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Two Rab7 isoforms, *EhRab7A* and *EhRab7B*, play distinct roles in biogenesis of lysosomes and phagosomes in the enteric protozoan parasite *Entamoeba histolytica*

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Summary

Rab7 small GTPase plays a crucial role in the regulation of trafficking to late endosomes, lysosomes and phagosomes. While most eukaryotes encode a single Rab7, the parasitic protist *Entamoeba histolytica* possesses nine Rab7. In this study, to understand the significance of the presence of multiple Rab7 isoforms, a role of two representative Rab7 isoforms, *EhRab7A* and *EhRab7B*, was investigated. *EhRab7B* was exclusively localized to acidic vacuoles containing lysosomal proteins, e.g. amoebapore-A and cysteine protease. This lysosome localization of *EhRab7B* was in good contrast to *EhRab7A*, localized to a non-acidic compartment in steady state, and only partially colocalized with lysosomal proteins. Overexpression of *EhRab7B* resulted in augmentation of late endosome/lysosome acidification, similar to the *EhRab7A* overexpression. Expression of *EhRab7B*-GTP mutant caused dominant-negative phenotypes including decrease in late endosome/lysosome acidification and missecretion of lysosomal proteins, while *EhRab7A*-GTP enhanced acidification but did not affect either intracellular or secreted cysteine protease activity. Expression of either *EhRab7B* or *EhRab7B*-GTP mutant caused defect in phagocytosis, concomitant with the disturbed formation and disassembly of prephagosomal vacuoles, the compartment previously shown to be linked to efficient ingestion.

Altogether, these data indicate that the two Rab7 isoforms play distinct but co-ordinated roles in lysosome and phagosome biogenesis.

Introduction

Lysosomes serve as a compartment to degrade endocytosed materials with various hydrolytic and degradative proteins. Lysosomes also play a role as a compartment to process, activate and store proteins secreted extracellularly (Mullins and Bonifacino, 2001; Bowers and Stevens, 2005). Among a number of molecules involved in the lysosome biogenesis, one of the most important players is Rab7 small GTPase (Mullins and Bonifacino, 2001). Roles of Rab7 are significantly divergent between organisms and cell types; Rab7 plays a role on several distinct steps of endosomal or lysosomal trafficking (Feng *et al.*, 1995; Meresse *et al.*, 1995; Vitelli *et al.*, 1997; Bucci *et al.*, 2000). In baby hamster kidney cells, Rab7 was shown to mediate the early-to-late endosomal transport (Feng *et al.*, 1995; Vitelli *et al.*, 1997), whereas in HeLa cells, Rab7 was mainly associated with lysosomes and involved in lysosome acidification and transport of lysosomal proteins, but not of late endosomal proteins (Meresse *et al.*, 1995; Bucci *et al.*, 2000). Moreover, Rab7 was also shown to be required for fusion of late endosomes and lysosomes with primary phagosomes in professional phagocytes (Vieira *et al.*, 2003). In yeast, Ypt7p, the yeast Rab7 homologue, was also shown to be involved in transport from the late endosomes to the central vacuole, the yeast lysosome equivalent, and to be required for homotypic fusion of the vacuoles (Wichmann *et al.*, 1992; Schimmoller and Riezman, 1993; Haas *et al.*, 1995).

While many uni- and multicellular eukaryotes including *Saccharomyces cerevisiae*, *Trypanosoma brucei*, *Plasmodium falciparum*, *Caenorhabditis elegans*, *Drosophila melanogaster*, human, encode a single Rab7 (Pereira-Leal and Seabra, 2001; Quevillon *et al.*, 2003; Ackers *et al.*, 2005; Berriman *et al.*, 2005), some protozoan parasites including *Trichomonas vaginalis* and *Entamoeba histolytica* have three to nine Rab7 isoforms (Lal *et al.*, 2005; Saito-Nakano *et al.*, 2005), which is similar to plants such as *Lotus japonicus* and *Arabidopsis thaliana*, having four

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to eight Rab7 isotypes (Borg *et al.*, 1997; Pereira-Leal and Seabra, 2001). In *L. japonicus*, some of Rab7 isotypes were expressed in a tissue-specific manner (Borg *et al.*, 1997), and also in *A. thaliana*, one of Rab7 isotypes was expressed tissue-specifically and its expression was induced by stress (Mazel *et al.*, 2004). However, the functional differences between Rab7 isotypes and biological significance of the redundancy in a unicellular organism have not been elucidated.

The unicellular enteric protist *E. histolytica* causes an estimated 50 million cases of amoebic dysentery, colitis and liver abscess in human, which leads to 100 000 deaths annually (Haque *et al.*, 2003; Huston, 2004). Among several factors including galactose/N-acetylgalactosamine (Gal/GalNAc)-inhibitable lectin (Vines *et al.*, 1998), the membranolytic peptide amoebapore (AP) (Leippe, 1999), and lysosomal hydrolase cysteine proteases (CP) (Que *et al.*, 2002) implicated for the multifactorial virulence mechanisms of *E. histolytica*, CPs are considered to be largely attributed to the pathogenesis of the parasite. Therefore, lysosome biogenesis that controls transport, maturation and secretion of CPs likely plays an important role in pathogenesis as well as housekeeping functions unrelated to parasitism and virulence in this organism (Nozaki and Nakada-Tsukui, 2006). *E. histolytica* has the largest number (96–106) of Rab GTPases, including nine of Rab7 isotypes, among organisms whose genome sequences are available (Welter *et al.*, 2002; Lal *et al.*, 2005; Saito-Nakano *et al.*, 2005). We have previously shown that one of Rab7 isotypes, *EhRab7A*, is involved in the transport of CPs, e.g. CP2, and AP to phagosomes via prephagosomal vacuoles (PPV), which are formed accompanied with phagocytosis, and likely serves to process, activate and store these lysosomal proteins prior to targeting to phagosomes (Saito-Nakano *et al.*, 2004). *EhRab7A* also regulates recycling of a CP receptor from phagosomes to the *trans*-Golgi network via interaction with the retromer-like complex (Nakada-Tsukui *et al.*, 2005; Nozaki and Nakada-Tsukui, 2006). However, a role of other Rab7 isotypes has not been elucidated. In this report, we describe that two Rab7 isotypes, *EhRab7A* and *EhRab7B*, play distinct but co-ordinated roles in lysosome biogenesis. To our knowledge, this is the first demonstration of distinct roles of Rab7 isotypes in lysosome and phagosomal biogenesis of unicellular organisms.

Results

All nine *EhRab7* isotypes are expressed under axenic culture conditions

Entamoeba histolytica encodes nine Rab7 isotypes, designated as *EhRab7A* to *EhRab7I* (Saito-Nakano *et al.*,

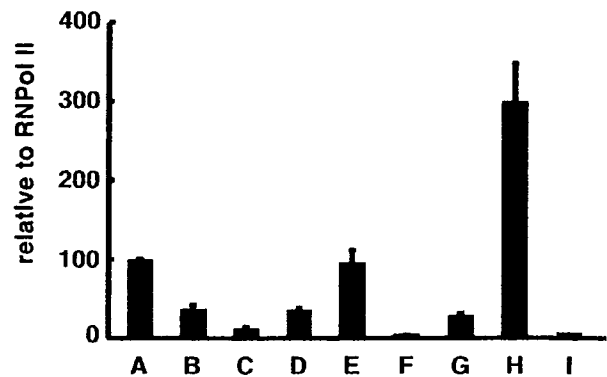


Fig. 1. Expression of nine *EhRab7* isotypes under standard axenic culture conditions. The quantitative RT-PCR was performed using mRNA from the amoeba trophozoites cultivated axenically, and the amount of mRNAs of each isotype was normalized relative to the amount of RNA polymerase II 15 kDa subunit. Relative values are shown in percentages. Error bars represent SD of two independent experiments.

2005), which is in marked contrast to mammals and yeasts, where only one Rab7/Ypt7p is encoded. These Rab7 isotypes showed 40–64% mutual identities and 32–56% identities to Rab7/Ypt7 homologues in other organisms, and designated alphabetically in a descending order of percentage identity to human Rab7 or yeast Ypt7. To validate that these Rab7 isotypes are transcribed, we measured the steady-state level of their transcripts under the axenic culture conditions. Quantitative real-time PCR (RT-PCR) showed that all nine *EhRab7* isotypes are expressed above the measurable level, verifying that none of these *EhRab7* genes is a pseudogene (Fig. 1). Six isotypes, i.e. *EhRab7A*, B, D, E, G and H, are expressed at the level of 0.3–3-fold of RNA polymerase II 15 kDa subunit while the three other isotypes were expressed at the lower level. The steady-state level of transcripts of *EhRab7F* and I was very low but reproducibly detectable (3.8% and 5.3% of RNA polymerase II 15 kDa subunit respectively). As *EhRab7B*, previously referred as 'a homologue of *Dictyostelium Rab7D*', was shown to be upregulated in the amoebae derived from an infected animal (Bruchhaus *et al.*, 2002), we also measured the level of steady-state transcripts of *EhRab7* isotypes in the animal liver-derived highly virulent HM1 strain (Mitra *et al.*, 2006). However, all *EhRab7* isotypes including *EhRab7B* remained unchanged upon the animal infection (data not shown). This result is consistent with our previous data showing that the amount of *EhRab7* isotypes associated with phagosomes were comparable between axenically cultured avirulent and animal-passaged highly virulent strains (Okada *et al.*, 2006). In this work, we describe characterization of *EhRab7A* and *EhRab7B*, and studies on the other *EhRab7* isotypes will be described elsewhere.

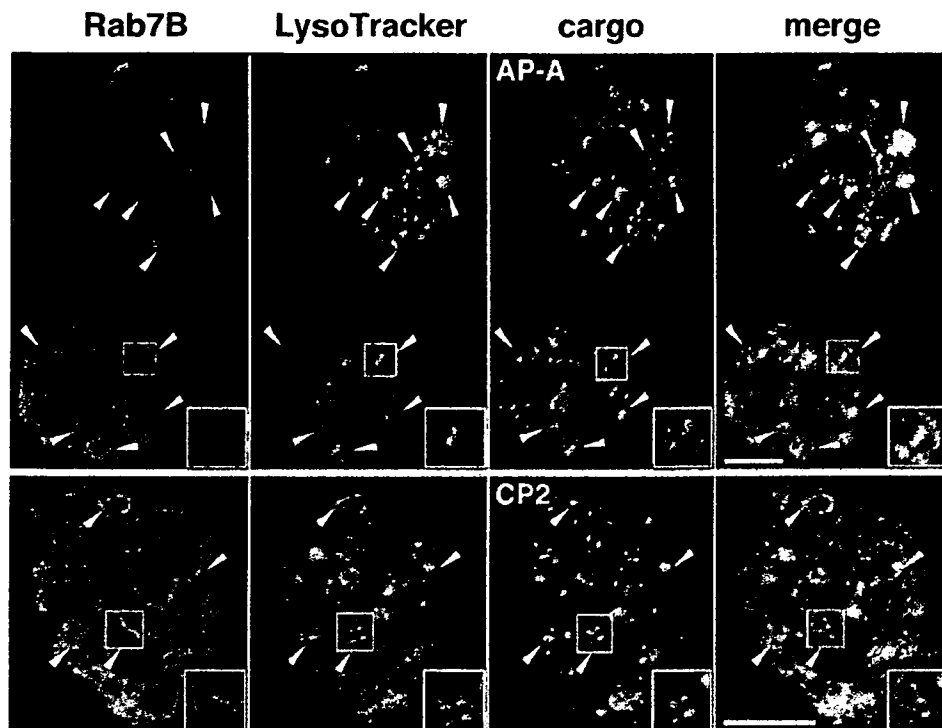


Fig. 2. Immunofluorescence analysis of *EhRab7B*. The HA-tagged *EhRab7B*-overexpressing transformant was incubated with LysoTracker Red, and subjected to immunofluorescence assay using anti-HA antibody and either anti-AP-A (upper panels) or anti-CP2 antibody (lower panels). Arrowheads indicate representative *EhRab7B*-positive vacuoles containing both LysoTracker and AP-A (upper) or both LysoTracker and CP2 (lower). Insets show magnified images of selected *EhRab7B*-positive vacuoles. Bars, 10 μ m.

EhRab7B is associated with late endosomes/lysosomes and is likely involved in lysosomal maturation

We examined subcellular localization of *EhRab7B* by immunofluorescence assay using a stable transformant that constitutively expressed three tandem haemagglutinin (3HA)-tagged *EhRab7B* (Fig. 2). In the transformant, *EhRab7B* was found to be associated with 1–4 μ m vesicles/vacuoles. Almost all ($93\% \pm 0.7\%$) *EhRab7B*-positive vesicles/vacuoles contained degradative proteins represented by AP-A and CP2, as well as LysoTracker Red, a membrane diffusible probe accumulated in acidic compartments (Bucci *et al.*, 2000). Contrarily, less than 50% of *EhRab7A*-positive vacuoles, when over-expressed, contained LysoTracker Red (Nakada-Tsukui *et al.*, 2005), suggesting that *EhRab7B* is probably located downstream of *EhRab7A* in the maturation of the post-Golgi compartment to lysosomes. The *EhRab7B*-associated vacuoles typically contained multi-vesicular structures that included the lysosome-resident proteins and the marker (Fig. 2, insets), which is similar to the structures previously demonstrated in the *EhRab7A* vacuoles containing endosomes enclosing the fluid-phase marker (Saito-Nakano *et al.*, 2004).

We also examined the localization of *EhRab7B* using the wild-type trophozoites and the anti-*EhRab7B* anti-

body affinity purified by the antigen-immobilized column. Immunoblot assay using anti-*EhRab7B* antibody showed a single 23 kDa band in the lysate of the wild-type trophozoites, and 23 and 27 kDa bands in the lysate of the *EhRab7B*-overexpressing transformant. The 27 kDa band was also detected with anti-HA antibody, suggesting that the 27 kDa band corresponds to the exogenous epitope-tagged *EhRab7B* (Fig. 3A). We roughly estimated by measuring signal of the bands by chemiluminescence assay that the amount of the epitope-tagged *EhRab7B* was eightfold higher than that of the endogenous protein (Fig. 3A). Immunofluorescence imaging with the affinity-purified anti-*EhRab7B* IgG revealed that intrinsic *EhRab7B* was associated with the periphery of lysosomes in wild-type cells (Fig. 3B). The localization of the intrinsic *EhRab7B* was similar to, but slightly different from that of the tagged-*EhRab7B* in the transformant. In the wild-type cell, enlarged lysosomes, often observed in the tagged-*EhRab7B*-expressing transformant (Fig. 2), were occasionally detected. Endogenous *EhRab7B*-associated vesicles/vacuoles were often ($93.5\% \pm 7.6\%$) associated with LysoTracker (Fig. 3B). We also verified that the apparent localization of *EhRab7B* in the epitope-tagged *EhRab7B*-expressing transformant demonstrated with anti-*EhRab7B* antibody was indistinguishable from that using anti-HA antibody

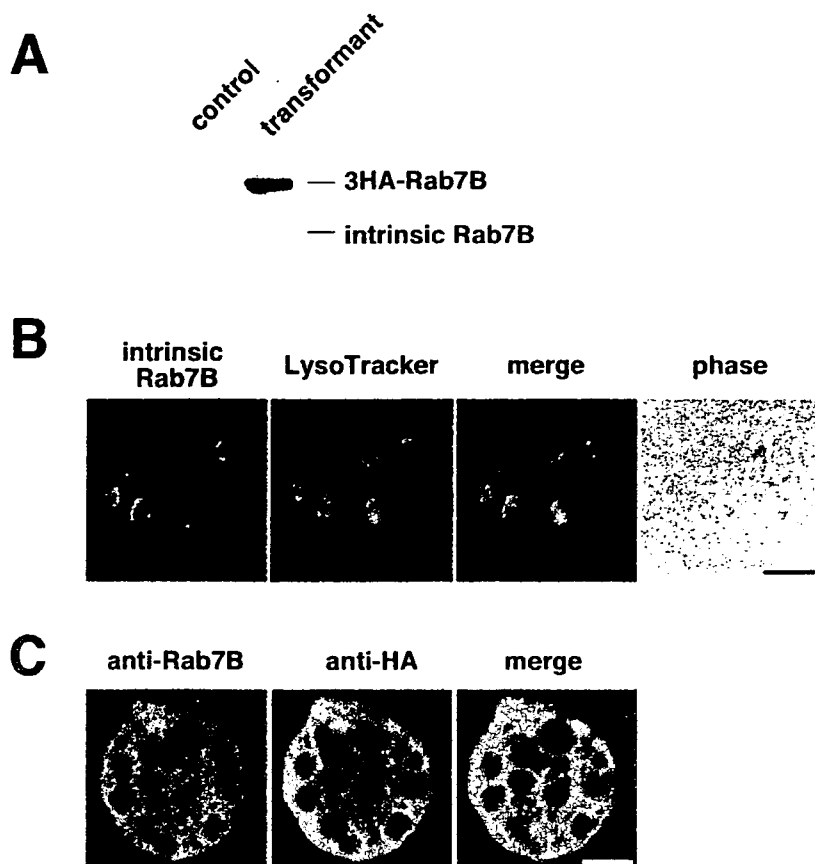


Fig. 3. Detection of intrinsic and epitope-tagged *EhRab7B* in wild-type and transformant trophozoites.

A. Immunoblot analysis of intrinsic and exogenous *EhRab7B* in wild-type cells (left) and the HA-tagged *EhRab7B*-overexpressing transformant (right) using affinity-purified anti-*EhRab7B* antibody.

B. Immunofluorescence imaging of intrinsic *EhRab7B* in wild-type cells. Lysosomes were stained with LysoTracker Red (red) and intrinsic *EhRab7B* was visualized with anti-*EhRab7B* antibody (green).

C. Detection of *EhRab7B* with anti-*EhRab7B* (green) and anti-HA (red) antibodies in the HA-tagged *EhRab7B*-overexpressing transformant. Bars, 10 μ m.

(Fig. 3C). Taken together, these data suggest that *EhRab7B* is primarily associated with late endosomes/lysosomes, and involved in the maturation of the acidic compartment, and that overexpression of *EhRab7B* caused enhancement of late endosome/lysosomal fusion and enlargement of lysosomes.

To investigate a role of *EhRab7B* in lysosome maturation, the total cellular acidity of the *EhRab7B*-overexpressing and control transformants was measured by fluorescence-activated cell sorter (FACS) analysis of the LysoTracker-stained cells (Fig. 4). The LysoTracker staining significantly increased by *EhRab7B* overex-

pression; the peak channel increased from 29 ± 4.5 in the control transformant to 43 ± 2.1 in the *EhRab7B*-overexpressing transformant (Fig. 4, left; $P = 0.038$ by Student's *t*-test), indicating that *EhRab7B* overexpression increased the volume of the acidic compartment, which is likely attributable to enhanced homotypic or heterotypic lysosome fusion. Similarly, overexpression of *EhRab7A* resulted in an augmented formation of *EhRab7A*-positive vesicles/vacuoles and an increased cellular acidity (Nakada-Tsukui *et al.*, 2005). Expression of a GTP-form (H69L), corresponding to human Rab7-GTP mutation, of *EhRab7B* (*EhRab7B*-GTP) slightly reduced the total cel-

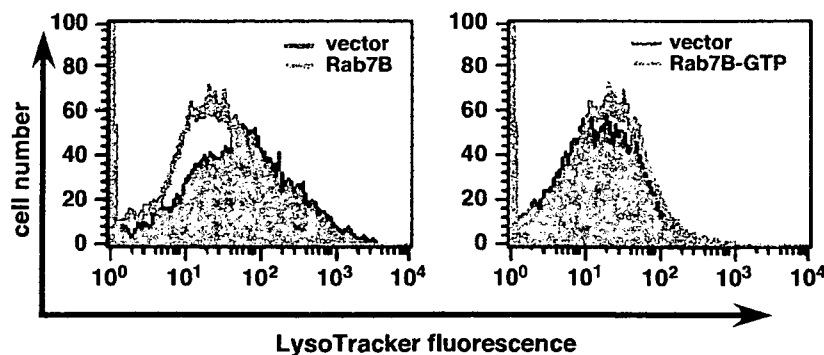


Fig. 4. Histograms of LysoTracker-stained trophozoites of *EhRab7B*- (left panel, purple), *EhRab7B*-GTP-overexpressing (right panel, purple), and control (vector) (both panels, green) transformants by FACS analysis. The transformants were stained with 2 μ M LysoTracker Green for 30 min and then analysed on FACS.

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lular acidity (peak channel, 24 ± 3.5 ; $P=0.04$ versus the control transformant, Fig. 4, right), which is likely a dominant-negative effect. In contrast, expression of *EhRab7A-GTP* further increased the cellular acidity (data not shown), similar to human Rab7-GTP mutant (Bucci *et al.*, 2000).

EhRab7B-GTP form mutant is partially defective in membrane association

Function of Rab proteins is modulated by hydrolysis and exchange of bound guanine nucleotides (i.e. GTP-bound active and GDP-bound inactive states) (Novick and Zerial, 1997). A majority of GTP-bound Rab proteins are associated with the membrane, and potentially capable of interacting with effectors, while GDP-bound Rab proteins are complexed with GDP-dissociation inhibitor and localized in the cytosol. To better understand the cause of the acidification defect caused by *EhRab7B-GTP*, we fractionated the total lysate prepared by mechanical homogenization. Immunoblot analysis revealed that only a half ($58\% \pm 5.6\%$) of *EhRab7B-GTP* was recovered in the 100 000 *g* pellet (membrane) fraction, while a majority ($86\% \pm 3.5\%$) of wild-type *EhRab7B* was detected in this fraction (Fig. 5). These results indicate that membrane association of *EhRab7B-GTP* form is partially hampered.

Immunofluorescence imaging of the *EhRab7B-GTP*-expressing transformant (Fig. 6A) showed that *EhRab7B-GTP* was localized in the cytosol or tiny vesicles throughout the cell in steady state. The *EhRab7B-GTP* colocalization with the compartment associated with the lysosomal proteins and marker (AP-A, CP2, and LysoTracker) was less pronounced (Fig. 6B) than that for the wild-type *EhRab7B* (Fig. 2). These results were consistent with the defect of membrane association of *EhRab7B-GTP* (Fig. 5).

Expression of *EhRab7B-GTP* form mutant causes missorting of lysosomal proteins

To reveal the precise role of *EhRab7B* in lysosome biogenesis, we next examined if transport of lysosomal cargo proteins, i.e. AP-A and CP2, is affected by overexpression of *EhRab7B* wild type or GTP-form mutant. AP-A and CP2 were very well colocalized with LysoTracker in the *EhRab7B*-overexpressing transformant (see above, Fig. 2A). In the *EhRab7B-GTP* transformant, the colocalization of the lysosomal cargo proteins and LysoTracker remarkably decreased (Fig. 6B; $P=0.013$ or 0.007 for CP2 or AP-A respectively), suggesting that *EhRab7B-GTP* expression caused either hindrance of transport or mistargeting of the lysosomal proteins.

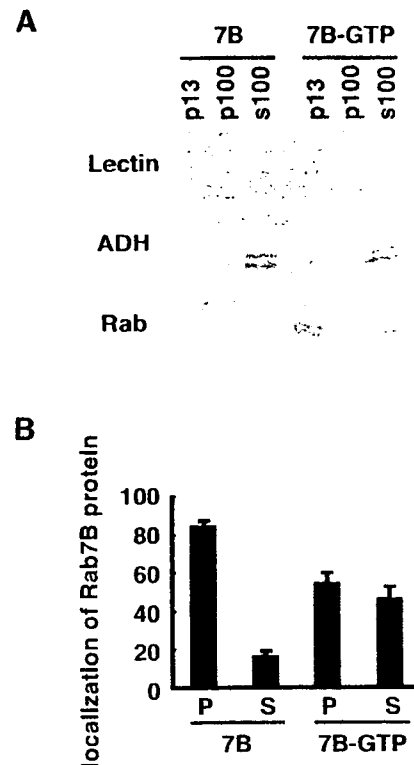


Fig. 5. Subcellular fractionation of *EhRab7B* and *EhRab7B-GTP*. **A.** Fractionation of the lysates from the *EhRab7B* and *EhRab7B-GTP* transformants. Amoebic total homogenate was separated into low-speed pellet (p13), high-speed pellet (p100) and supernatant (s100) fractions, and these fractions were subjected to immunoblot analyses using the following antibodies: anti-HA antibody to probe *EhRab7B* and *EhRab7B-GTP* (Rab), anti-Gal/GalNAc-inhibitable lectin antibody (Lectin), anti-alcohol dehydrogenase (ADH) antibody, the latter two of which were used as a marker for the membrane or cytosolic protein respectively. **B.** Quantification of *EhRab7B* and *EhRab7B-GTP* in the fractions separated by differential centrifugation as in (A) by chemiluminescence measurement with LAS3000 Lumi-Imager.

We next measured both secreted and intracellular CP activities of the *EhRab7B*-, *EhRab7B-GTP*-overexpressing, and control transformants. The CP activity secreted to the medium by the *EhRab7B-GTP* transformant was 4.3-fold higher than the control transformant (Fig. 6C, right) ($P=0.0016$). Moreover, the *EhRab7B-GTP* transformant had a 38% less total intracellular CP activity than the control transformant ($P=0.012$) (Fig. 6C, left). In contrast, neither secreted nor intracellular CP activity significantly changed in the *EhRab7B*-overexpressing transformant. To ensure CP production *per se* was not affected by *EhRab7B-GTP* overexpression, the steady-state amount of the three major CP (CP1, CP2 and CP5) mRNA was measured by quantitative RT-PCR. The steady-state level of CP1, CP2 or CP5 mRNA remained unchanged in the *EhRab7B-GTP* transformant compared with the control transformant

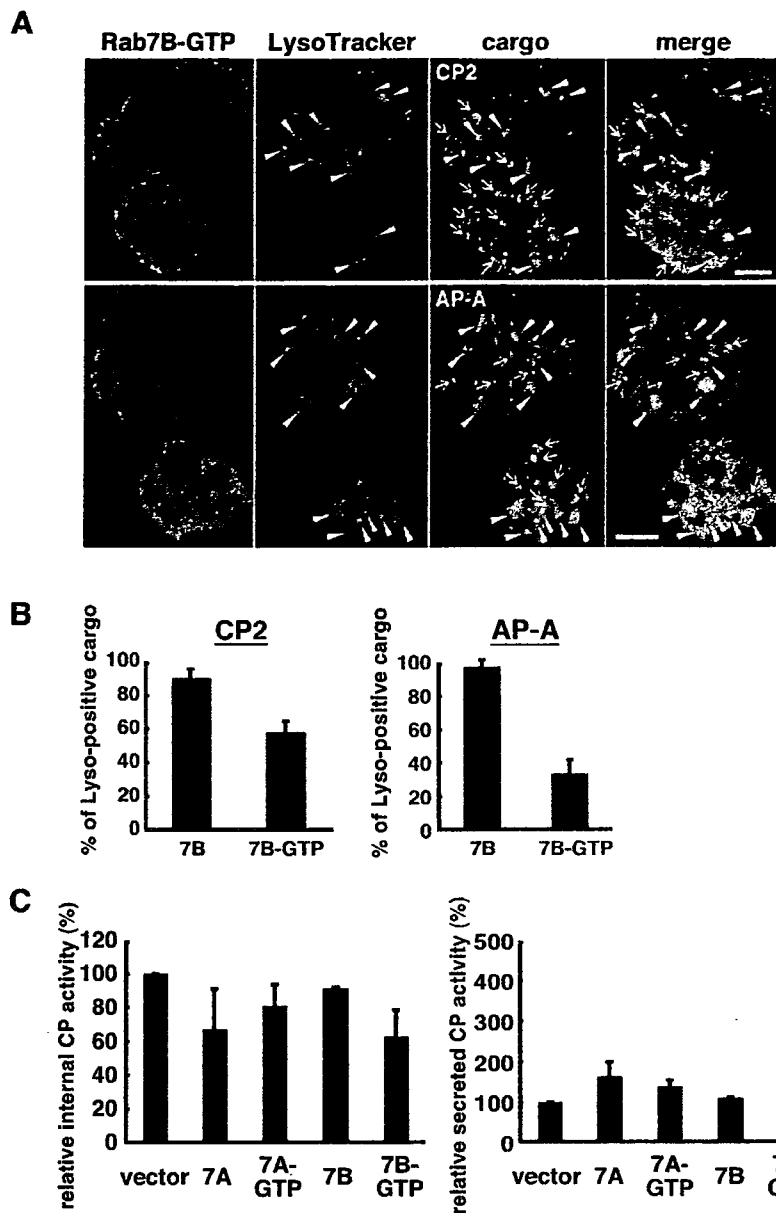


Fig. 6. Localization of *EhRab7B*-GFP and effects of *EhRab7B* overexpression on CP transport to lysosomes and CP activity. **A.** Immunofluorescence assay of *EhRab7B*-GFP. Colocalization of lysosomal cargo proteins (blue), CP2 (upper panels) and AP-A (lower panels), with LysoTracker (red) in the *EhRab7B*-GFP (green)-expressing transformant. Arrowheads indicate cargo proteins colocalized with LysoTracker. Arrows indicate cargo proteins not associated with LysoTracker. Bars, 10 μ m. **B.** Measurement of cargo protein transport to lysosomes in the *EhRab7B* and *EhRab7B*-GFP transformants. Percentages of LysoTracker-positive vesicles/vacuoles of all cargo-positive vesicles/vacuoles are shown. **C.** CP activity in the whole lysate (left) and secreted to the medium (right) in the *EhRab7A* ('7A'), *EhRab7A*-GFP ('7A-GTP'), *EhRab7B* ('7B'), *EhRab7B*-GFP ('7B-GTP') and control ('vector') transformants. CP activity is shown in percentage relative to that of the control transformant. Error bars represent SD of two independent experiments.

(113%, 86% or 91% of the mRNA level of the control respectively; data not shown). Together with the fact that *EhRab7B* overexpression enhanced maturation and/or fusion of the acidic compartment whereas *EhRab7B*-GFP conferred the opposite effect (Fig. 4), these data indicate that *EhRab7B* may mediate trafficking of lysosomal proteins to the storage compartment. In contrast, overexpression of either *EhRab7A* or *EhRab7A*-GTP caused the less magnitude (< twofold) of changes of intracellular and secreted CP activity, which is consistent with the premise that *EhRab7B* mediates a transport stage closer to lysosomes than that mediated by *EhRab7A*.

EhRab7B and *EhRab7A* are localized to distinct but significantly overlapping compartments

We have previously shown that *EhRab7A* is associated with the post-Golgi compartment, but not the acidic compartment in steady state (Saito-Nakano *et al.*, 2004). To clarify the difference of subcellular localization between *EhRab7A* and *EhRab7B*, localization of *EhRab7A* and *EhRab7B* was simultaneously visualized using the *EhRab7B*-overexpressing transformant (Fig. 7A). In steady state, vacuoles associated with either *EhRab7A* or *EhRab7B*, or both were observed. Approximately one

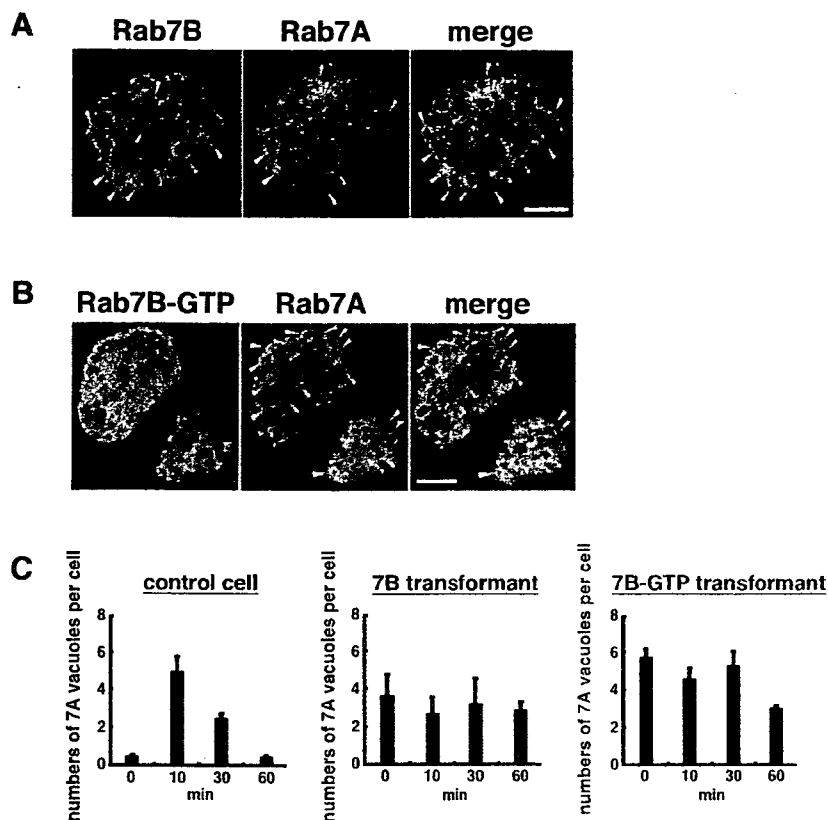


Fig. 7. Subcellular localization of *EhRab7B* and *EhRab7A* and effects of *EhRab7B* overexpression on PPV formation.

A and **B.** Immunofluorescence images of *EhRab7B*, *EhRab7B*-GTP and *EhRab7A*. The HA-tagged *EhRab7B*- (**A**) or *EhRab7B*-GTP (**B**)-overexpressing transformant was probed with anti-HA (green) and anti-*EhRab7A* (red) antibodies to simultaneously visualize *EhRab7B* (**A**) or *EhRab7B*-GTP (**B**) and *EhRab7A* respectively. Green or red arrowheads indicate the vacuoles stained solely with either anti-*EhRab7B* or *EhRab7A* antibody respectively. Vacuoles simultaneously stained with both anti-*EhRab7B* and *EhRab7A* antibodies are marked with yellow arrowheads. Bars, 10 μ m. **C.** The number of *EhRab7A*-positive vacuoles at 10, 30 and 60 min after phagocytosis of erythrocytes in the control, *EhRab7B*- and *EhRab7B*-GTP-overexpressing transformants.

fourth ($28\% \pm 4.2\%$) of *EhRab7B*-positive vacuoles were associated with *EhRab7A*. Conversely, about a half ($60\% \pm 13\%$) of *EhRab7A*-positive vacuoles were associated with *EhRab7B*. The compartment co-associated with both *EhRab7A* and *EhRab7B* is likely the transitional compartment. The average diameter of *EhRab7A*- or *EhRab7B*-positive vacuoles was 3.5 ± 0.3 or 3.4 ± 0.1 μ m respectively. Localization of *EhRab7A* and *EhRab7B* was also clearly different during phagocytosis (Fig. 8A). *EhRab7B* was not associated with erythrocyte-containing phagosomes whereas *EhRab7A* was often localized to them (Saito-Nakano *et al.*, 2004). In addition, *EhRab7B* was not associated with one of the retromer-like complex, Vps26, which was shown to be colocalized with *EhRab7A* (Nakada-Tsukui *et al.*, 2005) (Fig. 8B).

EhRab7B plays a role in the formation of PPV, phagosomal acidification, and degradation of its content

We previously reported that PPV is the *EhRab7A*-associated preparatory vacuole, formed in response to phagocytosis stimuli, and is necessary for efficient phagocytosis (Saito-Nakano *et al.*, 2004). *EhRab7A*-positive PPVs were not present before the addition of erythrocytes, emerged at 10 min after phagocytosis, and disappeared at 30–60 min in the control transfor-

mant ('control cell') (Fig. 7C, left). On the other hand, in the *EhRab7B* or *EhRab7B*-GTP transformants, an average number of 3.3 ± 1.5 or 5.6 ± 2.3 *EhRab7A*-positive PPVs per trophozoite were formed in steady state respectively (Fig. 7A–C). This result indicates that overexpression of *EhRab7B* or *EhRab7B*-GTP induced the formation of PPVs without phagocytosis-linked stimuli (e.g. attachment). Moreover, the number of PPVs in the *EhRab7B*- or *EhRab7B*-GTP-expressing transformant remained unchanged during erythrocyte phagocytosis (Fig. 7C, middle and right), which was in good contrast to the time-dependent emergence and disappearance of PPV in the course of phagocytosis (Saito-Nakano *et al.*, 2004; Fig. 7C, left). Next, we tested if the *EhRab7B*- and *EhRab7B*-GTP-expressing transformants, both of which showed defect in the erythrocyte-induced formation of PPVs, are defective in engulfment *per se*. Overexpression of *EhRab7B*-GTP or *EhRab7B* wild-type, to a less degree, resulted in the reduction of yeast phagocytosis (Fig. 9A). These data agreed with the premise that the interference of the regulation of the PPV formation hindered engulfment, which is similar to the case seen for *EhRab5*-GTP (Saito-Nakano *et al.*, 2004).

Acidification and degradation of the content in phagosomes well correlated (Mitra *et al.*, 2005; 2006). We next

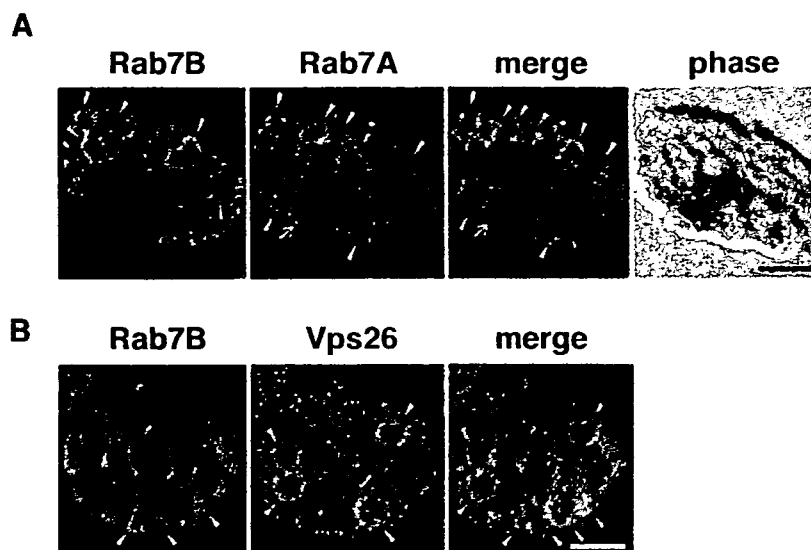


Fig. 8. Immunofluorescence imaging of *EhRab7A*, *EhRab7B* and retromer-like complex during erythrophagocytosis.

A. Localization of *EhRab7A* and *EhRab7B* during erythrophagocytosis. The transformant was cultivated with erythrocytes for 30 min and *EhRab7A* (red) or HA-tagged *EhRab7B* (green) was detected with anti-*EhRab7A* or anti-HA antibody respectively. *EhRab7A*-single positive, *EhRab7B*-single positive, or double-positive vacuoles were shown in red, green or yellow arrowheads respectively. Note that a phagosome containing an erythrocyte (an red arrow, stained black with diaminobenzidine) is associated with *EhRab7A*, but not *EhRab7B*.

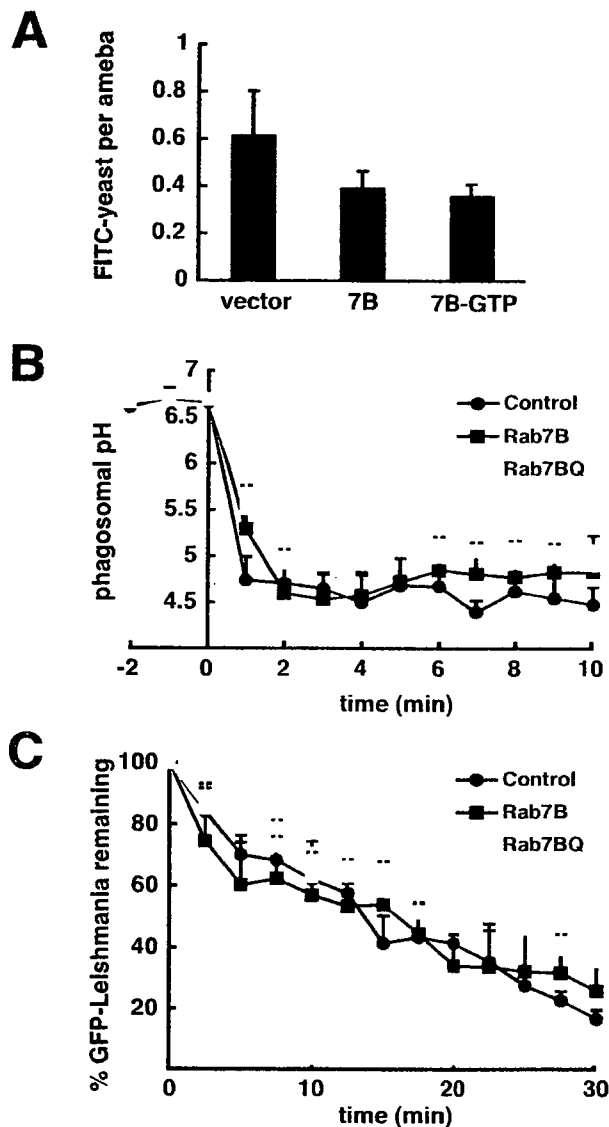
B. Lack of colocalization of *EhRab7B* and Vps26, one of the components of the retromer-like complex, which was previously shown to be the *EhRab7A* effector. Note that *EhRab7B* (green) did not colocalize with Vps26 (red), in contrast to colocalization of Vps26 and *EhRab7A* (Nakada-Tsukui *et al.*, 2005). Bars, 10 μ m.

examined if expression of *EhRab7B* or *EhRab7B*-GTP affects phagosomal acidification and degradation of ingested materials (Fig. 9B and C). Phagosomes of the *EhRab7B*-GTP transformant were less acidic (the average pH of phagosomes of 2–10 min post ingestion, 5.01 ± 0.10) than that of the mock vector control transformant (4.58 ± 0.11 , $P = 0.00028$) (Fig. 9B). Moreover, *EhRab7B*-GTP transformant showed approximately 25% reduced degradation as measured with decay of GFP fluorescence of ingested GFP-expressing *Leishmania* promastigotes ($1.80\% \pm 0.32\%$ GFP degradation per min), when compared with the vector control transformant ($2.40\% \pm 0.25\%$ degradation per min; $P = 0.025$) (Fig. 9C). These results are consistent with the premise that *EhRab7B*-GTP overexpression caused defect in lysosomal acidification and transport of lysosomal proteins (Figs 4 and 6). In contrast, *EhRab7B* overexpression, which resulted in enhancement of lysosomal fusion and increase of the lysosome volume, caused no significant change in phagosome pH and degradation kinetics. The average phagosome pH of 2–10 min post ingestion was 4.72 ± 0.12 in the *EhRab7B*-overexpressing transformant ($P > 0.05$ versus the control transformant). Degradation within phagosomes in the *EhRab7B* transformant ($2.00 \pm 0.37\%$ degradation per min) was only slightly reduced compared with the mock vector control ($P > 0.05$ versus the control transformant).

Discussion

In the present study, we described the functional differences of Rab7 isotypes in this medically important protozoan parasite. As far as we are concerned, this is the first report on the functional differences between Rab7 isotypes in not only protists, but also unicellular eukaryotes. Rab7 GTPase has been implicated in trafficking of at least three steps in different organisms, i.e. early endosomes to late endosomes in BHK cell (Feng *et al.*, 1995; Vitelli *et al.*, 1997), late endosomes to lysosomes in HeLa cell (Meresse *et al.*, 1995; Bucci *et al.*, 2000), and homotypic lysosome fusion in *S. cerevisiae* (Wichmann *et al.*, 1992; Schimmoller and Riezman, 1993; Haas *et al.*, 1995). Our data presented here are consistent with the notion that *EhRab7B* is localized to late endosomes/lysosome and involved in the formation of or fusion to lysosomes, whereas *EhRab7A* is associated with the post-Golgi compartment containing cargos destined to lysosomes, and involved in the fusion to late endosomes. There was no precedent where two Rab7 isotypes are involved in the trafficking of lysosomal proteins from the post-Golgi to lysosomes/phagosomes in a sequential and co-ordinated fashion, as shown in this study.

We have demonstrated that the two representative Rab7 isotypes, *EhRab7A* and *EhRab7B*, showed differences in localization and role in biogenesis of lysosomes



and phagosomes. First, as mentioned above, while *EhRab7A* is primarily localized in the post-Golgi compartment (Saito-Nakano *et al.*, 2004; Nakada-Tsukui *et al.*, 2005), *EhRab7B* is almost exclusively localized to late endosomes/lysosomes (Fig. 2). Second, while *EhRab7A* is transported to phagosomes containing erythrocytes after 30 min of phagocytosis (Saito-Nakano *et al.*, 2004), *EhRab7B* is not trafficked via or to erythrocyte-containing phagosomes (Fig. 8A). Third, overexpression of *EhRab7B-GTP* dramatically decreased intracellular CP activity and enhanced secretion of CP activity into the medium, while overexpression of *EhRab7A* or *EhRab7A-GTP* affected intracellular and secreted CP activity only marginally (Fig. 6C). Fourth, *EhRab7A* regulates retrograde transport of a putative hydrolase receptor from phagosomes to the *trans*-Golgi network via interaction with

the retromer-like complex (Nakada-Tsukui *et al.*, 2005), while *EhRab7B* neither interacts with the retromer-like complex nor is associated with the process (Fig. 8B). On the other hand, overexpression of these two Rab7 isoforms led to apparently similar consequences. Overexpression of *EhRab7A* or *EhRab7B* caused increase of the cellular acidity, consistent with the notion that *EhRab7A* or *EhRab7B* is involved in maturation of and fusion to late endosomes or lysosomes respectively. Neither *EhRab7A* nor *EhRab7B* overexpression caused defect in endocytosis or growth (data not shown), suggesting lack of association of these Rab7 isoforms with initial phase of endocytosis or recycling.

It is conceivable that *EhRab7A* and *EhRab7B* share common effectors, and transmit signal for divergent pathways because the effector domain of these two Rab7 isoforms showed 90% identity [YKATIGADFL, a.a. 36–45 of *EhRab7A*; YKATIGADFM, a.a. 39–48 of *EhRab7B*; substituted amino acids are shown in *italic*] (Saito-Nakano *et al.*, 2005). Mechanisms by which activation of *EhRab7B* leads to recruitment and activation of *EhRab7B* may exist, as shown for the case of endosome maturation in mammalian cells, where Rab5 recruited to early endosomes initiates recruitment of the HOPS complex, an effector complex of Rab7 essential for lysosome fusion (Eitzen *et al.*, 2000), and Rab7-guanine nucleotide exchange factor in the complex further activates Rab7 for following maturation of endosomes (Rink *et al.*, 2005).

The decrease of the cellular acidity caused by *EhRab7B-GTP* expression may be at least partially attributable to its disrupted membrane association of this

the kinetics of degradation of GFP-expressing *Leishmania* promastigotes in the *EhRab7B*-expressing (black squares), *EhRab7B-GTP*-expressing (grey squares) and control (black circles) transformants. Trophozoites were mixed with FITC-labelled yeasts at 1:10 ratio on a glass bottom culture dish, enclosed with a coverslip, and allowed to ingest yeasts at 33°C. Trophozoites containing a single yeast were selected and phagosomal pH was measured at 1 min intervals for 3 h with time-lapse video microscopy on a Leica AS MDW. Only data for the first 10 min are shown. Data represent the average of 10 independent phagosomes.

the kinetics of degradation of GFP-expressing *Leishmania* promastigotes in the *EhRab7B*-expressing (black squares), *EhRab7B-GTP*-expressing (grey squares) and control (black circles) transformants. Trophozoites were incubated with live GFP-*Leishmania* promastigotes at 1:5 ratio and images were captured at 30 s intervals to measure the GFP fluorescence intensity. Data of the average of 10 independent phagosomes at 2.5 min intervals are shown.

mutant. In HeLa cell, expression of Rab7-GTP conferred dominant active phenotypes, e.g. augmented lysosomal fusion and formation of enlarged lysosomes (Bucci *et al.*, 2000). The unexpected dominant-negative phenotypes such as reduction of the lysosome acidity, CP and AP-A transport to lysosomes, and phagosome acidification and degradation, observed in the *EhRab7B*-GTP mutant, was also observed in the case of *EhRab5*-GTP overexpression, which caused a defect in the formation of PPV and phagocytosis efficiency (Saito-Nakano *et al.*, 2004). Alternative explanations for the dominant-negative phenotype include: *EhRab7B*-GTP elicited irreversible recruitment of and binding to the HOPS complex, or its amoebic equivalent, which interfered with downstream maturation due to incompetence of GTP hydrolysis (Bowers and Stevens, 2005). Similarly, it was shown that Ypt7-GDP mutant was unable to recruit the HOPS complex in yeast, and incompetent to initiate vacuole docking and fusion (Eitzen *et al.*, 2000).

Mislocalization of lysosomal cargos to non-acidified compartments observed in the *EhRab7B*-GTP-expressing transformant (Fig. 6B) is similar to the previous demonstration that expression of a Rab7 mutant inhibited lysosomal acidification, due to perturbation of V-ATPase (Bucci *et al.*, 2000). In yeast, defects in genes involved in transport from the *trans*-Golgi to the vacuole showed missecretion of vacuolar proteases to the medium (Bowers and Stevens, 2005). Although mechanisms of the CP missecretion to the extracellular milieu is not well understood, it is conceivable to hypothesize that mislocalized lysosomal proteins are transported to the plasma membrane through recycling pathway mediated by *EhRab11B*, which plays a substantial role in the secretion of CPs (Mittra *et al.*, 2007).

Overexpression of *EhRab7B* or *EhRab7B*-GTP caused reduction of the phagocytosis efficiency. In addition, attachment-dependent formation and disintegration of PPVs were interrupted by overexpression of either *EhRab7B* or *EhRab7B*-GTP (Fig. 7C). In wild-type amoebae, PPVs emerged in a contact-dependent manner, and disappeared after 20–30 min after phagocytosis (Saito-Nakano *et al.*, 2004). In contrast, in the *EhRab7B*- or *EhRab7B*-GTP-overexpressing transformant, PPVs were formed in quiescent state, and the formation and disassembly of PPVs were not controlled in a course of phagocytosis (Fig. 7C). These data are consistent with the notion that *EhRab7B* is involved in the signalling associated with phagocytosis. *EhRab7B*-GTP expression also caused defect in phagosome acidification, which correlated well with retardation in the degradation of the content within phagosomes (Fig. 9B and C). The negative effects of *EhRab7B*-GTP on phagosome functions can be explained as a decreased efficiency of recruitment of V-ATPase and

transport of digestive proteins to lysosomes and phagosomes.

Five of Rab7 isotypes (*EhRab7A*, B, C, D and E) were identified from the latex bead-containing phagosomes isolated by flotation centrifugation on a sucrose step gradient (Okada *et al.*, 2005; 2006) and three of them (Fig. 7A, B and D) were also identified from phagosomes containing human serum-coated magnetic beads (Marion *et al.*, 2005). These *EhRab7* isotypes revealed remarkable stage-dependent recruitment to phagosomes during maturation. e.g. *EhRab7A* and *EhRab7E* are constitutively associated with phagosomes while *EhRab7B*, *EhRab7C* and *EhRab7D* were detected in an early (0–30 min) to intermediate phase (60 min). Thus, it is conceivable that that these *EhRab7* isotypes are sequentially and co-ordinately involved in phagosome biogenesis. Other not-yet-characterized phagosome-associated *EhRab7* isotypes, i.e. *EhRab7C*, 7D and 7E, likely play an independent role in the lysosome/phagosome trafficking in this organism. Finally, the multiplicity and diversity of *EhRab7* isotypes reflect the complexity and biological importance of endosomal-lysosomal trafficking and phagosome biogenesis in this organism, which may be related to parasitism and virulence of this medically important parasite.

Experimental procedures

Culture

Trophozoites of the *E. histolytica* isolate HM-1:IMSS cl6 (Diamond *et al.*, 1972) were cultured axenically in BI-S-33 medium at 35°C as described previously (Diamond *et al.*, 1978).

Quantitative RT-PCR

mRNA expression of nine *EhRab7* genes (Saito-Nakano *et al.*, 2005) and three major CPs (CP1, CP2 and CP5) was analysed by quantitative RT-PCR analysis essentially as previously described (Gilchrist *et al.*, 2006) with some modifications. RNA polymerase II served as an internal control (GenBank accession number, XP_649091) (Gilchrist *et al.*, 2006). Primers used were 5'-gctgaacaatgggttcagaacat-3' and 5'-caaaagctgattgccctgttga-3' (*EhRab7A*, GenBank Accession No. AB054583); 5'-gaccaattaaggcaatgggtgtgt-3' and 5'-acacaatcatctglagctc taa-3' (*EhRab7B*, AB186363); 5'-gcaaaagattgggtgaaataat-3' and 5'-gaaccaaataagagctgtttaa-3' (*EhRab7C*, AB186364); 5'-gaacaagcagcagaatgggtgtaa-3' and 5'-aagaagaaggagggtgtgctaa-3' (*EhRab7D*, AB186365); 5'-tctgatgtaaaacaatgggtgaa-3' and 5'-aaaaaagaaggagggtgttga-3' (*EhRab7E*, AB186366); 5'-gctgtgatgattggattcaattt-3' and 5'-gltgaaacagcgccttltgtaa-3' (*EhRab7F*, AB186367); 5'-gtttcaactgaaagtgctcgtcaa-3' and 5'-ttaacaacaaccttcagactt-3' (*EhRab7G*, AB186368); 5'-gttgataaaag tcaagaagagta-3' and 5'-tcaacaacattgttttltgtaac-3' (*EhRab7H*, AB186369); 5'-gatgaagaagaacaagtagtttt-3' and 5'-tcaacaacaac tcttttaacctt-3' (*EhRab7I*, AB197056); 5'-caatgcaagaataactat tttgca-3' and 5'-tcagagattcaaccaccagttgg-3' (CP1, XM_645064);

5'-aatgcaagaataacttttgc-3' and 5'-lcaaagatattgaacgccagttgg-3' (CP2, XM_645550); 5'-aaagaatgtcatcaactcagctt-3' and 5'-ttaagcatcagcaacccaactgg-3' (CP5, XM_645845); and 5'-gatc caacatacctaaacaaca-3' and 5'-tcaattatttctgaccgcgttc-3' (RNA polymerase II). Parameters used are: an initial step of denaturation at 95°C for 9 min, followed by 40 cycles of denaturation at 94°C for 30 s, annealing at 50°C for 30 s, and extension at 65°C for 1 min. A final step at 95°C for 9 s, 60°C for 9 s, and 95°C for 9 s was used to remove primer dimers.

Plasmid constructs

A 624 bp DNA fragment containing *EhRab7B* coding sequence was amplified by PCR from *E. histolytica* cDNA library (Nozaki *et al.*, 1998) using a pair of appropriate primers with restriction enzyme sites. The amplified fragment was cloned into the BglII-XhoI sites of pEhEx (Nozaki *et al.*, 1999), and 3HA-tag was inserted at the amino terminus of *EhRab7B* gene essentially as described previously (Saito-Nakano *et al.*, 2004). The final plasmid to express 3HA-*EhRab7B* in trophozoites was designated pH7B. A plasmid to express *EhRab7B* H69L mutant was constructed by PCR-mediated mutagenesis (Landt *et al.*, 1990) and designated pH7BL. A coding region of monomeric red fluorescence protein (mRFP1) was amplified by PCR using mRFP1-pRSETB plasmid (a kind gift from Atsushi Miyawaki) (De Ray *et al.*, 2004) as a template, and cloned into pKT-3M (Saito-Nakano *et al.*, 2004), which contained the cysteine synthase promoter, 3myc-tag, SmaI and XhoI restriction sites to produce pKT-MR. A coding sequence lacking the stop codon of *EhRab7B* wild type or H69L mutant was ligated into SmaI-XhoI sites of pKT-MR in frame to the coding region of mRFP1 at the amino terminus to produce pKT-RFP7B and pKT-RFP7BL respectively. The plasmids were introduced into trophozoites by liposome-mediated transfection as previously described (Nozaki *et al.*, 1999; Saito-Nakano *et al.*, 2004), and stable transformants were cultured in the medium containing 6 (for pH7B, pH7BL and pEhEx) or 40 µg ml⁻¹ Geneticin (Life Tech Oriental) (for pKT-RFP7B, pKT-RFP7BL and pKT-MR).

Production of antibody

Antiserum was raised against recombinant *EhRab7B* in rabbits commercially (Kitayama-Rabes, Japan). IgG was further purified using HiTrap NHS-activated HP column (Amersham) coupled with purified recombinant *EhRab7B* according to the manufacturer's instruction.

Indirect immunofluorescence

Indirect immunofluorescence assay was conducted as previously described (Saito-Nakano *et al.*, 2004). Trophozoites were transferred to 8 mm round wells on a slide glass, fixed, permeabilized, and reacted with anti-HA 16B12 monoclonal antibody to detect HA-tagged *EhRab7B* wild type and *EhRab7B*-GTP mutant (Berkeley Antibody), anti-CP2 (a gift from Iris Bruchhaus and Egbert Tannich) (Hellberg *et al.*, 2000), anti-AP-A (a gift from Matthias Leippe) (Leippe *et al.*, 1991), or anti-*EhRab7A*, anti-*EhRab7B* antibody (Saito-Nakano *et al.*, 2004). Acidic compartments of trophozoites were stained with LysoTracker Red DND-99 (Invitrogen) at 35°C for 12 h.

Flow cytometry

Trophozoites were incubated in BI-S-33 medium containing 2 µM LysoTracker Green (Invitrogen) at 36°C for 30 min, washed with cold phosphate-buffered saline (PBS), and analysed by FACS using FACS Calibur (Becton Dickinson, San Jose, CA) as previously described (Nakada-Tsukui *et al.*, 2005).

Subcellular fractionation

Approximately 3 × 10⁵ amoeba cells were washed with cold PBS containing 2% glucose, resuspended in homogenization buffer (250 mM sucrose, 50 mM Tris, pH 7.5, 50 mM NaCl, 0.1 mg ml⁻¹ E-64), and homogenized on ice with 30 strokes by a Dounce homogenizer with a tight fitting pestle as described (Okada *et al.*, 2005). After unbroken cells were removed by centrifugation at 4500 g for 2 min, the supernatant was centrifuged at 13 000 g at 4°C for 10 min to obtain the pellet (p13) and supernatant (s13) fractions. The s13 fraction was further separated by centrifugation at 100 000 g at 4°C for 1 h to obtain the pellet (p100) and soluble (s100) fractions. These fractions were subjected to immunoblot analyses with anti-HA, anti-intermediate subunit of Gal/GalNAc-inhibitable lectin (a gift from Hiroshi Tachibana) (Cheng *et al.*, 1998), or anti-alcohol dehydrogenase antibody (Sanuki *et al.*, 2001).

CP assay

Approximately 4 × 10⁵ trophozoites were incubated in 100 ml of Opti-MEM medium (Invitrogen), supplemented with 137 mM cysteine and 19 mM ascorbic acid, pH 6.8, on a 96 well micro plate at 35°C for 1 h. After incubation, the culture supernatant was recovered and trophozoites were removed from the micro plate by incubation on ice. CP activity was measured using z-Arg-Arg-7-amino-4-trifluoromethylcoumarin substrate as described (Nakada-Tsukui *et al.*, 2005).

Measurement of phagocytosis efficiency, and acidification and degradation within phagosomes

Phagocytosis of yeasts was monitored as described (Mitra *et al.*, 2005; 2006) with some modifications. Trophozoites transfected with pKT-MR, pKT-RFP7B or pKT-RFP7BL were first monitored for mRFP1 fluorescence to select cells that expressed a high level of mRFP1-*EhRab7B* wild type or GTP mutant. Kinetics of acidification of phagosomes and degradation of their contents was monitored using fluorescein isothiocyanate (FITC)-labelled yeasts and GFP-expressing *Leishmania amazonensis* promastigotes respectively, using pKT-MR, pKT-RFP7B or pKT-RFP7BL expressing cells as described previously (Mitra *et al.*, 2005; 2006).

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