrating cells, integrin recycling via a fast and Rab4-dependent, as well as a slow and Rab11-dependent recycling route, is the driving force to continuously assemble and disassemble FAs in the leading edge enabling forward movement (De Franceschi et al. 2015; Shafaq-Zadah et al. 2016). Additionally, integrin-dependent adhesion to collagen type-1 matrix protein stimulates MT1-MMP translocation, from the intracellular biosynthetic-storage compartment and by a Rab8-dependent exocytosis, to surface structures that promote invasion of MDA-MB-231 tumor cells (Bravo-Cordero et al. 2007). However, additional Rab GTPases (Rab2, Rab5, Rab7, Rab14) and the internalization process could also regulate MT1-MMP activity at the plasma membrane in other settings (Frittoli et al. 2011; Wiesner et al. 2013; Williams and Coppolino 2011; Castro-Castro et al. 2016; Kajiho et al. 2016). Interestingly, from the point of view of endosomal signaling, integrins bind distinct sets of proteins when located at the plasma membrane or in endosomes. Consequently, this elicits different signal output in endosomes: activation of focal adhesion kinase (FAK), Akt, ERK, and suppression of anoikis (Alanko et al. 2015; Alanko and Ivaska 2016).

In summary, in this section we have given an overview how the endo/lysosomal system provides membranous platforms to regulate spatiotemporal signaling in cells (Flinn et al. 2010; Gould and Lippincott-Schwartz 2009; Kermorgant and Parker 2008; Lobert and Stenmark 2011; Ohashi et al. 2011; Palamidessi et al. 2008; Platta and Stenmark 2011; Sorkin and von Zastrow 2009; Taub et al. 2007). In the following, we will discuss in more detail how the endosomal localization of several small GTPases proteins of the Ras superfamily actively participates to control cellular processes like proliferation and cell mobility.

3.2 Signaling of the Small GTPases Ras and Rac1 from Endosomes

The Ras superfamily of GTPases comprising a total of 150 members is also known as small GTPases due to their small molecular weight (20–40 kDa). They are classified into six subfamilies: Ras, Rho, Rab, Arf, Ran, and Galpha subunits (Flinn et al. 2010; Rojas et al. 2012). The Rho family members control cytoskeleton dynamics and cellular mobility, while Rab and Arf proteins modulate formation and transport of intracellular vesicles, including exo- and endocytosis. The Ran family coordinates nuclear transport processes, and Galpha subunits manage GPCR signaling. Finally, Ras GTPases are located upstream signaling cascades such as the Raf-1/MAPK pathway that is known to regulate transcription relevant for proliferation and differentiation processes among others.

Rac1, which will be discussed in more detail in Sect. 3.2.2, belongs to the Rho subfamily and within the Ras subfamily there are four isoforms (HRAS, NRAS, KRAS4A, and KRAS4B). All of them have in common a module called the G-domain, which adopts an α/β topology and contains 60–180 residues, responsible for nucleotide (GTP)-dependent conformational changes of two internal regions named switch region I (residues 30–38) and switch region II (residues 59–67) (Wittinghofer and Vetter 2011). The ability to bind GTP and the concomitant conformational changes associated with GTP or GDP binding enables Ras proteins to act as binary molecular switches, active when GTP is bound to the G-domain and inactive when GDP is associated with the G-domain. In the active state (GTP-bound), GTPases interact and activate a plethora of different effectors with different functions, including Raf-1, phosphoinositide 3-kinase (PI3K), RAL guanine nucleotide dissociation stimulator (RalGDS), T lymphoma invasion and metastasis-inducing 1 (TIAM1), WASP-family verprolin-homologous protein (WAVE,) and others. The active and inactive state cycle is controlled by guanine exchange factors (GEFs) which facilitate the exchange of GDP for GTP. The ability of GEFs to remove GDP enables more efficient GTP binding which is found at approximately tenfold higher concentrations compared to GDP in the cytosol. On the other hand, GTPase activating proteins (GAPs) increase the intrinsic GTP hydrolyzing capacities of GTPases to ensure rapid inactivation (Rajalingam et al. 2007; Downward 1996; Marshall 1996). Both, GEFs and GAPs, are spatially and temporally modulated by external stimuli and signaling molecules (Bos et al. 2007).

Given their prominent localization at the plasma membrane and proximity to RTKs and GPCRs, Ras GTPases are key players in the initial steps of signaling cascades generated at the cell surface and therefore control important processes such as proliferation, differentiation, apoptosis, cytoskeleton dynamics or cell motility (Malumbres and Barbacid 2003). However, critical for the “signaling endosome” concept, the presence of Ras proteins in the endosomal compartment makes them the key transducers of the signaling events generated by active receptors along endocytic pathways. As outlined in the following sections in more detail, Ras and Rac1 signaling from endomembranes, in particular from endosomes, have been associated with

proliferation, apoptosis, and/or cellular migration. Nevertheless, it should be noted that some caution should be taken when referring to the conclusions based on Ras and Rac1 signaling from endosomes as the majority of published data has been obtained from model systems that often express unphysiologically high levels of receptors and signaling components.

3.2.1 *Ras Signaling from Endosomes*

3.2.1.1 The Ras Family

In human cells, Ras isoforms are encoded by three genes: *KRAS* (Kirsten rat sarcoma viral oncogene homolog), *NRAS* (Neuroblastoma RAS viral (v-ras) oncogene homolog), and *HRAS* (Harvey rat sarcoma viral oncogene homolog). This gives rise to 4 different Ras isoforms (~21 kDa): HRas, NRas, KRas4A, and KRas4B (referred to as KRas), the latter two being derived from alternative RNA splicing. Since Ras proteins control proliferation, survival and migration, missense mutations at position G12, G13, and Q61 result in gain-of-function Ras mutants that confer oncogenic activity. All these mutations impair Ras-GTP hydrolysis by inhibiting its intrinsic GTPase activity. Consequently, this interferes with the action of GAPs and Ras remains in a constitutively active state. Hence, oncogenic Ras mutant hyperactivity contributes to the initiation and progression of a large variety of human cancers (~25% of human cancers, with KRas being the most frequently mutated isoform) (Hobbs et al. 2016; Barbacid 1987; Bos 1989; Malumbres and Barbacid 2003; Rajalingam et al. 2007; Newlaczyl et al. 2014).

Given their prominent contribution to the development of tumorigenic events, much effort over the years aimed to unravel the structure, localization and differential function of the Ras isoforms. Structural analysis first revealed that all Ras isoforms shared a highly conserved and nearly identical globular N-terminal domain (residues 1–165), which binds nucleotides and the majority of Ras effectors (see Sects. 3.2.1.3 and 3.2.1.4). However, as described in more detail below, important differences were found in the C-terminal domain (last 24–25 residues), named the hypervariable region (HVR), which is posttranslational modified and responsible for differential subcellular localization and as a result differential signaling among the Ras isoforms (Barbacid 1987; Hancock 2003; Mor and Philips 2006; Fotiadou et al. 2007; Calvo et al. 2010; Eisenberg and Henis 2008; Prior and Hancock 2012). For instance, in cell culture, KRas activates the small GTPase Rac1 more efficiently than HRas because of their differently membrane anchoring and localization, which is consequently translated in more efficient KRas induction of membrane ruffling, pinocytosis, cell motility, and cell survival than HRas (Walsh and Bar-Sagi 2001).

3.2.1.2 Synthesis, Processing, and Trafficking of Ras Isoforms to the Plasma Membrane

Ras proteins are synthesized in the cytosol as globular hydrophilic proteins (188 amino acids in the case of KRas and 189 for all other Ras isoforms) containing a C-terminal CAAX motif (C, cysteine; A, aliphatic residue; X, any residue); being CVLS, CVVM and CVIM for H-, N-, and KRas, respectively. This CAAX sequence is essential for subsequent posttranslational modifications of Ras and its successive targeting to different cellular membranes. Because Ras proteins contain a methionine or a serine as last amino acid (X residue), this CAAX sequence is specifically recognized by a farnesyl transferase in the cytosol, which irreversibly incorporates a farnesyl group (15-carbons isoprenyl) to the cysteine C186, and C185 in KRas. Farnesylation allows Ras proteins to insert and localize on the endoplasmic reticulum membrane for subsequent CAAX modifications which includes AAX hydrolysis by Ras-converting enzyme 1 (Rce1) and the methylation of the remaining farnesylcysteine residue by Isoprenylcysteine carboxyl methyltransferase (Icmt) (Fehrenbacher et al. 2009) (see [1] in Fig. 3.1). Strikingly, despite all these posttranslational modifications occurring for each Ras isoform, H-, N-, and KRas then follow different routes from the ER to the plasma membrane (Mor and Philips 2006).

Although farnesylcysteine methylation is an essential prerequisite, it is not sufficient for cell surface delivery, and Ras needs a second signal to finally reach the plasma membrane or other organelles like endosomes. In the case of KRas, this second signal is a polybasic region (PBR) composed of six basic lysine residues near the farnesylcysteine in the HVR. This PBR motif electrostatically interacts with anionic phospholipids in membranes, such as phosphatidylinositol-4,5-bisphosphate PtdIns (4,5)P₂, the phosphatidylinositol-3,4,5-trisphosphate PtdIns (3,4,5)P₃ or phosphatidylserine (PS) (Hancock et al. 1990; Cho et al. 2012; Apolloni et al. 2000; Heo et al. 2006; Yeung et al. 2008; Gelabert-Baldrich et al. 2014). Hence, through a yet still not well-defined Golgi exocytic-independent route that likely involves the above-mentioned electrostatic interactions both signals (farnesyl lipid group and PBR) contribute to direct KRas from the ER to the plasma membrane (Apolloni et al. 2000; Magee and Marshall 1999) (see [2] in Fig. 3.1). The molecular machinery that regulates this trafficking route is also not well known and includes the possibility of a passive electrostatic switch. Alternatively, recent results from the Bastiaens group suggest that the delta-subunit of phosphodiesterase 6 (PDE6- δ), or maybe other chaperone-like proteins, act as a cytosolic solubilization factor and its binding to the farnesyl moiety of KRas could then facilitate KRas trafficking to the plasma membrane. Once at the plasma membrane, the highest electrostatic interaction exerted by acid phospholipids could compete and displace PDE6- δ from KRas, favoring its incorporation or insertion into the inner leaflet of the cell surface phospholipid bilayer (Schmick et al. 2015).

Much different to the complex regulation of KRas translocation to the cell surface, the second signal for targeting H-, N-, and spliced KRas4A proteins to the plasma membrane is represented by the reversible addition of one or two palmitoyl groups at additional cysteine residues adjacent to the CAAX motif. A palmitoyl-transferase

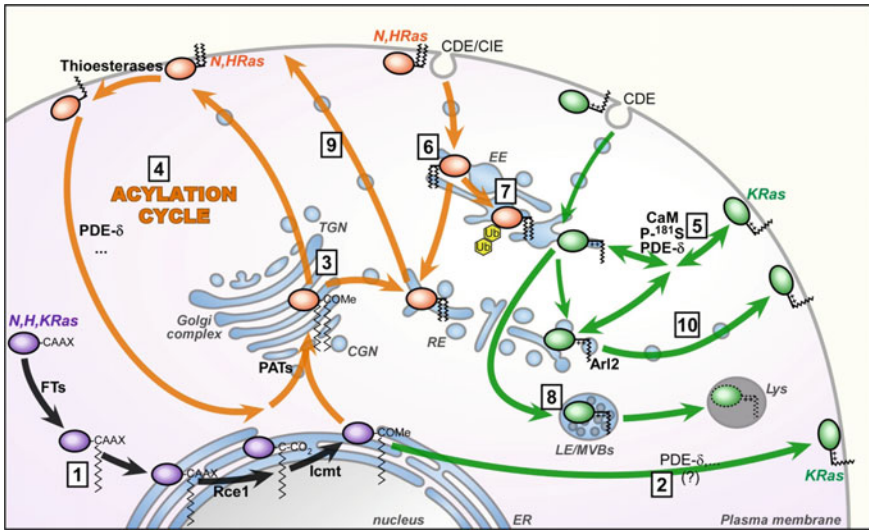


Fig. 3.1 Different routes to the plasma membrane and through the endocytic compartment followed by the Ras isoforms. Once synthesized in the cytosol, Ras isoforms are cysteine farnesylated in their terminal CAAX motif by farnesyl transferases (FTs). This is followed by further posttranslational modifications mediated by Ras-converting enzyme 1 (Rce1) and Isoprenylcysteine carboxyl methyltransferase (Icmt) in the endoplasmic reticulum (ER) [1]. This scheme recapitulates the following traffic routes for the different Ras isoforms: H- or NRas trafficking is shown in orange and KRas trafficking is depicted in green. KRas reaches the PM by still not well-defined non-vesicular routes that likely involve chaperone proteins like PDE- δ [2]. In contrast, H- and NRas use the vesicular exocytic pathway via Golgi and/or Golgi and recycling endosomes (RE) to the plasma membrane (PM) [3]. H- and NRas switch between PM and the Golgi by the action of thioesterases at the PM and palmitoyl-transferases (PATs) at the Golgi, which is known as the acylation cycle [4]. Moreover, from the PM, H-, and NRas can be internalized via CDE or CIE pathways to reach early endosomes (EEs) [6], where they can either be recycled back to PM through RE [9] or remain retained when ubiquitinated [7]. On the other hand, KRas can also use the vesicular CDE pathway but the bidirectional movement of KRas between PM and endosomal compartments is mainly accomplished through an electrostatic switch modulated by serine phosphorylation (P- 181 S) or binding proteins, like CaM or PDE- δ , to its hypervariable region [5]. KRas can also return back from RE to the PM via an Arl2-dependent vesicle transport route [10]. In contrast to H- and NRas, KRas moves to late endosome/multivesicular bodies (LE/MVBs) on route for degradation in lysosomes (Lys) [8]

enzyme localized in the Golgi/ER is responsible for palmitoylation of HRas at C181 and C184, NRas at C181 and KRas4A at C180 (Hancock et al. 1989; Swarthout et al. 2005). This modification stabilizes the membrane interaction of these Ras isoforms and favors its transport to the plasma membrane through vesicle carriers following the exocytic pathway from the TGN (Choy et al. 1999). In some cases this includes trafficking through REs, which act as a way-station for palmitoylated H- and NRas proteins as they move along the post-Golgi exocytic pathway to the plasma membrane (Misaki et al. 2010) (see [3] in Fig. 3.1). Palmitoylation being

decisive for these Ras proteins to reach the plasma membrane was experimentally evidenced in live cell imaging, where green fluorescent protein (GFP)-tagged and palmitoyl-deficient Ras mutants were mislocalized in the ER and Golgi and lacked delivery to the plasma membrane (Hancock et al. 1989; Choy et al. 1999). Note that palmitoylation also contributes to certain levels of diversity in the Ras family. While di-palmitoylated HRas is strongly associated with membranes and can efficiently follow the slow exocytic transport to the plasma membrane, the mono-palmitoylated N- and KRas4A isoforms need additional hydrophobic/basic amino acid sequences (Laude and Prior 2008). The different mechanisms that contribute to Ras processing associated with different trafficking routes are depicted in Fig. 3.1.

One can envisage that the differential contribution of the various CAAX motifs, posttranslational modifications (farnesylation, palmitoylation), together with HVR sequence variations, will impact on their spatiotemporal distribution, with consequences for their ability to activate effector pathways. Hence, the possibility to uncover underlying principles for the creation of signal diversity prompted researchers to extensively examine the distribution of Ras isoforms at the plasma membrane. Indeed, subcellular fractionation as well as advanced imaging identified that once at the plasma membrane, Ras isoforms display distinct localizations in specific membrane subdomains. Moreover, it is now believed that active and inactive Ras proteins are organized in nanoclusters, containing 6–7 Ras proteins per nanocluster. Over the years, it has become clear that these clusters highly depend on the distribution of lipids within the membrane. HRas is the best-characterized member of the Ras family in this context, with HRas-GTP nanoclusters being found in disordered (fluid, cholesterol-poor) domains (Prior et al. 2003; Zhou and Hancock 2015). In contrast, HRas GDP clusters are mainly localized in cholesterol- and sphingolipid-rich domains (lipid rafts). While NRas seems to distribute similar to HRas, KRas is predominantly localized outside lipid rafts. In addition, a distinct cohort of phospholipids, in particular phosphatidylserine, but also phosphatidic acid and phosphatidylinositides contribute to the spatial segregation of Ras isoforms. The different distribution of active and inactive Ras proteins implicates lateral movement of Ras isoforms in the plasma membrane. As Ras activity is determined by GTP/GDP exchange, the localized recruitment and activity of GEFs and GAPs appears critical to ensure the transient nature of Ras nanoclusters (Grewal and Enrich 2006). Interestingly, a specialized form of lipid raft, caveolae, seems to critically translate environmental cues, such as mechanical stress, into the remodeling of lipids at the plasma membrane that in turn extensively modulate the organization of Ras nanoclusters (Ariotti et al. 2014). As such, caveolin-1 deficiency or downregulation of cavin-1, another structural component of caveolae, alters phosphatidylserine distribution at the plasma membrane, which correlates with enhanced KRasG12V nanoclustering and MAPK signaling. Yet lateral segregation of HRas was abolished, thereby compromising signal output from HRasG12V nanoclusters (Ariotti et al. 2014).

In addition to their differential distribution at the cell surface outline above, the different posttranslational modifications of each Ras isoforms affect also the association dynamics of cytosolic Ras protein pools with the plasma membrane. It was

originally postulated that all Ras isoforms display stable membrane association, moving by lateral diffusion as described above (Niv et al. 1999, 2002). However, under certain conditions or upon specific posttranslational modifications, Ras localization at the plasma membrane switches from lateral diffusion to exchange dynamics with cytoplasmic Ras protein pools (Vartak and Bastiaens 2010). As described above, activation of H- and NRas, via GTP-induced conformational changes, leads to their exchange between lipid rafts and non-rafts (Gorfe et al. 2007). Yet, H- and NRas can also dissociate from the plasma membrane in a process known as the acylation cycle, which involves the depalmitoylation of cysteine residues in their HVR domain that is independent of the activation state of Ras (Rocks et al. 2005, 2010). This non-vesicular pathway is mediated by acyl protein thioesterases in the plasma membrane rapidly returning Ras to the diffusing low-membrane affinity farnesylated Ras pool in the cytoplasm. It is yet unclear how the cell translates the intricate network of cellular and environmental signals to provide the balance between lateral diffusion at the plasma membrane or diffusion into the cytosol, but one modulating factor could be the interaction of the Ras-farnesyl group with PDE- δ when Ras proteins are depalmitoylated (Vartak and Bastiaens 2010; Chandra et al. 2011; Goodwin et al. 2005). This could enable protein acetyltransferase (PAT) enzymes to trap depalmitoylated Ras specifically in Golgi/ER membranes, where another round of palmitoylation and trafficking through the exocytic pathway may then be required to ensure the return to the plasma membrane (Rocks et al. 2005; Schmick et al. 2015) (see [4] in Fig. 3.1).

While a general concept of diffusion dynamics for H- and NRas seems to be emerging, the data on trafficking dynamics of KRas to and from the plasma membrane is more complex and in part controversial. Initially, it was proposed that the half-time for KRas membrane desorption was in the order of minutes or even longer, which was in consonance with a postulated stable plasma membrane association regulated by lateral diffusion (Silvius et al. 2006; Niv et al. 1999, 2002). Lately, Silvius et al. (2006), using an inducible heterodimerization technique between ectopically expressed KRas and a complementary binding partner confirmed predominant KRas association with the plasma membrane under basal conditions. Yet, this included a continuous cycling of KRas on and off the membrane in an interval of minutes. Further results from Yokoe and Meyer indicate that the rate of KRas exchange between plasma membrane and cytoplasm may be even more rapid, within seconds (Yokoe and Meyer 1996). In line with these findings, *in vitro* studies demonstrated that the PBR of KRas associates with lipid bilayers in a rapidly reversible manner with a half-time of seconds or less (Leventis and Silvius 1998). On the other hand, depending on the experimental settings and stimuli, desorption of KRas from the plasma membrane is also modulated by several KRas-interacting proteins, as such as PDE- δ , prenylated Rab protein acceptor protein 1, calmodulin (CaM), and galectin-3 (Chandra et al. 2011; Bhagatji et al. 2010; Elad-Sfadia et al. 2004; Figueroa et al. 2001; Fivaz and Meyer 2005; Lopez-Alcala et al. 2008; Nancy et al. 2002; Villalonga et al. 2001; Philips 2012). In addition, the protein kinase C (PKC)-mediated phosphorylation of active KRas at serine 181 (Ballester et al. 1987) affects the PBR net charge of KRas, thereby inducing an electrostatic switch that displaces KRas from the plasma membrane to endomembranes, including endosomes (Bivona et al. 2006;

Chandra et al. 2011). KRas phosphorylation at serine 181 inhibits CaM binding and accordingly, CaM efficiently interacts with non-phosphorylated KRas-GTP (Lopez-Alcala et al. 2008), an interaction that also favors KRas desorption from the plasma membrane (Bhagatji et al. 2010; Fivaz and Meyer 2005). In this context, elegant studies from Fivaz and Meyer revealed the physiological significance of these interactions in neuronal cells, as cell activation caused the translocation of KRas from the plasma membrane to endosomes through sequestration of the PBR-farnesyl motif in a Ca^{2+} /CaM-dependent manner (Fivaz and Meyer 2005) (see [5] in Fig. 3.1).

3.2.1.3 Ras Trafficking Along Endocytic Routes

Although Ras proteins are predominantly found at the plasma membrane to transduce signals received from surface receptors, substantial amounts of Ras proteins have also been identified in subcellular organelles where they can elicit several functions. Over the last decades, the combination of cellular fractionation techniques with newly developed advanced microscopy revealed the presence of Ras proteins in endosomal fractions, visualized their trafficking to endosomal structures in live cells, and provided extensive colocalization data with established markers of the different endocytic compartments (Lu et al. 2009; Moreto et al. 2008, 2009; Pol et al. 1998; Howe et al. 2001; Fivaz and Meyer 2005; Jiang and Sorkin 2002; Gomez and Daniotti 2007; Roy et al. 2002; Yeung et al. 2008; Hancock 2003; Gelabert-Baldrich et al. 2014; Choy et al. 1999; Zheng et al. 2012b; Prior and Hancock 2012). Most of the results have been obtained with ectopic expression of fluorescently tagged wildtype, active and inactive Ras mutant proteins in different cell types. Using advanced imaging like FRET, FRAP technology or in the case of KRas, RAICHU probes, these fusion constructs were critical tools to develop experimental approaches that were able to monitor the location and activity of Ras proteins over time in live and fixed cells. As the availability of sensitive antibodies specific for Ras isoforms and their activity remains an issue in the field, these fluorescently labeled Ras proteins have been proven very valuable. However, despite the great insights obtained with these methodologies, it should be noted that a lot of the conclusions drawn from these overexpression studies still lack validation for their endogenous counterparts.

In general, Ras proteins can be translocated from the plasma membrane to endosomes via two different routes. The pathway mainly used by H-, N-, and KRas4A is through endocytic vesicles derived from CDE and CIE pathways (Porat-Shliom et al. 2008; Howe et al. 2001; Gomez and Daniotti 2005; Jiang and Sorkin 2002; Roy et al. 2002) (see [6] in Fig. 3.1). The other route predominantly used by KRas involves desorption from the plasma membrane into the cytosol, followed by non-vesicular diffusion shuttling mechanism to endosomes (Gelabert-Baldrich et al. 2014; Fivaz and Meyer 2005; Yeung et al. 2008; Schmick et al. 2015) (see [5] in Fig. 3.1).

Endocytosed palmitoylated Ras proteins, via CDE or Arf6-dependent CIE encounter the EE or RE compartment in a process regulated by Rab5 or Rab11 GTPases (Gomez and Daniotti 2005; Porat-Shliom et al. 2008; Howe et al. 2001) (see [6] in Fig. 3.1). In EEs, H- and NRas can be mono- and di-ubiquitinated via

a lysine 63-linked chains on lysine 117, lysine 147, and lysine 170 independently of their activation state (Jura et al. 2006). This is not a degradative posttranslational modification but rather stabilizes these Ras isoforms in endosomes and inhibits their recycling to plasma membrane (Jura et al. 2006) (see [7] in Fig. 3.1). The HVR of these Ras proteins is not an obligatory acceptor for ubiquitin but participates in ubiquitination by the E3 ubiquitin ligase Rabex5 (Xu et al. 2010). Interestingly, activated Ras induces the recruitment of Rabex-5 to endosomes through a RAS and RAB interactor 1 (RIN1)-containing machinery. Consequently, this leads to Rab5 activation. Hence, through this complex interplay of Ras with ubiquitination and Rab5 activity, Ras modulates its own stability in endosomes (Zheng et al. 2012b; Ahearn et al. 2011). In addition, retention of Ras proteins in endosomes is also regulated by several members of the sorting nexin (SNX) family such as SNX17, SNX27, and SNX31, which bind PtdIns(3)P as well as active Ras on endosomes (Ghai et al. 2011).

In contrast to H- and NRas, KRas is mono-ubiquitinated via lysine 45-linked chain on lysine 104 and lysine 147 and this modification does not affect its endosomal trafficking but enhances interactions with several effectors (Sasaki et al. 2011). Overall, the endosomal localization of KRas is less prominent compared to H- and NRas isoforms, probably because KRas is less retained on endosomes and as a result faster recycling to the plasma membrane may occur (Vigil et al. 2010; Jiang and Sorkin 2002; Roy et al. 2002). Yet, despite the small amount of KRas in EE, KRas can also continue its journey to LE/MVBs and eventually into lysosomes following the degradative endocytic pathway (Lu et al. 2009) (see [8] in Fig. 3.1). This feature is strikingly different to H- and NRas, which are essentially found in EEs and REs following the recycling route to the plasma membrane (see [9] in Fig. 3.1). The trafficking of GFP-tagged KRas through these different compartments was confirmed by colocalization with established endocytic markers for EE, LE and LE/lysosomes (Lu et al. 2009). Moreover, subcellular fractionation identified approximately 10% of ectopically expressed GFP-KRas, but also endogenous KRas independent of its activation state, in purified EE and LE fractions (Lu et al. 2009; Gelabert-Baldrich et al. 2014). The trafficking routes that deliver KRas to LE and lysosomes are not fully resolved. As GFP-KRas is observed in clathrin-coated pits and vesicles, KRas may reach EE/LE/MVB/lysosomes via CDE and endosomal transport vesicles (Lu et al. 2009). However, FRAP microscopy implicated that delivery through transport vesicles accounted for only a minor proportion of GFP-KRas on endosomal membranes (Gelabert-Baldrich et al. 2014).

FRAP analysis identified a fast replenishment (half-time 1.3 s) of approximately 80% of the bleached GFP-KRas pool on endosomes. This indicates that KRas is highly dynamic, which is in agreement with a model of rapid diffusional incorporation from the cytoplasm. Strikingly different from KRas, the fluorescence recovery was negligible for GFP-H- and GFP-KRas4A, strongly supporting their dependence in slow vesicular transport (Gelabert-Baldrich et al. 2014).

Based on these findings, one can assume that cellular stimuli that lead to KRas serine 181 phosphorylation or promote association of known PBR/farnesyl-binding proteins to the active KRas (CaM, PRA1, PDE- δ) could regulate KRas interaction dynamics with endosomes by inducing electrostatic switch or membrane dissocia-

tion, respectively (Alvarez-Moya et al. 2011; Bhagatji et al. 2010; Fivaz and Meyer 2005; Lopez-Alcala et al. 2008; Chandra et al. 2011; Bivona et al. 2006). Indeed, FRAP microscopy in COS1 cells identified that the constitutively inactive KRas mutant KRasS17N was more immobile than the active mutant KRasG12V as a consequence that active KRas, but not the inactive, can bind CaM or can be posttranslationally modified via serine 181 phosphorylation (Gelabert-Baldrich et al. 2014) (see [5] Fig. 3.1).

As previously mentioned, the PDE- δ protein, through its interaction with the farnesyl group of KRas, regulates KRas localization and dynamics on endosomal membranes and plasma membrane. This interaction solubilizes KRas from endomembranes with low negatively charged surfaces, including EE membranes, leading to a redistribution of KRas to perinuclear RE membranes. The underlying mechanism for this redistribution was based on an activity in RE that displaced KRas from PDE- δ . Further studies then identified the Arf-like GTPase Arl2, which in its active form binds to an allosteric site on PDE- δ , thereby inducing a conformational change that unloads farnesylated cargo (Ismail et al. 2011). Finally, from RE, KRas follows the recycling pathway to the plasma membrane through vesicular transport (Schmick et al. 2015) (see [10] in Fig. 3.1). Trafficking of the different isoforms is summarized in Fig. 3.1.

3.2.1.4 Ras Signaling Pathways from Endosomes

Several studies identified upstream components of the Ras activation pathway on endosomes, including activated EGFR and adaptor proteins Shc/Grb2. This complex is able to recruit Sos1, facilitating GDP/GTP exchange for increasing Ras activity in the endosomal compartment (von Zastrow and Sorkin 2007; Vieira et al. 1996; Herbst et al. 1994; Jiang and Sorkin 2002; Wang et al. 2002). Ras activation on endosomes in live cells has been elegantly demonstrated using FRET microscopy, which allows the spatiotemporal analysis of interaction between molecules inside cells (Jiang and Sorkin 2002; Moreto et al. 2008; Miaczynska and Bar-Sagi 2010). This methodology is based on the energy transfer between two spectrally overlapping GFP variants in cells, for instance, Cyan/cerulean-FP acting as a donor and Yellow/Venus-FP as an acceptor of energy. In order to determine Ras activation utilizing FRET, one of the GFP variants were fused with Ras, while the other GFP variants was fused with the Ras-binding domain of the Raf1 effector. This approach appeared appropriate to detect Ras activation on endosomes (Lu et al. 2009; Jiang and Sorkin 2002; Gomez and Daniotti 2005; Misaki et al. 2010), in particular, as phosphorylated and activated Raf1 was present in purified endosomes from rat liver (Di Guglielmo et al. 1994; Pol et al. 1998). In addition, bimolecular fluorescent complementation (BiFC) microscopy has been also very useful to characterize several other Ras effectors that interact directly or in a protein complex with active Ras on endosomes, such as PI3K and Cdc42 (Tsutsumi et al. 2009; Chang and Philips 2006; Cheng et al. 2011). The BiFC technique relies on the fusion of the N- and C-terminal Venus fluorescent protein with Ras and the RBD of the selected effector,

respectively. Once both proteins interact, the Venus fluorophore rebuilds by complementation, generating a fluorescence signal that can be monitored using microscopy (Zheng and Chang 2014).

The FRET technology described above is based on the overexpression of two fluorescent proteins, often creating false FRET signals that did not correlate with endogenous Ras activation. Unimolecular FRET technology using Raichu probes provided a great advancement for the field. In this approach, YFP-KRas is fused to the CFP-tagged RBD of Raf-1 to provide a single ('biosensor') construct that upon KRas activation, allows intramolecular binding to Raf-RBD. This ultimately brought CFP and YFP in close proximity to create a detectable FRET signal. Using this Raichu probe, it has been demonstrated that EGF-induced activation of KRas in live cells (Lu et al. 2009; Kiyokawa et al. 2006; Mochizuki et al. 2001; Miaczynska and Bar-Sagi 2010).

Despite these findings, the general perception in the field still considers Ras activation at the plasma membrane rather than endosomal signaling as the driver of oncogenic events. However, in NIH3T3 cells, inhibition of Ras internalization to exclusively examine Ras signaling emanating from the cell surface was inefficient to effectively induce cell transformation (Cheng et al. 2011). In addition, a focus formation assay identified expression of endosomal GFP-Ras to produce more foci than the GFP transfected control (Aran and Prior 2013). Hence, endosomal Ras signaling seems to substantially contribute to oncogenic events. In the following, we will dissect some of the Ras isoforms and their effector pathways and endosomal locations that possibly contribute to cell transformation.

The identification of signal specificity within the Ras family has captivated the field for a long time, as the highly conserved effector binding G-domain in all active Ras (GTP-bound) isoforms is capable to interact with the same set of effectors (Wittinghofer and Herrmann 1995) to potentially elicit the same signaling output. Out of more than 20 known Ras effectors, Raf1 and PI3K have been the most extensively studied, driving MEK/MAPK and Akt signaling cascades that control proliferation and cell survival, respectively. Based on their similar binding behavior, it was initially proposed that Ras isoforms would have no preference to couple with either Raf1/MAPK or PI3K/Akt (Omerovic et al. 2008). However, more recent work revealed that depending on the activated Ras isoform, Raf1/MAPK and PI3K/Akt effector pathways appear to be differentially regulated on endosomes. This observation seems to be a consequence of the Ras isoform-specific posttranslational ubiquitin modifications discussed previously. The ubiquitination of H- and NRas on endosomes, which stabilizes their association with EE and simultaneously, reduces recycling to the plasma membrane (see Sect. 3.2.1.3), impairs interaction of H- and NRas with Raf1. Consequently, MAPK activation is reduced, yet PI3K/Akt activation is not affected (Xu et al. 2010; Yan et al. 2010; Jura et al. 2006). Hence, inhibition or overexpression of the ubiquitin ligase Rabex5, which is responsible for H- and NRas ubiquitination on endosomes, resulted in increased or attenuated Raf1/MAPK activation, respectively (Xu et al. 2010; Yan et al. 2010). In a much more complex scenario, Rin1, the GEF for Rab5, can bind HRas on endosomes and simultaneously stimulates Rab5-dependent endocytosis (Cheng et al. 2011; Tall et al. 2001). If the

latter then triggers Rabex5 recruitment, this could also lead to HRas ubiquitination, thereby generating a negative feedback mechanism for HRas/MAPK activation.

Despite the substantial amount of data generated from multiple research groups in recent years on Ras signaling from endosomes, including FRET microscopy demonstrating interaction of ectopically expressed HRas with Raf1 on endosomes (Jiang and Sorkin 2002), Sorkin and coworkers recently reported that endogenous HRas signals from receptors activated at the plasma membrane and not from internal membranes (Pinilla-Macua et al. 2016). These findings clearly challenge the now widely accepted concept of HRas-mediated Raf1/MAPK activation on endosomes highlighting the need for cautious interpretation of data based on ectopic Ras overexpression, which generate highly elevated Ras levels compared to their endogenous counterpart. Hence, future research with advanced technology that would clarify the signaling activities of endogenous HRas on endosomes is still required.

In contrast to the inhibitory impact of ubiquitination on H- and NRas activity, the same posttranslational modification enhances KRas activity. This increases interaction with Raf1 and PI3K, thus elevating signal output of MAPK and Akt pathways (Sasaki et al. 2011). Interestingly, HRas- and KRas-mediated activation of the Raf1/MAPK cascade varies in its dependence on endocytosis, CaM and PI3K activity (Roy et al. 2002; Moreto et al. 2008, 2009). Actually, inhibition of CaM and/or PI3K impairs recycling from EEs, which seems to be linked to HRas/MAPK inhibition (Roy et al. 2002). In fact, CaM inhibition generates enlarged endosomes by preventing the exit of endocytosed molecules, such as the EGFR, from EEs (Tebar et al. 2002) by a molecular mechanism that involves PKC- δ activity (Llado et al. 2004) and actin polymerization (Llado et al. 2008).

In COS1 cells, inhibition of endocytosis via overexpression of the dominant-negative dynamin mutant dynK44A, negatively affects HRas-dependent activation of Raf1 (Moreto et al. 2008). Although dynK44A may also affect other cellular processes, Omerovic et al. also demonstrated that inhibition of receptor internalization reduced H- and N-, but not KRas-mediated Raf1 activation (Omerovic et al. 2008). Together with reports demonstrating HRas and Raf1 interaction in Rab11-positive recycling endosomes after serum stimulation (Gomez and Daniotti 2005), this may suggest that Raf1 activation by HRas indeed occurs in endosomes. Taken together, current views favor divergent roles of endosomes in H/NRas-mediated Raf1/MAPK activation. Signal outcome, either abrogation or stimulation, could be explained by the existence of two different pools of H/NRas on endosomes: ubiquitinated Ras (Raf1/MAPK incompetent) and non-ubiquitinated Ras (Raf1/MAPK competent). The final signal output from H- and NRas on endosomes would then depend on the balance between these two Ras pools, which could be modulated differently by environmental signals, experimental settings, and the cell type.

Besides the differential regulation of Ras isoforms in EE described above, an additional layer of signal specificity is achieved through the localization of KRas, but not H- and NRas in LE/MVBs/lysosomes. In COS1 cells, Raichu probes revealed that EGF stimulation increased KRas activity in LE/MVBs, which in combination with Raf1 and the p14/MP1 scaffold for MEK and ERK (Teis et al. 2002), activates MAPK in this compartment (Lu et al. 2009).

Most interestingly, although the pool of ubiquitinated H- and NRas displays impaired MAPK activation in EEs, these isoforms are perfectly competent to activate the Rho-GTPase Cdc42, thus regulating Cdc42-dependent cytoskeletal rearrangements and cell transformation when they are endocytosed (Cheng et al. 2011; Cheng and Chang 2011). These findings complement Ras function in the fission Yeast *pombe*, which only express one Ras protein, Ras1. At the plasma membrane, Ras1 activates Byr2 (a MEKK homolog)/MAPK but on endomembranes, Ras1 activates Sed1, a GEF for Cdc42 but not MAPK. Thus, in endosomes Ras also activates the cytoskeleton to maintain an elongated morphology, cell polarity, and mitosis (Chang and Philips 2006; Onken et al. 2006). Strikingly, HRas-mediated Cdc42 activation also seems relevant *in vivo*, as expression of a constitutively active HRas mutant restricted to endomembranes induced tumors in nude mice by a mechanism comprising HRas/Cdc42 complex formation (Cheng et al. 2011). This interaction may be mediated by Dbl, one of several GEFs for Cdc42 (Cheng et al. 2011; Cerione 2004). Moreover, the presence of NRas-, and to a minor extent, KRas-containing Cdc42 complexes in these studies could indicate their contribution to tumor initiation (Cheng et al. 2011).

That Ras isoform signaling from endosomal compartments is intimately linked to the endocytic machinery is further highlighted by a screen for HRas effectors in endosomes using BiFC methodology. This study confirmed interaction of ubiquitinated HRas with Cdc42 and PI3K in this compartment (Zheng and Chang 2014; Tsutsumi et al. 2009), but also identified CHMP6/VPS20 and VPS4A as HRas interaction partners, all proteins of the ESCRT-III complex that controls recycling from endosomes to the plasma membrane (Zheng et al. 2012a). One could speculate that the latter interaction could increase recycling of HRas, but also other components of endosomes, such as growth factor receptors, to enhance and sustain growth factor signaling.

Finally, among the different Ras effectors, it is noteworthy to mention T lymphoma invasion and metastasis-inducing 1 (Tiam1) (Lambert et al. 2002), which is a specific GEF for the small GTPase Rac1 (Habets et al. 1994). Interestingly, endosomal Tiam1 activates Rac1 in this compartment, a prerequisite for the subsequent transport of active Rac1 to specific plasma membrane domains and the generation of lamellipodia in migrating cells (Palamidessi et al. 2008). Together with Tiam1 being required for the development of Ras-induced skin tumors (Malliri et al. 2002), this points at Tiam1 as a critical link between Ras and Rac1 in metastasis. The role of Rac1 on endosomes will be explained in more detail in the following section. Figure 3.2 summarizes endosome signaling outcome of different Ras isoforms.

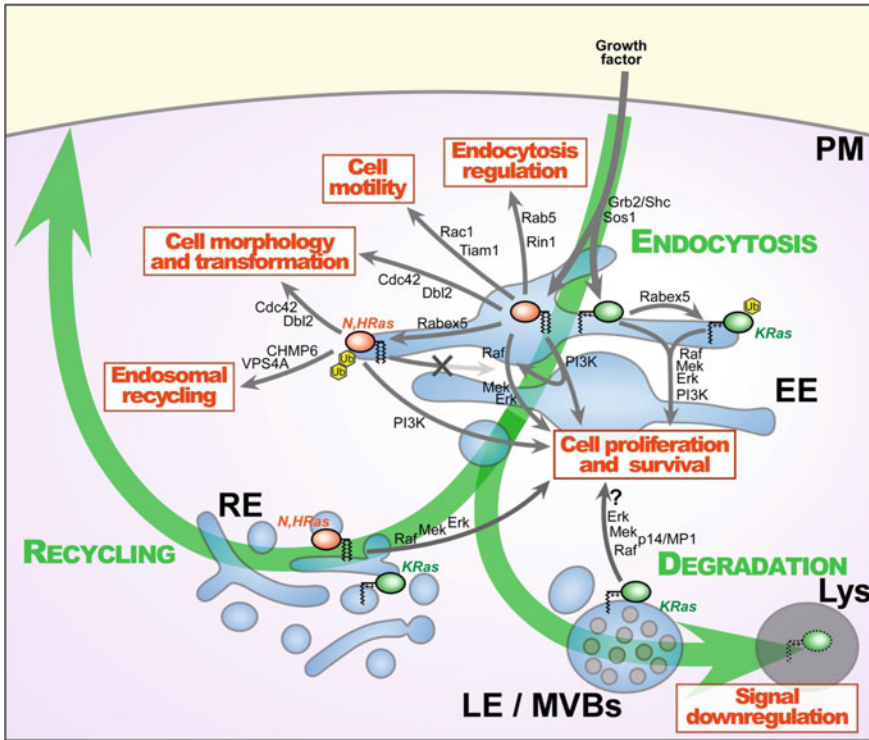


Fig. 3.2 Signaling pathways and outputs from endosomes generated by Ras GTPases. Growth factors induce Ras activation in early endosomes (EE) by recruiting the molecular machinery required for Ras-GTP loading, including adaptors Grb2, Shc, and the guanine exchange factor Sos1. In EE, activated H- or NRas (orange) and KRas (green) then signal through Raf1/Mek/Erk and PI3K/Akt pathways to regulate cell proliferation and survival, respectively. In the case of KRas, Erk activation is also elicited in late endosome/multivesicular bodies (LE/MVBs) through the Raf1/p14/MP1/Mek signaling cascade, which may also support cell proliferation. Furthermore, trafficking of KRas along the degradative route via LE/MVBs and lysosomes (Lys) finally down-regulates KRas signaling. In addition, once in EEs, Ras isoforms then also follow the recycling pathway back to the plasma membrane (PM). Along this route, activation of the Raf1/Mek/Erk cascade can occur in the recycling endosomal compartment (RE), which consequently impacts on cell proliferation. In the EE compartment, Ras regulates several cellular processes by activating GEFs of other signaling proteins. In particular, Ras stimulates Tiam1-mediated Rac1 activation for cell motility and Rin1-mediated Rab5 activation to increase endocytosis. In EEs, Ras isoforms could also become substrates for the ubiquitin ligase Rabex5 for ubiquitination. This posttranslational modification enables all Ras isoforms to enhance PI3K activation but differentially affects the ability of H-, N-, or KRas to regulate Raf1 activity. On the other hand, ubiquitinated H- and NRas, through CHMP6 and VPS4A, increase overall transport through the recycling pathway. Additionally, both ubiquitinated as well as non-ubiquitinated H- and NRas activate Cdc42, through the GEF Dbl2, which may control cell morphology and transformation

3.2.2 *Rac1 Signaling from Endosomes*

Rac proteins belong to the Rho subfamily within the Ras superfamily of small GTPases (Bishop and Hall 2000; Didsbury et al. 1989). Mammalian organisms express three Rac isoforms: Rac1, the focus of this chapter, is ubiquitously expressed, while Rac2 is mostly expressed in the hematopoietic lineage and Rac3 is only found in the central nervous system (Didsbury et al. 1989; Bolis et al. 2003). Together with Rho and Cdc42, Rac1 represents one of the three most extensively studied Rho family members, all well known to coordinate cytoskeleton dynamics that control the formation of stress fibers, filopodia, and lamellipodia, respectively, for cell mobility (Bishop and Hall 2000; Hall 1998; Ridley 2001).

By controlling the dynamics of the actin cytoskeleton, Rac1 regulates many cellular processes linked to cell motility, including cell spreading, adhesion, migration, and axonal growth, but also phagocytosis, macropinocytosis, pinocytosis or vesicular transport (Bosco et al. 2009; Ridley 2006; Heasman and Ridley 2008; Bustelo et al. 2007). Moreover, a wide range of cellular functions, not strictly related with the control of the cytoskeleton, have also been described for Rac1, such as cell survival, the control of gene expression, cell cycle, cell differentiation as well as proliferation (Bosco et al. 2009; Sahai and Marshall 2002; Bishop and Hall 2000). In this context, some mitogenic Rac1 activities can be attributed to signaling events downstream of oncogenic Ras (Samuel et al. 2011; Joneson et al. 1996; Qiu et al. 1995).

Hence, given the multiple functions of Rac1 in fundamental cellular processes, deregulation of Rac1 has been identified to significantly contribute to pathogenic events in several human diseases, including cardiovascular diseases, and metastatic dissemination during cancer progression (Marei and Malliri 2016; Sahai and Marshall 2002). Indeed, Rac1 is a potent regulator of epithelial-mesenchymal transition (EMT) and its reverse process, mesenchymal-epithelial transition (MET), both considered critical to guide cell migration and metastasis of epithelial tumors (Marei and Malliri 2016).

Although activating mutations of Rac1 have only been found with a very low frequency in lung, skin or breast cancer (Schnelzer et al. 2000; Davis et al. 2013), its significant contribution to cell motility, metastasis and cancer progression has been thoroughly demonstrated (Parri and Chiarugi 2010; Bosco et al. 2009; Marei and Malliri 2016). However, despite these pro-oncogenic activities, Rac1 and its GEF Tiam1 also protect against invasion by stabilizing cadherin-mediated cell—cell contacts (Marei and Malliri 2016), and restoring epithelial morphology in Ras-transformed Madin Darby canine kidney cells (Hordijk et al. 1997). It is believed that these pro- and anti-invasive Rac1 activities could be triggered by different stimuli, or response to changes in the surrounding microenvironment, such as cell interaction with the ECM or reflect differential effects of Rac1 activity in relation to the stage of tumor progression (Sander et al. 1998; Sahai and Marshall 2002; De Franceschi et al. 2015; Marei and Malliri 2016; Bosco et al. 2009).

3.2.2.1 Synthesis, Processing and Trafficking of Rac1

In the cytosol, Rac1 is synthesized as a hydrophilic protein and like the Ras isoforms, contains a C-terminal CAAX motif (CLLL). The final leucine residue allows its recognition by a geranylgeranyltransferase type I that covalently incorporates a geranylgeranyl group (20-carbons isoprenyl) to the cysteine residue of the CLLL recognition sequence (Reid et al. 2004). This first cytosolic posttranslational modification enables incorporation of Rac1 into ER membranes and the subsequent AAX hydrolysis, followed by methylation of the geranylgeranylated cysteine residue mediated by Rce1 and Icmt enzymes, respectively, similar to the processing of Ras isoforms described above (Sect. 3.2.1.2). Adding additional complexity in the regulation of Rac1 processing, localization and activity, interaction with Rho-GDP dissociation inhibitor (RhoGDI) proteins then facilitates solubilization of ER-associated Rac1 and consequently, Rac1 release into the cytosol (Bustelo et al. 2007; Hoffman et al. 2000; Marei and Malliri 2016).

Like all other Ras GTPases, Rac1 switches between the active GTP-bound and inactive GDP-bound form, a cycle controlled by several Rho-GEFs and Rho-GAPs that ensure the spatiotemporal regulation of Rac1 activity (Sahai and Marshall 2002). However, in striking contrast to the Ras isoforms, the interaction of RhoGDIs with Rac1, as well as the other members of the Rho family, provides an additional layer to control Rac1 activity. RhoGDIs mainly interact with the inactive Rac1 (GDP-bound) via the G-domain and the geranylgeranyl group, which weakens the membrane anchoring provided by the geranylgeranyl group, thereby solubilizing and sequestering the inactive Rac1 GTPase into the cytosol (Olofsson 1999; DerMardirossian and Bokoch 2005; Grizot et al. 2001). Extensive research over the years identified multiple regulatory circuits driven by growth factors and other external stimuli that can modify this interaction. For instance, RhoGDI can be phosphorylated by PKC or p21-activated kinase (PAK), decreasing its affinity for Rac1-GDP and allowing the insertion of the Rac1 prenyl group into the plasma membrane, followed by GEF-mediated activation of Rac1 (DerMardirossian et al. 2004; Price et al. 2003). Also, integrins can displace RhoGDIs by favoring Rac1 insertion into lipid rafts, specialized plasma membrane domains associated with Rac1 activation (del Pozo et al. 2000, 2002). This complex regulatory circuit is initiated by ECM proteins, fibronectins, first activating integrins in lipid rafts. This stimulates phospholipase D (PLD) and leads to the localized generation of PA in this membrane domain, which competes with RhoGDI for the binding to Rac1. Ultimately, this ensures the Rac1 prenyl group insertion into this membrane domain, which favors Rac1 activation and consequently cell spreading, lamellipodia and migration (Chae et al. 2008).

Within the hypervariable region and adjacent to the CAAX motif, Rac1 also harbors a polybasic region. Several reports demonstrate that this PBR electrostatically interacts with anionic membrane phospholipids, like PS, PtdIns(3,4,5)P₃, PtdIns(3,5)P₂, or PA, determining its localization in specific membrane domains under different physiological conditions (Michaelson et al. 2001; ten Klooster and Hordijk 2007; Finkielstein et al. 2006; Yeung et al. 2006; Chae et al. 2008). In addi-

tion, a proline-rich domain neighboring the PBR has been demonstrated to contribute to the targeting of Rac1 to cellular focal adhesions (ten Klooster et al. 2006).

Finally, Rac1 is also palmitoylated at the cysteine 178 amino acid, which greatly enhances Rac1 membrane stability and promotes its localization and functionality in cholesterol-rich plasma membrane domains (lipid rafts) (Navarro-Lerida et al. 2012). Similar to the Ras isoforms, at the plasma membrane Rac1 can be internalized through CIE transport vesicles reaching EEs and then LEs. The role of Rac1 endocytosis in signaling and its implication in the regulation of different cellular processes is detailed in the next section.

3.2.2.2 Signaling Pathways Regulated by Rac1 from Endosomes

As the genetic ablation of Rac1 in mice results in embryonic lethality (Sugihara et al. 1998) limited information of Rac1 function in vivo is available up to date, mostly relying on studies modulating Rac1 effector gene expression. Therefore, the current knowledge in the field is still based on the vast majority of Rac1 signaling studies performed in cell culture experiments using different cell types.

Signaling elicited by Rac1 effectors commonly are related to actin cytoskeleton rearrangements. One of the most extensively studied Rac1 effectors is PAK which phosphorylates LIM kinase and cortactin, among others, to coordinate actin polymerization (F-actin) at the plasma membrane in a multifactorial process that includes the actin-related protein-2/3 (Arp2/3) complex, Neural Wiskott–Aldrich syndrome protein (N-WASP)/WASP-family verprolin-homologous protein (WAVE), cofilin or dynamin proteins (Frost et al. 1998; Yang et al. 1998; Vidal et al. 2002; Webb et al. 2006; Sauvonnnet et al. 2005; Schafer et al. 2002; Grassart et al. 2010). In addition, another Rac1 effector determining actin dynamics is phosphatidylinositol-4-phosphate 5-kinase (Tolias and Carpenter 2000; Tolias et al. 2000; Vidal-Quadras et al. 2011; Weermink et al. 2004; Chao et al. 2010), which upon activation leads to increased production of PtdIns(4,5)P₂ at the plasma membrane (Doughman et al. 2003; Tolias et al. 2000; van den Bout and Divecha 2009; Shibasaki et al. 1997). On the other hand, Rac1 interacts and activates phospholipase C enzymes (Illenberger et al. 1998; Jezyk et al. 2006; Li et al. 2009), which hydrolyzes PtdIns(4,5)P₂ to generate diacylglycerol and PtdIns(3)P both well established second messengers. This rapid turnover of PtdIns(4,5)P₂ has been demonstrated to promote F-actin polymerization and cell migration (Li et al. 2009). The diversity and complexity of PIs modulating Rac1 signaling are further underscored with PI3K generating PtdIns(3,4,5)P₃ from PtdIns(4,5)P₂, which affects cell migration and cell survival controlled by Rac1 (Yang et al. 2011; Murga et al. 2002). Moreover, PtdIns(3,4,5)P₃ is able to recruit several Rac1-GEFs to the plasma membrane, providing multiple opportunities for positive feedback mechanisms between PI3K and Rac1 (Zhu et al. 2015; Ebi et al. 2013).

All of these Rac1 effectors are critical for actin organization at the plasma membrane, which in addition to controlling formation of membrane protrusions such as lamellipodia in migrating cells, also influences endocytosis (Lamaze et al. 1996;

Soriano-Castell et al. 2017). For instance, Rac1 impacts on CIE of receptors, such as IL-2R (Grassart et al. 2008; Lamaze et al. 2001), fluid phase ingestion, TrkA receptor internalization via macropinocytosis (Valdez et al. 2007), as well as phagocytosis of pathogens (Etienne-Manneville and Hall 2002; Criss et al. 2001). Interestingly, the recently identified novel Rac1 effector amyotrophic lateral sclerosis 2 (ALS2) gene, which is vital for motor neurons, is a Rab5-GEF driving Rac1 activation for macropinocytosis and the subsequent fusion of macropinosomes with EEs (Kunita et al. 2007).

As outlined above, membrane recruitment of Rac1 effectors is intimately linked to cholesterol- and sphingolipid-enriched domains, but is also strongly influenced by the distribution of phosphorylated derivatives of PI. All of these membrane lipids localize to distinct membrane domains at the plasma membrane and in endosomal compartments, contributing to the recruitment of distinct effectors that not only establish signaling platforms, but also control membrane dynamics. Thus, Rac1 does not only control endocytic transport (see above), but vice versa endocytic trafficking is also instrumental in modulating Rac1 activity. This intermingled connection between endocytic trafficking and signal output provides opportunity for localized Rac1 signaling within the endocytic compartment and has been thoroughly demonstrated for ectopically expressed and fluorescently tagged Rac1, Raichu sensors, or photoactivatable GFP-Rac1 by means of biochemical and microscopy techniques. For instance, endocytosis of activated growth factor receptor enabled Rac1 activation in EEs and LEs, while RE ensured the translocation of active Rac1 to specific plasma membrane domains to control decisive events enabling forward movement, such as cell–cell contact, focal adhesion dynamics, assembly and disassembly of invadopodia or lamellipodia membrane protrusion at the leading edge (Menard et al. 2014; Revach et al. 2016; Garcia-Weber and Millan 2016; Stasyk and Huber 2016; Miaczynska and Bar-Sagi 2010; De Franceschi et al. 2015; Zhou et al. 2007; Harrington et al. 2011). Indeed, Kermorgant and coworkers demonstrated that the signaling output from endosomes of activated HGF-R (Met) not only enables Rac1 activation in this compartment, but subsequently ensures redirection of active (GTP-bound) Rac1 to the plasma membrane to control cell migration (Barrow-McGee and Kermorgant 2014). This implicates Rac1 signaling events from endosomes as well as from the plasma membrane to cooperatively determine the migratory behavior of cells. Indeed, PI3K activity and the Rac1-GEF Vav2 in perinuclear endosomes are required to sustain Rac1 signaling output to efficiently activate cell migration and invasion (Menard et al. 2014; Joffre et al. 2011). Most strikingly, constitutively active and oncogenic Met mutants (M1268T and D1246N), which accumulate in endosomal compartments, are characterized by enhanced endosomal Rac1 activity, reduced actin stress fibers, and increased cell migration, highlighting the significant contribution of endocytosis, and endosomal Rac1 signaling to tumor progression and metastatic events (Joffre et al. 2011; Barrow-McGee and Kermorgant 2014).

Further underscoring endocytic trafficking substantially contributing to Rac1 activation, after growth factor-induced activation of motogenic receptors such as HGF-R, Rab5 activity, and CDE is required for Rac1 activation on EEs through the Rho-GEF Tiam1. Moreover, the recycling of active endosomal Rac1 back to the plasma mem-

brane, via the small GTPase Arf6, triggered the formation of actin-based migratory protrusions. This endocytic trafficking route of active Rac1 through Rab5- and Arf6-positive compartments seems to contribute to cell motility in a variety of tumor cells (Palamidessi et al. 2008). In support of the latter, it has been described that active Arf6 induces Rac1 activation through endosomal trafficking (Donaldson et al. 2009).

In other cell types and settings, the initiation of Rac1 signaling from endosomes does not always require growth factor activation. For example, in endothelial cells ECM-bound β 1-integrins recruit another member of the Ras superfamily, R-Ras, to nascent adhesions in lamellipodia, which promotes β 1-integrin and R-Ras internalization by a Rab5-dependent pathway. Once endocytosed, R-Ras then activates Rac1 through Tiam1, followed by active Rac1 redirection to the plasma membrane to control cell adhesion and morphogenesis (Sandri et al. 2012). Similarly, TrkB receptor-mediated activation of PI3K and Tiam1/Rac in endosomes is essential to mediate the chemotactic response of the brain-derived neurotrophic factor (Zhou et al. 2007).

While the majority of Rac1 signaling events described above seem to occur predominantly in EE and RE compartments, Rac1 activity has also been associated with proteins and events located in LE. Along this line, the small GTPase Rab7, an established LE marker that controls late endocytic trafficking, directly interacts with Rac1 and both proteins colocalize in endosomes at the perinuclear region and on vesicles near the plasma membrane. It has been recently demonstrated that Rab7 enables Rac1 activation and promotes Rac1 delivery to the plasma membrane to stimulate cell migration (Margiotta et al. 2017). Moreover, Rab7 and Rac1 association also facilitates endosomal transport, through microtubules and actin filaments, in the context of ruffled border formation in osteoclasts, E-cadherin turnover, and stability of cell-cell contacts (Sun et al. 2005; Frasa et al. 2010).

In the LE compartment, the small GTPase RhoB acts as a negative regulator of Rac1 activity. Hence, inhibition of RhoB induced Rac1 activity and consequently lamellipodia protrusion (Garcia-Weber and Millan 2016). In contrast, active RhoB retained Rac1 in intracellular endosomal localizations and prevented Rac1 activation and its recycling to the cell border, blocking Rac1-dependent endothelial barrier reformation and stabilization of cell-cell junctions (Marcos-Ramiro et al. 2016). These findings are in consonance with the protective effect of HGF-induced and Tiam1-dependent Rac1 activation on endothelial cell barrier function, also requiring the Rac1 effector cortactin and a formation of a cortical actin ring (Birukova et al. 2007). Other negative Rac1 regulators include Rab11-family interacting protein 3 (FIP3). In T-cells, this interaction diverts Rac1 to a Rab11-positive recycling perinuclear endosomes, restricting access of Rac1 to the plasma membrane. In fact, FIP3 silencing induced T-cell spreading, a process that is controlled by Rac1, suggesting endosomal trafficking of Rac1 to regulate T-cell spreading in the immunological synapse (Bouchet et al. 2016).

Finally, it should be noted that the localization of intracellular Rac1 regulators may include players not restricted to the EE, RE, and LE compartments. This includes Rab8, which has been implicated in exocytic/recycling membrane trafficking, but also actin and microtubule cytoskeletal rearrangements (Hattula et al. 2006; Huber

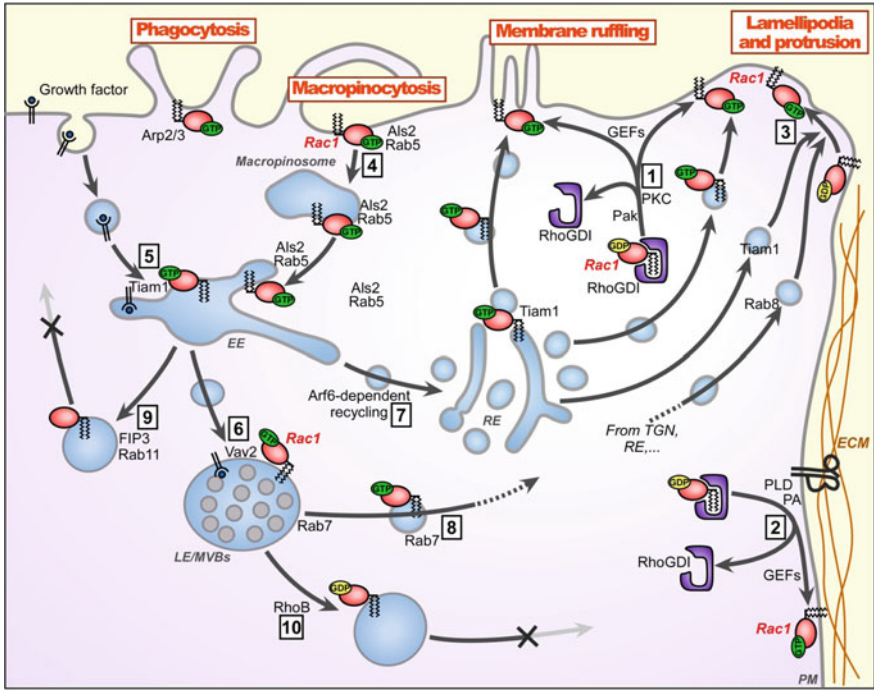


Fig. 3.3 Involvement of the endosomal compartment in Rac1 activation and trafficking to plasma membrane. This scheme illustrates the current knowledge on Rac1 activation on endosomes and Rac1 transport to the plasma membrane (PM) to regulate actin dynamics. In the cytosol, inactive Rac1 (GDP-bound, yellow) is sequestered and maintained soluble by RhoGDI. RhoGDI could be released by phosphorylation through activated p21-activated kinase (PAK)/protein kinase C (PKC) [1]. Alternatively, RhoGDI can be released by activated integrins bound to the extracellular matrix (ECM) upon phospholipase D (PLD) activation and generation of phosphatidic acid (PA), which competes with RhoGDI for Rac1 binding [2]. This allows the insertion of Rac1 at the PM and its interaction with GEFs, which are recruited to the PM by vesicular transport [3] or by interaction with elevated phosphoinositides at the PM. This interaction consequently leads to Rac1 activation (GTP-bound, green). At the PM, active Rac1 regulates cytoskeleton dynamics which controls phagocytosis, macropinocytosis, membrane ruffling, protrusion and lamellipodia formation. Exemplifying the multiple links between Rac1 activity and endocytosis, the Rac1-effector Als2 is a Rab5-GEF, which together with Rac1-induced actin rearrangements, activates macropinocytosis and the subsequent fusion of macropinosomes with early endosomes (EE) [4]. Endocytic membrane compartments and vesicular transport are also critical for Rac1 activation and its redirection to specific PM domains to exert the above-mentioned functions. Growth factor stimulation induces Rac1 activation in EEs and late endosomes (LEs/MVBs) by the GEFs Tiam1 [5] and Vav2 [6], respectively. Thereafter, recycling from these compartments by Arf6 [7], via the recycling compartment (RE), and Rab7 [8] redirects active Rac1 to specific domains at the PM. In addition, the Rab11 effector FIP3 in EEs [9] and the GTPase RhoB in LE/MVBs [10] have also been reported to deliver Rac1 to associated sequestering endocytic vesicles, which inactivate Rac1 by impairing its recycling to the PM

et al. 1993; Peranen et al. 1996; Roland et al. 2007). Rab8 localizes to vesicular structures, including RE and LE, but also the Golgi region, and peripheral membrane ruffles, and increases Rac1 activity and Tiam1/Rac1 mobilization from intracellular compartments to cortical locations to maintain directionality of migrating cells by enabling focal adhesion turnover and actin polymerization (Bravo-Cordero et al. 2016).

In summary, the aforementioned results exemplify and highlight the role of the endocytic system to regulate spatiotemporal Rac1 functionality. Several of these results have been illustrated in Fig. 3.3.

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