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The vacuolar (H\(^+\))-ATPase (V-ATPase) is an important proton pump, and multiple critical cell-biological processes depend on the proton gradient provided by the pump. Yet, the mechanism underlying the control of the V-ATPase is still elusive but has been hypothesized to involve an accessory subunit of the pump. Here we studied as a candidate V-ATPase regulator the neuroendocrine V-ATPase accessory subunit Ac45. We transgenically manipulated the expression levels of the Ac45 protein specifically in Xenopus intermediate pituitary melanotrope cells and analyzed in detail the functioning of the transgenic cells. We found in the transgenic melanotrope cells the following: i) significantly increased granular acidification; ii) reduced sensitivity for a V-ATPase-specific inhibitor; iii) enhanced early processing of proopiomelanocortin (POMC) by prohormone convertase PC1; iv) reduced, neutral pH–dependent cleavage of the PC2 chaperone 7B2; v) reduced 7B2-proPC2 dissociation and consequently reduced proPC2 maturation; vi) decreased levels of mature PC2 and cortin (POMC) by prohormone convertase PC1; and vii) increased sensitivity for the V-ATPase-specific inhibitor. Together, our results show that the V-ATPase accessory subunit Ac45 represents the first regulator of the proton pump and controls V-ATPase-mediated granular acidification that is necessary for efficient prohormone processing.

INTRODUCTION

The vacuolar (H\(^+\))-ATPase (V-ATPase) is a proton pump that is crucial for a wide variety of biological processes, such as bone resorption by osteoclasts (Xu \textit{et al.}, 2007), maintenance of the acid-base balance by the renal alpha intercalated cells (Brown and Breton, 2000; Wagner \textit{et al.}, 2004), embryonic left-right patterning (Adams \textit{et al.}, 2006), and Wnt signaling during anterior-posterior patterning (Cruciat \textit{et al.}, 2010). Moreover, intracellular events such as membrane trafficking, receptor-mediated endocytosis, lysosomal hydrolysis, neurotransmitter uptake and release, and prohormone processing also highly depend on a low intragranellar pH provided by the V-ATPase (Schoonderwoert et al., 2001; Nishi and Forgac, 2002; Paroutis \textit{et al.}, 2004).

Prohormone processing to peptide hormones occurs in the regulated secretory pathway via endoproteolytic cleavage at pairs of basic amino acid residues by the prohormone convertase 1/3 (hereafter referred to as PC1) and prohormone convertase 2 (PC2) (reviewed by Hook \textit{et al.}, 2008). The maturation of the proform of PC1 takes place in the ER (Zhou and Mains, 1994), whereas proPC2 maturation occurs later in the secretory pathway, namely in the more acidic trans-Golgi network (TGN) and secretory granules (Zhou and Mains, 1994; Muller \textit{et al.}, 1997). Furthermore, the regulation of proPC2 transport and maturation by its chaperone 7B2 (Barbero and Kitabgi, 1999; Mbikay \textit{et al.}, 2001) as well as the enzymatic activities of PC1 and PC2 are highly dependent on the local intragranellar pH (Anderson and Orci, 1988; Tanaka \textit{et al.}, 1997; reviewed by Schoonderwoert and Martens, 2001). Thus, correct prohormone processing is critically relying on the supply of the proper pH to the various subcompartments of the regulated secretory pathway and therefore on the regulation of the V-ATPase.

At present, surprisingly little is known regarding the mechanism controlling the proton pump. A general mechanism of V-ATPase regulation may be represented by the coupling and uncoupling of its two main sectors (Beyenbach and Wieczorek, 2006), namely the cytoplasmic V1-sector responsible for energy delivery by ATP hydrolysis and the membrane-bound V0-sector that harbors the rotary mechanism to translocate protons across a membrane (reviewed by Jefferies \textit{et al.}, 2008). In the secretory pathway, the regulation and targeting of the pump has been hypothesized to be accomplished by an accessory subunit of the V-ATPase (Su-
Subunit Ac45 Regulates the V-ATPase

Brain-pituitary preparations were dissected from juvenile transgenic frogs and fixed in 4% paraformaldehyde in phosphate-buffered saline (PBS, pH 7.4). After cryo protection in 10% sucrose-PBS, sagittal 20-μm cryo sections were mounted on poly-L-lysine–coated slides and dried for 2 h at 45°C. For immunohistochemistry, sections were rinsed for 30 min in 50-μM Tris-buffered saline (pH 7.6) containing 150 mM NaCl and 0.1% Triton X-100 (TBS-TX). To prevent nonspecific binding, blocking was performed with 0.5% BSA in TBS-TX. Sections were incubated with anti-POMC (ST62, 1:2000) antibodies for 2 h in TBS-TX containing 0.5% BSA. After rinsing with TBS-TX, a secondary antibody, Goat-anti-Rabbit-Alexa Fluor 568 (Molecular Probes, Eugene, Oregon, USA) at a dilution of 1:100, was applied and sections were incubated for 1 h at 37°C. After an additional washing step, the sections were mounted in Moviol (Calbiochem, La Jolla, CA) containing 2.5% sodium azide and coveredslips. Immunofluorescence was viewed under a Leica DMRA fluorescence microscope.

**Measurement of Intragranular Acidification**

To study granular activation, the 3-(2,4-dinitroanilino)-3’-aminomethyl-dipropylamine (DAMP) method of Orri (Orri et al., 1986) was applied with slight modifications. After dissection, neurotransmitter lobes (NILs) of wild-type and transgenic Xenopus were preincubated for 60 min in Ringer’s/BSA. To further control NILs were preincubated in Ringer’s/BSA containing 1 μM bafilomycin A1 (Sigma-Aldrich, St. Louis, MO) and transferred to Ringer’s/BSA containing 60 μM DAMP (Molecular Probes, Eugene, OR), incubated for 2 h at 22°C and fixed in Karnovsky’s Fixative (2% paraformaldehyde, 2% glutaraldehyde in phosphate buffered pH 7.4). The tissue was rapidly frozen and immersed in acetone containing 0.5% uranyl acetate as fixation agent at −90°C. The temperature was raised stepwise to −4°C and the tissue was then infiltrated with Locryl (Vitrogon Carlsbad USA). 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 contrasting steps. After washing with distilled water, sections were contrasted in uranyl acetate and studied using a Jeol transmission electron microscopy (TEM) 1010 electron microscope. For quantification, gold particles in dense-cored granules were counted and the surfaces of the granules were measured using the ImageJ free software package.

**Metabolic Cell Labeling and Immunoprecipitations**

For radioactive labeling of newly synthesized proteins, freshly isolated Xenopus NILs were preincubated for 10 min in Ringer’s medium (112 mM NaCl, 2 mM KCl, 1.0 mM CaCl2, 1.5 mM HEPES pH 7.4, 2 μg/ml glustaride, 1 μg/ml BSA) containing 0.3 mg/ml BSA (Ringer’s/BSA), then incubated in Ringer’s/BSA containing 1.7 μCi/ml Tran32S label (MP Biomedicals) for indicated time periods and subsequently chased in 50 μl Ringer’s/BSA supplemented with 0.5 mM L-methionine as described previously (Bouw et al., 2000; Sterenberg et al., 2001; van Rosmalen and Martens, 2007; Stratting and Martens, 2009). Chase incubations were in the absence or presence 0.25 μM and 0.5 μM bafilomycin A1 (Sigma). Lobes were lysed in 100 μl lysis buffer (50 mM HEPES pH 7.4, 140 mM NaCl, 0.1% Triton-X100, 1% Tween-20, supplemented with Complete protease inhibitor mix (Roche Diagnostics, Mannheim, Germany), and lysates and media were cleared by centrifugation (13,000g; 7 min) and directly analyzed by SDS-PAGE. The gel migration positions of 37-kDa POMC, 18-kDa POMC, the various PC2 forms, and the GFP-Ac45 protein corresponded to those previously observed (Braks and Martens, 1994; Holthuis et al., 1995; Jansen et al., 2008). POMC represents more than 80% of all newly synthesized melanotrope proteins (Holthuis et al., 1995) allowing its direct analysis (i.e., no need for immunoprecipitation). The amounts of newly synthesized 37-kDa POMC and 18-kDa POMC were quantified by a Phosphoimager (Bio-Rad), need for immunoprecipitation). The amounts of newly synthesized 37-kDa POMC and 18-kDa POMC were quantified by a Phosphoimager (Bio-Rad), need for immunoprecipitation). The amounts of newly synthesized 37-kDa POMC and 18-kDa POMC were quantified by a Phosphoimager (Bio-Rad), need for immunoprecipitation). The amounts of newly synthesized 37-kDa POMC and 18-kDa POMC were quantified by a Phosphoimager (Bio-Rad), need for immunoprecipitation). The amounts of newly synthesized 37-kDa POMC and 18-kDa POMC were quantified by a Phosphoimager (Bio-Rad), need for immunoprecipitation). The amounts of newly synthesized 37-kDa POMC and 18-kDa POMC were quantified by a Phosphoimager (Bio-Rad), need for immunoprecipitation). The amounts of newly synthesized 37-kDa POMC and 18-kDa POMC were quantified by a Phosphoimager (Bio-Rad), need for immunoprecipitation).
Western Blot Analysis

Freshly dissected NILs were homogenized in 100 μl lysis buffer and 20% of the lysates was denatured, separated on SDS-PAGE and transferred to nitrocellulose or PVDF membrane. Following blocking, blots were incubated with anti-POMC (1:6,000), anti-PC2 (1:3,000), anti-PC1 (1:1,000), or anti-calnexin (1:10,000) rabbit antisera and with secondary peroxidase-conjugated Goat-anti-rabbit antibody followed by chemiluminescence. Signals were detected and quantified using a BioImaging system with Labworks 4.0 software (UVP Bioimaging systems, Cambridge, UK). Calnexin was used as a reference because expression levels of this protein were unaffected by our transgenic manipulations (van Rosmalen and Martens, 2007 and our unpublished observations).

Supernusion and α-MSH Radioimmunoassay

NILs were isolated from wild-type and Ac45-transgenic Xenopus and transferred to Ringer’s solution in superfusion chambers. The NILs were then superfused in Ringer’s supplemented with 1 μg/ml ascorbic acid at a rate of 30 μl/min. 7.5-min fractions were collected and stored on ice. Fifty microliters of each fraction was used in an α-MSH RIA (van Zoest et al., 1989). In short, 125I labeled α-MSH (10,000 cmap/100 μl) was diluted in 90 ml VAT-buffer (0.02 M Veronal, 0.2 g/l sodium azide, 0.3% BSA, 100 IU/ml trasylol, pH 8.6) and rabbit α-MSH antiserum L9 (1:6,000) (van Zoest et al., 1989) in 180 ml VAT buffer and pooled (RIAmix). Fifty microliters of each superfusion fraction was incubated with 450 μl RIAmix for 48 h at 4°C. An α-MSH standard dilution series (100 pg/μl to 0 pg/μl) was included. Reactions were stopped by adding 1 ml precipitation mix (30% polyethylene glycol, 4.8% chicken egg albumin), mixed, and pelleted (20 min, 4000 rpm, Jouan CR 4.11 with an E4 swingout rotor, 4°C). Radioactivity was measured using a 2 Clinigamma counter (LKB Wallac). Two independent experiments, n = 4 wt NILs, n = 4, Ac45-transgenic NILs, per experiment were performed. The supernusion experiment, NILs were recovered, homogenized in lysis buffer, and the lysates were subjected to Western blot analysis with anti-calnexin antibodies to measure the relative amounts of melanotrope cells.

Statistics

Data are presented as means ± SEM. Statistical evaluation was performed using an unpaired Student’s t test.

RESULTS

Generation of Transgenic Xenopus laevis Expressing Excess Ac45 Specifically in the Intermediate Pituitary Melanotrope Cells

We performed stable Xenopus transgenesis using a 529-bp fragment of the POMC gene promoter (Figure 1A) to drive transgenic Ac45 expression specifically to the neuroendocrine melanotrope cells. The length of the POMC promoter fragment was such that transgene expression was observed only in the melanotrope cells and not in other POMC-expressing cell types such as the corticotrope cells in the anterior pituitary or hypothalamic neurons (Jansen et al., 2002). Independent transgenic Xenopus lines were established, expressing Ac45 fused to the GFP. Direct fluorescence microscopy on pituitaries of adult Ac45-transgenic animals clearly showed that the transgene expression was exclusively in the intermediate pituitary melanotrope cells (Figure 1B) and the specificity was confirmed by the colocalization of the transgene product with the main melanotrope secretory cargo protein POMC (Figure 1C).

The Ac45-transgene product was targeted to secretory granules and efficiently transported through the secretory pathway to the plasma membrane where it was colocalized with the endogenous V-ATPase (Jansen et al., 2008). Furthermore, the Ac45-transgenic cells were characterized by a higher abundance of immature secretory granules and harbored an increased Ca2+-dependent secretory efficiency (Jansen et al., 2008). To examine the effect of excess Ac45 on granular acidification and propertion processing in the regulated secretory pathway, we analyzed melanotrope cells that expressed an ~10 times excess of the Ac45 protein (line #533, Jansen et al., 2008).

Statistics

Data are presented as means ± SEM. Statistical evaluation was performed using an unpaired Student’s t test.
transgenic melanotrope cells resulted in a decreased intragranular pH.

Excess Ac45 Affects the Sensitivity of the Melanotrope Cells for the V-ATPase–Specific Inhibitor Bafilomycin A1

We then examined the V-ATPase system by establishing the effect of the V-ATPase-specific inhibitor bafilomycin A1 on processing of newly synthesized proproteins in the transgenic Xenopus melanotrope cells. In the early secretory pathway of Xenopus melanotrope cells, 37-kDa POMC is processed by PC1 into 18-kDa POMC, representing the N-terminal portion of the POMC molecule and containing the only N-glycosylation site in the POMC molecule (Martens et al., 1982; Ayoubi et al., 1990). We decided to use bafilomycin A1 because the action of this inhibitor toward the V-ATPase has been well characterized (Bowman and Bowman, 2002; Huss et al., 2002; Bowman et al., 2006). Interfering with neuroendocrine V-ATPase activity through its inhibition by bafilomycin A1 greatly reduced prohormone trafficking and processing and the secretion of peptide hormones via the regulated secretory pathway (Tanaka et al., 1997; Schoonderwoert et al., 2000). The 37-kDa POMC protein and the ~75-kDa proform of PC2 clearly represent the majority (~90%) of the newly synthesized protein pool in the Xenopus melanotrope cells (Holthuis et al., 1995) and their subsequent processing products have been previously characterized (Braks and Martens, 1994; Holthuis et al., 1995). We therefore focused on the processing of these two proteins.

In wild-type Xenopus melanotrope cells, bafilomycin A1 inhibited the proteolytic processing of newly synthesized 37-kDa POMC and of ~75-kDa proPC2, resulting in an accumulation of 37-kDa POMC and 71-kDa PC2 clearly represent the majority (~90%) of the newly synthesized protein pool in the Xenopus melanotrope cells (Holthuis et al., 1995) and their subsequent processing products have been previously characterized (Braks and Martens, 1994; Holthuis et al., 1995). We therefore focused on the processing of these two proteins.

Figure 2. Excess Ac45 causes enhanced intragranular acidification in transgenic melanotrope cells. (A) Immunogold labeling of ultrathin sections of DAMP-incubated wild-type (wt) or Ac45-transgenic (tg) Xenopus melanotrope cells with the anti-DNP antibody in combination with 10-nm protein-A gold. Gold labeling was predominantly found in the secretory granules (arrows) and lysosomes (L). Bars equal 200 nm. (B) Quantification of intragranular DAMP accumulation. The number of gold particles per μm² found in 205 wt and 206 tg dense-core secretory granules of 20 randomly selected wt or tg melanotrope cells from three wt or tg frogs.
Excess Ac45 Affects the Steady-State Level of PC2 but not of PC1 or POMC

Having established that excess Ac45 affected the V-ATPase system, we then studied the steady-state levels of POMC, PC1, and PC2. Quantitative Western blot analysis revealed no significant differences in the expression levels of POMC, PC1, as compared with the reference protein, the ER chaperone calnexin (Figure 4, A and B). Intriguingly, in the Ac45-transgenic NILs we found an ∼75% reduction of the steady state PC2 expression level compared with that in wild-type NILs (Figure 4, A and C). Apparently, the decrease in intragranular pH caused by the excess of Ac45 provided a change in microenvironment of the secretory pathway affecting the steady state expression level of mature PC2 but not of PC1 and POMC.

Excess Ac45 Increases the Rate of the Early Endoproteolytic Cleavage of Newly Synthesized 37-kDa POMC to 18-kDa POMC

To examine the effect of the excess of Ac45 on the processing of newly synthesized 37-kDa POMC in the regulated secretory pathway, we performed metabolic cell labeling studies on wild-type and Ac45-transgenic NILs. In addition to the biosynthetically active melanotrope cells of the intermediate lobe, the *Xenopus* NIL consists of nerve terminals of hypothalamic origin (the neural lobe) and because the nerve terminals are biosynthetically inactive the radiolabeled proteins are synthesized by the melanotropes. Following a 30-min pulse incubation of wild-type NILs, clearly the most prominent newly synthesized product was 37-kDa POMC that during the subsequent chase periods was converted into 18-kDa POMC. The 18-kDa POMC product was subsequently secreted into the incubation medium (Figure 5A). After a 30-min pulse metabolic labeling of the Ac45-transgenic NILs, the biosynthesis of the newly synthesized proteins was similar to that in the wild-type NILs. However, during the chase periods the transgenic cells had converted clearly more 37-kDa POMC into 18-kDa POMC, resulting in an ∼3 times higher 18K/37K ratio (Figure 5B). Moreover, the release of 18-kDa POMC by the transgenic cells started already during the 120-min chase, whereas 18-kDa POMC secretion by the wild-type cells was detected only after 180 min of chase. After the 180-min chase period, the amount of 18-kDa POMC released into the incubation medium by the transgenic cells was ∼3 times higher than that released by wild-type cells (Figure 5B). These results suggest that excess Ac45 increased the rate of POMC processing in the secretory pathway.

Excess Ac45 Affects ProPC2 Maturation, 7B2 Cleavage, and ProPC2–7B2 Interaction

Biosynthetic labeling studies combined with anti-PC2 immunoprecipitations revealed that the newly synthesized expression levels of proPC2 did not differ between wild-type and Ac45-transgenic melanotrope cells (Figure 6A). After a 20-min pulse/45-min chase period, no proPC2 conversion was observed in both wild-type and the Ac45-transgenic cells. However, after a 90-min chase period, in the transgenic cells proPC2 conversion was clearly delayed compared with that in wild-type cells, resulting in an ∼2.5 times lower ratio of mature to proPC2 in the transgenic melanotropes (Figure 6, A and B).

Figure 4. Steady-state PC2 protein expression levels are lower in Ac45-transgenic melanotrope cells. (A) Western blot analysis of total proteins extracted from wild-type and Ac45-transgenic neurointermediate lobes of black-adapted *Xenopus* using various antibodies. (B–C) Steady-state protein levels of POMC (B), and PC2 (C) are presented in arbitrary units (AU) relative to the steady-state levels of calnexin.

Transport and activation/maturation of PC2 depends on its neuroendocrine chaperone 7B2 (Mbikay *et al*., 2001). We therefore also compared the fate of 7B2 in wild-type and Ac45-transgenic melanotrope cells using metabolic cell labeling and immunoprecipitations for 7B2. The expression levels of newly synthesized 25-kDa 7B2 (pro7B2) were similar between wild-type and the transgenic cells (Figure 6C). In wild-type cells, newly synthesized 25-kDa 7B2 was gradually converted to its 18-kDa processed form (Figure 6C). However, in the Ac45-transgenic cells, 7B2 processing was delayed resulting in the sustained presence of the intact 7B2 25-kDa form during the subsequent chase periods (Figure 6C). Interestingly, after a 60-min chase period, also in the transgenic melanotrope cells most 25-kDa 7B2 was converted to its 18-kDa form.

Because the processing of 7B2 takes place in the Golgi compartment (Paquet *et al*., 1994), the delay in 7B2 processing was apparently caused in the early secretory pathway. We therefore focused on 7B2 processing and its binding to...
proPC2 during the first hour after the start of its synthesis. Indeed, after a 20-min pulse/45-min chase period, a significant reduction in 7B2 processing was observed in the Ac45-transgenic melanotrope cells (Figure 6, C and D). We then performed coimmunoprecipitation experiments under native conditions to study the proPC2/7B2 complex. Interestingly, the lower rate of 7B2 processing in the Ac45-transgenic cells (Figure 6, C and D) resulted in a slight increase of 25-kDa 7B2 coimmunoprecipitating with proPC2 after the 45-min chase period (Figure 6, E and F). We conclude that manipulation of the V-ATPase system in the regulated secretory pathway by excess Ac45 results in a slower degree of proPC2 maturation, a slower processing of 7B2, and a sustained proPC2-pro7B2 interaction in the secretory pathway.

Excess Ac45 Decreases the Secretion of α-MSH

The initial processing of 37-kDa POMC to 18-kDa POMC is an early, PC1-mediated endoproteolytic cleavage taking place in the TGN/immature secretory granules (Ayoubi et al., 1990; Berghs et al., 1997), and the rate of this processing event is increased in the Ac45-transgenic melanotrope cells (Figure 5). Subsequent processing events result in the generation of the main melanotrope hormone α-MSH and are mediated by PC2 in the later stages of the secretory pathway, namely in the acidic secretory granules (Berghs et al., 1997). Superfusion experiments combined with an α-MSH radioimmunoassay (van Zoest et al., 1989) revealed that α-MSH secretion was decreased ~40% (Figure 7A); the number of transgenic and wild-type melanotrope cells superfused was similar (Figure 7B). Thus, excess Ac45 reduced the amount of α-MSH secreted, presumably as a consequence of the observed lower degree of proPC2 conversion to mature PC2 in the Ac45-transgenic cells.

DISCUSSION

To study the role of the V-ATPase accessory subunit Ac45 and the regulation of the V-ATPase pump, we generated transgenic Xenopus expressing the Ac45 protein specifically in the melanotrope cells and examined the effect of the excess of Ac45 on granular acidification and prohormone processing. Excess Ac45 increased intravesicular acidification because a clearly higher number of gold particles was found in vesicles of the Ac45-transgenic melanotrope cells (595 per μm²) than in the granules of wild-type melanotropes (248 per μm²). The number of gold particles per μm² found in the wild-type granules is in line with that detected in POMC-containing vesicles of mouse corticotrope AtT-20 cells (~250 per μm²) (Tanaka et al., 1997). Thus, the intravesicular pH is comparable between these two neuroendocrine and POMC-producing cell types. Application of the formula of Orci (Orci et al., 1986) to estimate the pH in acidic subcellular organelles on the basis of the density of gold particles due to DAMP accumulation indeed revealed a substantial reduction (~0.4 pH unit) in the average intragranular pH in the transgenic melanotrope cells when compared with that in granules of wild-type melano-
The fact that in the transgenic cells the specific V-ATPase inhibitor bafilomycin A1 less effectively interfered with proPC2 maturation and POMC processing than in wild-type cells also points to an increased V-ATPase activity and thus a lower pH in the TGN/immature secretory granules. Interestingly, disruption of the gene encoding the proprotein cleavage enzyme furin in mouse pancreatic β-cells resulted in an impaired intragranular acidification in these cells (Louagie et al., 2008). Furin is thought to cleave the Ac45 protein into its functional form, and therefore Louagi et al. speculated that a lack of functional Ac45 may have caused the observed decrease in granular acidification (Louagie et al., 2008). Our results now provide direct evidence for an important role of Ac45 in granular acidification. Intriguingly, a proper intracellular pH is also crucial for correct early embryonic development (Allan et al., 2005; Adams et al., 2006; Liegeois et al., 2006; Nuckels et al., 2009; Cruciat et al., 2010) and may well explain the fact that our ablation of the Ac45 gene in the mouse led to early embryonic lethality (Schoonderwoert and Martens, 2002).

We recently found that in the Ac45-transgenic Xenopus melanotrope cells not only the plasma membrane morphology was affected, but also that vesicle biogenesis and the secretory efficiency were enhanced (Jansen et al., 2008). The present results show that excess Ac45 also causes a lower pH in subcompartments of the regulated secretory pathway, a situation that is beneficial for the formation of immature secretory granules (Chanat and Huttner, 1991; Tapon et al., 2005). In addition, the more acidified secretory pathway subcompartments affected proprotein processing. Because only the steady-state level of mature PC2 and not that of mature PC1 was decreased, the pH in the ER, the site of

![Figure 6](image-url)

**Figure 6.** ProPC2 maturation and pro7B2 processing are delayed in Ac45-transgenic melanotrope cells. (A) Wild-type (wt) and Ac45-transgenic (tg) neurointermediate lobes (NILs) were pulse labeled for 20 min and subsequently chased for indicated time periods. After protein extraction, immunoprecipitation analyses were performed using an anti-PC2 antibody. (B) Quantification of PC2 maturation was calculated from the matPC2:proPC2 ratio. (C) Pulse-chase-labeled NIL proteins were immunoprecipitated using an anti-7B2 antibody. (D) Quantification of 7B2 processing was calculated from the 18-kDa 7B2:25-kDa 7B2 ratio. Shown are the means ± SEM (n = 4). Significant differences are indicated by *(p < 0.05). (E) Pulse-chase-labeled NIL proteins were extracted under native conditions, and proPC2 and 7B2 were communoprecipitated under native conditions using an anti-PC2 antibody; the PC2 gel was exposed for one day and the 7B2 gel for 12 d. (F) Quantification of the amount of 25-kDa 7B2 binding to proPC2 was calculated from the 25-kDa 7B2: proPC2 ratio; the difference was not statistically significant (p = 0.3).
proPC1 maturation (Zhou and Mains, 1994), likely remained unaffected.

In biosynthetic pulse-chase studies on metabolically labeled melanotrope cells, we focused on the fate of newly synthesized POMC, the prohormone that represents 80% of all radiolabeled proteins produced in the melanotropes. The transgenic manipulation did not affect the level of newly synthesized 37-kDa POMC but caused a higher rate of processing of the prohormone to the 18-kDa POMC cleavage product and consequently more 18-kDa POMC was secreted by the transgenic than the wild-type cells. This first POMC cleavage event is thought to be accomplished by PC1 and occurs in the TGN/immature secretory granules (Berghs et al., 1997). Thus, the excess of Ac45 apparently provided an attractive microenvironment for proPC1 enzyme activation (which has a pH optimum of 6.0, Cameron et al., 2001) that led to efficient early POMC processing to 18-kDa POMC. In addition, or alternatively, the observed increased levels of intracellular and secreted 18-kDa POMC may have been caused by reduced PC2-mediated cleavage of this N-terminal portion of POMC to γ-MSH, due to the low levels of mature PC2. Likewise, reduced PC2-mediated processing of the C-terminal part of POMC may well have led to the significantly lower amounts of another form of MSH, namely of the main melanotrope bioactive peptide α-MSH (Figure 8).

Earlier studies have shown that the proteolytic maturation and processing activity of the PC2 enzyme highly depend on a correct local pH (Lamango et al., 1999; Li et al., 2003). It is therefore not surprising that less amounts of mature PC2 were found in the Ac45-transgenic cells. The reduced PC2 cleavage activity led to less hormone-producing POMC processing events in the late secretory pathway. In the transgenic cells, the activities of other late-acting POMC processing enzymes may be affected as well, including the activity of the recently described cysteine protease cathepsin L (Funkelstein et al., 2008). Moreover, the time period for these late processing events is likely reduced due to the increased secretory efficiency of the transgenic cells (Jansen et al., 2008). Interestingly, in the furin/mouse pancreatic β-cells with a distorted granular pH the rate of proPC2 maturation was also decreased and consequently a lower degree of proinsulin II processing was observed (Louagie et al., 2008).

In the Ac45-transgenic melanotrope cells, the degree of proteolytic cleavage of 7B2, an event taking place in the TGN and thought to be executed by furin (Paquet et al., 1994), was clearly reduced, resulting in higher levels of intact 7B2 and prolonged 7B2-proPC2 binding. Because furin displays its highest activity at neutral pH (Hatsuzawa et al., 1992), it is likely that in the more acidic environment of the transgenic cells this proprotein cleavage enzyme is less active, leading to the sustained 7B2-proPC2 interaction and ultimately to the observed low levels of mature PC2.

In conclusion, our results show for the first time a central role for the Ac45 protein in controlling and assisting the V-ATPase, thereby greatly affecting granular acidification and subsequent proprotein processing in the regulated secretory pathway. Moreover, our results suggest that other V-ATPase accessory subunits may have an important role as well in cell- and cell organelle-specific targeting and regulation of the V-ATPase.

![Figure 7.](image)

**Figure 7.** Ac45-transgenic melanotrope cells secrete less α-MSH than wild-type cells. (A) Wild-type (wt) and Ac45-transgenic (tg) neurointermediate lobes were isolated and directly superfused. To measure the amount of α-MSH released into the medium, fractions of the superfusion medium were collected and subjected to an α-MSH radioimmunoassay. The average α-MSH release during a ~50-min period (7 fractions) was measured. The amount of α-MSH released was normalized for calnexin levels (see B) and the release of α-MSH by wild-type cells was set to 100%. Shown are the means ± SEM (n = 4). Significant difference is indicated by * (p < 0.05). (B) To estimate the number of wt and tg melanotrope cells, after superfusion the amount of the reference protein calnexin was determined by Western blot analysis.

![Figure 8.](image)

**Figure 8.** Processing of POMC by PC1 and PC2. Simplified version of the POMC processing scheme of Bicknell (Bicknell, 2008). Only the cleavage events pertinent to the present study are indicated. Filled dot, N-linked glycosylation site; MSH, melanophore-stimulating hormone; JP, joining peptide; CLIP, corticotropin-like intermediate lobe peptide.
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