The molecular and biochemical basis of nonshivering thermogenesis in an African endemic mammal, *Elephantulus myurus*

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**The success of early mammals is often attributed to the ability to produce heat endogenously through nonshivering thermogenesis (NST)** (6, 24). In eutherian mammals, NST is known to occur in brown adipose tissue (BAT), in which uncoupling protein 1 (UCP1) works to generate heat instead of ATP (6, 13, 15, 36). However, the often repeated statement that all eutherians exhibit BAT is based on only a few representatives of the subclass. Until recently, UCP1 was thought to be associated exclusively with NST in eutherian mammals. However, it has been demonstrated by conserved synteny that UCP1 appears in the vertebrate line as early as before the divergence of ray-finned and lobe-finned fishes (17), although a thermogenic function of fish UCP1 is unlikely. This finding begs the question of where in the vertebrate lineage UCP1 gained a thermogenic function as well as the adaptive significance of UCP1 presence.

**Within the Marsupialia and the Monotremata, the presence and function of UCP1 remain controversial.** The elephant shrews belong to the Afrotheria, a group of mammals thought to be at the base of the eutherian radiation (35). Their phylogenetic placement thus makes them an excellent model in the quest for the presence of UCP1- and BAT-mediated thermogenesis. In addition, the rock elephant shrew, *Elephantulus myurus*, shows a pronounced thermogenic response to norepinephrine (NE) injection (28), which is often taken as an indicator of BAT-mediated NST (5, 6). However, at present, it is unclear whether this NE-induced thermogenesis observed in *E. myurus* is indicative of classical NST and whether it is of any adaptive value, that is, can be recruited in the cold.

**Classical, adaptive, cold-mediated NST is accompanied by a pronounced recruitment of BAT and enhanced thermogenic capacity** (6, 12, 15, 20). This adaptive thermogenic capacity is evident as changes in physiological and biochemical parameters, such as high mitochondrial density and respiratory capacity in BAT, a high UCP1 concentration in BAT mitochondria of cold-acclimated mammals (19, 20), as well as a higher metabolic response to NE injection compared with warm-acclimated animals. Furthermore, in rodents, UCP1 increases proton leak in the presence of free-fatty acids, in a GDP-sensitive manner (32). In addition, basal metabolic rate (BMR) is increased in the cold, a response thought to be associated with increased blood flow to intestinal organs and increased peripheral vascularization (10).

**Drastic seasonal changes in thermogenic capacity are often associated with high-latitude species.** However, it is becoming increasingly clear that phenotypic plasticity is selected for even in those species from tropical and subtropical environments because plasticity allows organisms to match environmental variability at an ecological scale (25, 26, 31). We might therefore expect the African-endemic elephant shrews to exhibit adaptive changes in their thermogenic properties during warm and cold acclimation.

**The aim of the study was therefore twofold. First, we aimed to elucidate the molecular and biochemical basis of nonshivering thermogenesis in the rock elephant shrew, *E. myurus*.** Our approach was to investigate the occurrence of BAT and the patterns of tissue expression of UCP1 in *E. myurus*, as well as to characterize UCP1 function by measuring the proton leak kinetics of isolated BAT mitochondria. Second, we investigated whether parameters associated with thermoregulation and cold adaptation, such as BMR, NST capacity, amount of UCP1, and cytochrome c oxidase activity, were regulated in response to cold and warm acclimation.

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MATERIALS AND METHODS

Study animals. Adult E. myurus (n = 12) were captured on the MacKay farm, 17 km east of Estcourt (28°56’749’S 30°00’848’E), KwaZulu-Natal, South Africa, in June 2006. They were then flown to Germany and housed in the Department of Animal Physiology, Philippi Universität Marburg. Within 3 wk of arrival, three of the animals died, presumably because of stress associated with capture and handling.

The animals were individually housed in large Makrolon Type IV cages and provided with sawdust bedding and nesting boxes. They were maintained at 24°C under a 12:12 light-dark photoperiod. Food and water were available ad libitum throughout the study. The animals were fed ProNuto, a commercial high-protein cereal (22% protein, 59% carbohydrate, and 6% fat) mixed with water. This diet was alternated with canned dog food and was supplemented with fresh lettuce and cockroaches. The food was replenished once every 24 h.

Experimental sequence. All experiments complied with the German Animal Welfare Laws, were approved by the university’s local animal care and use committee, and are fully compliant with the American Physiological Society’s “Guiding Principles for Research Involving Animals and Human Beings.”

The metabolic measurements were made in October–December 2006. Our approach was to first measure BMR and NST capacity of animals acclimated to 24°C, after which the animals were divided into two groups, the warm-acclimated (WA) group (n = 4) at 28°C and the cold-acclimated (CA) group (n = 5) at 18°C. We expected that both BMR and NST capacity would increase and decrease under cold and warm acclimation, respectively. The BMR of the animals was measured at 31°C. This temperature is within the known thermoneutral zone for this species (23). After measurement of BMR, the NST capacity of the animals was tested by measurement of the metabolic response to NE injection. The animals were then maintained at their respective acclimation temperatures for at least 3 wk before repeat measurement of BMR, and NST capacity measurements were made. After 4 wk, the animals were killed so as to ascertain the biochemical and molecular basis of nonshivering thermogenesis in this species.

Measurement of BMR and NST capacity. Animals were placed in 1.8-liter metabolic chambers inside a constant environment cabinet. Oxygen consumption ($\dot{V}O_2$) was measured using an open-flow system using an electrochemical analyzer (S-3AII, Ametek). Air was pumped through the metabolic chambers at flow rates ~50 l/h. The use of solenoid relay valves for each chamber allowed us to measure three animals and a control channel sequentially in 1-min intervals. Measurements were therefore obtained for each animal every 4 min. During the determination of NST capacity, we measured single animals and therefore increased the resolution of measurement to 2 min. Further details of the respirometry system have been described previously by Heldmaier and Ruf (11).

All metabolic measurements were made during the daytime, the known rest phase for this species (30). On each measurement day, animals were removed from their cages around 0900, and measurements commenced shortly thereafter. The animals were kept in the metabolic chambers for at least 6 h, and the BMR was taken as the mean of the three lowest consecutive measurements, equivalent to 12 min, obtained during the last 2 h of data measurements. The length of time spent in the metabolic chambers coupled with the fact that the animals were not fed before measurement ensured that the animals were postabsorptive at the time of BMR determination. Animals were allowed at least 3 days of recovery from BMR measurements, after which their capacity for NST was determined through the injection of NE.

The measurements of response to NE were made at 25°C, so as to avoid hyperthermia (31). We used 85% of the dose recommended by Wunder and Gettinger (0.458 mg/kg; Ref. 36) because Mzilikazi and Lovegrove (30) demonstrated that the maximal NE-induced thermogenesis in this species can already be elicited at this dose. Animals were injected with NE at least 2 h after they were initially placed in the respirometers. For each animal, the NST capacity was determined as the difference between the highest NE-induced $\dot{V}O_2$ and the BMR.

Cloning of Ucp1 cDNA and phylogenetic inference. Total RNA was isolated from selected tissues, and cDNA was synthesized as described previously (16). Primers were deduced from the lower hedgehog telec (Echinops telfairi) genome found at www.ensembl.org. Primers (forward: 5’-GACTATGGGGTGGAAGATCCTT-3’; reverse: 5’-AAGGCCCAGGCGCTTTGTTG-3’) were used for PCR on cDNAs of the interscapular fat deposit of E. myurus. Forty cycles of denaturation at 94°C (1 min), annealing at 59°C (1 min), and elongation at 72°C (1 min) were performed. A final extension at 72°C was applied for 10 min and followed by rapid cooling to 4°C. The PCR product was gel purified and ligated into a pJE1/blunt cloning vector (Fermentas). Inserts were sequenced using vector-based primers.

Three plant UCPs, three bird UCPs, 22 UCP2, 16 UCP3, and 22 UCP1 sequences, including the novel E. myurus sequence, were aligned and subjected to phylogenetic analysis using neighbor-joining method as described previously (16). For bootstrap analysis, the alignment data set was shuffled 1,000 times. The phylogenetic tree was derived from 1,000 bootstrap-replicated neighbor-joining trees. Bootstrap values were calculated from the neighbor-joining trees with 1,000 replications for support at each node. Clusters were considered significantly different when the bootstrap value was >70%.

Immunological detection of UCP1. Samples of frozen tissues were homogenized in sample buffer (100 mM KH2PO4/K2HPO4, 2 mM EDTA pH 7.5), after which the protein concentration was determined by the Bradford method. Protein samples were then run on a SDS-polyacrylamide gel (3% stacking gel and 12.5% running gel). The protein was then transferred to a nitrocellulose membrane (Hybond-N, Amersham), and UV cross-linked. All blots were hybridized with probes corresponding to the cDNA sequences of E. myurus UCP1. The cDNA probes were labeled by random priming with [α-32P]dATP. Nonspecific binding was blocked in BSA solution (0.5 M Na2HPO4/NaH2PO4, pH 7.0, 1 mM EDTA, pH 8.0, 0.7% SDS, 1% BSA) for at least 1 h and hybridized overnight at 63°C with the 32P-labeled probe. After hybridization, the blots were washed with 2× SSC/0.1% SDS for 30 min, 1× SSC/0.1% SDS for 10 min, 0.5× SSC/0.1% SDS for 10 min and 0.1× SSC/0.1% SDS for 10 min at room temperature. Signal intensities were then monitored by exposure to a PhosphoScreen (Molecular Dynamics). The hybridized blots were then detected by phosphor imaging (Storm 860, Molecular Dynamics), and the signal intensities were quantified using ArrayVision 7.0 (Imaging Research). Signal intensities were normalized to ethidium-bromide-stained 28S rRNA.

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Isolation of interscapular fat mitochondria. Clearly identifiable fat deposits from the interscapular region were excised from the animal and quickly transferred to an excess of ice-cold isolation medium A [250 mM sucrose, 10 mM TES, 1 mM EDTA, 0.4% (wt/vol) BSA, pH 7.2]. The tissue was then minced in the buffer, on ice, with fine scissors. The tissue was then transferred to a glass-Teflon homogenizer. The tissue was homogenized with 6 strokes of a loose-Teflon pestle, filtered through a layer of gauze, and centrifuged for 10 min at 8,740 g. The lipid layer was removed through aspiration, the supernatant was discarded, and the lipid remaining on the inside walls of the tube was removed using tissue paper. The mitochondria pellet was suspended in isolation medium B (250 mM sucrose, 10 mM TES, 1
mM EGTA, 0.4% wt/vol BSA, pH 7.2) and centrifuged at 950 g for 10 min, and the resulting supernatant was transferred to a new tube and centrifuged at 8,740 g for 10 min. The final mitochondrial pellet was suspended in a buffer containing 100 mM KCl, 20 mM TES, 1 mM EGTA, pH 7.2). Protein concentration was determined using the Biuret method.

Isolation of liver mitochondria. The liver was removed and immediately placed in ice-cold isolation medium (250 mM sucrose, 5 mM Tris·HCl, 2 mM EGTA, pH 7.4). The tissue was minced with scissors and disrupted using a Dounce homogenizer with a medium-fitting pestle. The homogenate was centrifuged at 8,500 g for 10 min at 4°C, and the pellet was resuspended in isolation medium and spun at 1,047 g for 10 min. The resulting supernatant was subjected to a high-speed centrifugation at 950 g for 10 min, and the resulting supernatant was transferred to a new tube and centrifuged at 8,740 g for 10 min. The final mitochondrial pellet was resuspended in a minimal volume of isolation medium. The high-speed cycle (11,630 g, 10 min) was repeated twice, and the final pellet was resuspended in a minimal volume of isolation medium. Protein concentration was determined using the Biuret method.

Protein leak kinetics: measurement of oxygen consumption and membrane potential. Oxygen consumption of BAT mitochondria was measured using a Clark-type electrode (Rank Brothers), maintained at 37°C, and calibrated with air-saturated medium [50 mM KCl, 5 mM TES, 2 mM MgCl₂, 6 mM H₂O, 4 mM KH₂PO₄, 1 mM EGTA, 0.4% (wt/vol) BSA, pH 7.2]. For the liver mitochondria, the measuring medium contained 120 mM KCl, 5 mM KH₂PO₄, 3 mM HEPES, 1 mM EGTA and 0.3% (wt/vol) BSA, pH 7.2. The measuring medium was assumed to contain 406 nmol oxygen/ml (33). Oxygen consumption and membrane potential were measured simultaneously using an electrode sensitive to the potential-sensitive probe, TPMP⁺ (triphosphorylmethylphosphonium), a method previously described (1, 3).

Briefly, the kinetics of the mitochondrial proton leak were measured by determining the dependence of the respiratory rate required to drive the proton leak on membrane potential. BAT and liver mitochondria were incubated at protein levels of 0.3 mg/ml and 0.7 mg/ml, respectively, in 2.5 ml of medium containing 8 μM rotenone to inhibit complex I, (4 μg/ml) oligomycin to inhibit phosphorylation of ADP and (110 ng/ml) nigericin to abolish ΔpH. The TPMP⁺ electrode was calibrated with sequential additions up to 2.5 μM TPMP⁺. Succinate (6 mMol/l) was provided as the substrate for respiration. Oxygen consumption and membrane potential were titrated through sequential steady states by successive additions of malonate up to 2 mM for BAT mitochondria and up to 4 mM for liver mitochondria. Finally, 0.3 μM FCCP was added to dissipate the mitochondrial membrane and release all of the TPMP⁺ from the mitochondria, allowing for correction of baseline drift. Respiration at each steady state was then plotted against the appropriate membrane potential so as to display the dependence of proton leak rate on potential.

We were interested in whether the presence of UCP1 in the BAT of E. myurus was associated with uncoupled respiration (proton leakage), representing the molecular mechanism of NST. Proton leakage catalyzed by UCP1 has two distinct characteristics: inhibition by purine nucleoside di- or triphosphates, as well as activation by fatty acids (32). We, therefore, investigated whether the proton leak kinetics in Elephant shrew BAT mitochondria were affected by GDP and palmitate in CA and WA elephant shrews.

Cytochrome c oxidase activity measurements. Cytochrome c oxidase (COX) activity was measured polarographically (34) in BAT mitochondria, BAT, liver, and skeletal muscle tissue homogenates. All tissues were weighed and then homogenized in tissue buffer containing 100 mM KH₂PO₄/K₂HPO₄, 2 mM EDTA, pH 7.5. The homogenate was incubated at 25°C with 1 ml air-saturated medium (79 mM K₂HPO₄ × 3H₂O, KH₂PO₄, 5 mM EDTA-Na₂, pH 7.4) assumed to contain 479 nmol O₂/ml with 43 μl 3 mM cytochrome c, and 71 μl of 0.25 M ascorbic acid added. The tissue homogenate was diluted 1:2 up to 1:6 for BAT, liver, and skeletal muscle, and 1:15 for BAT mitochondria, with polyoxyethyleneether W1, 1.5% (wt/vol) no longer than 10 min before the assay.

All mean values are reported ± SE. Differences between groups were analyzed using t-tests, paired t-tests, and ANOVAs as appropriate.

RESULTS

Body mass. The mean ± SE body mass of all of the animals acclimated to 24°C was 63.5 ± 2.1 g. After 3 wk of respective acclimation temperature, the body mass of both WA and CA had decreased to 59.2 ± 3.1 and 59.4 ± 1.8 g, respectively, and did not differ significantly between the groups (t = 0.07; P > 0.05).

Basal metabolic rate and nonshivering thermogenesis. The mean BMR of all animals acclimated to 24°C was 1.23 ± 0.03 ml O₂·g⁻¹·h⁻¹ There was no significant difference in the BMR of the two groups before they were transferred to their respective acclimation temperatures. However, there was a pronounced cold acclimation effect on the BMR of the rock elephant shrews (Fig. 1). Except for one individual, the WA animals either maintained the same BMR as at 24°C or decreased BMR. Overall, the BMR of the WA group (1.31 ± 0.07 ml O₂·g⁻¹·h⁻¹) was not significantly different than that measured at 24°C. In contrast, all the CA animals exhibited a significant increase in BMR (1.64 ± 0.04 ml O₂·g⁻¹·h⁻¹). This BMR increase was on average 37.9 ± 1.6% and ranged from 35 to 42%. Overall, there was a significant difference in
the BMR of cold- and warm-acclimated animals ($t = 4.65; P = 0.002$).

The injection of NE caused an increase in $V_O_2$, which was observed within 45 min of administration. These high metabolic rates following NE injection were not associated with activity, as the animals typically spread out their bellies on the metabolic chambers, presumably to dissipate heat. The increase in $V_O_2$ caused by NE injection was in most cases up to 4 times that of BMR values. The NST capacity for all animals at $24^\circ C$ was $2.75 \pm 0.69 \text{ ml} \text{ O}_2 \cdot \text{g}^{-1} \cdot \text{h}^{-1}$, and there were no differences in the NST capacity of the animals that were placed in the respective acclimation groups (data not shown). Surprisingly, cold acclimation did not lead to an increase in the NST capacity of rock elephant shrews (Fig. 1; $2.65 \pm 0.65 \text{ ml} \text{ O}_2 \cdot \text{g}^{-1} \cdot \text{h}^{-1}$). Similarly, warm acclimation did not lead to a decrease in the NST capacity ($2.53 \pm 0.18 \text{ ml} \text{ O}_2 \cdot \text{g}^{-1} \cdot \text{h}^{-1}$). Overall, there were no significant differences in NST capacity of cold- and warm-acclimated animals ($t = -0.09; P = 0.93$).

Cloning of the UCP1 cDNA and phylogenetic inference. We amplified a 726-bp cDNA fragment by RT-PCR from the interscapular fat depot (Genbank Acc. No EF 121740), which had the characteristics of eutherian brown fat, extensive blood supply, as well as abundant mitochondria, giving it a brownish color. For classification of the deduced $E. \text{myurus}$ UCP1 protein sequence and its relationship to other homologs, we performed phylogenetic analyses and generated a tree. Phylogenetic inference revealed that $E. \text{myurus}$ UCP1 groups among other known eutherian UCP1 orthologs (Fig. 2). It is most closely related to the tenrec UCP1 sequence with 81% amino acid identity, has 76% identity to mouse UCP1, 55% identity to mouse UCP2, and 53% to mouse UCP3.

UCP1 expression patterns and regulation. We analyzed the tissue distribution of UCP1 both at the mRNA, as well as the protein level in the elephant shrews. Northern hybridization of total RNA with a $E. \text{myurus}$ UCP1 cDNA probe selectively detected a transcript in interscapular adipose tissue but not in WAT or any of the other tissues dissected from $E. \text{myurus}$ (Fig. 3A). Accordingly, on Western blots our polyclonal hamster UCP1 antibody only detected a 32-kDa protein in the interscapular fat pad (Fig. 3B). Weak signals detected in the other tissues represent cross-reactivity of the antibody, with unknown proteins of different molecular mass. Cold acclimation did not increase UCP1 mRNA expression in the interscapular fat (Fig. 3C; CA $= 0.7 \pm 0.1$, WA $= 1.0 \pm 0.2$; $t = -1.24, P = 0.25$). We then analyzed the UCP1 concentration in protein extracts prepared from tissue homogenates (Fig. 3D) and in isolated mitochondria (Fig. 3E). The UCP1 protein levels in the interscapular fat of warm- and cold-acclimated elephant shrews was not significantly different (CA $= 1.0 \pm 0.1$, WA $= 1.1 \pm 0.1$; $t = -0.51, P = 0.62$).

COX activity. The enzyme COX is a reliable indicator of respiratory capacity in a tissue. We, therefore, investigated whether there were differences in COX activity in the BAT, liver, and skeletal muscle of CA and WA animals. COX activity was highest in BAT, followed by skeletal muscle and the lowest enzyme activity was observed in the liver (Fig. 4A). However, none of the tissues showed increased COX activity during cold acclimation. In addition to investigating COX activity at the tissue level, we also measured COX activity in BAT mitochondria. There was a tendency toward increased activity in the mitochondria of CA animals, although this did not amount to a statistically significant difference (Fig. 4B; $t = -1.29, P = 0.24$). We also compared state 4 respiration (in the presence of 5 mM GDP) of BAT mitochondria from CA and WA animals. The state 4 respiration of CA mitochondria ($151.9 \pm 4.4 \text{ nmol} \text{ O}_2 \cdot \text{min}^{-1} \cdot \text{mg protein}^{-1}$) was significantly higher than that of WA animals ($130.3 \pm 7.1 \text{ nmol} \text{ O}_2 \cdot \text{min}^{-1} \cdot \text{mg protein}^{-1}$) ($t = 2.72, P = 0.03$), suggesting a higher respiratory capacity.
in CA animals (Fig. 4 C). There were no differences in the state 4 respiration of liver mitochondria from CA (54.4 ± 6.1 nmol O$_2$ min$^{-1}$ mg protein$^{-1}$) and WA (55.9 ± 6.7 nmol O$_2$ min$^{-1}$ mg protein$^{-1}$) animals ($t = -0.16$, $P = 0.87$).

Proton leak kinetics and functional characterization of UCP1. First, we titrated the effect of GDP on mitochondria isolated from BAT and liver of rock elephant shrews. Because proton leak is a nonlinear function of membrane potential, we compared the oxygen consumption driving the proton leak at a common membrane potential of 135.3 mV in the presence of 0, 1, 3, and 5 mM GDP. There was a clear sensitivity of proton conductance to GDP presence in BAT mitochondria, whereas this sensitivity could not be discerned on liver mitochondria (Fig. 5A). In the absence of GDP, the oxygen consumption required to balance the proton leak in BAT mitochondria was quite substantial and decreased with increasing GDP concentration (Fig. 5B).

The addition of 100 μM palmitate increased proton conductance (Fig. 6). In the absence of GDP, palmitate almost completely dissipated the membrane potential, while stimulating respiration. We therefore used 3 mM GDP in our assay. Under this condition, palmitate caused a strong increase in proton...
leakage, as evidenced by the increased oxygen consumption and decreased membrane potential. At 3 mM GDP, the proton leak induced by palmitate was even higher than that observed in the absence of GDP (0 mM) and palmitate. However, palmitate had no discernible effect on oxygen consumption of liver mitochondria (Fig. 6). The increased proton leakage due to palmitate combined with the observed GDP inhibition was consistent with an uncoupling function of UCP1.

There always remains the possibility that the GDP-sensitive proton conductance in the BAT mitochondria was due to the adenine nucleotide translocase (ANT), a mitochondrial anion carrier that exchanges ADP for ATP across the mitochondrial inner membrane (3, 9). ANT can be potently inhibited by carboxyatractylate (CAT). As the uncoupling effect of ANT is so strong in rat liver and kidney mitochondria, Skulachev and colleagues (18) have suggested that the recoupling effect of GDP on mitochondria cannot be considered as a specific probe for the involvement of a UCP in fatty acid-mediated uncoupling and that GDP suppresses ANT function. However, the addition of 2.5 μM CAT in the absence of GDP did not result in any observable change in proton conductance in BAT mitochondria of cold-acclimated E. myurus. In fact, in the presence of CAT (no GDP), the BAT mitochondria were more uncoupled than when 1 mM GDP was present in our assay (data not shown). This suggests that the proton leakage induced by fatty acids in this study was mediated by UCP1 and not by ANT. In addition, 5 mM ADP had an effect even more potent than that of 5 mM GDP, demonstrating strong purine nucleotide sensitivity.

We then compared kinetics of proton conductance in BAT mitochondria from CA and WA animals. The oxygen consumption driving the proton leak in the absence of ATP synthesis was plotted against different membrane potentials imposed by malonate titration of succinate oxidation to display the kinetic dependence of proton leak on its driving force, the membrane potential at 37°C. We then assessed similarities and differences in proton leak rate curves by the overlap or non-overlap of SE bars, as has been done in other studies (2, 4, 14).

In agreement with our other results, the proton leak curves of BAT mitochondria overlapped for cold- and warm-acclimated animals, indicating similar proton leak kinetics under the two acclimation treatments (Fig. 7), suggesting that BAT mitochondria from CA animals were no more uncoupled than those from WA animals. Similarly, there were no significant differences in the proton leak kinetics of liver mitochondria between groups (data not shown).

DISCUSSION

The overall aim of this study was to elucidate the basis of nonshivering thermogenesis in the rock elephant shrew, E. myurus by integrating measurements at the molecular, subcellular, tissue, and whole animal levels. We have demonstrated the presence of the Ucp1 gene, as well as its protein UCP1, whose expression was BAT specific in a member of the Afrotheria. The ortholog of UCP1 has already been demonstrated in fish, although a thermogenic role in ectotherms is unlikely (17). It is therefore imperative that in addition to showing the occurrence of UCP1, uncoupling thermogenic function should also be demonstrated if it is to be implicated in nonshivering thermogenesis. We therefore characterized the function of UCP1 and investigated proton leak kinetics and demonstrated that the addition of fatty acids to isolated BAT mitochondria increases proton conductance in a GDP-sensitive manner. To fully display thermogenesis, an organ requires high oxidative capacity to oxidize metabolic substrates and a leak (such as UCP1 to release heat) to uncouple oxidative phos-
phorylation (20). We demonstrated that BAT of the elephant shrew displays highest oxidative capacity compared with skeletal muscle and liver. Taken together, our data show that in this ancient eutherian, UCP1 has a thermogenic function and that NST in the elephant shrew occurs in BAT and is UCP1 mediated.

We expected adaptive recruitment of thermogenic capacity during cold acclimation, the hallmarks of which are increases in the expression of the Ucp1 gene with its associated UCP1 and mitochondrial biogenesis (19). We found no evidence of recruitment of cold-induced thermogenic capacity in BAT when investigating NE-induced response, Ucp1 mRNA, mitochondrial UCP1 levels, and amounts of tissue UCP1 in rock elephant shrews. We also could not find any differences in the rate of proton leakage from mitochondria of cold- and warm-acclimated animals. Instead, of all the parameters considered, the principal adjustment in response to cold acclimation was only evident in BMR and state 4 respiration rate of BAT mitochondria.

Although in highly seasonal species such as the Djungarian hamster, uncoupled respiration has a dominating role during cold acclimation, with the total amount of UCP1 in BAT estimated to increase by a nearly 20-fold magnitude (10), it has been widely documented that small mammals increase their BMR in response to cold acclimation (7, 22, 31). This elevated BMR is thought to improve total thermogenic capacity, as well as extend the thermoneutral zone to lower ambient temperatures (T_is) and is partly associated with blood distribution to the intestinal organs, whose metabolic activities are presumably increased (10).

The higher state 4 respiration suggests a higher respiratory capacity in the BAT mitochondria of cold-acclimated animals. Cytochrome c oxidase is a marker enzyme for the inner mitochondrial membrane and can be used to estimate the amount of mitochondrial protein in BAT and respiratory capacity of mitochondria (19). Increased COX activity also points toward increased respiratory capacity and is often accompanied by a pronounced stimulation of UCP1 gene expression, thus elevating the capacity of BAT for NST (21). The high COX activity in BAT compared with skeletal muscle and liver does support a thermogenic function of this tissue. In addition, although there were no significant differences in COX activity between groups, both at tissue and mitochondrial level, we did find a tendency toward higher respiratory capacity in the BAT mitochondria of cold-acclimated animals.

It is tempting to ask whether pronounced differences might have been observed between the two groups had the animals in the cold acclimation group been placed at a much lower ambient temperature or cold- or warm-acclimated for a longer period. It is true that in most studies, animals are often acclimated to ambient temperatures below 10°C and that acclimating our animals to lower ambient temperatures for a longer period might have yielded significant differences between the two groups. Nevertheless, comparable temperature gradients such as used in this study have been shown to induce changes in thermogenic capacity of mice. For example, mice that were acclimated to 21°C and then transferred to 33°C decreased BAT mass, mitochondrial protein, and UCP1 content within 48 h (8).

We are interested in the extent to which ambient temperature fluctuations influence physiological responses of animals in their natural habitats. We therefore considered that placing the animals at lower ambient temperatures may not necessarily have been ecologically relevant because even in winter in their natural habitat, the rock elephant shrews would not experience consistently low ambient temperatures. Instead, in its natural range, this species is exposed to fluctuating diel ambient temperature cycles, with cool nights (~5°C) and warm days (>20°C). We suggest that the animals may not have increased their thermogenic capacity during our cold acclimation conditions simply because NST is not an exclusive source of heat gain for this species. In fact, it has been shown previously that during the winter, when E. myurus use daily torpor, they accrue significant energy saving by exogenous passive heating during arousal from torpor (27, 29). The apparent lack of NST recruitment may therefore be explained simply by considering the ambient temperature cycles that occur in this species’ natural habitat. In addition, Lovegrove et al. (23) predicted that metabolic rate of E. myurus acclimated to 18°C was 3.01 ± 0.15 ml O_2·g^{-1}·h^{-1} at 0°C (Fig. 5C; 23). Because there were no differences in NST capacity of cold- and warm-acclimated animals in this study, we pooled our results and found that the mean maximum NE-induced oxygen consumption was 4.03 ± 0.22 ml O_2·g^{-1}·h^{-1}. This implies that at 28°C, E. myurus have already acquired BAT, providing them with enough NST capacity to deal with T_is below freezing. Because T_is seldom decrease below 0°C in E. myurus’s natural habitat, the BAT recruited at 28°C is sufficient for survival and meets their ecological requirements. On the other hand, the maintenance of functional BAT at high T_is (28°C) might allow them to deal with unpredictable and aseasonal cold spells known to occur in this species’ range.

In nature, ambient temperature and photoperiod often act in concert to bring about seasonal physiological adjustments. In retrospect, it remains possible that had we coupled cold and warm acclimation with short and long photoperiod, respectively, we might have observed some differences between the two groups. Nevertheless, in a study investigating phenotypic plasticity of physiological variables between species, Lovegrove (22) found that after controlling for latitude and phylogenetic effects, the seasonal changes in NST could not (as yet) be reliably associated with any independent predictor variable.

In conclusion, we show that BAT and functional UCP1 are already present in the rock elephant shrew, a member of the Afrotheria and a basal eutherian mammal, although they did not show any evidence of additional recruitment of NST capacity when cold acclimated. This does not necessarily mean that NST is not adaptive in this species. We suggest that what is likely to be most informative regarding the seasonal regulation and the adaptive nature of thermoregulatory parameters in any species will be to capture free-ranging individuals, during the different seasons, and immediately measure the parameters of interest without prior acclimation. An understanding of interseasonal and interannual plasticity in physiological responses is likely to be important during seasonal climate perturbations, resulting from large-scale climate anomalies.

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