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BROWN AND BEIGE ADIPOSE TISSUES IN HEALTH AND DISEASE

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Abstract

Brown and beige adipocytes arise from distinct developmental origins. Brown adipose tissue (BAT) develops embryonically from precursors that also give to skeletal muscle. Beige fat develops postnatally and is highly inducible. Beige fat recruitment is mediated by multiple mechanisms, including de novo beige adipogenesis and white-to-brown adipocyte transdifferentiation. Beige precursors reside around vasculatures, and proliferate and differentiate into beige adipocytes. PDGFR α ⁺Ebf2⁺ precursors are restricted to beige lineage cells, while another PDGFR α ⁺ subset gives rise to beige adipocytes, white adipocytes, or fibrogenic cells. White adipocytes can be reprogramed and transdifferentiated into beige adipocytes. Brown and beige adipocytes display many similar properties, including multilocular lipid droplets, dense mitochondria, and expression of UCP1. UCP1-mediated thermogenesis is a hallmark of brown/beige adipocytes, albeit UCP1-independent thermogenesis also occurs. Development, maintenance, and activation of BAT/beige fat are guided by genetic and epigenetic programs. Numerous transcriptional factors and coactivators act coordinately to promote BAT/beige fat thermogenesis. Epigenetic reprogramming also influences expression of brown/beige adipocyte-selective genes. BAT/beige fat is regulated by neuronal, hormonal, and immune mechanisms. Hypothalamic thermal circuits define the temperature setpoint that guides BAT/beige fat activity. Metabolic hormones, paracrine/autocrine factors, and various immune cells also play a critical role in regulating BAT/beige fat functions. BAT and beige fat defend temperature homeostasis, and regulate body weight and glucose and lipid metabolism. Obesity is associated with brown/beige fat deficiency, and reactivation of brown/beige fat provides metabolic health benefits in some patients. Pharmacological activation of BAT/beige fat may hold promise for combating metabolic diseases.

INTRODUCTION

Brown adipose tissue (BAT) and beige fat defend body temperature homeostasis, regulate energy balance and body weight, and influence glucose and lipid metabolism in rodents. BAT develops embryonically, while beige fat is induced in white adipose tissue (WAT), termed browning of WAT, in postnatal life (239, 338). Albeit they arise from distinct developmental origins and are located in different anatomic regions, brown adipocytes and beige adipocytes (also called brite adipocytes) exhibit many common morphologic and metabolic characteristics, including multilocular lipid droplets, dense mitochondria, and expression of uncoupling protein 1 (UCP1). UCP1 resides in the inner mitochondrial membrane, and UCP1-mediated mitochondrial thermogenesis is a hallmark of both brown and beige adipocytes (339). In humans, BAT is abundant in infancy, but regresses in

adulthood. However, a considerable number of bioactive brown/beige adipocytes, which are scattered in broad regions, are detected in human adults and increases after cold exposure (57, 317, 321). Brown and beige adipocytes are speculated to have similar metabolic functions in humans as in rodents (58, 140, 338, 339). In this review article, I summarize recent advances about brown and beige adipocytes, and speculate on their therapeutic potential in combating obesity, type 2 diabetes, and nonalcoholic fatty liver disease (NAFLD).

BROWN AND BEIGE FAT FUNCTIONS

BAT and beige fat have distinct functions from WAT. WAT serves as an energy store for the body where excess chemical energy is stored as triacylglycerol (TAG). In contrast, both BAT and beige fat are highly metabolically active and utilize chemical energy for heat production. BAT and beige fat thermogenesis play a critical role in body temperature homeostasis, energy homeostasis, and body weight control. Recent findings also highlight the metabolic function of BAT and beige fat, raising the possibility that they may serve as a potential therapeutic target for metabolic diseases.

Body temperature homeostasis.

Warm-blooded animal species, such as mammals, evolve a complex thermoregulatory mechanism to maintain their own internal body temperature within a narrow range, regardless of fluctuating external temperatures. Body temperature homeostasis is critical for survival of these animal species, because vital physiological processes, particularly those involving enzyme-mediated biochemical reactions, are temperature-sensitive and disrupted when body core temperature is aberrantly high or low. In rodents, BAT and beige fat are indispensable for the maintenance of body temperature homeostasis. In humans, BAT is abundant in infancy and likely to regulate temperature homeostasis in a similar fashion; however, BAT declines in adulthood, and behavior adaptations (e.g. clothing) become a predominant way to maintain temperature homeostasis.

Cold exposure is the most powerful stimuli for heat production to keep the body core temperature at a relative stable level. Skeletal muscle shivering and nonshivering thermogenesis (also called adaptive thermogenesis) account for heat production during cold exposure. Using genetic approaches, it was demonstrated that ablation of both BAT and beige fat completely abolishes adaptive thermogenesis, rendering BAT- and beige fat-deficient mice fatal hypothermia upon cold exposure (192). These findings underscore the essential role of BAT and beige fat in the maintenance of rodent body temperature homeostasis. BAT has special physiological characteristics facilitating its thermogenesis function. It has dense vasculatures that allow an efficient delivery of metabolic fuel to BAT and a rapid heat dissemination. BAT is extensively innervated by the sympathetic nervous system (SNS) (211). Cold exposure rapidly activates the SNS and increases SNS inputs into the BAT, thereby stimulating BAT thermogenesis (211). Both brown and beige adipocytes express uncoupling protein 1 (UCP1), their signature mark. UCP1 is a proton channel resided in the inner mitochondrial membrane. Activated UCP1 allows energy-charged protons to leak across the inner mitochondrial membrane, thereby uncoupling oxidative

phosphorylation from ATP synthesis and dissipating chemical energy as heat. Genetic deletion of *UCP1*, like ablation of BAT and beige fat, severely inhibits cold adaptive thermogenesis, and *UCP1*-null mice develop fatal hypothermia upon cold exposure (75, 98). These results underscore the importance of UCP1-mediated thermogenesis in the maintenance of temperature homeostasis. Notably, *UCP1*-null mice gradually gain the ability to defend their body temperature after cold acclimation (75, 98), suggesting that chronic cold stress activates an adaptive UCP1-independent thermogenic mechanism that compensates for loss of UCP1. Importantly, cold exposure similarly activates brown and beige adipocytes in human adults, leading to an increase in energy expenditure (132, 232, 355). These exciting findings suggest that a SNS-BAT/beige fat axis also operate in human adults to promote energy expenditure.

Energy homeostasis and body weight.

Energy expenditure counterbalances energy intake, thus maintaining body weight at a relatively stable level. Energy imbalance results in obesity, which becomes a global epidemic (264). Mounting evidence supports the notion that BAT- and beige fat-mediated thermogenesis contributes to energy expenditure and protects against obesity. In line with this notion, a variety of metabolic hormones, metabolites, and nutrients are able to stimulate brown and/or beige adipogenesis (276); BAT and beige fat in turn mediate, at least in part, diet-induced thermogenesis, thus counteracting weight gain (85, 262, 270, 340). Using either pharmacological or genetic approaches, activation of BAT and beige fat thermogenesis considerably induces weight loss in rodents (275, 319). Conversely, ablation of BAT and beige fat results in severe obesity in mice (192). Importantly, activating brown and beige adipocytes, by either chronic cold exposure or pharmacological interventions, also decreases body weight and adiposity in human adults in a similar fashion (284, 355). It is becoming increasingly appreciated that recruitment and thermogenic activation of brown and beige adipocytes provide metabolic health benefits for both rodents and humans in the context of obesity and metabolic diseases.

Glucose and lipid homeostasis.

Body weight and adiposity profoundly influence glucose and lipid metabolism, and obesity is a primary risk factor for metabolic diseases, including type 2 diabetes, dyslipidemia, nonalcoholic fatty liver diseases (NAFLD). Given their important role in regulating energy expenditure and body weight, it is not surprising that BAT and beige fat are involved in the regulation of metabolic homeostasis. Interestingly, BAT and beige fat are also able to regulate glucose and lipid metabolism by a body weight-independent mechanism. Adoptive transplantation of BAT grafts normalizes hyperglycemia and substantially improves glucose intolerance in recipient mice with either streptozotocin-induced or genetic type 1 diabetes (105, 106). BAT transplantation also attenuates insulin resistance in recipient mice with high fat diet (HFD)-induced obesity (287). However, the underlying mechanism of BAT-induced improvement in insulin sensitivity and glucose metabolism remains elusive.

BAT and beige fat primarily use fatty acids to fuel their thermogenesis. Lipids are delivered to BAT and beige fat either as nonesterified free fatty acids (FFAs) or in TAG-rich lipoprotein particles. Notably, BAT and beige fat abundantly express and secrete lipoprotein lipase

(LPL), which is upregulated by cold exposure (17, 38). LDL hydrolyzes TAG-rich lipoproteins to release FFAs which are taken into brown and beige adipocytes via CD36, a plasma membrane FFA transporter (17, 38, 66). BAT also expresses angiopoietin-like protein 4 (ANGPTL4), an endogenous LDL inhibitor; cold exposure downregulates BAT ANGPTL4, thereby further increasing LPL activity, LDL-mediated catabolism of lipoprotein particles (66). It is emerging that BAT and beige fat play a critical role in the maintenance of blood TAG homeostasis. Importantly, human brown and beige fat are likely to regulate glucose and lipid metabolism in a similar fashion (25, 46, 47, 117).

Endocrine functions.

It is well established that WAT secretes numerous metabolic hormones and mediators (collectively called adipokines), including leptin and adiponectin, and these adipokines help govern energy and nutrient metabolism. Likewise, brown and beige adipocytes also secrete leptin and adiponectin. Given their small mass relative to WAT, brown and beige fat is unlikely to be an important source of circulating leptin and adiponectin in humans. Additionally, brown and beige adipocytes secrete several specific adipokines, including neuregulin 4, IGF-1, FGF21, and interleukin (IL) 6 (62, 87, 105, 149, 287, 324). Neuregulin 4 suppresses hepatic lipogenesis as an endocrine hormone (324). FGF21 and IL6 promotes brown and beige adipocyte thermogenesis in a paracrine/autocrine fashion (87, 128, 158). IGF-1 is believed to be involved in reducing hyperglycemia by BAT in mice with type 1 diabetes (105). BAT and beige fat-derived metabolic factors are gaining increasing attention for their anti-obesity, anti-hyperglycemia, and/or anti-insulin resistance activities.

BROWN AND BEIGE FAT THERMOGENESIS

BAT and beige fat are distinguished from WAT by their high levels of metabolic rates and thermogenic capability (17, 287). BAT and beige fat possess multiple characteristic and thermogenic-promoting properties, including dense mitochondria, thermogenic UCP1, and multilocular lipid droplets that supply chemical fuel. UCP1-mediated thermogenesis is a hallmark of BAT and beige fat; however, recent findings indicate that brown and beige adipocytes also carry out thermogenesis by additional UCP1-independent mechanisms. Furthermore, mitochondrial dynamics, lipid droplet dynamics, and metabolic fuel mobilizations all profoundly influence brown and beige adipocyte thermogenesis.

UCP1-dependent thermogenesis.

UCP1 is commonly used as molecular marker to identify brown and beige adipocytes. It resides in the inner mitochondrial membrane and binds to cardiolipin, a mitochondrial-restricted membrane lipid species (175). UCP1 is absent in brown and beige progenitor cells, and its expression increases progressively during brown and beige adipogenesis under the control of brown/beige adipocyte-selective genetic programs (258, 339). Notably, cold exposure dramatically increases UCP1 expression in beige fat and substantially increases UCP1 in BAT through the SNS- β adrenergic signaling axis in mice (145). Thyroid hormones also potently stimulate UCP1 expression, increasing BAT thermogenesis (249). In addition to its levels, UCP1 thermogenic activity is also regulated by multiple factors. In quiescent brown and beige adipocytes, purine nucleotides (di- and triphosphates) bind to UCP1 and

inhibit its thermogenic activity (279). In contrast, polyunsaturated fatty acids, either internally generated from lipid droplets via lipolysis or externally obtained through CD36-mediated FFA uptake, bind to UCP1 and activate its thermogenic activity (19, 81). Cold exposure rapidly increases the levels of reactive oxygen species (ROS) in BAT, and ROS in turn induces sulfenylation of UCP1 at Cys253, enhancing UCP1 thermogenic activity (48). Notably, UCP1 activation reduces mitochondrial superoxide production in BAT (226), suggesting that UCP1 functions as a component of the oxidative defense system. Indeed, chronic cold exposure markedly increases oxidative stress in *UCP1* knockout (KO) but wild type (WT) mice (288). Albeit *UCP1* KO mice develop fatal hypothermia when exposed to cold temperature for the first time (75, 97, 98, 125, 202), they progressively regain their abilities to defend the core body temperature against external cold environments after a chronic cold acclimation (98, 208, 313). These observations indicate that UCP1-independent thermogenic mechanisms exist and are activated to compensate for loss of UCP1 in *UCP1* KO mice during cold acclimation.

UCP1-independent thermogenesis.

Several UCP1-independent mitochondrial processes have been demonstrated in brown and beige adipocytes to dissipate chemical energy as heat, contributing to adaptive thermogenesis. HFD feeding increases adipose expression of adenine nucleotide translocase 2 (ANT2), an inner mitochondrial membrane conduct that allows energy-charged protons to leak across, thus promoting diet-induced thermogenesis (31, 179). BAT, beige fat, and liver secrete peptidase M20 domain containing 1 (PM20D1), an enzyme that catalyzes condensation of fatty acids and amino acids to produce *N*-acyl amino acid products (189). *N*-acyl amino acids (e.g. Phe and Leu) directly bind to mitochondria and function as endogenous uncouplers to promote mitochondrial respiration and thermogenesis (189). ATP-Mg²⁺/P(i) solute transporters (Slc25a25) dissipate chemical energy as heat during shuttling ATP-Mg²⁺ and P(i) across the inner mitochondrial membrane (8). Cold exposure stimulates mitochondrial creatine kinase activity in beige adipocytes, and a mitochondrial creatine kinase-mediated futile cycle of creatine metabolism promotes thermogenesis independently of UCP1- (148).

Mitochondrial fission and fusion.

Brown and beige adipocytes have a high level of mitochondrial content, contributing to high metabolic rates in these cells. Mitochondrial respiration is profoundly influenced by mitochondrial dynamics (i.e. fission and fusion). Mitochondrial fission and fusion are controlled by distinct molecular machinery. Drp1 is a master regulator of mitochondrial fission and fragmentations (139, 356); in contrast, mitofusin 1 (Mfn1), Mfn2, and Opa1 promote mitochondrial fusion and branching (285). Cold exposure rapidly stimulates Drp1-mediated mitochondrial fission and fragmentations in BAT via the SNS (335). Inhibition of mitochondrial fission, by either overexpressing dominant negative Drp1 or blocking OMA1-mediated degradation of Opa1, substantially decreases brown adipocyte thermogenesis (248, 335). Conversely, forcing mitochondrial fission through silencing Mfn2 increases brown adipocyte thermogenesis (335). However, molecular connections between mitochondrial dynamics and the UCP1-dependent and UCP1-independent thermogenic machinery remain unknown. Perhaps, mitochondrial fission increases mitochondrial number as well as

mitochondrial respiration capability, thereby enhancing thermogenesis. In line with this notion, blocking adipose mitophagy (increase mitochondria), using adipocyte-specific deletion of *ATG7*, increases beige adipogenesis and BAT thermogenesis, and protects against HFD-induced insulin resistance and glucose intolerance in mice (283). In contrast, increasing mitophagy is likely to be a driving force for re-whitening (inactivation) of beige adipocytes (5).

Lipid droplets and fuel mobilization.

Lipid droplet size and morphology are drastically different between WAT and BAT. White adipocytes have a large unilocular lipid droplet per cell; in contrast, brown and beige adipocytes have multilocular lipid droplets, and their sizes vary, depending on cell thermogenic states. Lipid droplets are coated with lipid droplet proteins, including perilipin (Plin) family members and Cide family members. Brown and beige adipocyte lipid droplets contain abundant Plin1, Plin2, Plin5, and cidea, and these lipid droplet proteins play a critical role in regulating lipolysis (59, 223, 336, 348, 357).

Lipid droplet lipolysis has been extensively examined in white adipocytes. It is composed of a chain of biochemical reactions catalyzed by cytoplasmic lipases. Adipose TAG lipase (ATGL) catalyzes the first step of lipolysis to generate diacylglycerol (DAG) and FFAs from TAG in lipid droplets (366). Hormone-sensitive lipase (HSL) hydrolyzes DAG to generate monoacylglycerol (MAG) which is completely hydrolyzed by MAG lipase (MAGL) to release free glycerol and FFAs. Interestingly, adipocyte-specific deletion of *ATGL* impairs thermogenesis in mice (2). Conversely, adipocyte-specific overexpression of ATGL increases both body core temperature and energy expenditure (3). These findings suggest that ATGL-mediated lipolysis is a regulatory node of BAT and beige fat thermogenesis and energy expenditure. We recently reported that Snail1, a transcriptional repressor, potently suppresses ATGL expression and ATGL-mediated lipolysis in adipocytes (292). ATGL activity is regulated by both positive (e.g. CGI-58) and negative (e.g. G0S2) regulators as well as by lipid droplet proteins (101, 168, 349, 352). It is very important to fully delineate a lipid droplet-lipolysis-mitochondrial thermogenic machinery axis in brown and beige adipocytes in the context of energy imbalance and obesity in the future.

FFAs are the primary products of lipid droplet lipolysis, and are likely to promote BAT and beige fat thermogenesis by multiple mechanisms. FFAs serve as critical chemical fuel to drive mitochondrial respiration and thermogenesis. Interestingly, lipid droplets directly bind to mitochondria in brown adipocytes (357), likely facilitating delivery of FFAs to mitochondria. FFAs are transported by carnitine palmitoyltransferase (CPT) 1 and CPT2 across the inner mitochondrial membrane into the mitochondrial matrix where FFAs are metabolized through β oxidation to release chemical energy. Adipocyte-specific ablation of CPT2, which blocks FFA utilization by adipocytes, severely impairs cold-induced adaptive thermogenesis in mice (170). Furthermore, genetic inactivation of either the long chain acyl CoA dehydrogenase or the short chain acyl CoA dehydrogenase, two enzymes that catalyze FFA β oxidation, also markedly impairs cold adaptive thermogenesis in mice (102). SIRT3 is a mitochondrial enzyme that deacetylates and stimulates the long chain acyl CoA dehydrogenase, and deletion of *SIRT3* impairs cold adaptive thermogenesis in mice (123).

Together, these findings strongly argue for the notion that FFA delivery to mitochondria and subsequent β oxidation are a determinant of BAT and beige fat thermogenesis and energy expenditure.

FFAs activate UCP1 as discussed above, further stimulating BAT and beige fat thermogenesis. In addition, FFAs are known by their ability to stimulate nuclear hormone receptors PPAR α and PPAR δ as endogenous ligands. PPAR α and PPAR δ activate genomic programs that promote mitochondrial biogenesis and mitochondrial thermogenesis (212). Thus, FFAs connect lipid droplets, mitochondria, and the nucleus, coordinating and promoting thermogenic programs in brown and beige adipocytes.

Glucose uptake and FFA uptake.

BAT is one of the organs with the highest glucose and FFA uptake per cell in rodents and humans (17, 57, 287, 317, 321). Lipid droplets directly provide FFAs to fuel mitochondrial thermogenesis in brown and beige adipocytes, and need to be recharged with lipid fuel that is obtained from the blood. Brown adipocyte glucose uptake is mediated by plasma membrane Glut1 and Glut4 (136, 341). Glucose is converted into FFAs through lipogenesis. FFA uptake is mediated by plasma membrane CD36 and FATP1 in brown and beige adipocytes. Deletion of *CD36* or *FATP1* impairs cold adaptive thermogenesis in mice (7, 243, 342), indicating that FFAs serve as predominant chemical fuel for BAT and beige fat. Interestingly, cold exposure increases expression of genes responsible for replenishing lipid droplets in BAT, including the genes that mediate glucose uptake, lipogenesis, and TAG synthesis (*Glut1*, *Glut4*, *hexokinase*, *PFK1*, *PDHa1*, *FAS*, glycerol kinase, *PEPCK*, *GPAT3*, *Dgat1*, *Dgat2*) (166). PPAR α or PPAR γ agonists, which promote differentiation of human mesenchymal stem cells into brown/beige adipocytes, also stimulate expression of genes responsible for lipolysis, de novo lipogenesis, TAG synthesis, and lipid droplet formation (16). Therefore, lipid droplet dynamics, including lipid droplet lipolysis and replenishment, are likely to play an important role in regulating BAT and beige fat thermogenesis.

BAT AND BEIGE FAT DEVELOPMENT

BAT and beige fat development is best understood in rodents. BAT develops embryonically while beige fat develops postnatally (263). BAT mass is maintained at relatively stable levels by a homeostatic mechanism in adulthood; in contrast, beige fat is barely detectable at thermoneutrality and highly induced by cold exposure (18, 103, 338, 339). Furthermore, brown and beige adipocytes arise from completely different progenitor/stem cell origins.

BAT.

Mouse or rat interscapular BAT develops between E15–16, and markedly increases between P15–21 (130, 331). Functional transformation occurs two days before birth (E18–19), generating thermogenic-competent UCP1⁺ brown adipocytes (94, 130). A common Myf5⁺ (and Pax7⁺) progenitor population is believed to give rise to both BAT and skeletal muscle in mice (180, 274). In line with this notion, the gene expression profiles of BAT contain a skeletal muscle gene expression signature (301). A further differentiated Myf5⁺PDGF α ⁺ subset is committed to the BAT lineage during fetal development (331). In adults, BAT

homeostasis is maintained by proliferation and differentiation of BAT progenitors, which appear to reside at the dorsal edge of iBAT (177).

Beige fat.

Beige adipocytes are distributed in broad areas, including sWAT, perivascular adipose tissue, and skeletal muscle in mice (4, 43, 55, 88). They are detected in the cervical-supraclavicular, shoulder-blades, cervical, axillary, mediastinal, paravertebral, perirenal, and peri-aortic regions in humans (256, 338). Notably, beige adipocytes are heterogeneous populations with regard to their metabolic properties and gene expression profiles (176). Beige adipocyte heterogeneity is profoundly influenced by the nature of its inducers (e.g. β 3 adrenergic agonists vs PPAR γ agonists) (325). The mechanism of beige fat development (also referred to as beige adipocyte recruitments or browning of WAT) remains elusive, and three models receive great attention.

De novo beige adipogenesis.—In this model, beige fat inducers are believed to stimulate beige fat progenitor expansion and differentiation into mature beige adipocytes. Beige progenitor cells are believed to reside in adipose vasculatures (a progenitor/stem cell niche) where the local microenvironments help preserve the stemness of beige progenitor/stem cells and facilitate de novo beige adipogenesis upon stimulation (23, 190, 205, 307). Indeed, cold exposure or β 3 adrenergic agonist stimulation increases beige precursor proliferation and differentiation into beige adipocytes in mice (329, 338). Human beige precursors are also associated with adipose vasculatures (205). Albeit the precise identity of beige progenitor/stem cells remains elusive, a number of molecular markers has been shown to be linked to beige precursors. Adipose vasculature mural cells expressing smooth muscle actin (SMA), Myh-11, or PDGFR α are able to proliferate and differentiate into beige adipocytes in vitro and in vivo (23, 178, 190). Interestingly, beige fat displays a smooth muscle-like signature of gene expression profiles (190), suggesting a potential lineage relationship between beige adipocytes and smooth muscle cells. Diverse beige progenitor lineages may exist; in mice, both beige adipocyte-specific progenitors and beige/white adipocyte-bipotent PDGFR α ⁺ progenitors have been reported (60, 178, 338). Notably, a subpopulation of PDGFR α ⁺ mesenchymal progenitors (PDGFR α ⁺CD9^{high}) also differentiates into fibrogenic cells in obesity, promoting adipose tissue fibrosis (201).

White-to-beige adipocyte transdifferentiation.—It has long been believed that mature white adipocytes and beige adipocytes can be converted between each other (i.e. transdifferentiation) under certain conditions. Cold exposure or β adrenergic agonist stimulation was reported to induce white-to-beige adipocyte transdifferentiation in mice and rats (15, 121). Lineage tracing studies reveal that the majority of UCP1⁺ beige adipocytes in inguinal WAT, induced by a short-term cold exposure or β adrenergic agonist stimulation, arise from pre-existing white adipocytes that express adiponectin, a molecular marker of mature adipocytes (177, 322). Moreover, UCP1⁺ beige adipocytes can be reverted back into UCP1⁻ white adipocytes in mice housed at thermoneutrality following cold exposure (5, 259), and beige-to-white adipocyte transdifferentiation is facilitated by mitophagy (5).

Activation of dormant beige adipocytes.—Beige adipocytes may also exist in inactive (dormant) and active states. Dormant beige adipocytes resemble white adipocytes in morphology and some chemical and metabolic properties (e.g. unilocular lipid droplets, lacking UCP1), but they are distinct in developmental origins from white adipocytes. Dormant beige adipocytes can be rapidly activated to become active UCP1⁺ beige adipocytes upon cold exposure temperature or β adrenergic stimulation (259), accounting for, at least in part, recruitments of beige fat. It is worth mentioning that current methods are unable to distinguish white-to-beige adipocyte transdifferentiation from dormant beige adipocyte activation.

GENETIC AND EPIGENETIC REGULATION OF BROWN AND BEIGE FAT THERMOGENESIS

BAT development and beige fat recruitment are controlled by lineage-specific genetic programs. Notably, many transcription factors regulate the development, maintenance, and/or activation of both BAT and beige fat in a similar fashion. Recent research also underscores the importance of epigenetics in BAT and beige fat biology.

Zfp423.

Zfp423 is a transcription factor highly expressed in adipocyte precursors (109, 322). It activates expression of PPAR γ , thereby promoting commitment of progenitors to white or brown preadipocyte (108). Notably, Zfp423 also binds to early B-cell factor 2 (Ebf2) and inhibits the ability of Ebf2 to stimulate Prdm16 expression and beige adipogenesis (281). Zfp423 is also expressed in mature adipocytes, and its levels are higher in WAT than in BAT (281). Downregulation of Zfp423 induces a white-to-beige adipocyte conversion in mice (281).

Zfp516.

Cold exposure stimulates expression of Zfp516 in BAT that binds to Prdm16 and stimulates *UCP1* transcription (64, 267). In agreement with these findings, adipocyte-specific overexpression of Zfp516 increases brown adipogenesis in mice (64). Global deletion of *Zfp516* results in embryonic lethality, and BAT mass is dramatically reduced in *Zfp516*-null fetuses (64).

Ebf2.

Ebf2, in contrast to Zfp432, is expressed at higher levels in BAT than in WAT (250). Ebf2 stimulates, in conjunction with PPAR γ , expression of both Prdm16 and UCP1 in brown adipocyte cultures (250). In line with these findings, adipocyte-specific overexpression of Ebf2 promotes beige adipogenesis and protects *Ebf2*-transgenic mice from HFD-induced obesity (289). Mice with global deletion of *Ebf2* die soon after birth (53), and brown preadipocytes derived from *Ebf2* null embryos have reduced ability to differentiate into brown adipocytes (250). Several factors are known to regulate the development and function of BAT and/or beige fat through Ebf2. Zfp432 suppresses beige fat function by binding and inhibiting Ebf2 transcriptional activity as discussed above. Similarly, inhibitor of DNA

binding 1 (Id1) also binds to Ebf2 and suppresses Ebf2 transcriptional activity, and adipocyte-specific overexpression of Id1 exacerbates age-induced or HFD-induced obesity (237). In contrast, a long noncoding RNA Blnc1 binds to Ebf2 and enhances Ebf2-stimulated expression of thermogenic genes in brown and beige adipocytes (363).

PPAR family members (γ , α , and δ).

PPAR γ is a core transcription factor required for white adipogenesis (258). Interestingly, PPAR γ agonists potently increase *de novo* beige adipogenesis and white-to-beige adipocyte transdifferentiation in both rodents and humans (16, 188, 229, 239). The ability of PPAR γ to stimulate preadipocyte differentiation into either white or brown/beige adipocytes appears to be determined by its associated coactivators. When associated with Prdm16, PPAR γ stimulates expression of brown/beige adipocyte-selective genes and represses white adipocyte-specific genes (245). Interestingly, Sirt1 deacetylates PPAR γ (Lys268 and Lys293), which promotes binding of PPAR γ to Prdm16 in brown/beige adipocytes (245). In contrast, binding to TLE3 allows PPAR γ to suppress expression of brown/beige adipocyte-selective genes and stimulate white adipocyte-selective genes (320). Moreover, TLE3 and Prdm16 compete for the same binding sites in PPAR γ (320).

PPAR α is well known to stimulate fatty acid β oxidation and mitochondrial respiration (212). Activation of PPAR α has been reported to promote a white-to-beige adipocyte conversion and BAT and beige fat thermogenesis (16, 127). Consistently, PPAR α directly stimulates expression of PGC1 α and Prdm16, two coactivators that promote brown and beige adipocyte thermogenesis (127). PPAR α binds to period 2 (Per2), a circadian clock protein that acts as a PPAR α coactivator to enhance brown/beige adipocyte activity (44), likely linking to a circadian control of BAT and beige fat activities.

PPAR δ , like PPAR α , also promotes BAT and beige fat thermogenesis in mice (332). Of notice, PPAR γ , PPAR α , and PPAR δ can be activated by lipid ligands produced from lipid droplet lipolysis (212); therefore, these nuclear hormone receptors are likely to be involved in mediating crosstalk between lipid droplets, the nucleus, and mitochondria to coordinate brown/beige adipocyte thermogenic processes.

Additional nuclear hormone receptors.

Estrogen-related receptor β (ERR β), ERR γ , and nuclear receptor-4A member NOR-1 all are able to stimulate UCP1 expression and brown/beige adipocyte thermogenesis (67, 90, 164). Cold exposure activates the protein kinase A (PKA)/p38 cascade, and p38 activates ERR β and ERR γ to stimulate expression of UCP1 and other thermogenic genes, increasing BAT thermogenesis (90). ERR γ binds a corepressor SHP that inhibits the ability of ERR γ to activate the *PGC1 α* promoter, and deletion of *SHP* increases PGC1 α levels in BAT and energy expenditure and protects *SHP* null mice from diet-induced obesity (327). Activation of the retinoic acid receptor (RAR) by retinaldehydes stimulates beige adipogenesis and adaptive thermogenesis in mice (151). In contrast to the above nuclear receptors that stimulate BAT and beige fat thermogenesis, activation of LXR α or Vitamin D receptors inhibits UCP1 expression and brown and beige adipocyte thermogenesis (200, 326). LXR α

binds to receptor-interacting protein 140 (RIP140) corepressor and recruits RIP140 to the *UCP1* promoter, inhibiting *UCP1* expression in BAT (326).

C/EBP family members (α , β , and δ).

C/EBP family members are core adipogenic transcription factors (258). Deletion of *C/EBP α* blocks WAT but not BAT development (184), suggesting that *C/EBP α* is dispensable for BAT. Using an inducible, adipocyte-specific knockout system, *C/EBP α* was reported to be required for white adipogenesis in adult mice; surprisingly it is dispensable for fetal/early postnatal WAT development (330). Cold-induced beige adipogenesis is also independent of *C/EBP α* (330).

Deletion of both *C/EBP β* and *C/EBP δ* , in contrast to *C/EBP α* , blocks BAT development in mice (298), indicating that these two transcription factors are indispensable for BAT and beige fat development, maintenance, and/or function. *C/EBP β* binds to *Prdm16* that acts as a coactivator for *C/EBP β* to promote brown and beige adipogenesis (143). *C/EBP β* is likely to serve as a regulatory hub for BAT and beige fat thermogenesis. In line with this notion, *Plac8* activates *C/EBP β* expression, and deletion of *Plac8* impairs beige adipogenesis and adaptive thermogenesis, promoting obesity (142). In contrast, *Hoxc8* suppresses *C/EBP β* expression and brown adipogenesis (210). *C/EBP β* is also involved in mediating microRNA regulation of BAT and beige fat activities. miR-196a upregulates *C/EBP β* by suppressing expression of *Hoxc8*, increasing beige adipogenesis (210). miR-155 suppresses *C/EBP β* expression, and ablation of miR-155 increases brown and beige adipogenesis in mice (45).

Circadian clock proteins.

Cold exposure stimulates *Per2* expression in BAT via heat shock factor 1 (HSF1), and *Per2* null mice are cold sensitive (44). *Per2* increases *UCP1* expression by acting as a PPAR α coactivator as discussed above. *Rev-erba* levels are higher in BAT than in WAT, and deletion of *Rev-erba* impairs BAT development in mice (217). Surprisingly, the other group reported that *Rev-erba* directly represses *UCP1* expression, and deletion of *Rev-erba* improves cold tolerance in mice (92). *Rev-erba* deficiency also abolishes normal rhythms of body temperature and BAT activity (92).

***Prdm16*.**

Prdm16 has gained great attention by its ability to promote commitment of Myf5⁺ progenitor cells to brown adipocyte lineage (274). Mechanistically, *Prdm16* acts as a cofactor for multiple transcription factors (e.g. PPAR γ , *C/EBP β* , *Zfp516*) to stimulate *UCP1* expression and thermogenesis in brown and beige adipocytes (64, 143, 245). *Prdm16* is able to suppress expression of negative regulators of BAT and beige fat, thereby promoting BAT and beige fat activities. A Rb family member p107 is expressed in adipose precursors and represses their differentiation into brown adipocytes, and p107-deficient stem cells uniformly give rise to brown adipocytes (63). PRDM16 binds to the *p107* promoter and suppresses p107 expression (63). Additionally, *Prdm16* also represses expression of white adipocyte-selective genes (118), likely preserving brown and beige adipocyte phenotypes. In line with these findings, adipocyte-specific overexpression of *Prdm16* robustly induces beige

adipogenesis and protects *Prdm16* transgenic mice from HFD-induced obesity and insulin resistance (275).

Numerous factors regulate brown and beige adipocyte thermogenesis through modulating *Prdm16* expression and/or its transcriptional activity. Euchromatic histone-lysine *N*-methyltransferase 1 (EHMT1) and MED1 bind to *Prdm16* and activate expression of UCP1 and other brown/beige adipocyte-selective genes (118, 119, 133, 228). Deletion of *EHMT1* in either *Myf5*⁺ brown adipocyte precursors or adiponectin⁺ adipocytes impairs brown and beige adipogenesis and cold adaptive thermogenesis in mice (228). PPAR α , PPAR γ , and IRF4 stimulate PRDM16 expression, which explains, at least in part, the ability of these proteins to stimulate brown and/or beige adipogenesis and thermogenesis (127, 160, 229). In contrast, CtBP1, CtBP2, and TLE3 bind to *Prdm16* and inhibit its ability to stimulate expression of brown and beige adipocyte-selective genes and thermogenesis (144, 320). miR-133 binds to the 3' UTR of *Prdm16* and downregulates *Prdm16* expression (305, 354). Cold exposure decreases miR-133 expression, thereby contributing to upregulation of *Prdm16* and recruitments of BAT and beige fat in mice (305, 354).

Given its roles in promoting commitment to the brown preadipocyte lineage and brown adipocyte thermogenesis, it is surprising that *Prdm16* deficiency either in *Myf5*⁺ brown precursors and their progeny brown adipocytes or in adiponectin⁺ adipocytes (e.g. white, brown, and beige adipocytes) does not alter BAT development and BAT thermogenesis in mice (51, 118). Notably, adipocyte-specific deletion of *Prdm16* completely blocks cold-induced recruitment of UCP1⁺ beige fat in mice, leading to the notion that *Prdm16* is required for beige adipogenesis but not for brown adipogenesis (51). Additionally, *Prdm16*-deficient brown adipocytes progressively lose their thermogenic capability during aging and become white adipocyte-like cells, suggesting that *Prdm16* plays an important role in preserving brown and beige adipocyte phenotypes in aged mice (118).

PPAR γ coactivator-1 α (PGC1 α).

The PGC1 coactivator family contains three members of PGC1 α , PGC1 β and PRC (also called PPRC1) which are known to promote mitochondrial biogenesis and respiration (183). The *PGC1 α* gene encodes a long and a short (NT-PGC1 α)²⁵⁴ variant via mRNA alternative splicing, and both variants are able to promote brown adipocyte thermogenesis (42). Cold exposure increases PGC1 α expression in BAT in mice and in subcutaneous fat in humans (150, 170). PGC1 α stimulates UCP1 expression and thermogenesis in brown and beige adipocytes by acting as a coactivator for many transcription factors, including PPAR family members, C/EBP family members, Tbx15, N-arginine dibasic convertase (Nrd1/NRDC, also called nardilysin), and IRF4 (91, 122, 160). It also binds to *Prdm16*, stimulating expression of brown and beige adipocyte-selective genes (144).

Many cellular factors are believed to regulate brown and beige fat thermogenesis through modulating, at least in part, PGC1 α expression and/or its transcriptional activity. CREB, ATF2, and ERR γ directly stimulate *PGC1 α* expression in brown and/or beige adipocytes (34, 197, 327). In contrast, Foxa3, pRb, and SHP bind to the *PGC1 α* promoter and suppress *PGC1 α* transcription, thereby inhibiting brown and beige adipocyte activity (197, 272, 327). Smad3 also suppresses PGC1 α expression, and deletion of *Smad3* enhances beige

adipogenesis and protects *Smad3* null mice from diet-induced obesity and insulin resistance (347). Twist-1 and RIP140 directly bind to PGC1 α and inhibit the ability of PGC1 α to stimulate expression of UCP1 and other brown and beige adipocyte-selective genes (49, 113, 234). PGC1 α activity is also regulated through posttranslational modifications. SIRT2 deacetylates and activates PGC1 α , promoting mitochondrial biogenesis and β oxidation (163). HIF1 α directly suppresses expression of SIRT2 and SIRT2-mediated activation of PGC1 α (163), and adipocyte-specific deletion of *HIF1 α* or *ARNT* (the HIF1 α partner) increases energy expenditure, contributing to protection against diet-induced obesity and insulin resistance in the mutant mice (141, 163). p38 MAPK phosphorylates PGC1 α , which increases PGC1 α stability as well as the ability of PGC1 α to stimulate UCP1 expression and mitochondrial respiration in brown adipocytes (34, 242).

Given the profound effects of PGC1 α on UCP1 expression and mitochondrial respiration, it is surprising that adipocyte-specific deletion of *PGC1 α* only slightly impairs BAT function (157). Perhaps PGC1 β , PRC, and/or other related molecules compensate for loss of PGC1 α in *PGC1 α* null mice.

Epigenetic regulation of BAT and beige fat functions.

Recent research highlights the importance of epigenetics in the regulation of the development, maintenance, and activation of BAT and beige fat. Brown adipocyte differentiation is associated with increased expression of Jmjd3 (a H3K27me3 demethylase), ubiquitously transcribed tetratricopeptide repeat on chromosome X (UTX, demethylating H3K27me2–3), and lysine-specific histone demethylase 1 (LSD1, demethylating both H3K4me1–3 and H3K9me1–3) (235, 267, 359). Jmjd3 and UTX demethylate H3K27me3, a repressive epigenetic mark, at the promoters of *UCP1* and other brown adipocyte-selective genes, thereby upregulating these genes (235, 359). Cold exposure or β 3 agonist stimulation increase LSD1 expression in iWAT (71). LSD1 appears to directly promote recruitments/activation of BAT and beige fat; in line with this notion, brown/beige adipocyte-specific deletion of *LSD1* impairs both brown and beige adipogenesis, decreases energy expenditure, and increases adiposity in mice (72, 267), whereas global overexpression of LSD1 increases browning of WAT and protects *LSD1* transgenic mice from HFD-induced obesity (71). Cold exposure stimulates PKA-mediated phosphorylation of Jmjd1a (also known as Jhdm2a or Kdm3a) and activates Jmjd1a (1). Activated Jmjd1a binds to the *UCP1* promoter and demethylates repressive H3K9me2, and deletion of *Jmjd1a* impairs BAT lipolysis and oxygen consumption, resulting in reduced energy expenditure, adult onset obesity, and hyperlipidemia in mice (299). MLL4 (also called KMT2D) is a H3K4me1–2 methyltransferase, and deletion of *MLL4* in Myf5⁺ brown precursors and their progeny brown adipocytes impairs brown adipogenesis in mice (171). MLL4 is recruited to adipogenic enhancers through its interactions with C/EBP β (171). Rreb1 recruits Jmjd3 to the *UCP1* promoter (235). LSD1 is recruited to brown/beige adipogenic enhancers through its interactions with transcription factors Nrf1 and Zfp516 (71, 267). Cold exposure decreases histone deacetylase 1 (Hdac1) levels in BAT, and β adrenergic signaling decreases the binding of Hdac1 to the *UCP1* and *PGC1 α* promoters in brown adipocytes, leading to an increase in active epigenetic H3K27ac mark (181). Concurrently, β adrenergic signaling stimulates dissociation of enhancer of zeste homologue (Ezh2) and suppressor of zeste 12

(SUZ12), leading to a decrease in repressive epigenetic mark H3K27me3 at the *UCP1* and *PGC1a* promoters (181).

Aside from histone modifications, DNA methylations are also involved in regulating BAT and beige fat function. Activation of APMK α 1, which stimulates brown/beige adipocyte activity as described later, increases α -ketoglutarate (α KG) levels (351). α KG activates Tet DNA demethylases, leading to DNA demethylation at the *Prdm16* promoter, thereby enhancing Prdm16 expression and brown adipogenesis (351).

NEURAL REGULATION OF BROWN AND BEIGE FAT THERMOGENESIS

The core body temperature is maintained at a relatively stable level by a homeostatic mechanism, which is guided by a temperature setpoint. The hypothalamic temperature-regulating center is believed to define the body temperature setpoint. A deviation from the temperature setpoint rapidly triggers thermal responses (i.e. heat production vs heat loss) to defend body temperature homeostasis. In rodents, adaptive thermogenesis by BAT and beige fat plays an essential role in combating cold environments to keep the core body temperature close to the temperature setpoint. Information about ambient cold temperature is transmitted into the hypothalamic temperature-regulating center where a complex thermal circuitry integrates thermal information as well as internal inputs related to body metabolism and physiologic states. The hypothalamic outputs determine the activities of the SNS and the hypothalamic-pituitary-thyroid (HPT) axis that in turn control BAT and beige fat functions. It is worth mentioning that the hypothalamic thermal circuits also mediate social stress-induced thermogenesis as well as infection-induced fever (147, 186, 211, 361).

The core thermal circuitry.

Skin transient receptor potential M8 (TRPM8) cation channels function as cutaneous cold receptors to detect ambient cold temperature and encode cold information (203). TRPV3 and TRPV4 channels are warm receptors and encode warm information (211). Primary temperature-sensing neurons are located in the dorsal root ganglia (DRGs) and transmit thermal information into the central nervous system (CNS) (Fig. 1). Primary thermoreceptive afferent fibers are predominantly myelinated A δ fibers and synapse on lamina I thermoregulatory glutamatergic neurons in the spinal (or trigeminal) dorsal horns (311). The spinal or trigeminal second-order neurons project to the lateral parabrachial nucleus (LPB) where they synapse on glutamatergic neurons (211, 311). LPB glutamatergic neurons project to in the median preoptic subnucleus (MnPO) of the preoptic area (POA) where they synaptically activate GABAergic neurons (211, 311). MnPO GABAergic neurons innervate and inhibit warm sensitive GABAergic neurons in the medial preoptic area (MPA) (311). MPA GABAergic neurons project to the dorsomedial hypothalamus (DMH)/dorsal hypothalamic area (DHA) where they inhibit glutamatergic neurons (Fig. 1) (311). DMH/DHA glutamatergic neurons project to the rostral raphe pallidus (rRPa), raphe magnus nucleus, and the parapyramidal area (PaPy), and monosynaptically activate BAT premotor neurons in these areas (211, 311). BAT premotor neurons consist of glutamatergic and serotonergic subpopulations, and both project to the intermediolateral nucleus (IML) of the thoracolumbar spinal cord where they activate BAT preganglionic neurons, stimulating

BAT thermogenesis (Fig. 1) (211, 216, 311). The DMH/DHA/rRPa circuits also mediate social defeat stress-induced, in addition to cold stress-induced, BAT thermogenesis in rats (147, 186).

Bacterial infection commonly causes fever by raising the hypothalamic temperature setpoint. The core thermoregulatory circuitry also mediates pyrogen-induced BAT thermogenesis and fever (211). Pyrogens (e.g. TNF α , and IL1 β) stimulate production of prostaglandin E2 (PGE2) from the brain vasculature, and PGE2 in turn induces fever by activating ER3 receptors on warm-sensitive GABAergic neurons in the POA (311). Notably, histaminergic inputs to POA neurons also increase BAT thermogenesis in mice by activating H1 and H3 receptors (211, 278).

Hypothalamic thermal circuits.

Aside from the POA and DMH/DHA, many other hypothalamic nuclei, including the arcuate nucleus (ARC), ventromedial hypothalamus (VMH), lateral hypothalamus (LH), and paraventricular hypothalamus (PVH), are also involved in regulating BAT and beige fat thermogenesis (6, 9, 41, 50, 76, 153, 159, 162, 211, 222, 238, 247, 296, 303, 323). ARC POMC neurons and RIP neurons stimulate, while ARC AgRP neurons inhibit, BAT and beige fat energy expenditure (9, 50, 76, 159, 162, 211, 247, 303). RIP neurons and AgRP neurons project to the PVH that mediates the thermal action of these two neuronal subpopulations; in contrast, POMC neurons stimulate BAT and beige fat activities through PVH-independent circuits (14, 159, 261, 282). The PVH contains heterogeneous neuronal subpopulations, and the BDNF, oxytocin, and CRF subsets are able to stimulate BAT and beige fat thermogenesis via the SNS (6, 41, 211, 296, 323). ARC POMC neurons activate MC4R signaling in the LH (209). LH orexin neurons project to the rRPa and the PaPy where they activate BAT premotor neurons, thus increasing BAT thermogenesis (211, 310). It is likely that POMC neurons stimulate BAT and beige fat activities at least in part by stimulating LH orexin neurons (209). Notably, orexin neurons are required for social stress-induced thermogenesis in mice (361).

Multiple hormonal and nutrient signals stimulate BAT and beige fat energy expenditure through the hypothalamic circuitry. Leptin stimulates LepRb neurons in the ARC (e.g. POMC, AgRP, and RIP neurons) (68, 159), DMH (PrRP neurons) (69, 76), and MnPO (warm sensitive glutamatergic neurons) (358, 362). These LepRb neural circuits are likely to act coordinately to mediate leptin-stimulated energy expenditure. Central insulin stimulates ARC neurons and promotes beige fat recruitments (68). Estrogens activate ER α signaling in the VMH, increasing BAT and beige fat thermogenesis (345). Deletion of *ER α* in Sim1-expressing neurons (the PVH and medial amygdala) decreases energy expenditure and increases adiposity (343), suggesting that estrogen signaling in these neurons also promote thermogenesis. Central thyroid hormones and urocortin-3 stimulate VMH circuits and increase BAT and beige fat energy expenditure (165, 191). Central FGF21 also increases energy expenditure (268). Thus, it is likely that these hormonal and nutritional signals help determine the CNS temperature setpoints through modulating the activity of the hypothalamic thermal circuits.

Medullary thermal circuits.

The ventrolateral medulla (VLM) and the nucleus tractus solitarius (NTS) also profoundly influence BAT and/or beige fat premotor neuron activity, thereby modulating thermogenesis and energy expenditure. VLM catecholaminergic neurons project to the rRPa and inhibit BAT premotor neurons via α_2 adrenergic receptors (198), and stimulation of VLM or A1/C1 catecholaminergic neurons rapidly inhibits sympathetic inputs to BAT and decreases BAT thermogenesis (36, 211).

The NTS is known to integrate satiety signals which are relayed to the brain from the gastrointestinal (GI) tract via vagal afferent nerves. Many satiety hormones stimulate BAT and beige fat thermogenesis (273); moreover, duodenal lipid sensing stimulates BAT thermogenesis via NTS circuits (26). NTS GABAergic neurons directly project to rRPa, inhibit BAT premotor neurons, and decrease BAT thermogenesis (36, 159). Notably, the NTS also contains BAT sympathoexcitatory neurons (311). A GI-NTS-rRPa-BAT axis is emerging and is likely to be involved in mediating diet-induced thermogenesis.

SNS-BAT and SNS-beige fat cascades.

We have discussed that the SNS outflow to BAT is a driving force for BAT activation. Moreover, tonic sympathetic inputs are also required for BAT maintenance and homeostasis, as demonstrated by BAT atrophy when it is denervated (271). Further underscoring the importance of the SNS inputs to BAT, deletion of dopamine β -hydroxylase, which catalyzes neurotransmitter norepinephrine synthesis, blocks BAT thermogenesis (300).

The SNS promotes BAT and beige fat thermogenesis by multiple mechanisms. Norepinephrine stimulates β_1 , β_2 , and β_3 adrenergic receptors in brown and beige adipocytes. Deletion of β_1 or β_3 adrenergic receptors partially impairs BAT and beige fat thermogenesis (295, 312), and ablation of all three isoforms causes dysfunction of BAT and beige fat to the highest level relative to ablation of individual isoforms (12). Thus, β_1 , β_2 , and β_3 adrenergic receptors all are involved in mediating sympathetic stimulation of BAT and beige fat thermogenesis. Activation of β_1 , β_2 , or β_3 adrenergic receptors stimulates the cAMP/PKA/p38 MAPK pathway, which is responsible for stimulating UCP1 expression, mitochondrial respiration, and thermogenesis in brown/beige adipocytes (34, 35, 242). Activation of the cAMP/PKA pathway also rapidly stimulates phosphorylation and activation of Drp1, thus promoting Drp1-mediated mitochondrial fission (335). Mitochondrial fission further increases brown and beige adipocyte thermogenesis (335). Notably, brown and beige adipocyte β adrenergic sensitivity declines in obesity (37), which may account for, at least in part, a reduction in energy expenditure under these conditions. The cAMP/PKA pathway is negatively regulated by phosphodiesterases (PDEs) that degrade cAMP. Pharmacological inhibition of PDE10A or deletion of *PDE10A* increases beige adipogenesis and energy expenditure in mice (115, 218). Furthermore, activation of α_2 adrenergic receptors, unlike β adrenergic receptors, inhibits brown adipocyte thermogenesis (367). These findings raise the possibility that upregulation of PDE10A or related negative regulators of the adrenergic receptor/cAMP/PKA pathway may contribute to blunted thermal responses of BAT and beige fat to sympathetic inputs in obesity.

Sympathetic postganglionic neurons also release coneurotransmitters into BAT and/or beige fat, including adenosine that activates adenosine A_{2A} receptors (96). A_{2A} receptor agonists stimulate BAT thermogenesis and beige fat recruitment; conversely, pharmacological or genetic inactivation of A_{2A} receptors decreases BAT thermogenesis in mice (96). Connexin 43 is an important gap junction protein; interestingly, brown/beige adipocyte-specific ablation of connexin 43 impairs cold-induced beige adipogenesis (365). These findings raise a possibility that gap junctions may mediate a fast propagation of neuronal signals in BAT to allow a rapid, robust thermal response to cold stress.

Sympathetic inputs are also able to potentiate the thermal responses of brown and beige adipocytes to other thermogenic factors. For instance, activation of the β adrenergic receptor/cAMP/PKA pathway robustly increases expression of type 2 iodothyronine deiodinase (*Dio2*) (61). *Dio2* catalyzes a conversion of prohormone thyroxine T4 to bioactive T3, and deletion of *Dio2* impairs cold adaptive thermogenesis in mice (61). Additionally, sympathetic inputs to BAT stimulate de novo brown adipogenesis via β 1 adrenergic receptor pathways (177). Sympathetic inputs also stimulate local release of paracrine and/or autocrine factors (e.g. FGF21, prostaglandins) that stimulate brown and beige adipocyte thermogenesis (62, 318). Furthermore, the SNS is likely to mediate cold-stimulated secretion of endocrine hormone natriuretic peptides (NPs) from the heart, and NPs in turn stimulate BAT thermogenesis (28).

The HPT axis.

The HPT axis is known to determine basal metabolic rates (126). Thyrotropin-releasing hormone (TRH) neurons in the PVH receive neural inputs from the NTS, ARC, and DMH (82, 83, 169, 269), and projects to the median eminence where they release TRH. TRH is delivered to the pituitary gland via the hypophyseal portal system and stimulates thyrotrope cells in the anterior pituitary gland to secrete thyroid-stimulating hormone (TSH). TSH is transported in the blood to the thyroid gland where it stimulates production and secretion of thyroid hormones thyroxine (T4) and triiodothyronine (T3). T4 is converted to active T3 by *Dio2* inside brown and beige adipocytes. T3 directly stimulates UCP1 expression and mitochondrial biogenesis via its nuclear receptors TR α and TR β in brown and beige adipocytes (172, 249, 255). TR α signaling also augments the thermogenic response of BAT to β adrenergic stimulation (255). Notably, leptin stimulates release of TRH both directly by activating LEPRb in TRH neurons and indirectly by activating ARC POMC neurons that innervate TRH neurons (93, 107, 120, 131). Oxysterols activate LXR α and LXR β as ligands, and deletion of *LXR α* and *LXR β* enhances TRH neuronal activity and increases beige adipogenesis (204). Thus, the HPT axis appears to link nutrient metabolism to BAT and beige fat energy expenditure. It is worth mentioning that the SNS and the HPT systems are likely to act coordinately/synergistically to promote BAT and beige fat thermogenesis.

HUMORAL REGULATION OF BROWN AND BEIGE FAT THERMOGENESIS

Numerous endocrine, paracrine, and autocrine factors have been demonstrated to regulate the development, maintenance, and function of BAT and beige fat. These factors are secreted by a variety of tissues and organs, including the pancreas, liver, GI tract, heart, adipose

tissue, skeletal muscle, and the immune system. These humoral regulators, in conjunction with the SNS system, dynamically regulate BAT and beige fat activities, maintaining body temperature homeostasis and energy balance.

Endocrine regulators.

Insulin.—Insulin receptor expression increases during brown adipocyte differentiation, and deletion of insulin receptors dramatically impairs brown adipocyte differentiation in vitro (77). In line with these findings, deletion of insulin receptors specifically in Myf5⁺ brown precursor cells substantially decreases BAT mass in mice (196). Furthermore, deletion of insulin receptors in UCP1⁺ brown/beige adipocytes also decreases BAT mass (104). Deletion of insulin receptors in adiponectin⁺ adipocytes (white, brown, and beige adipocytes) also decreases BAT mass and impairs cold adaptive thermogenesis in mice (30). These genetic data suggest that insulin signaling is required not only for brown adipogenesis and BAT development but also for the maintenance of the thermogenic and metabolic phenotypes of BAT, and perhaps also beige fat.

Insulin receptors bind to both IRS1 and IRS2 that mediate activation of the PI 3-kinase/Akt pathway; however, IRS1 but not IRS2 appears to mediate stimulation of brown adipogenesis by insulin (79, 80). Insulin stimulates UCP1 expression in brown adipocyte cultures in a PI 3-kinase- and Akt-dependent manner (79, 219, 314). Adipocyte-specific ablation of p110 α , a catalytic subunit of PI 3-kinase, decreases BAT UCP1 expression, BAT thermogenesis, and energy expenditure, and promotes obesity, glucose intolerance, and liver steatosis in mice (219). Insulin activates TORC1 via the PI 3-kinase/Akt pathway. Importantly, adipocyte-specific ablation of raptor, an essential component of the TORC1 complex, inhibits β adrenergic-stimulated beige adipogenesis in mice (306). Thus, the IRS1/PI 3-kinase/Akt/TORC1 pathway appears to be indispensable for insulin to promote BAT and beige fat function. TORC1 phosphorylates and inhibits 4E-BP1. Deletion of *4E-BP1* increases beige adipogenesis and metabolic rates and decreases adiposity in mice (309), indicating that 4E-BP1 is a negative regulator of beige fat. It is likely that the insulin/IRS1/PI 3-kinase/Akt/TORC1 pathway disinhibits BAT and/or beige fat by suppressing 4E-BP1. Aside from cell-autonomously promoting brown and beige adipocyte function, insulin is also able to stimulate BAT and beige fat thermogenesis indirectly by regulating hypothalamic circuits (33, 68).

Glucagon.—Deletion of *glucagon* impairs cold adaptive thermogenesis in mice, suggesting that glucagon promotes BAT thermogenesis in mice (155). (155). Glucagon stimulates FGF21 secretion from the liver in both rodents and humans (10, 112). FGF21 is known to stimulate BAT and beige fat thermogenesis (87, 128), which may be involved in mediating glucagon-stimulated thermogenesis. Notably, deletion of the *glucagon* gene also abolishes expression of glucagon-like peptide 1 (GLP-1) and GLP-2, (155), and the relative contributions of glucagon, GLP-1, and GLP-2 to BAT and beige fat thermogenesis remain unclear.

Glucocorticoids.—Cold stress activates the hypothalamic-pituitary-adrenal axis, increasing plasma ACTH and corticosterone levels (316). BAT expresses glucocorticoid

receptors (84), suggesting that brown adipocytes are regulated directly by stress hormones. Notably, glucocorticoids have the opposite effects on brown and beige adipocytes between rodents and humans. Corticosterone inhibits UCP1 expression in mouse brown adipocyte cultures (316), and a chronic corticosterone treatment inhibits brown/beige fat activity in cold-exposed mice (315). In contrast, glucocorticoids enhance the ability of isoprenaline to stimulate UCP1 expression and mitochondrial respiration in human primary brown adipocyte cultures, and glucocorticoid treatment increases BAT activity in healthy men (252).

Liver-secreted regulators.—The liver is the main source of circulating fibroblast growth factor (FGF) 21 (13, 135). Plasma FGF21 levels correlate with BAT activity in humans (116). FGF21 treatment stimulates BAT and beige fat thermogenesis (74, 128). Conversely, deletion of *FGF21* impairs beige adipogenesis and cold adaptive thermogenesis in mice (87). Protein restriction increases energy expenditure in a FGF21-dependent manner in mice (167). Of notice, adipose tissue and skeletal muscle also secrete FGF21 that enhances BAT and beige fat thermogenesis (87, 149, 174). The liver synthesizes bile acids exclusively by hepatocytes. Bile acids increase BAT thermogenesis by activating TGR5 receptors in brown and beige adipocytes (333). Additionally, bile acids also stimulate the GI tract to secrete FGF15/19 (134). FGF15/19 promotes BAT and beige thermogenesis as discussed below. The liver oxidize FFAs to produce ketone bodies, and ketone bodies (e.g. β -hydroxybutyrate) are able to stimulate browning of WAT and BAT/beige fat thermogenesis (39, 286).

Skeletal and cardiac muscle-secreted factors.—Exercise or cold-stimulated shivering stimulates skeletal muscle to release a number of endocrine factors that promote BAT and beige fat activities. Exercise or cold-induced shivering stimulates expression of irisin (derived from *FNDC5* mRNA) in skeletal muscle (29, 174, 338). Irisin is able to stimulate BAT thermogenic activity in mice (29, 338). However, it was also reported that exercise does not increase *FNDC5* expression, and recombinant irisin does not promote human brown adipocyte differentiation (254). Exercise or cold exposure was reported to stimulate skeletal muscle and adipose tissue to secrete meteorin-like (*Metnl*) that stimulates beige fat thermogenesis (253). Surprisingly, overexpression of *Metnl* (driven by the *aP2* promoter) does not increase beige adipogenesis in *Metnl* transgenic mice (182). Skeletal muscle secretes IL6 that enhances beige fat activity, and deletion of *IL6* blocks exercise-induced beige adipogenesis (158). Cold exposure increases the circulating levels of cardiac natriuretic peptides that stimulate brown adipocyte mitochondrial biogenesis and BAT thermogenesis through activating the p38 MAPK pathway in brown adipocytes (28).

Exercise was reported to increase brown precursor numbers and BAT thermogenesis in mice (29, 344); however, chronic exercise was also reported to decrease UCP1 and PGC1 α expression and BAT thermogenesis in rats (340). But prolonged exercise training increases browning of WAT and beige fat thermogenesis in both mice and rats (158, 340).

GI-secreted regulators.—The GI tract is like to be involved in mediating diet-induced thermogenesis. It secretes various satiety factors that regulate BAT and beige fat activities via the vagal-brain axis as described above. Small intestines secrete FGF15/19 in the postprandial period (134), and food ingestion increases FGF15/19 secretion and circulating

FGF15/19 levels (241). Transgenic overexpression of FGF15/19 increases BAT mass and energy expenditure (302). The GI tract is an important source of circulating serotonin, and fasting increases serotonin secretion from the GI tract (291). Serotonin directly suppresses brown and beige adipocyte activation (54), and pharmacological inhibition of serotonin synthesis induces beige adipogenesis and enhance BAT and beige fat thermogenesis in mice (54, 227). Circulating serotonin levels are lower in the fed state and markedly increase during chronic fasting (291), which may help explain, at least in part, diet-induced thermogenesis. Notably, depletion of gut microbiota increases browning of WAT in both lean and obese mice, leading to improved glucose tolerance and insulin sensitivity (290). These findings suggest that the gut/microbiota/beige fat axis exists and modulates energy and glucose homeostasis.

Renal factors.—Erythropoietin (EPO) is secreted mainly by the kidney and promotes beige adipogenesis (328). Adipocyte-specific deletion of EPO receptors decreases energy expenditure, thereby exacerbating HFD-induced obesity and insulin resistance (328). EPO receptors activate the JAK/STAT3 pathway. Interestingly, BAT thermogenesis is impaired in mice with *Tyk2*-deficiency, and adipocyte-specific expression of constitutively active STAT3 reverts impairment in BAT of *Tyk2* null mice (65). *Tyk2* dimerizes with JAK1 or JAK2 that in turn phosphorylates and activates STAT3 to promote brown adipogenesis and BAT thermogenesis in mice (251). Thus, EPO stimulates BAT and beige fat thermogenesis, likely by activating the JAK/STAT3 pathway in brown and beige adipose lineage cells. It is worth mentioning that the JAK/STAT3 pathway is also activated by IL6 and other cytokines, raising the possibility that the JAK/STAT3 pathway in BAT and beige fat may also mediate the thermal action of these cytokines.

Paracrine/autocrine factors

Bone morphogenetic proteins (BMPs) and related cytokines.—Both brown preadipocytes and adipocytes express BMP4 and BMP7 (110, 236), and cold exposure or HFD feeding also stimulates expression of BMP8B in BAT (334). BMP4, BMP7, and BMP8B all promote brown and beige adipogenesis in mice (27, 110, 244, 308, 334). BMP7 also stimulates fatty acid uptake into brown adipocytes (304). BMP4 and BMP7 bind to BMPRII receptors and stimulate the Smad1/5/8 pathway, which mediates their stimulation of brown and beige adipogenesis (271, 308). In contrast, myostatin and TGF β 1, two BMP-related cytokines, inhibit BAT and beige fat function, presumably by activating the ActRIIB/Alk4/5/Smad2/3 pathway (89, 347, 360).

Vasculature-derived factors.—Cold exposure or β adrenergic agonist stimulation induces angiogenesis in both WAT and BAT (277, 346), facilitating fuel delivery, heat dissipation, and thermogenesis. VEGF-A is a key angiogenic growth factor, and overexpression of VEGF-A either in all adipocytes or in UCP1⁺ brown and beige adipocytes increases adipose vascularization, beige adipogenesis, and BAT and beige fat thermogenesis in mice (73, 293, 294). Conversely, inhibition of adipose angiogenesis by deleting endothelial *VEGFR2* impairs β adrenergic-stimulated beige adipogenesis and nonshivering thermogenesis (277, 346). A reduction in vascularization and blood flow is expected to induce hypoxia and activation of HIF1 α , and adipocyte-specific ablation of HIF1 α or its

binding partner ARNT increases energy expenditure in mice (141, 163), suggesting that the hypoxia-HIF1 α axis suppresses the recruitments and activities of BAT and/or beige fat.

Endothelial cells are known to synthesize nitric oxide (NO), and NO is able to promote mitochondrial biogenesis in brown adipocytes (221). NO activates soluble guanylyl cyclase (sGC) that catalyzes cGMP synthesis. Genetic ablation of the β 1 subunit of sGC impairs BAT thermogenesis in mice (124). cGMP stimulates protein kinase G (PKG). Activation of the cGMP/PKG pathway promotes brown adipogenesis as well as mitochondrial biogenesis and UCP1 expression in brown adipocytes (111, 124, 207). Thus, the endothelial cell/NO/sGC/cGMP/PKG axis may exist and promote BAT and/or beige fat thermogenesis.

Lipid regulators.—Cold exposure or β adrenergic agonist stimulation increases expression of cyclooxygenase 2 (COX2), the rate-limiting enzyme of the prostaglandin synthesis pathway, in adipose tissue (318). Pharmacological inhibition of COX2 or genetic deletion of *COX2* attenuates BAT and beige fat thermogenesis stimulated by either cold exposure or β adrenergic agonist stimulation, and attenuates HFD-induced obesity (199, 318). In line with these findings, adipose PGE2 directly stimulates beige adipogenesis by stimulating EP4 signaling (199). Additionally, central PGE2 acts as a pyrogenic mediator to stimulate hypothalamic thermal circuits via ER3, inducing fever (311).

PDGF-CC and Slit2.—Both brown and beige precursor cells express PDGFR α as discussed above. PDGF-CC is able to stimulate both PDGFR α homodimers and PDGF α / β heterodimers, and it also stimulates differentiation of PDGFR α ⁺ progenitors into beige adipocytes (277). In line with this finding, deletion of *PDGF-C*, or pharmacological blockage of PDGFR α or PDGR β , inhibits β adrenergic-stimulated beige adipogenesis in mice (277). However, activation of PDGFR α signaling was also reported to stimulate differentiation of adipose mesenchymal progenitors into fibrotic cells at the expense of suppressing adipogenesis (138). Interestingly, a recently study reported an identification of PDGFR α ⁺CD9^{high} and PDGFR α ⁺CD9^{low} subsets in adipose tissue (201). The PDGFR α ⁺CD9^{high} mesenchymal progenitors differentiate into fibrogenic cells, whereas the PDGFR α ⁺CD9^{low} subset differentiate to adipocytes (201). Thus, the relative abundance of these two subpopulations is likely to a determinant for the outcome of adipose PDGF signaling.

Adipose extracellular matrix (ECM) also influences beige adipogenesis. Adipocytes express and secrete Slit2, an ECM protein (297). A C-terminal fragment of Slit2 is generated endogenously and promotes beige fat recruitment and thermogenesis in mice, presumably by activating the PKA pathway (297).

Wnt, Notch, and hedgehog signaling.—Wnt is well known to suppress white adipocyte differentiation (260). Similarly, overexpression of Wnt10b in UCP1⁺ cells inhibits BAT activity and blocks beige fat development in *Wnt10b* transgenic mice (146). Conversely, blocking Wnt signaling enhances differentiation of inguinal preadipocytes into beige adipocyte (187). Notch or hedgehog signaling, as Wnt signaling, also inhibits brown and beige adipogenesis (24, 224).

Diets and metabolic states.

Food intake is well known to increase nonshivering thermogenesis in rodents and humans (262, 270). Ingestion of energy dense food (e.g. HFD) further increases BAT and beige fat thermogenesis (340). Perhaps, diet-induced thermogenesis is a physiological adaptation to combat weight gain and obesity. Notably, dietary constituents greatly influence BAT and beige fat activity. Feeding a ketone ester diet promotes UCP1 expression and mitochondrial biogenesis in BAT, increasing BAT thermogenesis in mice (286). Feeding protein-restricted diets also increases energy expenditure in mice (167). Lactate acts in concert with PPAR γ agonists to promote browning of WAT in mice (39).

AMPK is believed to be an intracellular energy sensor to monitor metabolic states. Basal AMPK activity in BAT is high and further increases by chronic cold exposure in mice (215). Prolonged activation of AMPK, by AICAR treatment, induces browning of WAT and body weight loss in mice (319). AMPK is inhibited by folliculin (11), and adipocyte-specific deletion of folliculin increases AMPK activity, browning of WAT, energy expenditure, and protects against HFD-induced obesity and insulin resistance in mice (350). Adipocyte specific deletion of *Ip6k1* also increases adipose AMPK activity, browning of WAT, and energy expenditure, and attenuates HFD-induced obesity in mice (364). α -ketoglutarate (α KG) is a TET demethylase cofactor and promotes active DNA methylation at the *Prdm16* promoter (351). AMPK α 1 increases α KG levels, likely through downregulating IDH2, thereby stimulating *Prdm16* expression and brown adipogenesis (351). In line with these findings, adipocyte-specific deletion of both *AMPK β 1* and *AMPK β 2* impairs both BAT thermogenesis and browning of WAT, and exacerbates HFD-induced insulin resistance and liver steatosis (213). Surprisingly, adipocyte-specific deletion of both *AMPK α 1* and *AMPK α 2* increases FFA β oxidation and energy expenditure and decreases adiposity in mice (154). The reason for the discrepancy between mice with *AMPK β 1/ β 2* deficiency and mice with *AMPK α 1/ α 2* deficiency remains elusive.

REGULATION OF BROWN AND BEIGE FAT THERMOGENESIS BY THE IMMUNE SYSTEM

Metabolic inflammation has been extensively examined in the context of overnutrition states. Chronic, low-grade adipose inflammation is associated with obesity, and is believed to induce insulin resistance (129). Numerous innate immune cells are recruited into WAT where they orchestrate metabolic inflammation (also referred to as metaflammation or sterile inflammation) in obesity (95, 129, 193, 231). It is emerging that immune cells, particularly innate immune cells, play an important role in de novo beige adipogenesis and beige fat thermogenesis. However, metaflammation in BAT remains poorly understood.

Macrophages.

In WAT, M1-polarized macrophages are believed to promote insulin resistance while M2-polarized macrophages counteract the action of M1 macrophages and improve insulin sensitivity (95, 129, 193, 231). Similarly, M1 and M2 macrophages appear to have opposing actions in BAT and/or beige fat. Clodronate liposome-induced depletion of M1 macrophages increases UCP1 expression in BAT and beige fat in mice with HFD-induced obesity (266).

M1 macrophages secrete a variety of proinflammatory cytokines and chemokines, including TNF α and IL1 β . IL1 β directly inhibits brown adipocyte differentiation in vitro (214). TNF α suppresses expression of β 3 receptors in mouse adipocytes, thus attenuating β adrenergic signaling (21), and TNF α treatment attenuates cold-induced UCP1 expression in both BAT and iWAT in C57BL mice (265). A chronic treatment with a low dose of lipopolysaccharides (LPS), which stimulate M1 polarization, impairs beige adipogenesis and induces hypothermia in C57BL mice (230). LPS also suppresses BAT activity via Toll-like receptor 4 (TLR4) (214, 230). In stark contrast, M2 macrophages, which are detected in BAT and increase during cold exposure, stimulate BAT thermogenesis in mice by releasing catecholamines (220). Genetically blocking M2 polarization (deleting IL4/13, IL4R α , or STAT6) impairs cold-induced beige adipogenesis in mice (246). We recently found that the IRE1 α branch of unfold protein response (UPR) profoundly influences M1 vs M2 polarization and BAT and beige fat thermogenesis. Myeloid cell-specific deletion of *IRE1 α* promotes M2 polarization while suppressing M1 macrophages in mice with diet-induced obesity, increases BAT and beige fat thermogenesis, and protects against diet-induced obesity and insulin resistance (280).

Eosinophils.

Cold exposure promotes recruitment of eosinophils into mouse adipose tissue (253). Eosinophils express IL4 that stimulates M2 polarization of macrophages by activating the STAT6 pathway (337). Depletion of eosinophils impairs cold-induced beige adipogenesis and adaptive thermogenesis through blocking M2 polarization (246). Additionally, IL4 is also believed to directly stimulate PDGFR α ⁺ precursors and induce beige adipogenesis by activating the IL4R α /STAT6 pathway (173). Notably, chronic caloric restriction, which is known to improve metabolic health conditions and extend lifespan, increases beige adipogenesis in mice, accompanied by increased eosinophil infiltration, type 2 cytokine signaling, and M2 macrophage polarization in WAT (78). Deletion of *IL4* or *STAT6* prevents caloric restriction-induced browning of WAT and metabolic improvements (78). Interestingly, depletion of gut microbiota, by either antibiotic treatment or housing at germ-free conditions, increases adipose eosinophils, M2 macrophages, and expression of type 2 cytokines (e.g. IL4, IL5, IL13), leading to an increase in browning of WAT and improvement in glucose tolerance and insulin resistance in obese mice (290). These findings raise the intriguing possibility that gut microbiota may modulate energy balance and glucose metabolism through the immune system-BAT/beige fat axis.

Group 2 Innate lymphoid cells (ILC2s).

ILC2s are detected in adipose tissue (32), and activation of adipose ILC2s robustly promotes beige adipogenesis in mice (32, 173). ILC2s secrete IL5 and IL13 that stimulate eosinophils (173). Eosinophils release IL4 that is able to stimulate proliferation and commitment of PDGFR α ⁺ precursors to beige adipocyte lineage as discussed above. The ILC2/eosinophil/IL4 axis is proposed to explain stimulation of de novo beige adipogenesis by ILC2s (173); however, it was also reported that ILC2s elicit beige adipogenesis by an eosinophil- and IL4R α -independent mechanism (32). ILC2s secrete methionine-enkephalin peptides that are responsible for recruitment of beige fat in mice (32). The reason for the discrepancy between these studies remains unclear. Of notice, adipose ILC2s decrease in

obese mice and obese humans (32), which may explain, at least in part, impaired beige adipogenesis in obesity.

iNKT cells.

Adipose tissue contains iNKT cells, and activation of iNKT by α GalCer increases beige adipogenesis and energy expenditure and decreases adiposity in obese mice (194). Adipose iNKT number is lower in obese mice and obese humans relative to lean controls (195), which may also contribute to impaired beige adipogenesis in obesity.

Mast cells.

Mast cells secrete histamine and IL4, both of which are able to stimulate browning of WAT (86). Mast cells are likely to be involved in mediating seasonal beige adipogenesis in the winter in humans (86).

IL33.

IL33 is secreted by a variety of cell types, including fibroblasts, immune cells, endothelial cells, and epithelial cells (206). Deletion of *IL33* impairs beige adipogenesis, decreases energy expenditure, and promotes obesity in mice (32). IL33 activates adipose ILC2s which in turn stimulate beige adipogenesis (32, 173). IL33 also directly regulates the behavior of brown and beige lineage cells (225). IL33 signaling appears to be required for *UCP1* mRNA splicing, and deletion of *IL33* or its receptor *ST2* blocks UCP1 protein synthesis in both brown and beige adipocytes (225).

TNF α and IL1 β .

These two cytokines serve as key pyrogens in infection, and induce fever through activating the hypothalamic thermal circuits (211, 311).

BROWN AND BEIGE FAT DYSFUNCTION IN METABOLIC DISEASES

Mounting evidence suggests that deficiency and dysfunction of BAT and beige fat increase susceptibility to obesity and metabolic diseases. In mice with obesity, activation of BAT and beige fat, by genetic manipulation, cold exposure, or pharmacological interventions, substantially improves metabolic health conditions, including reducing body weight, insulin resistance, and glucose intolerance. Cold exposure or pharmacological interventions similarly activate brown/beige adipocytes and improve metabolic health in some patients with obesity and metabolic disease (117, 232, 317, 355). It is worth mentioning that the same treatments do not have the metabolic beneficial effects on other patients (150), and the underlying reason for the discrepancy between different individuals remains elusive. Interestingly, cold exposure increases energy expenditure, whole body glucose disposal, fatty acid β oxidation, and insulin sensitivity in BAT-positive, but not BAT-negative, individuals (46). These findings further underscore the metabolic importance of BAT in humans.

Obesity.

The anti-obesity and anti-type 2 diabetes functions of BAT and beige fat are convincingly demonstrated by the findings that genetic ablation of UCP1⁺ brown and beige adipocytes induces severe obesity, insulin resistance, and hyperglycemia in mice (192). In humans, obesity is associated with lower levels of brown/beige fat activity (25, 57, 317), further supporting the notion that brown/beige fat deficiency and dysfunction are a risk factor for obesity and metabolic disorders.

Protection against obesity by UCP1-dependent and UCP1-independent energy expenditure.—Adipocyte-specific overexpression of UCP1 decreases fat mass in *aP2-UCP1* transgenic mice (161). These findings suggest that activation of UCP1-mediated thermogenesis in fat is sufficient to protect against obesity. However, ablation of UCP1, unlike ablation of BAT and beige fat, does not induce obesity and insulin resistance in mice (75, 137). Notably, *UCP1*-null mice develop more severe obesity relative to wild type mice when housed at thermoneutrality (85). As discussed before, *UCP1*-null mice develop UCP1-independent thermogenesis that compensates for loss of UCP1 and protects against obesity (185, 313). UCP1-independent thermogenesis is inactive at thermoneutrality, which helps explain why *UCP1*-null mice develop obesity at thermoneutrality but not in cold-stressed conditions. Thus, defects in both UCP1-dependent and UCP-independent thermogenesis are likely to pose a risk for obesity and metabolic diseases.

BAT vs beige fat.—In rodents, inactivation of BAT is known to robustly induce a compensatory recruitment of beige fat. BAT atrophy, induced by BAT denervation, potently induces beige adipogenesis in mice (271). Deletion of *BMPRIA* or insulin receptors in *Myf5*⁺ brown progenitor cells impairs BAT development; similarly, BAT paucity markedly increases beige adipogenesis and beige fat recruitment in these mutant mice (196, 271). Beige adipocytes are believed to provide equal or even better metabolic health benefits in BAT-deficient animals (271).

Human BAT was reported to express beige markers (338); however, an independent study suggests that BAT in adult humans resembles classical BAT in rodents (58). Gene expression profile analysis reveals that in adult humans, BAT consists of both classical brown adipocytes and recruitable beige adipocytes (140). Furthermore, beige progenitors was also identified in human skeletal muscle in addition to adipose tissue (55).

Aging-associated dysfunction BAT and beige fat.—BAT activity progressively declines during aging in rodents and humans (100, 256). Aging is also associated with loss of beige regenerative capacity and beige adipocytes (100), and beige adipogenic capability markedly declines in aged mice (257).

Multiple mechanisms are likely to attribute to aging-associated deficiency of BAT and beige fat. Aged beige progenitors display characteristics of cellular senescence in both mice and humans, and beige progenitor senescence contributes to failure of beige adipogenesis in old mice (22). Aging is associated with decreased sympathetic inputs to subcutaneous adipose tissue (257), likely decreasing beige thermogenesis. Furthermore, β adrenergic sensitivity

in WAT and BAT is also impaired in mice with HFD-induced obesity (52). In humans, BAT develop resistance to sympathomimetic ephedrine in obesity (37).

Diabetes.

Obesity is a primary risk factor for insulin resistance and type 2 diabetes. Given that BAT and beige fat have anti-obesity function, it is not surprising that they also protect against insulin resistance and type 2 diabetes. Indeed, cold acclimation, which activate BAT and beige fat as discussed before, was reported to improve insulin sensitivity in some patients with type 2 diabetes (117). BAT mass and activity are lower in patients with type 2 diabetes relative to normal subjects (25), raising the possibility that deficiency of BAT and beige fat may increase susceptibility to insulin resistance and type 2 diabetes. Notably, cold exposure increases whole body glucose disposal and insulin sensitivity only in brown/beige adipocyte-positive men but not in brown/beige adipocyte-deficient men (46). These observations further demonstrate that activation of BAT and beige fat indeed improves insulin resistance and glucose metabolism in some patients with diabetes. Notably, adoptive transplantation of BAT also reverts hyperglycemia and glucose intolerance in recipient mice with type 1 diabetes (106). Thus, BAT and beige fat combats hyperglycemia and glucose intolerance by both insulin-dependent and insulin-independent mechanisms. However, the mechanism by which BAT and beige fat improve glucose metabolism in the absence of insulin remains elusive.

Hyperlipidemia.

Ablation of BAT and beige fat results in hyperlipidemia in both male and female mice (192), indicating that BAT and beige fat play a critical role in maintaining TAG homeostasis in the circulation. Mechanistically, brown and beige adipocytes robustly catabolize TAG-rich lipoproteins in the blood. Cold exposure or $\beta 3$ adrenergic agonist stimulation increases expression of LDL while suppressing ANGPTL4 (a LPL inhibitor) in BAT, thereby increasing LPL-mediated catabolism of TAG-rich lipoproteins to produce FFAs and LDL remnants (17, 20, 66). Brown and beige adipocytes take up FFAs via CD36 and oxidize them to fuel thermogenesis, while the liver clears plasma LDL remnants (17, 20). Notably, in *ApoE*-null or *Ldlr*-null mice that have impaired liver clearance of LDL remnants, cold exposure accelerates atherosclerotic lesions (70). Thus, BAT and beige fat act in concert with the liver to protect against atherosclerosis.

NAFLD.

Given that obesity is a critical risk factor for NAFLD, BAT and beige fat are expected to protect against NAFLD owing to their anti-obesity action. Moreover, BAT and beige fat primarily utilize FFAs to fuel their thermogenesis; hence, activation of BAT and beige fat are expected to decrease both circulating FFA levels and uptake of FFAs into the liver, thereby protecting against liver steatosis. In line with this notion, activation of BAT and beige fat protects against NAFLD in mice, whereas inhibition of BAT and beige fat has the opposite effect (99, 114, 195, 219, 281). Notably, BAT activity is associated with reduced risk for NAFLD (233, 353), suggesting that BAT activation similarly protects against NAFLD in humans. Furthermore, BAT volumes correlate with cold-stimulated lipolysis and FFA oxidation in humans (47), supporting the notion that human BAT and beige fat are also

important consumers of circulating FFAs. Thus, the anti-liver steatosis function of BAT and beige fat is likely to be conserved from rodents to humans.

Cancer-associated cachexia.

Cancer is associated with increased beige adipogenesis and energy expenditure, contributing to weight loss (156, 240). Tumor cells secrete parathyroid-hormone related protein (PTHrP), and PTHrP promotes beige adipogenesis and beige fat thermogenesis (156). Cancer is associated with chronic inflammation and elevation of IL6, and IL6 stimulates beige adipogenesis and BAT and beige fat thermogenesis, contributing to cancer-associated cachexia (240).

BAT and beige fat as potential therapeutic targets.

Obesity and metabolic disease are becoming global epidemics; however, treatment options are limited. Recent advances in our understanding of brown and beige adipocytes raise the possibility that BAT and beige fat may serve as potential therapeutic targets for treating obesity and/or metabolic disorders.

Target brown/beige adipocyte mitochondria.—Mitochondrial respiration (both UCP1-dependent and UCP1-independent) is responsible for thermogenesis. Therefore, mitochondrial biogenesis, dynamics, quality control, and/or metabolic pathways in brown and beige adipocytes may serve as potential targets.

Target brown/beige adipocyte lipid droplets—Lipid droplet lipolysis releases FFAs that directly fuel mitochondrial respiration. FFAs also activate UCP1 and stimulate the genetic programs to further increase thermogenesis in brown and beige adipocytes as discussed before. Thus, molecular regulators, which govern lipolysis, lipid droplet replenishment, and lipid droplet dynamics, may serve as potential targets.

Target reprogramming of adipocytes.—It is increasingly recognized that white-to-brown adipocyte transdifferentiations occur under certain conditions (71, 275, 281, 289). Given a large WAT mass in the body, a white-to-brown adipocyte conversion is expected to provide a considerable resource for brown/beige adipocyte recruitments. However, the underlying molecular mechanism of white-to-brown adipocyte transdifferentiations remain elusive, limiting our ability to explore this approach in the translational settings.

Target de novo brown and beige adipogenesis.—Obesity and aging are associated with a decline in the capacity of de novo brown and beige adipogenesis. Brown and beige precursor senescence contributes to reduced beige fat regenerative capability under these conditions as discussed before. Therefore, inhibiting brown and/or beige precursor senescence, preserving brown and/or beige precursor pool size, and facilitating brown and beige adipocyte differentiation are expected to improve metabolic health.

Target adipose β adrenergic signaling.—Chronic β 3 adrenergic agonist treatment attenuates HFD-induced obesity in mice (52, 137). Increasing β adrenergic sensitivity, using adipocyte-specific overexpression of FoxC2 (increasing PKA RI α), induces beige

adipogenesis and protects *FoxC2* transgenic mice from HFD-induced obesity and insulin resistance (40, 152). These findings provide proof of concept evidence for the notion that β adrenergic agonists and/or sensitizers may have translational significance in treating obesity and/or metabolic disorders.

Behavior interventions.—A chronic cold exposure activates brown/beige fat, promoting weight loss and improving insulin sensitivity in both rodents and humans (56, 117, 166, 355). Exercise increases beige adipogenesis in rodents (29, 340, 344). Caloric restriction also increases beige adipogenesis (78). It is worth mentioning that genetic variations may influence the metabolic outcomes of these behavior interventions.

CONCLUSIONS

Albeit they develop from different cellular origins, brown and beige adipocytes display similar thermogenic characteristics, are controlled by similar genetic and epigenetic programs, and are regulated by similar neuronal, hormonal, and immune mechanisms. They similarly defend body temperature homeostasis and regulate energy, glucose, and lipid homeostasis. It is emerging that dysfunctions of BAT and beige fat development, maintenance, and/or activation contribute to metabolic disorders, at least in a subpopulation. As such, reactivation of brown and beige adipocytes provides metabolic health benefits in some patients with obesity or type 2 diabetes. We have made a tremendous progress in the understanding of BAT and beige fat biology; however, we are also facing exciting challenges. The nature and the relative contribution of UCP1-independent thermogenesis to energy balance remain elusive. The molecular identities of brown and beige progenitor/stem cells, the chemical niches for brown and beige progenitor/stem cells, and the genetic and epigenetic programs governing individual differentiation steps, are ill-defined. The molecular events that determine brown and beige precursor stemness, regulate brown and beige precursor senescence, preserve brown and beige precursor pool size, and trigger their proliferation and differentiation are poorly understood. The molecular and cellular processes that guide transdifferentiation between white and brown adipocytes are largely unknown. It remains to be determined if and how beige adipocytes, which are intertwined with white adipocytes, influence WAT metabolic and immune homeostasis. We need to answer these exciting questions in order to achieve the goal of targeting BAT and beige fat for obesity, diabetes, and/or NAFLD treatments.

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DIDACTIC SYNOPSIS

Major teaching points:

- Understanding of the development, maintenance, and activation of brown fat and beige fat is critical to appreciate body temperature homeostasis, energy balance, and body weight control.
- Understanding of the thermogenic machinery is necessary to explain the metabolic function of brown fat and beige fat.
- Understanding of neuronal, humoral, and immune regulation of brown fat and beige fat is important to appreciate the role of brown fat and beige fat in obesity and metabolic disease development.
- Understanding of adipose signaling pathways, genetic programs, and epigenetic reprogramming is critical to appreciate brown and beige adipogenesis.
- Understanding of human brown/beige fat characteristics is important to guide development of new obesity and metabolic disease therapies.

CROSS-REFERENCES (5 CHP)

1. Beige adipose tissue in health and disease
2. Central nervous system regulation of brown adipose tissue
3. Contribution of adipose tissue to development of diabetes
4. Hormonal regulation of adipogenesis
5. Innate immune system in adipose tissue

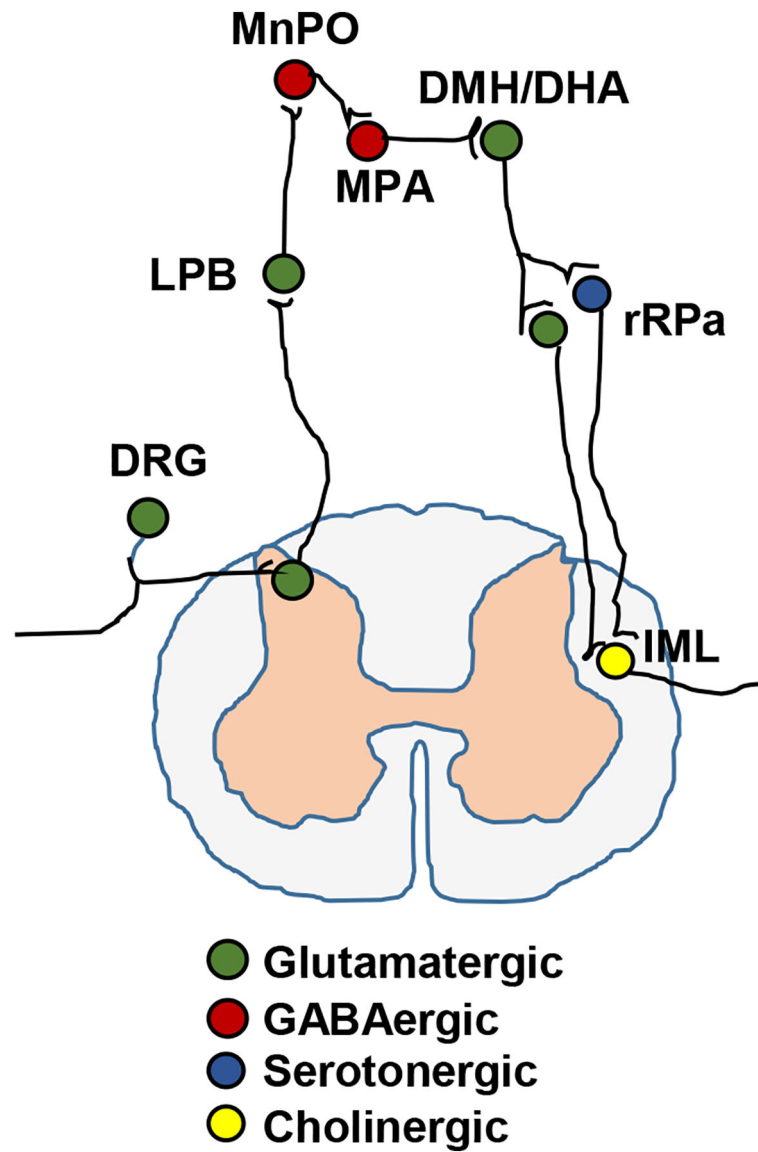


Figure 1. A schematic representation of the core thermal circuitry.
 DRG: dorsal root ganglia. LPB: lateral parabrachial nucleus. MnPO: median preoptic subnucleus. MPA: medial preoptic area. DMH/DHA: dorsomedial hypothalamus/dorsal hypothalamic area. rRPa: the rostral raphe pallidus. IML: intermediolateral nucleus.