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Disparate Effects of p24α and p24δ on Secretory Protein Transport and Processing

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INTRODUCTION

The secretory pathway consists of a number of distinct membrane-bounded subcompartments that have specialized functions in the process of protein biosynthesis [1]. Proteins that pass through the subcompartments undergo various posttranslational modifications (e.g. glycosylation, sulfation and proteolytic cleavage) that are essential for their biological activity. The biosynthetic process includes the selective packaging of proteins from the endoplasmic reticulum (ER) into vesicles for delivery to the subcompartments. Members of the p24 family of type-I transmembrane proteins are thought to be somehow involved in endoplasmic reticulum (ER)-to-Golgi protein transport. A subset of the p24 proteins (p24α, -β, -γ and -δ) is upregulated when Xenopus laevis intermediate pituitary melanotrope cells are physiologically activated to produce vast amounts of their major secretory cargo, the prohormone proopiomelanocortin (POMC). Methodology/Principal Findings. Here we find that transgene expression of p24α or p24δ specifically in the Xenopus melanotrope cells in both cases causes an effective displacement of the endogenous p24 proteins, resulting in severely distorted p24 systems and disparate melanotrope cell phenotypes. Transgene expression of p24α greatly reduces POMC transport and leads to accumulation of the prohormone in large, ER-localized electron-dense structures, whereas p24δ transgenesis does not influence the overall ultrastructure of the cells nor POMC transport and cleavage, but affects the Golgi-based processes of POMC glycosylation and sulfation. Conclusions/Significance. Transgenic expression of two distinct p24 family members has disparate effects on secretory pathway functioning, illustrating the specificity and non-redundancy of our transgenic approach. We conclude that members of the p24 family furnish subcompartments of the secretory pathway with specific sets of machinery cargo to provide the proper microenvironments for efficient and correct secretory protein transport and processing.


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be modulated by placing the frogs on a white (inactive melanotrope cells) or black (highly active melanotrope cells) background. The manipulation of the activity of the melanotrope cells is strictly regulated by inhibitory and stimulatory neurons of hypothalamic origin. Upon activation, the melanotrope cells produce and proteolytically cleave vast amounts of the prohormone proopiomelanocortin (POMC), the precursor of a number of bioactive peptides, including α-MSH (reviewed in [17]). In the activated melanotrope cells, proteins upregulated together with POMC are thought to play a role in the biosynthesis of the prohormone [18] and include a subset of p24 proteins, namely p24α3, p24β1, p24γ3 and p24δ2. Two other members of the p24 family (p24γ2 and p24δ1) are expressed in the melanotrope cells as well, but not coordinately with POMC [19]. To examine the role of p24 in the biosynthesis of POMC, we chose to generate and analyze Xenopus lines with transgene expression of p24α3 or p24δ2, i.e. two p24s of the upregulated set. We used a POMC gene promoter fragment to target the expression of the transgenes specifically to the melanotrope cells [20], leaving the regulation of these cells by hypothalamic neurons intact. We find that the p24α3- and p24δ2-transgenic frogs have distinct melanotrope cell phenotypes in that POMC transport and processing was differently affected, allowing us to conclude that p24α3 and p24δ2 have non-redundant roles in maintaining the functional and structural integrity of the secretory pathway.

RESULTS
Generation of Xenopus laevis with stable transgene expression of p24α3 or p24δ2 specifically in the melanotrope cells
For our functional studies on p24, we generated Xenopus laevis transgenic for the p24α3 or the p24δ2 protein. In order to drive transgene expression specifically to the melanotrope cells of the Xenopus intermediate pituitary, we made DNA-constructs containing a 529-bp Xenopus laevis POMC gene A promoter fragment (pPOMC [20]) in front of Xenopus laevis p24α3 or p24δ2 cDNA. To allow direct selection of embryos expressing the transgene, we fused GFP to the C-terminus of p24α3 and p24δ2. The linearised DNA-constructs (pPOMC-p24α3-GFP, Figure 1A or pPOMC-p24δ2-GFP, Figure 1B) were mixed with wild-type Xenopus sperm nuclei and the mixtures were microinjected into unfertilized wild-type Xenopus laevis eggs. We generated three independent transgenic F0 lines with transgene expression of p24α3 or p24δ2, and the majority of the transgene product was found readily and directly be observed in living tadpoles (Figure 1C) and in adult frogs after lifting the brain (Figure 1D).

We (in line #124 p24δ2-transgenic Xenopus [21]) and others (in heterozygous p24 knock-out mice [16], by p24 knock-down in mammalian cells in culture [22,23] and in p24 knock-out yeast [7,8]) have observed that manipulation of the expression of a single p24 family member interferes with the endogenous p24 system and affects the steady-state levels of the other p24 family members. We therefore studied in the melanotrope cells of the three p24α3- and four p24δ2-transgenic Xenopus lines the steady-state levels of members of the endogenous p24 protein family. In the melanotrope cells of the three lines transgenic for the p24α3-GFP fusion protein, the transgene product effectively displaced the endogenous p24α3, β1, γ3, δ1 and δ2 proteins (75–90% displacement; n = 4; Figure 2A and data not shown). We selected line #55 to further study the effect of p24α3 transgene expression on the functioning of the melanotrope cells. In the transgenic melanotrope cells of line #224, the p24α3-GFP fusion protein displaced the endogenous p24 proteins similarly effective (70–98% displacement; n = 4; Figure 2A). This degree of displacement was higher than that in the previously described p24δ2-transgenic melanotrope cells of lines #115, #124 and #125 [21]. We therefore decided to select p24δ2-transgenic line #224 for further functional analysis. Surprisingly, whereas the level of expression of the p24α3-GFP fusion protein was ~6 times lower than that of p24δ2-GFP (n = 11; Figure 2B), the p24α3 and p24δ2 fusion proteins were similarly effective in displacing the endogenous p24 proteins.

We next investigated the localization of the fusion proteins within the transgenic melanotrope cells by immuno-electron microscopy (IEM) using an anti-GFP antibody. In the p24α3-transgenic melanotrope cells, the majority of the transgene product was found in ER-localized electron-dense structures (Figure 2C) in which we also observed POMC (see below). In the p24δ2-transgenic cells, the gold-label was detected mostly on the ER and the Golgi (Figure 2D), indicating cycling of the fusion protein between these compartments and in line with our previous observation of ER/Golgi localization of the transgene product in line #124 p24δ2-transgenic melanotrope cells [21] and consistent with the localization of endogenous p24 proteins (reviewed in [3]).

Figure 1. Generation of Xenopus with transgene expression of p24α3 or p24δ2 specifically in the melanotrope cells. (A and B) Schematic representation of the linear injection fragments pPOMC-p24α3-GFP (A) and pPOMC-p24δ2-GFP (B) containing a Xenopus POMC gene promoter fragment (pPOMC) and the protein-coding sequence of p24α3-GFP (transgenic lines #605, #602 and #600) or p24δ2-GFP (lines #125, #115, #124 and #224); pPOMC drives transgene expression specifically to the melanotrope cells. (C) Pituitary-specific GFP-fluorescence (arrows) in living tadpoles transgenic for p24α3 (line #55) or p24δ2 (line #224); G, gut; E, eye; N, nose. (D) Fluorescence in the intermediate lobe (IL) and not in the anterior lobe (AL) of the pituitary of adult frogs transgenic for p24α3 (#55) or p24δ2 (#224). doi:10.1371/journal.pone.0000704.g001
Together, the studies on the steady-state p24 protein levels showed that in the p24α3- and p24δ2-transgenic melanotrope cells the entire set of endogenous p24 proteins was nearly completely displaced by the transgene product and therefore the fusion protein was essentially the only p24 protein available to the transgenic cells.

**Steady-state levels of secretory cargo proteins in the transgenic Xenopus melanotrope cells**

To study the effect of the transgene expression of p24α3 or p24δ2 on the functioning of the secretory pathway, we first examined the steady-state levels of the soluble secretory cargo proteins POMC and its processing enzyme prohormone convertase PC2 in the transgenic melanotrope cells. Western blot analysis revealed that the levels of the 37K POMC prohormone were significantly increased in the p24α3-transgenic cells (~11-fold; n = 6), whereas in the p24δ2-transgenic cells the steady-state levels of 37K POMC were not affected (n = 6; Figures 3). Furthermore, the proenzyme form of PC2 was detected only in the p24α3-transgenic melanotrope cells, and not in wild-type and the p24δ2-transgenic cells (Figure 3). We then studied the steady-state levels of a transmembrane cargo protein, namely of the type-I transmembrane protein amyloid-β precursor protein (APP). *Xenopus* APP is synthesized as an ~100K N-linked glycosylated protein that in the Golgi is converted into an ~110K O-glycosylated mature protein [24]. Western blot analysis using anti-APP antibodies showed in wild-type cells an ~5.4-fold (n = 4) higher amount of 110K APP than the level of immature 100K APP. In the p24α3-transgenic cells, the level of immature 100K APP was clearly increased (~1.9-fold; n = 4), such that the ratio between 110K and 100K APP was ~2.8 (n = 4), whereas the ratio between both forms as well as the total amount of APP were not significantly affected in the p24δ2-transgenic cells (n = 4; Figure 3). Thus, increased steady-state levels of the unprocessed forms of both soluble (POMC, pro-PC2) and transmembrane (APP) cargo proteins were detected in the p24α3-, but not in the p24δ2-, transgenic melanotrope cells.

Unfortunately, the use of a battery of antibodies against multiple mammalian ER and Golgi enzymes and matrix proteins did not allow us to determine the steady-state levels of these proteins in the transgenic cells because of the inability of the antibodies to cross-react with the *Xenopus* orthologs.
We next investigated the peptides produced by POMC cleavage through matrix-assisted laser-desorption-ionization time-of-flight mass spectrometry (MALDI-TOF MS). The POMC-derived peptides des-N-α-acetyl-α-MSH (the nonacetylated form of α-MSH), α-MSH, γ1-MSH, β-MSH and two corticotrophin-like intermediate lobe peptides (CLIP A and B) were found in wild-type melanotrope cell extracts as well as in samples from the p24_a3- and p24_d2-transgenic cells (data not shown), indicating that both the p24_a3- and the p24_d2-transgenic melanotrope cells converted 37K POMC into the same set of bioactive peptides as the wild-type cells.

**Biosynthesis of POMC in the transgenic Xenopus melanotrope cells**

In view of the observed differences in the steady-state protein levels, we next wondered whether the biosynthetic activity for POMC production was affected in the transgenic melanotrope cells. From the pituitary (consisting of the pars nervosa, and the anterior and intermediate lobes), the anterior part can be dissected but the pars nervosa is intimately associated with the intermediate pituitary (the neuroendocrine melanotrope cells). For our studies, we therefore used the neurointermediate lobe (NIL; pars nervosa plus intermediate lobe) of the pituitary to study the biosynthetic events in the melanotrope cells. Since the Xenopus pars nervosa consists of biosynthetically inactive nerve terminals of hypothalamic origin, the radiolabelled proteins are synthesized exclusively by the melanotrope cells of the intermediate pituitary. Metabolic cell-labeling experiments revealed that following a 30-min pulse the patterns of newly synthesized proteins produced in the p24a3- and in the p24d2-transgenic melanotrope cells were similar to that in wild-type cells (data not shown). Thus, protein biosynthesis was not affected in the transgenic melanotrope cells. Following a 30-min pulse and a 3-hr chase period, we observed a clearly higher amount of newly synthesized 37K POMC remaining in the p24a3-transgenic than in wild-type cells (~3-fold; n = 10; Figures 4A and 4B). In contrast, following the pulse-chase incubation the amount of newly synthesized 37K POMC found in the p24d2-transgenic melanotropes was similar to that in wild-type cells (n = 6; Figures 4A and 4B). These observations are in line with the Western blot results showing higher steady-state levels of 37K POMC in the p24a3-transgenic melanotrope cells than in wild-type and the p24d2-transgenic cells (Figure 3). Thus, the levels of POMC biosynthesis were not changed in the melanotrope cells of the two transgenic lines, but the extent of POMC processing appeared to be affected in the p24a3-transgenic cells.

**Processing of newly synthesized POMC in the transgenic Xenopus melanotrope cells**

Because of the observed accumulation of POMC in the p24a3-transgenic melanotrope cells, we next studied the dynamics of POMC processing by performing pulse-chase metabolic cell labeling experiments. The first endoproteolytic cleavage of newly synthesized 37K POMC yields an ~18K POMC cleavage product that represents the N-terminal portion of 37K POMC and...
contains the only N-linked glycosylation site present in the \textit{Xenopus} POMC molecule [25]. In wild-type melanotrope cells, after a 30-min pulse and 3-hr chase period, two forms of 18K POMC are produced, a major product (~80%) indicated as 18K POMC and a minor (~20%), slightly slower migrating product that we previously designated 18K* POMC (Figure 4A; [21]). In the p24\textsubscript{2}-transgenic cells, the amounts of the 18K and the 18K* POMC processing products were clearly reduced (n = 6; Figures 4A and 4C), indicating less proteolytic processing of newly synthesized 37K POMC. In the p24\textsubscript{a3}-transgenic cells, whereas the amount of the 18K* POMC product was clearly increased (~3-fold; n = 6), the amount of the 18K POMC product was greatly diminished (~7-fold; n = 6), reducing the ratio 18K/18K* POMC from ~4 in wild-type cells to ~0.2 in the p24\textsubscript{a3}-transgenic cells (Figure 4C). In line #124 p24\textsubscript{a3}-transgenic cells, we have previously also observed a decrease in the 18K/18K* POMC ratio, albeit less pronounced [21]. The two forms of 18K POMC presumably differ in the sugar moieties added to their N-glycosylation sites, because deglycosylation of the newly synthesized melanotrope cell proteins with peptidyl N-glycosidase F (PNGaseF), an enzyme that removes all N-linked sugar groups from the protein backbone, caused a shift of both 18K and 18K* POMC to an ~15.5K product (Figure 5). These results suggest that only in the p24\textsubscript{a3} and not in the p24\textsubscript{2}-transgenic cells the glycosylation machinery was affected. Next, HPLC analysis was used to study the newly synthesized peptides resulting from the proteolytic cleavage of radio-labelled POMC. This analysis revealed that the proteolytic cleavage of newly synthesized POMC to des-\textalpha-MSH, \textalpha-MSH, the two forms of CLIP and the two forms of endorphin was similar in the transgenic and wild-type cells (data not shown), in line with the results obtained by mass spectrometry analysis of the steady-state peptides. Together, the biosynthetic studies on the processing of newly synthesized POMC showed that the processing rate was severely reduced in the p24\textsubscript{a3}-transgenic cells and that the glycosylation event was affected in the p24\textsubscript{2}-transgenic cells.

**Sulfation of newly synthesized POMC in the transgenic \textit{Xenopus} melanotrope cells**

In addition to N-linked glycosylation and proteolytic cleavage, POMC is posttranslationally modified by sulfation in the trans-Golgi network (TGN) of the \textit{Xenopus} melanotrope cells [26]. To examine whether sulfation of newly synthesized POMC was affected in the transgenic melanotrope cells, we pulse labeled the cells in the presence of both \textsuperscript{3}H-lysine and \textsuperscript{35}S-sulfate. The labeling with \textsuperscript{3}H-lysine allowed us to quantify the total amount of newly synthesized POMC and \textsuperscript{35}S-sulfate labeling revealed the degree of sulfation of the newly synthesized prohormone, 37K POMC sulfation was not affected in the p24\textsubscript{2}-transgenic cells, whereas we observed an ~3-fold increase in the sulfation of the prohormone in the p24\textsubscript{a3}-transgenic cells (Figure 6). Removal of the N-linked glycans from the sulfate-labeled 37K POMC with PNGaseF increased its electrophoretic mobility but did not affect the degree of sulfate labeling (data not shown), suggesting that the sulfate did not reside on the glycosidogroup. Together with the fact that the 18K POMC species were not sulfated and in line with the presence of a predicted tyrosine sulfation site in the C-terminal half of the \textit{Xenopus laevis} 37K POMC molecule (Sulfinator prediction program [27]), the sulfate label presumably resides on tyrosine residue 188 (SLELDY\textsuperscript{188}PEIDLDEDIED). The biosynthetic studies with \textsuperscript{35}S-sulfate thus showed that the level of POMC sulfation in the TGN was increased in the p24\textsubscript{2}-, but not the p24\textsubscript{a3}-, transgenic melanotrope cells.

**Electron and immuno-electron microscopy analysis of the transgenic \textit{Xenopus} melanotrope cells**

In view of the observed differences in POMC transport and processing, we decided to examine the ultrastructure of the transgenic cells by performing EM. Like in wild-type cells, in the p24\textsubscript{2}- and p24\textsubscript{a3}-transgenic melanotrope cells the rough ER was well developed. However, the p24\textsubscript{2}-transgenic cells contained the only N-linked glycosylation site present in the \textit{Xenopus} POMC molecule. Neurointermediate lobes (NILs) from wild-type frogs (wt) and frogs transgenic for p24\textsubscript{2} (#55) or p24\textsubscript{a3} (#224) were pulse labeled with \textsuperscript{35}S-Met/Cys for 30 min and subsequently chased for 3 hrs. Newly synthesized proteins extracted from the NILs were deglycosylated with PNGaseF (F) or control-treated (C), resolved by 20% SDS-PAGE and visualized by autoradiography; the #55 lanes were exposed three times longer than the other lanes. doi:10.1371/journal.pone.0000704.g005

**Figure 5.** Newly synthesized 18K and 18K* POMC differ in N-glycosylation. Neurointermediate lobes (NILs) from wild-type frogs (wt) and frogs transgenic for p24\textsubscript{2} (#55) or p24\textsubscript{a3} (#224) were pulse labeled with \textsuperscript{35}S-Met/Cys for 30 min and subsequently chased for 3 hrs. Newly synthesized proteins extracted from the NILs were deglycosylated with PNGaseF (F) or control-treated (C), resolved by 20% SDS-PAGE and visualized by autoradiography; the #55 lanes were exposed three times longer than the other lanes. doi:10.1371/journal.pone.0000704.g005

**Figure 6.** Sulfation of newly synthesized POMC in wild-type and transgenic \textit{Xenopus} intermediate pituitary cells. Neurointermediate lobes (NILs) from wild-type frogs (wt) and frogs transgenic for p24\textsubscript{2} (#55) or p24\textsubscript{a3} (#224) were pulse labeled with \textsuperscript{35}S-sulfate and \textsuperscript{3}H-lysine for 15 min. Newly synthesized proteins extracted from the NILs were resolved by 15% SDS-PAGE and the amount of \textsuperscript{35}S-sulfate labeling revealed the degree of sulfation of the newly synthesized prohormone, 37K POMC. Shown are the amounts of newly synthesized sulfated 37K POMC produced in the transgenic relative to wild-type NILs. Data are shown as means +/- SEM (wt, n = 7; transgenics, n = 5). *, p<0.05; n.s., not significant. doi:10.1371/journal.pone.0000704.g006
Figure 7. Electron microscopy analysis of wild-type and transgenic melanotrope cells. (A–C) Wild-type (wt; A1 and A2) intermediate pituitary cells showed a well-developed rough endoplasmic reticulum and extensive Golgi-ribbons. The p24a3-transgenic cells (#55; B1 and B2) contained Golgi mini-stacks and large electron-dense structures (EDS). The p24d2-transgenic cells (#224; C1 and C2) showed an ultrastructure similar to that of wild-type cells. The dotted lines highlight the outline of the Golgi. (D–F) Immuno-electron microscopy analysis of intermediate pituitary melanotrope cells from wt frogs (D), and frogs transgenic for p24a3 (#55; E) or p24d2 (#224; F) using an anti-POMC antiserum. Immunoreactivity was found in dense-core secretory granules (filled arrowheads) in wt and p24a3- and p24d2-transgenic cells and occasionally in newly forming secretion granules still attached to the trans-Golgi network (open arrowheads). In addition, in the p24a3-transgenic cells a strong POMC-immunolabeling was observed in the EDS, which were localized to the ER lumen (arrow) and occasionally in EDS newly forming within the ER lumen (open arrow). G, Golgi; L, lysosome; M, mitochondrion; N, nucleus; RER, rough endoplasmic reticulum; PM, plasma membrane; sg, immature secretory granules. Bars equal 1 μm (A–C); 500 nm (D–F).

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the ER and impaired the structural integrity of the Golgi apparatus, whereas the transgenic expression of p24β2 did not affect the ultrastructure of the cells.

DISCUSSION
The type-I transmembrane p24 proteins are abundantly present in ER- and Golgi-derived transport vesicles, and are therefore thought to play an important role in some aspect of cargo-selective transport through the early secretory pathway [2]. The complex and dynamic behavior of this protein family has hampered functional analyses. In this study, we used the Xenopus laevis intermediate pituitary melanotrope cells to explore the function of p24. The Xenopus melanotrope cells are well-defined neuroendocrine cells of which the biosynthetic and secretory activity can be physiologically induced by placing the frogs on a black background (for review, see [17]). Upon black-background adaptation, four p24 family members (p24αβ, p24ββ, p24γγ and p24δδ), but not p24γβ and p24δ1, are upregulated in the melanotrope cells together with the main secretory cargo protein POMC [19]. The specific upregulation of these four p24 proteins suggests that they are somehow involved in the biosynthesis of POMC. Of the four upregulated p24 proteins, we chose p24αβ and p24δ2 for our functional analyses and generated three independent stable transgenic lines expressing p24αβ and four independent stable p24δ2-transgenic lines, using a POMC gene promoter fragment [20] to drive transgene expression specifically to the melanotrope cells.

We showed in the transgenic Xenopus melanotrope cells a nearly complete displacement of the endogenous p24αβ, p24ββ, p24γγ, p24δ1 and p24δ2 proteins by both the p24αβ and the p24δ2-transgene product. This displacement effect is not in line with the result of the transient overexpression of TMP21 (p24δ1) or p24α (p24β1) in cultured tumor cells, which did not influence the steady-
state levels of p24a or TMP21 respectively [22]. This apparent discrepancy may have been caused by the transient nature of the overexpression in the tumor cells (in our transgenic system the overexpression was stable). To our knowledge, the effect of stable overexpression of an exogenous p24 protein on the endogenous p24 system has not been studied before. Yet, knockout or knockdown of a p24 member in yeast or mammalian cells has led to a reduction in the levels of other p24 proteins as well [7.8.16], At present, we can only speculate why the endogenous p24 proteins were displaced in the p24-d2-transgenic and p24-d2-transgenic Xenopus melanotrope cells. For instance, the amount of early secretory pathway membranes that can harbor p24 proteins may be limited and the relative levels of the various newly synthesized p24 family members expressed in a cell will then determine the final composition of the p24 system. In the transgenic melanotrope cells, the relatively high amount of newly synthesized transgenic product will occupy most of the available space, consequently leading to the displacement of the endogenous p24 proteins. Alternatively, since p24 protein stability depends on the presence of other p24 proteins and their interaction within p24 complexes [7.8.16], and the stable transgene expression in the Xenopus melanotrope cells disturbed the stoichiometry of the p24 system, the transgenic manipulation may well have resulted in altered p24 complex compositions. As a consequence, the endogenous p24 proteins would not be able to form their favored and thus stable complexes, leading to the observed reduced endogenous p24 protein levels. Remarkably, for unknown reasons the p24-d2-transgenic product displaced the endogenous p24 proteins more effectively than the p24-d2-transgenic product.

Irrespective of the explanation, the nearly complete displacement of the endogenous p24 proteins implies that in the p24-d2- and p24-d2-transgenic Xenopus melanotrope cells the p24 system consists essentially of only the p24-d2- and p24-d2-transgenic product respectively. This unique situation allowed us to search for the role of p24 by analyzing the functioning of the secretory pathway in the transgenic cells. For our functional analysis, we took advantage of the fact that the Xenopus melanotrope cells produce and process only major secretory cargo protein (POMC) and that in wild-type melanotrope cells the biosynthetic processes have been previously analyzed in detail [reviewed in [17]]. In the p24-d2-transgenic melanotrope cells, the amounts of newly synthesized POMC, the level of POMC sulfation as well as the ratio of 18K* to 18K-POMC were normal, but the rates of transport and proteolytic cleavage of 37K POMC were greatly reduced. The uncleaved POMC accumulated in large electron-dense structures in the transgenic melanotrope cells. For our functional analysis, we took advantage of the fact that the Xenopus melanotrope cells produce and process only one major secretory cargo protein (POMC) and that in wild-type melanotrope cells the biosynthetic processes have been previously analyzed in detail [reviewed in [17]]. In the p24-d2-transgenic melanotrope cells, the amounts of newly synthesized POMC, the level of POMC sulfation as well as the ratio of 18K* to 18K-POMC were normal, but the rates of transport and proteolytic cleavage of 37K POMC were greatly reduced. The uncleaved POMC accumulated in large electron-dense structures localized to the ER. Since these structures were present only in the p24-d2- and not in the p24-d2-transgenic melanotrope nor in Xenopus melanotrope transgenic for other (transmembrane) proteins (our unpublished observations), they were not merely a result of transgenic protein expression per se. Furthermore, in the p24-d2-transgenic cells the Golgi appeared as ministacks, whereas in wild-type and the p24-d2-transgenic cells this subcompartment was present as Golgi ribbons. An attractive explanation for these observations is that the excess of p24-d2 had affected the supply of the machinery cargo that is required for a correct microenvironment in the early secretory pathway with the consequence of an improper transport and accumulation of POMC, and an abnormal structural organization of the Golgi apparatus in the p24-d2-transgenic cells. In the p24-d2-transgenic melanotrope cells, the overall ultrastructure was not affected by the transgenic manipulation and the levels and rates of POMC synthesis, transport and cleavage were normal. Also, the steady-state and biosynthetic levels of the POMC-cleavage enzyme PC2 and the transmembrane cargo APP are similar in wild-type and the p24-d2-transgenic cells. However, higher amounts of the differentially glycosylated 18K* POMC-product and of sulfated POMC were found in the p24-d2-transgenic than wild-type or the p24-d2-transgenic cells. Since the processes of glycosylation and sulfation occur in the Golgi, it appears that excessive p24-d2 had resulted in an increased supply of the machinery cargo that is responsible for these processes in this subcompartment of the secretory pathway. Taken together, our results suggest that in the p24-d2- and p24-d2-transgenic melanotrope cells the microenvironments of, albeit different, subcompartments in the early stages of the secretory pathway were affected, pointing to a role for p24 proteins in the transport of subsets of machinery cargo and thus in furnishing specific subcompartments of the early secretory pathway.

In view of their structural similarity, the various p24 family members presumably have similar functions. Thus far, the p24 proteins have been mainly implicated in the selection and packaging of secretory cargo proteins (cargo receptor model; reviewed in [2]). However, if the p24 proteins were receptors for secretory cargo, it is not clear why in the Xenopus melanotrope cells four p24 proteins (p24a2, p24b1, p24y3, p24d2) are coordinately expressed with POMC, the major secretory cargo (the prohormone represents >80% of all newly synthesized proteins; [19]). Furthermore, if the four upregulated p24 proteins would function together as a heterotetrameric POMC receptor, one would not have expected to observe such different phenotypes for the p24-d2- and p24-d2-transgenic melanotrope cells. Reasoning along the same lines, the role suggested for p24 in vesicle biogenesis [5] appears to be improbable. Thus, the results of our study do not support a role for p24 in secretory cargo receptor or vesicle functioning, but rather are most consistent with a function in furnishing secretory pathway subcompartments. Our furnishing model is compatible with the results of other studies in which the expression of p24 was also manipulated. First, overexpressing p23 (p24 b1) or a p25 (p24 a2) mutant protein in cultured mammalian tumor cells resulted in the formation of Golgi mini-stacks and highly specialized lipid subdomains, respectively, leading the investigators to conclude that p24 proteins are involved in the formation of membrane subdomains in the early secretory pathway [13,14]. Second, antibodies against the cytoplasmic tails of p24a2, p24b1 or p24 (p24d2) inhibited the formation of transport carriers and cargo transport [10,12,28], consistent with a role for p24 in the supply of machinery cargo to ER-subdomains that are capable of forming transport carriers. Third, reducing the expression of Tmp21/p23 (p24d1) in mammalian cells in culture with siRNA led to an effect on the fate of the secretory cargo [22,23]. Fourth, the finding that in single and multiple yeast p24 knock-outs the vesicular incorporation and maturation of a specific set of secretory cargo proteins was reduced [6-9,15,29] is reminiscent of what we observed in the p24-d2-transgenic cells and may thus also be explained by an improper supply of subsets of machinery cargo involved in transport carrier formation or maturation of secretory cargo. In addition, these yeast knock-outs had defects in the retention of the ER-chaperones Kar2p (BiP) and protein disulfide isomerase, which may have been caused by an improper maintenance of the ER-retrieval machinery [8,15,29,30]. Fifth, the injection of antibodies against the cytoplasmic-tail of p23 (p24b1) into cultured mammalian tumor cells inhibited retrograde cargo transport due to a malfunctioning of the ER-retrieval machinery [31]. Indeed, p23 (p24b1) directly interacted with the KDEL-receptor, a component of the retrieval system [32]. Sixth, manipulation of p23 (p24b1) or p25 (p24d2) expression levels in cultured mammalian tumor cells affected the ER localization of the phosphatase machinery protein TC48 [33].
Seventh, in C. elegans mutated p24 proteins damaged the supply of machinery cargo involved in the quality control system, allowing the transport of a mutant cargo protein out of the ER [34]. Thus, the phenotypes displayed by the various cell types in which p24 expression had been manipulated are consistent with a role for p24 in the supply of machinery cargo to secretory pathway subcompartments. Such a role is supported by the results of our search of the BIOGRID database [35] for physical interactors with yeast p24 proteins revealing that, besides constituents of the COPI- and COPII-coat machinery, a substantial number of the interactors are components of the secretory pathway machinery, like membrane-lipid-synthesizing proteins and N- and O-glucosylation enzymes.

An intriguing extension of our model on the role of p24 concerns the recently proposed mechanism for the anterograde-directed bulk flow transport of secretory cargo with progressive en bloc protrusion from the ER, leading to the formation of large tubulo-saccular structures that transport the cargo to the Golgi apparatus [36]. In the so-called ER-exit sites (ERES) adjacent to the large cargo carriers, the COPII-system would recruit machinery needed to create a microenvironment in the ER and Golgi (e.g. a locally different pH or Ca²⁺ concentration) that facilitates efficient secretory cargo delivery to the newly forming transport carriers, and allows later trafficking and processing events [36]. For the Xenopus melanotrope cells, an attractive model for ER-to-Golgi secretory cargo transport may therefore involve an en bloc bulk-flow protrusion of POMC with each of the upregulated p24 family members recruiting a specific set of machinery cargo to the ERES in order to allow efficient transport and subsequent correct processing of POMC in the regulated secretory pathway of these neuroendocrine cells. Our model differs from the current models proposing a role for p24 as receptor for secretory cargo or in vesicle biogenesis, and will serve as a challenging foundation for future p24 research.

In summary, we explored the role of two p24 family members by applying a stable, cell-specific transgenic approach in a well-defined and physiologically relevant neuroendocrine cell model. Since both the p24α and as well as the p24α-transgenic melanotrope cells showed a nearly complete knockdown of the endogenous p24 proteins and still displayed disparate phenotypes, the observed effects are specific and caused by the transgene products rather than by the absence of the endogenous p24 proteins, indicating the selectivity and non-redundancy of our approach. We conclude that in the p24α-melanotrope cell phenotype an improper furnishing of machinery cargo to the early stages of the secretory pathway hampered transport of secretory cargo from the ER, whereas in the p24α-phenotype the supply of a different set of machinery cargo influenced post-translational secretory cargo modifications in the Golgi. Collectively, the results are thus most consistent with a role for p24 in furnishing the various subcompartments of the early secretory pathway with specific sets of machinery cargo in order to create the proper microenvironments for efficient and correct secretory cargo transport and processing to eventually generate bioactive proteins that function in the plasma membrane/extracellular matrix or are secreted into the extracellular space as biological signals.

MATERIALS AND METHODS

Animals

South African claw-toed frogs Xenopus laevis were bred and reared in the Central Animal Facility of the Radboud University (Nijmegen, The Netherlands). Animals were adapted to a black background for at least three weeks. All animal experiments were carried out in accordance with the European Communities Council Directive 86/609/EEC for animal welfare, permit RBD0166(H10) to generate and house transgenic Xenopus and permits RU-DEC 2003-53 and 2007-027 from the animal experiment committee of the Radboud University for the use of Xenopus laevis frogs.

Antibodies

The rabbit polyclonal antibodies against a region in the luminal part of Xenopus laevis p24α, against the C-terminal tail of Xenopus p24β, against part of the luminal region of Xenopus p24δ, against portions of the luminal and C-terminal regions of Xenopus laevis p24δ, (anti-1262N and anti-1262C respectively) and against the C-terminal region of Xenopus APP (C87) have been described previously [19,24,37]. We raised a polyclonal antibody against Xenopus p24β, by injecting rabbits with a recombinant protein encompassing the luminal domain of Xenopus p24β fused to GST. A polyclonal antibody against GFP was obtained from Dr. J. Fransen (NCMLS, Nijmegen, The Netherlands), against Xenopus POMC (ST62, recognizing only the precursor form) from Dr. S. Tanaka (Shizuoka University, Japan), against recombinant mature human PC2 from Dr. W.J.M. Van de Ven (University of Leuven, Belgium) and the monoclonal anti-tubulin antibody E7 was obtained from Dr. B. Wieringa (NCMLS, Nijmegen, The Netherlands) [38].

Generation of Xenopus laevis transgenic for p24α or p24δ

For the Xenopus transgenesis experiments, eggs were harvested from mature wild-type female Xenopus injected with 375 IU human chorionic gonadotropin hormone (Pregnyl; Organon, Oss, The Netherlands) 18 hrs before. The eggs were collected in 1xMMR (0.1M NaCl, 2mM KCl, 1 mM MgCl₂, 1.5mM CaCl₂, 5mM HEPES pH7.4) and dejellied in 2% L-cysteine/1 xMMR pH8.2.

To generate Xenopus laevis transgenic for p24α-GFP, a linear 2274-base pair SalI/NarI DNA fragment, containing a 529-base pair Xenopus POMC gene A promoter fragment (pPOMC [20]) and a cDNA encoding the Xenopus p24α protein (construct pPOMC-p24α-GFP) with the enhanced green fluorescent protein (GFP) protein fused in frame to its C-terminus (p24α-GFP fusion protein), was used for stable Xenopus transgenesis [39,40]. The linearized transgene DNA fragment was mixed with sperm nuclei prepared as described previously [20,40], incubated at room temperature (RT) for 15 min and injected into the unfertilized eggs. Normally cleaving embryos were selected at the 4-cell stage and grown in 0.1xMMR/6% Ficoll-400 (Sigma) with 50 µg/ml gentamycin (Gibco/BRL) at 18°C until gastrulation (stage 12 [41]) was reached and then in 0.1xMMR containing gentamycin at RT. In living stage-45 embryos [41] anesthetized with 0.25 mg/ml MS222 (3-aminobenzoic acid ethyl ester; Sigma) the presence of GFP fluorescence was examined using a Leica MZ FLIII fluorescence stereomicroscope and photographs were taken with a Leica DC200 color camera using the Leica DCview software. A number of injection rounds resulted in a number of F₀ animals expressing the fusion protein at various levels. F₁ transgenic Xenopus laevis offspring were generated by in vitro fertilization (IVF), either using pieces of testes from male transgenic frogs and eggs harvested from wild-type females or using pieces of testes from male wild-types and eggs from transgenic females. For IVF, the testes of male Xenopus frogs were isolated and incubated for 10 min with a monolayer of eggs harvested from females frogs injected with Pregnyl 18 hr before. 0.1xMMR was added and properly dividing embryos were selected and screened for GFP fluorescence as described above for F₀ tadpoles. To generate p24δ-transgenic
Xenopus, a linear 2166-base pair SalI/NotI DNA fragment (construct pPOMC-p24b-GFP), containing the Xenopus POMC gene A promoter (pPOMC [20]) and a cDNA encoding the Xenopus p24b protein with the enhanced GFP protein fused in frame to its C-terminus (p24b-GFP fusion protein), was used analogously to the method described above to generate the animals transgenic for p24b-GFP. A number of injection rounds resulted in a number of F0 animals transgenic for p24b-GFP and expressing the fusion protein at various levels. F1 transgenic Xenopus laevis offspring were generated by IVF, using pieces of testes from male transgenic frogs and eggs harvested from wild-type females.

Western blot analysis
Western blot analysis was performed as described previously [42]. Proteins on the blot were visualized by enhanced chemiluminescence using the Lumi-lightPLUS Western blotting substrate (Roche), detected in an Epi Chemi II Darkroom equipped with a 12-bit SensiCam CCD camera and quantified using the Labworks 4.0 program (UVP BioImaging systems, Cambridge, United Kingdom).

MALDI-TOF MS
Freshly dissected neurointermediate lobes (NILs) were homogenized on ice in cold 0.1% tri-fluoroacetic acid (TFA; mass spectrometry grade; Merck, Darmstadt, Germany) and kept on ice for 15 min. Subsequently, cell debris was pelleted by centrifugation (10 min, >15000xg, 4°C), and supernatants were collected and diluted in 0.1% TFA. The diluted homogenates, 1 μl was mixed with 10 μl of a saturated solution of α-cyano-4-hydroxy-cinnamic acid (CHCA; Sigma) in a 1:1 (v/v) acetonitrile (Sigma)/0.1% TFA mixture. A volume of 0.5 μl of this mixture was spotted on the sample plate and samples were measured in reflectron mode on a Bruker Biflex III machine (Bruker, FRG). The machine was calibrated with the reference peptides Bradykinin fragment 1–7 (757.3997Da; Sigma), Angiotensin II (1,046.5423Da; Sigma), synthetic peptide P14R(1,533,5852Da; Sigma) and human ACTH fragment 18–39 (2,463,1989Da; Sigma).

Pulse and pulse-chase analysis
For metabolic cell labeling, NILs from wild-type and transgenic Xenopus were mixed with 10 ml of a saturated solution of α-cyano-4-hydroxy-cinnamic acid, and diluted in 0.1% TFA. Of the diluted homogenates, 1 ml was for 15 min. Subsequently, cell debris was pelleted by centrifugation (10 min, >15000xg, 4°C), and supernatants were collected and diluted in 0.1% TFA. The diluted homogenates, 1 μl was mixed with 10 μl of a saturated solution of α-cyano-4-hydroxy-cinnamic acid (CHCA; Sigma) in a 1:1 (v/v) acetonitrile (Sigma)/0.1% TFA mixture. A volume of 0.5 μl of this mixture was spotted on the sample plate and samples were measured in reflectron mode on a Bruker Biflex III machine (Bruker, FRG). The machine was calibrated with the reference peptides Bradykinin fragment 1–7 (757.3997Da; Sigma), Angiotensin II (1,046.5423Da; Sigma), synthetic peptide P14R(1,533,5852Da; Sigma) and human ACTH fragment 18–39 (2,463,1989Da; Sigma).

HPLC
For the separation of the newly synthesized POMC-derived peptides, radiolabelled NIL lysates were subjected to HPLC analysis as described previously [44].

Transmission electron microscopy
For ultrastructural studies, NILs were freshly isolated from wild-type and transgenic Xenopus and fixed overnight at 4°C in 2% glutaraldehyde in 0.1 M phosphate buffer (PB, pH7.5). After rinsing in the same buffer, fixed tissues were osmicated for one hour in 1% osmium tetroxide in 0.1 M PB, rinsed in PB, dehydrated through graded series of alcohol and embedded in Epon 812. One-micron thick sections were cut, stained with toluidine blue and examined in a phase-contrast microscope (Diaphot 20, Leitz). Ultrathin sections were cut, double contrasted with uranyl-acetate/lead-citrate and photographed using a transmission electron microscope (JEOL1010).

Immuno-electron microscopy
For freeze substitution and low-temperature embedding, the tissue was rapidly frozen by a Leica EM High-Pressure Freezing system (HPF, Leica Microsystems) and transferred to the precooled chamber (−90°C) of a CS auto freeze substitution apparatus (Reichert-Jung, Germany). Freeze substitution was performed according to standard procedures. The tissue was immersed for 72 hours in acetone containing 0.5% uranyl acetate as fixing agent at −90°C and the temperature was then raised stepwise 4°C per hour to −45°C. Prior to infiltration with Lowicryl HM20 resin (Bio-Rad Richmond, California; USA), the tissue was washed several times with acetone at −45°C to remove water and excess uranyl acetate. The embedding process was carried out at −45°C in three stages, with a progressively increasing ratio of resin to acetone. Diffuse UV-radiation (360nm) was used to catalyze polymerization first at −45°C overnight and then at room temperature for 24 hrs. Thin sections were cut on a Reichert Ultracut-E and mounted on one-hole nickel grids coated with a formvar film.

For postembedding immunohistochemistry, ultrathin Lowicryl sections were washed for 10 min in phosphate buffered saline (PBS, pH 7.4) containing 0.1% sodium borohydride and 50 mM glycine, and for 10 min in PBS containing 0.5% BSA and 0.1% cold fish skin gelatine (PBG). For immunolabeling, sections were incubated overnight at 4°C in drops of PBG containing anti-GFP or anti-POMC antibody. Sections were washed for 20 min in PBG, incubated with protein A-labeled 10 nm gold markers, washed in PBS and postfixed with 2.5% glutaraldehyde in PB for 5 min to minimize loss of gold label during the contrast steps. After washing with distilled water, sections were contrasted in uranyl acetate and studied using a JEOL1010 TEM electron microscope.

Quantification and statistics
Statistical evaluation was performed using unpaired two-tailed t-tests. In those cases where the variances were significantly different, Welch’s correction was used. Calculations were performed using the GraphPad Prism 4 program (GraphPad Software).
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