

REVIEW



Rab proteins as major determinants of the Golgi complex structure

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ABSTRACT

GTP-ases of the Rab family (about 70 in human) are key regulators of intracellular transport and membrane trafficking in eukaryotic cells. Remarkably, almost one third associate with membranes of the Golgi complex and TGN (*trans*-Golgi network). Through interactions with a variety of effectors that include molecular motors, tethering complexes, scaffolding proteins and lipid kinases, they play an important role in maintaining Golgi architecture.

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Introduction

The Golgi complex is at the crossroad between the biosynthetic/secretory pathway and the endocytic pathway. Although it adopts an apparently stable organization (Golgi stacks) at the steady state, it is a highly dynamic organelle. For instance, Golgi resident enzymes have been proposed to recycle continuously to pre-Golgi compartments and the endoplasmic reticulum (ER), although the extent of this recycling is still a matter of debate.^{75,83} Late Golgi and TGN membranes are, at least in part, consumed to produce post-Golgi transport carriers. The morphology of the Golgi at steady state thus relies on a tightly regulated balance between membranes arriving or leaving at its *cis*-side and membranes arriving or leaving at its *trans*-side.

GTPases of the Rab family (about 70 members in human) are master regulators of vesicular transport and membrane trafficking in eukaryotic cells. By interacting with a wide variety of effectors, that include molecular motors, tethering complexes, scaffolding proteins and lipid kinases, they regulate virtually all transport steps of vesicular traffic between cell compartments, from the biogenesis of transport carriers to their movement along the cytoskeleton and their tethering with target membranes (for reviews, see^{34,82}). Remarkably, about one third of known human Rabs have been found associated with membranes at the ER/Golgi/TGN level (for review, see.⁴² Since they regulate in and out as well as intra-Golgi trafficking, Rab proteins are expected to have a major role in Golgi architecture and maintenance, and

functional alterations of several Rabs and Rab-interacting proteins, in particular Rab effectors, have been shown to disrupt Golgi morphology (see Fig. 1 and Table 1).

Several excellent reviews have recently addressed the role of Rab GTP-ases in Golgi organization and function.^{44,64,73} Our goal here is to summarize and discuss the recent literature on this topic. We will distinguish three groups of Rabs, those associated to the *cis*-side of the Golgi complex/intermediate compartment (IC), those associated towards the late Golgi/TGN/post-Golgi/endosome and secretory vesicles, and those primarily associated with Golgi membranes (“*bona fide*” Golgi Rabs).

- Pre-Golgi and cis-Golgi Rabs (Rab1, Rab2, Rab18, Rab41/Rab6d, Rab43)

The best known Rab that regulates pre-Golgi membrane trafficking events is Rab1 (Ypt1 in yeast *S. cerevisiae*). The Rab1 family comprises two isoforms with a high degree of sequence similarity (~92 and 86%, respectively), Rab1a and Rab1b. Rab1a and Rab1b have long been thought to fulfill redundant functions but a recent study suggests that it may not be the case as Golgi fragmentation induced by Rab1a siRNA cannot be rescued by overexpression of Rab1b.¹

Rab1b was originally found associated with ER and Golgi.⁶⁶ Later studies showed that Rab1a and Rab1b are predominantly associated with membranes of the so-called IC, an ERGIC53/p58 positive, network of

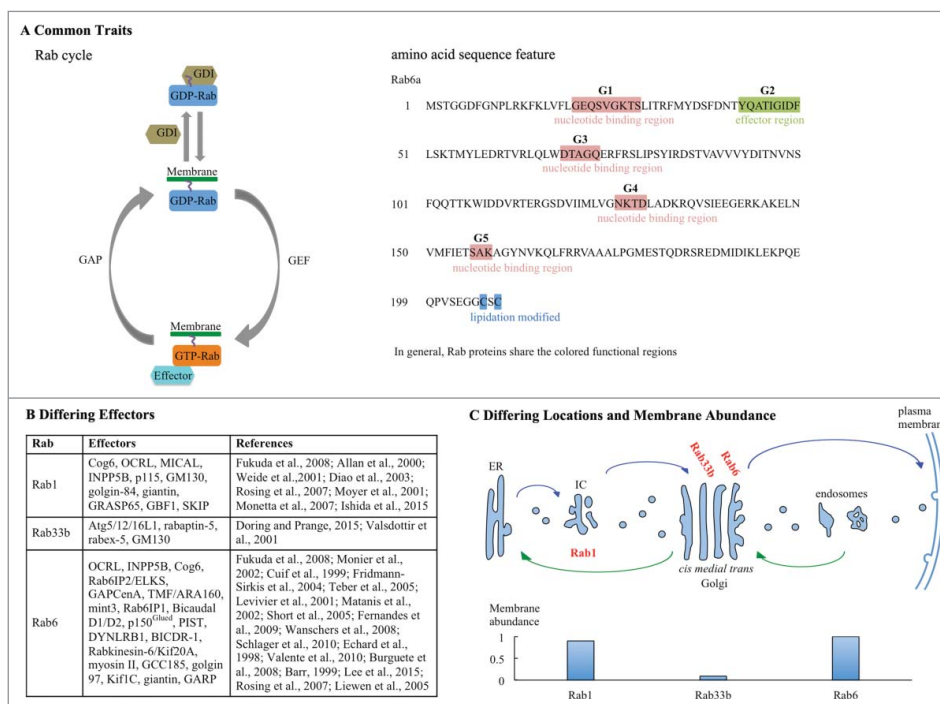


Figure 1. Illustrative shared and distinguishing traits of Golgi important Rab proteins. Rab proteins share a GTPase cycle between nucleotide-bound, membrane associated and –free states and functional amino acid motifs colored as indicated in (A). However, activated Rab proteins recruit distinct effectors to regulate their respective pathways (B). As indicated in (C). Rab proteins have distinct locations with respect to the Golgi complex and vary in abundance as quantified for purified cell fractions.^{8,10,13,15,17,19,21,22,28,30,39,40,41,54,56,57,58,68,76,79,86,90,93,94}

pleomorphic membranes located between ER exit sites (ERES) and Golgi.⁷² Whether IC is a transient and motile compartment that gives rise to *cis*-Golgi cisternae or whether it is a stable compartment connected by bi-directional vesicular traffic with ER and Golgi is still a matter of debate. Depending on the model, the functions of Rab1 could be slightly different: in the biogenesis of ER-derived COPII vesicles and the tethering of COPII vesicles and/or COPII positive IC membranes with *cis*-Golgi,² or primarily in the formation of membrane domains on the IC and of a specialized IC sub-compartment next to the centrosome called pcIC (for review, see⁷³).

As with Ypt1p in yeast,³⁷ Rab1, at least Rab1b, appears also to be involved in COPI-dependent retrograde transport between Golgi and ER.⁴ Rab1 function in this pathway could rely on its interaction with GBF1, the exchange factor for Arf1 involved in the biogenesis of COPI vesicles.⁴ Finally, Rab1 has also been shown to be involved in intra-Golgi transport⁶⁶ but this function remains poorly characterized, in Golgi bypass pathways,⁷¹ in transport of melanosomes,³⁵ and recently in actin-based remodeling of ER and Golgi membranes through its interaction with WHAMM.⁶⁹

The pivotal role of Rab1 in bi-directional transport between ER and Golgi explain why alteration of Rab1 function(s) has a strong effect on Golgi morphology. The

microinjection of GDP-bound form of Rab1a (S25N) or a mutant defective in guanine nucleotide binding (N124I) causes Golgi disassembly.⁹⁶ Similar effect is observed by overexpressing the dominant-negative forms of Rab1a and Rab1b^{61,66,88} or following Rab1 depletion by siRNA.⁵ Golgi collapse is also observed by overexpressing TBC1D20, a Rab1 GAP *in vivo*.³² However, Golgi collapse following inhibition of Rab1 function is stronger than that observed after the inhibition of the other players of the ER to Golgi transport pathways such as Sar1 or the tethering factor p115, a Rab1 effector.^{2,32} This is likely because Rab1 is not solely involved in ER to Golgi anterograde pathway (see above). The overexpression of Rab1b was also shown to cause Golgi enlargement.⁶⁷ Interestingly, this enlargement is likely due to increased expression of genes encoding proteins involved in membrane transport or Golgi structure, such as *GM130*, *GRASP65*, and *GRASP55*.⁶⁷

The role of Rab1 in the maintenance of Golgi architecture has been recently confirmed by two high-content siRNAs-based screens. In HeLa cells, depletion of Rab1a and Rab1b causes, similar to that of Rab2 (see below), a strong fragmentation of the Golgi complex.²⁵ Similar results were obtained in HeLa-S3 cells by Aizawa and Fukuda.¹

Another important player in pre-Golgi trafficking is Rab2. Rab2 family comprises two isoforms, Rab2a and Rab2b. As for Rab1, a recent study showed that Rab2a and

Table 1. Effect of altered rab expression on golgi ribbon organization.

Rab Localization	Overexpression			Golgi organization		Mutation
	Wild Type Rab	GTP-bound Rab	GDP-bound Rab	KD	KO	
Pre-Golgi and cis-Golgi						
Rab1	Golgi stable	Golgi unstable Golgi ribbon fragmentation	Golgi unstable, Golgi ribbon fragmentation	KD similar to overexpression results		NR
Rab2		Overexpression of the Rab2 GAP results in the accumulation of Golgi proteins in the ER.		Golgi ribbon fragments in response to Rab2a and Rab2b knockdown.		
Rab18	Golgi protein accumulation near ER exit sites with WT or GTP-bound Rab18		Golgi stable			
Rab41/Rab6dGolgi	Golgi stable		Golgi ribbon fragmentation			
Rab43	Golgi fragmentation		Golgi proteins redistribute to ER exit site adjacent			
Late Golgi/TGN and post Golgi						
Rab3	In most cases, depletion or alteration in function of these Rabs has little to no effect on Golgi organization. Summary outcomes are given for only those Rabs having a distinct effect.					
Rab7b						
Rab8						
Rab9a/b						
Rab10						
Rab11a						
Rab13						
Rab14						
Rab21						
Rab22b/Rab31	Golgi stable		TGN46 distribution disrupted	KD similar to overexpression results		
Rab29			Golgi stable			
Rab39a			Golgi unstable, TGN fragmentation			
"Bona fide" Golgi distal association						
Rab6	Golgi unstable Proteins relocalize to ER	Golgi unstable Proteins relocalize to ER	Golgi stable, if anything, more compact	Golgi stable, by EM longer stacks	KO embryonically lethal in mice, longer Golgi stacks in MEFs	NR
Rab19						
Rab30						
Rab33b	Golgi stable	Golgi unstable Golgi fragmentation and Golgi proteins relocalize to ER	Golgi stable	Golgi stable	NR	Rab protein mutations destabilizing mutations fragment Golgi and cause skeletal deformations in humans
Rab34						
Rab36						
Rab39b						
Abbreviations						
KD, knockout; KO, knockout; MEF, mouse embryonic fibroblasts; NR, no report						
References						
Pre-Golgi and cis Golgi Rabs						
Rab1 ^{1,2,5,6,1,6,6,88,96} Rab2 ^{22,25,1} Rab18 ¹⁴ Rab41/Rab6d ⁴² Rab43 ^{14,23,12}						
Late Golgi/TGN and post Golgi Rabs						
Rab3 ^{2,5} Rab8b ¹ Rab21 ^{2,5} Rab22b/Rab31 ^{2,5} Rab29 ⁹¹						
"Bona fide" Golgi distal associated Rabs						
Rab6 ^{6,49,84} , Rab33b ^{91,3,6,81,3,18,70}						

Rab2b may have non-redundant role in Golgi morphology, which is supported by the identification of Rab2b-specific effector, GARI-L4, involved in Golgi compaction.¹

Although the precise localization of Rab2 has been less investigated than that of Rab1, the two proteins appear to mainly associate with similar compartments at steady state, i.e. the IC and *cis*-Golgi membranes (for review, see⁷³). Rab2 was originally found to work, like Rab1, in the anterograde transport pathway between ER and Golgi.⁸⁸ However, later work suggested that Rab2 could primarily function in the opposite direction (Golgi to ER). In support of this hypothesis, Rab2 was shown to promote the formation of retrograde COPI vesicles, in conjunction with two of its known effectors, an atypical kinase C iota/lambda (aPKC) and glyceraldehyde-3 phosphate dehydrogenase (GAPDH).⁸⁹

Evidence also exists that Rab2 plays additional roles at the Golgi level. Active Rab2 (GTP-bound) was shown to directly interact with golgin-45 and both proteins form a complex with GRASP55.⁷⁸ Rab2 also interacts with other Golgins, including GCC185 and GMAP-210.^{33,80} Golgins are long coiled-coil proteins that specifically localize to *cis*, medial and *trans* Golgi membranes. An elegant recent study by Wong and Munro⁹⁷ showed that Golgins can, like tentacles, capture *in vivo* transport vesicles from different origins (ER or endosomes-derived as well as intra-Golgi vesicles) and thus act as tethers of transport vesicles with Golgi membranes. In addition to Rab2, Golgins bind several other Rabs (see below), mostly through their coiled-coil regions, but the significance of Rab binding remains unclear. Concerning Rab2, it was shown that GMAP-210 recruits transport vesicles via its N-terminus ALPS domain and that Rab2 binding occurs in the central coiled-coil region of GMAP-210 and downstream of vesicle tethering.⁷⁴ A tentative hypothesis is that Rab2 binding promotes a conformational change of GMAP-210, allowing the Rab2 positive transport vesicles to get closer to the Golgi membranes. Flexibility has been recently documented for another Golgin, GCC185.¹¹

In contrast to Rab1, the role of Rab2 in Golgi architecture has not been extensively investigated. However, the overexpression of the Rab2 GAP, TBC1D20, induces the redistribution of Golgi-resident enzymes to the ER.³² Depletion of golgin-45 disrupts the Golgi apparatus⁷⁸ and GMAP-210 is required for Golgi assembly.⁷⁴ Finally, Rab2 depletion by siRNAs was found to strongly disrupt the Golgi in the two high-content siRNAs-based screens mentioned above.

Three other proteins, Rab18, Rab43 and Rab41/Rab6d, have also been implicated in pre-Golgi trafficking events. Rab43 was found associated with several membranes (ER/Golgi in;¹⁴ medial Golgi in;¹² TGN in.²³ Several regulatory functions have thus been attributed to Rab43, including ER to Golgi anterograde trafficking,

perhaps through an interaction with the dynein/dynactin complex,¹⁴ retrograde transport between endosomes and TGN (using Shiga toxin as a marker of this pathway)²³ and anterograde trafficking of a subset of membrane cargo through the medial Golgi.¹²

Whatever at which steps of transport Rab43 exactly plays a role, the alteration of its function has strong effects on Golgi morphology. The overexpression of the dominant-negative mutant of Rab43 (GFP-Rab43-T32N) results in the redistribution of various Golgi/TGN markers, including GM130, Mannosidase II and TGN46 into scattered punctae colocalizing with ERES, a phenotype reminiscent of that obtained upon disruption of microtubules with nocodazole.¹⁴ High overexpression of GFP-Rab43 causes the fragmentation of ManII and giantin-positive compartments. Fragmentation of GM-130 and TGN46 positive compartments was also observed in cells overexpressing RN-tre, proposed to act as a GAP (GTP-ase activating protein) for Rab43 *in vivo*.³²

Less information is available on Rab18 and its exact function(s) remain(s) poorly characterized. Rab18 seems to be predominantly associated with ER membranes,^{14,26,47} and to lipid droplets.⁶³

Overexpression of GFP-Rab18 or the activated mutant Rab18 Q67L (but not GFP-Rab18S22N) causes a redistribution of Golgi markers near ER-exit sites (ERES) and Rab18 depletion fragments the Golgi.¹⁴ These findings support a role for Rab18 in COPI-independent Golgi to ER transport.¹⁴ Of note, the other functions attributed to Rab18 are regulation of lipid transport and ER architecture.^{26,47}

Rab41, also termed Rab6d,⁴³ shares 60% similarity with other members of the Rab6 family (80% in its central region). Depletion of Rab41 by siRNA or the overexpression of the GDP-bound forms inhibit transport of VSV-G between ER and Golgi without having an effect on retrograde transport between endosomes and Golgi.⁴³ Both treatments have a profound effect on the organization of the Golgi ribbon, which is fragmented into a cluster of punctate elements. This suggests a direct role of Rab41 in Golgi architecture. Recently, three Rab41 effectors were identified (dynactin 6, syntaxin 8, and Kif18A), and depletion of two of them (dynactin 6 and syntaxin 8) give a phenotype similar to Rab41 knock-down, suggesting that they are involved in Golgi organization.⁴⁵

- Late Golgi/TGN and post-Golgi Rabs (Rab3, Rab7b, Rab8, Rab9a/b, Rab10, Rab11a, Rab13, Rab14, Rab21, Rab22b/Rab31, Rab29, Rab39a)

Many Rabs have been associated to late Golgi/TGN compartments. They include Rab7b, Rab8, Rab9a/b, Rab10, Rab11a, Rab13, Rab14, Rab29, Rab31/Rab22b, and

Rab39a. However, these Rabs localize primarily to endosomal compartments (although their steady state localization may vary from one cell type to another), reflecting the dynamic nature of the interface between late Golgi/TGN membranes and endosomes.

Members of the Rab6 family also localize to late Golgi/TGN membranes and to post-Golgi vesicles. However, Rab6 does not associate with endosomal membranes and regulates intra-Golgi and Golgi to ER trafficking. Rab6 will be thus considered as a “bona fide” Golgi Rab (see next paragraph).

The Rab GTPases mentioned above have been implicated in many transport pathways that have been reviewed elsewhere.^{9,16,55,60,82} In most cases, the depletion or the alteration of the function (s) of these GTPases have no effect or much less pronounced effect on Golgi morphology than of those located at the ER-Golgi interface. This suggests that the regulation of membrane flux at the late Golgi/TGN-endosome interface is not playing a major role in the regulation of Golgi morphology. Alteration of Golgi morphology (Golgi fragmentation) have been however observed following Rab8a depletion¹ but the significance of this result remains unclear.

A role for Rab22b/Rab31 and Rab29 in TGN morphology have also been documented.^{59,92} However, the functions of these GTP-ases are very poorly known and how they regulate TGN morphology remain to be investigated.

Of note, it was recently shown, unexpectedly, that depletion of members of the Rab3 family (Rab3a-d) and that of Rab21, a protein that associates with early endosomes, affects Golgi morphology.²⁵ The possible reasons for such an effect are discussed in this article.

- “Bona fide” Golgi Rabs (Rab6, Rab19, Rab30, Rab33b, Rab34, Rab36, Rab39b)

Several Rab proteins localize almost exclusively to the Golgi and might well be considered to be « bona fide » Golgi Rabs. They include Rab19, Rab30, Rab33b, Rab34, Rab36, and Rab39b. Rab34 and Rab36 interact with the Rab7a effector RILP and regulate the spatial distribution of late endosomes, lysosomes and melanosomes.⁵¹ Rab39b is preferentially expressed in brain and mutations in the *RAB39b* gene are associated with neuronal diseases²⁷. Rab39b was recently shown to regulate ER to Golgi trafficking of the GluA2 receptor.⁵² Very little is known about Rab19 and Rab30 functions. To our knowledge, the contribution of Rab19, Rab30, Rab34, Rab36 and Rab39b to Golgi architecture has not been investigated, except for Rab30 whose depletion impacts Golgi morphology.³⁸ Of note, Rab19 and Rab30 interact with Golgins.⁸⁰

The Rab33 family comprises two isoforms, the b isoform being ubiquitously expressed at relatively low levels²⁸ while the a isoform is only expressed in brain and cells of the immune system. Rab33b localizes to the medial Golgi cisternae.¹⁰¹ Rab33b has been implicated in Golgi-to-ER retrograde transport^{36,90} but also in autophagy as it directly interacts with Atg16L.²⁴

The overexpression of wild-type Rab33b or its GTP-locked form induces the redistribution of Golgi enzymes into the ER.^{36,91} Evidence exists for a functional connection between Rab6 (see below) and Rab33b, possibly through a Rab6/Rab33b « cascade ». This Rab cascade may contribute to Golgi compartmentalization and membrane domain formation as suggested by Pfeiffer.⁶⁵ These points are discussed in detail in a recent review.⁴⁴ In humans, mutations in Rab33b that affect GTP-binding results in vastly decreased protein abundance and defects in skeletal formation and early death.^{3,18}

The best studied Golgi associated protein Rab, and the most abundant, is Rab6 (Ypt6p in yeast). We take this example as being illustrative of the extent to which we understand the relative role of local Rab recruited protein machines in Golgi structure/function relationships.

The type member of the Rab6 family, Rab6A, was discovered almost 30 years ago^{29,100} and the encoding gene has been shown to be essential to mammalian development *in utero*.⁷⁷ The Rab6 family comprises 4 proteins, named Rab6A, Rab6A', Rab6B and Rab6C. Rab6A' is generated by alternative splicing of the *RAB6A* gene and differs from Rab6A by only three amino acids.²⁰ Both proteins are ubiquitously expressed and are together the most abundant Golgi-associated Rab protein.²⁸ Rab6B is encoded by a separate gene and is mostly expressed in neurons and neuroendocrine cells.⁶² The exact function of the neuronal isoform Rab6B is unknown. *RAB6C* is a primate-specific retrogene transcribed in a limited number of human tissues. It encodes a protein with altered biochemical properties compared to other Rab6 isoforms that localizes to centrosome and is involved in cell cycle progression.⁹⁹ A slightly more distant protein, Rab41, can be considered to be a 5th member of the Rab6 family.⁴³

Numerous studies have established the essential role played by Rab6A/A' in the regulation of several transport steps at the level of the Golgi complex, including retrograde transport between endosomes and the endoplasmic reticulum via the Golgi complex, anterograde transport between Golgi and the plasma membrane, as well as in the homeostasis of Golgi membranes.^{31,46,48,49,50,84,95} As expected, these multiple roles in Rab6 in Golgi derived trafficking are then mediated by the recruitment of a wide array of Rab6 effector proteins to the Golgi complex. At least 15 different Rab6 effectors

have been identified.^{7,30} In a manner not well understood yet, effector recruitment must be localized and context sensitive. In brief, Rab6 can and does promote the formation of localized, multicomponent protein machines that initiate and sustain individual Golgi trafficking pathways. Probably the best studied case is the myosin II, Rab6, Kif20A complex at the trans Golgi/TGN. This complex forms locally and promotes the extension of Golgi derived tubules and the eventual release of vesicles,^{53,54}). In the depth study of this complex holds great promise of answering the question of how local, context sensitive Rab action can occur. This is an important and general problem in both secretory and endocytic pathways as Rab protein in general have many effectors.

Considering the numerous roles of Rab6 in Golgi associated trafficking events, one might expect that Rab6 depletion or alteration of its functional state would produce little net effect on Golgi morphological organization as the various individual effects would cancel one another out. In the case of Rab6 inactivation, GDP-locked Rab6 T27N overexpression^{36,48,85,98} or Rab6 depletion through siRNA treatment,^{84,97} the effects seen by light microscopy appear slight. There is a slight compaction of the juxtannuclear Golgi ribbon and a delay, but no strong inhibition, in anterograde and retrograde transport through the organelle (e.g.⁸⁴). The length of cisternae however increases by about 2x fold in si-RNA depleted cells and in MEFs derived from Rab6 knock-out mice.^{6,84} In HeLa cells, Rab6 depletion also leads to an increase in the number of Golgi stacks.⁸⁴ Considering the wide variety of trafficking pathways supported by Rab6, this outcome might well be considered to be the expected result. Both anterograde and retrograde trafficking pathways should be slowed. In net, the balance between trafficking pathways appears to be roughly maintained. However, in striking contrast, overexpression of wild type Rab6 or GTP-locked Rab6 results in a BFA-like Golgi phenotype; Golgi resident proteins redistribute to the endoplasmic reticulum,^{36,49} a result that strongly indicates a preferential biasing of Golgi trafficking pathways towards retrograde trafficking to the ER. How might this outcome be explained? We propose that the most plausible explanation is that the binding constants of various Rab6 effectors varies significantly and hence as the expression of wild-type or GTP-locked Rab6 is increased the importance of relatively weak or minor pathways is over emphasized. If so, this would suggest that the effector(s) prompting retrograde trafficking to the ER have comparatively low binding constants. To date the determination of effector has been a qualitative, yes or no, experiment. Comparative quantitative data on effector binding might well make possible a

systems biology approach to the prediction of the various pathways as Rab6 is titrated.

- Conclusions and perspectives

The roughly 20 Rab GTPases discussed here relative to the regulation and maintenance of Golgi complex structure all share certain common features such as the underlying biochemistry of the GTPase cycle and shared protein sequence and folding features (Fig. 1A). Initially, these common features were very helpful in the search for new family members, an important stage in the development of the field. However, as should be apparent from our enumeration of the roles and functions of varied Golgi-associated Rab proteins, the challenge today is different. A major aspect is to understand how individual Rab proteins modulate the activity of distinct and context-sensitive protein machines while at the same time giving attention to how multiple machines can be integrated to give functionality within the cell, for example, to determine Golgi complex structure. To understand the even simplified individuality apparent and summarized in Fig. 1B-C, we suggest that research efforts must go to both “drilling down” at the level of individual process and biochemistry and integrating through a systems biology approach quantification determinations and modeling to reveal patterns of action and how they change with increased or decreased Rab protein levels. Hence, we suggest in the previous section of this review that Rab6 and an individual context sensitive process such as myosin II dependent vesicle formation may be an attractive example for the drill down approach. On the other hand, the question of how Rab6 overexpression leads to Golgi protein redistribution to the ER rather than transport to the plasma membrane, endosomes or lysosomes likely will require an integrative systems biology approach. We suggest in this case that weaker interactions are “ratched up” and determinative. This preferential ratching up then leads to redistribution to Golgi proteins to the ER. We note that today that there is no quantitative data to indicate the existence of weaker or stronger interactions that might be preferentially modulation in the overexpression case.

In sum, today we can only give the reader the qualitative answer that the role of Rab proteins in Golgi structure relies on their role in trafficking. We project that an understanding of specific, locality-sensitive roles of Golgi-associated Rabs will be a step towards transforming this situation. We suggest that the Rab6/myosin II interaction at the *trans*-Golgi/TGN is apt to be an illustrative example. Furthermore, an integrated understanding of the relative role of Rabs and in particular Rab effectors is likely in comparison to require quantitative

data from which model(s) of predictive value regarding Golgi phenotype could be made. Again, this would be a transformative step. In conclusion, we predict in 10 years that a review such as this will be a quantitative statement of how an individual Rab protein through multiple effectors produces an integrated Golgi phenotype. Considering the magnitude of the task, that outcome will likely require the effort of multiple laboratories.

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