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**DISRUPTION OF OLIGOMERIZATION INDUCES NUCLEO-CYTOPLASMIC
SHUTTLING OF LEUKEMIA-ASSOCIATED RHOGEF**

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ChFP, cherry fluorescent protein; DH, Dbl homology; G protein, guanine nucleotide-binding protein; GPCR, G protein-coupled receptor; GAP, GTPase activating protein; GEF, guanine-nucleotide exchange factor; RGS, regulator of G protein signaling; LARG, leukemia-associated RhoGEF; MLL, mixed lineage leukemia; NES, nuclear export sequence; NLS, nuclear localization sequence; NPC, nuclear pore complex; PH, pleckstrin homology; PRG, PDZRhoGEF; SRE, serum response element

Abstract

The rgsRhoGEFs comprise a subfamily of three guanine nucleotide exchange factors, which function in linking heterotrimeric G-proteins to the monomeric RhoGTPase. Here we reveal the novel finding that oligomerization of leukemia-associated RhoGEF (LARG) functions to prevent nucleo-cytoplasmic shuttling and to retain LARG in the cytoplasm. We establish that oligomerization is mediated by a predicted coiled-coil sequence (amino acids 1507-1520) in the extreme C-terminus of LARG and that substitution of isoleucines 1507/1510 with alanines disrupts homo-oligomerization and leads to nucleo-cytoplasmic shuttling via the CRM1 nuclear transport pathway. Also, we demonstrate that induced dimerization of an otherwise nuclear monomeric LARG mutant promotes cytoplasmic localization. Furthermore, we establish that nuclear import of monomeric LARG is mediated by the nuclear localization sequence ²⁹PTDKKQK³⁵ in the extreme N-terminus. We propose that nucleo-cytoplasmic shuttling provides a mechanism for spatially regulating the activity of LARG towards its cytoplasmic targets as well as potentially new nuclear targets.

Introduction

Rho, together with Rac and Cdc42, belongs to the Rho-family of small monomeric GTPases and functions in regulating several cellular processes such as cell movement, survival, cell-cycle, and gene transcription (Rossman et al., 2005; Schmidt and Hall, 2002a). Like all GTPases, Rho cycles between an inactive GDP-bound state and an active GTP-bound state. The GDP/GTP cycle of Rho is regulated by guanine nucleotide exchange factors (GEFs), which catalyze the exchange of GDP for GTP leading to the activation of downstream effector pathways, and GTPase activating proteins (GAPs), which catalyze the hydrolysis of GTP. Rho activation is mediated by several cell-surface receptors including many heterotrimeric G-protein coupled receptors (GPCRs) (Fukuhara et al., 2001; Sah et al., 2000; Seasholtz et al., 1999), as well as growth factor receptors (Taya et al., 2001), and the semaphorin-4D receptor (Basile et al., 2004).

The oncogenic potential of Rho GTPases has been revealed by several studies (Dhanasekaran and Prasad, 1998; Fukuhara et al., 2001; Sahai and Marshall, 2002). RhoGTPases have also been shown to mediate heterotrimeric G-protein induced cell transformation (Fromm et al., 1997). A subfamily of RhoGEFs consisting of p115RhoGEF, PDZ-RhoGEF (PRG), and leukemia-associated RhoGEF (LARG) interact with $G\alpha_{12}$ and $G\alpha_{13}$ leading to Rho activation and thereby coupling heterotrimeric G-protein signaling to Rho signaling (Fukuhara et al., 2000; Fukuhara et al., 1999; Hart et al., 1998; Kozasa et al., 1998; Suzuki et al., 2003). Interactions of p115RhoGEF, PRG, and LARG with $G\alpha$ occur through regulator of G-protein signaling (RGS) domains, a

distinct feature of the proteins in this subfamily of RhoGEFs (rgsRhoGEFs). Like all RhoGEFs, p115RhoGEF, PRG, and LARG contain a DH (Dbl homology) and a PH (Pleckstrin homology) domain, which mediate the exchange activity on Rho. In addition, LARG and PRG contain PDZ domains which have been shown to be involved in cell-surface receptor coupling (Taya et al., 2001; Yamada et al., 2005).

LARG is one of the very few RhoGEFs that have been found mutated in human cancers. The gene for LARG was identified as a fusion partner with the mixed lineage leukemia gene (MLL) in a patient with acute myeloid leukemia (Kourlas et al., 2000). MLL re-arrangements are common in both primary and secondary leukemias and recent studies have reported additional cases of MLL-LARG fusions (Shih et al., 2006; Tyybakinoja et al., 2006). The activity of the MLL-LARG has not been investigated; however the chimeric protein lacks the N-terminus of LARG, and numerous studies indicate that both the N-terminus and C-terminus of several Rho GEFs often contain regulatory sequences that regulate RhoGEF activity by determining intramolecular inhibitions, protein-protein interactions, and RhoGEF re-location in response to stimuli (Schmidt and Hall, 2002a). Current models on the mechanisms of function of RhoGEFs uphold a requirement for translocation to membranes or cytoskeletal structures in response to stimuli. However, studies with two Rho specific GEFs, Net1 and Ect2, have revealed nucleo-cytoplasmic shuttling as a mechanism that tightly regulates their activity (Schmidt and Hall, 2002b; Tatsumoto et al., 1999).

This study provides the first insight into mechanisms regulating the subcellular distribution of LARG. We identify a coiled-coil sequence in the extreme C-terminus of LARG that mediates homo-oligomerization and cytoplasmic retention, and a nuclear

localization sequence (NLS) in the extreme N-terminus. Our results using mutations that disrupt the oligomerization of LARG and constructs that allow for induced dimerization of LARG, suggest a novel model of LARG localization in which LARG oligomers are retained in the cytoplasm, whereas LARG monomers undergo nucleo-cytoplasmic shuttling. Taken together our findings raise the interesting possibility that signaling functions of LARG may be regulated by compartmentalized localization of this protein in the nucleus and the cytoplasm.

Materials and Methods

Cell culture and transfection. COS-7 cells were maintained in Dulbecco's modified Eagle's medium (DMEM) containing 10% fetal bovine serum, and penicillin-streptomycin. Unless otherwise noted cells were plated in 10 cm or 6-well plates 24 h prior to transfection. Cells were transfected with either 1 μ g of DNA/well of 6-well plate or 9 μ g DNA in a 10 cm plate using FuGENE 6 (Roche Diagnostics, Indianapolis, IN), according to manufacturer's protocol.

Reagents and expression plasmids. Leptomycin B was purchased from Biomol International (Plymoth Meeting, PA). The ArgentTM Regulated Heterodimerization Kit was a kind gift from Ariad Pharmaceuticals (Cambridge, MA, <http://www.ariad.com>). The reporter plasmid that expresses the luciferase gene under the control of serum response element (SRE), termed pSRE-Luc, was purchased from Stratagene (La Jolla, CA).

For the construction of GFP fused to LARG FL, LARG Δ C (amino acids 1-1160), LARG Δ N (amino acids 359-1544), LARG Δ N/ Δ C (amino acids 359-1160), LARG (amino acids 1-1240), LARG (amino acids 1-1340), LARG (amino acids 1-1440), or LARG (amino acids 1-1490), forward and reverse primers containing a 5' XhoI site and a 3' BamHI site were used to amplify LARG from pcDNA3-MycLARG. Following digestion with XhoI and BamHI, the PCR generated fragments were ligated into pEGFP-CI. Sequential PCR was used to generate the chimeric GFP-L_NPRG Δ C where the N-terminus of PRG has been replaced with the N-terminus of LARG. The Stratagene QuickChange site-directed mutagenesis kit was used to create GFP-LARG Δ C-2Q, GFP-LARG Δ C-2E, GFP-LARG FL-2IA, and GFP-LARG FL-2IA/2Q. FRB and FKBP, from

pC₄R_HE and pC₄EN-F1 (Ariad Pharmaceuticals, Cambridge, MA) respectively, were amplified with forward and reverse primers containing a 5' BamHI site and a 3' SalI site for subcloning into a pEGFP-C1-LARG Δ C construct where a SalI site was introduced downstream from the BamHI site by QuickChange site directed mutagenesis. mCherry fluorescent protein (ChFP) fused to LARG FL or LARG-2IA was constructed by replacing the GFP coding sequence in pEGFP-C1-LARG FL and pEGFP-C1-LARG-2IA with the mCherry coding sequence from pmCherry-C1, through digestion with NheI and BspEI. For the generation of GFP fused PRG forward and reverse primers containing a 5' XhoI and a 3' EcoRI site were used to amplify PRG from pcDNA3-MycPRG (Banerjee and Wedegaertner, 2004) for subcloning into pEGFP-C1. For the construction of LARG with a GFP fused to its C-terminus, forward and reverse primers containing a 5' BamHI site and a 3' NotI site respectively were used to amplify LARG from pcDNA3-MycLARG. Following digestion with BamHI and NotI, the PCR generated fragments were ligated into pIC111.

The expression vector for ChFP_{2x}, containing a tandem repeat of the mCherry protein (Shaner et al., 2005) was generated in two steps. First, the mCherry coding sequence was PCR amplified from pRSET-B-mCherry using primers containing a 5' NheI site and a 3' Bgl II, and then subcloned into pEGFP-C1 to replace the EGFP coding sequence. Second, the mCherry coding sequence was PCR amplified using primers containing a 5' Bgl II site and a 3' Hind III site, and then subcloned into the corresponding restriction sites of pmCherry-C1 to produce pChFP_{2x}. Complementing single stranded oligonucleotide sequences for three repeats of the nuclear localization sequence of SV40 in tandem, SV40NLS_{3x}, and linker, with 5' EcoRI and 3' SalI

overhangs were annealed to generate double stranded sequences for subcloning into pChFP2x to generate pChFP_{2x}-SV40NLS_{3x}. ChFP_{2x}-LARG(29-35), ChFP_{2x}-LARG(21-41), ChFP_{2x}-LARG(15-41) were constructed by subcloning double stranded corresponding sequences and linker, with 5' EcoRI and 3' SalI overhangs as generated by annealing single stranded complementary sequences. The correct DNA sequence of the mutants was confirmed by DNA sequencing of the entire open reading frame (Kimmel Cancer Institute Nucleic Acid Facility). mCherry cDNA was provided by R. Tsien. pcDNA3-MycLARG was a gift from T. Kozasa, whereas pKH3-HA-RanWT, and pKH3-HA-RanG19V were gifts from I. Macara. The HA epitope (DVPDYA)-tagged pcDNA3HA α_{13} wt and pcDNA3HA α_{13} QL were gifts from J. S. Gutkind.

Co-Immunoprecipitations. Cos-7 cells in 10 cm plates were transfected with the indicated constructs. 24-48 h after transfection cells were washed twice with ice cold PBS and lysed with 0.5 ml of lysis buffer (20mM HEPES pH 7.4, 0.5% Triton X-100, 100 mM NaCl, 2.5 mM MgCl₂, 1mM EDTA, 5 μ g/ml leupeptin and aprotinin, 1mM PMSF, 25mM β -glycerophosphate, 1mM sodium orthovanadate) on ice. Following lysis, cell lysates were centrifuged at 13000 rpm for 5 min at 4°C. 5.75 μ g of an anti-GFP goat polyclonal antibody (Rockland, Gilbertsville, PA) was added, and the supernatants were tumbled for 1 h at 4°C. Next, 30 μ l of Protein A/G Plus agarose (Santa Cruz Biotechnology, Santa Cruz, CA) were added, and samples were tumbled for 2 h at 4°C. Co-immunoprecipitation samples were subjected to SDS-PAGE, transferred to PVDF and probed with 0.2 μ g/ml of an anti GFP rabbit polyclonal antibody (Santa Cruz Biotechnology, Santa Cruz, CA) or with 0.04 μ g/ml ChFP rabbit polyclonal antibody (Chemicon International, Temecula, CA), followed by horseradish peroxidase-conjugated

anti-rabbit antibody (Promega, Madison, WI). The blots were visualized using SuperSignal West Pico (Pierce Chemical, Rockford, IL).

Cell Imaging. Cos-7 cells were grown on coverslips in 6-well plates and were transfected for 24 or 48 h as indicated. For the effect of LMB on protein localization, LMB was added at 20 ng/ml for 2 h before fixation or live cell imaging. Fixation and staining have been previously described (Grabocka and Wedegaertner, 2005) but briefly cells were fixed with 3.7% formaldehyde in PBS for 15 min, washed and then incubated in blocking buffer containing 2.5 % nonfat milk in TBS-1 % Triton X-100. Cells were then incubated with 12CA5 mouse monoclonal antibody in blocking buffer for 1 h and then with Alexa Fluor 594 goat anti-mouse (Molecular Probes, Eugene, OR) secondary antibody in blocking buffer for 30 min. The coverslips were thereafter washed with TBS/1% Triton X-100, rinsed with distilled water and mounted on glass slides with 20 μ l of Prolong Antifade reagent (Molecular Probes, Eugene, OR). For DAPI staining, coverslips were incubated with 0.1 μ g/ml of DAPI (Molecular Probes, Eugene, OR) in PBS for 5 min following fixation or secondary antibody incubation and washes.

Representative images were acquired using an Olympus BX-61 upright microscope with an ORCA-ER (Hamamatsu, Bridgewater, NJ) cooled charge-coupled device camera controlled by Slidebook version 4.0 (Intelligent Imaging Innovations, Denver, CO). Images of fixed cells were captured with an Olympus PlanApo 60x/ N.A. 1.4 Oil objective. Live cell images were captured with a water immersion objective (Olympus LUMPlanFl 60x/0.9w). Images were processed with Adobe Photoshop.

SRE-mediated luciferase gene transcription assay. Cos-7 cells were plated in 6-well plates in serum supplemented DMEM for 24 h. Cells were then switched to serum free

DMEM and transfected with 0.05 μ g of pSRE-Luc, 0.1 μ g pCMV- β -gal, pcDNA3 and GFP-LARG or GFP-PRG constructs as indicated. 24 h after transfection cells were washed with ice-cold PBS and lysed using reporter lysis buffer according to the manufacturer's protocol (Promega, Madison, WI). 20 μ l of the lysates were mixed with 50 μ l of the luciferase substrate (Promega, Madison, WI) at room temperature. Luciferase activity was determined by measuring luminescence intensity. The β -galactosidase activities were determined by the colorimetric method and were used to normalize transfection efficiencies. SRE-readouts were also normalized for expression differences as determined by densitometry readings of Western Blots for GFP-LARG or GFP-PRG probed with anti-GFP rabbit polyclonal antibody.

Results

Deletion of the C-terminus of LARG induces nuclear localization. Recent work has shown that deletion of the C-terminus of rgsRhoGEFs disrupts their ability to homo- and/or hetero-oligomerize and enhances their ability to activate Rho mediated SRE-gene transcription (Chikumi et al., 2004). As a first step in identifying regulatory elements defining the subcellular distribution of LARG, constructs encoding GFP fused to the N-terminus of LARG full-length (FL) and the C-terminal deletion LARG Δ C were generated (Fig.1A). Due to the similarity in size and function between PRG and LARG, constructs encoding GFP-PRG FL and PRG Δ C were prepared (Fig.1A). After expression in Cos-7 cells, GFP-LARG FL was found mainly in the cytoplasm (Fig.1B, GFP panel) as indicated by the presence of a nuclear shadow and the decrease in GFP fluorescence towards the cell periphery. Myc-LARG FL in which a Myc-tag has been fused to the N-terminus of LARG, and LARG FL-GFP, where GFP has been fused to the C-terminus of LARG, display identical cytoplasmic localizations (Supplementary Figure 1). In addition, endogenous LARG also exhibits a predominantly cytoplasmic distribution (Supplementary Figure 1). GFP-PRG FL exhibits the characteristic cytoplasmic as well as peri-PM localization (Banerjee and Wedegaertner, 2004) indicated by the sharp staining at the cell periphery (Fig.1B, GFP panel), and co-localization with cortical actin revealed by phalloidin staining (data not shown) distinct from the cytoplasmic only distribution of GFP-LARG FL. Co-immunoprecipitation studies also revealed that GFP-LARG FL in contrast to GFP-PRG FL, does not interact with actin (data not shown). Thus, association with actin structures is not a feature of GFP-LARG FL.

Surprisingly, GFP-LARG Δ C displayed a strong nuclear localization (Fig.1B, GFP panel) as confirmed by identification of nuclei with DAPI staining (Fig 1B, DAPI panel). In contrast, the C-terminal truncation of PRG did not promote nuclear localization; GFP-PRG Δ C retained cytoplasmic and peri-PM staining (Fig.1B).

Next, we examined the ability of GFP LARG FL and GFP-LARG Δ C to interact with activated α_{13} by assaying for PM recruitment. Previous work has demonstrated that expression of a mutationally activated α_{13} leads to the PM translocation of an otherwise cytoplasmic p115RhoGEF (Bhattacharyya and Wedegaertner, 2000; Bhattacharyya and Wedegaertner, 2003; Grabocka and Wedegaertner, 2005), but a similar PM recruitment of LARG has not been tested. Co-expression of α_{13} wt (HA panel) had no effect on the localization of GFP-LARG FL, or GFP-LARG Δ C (Fig.1C, GFP panel). However, expression of constitutively active HA- α_{13} QL (Fig.1C, HA panel) induced PM recruitment of GFP-LARG FL or GFP-LARG Δ C (Fig.1C, GFP panel). Furthermore, α_{13} E229KQL, a mutant of α_{13} which we have previously demonstrated to be deficient in interacting with and inducing the PM translocation of p115RhoGEF (Grabocka and Wedegaertner, 2005), was also deficient in inducing the PM translocation of GFP-LARG FL or GFP-LARG Δ C (data not shown). In addition to demonstrating that both GFP-LARG FL and GFP-LARG Δ C redistribute in response to α_{13} QL, the proper signaling function of the LARG constructs was confirmed. GFP-LARG FL and GFP-PRG FL activated SRE-mediated gene transcription, and C-terminal deletion results in a further 2 to 5-fold increase in activity, similar to a previous report (Supplemental figure 2) (Chikumi et al., 2004). Thus, the above results (Fig.1C, and Supplemental figure 2) suggest that GFP-LARG Δ C retains stability and structural integrity.

The key finding in Fig.1 is that removal of the C-terminal 384 amino acids of LARG results in strong nuclear localization rather than the cytoplasmic localization of GFP-LARG FL. Moreover, the nuclear localization of GFP-LARG Δ C but not GFP-PRG Δ C (Fig.1B) indicates a unique role of the C-terminus of LARG in regulating subcellular localization. These results further suggest that some aspect of the C-terminus of LARG functions as a cytoplasmic retention signal.

A predicted coiled coil domain in the extreme C-terminus of LARG mediates its homo-oligomerization. Previous work showed that the C-terminus of LARG was required for its oligomerization (Chikumi et al., 2004) and results in Fig. 1 indicate that the C-terminus is required for cytoplasmic retention; thus a logical prediction is that oligomerization functions to prevent nuclear localization of LARG. A previous study (Chikumi et al., 2004) did not define the structural requirements or sequence motifs in the C-terminus that mediate oligomerization of LARG, and therefore we first sought to understand the mechanism in order to more precisely disrupt LARG oligomerization. Interestingly, a recent report revealed that Lsc, the murine ortholog of p115RhoGEF, oligomerizes through a coiled-coil domain in its C-terminus (Eisenhaure et al., 2003). COILS (Lupas et al., 1991) predicts several potential coiled-coil domains in LARG (Fig.2A) characterized by heptad repeats (each heptad is designated by residues *a-g*) with hydrophobic residues *a* and *d* comprising the putative helix interface, and hydrophilic residues *b,c,e,f,g* in the solvent-exposed region (Lupas, 1997). Amino acids 1507-1520 in the extreme C-terminus of LARG appear to constitute a coiled-coil sequence of two heptad repeats (Fig.2A). To test whether this predicted coiled-coil domain is required for oligomerization of LARG isoleucines at position 1507 and at position 1510 were

substituted with alanines (termed 2IA mutation), and co-immunoprecipitation experiments were performed. Cos-7 cells expressing both GFP-LARG FL and ChFP-LARG FL, where the mCherry fluorescent protein has been fused to LARG, were lysed, and GFP-LARG FL was immunoprecipitated with an anti-GFP antibody. (Fig.2B). ChFP-LARG FL is detected in the GFP-LARG FL immunoprecipitate indicating that, as expected, LARG FL homo-oligomerizes (Fig.2B). In contrast, the 2IA mutation strongly disrupted oligomerization, as revealed by the lack of co-immunoprecipitation of ChFP-LARG FL-2IA with GFP-LARG FL-2IA (Fig. 2B). GFP-LARG FL-2IA is able to activate Rho-mediated SRE-luciferase gene transcription to similar levels as GFP-LARG FL (Fig.2C) suggesting that the 2IA mutation does not disturb the structural folding LARG. In summary, the coiled-coil domain prediction and the demonstration that the point mutations of isoleucines 1507 and 1510 disrupt LARG-LARG interaction (Fig. 2A and 2B) strongly suggests that the short coiled-coil domain in the extreme C-terminus mediates oligomerization of LARG.

Oligomerization of LARG determines its cytoplasmic retention. To assess whether the C-terminal coiled-coil domain-mediated oligomerization regulates the cytoplasmic retention of LARG, we examined the subcellular distribution of monomeric GFP-LARG FL-2IA. Surprisingly, the steady state distribution of monomeric GFP-LARG FL-2IA is cytoplasmic (Fig.3A, *middle panel*) similar to oligomeric GFP-LARG FL. (Fig.3A, *upper panel*). This cytoplasmic localization of GFP-LARG FL-2IA is in contrast to the strong steady state nuclear localization of GFP-LARG Δ C (Fig.1B). However, this apparent paradox was resolved through the use of Leptomycin B (LMB), an inhibitor of the CRM1/Exportin 1 nuclear export pathway. When Cos-7 cells

expressing GFP-LARG FL-2IA were treated with LMB for 2h, GFP-LARG FL-2IA displayed a dramatic accumulation in the nucleus (Fig.3A, *middle panel*). The effect of LMB was quantitated by scoring cells for the following subcellular distribution phenotypes: N<C for higher fluorescence intensity in the cytoplasm, N=C for equal fluorescence intensity in the nucleus and cytoplasm, and N>C for higher fluorescence intensity in the nucleus (Fig.3B). In the absence of LMB about 80% of the cells expressing GFP-LARG FL-2IA show the N<C phenotype, but treatment with LMB for 2 h drastically reduces the N<C phenotype to only about 10% of the cells. In addition, LMB treatment increases the N=C phenotype to approximately 80% from only about 20% of the cells with this phenotype in the absence of LMB. As a positive control, GFP-arrestin3 showed the N>C phenotype in the majority of the cells following LMB treatment (Wang et al., 2003) compared to the predominant N<C in the absence of LMB (Fig.3B, *lower panel*).

In contrast to the effect of LMB on monomeric GFP-LARG FL-2IA, LMB treatment did not change the predominantly cytoplasmic distribution of GFP-LARG FL (Fig.3B, *upper panel*). It remained mostly cytoplasmic even after 16 h of LMB treatment (data not shown). Thus, GFP-LARG FL does not appear to undergo nucleocytoplasmic shuttling, at least under the conditions of these experiments. However, disruption of oligomerization of LARG by the two isoleucine to alanine point mutations prevents cytoplasmic retention of LARG and promotes nucleocytoplasmic shuttling, as revealed by LMB treatment (Fig. 3A-B).

Why does GFP-LARG Δ C reside strongly in the nucleus but GFP-LARG FL-2IA apparently shuttles in and out of the nucleus with a strongly cytoplasmic steady state

distribution? A likely reason is that GFP-LARG Δ C translocates into the nucleus due to a lack of oligomerization but has a defect in nuclear export and thus shows nuclear accumulation in the absence of LMB. Nuclear export is addressed below. Regardless, the key finding in this set of experiments is that disruption of oligomerization of full-length LARG allows nucleocytoplasmic shuttling.

To further test the proposal that oligomerization functions to retain LARG in the cytoplasm, we asked whether induced dimerization of a monomeric LARG would prevent its nuclear localization. We selected to induce dimerization of LARG Δ C, due to its readily observable strong nuclear localization, using an analog of the synthetic bivalent-dimerizing-ligand rapamycin and the rapamycin-binding proteins FRB and FKBP (Banaszynski et al., 2005; Muthuswamy et al., 1999; Paulmurugan and Gambhir, 2005). GFP-LARG Δ C chimeras containing the FKBP protein or a FRB domain (Fig.4A) were transfected into Cos-7 cells in the presence or absence of the rapamycin analog AP21967 for 24 h. Treatment with the dimerizer AP21967 caused a strong decrease in nuclear localization (Fig.4C). Live cells were also scored for subcellular distribution phenotypes (Fig.4B). Treatment with AP21967 resulted in an approximately 4 fold increase in the N<C phenotype (from ~6% to ~23%) and 2 fold increase in the N=C phenotype (from ~22% to ~50%) compared to non-treated cells expressing GFP-LARG Δ C-FRB and GFP-LARG Δ C-FKBP (Fig.4C). This increase in the N<C and N=C phenotypes is paralleled by the decline in the N>C phenotype from 72% in non-treated cells, to only 26% in treated cells expressing GFP-LARG Δ C-FRB and GFP-LARG Δ C-FKBP (Fig.4B). Also, GFP-LARG Δ C-FRB or GFP-LARG Δ C-FKBP, when expressed individually, localize to the nucleus in the presence or absence of AP21967 (data not

shown). Thus, induced dimerization of GFP-LARG Δ C strongly reduces its ability to translocate to the nucleus. The nuclear GFP-LARG Δ C-FRB and GFP-LARG Δ C-FKBP in the presence of AP21967 may reflect GFP-LARG Δ C-FRB or GFP-LARG Δ C-FKBP that are present as monomers and/or dimers with a weak ability to be imported into the nucleus.

In summary, these results demonstrate that whereas mutationally disrupting the ability of the GFP-LARG FL to oligomerize leads to its nucleo-cytoplasmic shuttling (Fig.3A and 3B), inducing dimerization of the monomeric and strongly nuclear LARG Δ C leads to its retention in the cytoplasm (Fig.4).

The N-terminus of LARG contains a functional NLS. Mutational disruption of oligomerization of full-length LARG allows nucleocytoplasmic shuttling suggesting that monomeric LARG is actively imported into the nucleus. Consistent with a model where monomeric LARG is actively imported instead of diffusing into the nucleus, nuclear import of GFP-LARG Δ C requires the Ran GTPase, as shown by inhibition of nuclear localization when a dominant interfering Ran mutant is expressed (Supplemental Figure 3B), and FRAP analysis (Supplemental Figure 3A) indicates that nuclear import appears to be a slow process.

Thus, we asked whether LARG contains a functional nuclear localization sequence (NLS). The classic NLS consists of either a short basic stretch of amino acids rich in lysines and arginines, or two basic stretches separated by about 10 non-conserved residues (bipartite NLS) (Jans et al., 2000). PSORTII predicts three NLSs in LARG: a 7 amino acid stretch ²⁹PTDKKQK³⁵, a 4 amino acid stretch ⁴⁵⁰KRRP⁴⁵³, and a bipartite NLS ⁵⁹³KRRGFPSILGPPRRPSR⁵⁶⁹ (Nakai and Horton, 1999). PRG and p115RhoGEF

are also predicted to contain nuclear localization signals. A comparison of the location of the NLS of LARG, PRG, and p115RhoGEF, reveals the extreme N-terminal NLS of LARG as unique. This, together with our observation that PRG Δ C (Fig.1A) and p115RhoGEF Δ C (Bhattacharyya and Wedegaertner, 2003), unlike LARG Δ C (Fig.1A) localize to the cytoplasm, led us to hypothesize that the N-terminus of LARG carries a functional NLS. Thus, we deleted both the N-terminus and the C-terminus of LARG generating a construct, GFP-LARG Δ N/ Δ C, consisting of amino acids 359-1160 (Fig.5A, *left panel*). When expressed in Cos cells GFP-LARG Δ N/ Δ C localizes to the cytoplasm (Fig.5A, *right panel*), indicating that deletion of the N-terminus prevents nuclear localization of the strongly nuclear GFP-LARG Δ C. GFP-LARG Δ N, where only the N-terminus of LARG has been removed, also localizes to the cytoplasm (Fig.5A, *right panel*). Interestingly, GFP-L_NPRG Δ C, where the N-terminus of PRG has been replaced with the N-terminus of LARG, and the C-terminus has been deleted exhibits a strong nuclear localization (Fig.5A, *right panel*) unlike the cytoplasmic/cortical actin localization of GFP-PRG Δ C (Fig.1). Thus, these results involving deletion of the N-terminus of LARG and swapping the N-terminus of LARG into PRG Δ C are consistent with the prediction that the N-terminus of LARG carries a functional NLS.

To more precisely define the predicted N-terminal NLS of LARG, the positively charged lysines at position 32 and 33 (Fig.5B) were substituted with glutamines (2Q). The 2Q mutation was introduced into the background of GFP-LARG FL-2IA and GFP-LARG Δ C. GFP-LARG FL-2IA/2Q retains a cytoplasmic localization upon LMB treatment (Fig.5C), in contrast to GFP-LARG FL-2IA, which shows a significant nuclear localization following LMB treatment (Fig.3A). Moreover, the 2Q mutation prevents

nuclear localization of GFP-LARG Δ C; GFP-LARG Δ C-2Q displays a cytoplasmic localization (Fig.5C). Importantly, these results demonstrate that lysines 32 and 33 are necessary for the nucleocytoplasmic shuttling of full-length monomeric LARG, *i.e.*, GFP-LARG FL-2IA, suggesting that these lysines are critical components of a NLS.

Next, we investigated whether the N-terminal NLS of LARG could target an unrelated protein to the nucleus. The mCherry fluorescent protein (ChFP) appears as a good candidate for this purpose since it does not contain any NLSs or NESs. Due to its small size (about 28kd), which allows for passive diffusion into the nucleus, a significant portion of ChFP localizes to the nucleus (data not shown) making it difficult to visualize NLS-induced nuclear localization. To overcome this problem we constructed a mCherry fluorescent fusion protein ChFP_{2x}, consisting of two repeats of the mCherry, which allowed for a stronger cytoplasmic content as detected in live cells expressing ChFP_{2x} (Fig.5D). ChFP_{2x}-LARG(29-35) consisting of the mCherry fusion protein and the putative NLS of LARG showed a similar distribution to ChFP_{2x}, although a control, ChFP_{2x}-SV40NLS_{3x}, which contains three repeats of the NLS of SV40 shows a completely nuclear distribution (Fig.5D). Thus, we examined whether additional amino acids were necessary to define a functional NLS of LARG. When LARG amino acids 22-41 were fused to ChFP_{2x} only a small increase in nuclear localization was observed (data not shown); however, a fusion protein of ChFP_{2x} with amino acids 15-41 of LARG exhibited a nuclear distribution similar to ChFP_{2x}-SV40NLS_{3x}. Thus, the short basic stretch of amino acids 29-35 of LARG requires additional N-terminus basic residues in the linear sequence of LARG in order to target an unrelated protein into the nucleus. This may reflect the minimum number of residues required for the proper folding of the NLS

as well as suggest that the functional NLS of LARG may conform to a bipartite nature. Taken together, the experiments in Figure 5, demonstrate a functional NLS in the extreme N-terminus of LARG.

The C-terminus is required for nuclear export of monomeric LARG. Lastly, we asked whether we could define regions of the protein that are involved in nuclear export of nucleocytoplasmic shuttling forms of LARG. The strong nuclear localization of GFP-LARG Δ C compared to the much stronger cytoplasmic steady state localization of GFP-LARG FL-2IA suggests that GFP-LARG Δ C undergoes either no nuclear export or nuclear export that is slower than import. Indeed, consistent with little or no nuclear export, following photobleaching of the cytoplasm of cells with GFP-LARG Δ C distributed in the cytoplasm and nucleus (similar to the image shown in Supplemental figure 3A) there was no significant recovery of fluorescence in the cytoplasm and/or loss of fluorescence in the nucleus over a time period of 1 h (data not shown).

To attempt to define further a role for the C-terminus in nuclear export, we analyzed a series of C-terminal deletions. Cells expressing GFP-LARG FL, GFP-LARG(1-1490), GFP-LARG(1-1440), GFP-LARG(1-1340), GFP-LARG(1-1240), or GFP-LARG Δ C were scored for the N<C, N=C, and N>C subcellular distribution phenotypes (Fig.6A). A key feature of the distribution phenotypes for the truncation mutants is the strong presence of the N=C phenotype for GFP-LARG(1-1340), GFP-LARG(1-1440) and GFP-LARG(1-1490). Whereas the N>C phenotype, as predominates in GFP-LARG(1-1240) and GFP-LARG Δ C, is consistent with a protein undergoing nuclear import but relatively slow nuclear export, the N=C phenotype is consistent with a protein undergoing nuclear export at a similar rate with nuclear import. Accordingly, the

strong presence of the N=C phenotype for GFP-LARG(1-1340), GFP-LARG(1-1440) and GFP-LARG(1-1490) suggests that these mutants are substantially exported out of the nucleus. Thus, we tested whether these deletion mutants were sensitive to LMB. Indeed, GFP-LARG(1-1340) shows an increased nuclear accumulation when cells are treated with LMB (Fig.6B). Taken together, these results indicate that removal of the 384 C-terminal amino acids of LARG prevents nuclear export, but smaller C-terminal deletions recover some nuclear export function. Thus, the C-terminus functions in mediating nuclear export of monomeric LARG. Analysis of the amino acid sequence of LARG for similarities with the leucine-rich CRM1 –dependent nuclear export signal (ϕ -x_{2,3}- ϕ -x_{2,3}- ϕ -x- ϕ ; ϕ =L,I,V,F,M, x=any amino acid) (Kutay and Guttinger, 2005) reveals a potential NES between amino acids 1242-1268 in LARG. However, though fusion of amino acids 1242-1268 of LARG to the otherwise mostly nuclear ChFP-LARG(15-41) led to an increase in cytoplasmic localization, extensive mutagenesis of leucine residues within amino acids 1242-1268 did not affect the localization of GFP-LARG-2IA (data not shown) indicating that these residues do not constitute an NES in the context of full length monomeric LARG. The C-terminus therefore, may contribute an NES that is not apparent in the linear amino acid sequence of LARG but that becomes available in the structural folding of the protein. Alternatively the C-terminus could mediate nuclear export of monomeric LARG through interaction(s) with other NES carrying protein(s).

Discussion

We have identified that a predicted coiled coil sequence comprised of amino acids 1507-1520 in the extreme C-terminus mediates the oligomerization of LARG. We determined that disruption of the coiled-coil domain by replacing both isoleucine 1507 and isoleucine 1510 with alanines strongly impairs the ability of LARG to oligomerize (Fig.2A-B) and confers upon LARG a nucleo-cytoplasmic shuttling ability (Fig.3). Also, we establish that monomeric GFP-LARG FL-2IA is imported into the nucleus via an extreme N-terminal NLS. Furthermore, following nuclear targeting, monomeric LARG is rapidly exported out of the nucleus via the CRM1 dependent nuclear export pathway.

Our results demonstrate that the extreme C-terminal and N-terminal sequences of LARG, function as key regulators of its localization. Nuclear versus cytoplasmic localization of LARG is determined by a tightly regulated interplay between the coiled-coil domain and a putative nuclear export sequence in the C-terminus and the NLS in the extreme N-terminus. Thus, the C-terminus coiled-coil domain of LARG, through its ability to oligomerize, functions as a cytoplasmic retention signal, and, although LARG carries a functional NLS in its N-terminus, it can only undergo nucleo-cytoplasmic shuttling when its ability to oligomerize has been disrupted. The mostly monomeric GFP-LARG-2IA mutant localizes to the nucleus upon inhibition of nuclear export by LMB while GFP-LARG FL remains cytoplasmic following LMB treatment (Fig.3B). In addition, forced dimerization of GFP-LARG Δ C-FRB/GFP-LARG Δ C-FKBP through the rapamycin inducible dimerization system, inhibits nuclear localization of GFP-LARG Δ C (Fig.4), consistent with a role for oligomerization in regulating nucleo-cytoplasmic shuttling of LARG. COILS predicts several other coiled-coil domains in the linear

sequence of LARG however removal of a short C-terminal stretch of amino acids including only the coiled-coil domain between amino acids 1507-1520 is enough to disrupt the cytoplasmic retention of LARG. Thus, although it is possible that additional coiled-coil domains in the linear sequence of LARG may participate in its oligomerization, the C-terminus coiled-coil domain represents the major determinant of oligomerization and cytoplasmic retention of LARG. Oligomerization may be a common mechanism for regulating nuclear transport of proteins. In addition to LARG, several proteins, including yeast Ste5, Smad4, and p53 have their nuclear transport regulated by oligomerization (Stommel et al., 1999; Wang and Elion, 2003; Watanabe et al., 2000).

We show that nuclear export of monomeric LARG, as revealed by the LMB sensitivity of GFP-LARG FL-2IA occurs via the CRM1 export pathway. LMB treatment also increased the nuclear localization of GFP-LARG(1-1340) (Fig.6B), GFP-LARG(1-1440), and GFP-LARG(1-1490) (data not shown). This, together with the distribution pattern of the series of truncation mutants where N=C is a dominant phenotype for GFP-LARG(1-1340), GFP-LARG(1-1440), and GFP-LARG(1-1490) (Fig.6A) indicate that the C-terminus mediates nuclear export of monomeric LARG. Mutagenesis of putative NESs in the linear sequence of LARG however, had no effect on the localization of monomeric GFP-LARG FL-2IA. Thus, the C-terminus could regulate nuclear export of monomeric LARG by mediating functionality of NESs not apparent in the linear sequence of LARG and/or participate in protein-protein interactions or modifications that regulate functionality of NES. Further studies will be needed to characterize the CRM1-dependent nuclear export mechanism of LARG.

The predicted N-terminal NLS (²⁹PTDKKQK³⁵) of LARG is necessary for the nuclear import of monomeric LARG as revealed by the cytoplasmic retention of GFP-LARG FL-2IA or GFP-LARGΔC mutants in which lysines 32 and 33 have been replaced with glutamines (Fig.5B-C) or glutamic acids (data not shown). However, the stretch of amino acids that is sufficient for nuclear import requires additional N-terminal basic residues. As shown in Fig.4D, fusion of LARG amino acids 29-35 or 21-35 to ChFP_{2x} does not promote nuclear localization, but ChFP_{2x}-LARG(15-41) shows a mostly nuclear distribution. A role for flanking residues in mediating import receptor binding is a feature of several nuclear cargo proteins (Jans et al., 2000). Alternatively, as the minimal stretch required for nuclear targeting contains two clusters of basic residues (amino acids 15-21 and 29-35) the functional NLS of LARG may be bipartite. Interestingly, the Net1 RhoGEF contains two N-terminal NLSs, while the Ect2 contains two NLSs located centrally in the linear sequence (Schmidt and Hall, 2002b; Tatsumoto et al., 1999). FRAP analysis (Supplemental Figure 3A) for GFP-LARGΔC reveals that its nuclear import as monitored in live cells is slow. Consistent with a slow import, inhibition of nuclear export of GFP-LARG FL-2IA results in a drastic increase only in the N=C phenotype as opposed to a large increase in the N>C phenotype which would indicate a faster nuclear import. LARG is a multidomain protein and as such it may participate in several protein interactions which could function in keeping LARG out of the nucleus and in cytoplasmic compartments or at the PM as indicated by the translocation of GFP-LARG FL or GFP-LARGΔC to the plasma membrane in the presence of α₁₃QL (Fig.1C).

It is well established that protein function is tightly regulated by temporal and spatial expression patterns. The ability of LARG to translocate to the nucleus may have

evolved as a means to control its ability to activate its cytoplasmic targets such as the Rho GTPase as has been previously suggested for the Net1 and Ect2 exchange factors (Schmidt and Hall, 2002b; Tatsumoto et al., 1999). A previous report showing higher activity of large C-terminal truncations of rgsRhoGEFs, raised the possibility that monomeric forms could be more active than the oligomeric forms (Chikumi et al., 2004). Our results for LARG instead suggest that C-terminal mediated oligomerization and regulation of activity are separable. Although the monomeric LARGAC displays higher signaling activity than LARG FL (Supplemental Figure 2), the monomeric LARG-2IA activates SRE-dependent gene transcription similarly to LARG FL (Fig.2C). A recent study reported similar results for Lsc, the murine ortholog of p115RhoGEF (Eisenhaure et al., 2003). Thus, our results with LARG and those reported for Lsc are consistent with the C-termini of rgsRhoGEFs having multiple regulatory functions. For LARG, the extreme C-terminus mediates oligomerization. Other C-terminal regions may also be responsible for regulating activity, possibly via intramolecular inhibition or by mediating interaction with additional proteins.

Additionally, the presence of LARG in the nucleus may indicate a nuclear specific function of this protein. Recent work has revealed that the rho-kinase ROCK2 localizes to the nucleus where it targets p300 for phosphorylation and regulates its acetyltransferase activity (Tanaka et al., 2006). Also, Rho and additional Rho-effectors such as PLD have been detected in the nucleus through fractionation studies (Balboa and Insel, 1995; Baldassare et al., 1997). Interestingly, several RGS proteins have been identified to localize to the nucleus, and although their nuclear functions are still emerging, several lines of evidence suggest that they can directly or indirectly regulate

gene transcription (Burchett, 2003). Remarkably the N-terminus of LARG, which we have identified to carry a functional NLS is absent from the MLL-LARG fusion protein (Kourlas et al., 2000; Popovic and Zeleznik-Le, 2005). It is tempting to speculate that in the MLL-LARG fusion protein, the NLS and DNA binding motifs of MLL (Li et al., 2005; Popovic and Zeleznik-Le, 2005) override the cytoplasmic retention signals of LARG and target MLL-LARG to the nucleus. Also, as proposed for many MLL-fusion partners (Li et al., 2005), LARG, through its ability to oligomerize, may also force oligomerization of MLL and lead to aberrant gene expression.

Numerous factors may function in disrupting oligomerization of LARG and inducing its nucleo-cytoplasmic shuttling. Such factors may include signals from cell surface receptor, protein kinases and phosphatases, protein modifications such as ubiquitination, as well as interactions with proteins that may function as anchors for a particular cellular compartment. It will be important to determine the cellular mechanisms that regulate oligomerization of LARG and other RhoGEFs.

Acknowledgements

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Footnotes

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Legends for Figures

Figure 1. Deletion of the C-terminus of LARG induces its nuclear localization. A) Schematic presentation of GFP-LARG FL (amino acids 1-1544), GFP-PRG FL (amino acids 1-1522), and ΔC truncation mutants (amino acids 1-1160). B) Cos-7 cells were transfected with 0.5 μg of the indicated LARG and PRG constructs and 0.5 μg pcDNA3. Cells were fixed 48 h after transfection. Localization of GFP-LARG and GFP-PRG constructs was visualized by the intrinsic fluorescence of GFP (GFP panel), whereas nuclei were visualized by staining of chromatin with DAPI (DAPI panel). Images are representatives of >100 cells analyzed in at least three independent experiments. Bars, 10.2 μm . C) $\alpha_{13}\text{QL}$ induces the translocation of GFP-LARG ΔC to the PM. Cells were transfected for 48 h with 0.5 μg of GFP-LARG FL or GFP-LARG ΔC and 0.5 μg of HA- $\alpha_{13}\text{wt}$ or HA- $\alpha_{13}\text{QL}$ as indicated. Localization of HA- α_{13} constructs was detected by immunostaining fixed cells with a mouse monoclonal anti-HA antibody (Anti-HA panel) followed by an Alexa-594 conjugated anti-mouse antibody. GFP-LARG FL, GFP-PRG FL, and ΔC mutants were visualized by intrinsic fluorescence of GFP, and nuclei were visualized by DAPI staining (DAPI panel). Images are representatives of >100 cells analyzed in each of at least three independent experiments. Bars, 10.2 μm .

Figure 2. Oligomerization of LARG is mediated by an extreme C-terminal coiled coil domain. A) Coils output for LARG as predicted by COILS 2.2 (MTIDK matrix, weighed) and amino acid sequence of the targeted coiled-coil. Mutated residues are indicated by asterisks (*). B) Substituting isoleucines 1507/1510 with alanines disrupts oligomerization of LARG. Cos-7 cells were transfected with GFP-LARG FL and ChFP-

LARG FL or GFP-LARG FL-2IA and ChFP-LARG FL-2IA, as indicated. 24 h after transfection cells were lysed and GFP-LARG FL or GFP-LARG FL-2IA were immunoprecipitated with a polyclonal anti-GFP antibody. Co-immunoprecipitates were separated by SDS-PAGE and immunoblotted with a polyclonal anti-ChFP antibody (anti-GFP IP, upper panel). Immunoblotting of the immunoprecipitates with a polyclonal anti-GFP antibody reveals similar amounts of immunoprecipitated GFP-LARG FL and GFP-LARG FL-2IA (anti-GFP IP, lower panel). Cell lysates were immunoblotted with an anti-ChFP antibody (TCL, upper panel) and an anti-GFP antibody (TCL, lower panel) to determine the expression levels of the ChFP and GFP constructs respectively. Results shown are representatives of at least three independent experiments. C) Monomeric GFP-LARG FL-2IA activates SRE-luciferase gene transcription similar to oligomeric GFP-LARG FL. Cos-7 cells were transfected with the indicated amounts of LARG constructs, pSRE-Luc, and pcDNA3. Cells were lysed 24 h after transfection and assayed for luciferase activity. Luciferase activity was normalized for expression differences as detected by densitometry readings of cell lysates immunoblotted with a polyclonal GFP antibody. Results are presented as fold increase over pcDNA3 transfected cells, and are the means \pm S.E from at least three independent experiments. There is no significant statistical difference between GFP-LARG FL and GFP-LARG FL-2IA.

Figure 3. Disruption of oligomerization induces nucleo-cytoplasmic shuttling of LARG. A) GFP-LARG FL-2IA localizes to the nucleus upon LMB treatment. Cos-7 cells transfected for 46 h with GFP-LARG FL, GFP-LARG FL-2IA, or GFP-Arrestin3 and

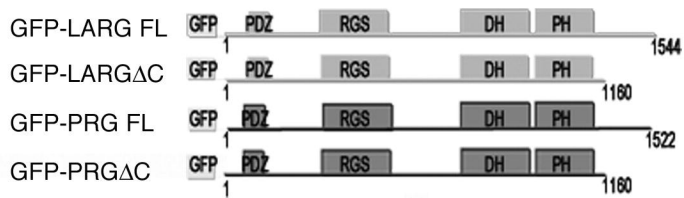
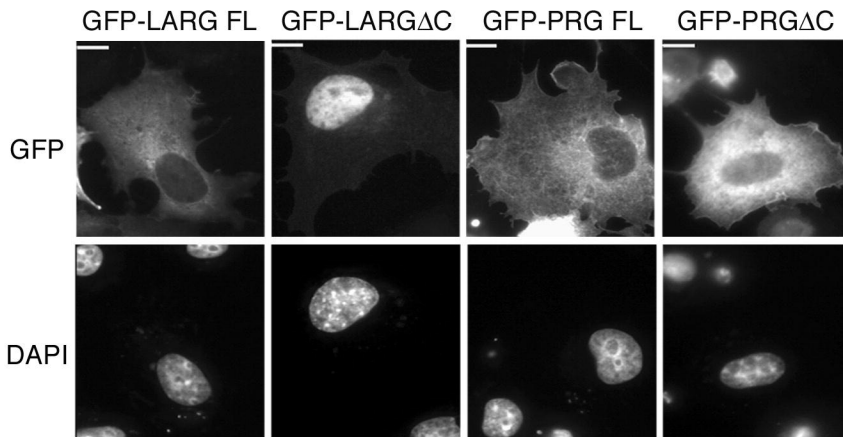
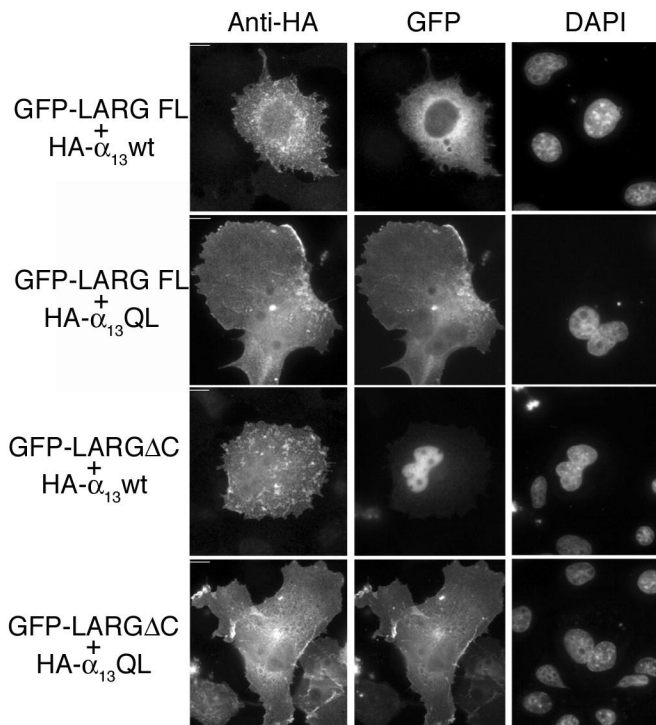
were incubated in the presence of 20 ng/ml LMB for the final 2 h. Cells were fixed and stained with DAPI and analyzed for the localization pattern of each mutant. Representative images of the dominant cellular distribution phenotype for each condition are shown. Bars, 10.2 μm . B) The nuclear fraction of GFP-LARG FL-2IA increases in the presence of LMB. Cellular distribution phenotypes were determined as listed: N=C cells showing equal fluorescence intensities in the nucleus and cytoplasm; N>C cells showing higher fluorescence intensity in the nucleus; N<C cells showing lower fluorescence intensity in the nucleus. Results are percentage of cells with each phenotype and are the means \pm S.E. from at least 100 cells analyzed in three independent experiments. Statistical differences between treated and non-treated cells for each phenotype, are indicated by asterisks (*two-tailed t-test*, ** $P<0.01$, * $P<0.05$).

Figure 4. Induced dimerization inhibits the nuclear translocation of GFP-LARG Δ C. A) Schematic representation of GFP-LARG Δ C fused to FRB or FKBP. B) Cos-7 cells were transfected with GFP-LARG Δ C-FRB and GFP-LARG Δ C-FKBP for 24 h in the presence of 100nM AP21967. Cellular distribution was determined by visualization of the intrinsic fluorescence of GFP in live cells. Distribution phenotypes were determined. Results are percentage of cells with each phenotype and are the means \pm S.E. from at least 100 cells analyzed in three independent experiments. Statistical differences between treated and non-treated cells for each phenotype, are indicated by asterisks (*two tailed t-test*, ** $P<0.01$, * $P<0.05$). C) Representative images of the dominant cellular distribution phenotype for each condition. Bars, 11 μm .

Figure 5. N-terminus of LARG contains the nuclear targeting motif. A) (*Left panel*) Schematic representation of LARG and PRG constructs used to determine the functional NLS of LARG. (*Right panel*) Plasmids encoding GFP-LARG Δ N, GFP-LARG Δ N/ Δ C, or GFP-L_N-PRG Δ C were transfected into Cos-7 cells. Cells were fixed 48 h after transfection and stained with DAPI. Images are representatives of >100 cells analyzed in each of three independent experiments. Bars, 10.2 μ m. B) Amino acid sequence of N-terminus of LARG containing the putative NLS ²⁹PTDKKQK³⁵ (highlighted in grey). Mutated residues are indicated by asterisks (*). C) Lysines at positions 32 and 33 are necessary for the nuclear localization of GFP-LARG FL-2IA and GFP-LARG Δ C. Cos-7 cells were transfected with a plasmid coding for GFP-LARG FL-2IA/2Q or GFP-LARG Δ C-2Q where lysines at positions 32 and 33 were substituted with glutamines. Cells were transfected for 48 h and incubated in the presence of 20ng/ml of LMB the last 2 h. Following fixation and DAPI staining cells were analyzed for the distribution pattern of GFP-LARG FL-2IA/2Q or GFP-LARG Δ C-2Q. Bars, 10.2 μ m. D) LARG amino acids 15-41 are sufficient to target an unrelated protein to the nucleus. Cos-7 cells were transfected with plasmids encoding ChFP_{2x}, ChFP_{2x}-SV40NLS_{3x}, ChFP_{2x}-LARG(29-35), and ChFP_{2x}-LARG(15-41). 48 h after transfection the localization pattern of the indicated constructs was observed in live cells by the intrinsic fluorescence of ChFP. The left panel shows differential interference contrast (DIC) images corresponding to the fluorescent images on the right panel. Bar, 11 μ m.

Figure 6. The C-terminus is required for nuclear export of monomeric LARG. A) Cos-7 cells transiently transfected for 48 h with the indicated constructs were fixed, stained with

DAPI, and scored for the listed phenotypes. Data is presented as percentage of cells with each phenotype and are the means +/- S.E. from three independent experiments. At least 100 cells were analyzed in each experiment. Two-tailed t-test analysis indicate statistical differences for N>C:N=C in all truncation mutants with a *P value*<0.01; N=C:N<C for GFP-LARG FL, GFP-LARG(1-1240) and GFP-LARGΔC with a *P value*<0.01, and GFP-LARG(1-1490), GFP-LARG(1-1440) and GFP-LARG(1-1340) with a *P value*<0.05; N>C:N<C for GFP-LARG FL, GFP-LARG(1-1440), GFP-LARG(1-1340), GFP-LARG(1-1240) and GFP-LARGΔC with a *P value*<0.01, and GFP-LARG(1-1490) with a *P value*<0.05. B) LMB treatment induces nuclear accumulation of GFP-LARG(1-1340). Cellular distribution phenotypes were determined. Results are percentage of cells with each phenotype and are the means +/- S.E. from at least 100 cells analyzed in three independent experiments. Statistical differences between treated and non-treated cells for each phenotype, are indicated by asterisks (*two tailed t-test*, ** *P*<0.01, * *P*<0.05).

A**B****C****Figure 1**

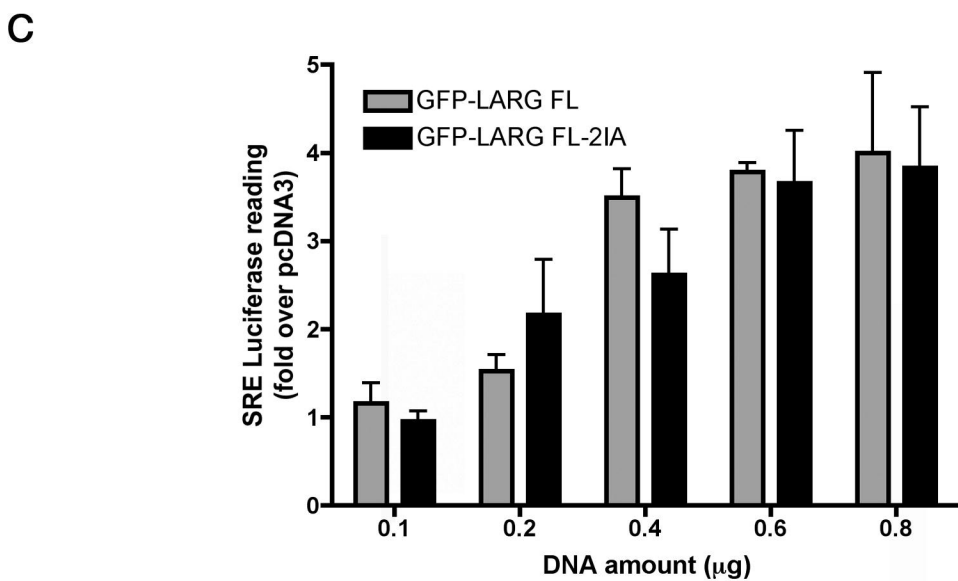
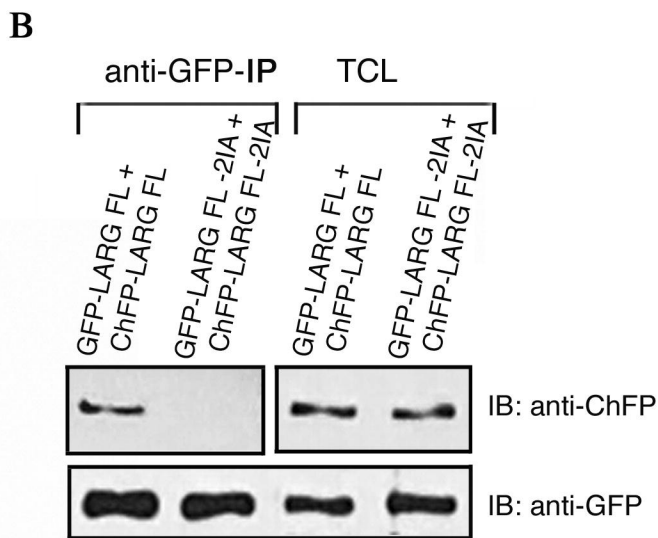
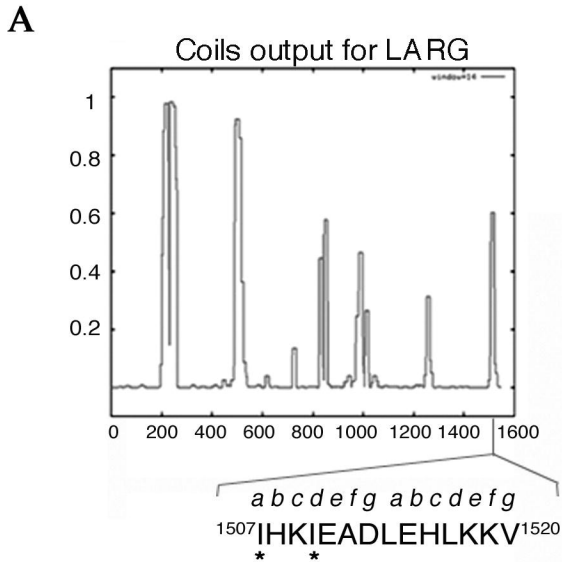


Figure 2

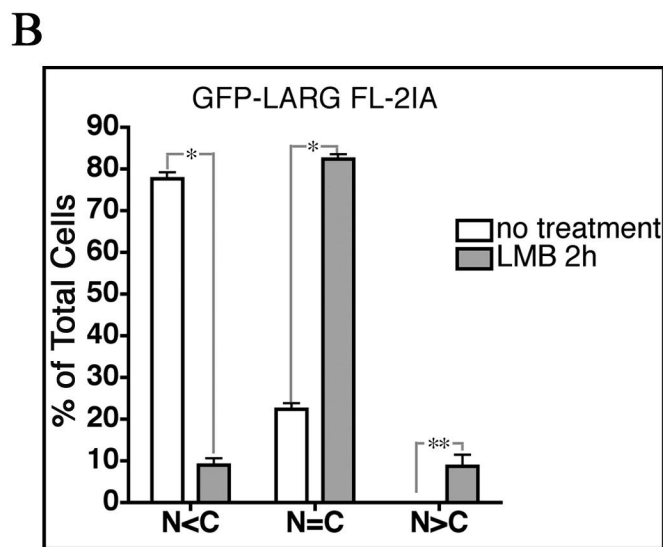
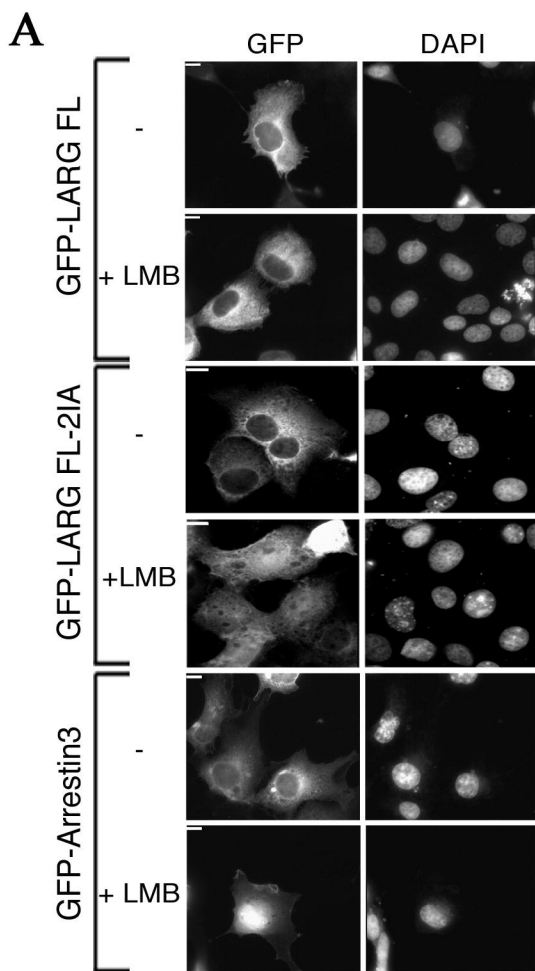


Figure 3

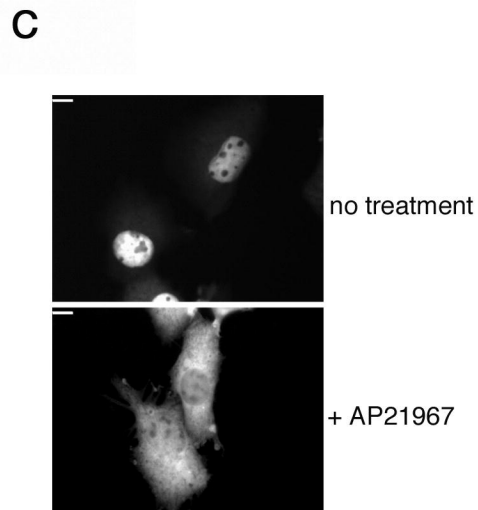
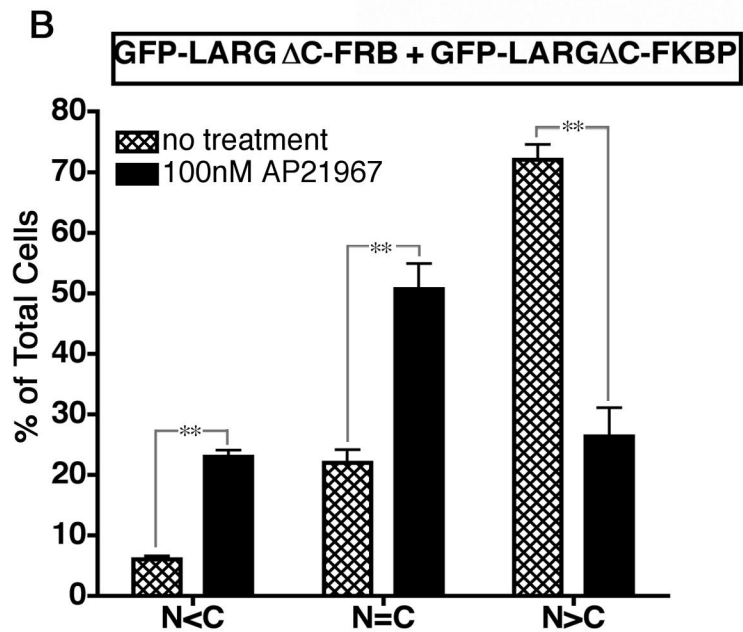
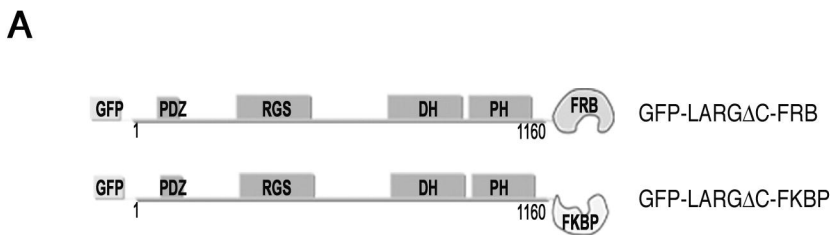
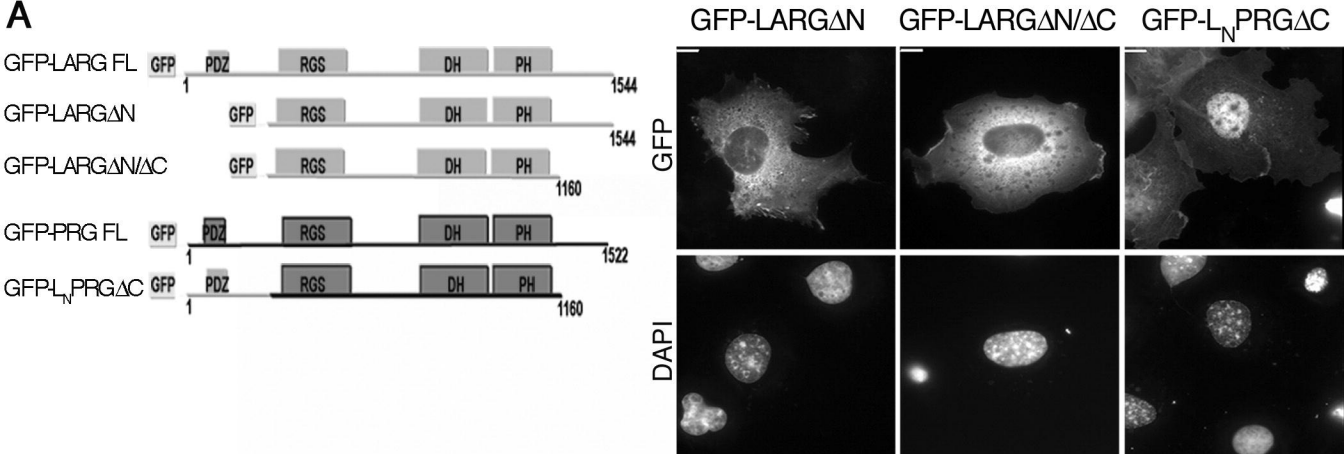


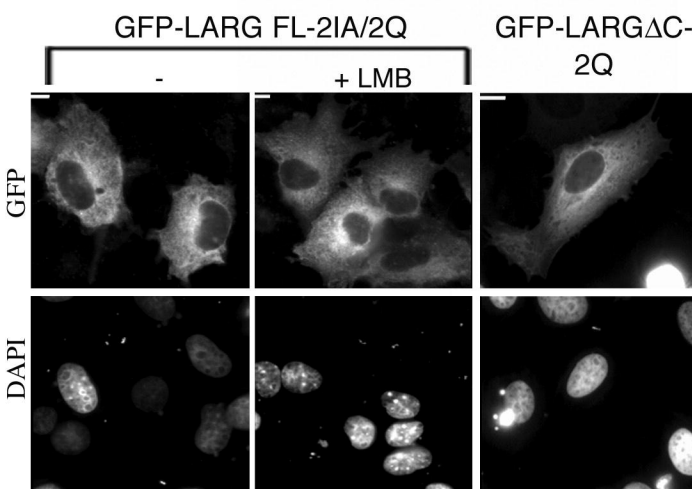
Figure 4



B

LARG 1MSGTQSTITDRFPLKKPIRHGSILNRESPTDKKQKVERIAS⁴¹
 **

C



D

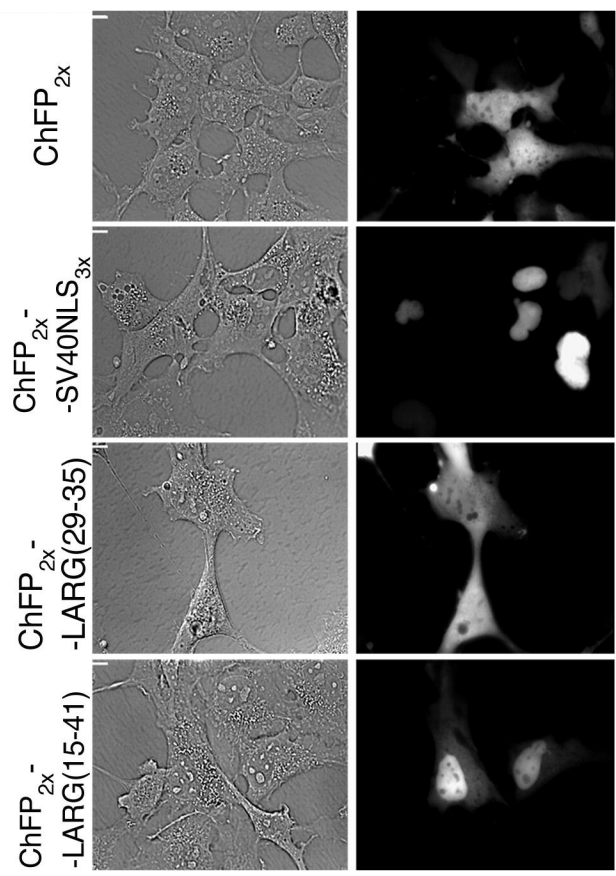
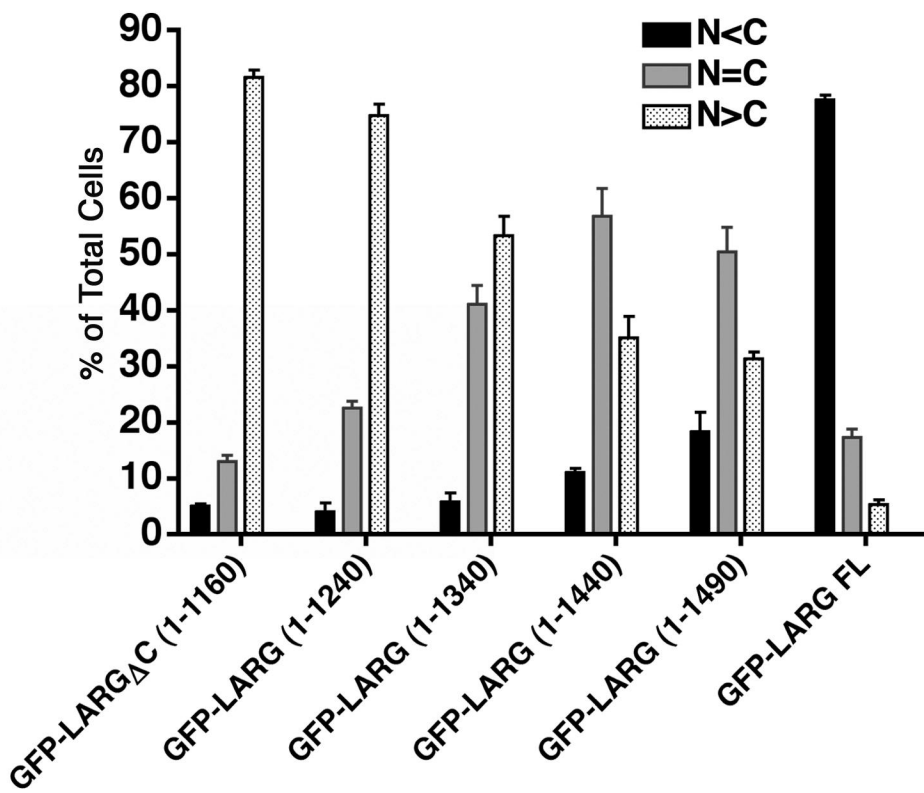


Figure 5

A



B

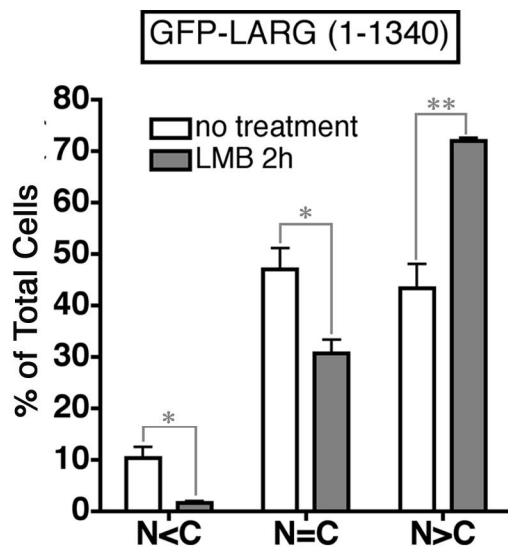


Figure 6