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1 **Abnormal mitochondrial functional markers in a rat model of “kidney yang deficiency” and**
2 **related metabolic disorders**

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17 **Keywords:** kidney yang deficiency, mitochondrial DNA, ATP, thermogenesis, PGC1 α

18

19 **Abstract**

20 The mitochondrion is the cellular ‘powerhouse’, generating ATP to support all physiological
21 functions and maintain core body temperature. In Chinese Medicine, the kidney is also
22 considered as the body’s ‘powerhouse’, in which a common pattern called Kidney Yang
23 Deficiency (KYD) describes a series of conditions suggesting energy shortage, eg. cold
24 intolerance, fatigue, and labor intolerance, with reduced blood corticosterone levels. We
25 hypothesized that KYD may be linked to impaired mitochondrial function in thermogenesis
26 and metabolic tissues, therefore making them also prone to metabolic disorders. A rat model
27 of KYD was used, which was established using Sprague Dawley rat dams with warm
28 preference subjected to herbal treatment that can suppress Kidney Yang. The human relevance
29 was confirmed by reduced serum corticosterone levels, and increased preference for warm
30 location. KYD Rats were underdeveloped. ATP production was reduced in the brown fat, but
31 increased in the muscle. However, oxidative phosphorylated complexes to generate ATP and
32 mitochondrial biogenesis marker were reduced in both tissues. When the second insult of high-
33 fat diet (HFD) was introduced, KYD rats gained less weight yet developed more severe lipid
34 and glucose metabolic disorders. This may be driven by dysregulated liver gluconeogenesis
35 marker FOXO1 and lipid metabolic regulator CYP7A1. In conclusion, KYD rats exhibited
36 reduced mitochondrial function in the brown fat, but were partially compensated by skeletal
37 muscle, associated with the phenotype of warm preference and metabolic disorder, which was
38 further exacerbated by additional HFD consumption. Future studies can focus on treatment
39 targeting mitochondria function to reverse this phenotype.

40

41 **1. Introduction**

42 The mitochondrion is the cellular ‘powerhouse’, which is essential to generate the energy substance
43 ATP to support all physiological functions. The heat generated during this process also contributes
44 to the maintenance of core body temperature. As such, mitochondrial density is higher in energy-
45 demanding and heat-generating organs, such as the skeletal muscle and brown adipose tissue (BAT)
46 (Chan et al., 2020). The production of ATP through oxidative phosphorylation (OXPHOS) takes
47 place at the cristae of the mitochondrion and is facilitated by OXPHOS complexes I-V. OXPHOS
48 Complex(C) I is an L shaped protein that acts as the first entry point of electrons in the respiratory
49 chain. OXPHOS CII is the second entry for electrons to the respiratory chain. OXPHOS CIII
50 facilitates electron transfer to OXPHOS CIV. The generated protons from OXPHOS CI to CIV drive
51 ATP synthase in OXPHOS CV (Dudkina et al., 2010). Mitochondrial dysfunction has been found to
52 contribute to various disease conditions, including cognitive disorders, metabolic disorders, and
53 kidney disease (Chan et al., 2016; Chan et al., 2017b; Li et al., 2019a; Li et al., 2019b). Mitochondrial
54 dysfunction can occur as a consequence of the disease, for example in many smoking related diseases,
55 oxidative stress damages mitochondria and results in dysfunction. However, it is now recognized that
56 genetic causes of mitochondrial dysfunction can cause a rare and often inheritable disease called
57 mitochondrial disease, in which patients suffer from fatigue, weakness, and various organ
58 dysfunctions, such as diabetes mellitus and impairment of growth. Mitochondrial disease has a range
59 of severities from relatively mild characterized by unexplained fatigue to severe life limiting disease.

60 In Chinese Medicine, what is referred to as the kidney is not the same solid organ as the kidney in
61 human anatomy, but is considered as the ‘powerhouse’ for the whole body as the primary source of
62 energy and heat, regulating multiple functions, including reproduction and development. Interestingly,
63 a condition in Chinese Medicine called ‘Kidney Yang’ deficiency (KYD) displays some similar
64 symptoms of energy shortage to mitochondrial disease, including fatigue, labor intolerance, cold
65 hypersensitivity (the inability to tolerate cold conditions as a result of the inability to heat the body,
66 especially in the lower limbs), reduced libido and fertility (Zhao et al., 2016); however generally
67 KYD represents mild diseases. The phenotype of KYD also tends to have a familiar heritage, although
68 no specific gene mutation has been reported to date.

69 Given the role of the mitochondria to produce energy in the form of ATP and produce most of the
70 bodies heat requirements in humans, and fact that mitochondrial disease is inheritable, it has striking
71 similarities to KYD, in that, in KYD the main diagnostic symptoms are “energy shortage” and “cold
72 hypersensitivity” and it is also an inheritable condition. It is therefore a reasonable hypothesis to
73 propose that mitochondrial dysfunction is the key to the development of KYD.

74 In Chinese Medicine theory, it is believed that prolonged exposure to a cold environment or regular

75 consumption of cold/frozen food (eg. ice-creams) can lead to KYD (Wang et al., 2006;Dashtdar et
76 al., 2016;Zhu et al., 2018). As such herbal medicines with warm properties are commonly used to
77 treat such conditions (Hempfen and Fischer, 2009). It has been shown that prolonged hypothermia
78 may increase oxidative stress, resulting in irreversible impairment in mitochondrial function (Mollica
79 et al., 2005;Hendriks et al., 2019). Furthermore, therapeutic hypothermia has been shown to reduce
80 mitochondrial function (Pamenter et al., 2018). Interestingly in people with mitochondrial diseases,
81 it has been observed that the brain is hypothermic (Rango et al., 2014). If the damaged mitochondria
82 are the result of altered mitochondrial DNA, it is possible that impaired mitochondria would be
83 inherited from the mother to the children.

84 Previous studies employing the medical examinations for endocrine function found that patients with
85 KYD commonly have reduced urine levels of 17-hydroxycorticosteroids (17-OHCS, a metabolic
86 product of cortisol) with or without reduced serum triiodothyronine (T3) level (Sheng et al.,
87 1979;Shen, 1999;Zhao et al., 2013;Malikov, 2016;Tang et al., 2018). In the clinic, reduced cortisol
88 levels can also contribute to weakness, fatigue, weight loss, and gastrointestinal problems (Adam et
89 al., 2017;Jang et al., 2018). Low serum T3 levels can lead to symptoms like cold sensitivity, edema,
90 weight gain, and muscle weakness (Ruiz-Núñez et al., 2018). However, the clinical features of
91 patients with KYD only have selected symptoms mentioned above and the hormone levels do not
92 warrant replacement therapies, suggesting neither cortisol nor T3 disorders are the primary cause of
93 symptoms in patients with KYD. Other mechanisms are underlying the pathological process of this
94 condition, which are unclear. Understanding such mechanisms can better guide the use of
95 complementary treatment strategies.

96 The heat generated during ATP synthesis in the mitochondria contributes to core body temperature
97 and muscle shivering is an essential mechanism with exposure to a cold environment (Rajagopal et
98 al., 2019). Mitochondrial number insufficiency and/or dysfunction most likely plays a major role to
99 determine the phenotype of KYD, particularly in thermogenesis tissue BAT and skeletal muscle.
100 Therefore, we hypothesized that the mechanisms underlying the pathophysiology of KYD are due to
101 the dysfunction of mitochondria or a reduced mitochondrial number in the BAT and skeletal muscles.
102 We chose rats with warmth preference as the breeders. Living and working in icy climates can allow
103 the cold to enter the body to quench the ‘fire’ energy causing Yang deficiency in the kidney, the
104 body’s powerhouse (Lyttleton, 2013b). Huang Bai is commonly used in Chinese medicine to correct
105 excess kidney yang energy and overdose can cause the deficiency of yang energy, as KYD. Therefore,
106 both were used in the dams to reinforce the KYD phenotype. We aimed to investigate the changes in
107 body temperature, cold preferences, mitochondrial functional markers, and DNA copy numbers in a
108 rat model of KYD. As mitochondria play a key role in metabolic homeostasis, we also examined lipid

109 and glucose metabolic profiles in KYD rats. In addition, mitochondrial function is vital for nutrient
110 metabolism (Mollica et al., 2005;Yoon et al., 2010;Miotto et al., 2018). Mitochondrial dysfunction is
111 well known to cause metabolic disorders, such as glucose intolerance (high risk of type 2 diabetes)
112 and dyslipidemia (risk for cardiovascular diseases) (Lionetti et al., 2007;Koves et al., 2008;Yoon et
113 al., 2010;Pinti et al., 2019;You et al., 2020). Therefore, we further hypothesized that rats with KYD
114 phenotype have a higher risk to develop metabolism disorders if a second insult is implemented. To
115 address this hypothesis, we fed the rats with a high-fat diet (HFD) from weaning for 10 weeks and
116 measured their glucose and lipid profile.

117 **2. Methods**

118 **2.1 Animals**

119 The study was approved by the Animal Ethics Committee of the Chengdu Dossy Experimental
120 Animal Co., Ltd (SCXK (Chuan) 2015-030) where the experiments were performed. A KYD
121 deficiency model was established in both male and female Sprague Dawley rats (10 weeks, Chengdu
122 Dossy Experimental Animal Co., Ltd) according to Chinese Medicine theory. The sires and dams
123 were first screened by the Hot Plate Test. Briefly, rats were allowed to choose to sit/lay on the hot
124 plate set to a temperature of 25°C or 40°C for 10 min. In the literature, the preferred temperature for
125 the rat is 24-27°C (Ray et al., 2004). The percentage of time spent at 40°C end reflects the preference
126 for hot temperatures. The rats which spent more than 20% of the 10 minutes at 40°C were selected
127 for further experimentation. The KYD phenotype was further reinforced by cold exposure (ambient
128 temperature 5-8°C, 2h/day) and the supplement of Huang Bai (*Cortex Phellodendri*) in the diet
129 (0.108g/100g chow) in the dams during pregnancy, as previously published (Li et al., 2014). This
130 dose was calculated based on the dose (12g raw herb/day) for human adults according to Chinese
131 Pharmacopoeia and the ratio of body surface area of humans and rats (0.018). Offspring with positive
132 KYD phenotypes from two consecutive generations were kept as KYD rat strain. To validate the
133 relevance of the rat phenotype to human KYD, the offspring were subjected to the Hot Plate Test at
134 12 weeks of age to evaluate their preference for hot environments. Blood corticosterone and T3 levels
135 were also measured (See the ‘Biochemical assays’)

136 **2.2 Experimental study**

137 At 13 weeks, male offspring were fasted overnight, and the tissues were harvested between 8:00-
138 10:00h. After anesthesia (2% Pentobarbital sodium 40mg/kg), the rectal temperature was measured,
139 followed by cardiac puncture for blood. Blood glucose was immediately measured using a glucose
140 meter (Accu-Check®, Roche Diagnostics, NJ, USA). The plasma was kept at -20°C for hormone and
141 lipid analysis. Brown fat, retroperitoneal white fat, kidney, liver, and skeletal muscle were collected

142 and weighed. Brown fat and skeletal muscle were snap-frozen and kept at -80°C.

143 Considering the vital role of mitochondria in nutrient metabolism, we further examined if the
144 phenotype will increase the risk of metabolic disorders. In a different cohort (n=6), weaning male rat
145 offspring (3 weeks old) were fed a pellet HFD (43% fat, 20kJ/g, Xutong Biological Ltd. Jiangsu,
146 China, following the recipe from our previous studies (Chen et al., 2014;Chen et al., 2018a;Chen et
147 al., 2018b;Komalla et al., 2020)) for 10 weeks. Their littermates were fed the standard rodent chow
148 (14% fat, 12kJ/g). This yielded 4 groups, Control-chow, KYD-chow, Control-HFD, and KYD-HFD.
149 Body weight and food intake were measured every fortnight.

150 **2.3 Biochemical assays - ELISA**

151 All blood markers were measured by ELISA in plasma using commercially available kits following
152 the manufactures' instructions. Briefly, for the corticosterone assay, plasma was diluted (1:10) before
153 the incubation estimation of levels using the Rat corticosterone ELISA kit, Shanghai Westang
154 Biotechnology, Shanghai, China. The ELISA plate was measured at an OD of 450nm (Synergy H1
155 microplate reader, BioTek, US). For the T3 assay, plasma samples (50ul) were used in the Total T3
156 ELISA assay (IBL International, Hamburg, Germany) and the plate read as above. LDL
157 measurements were made in plasma samples (5ul). Samples were first incubated with the AAP
158 solution (Shanghai Westang Biotechnology) and the first optical density (OD1) was measured, this
159 was followed by the incubation with enzyme conjugate for the measurement of the second optical
160 density (OD2) at 550nm. The difference between OD2 and OD1 was used to calculate LDL
161 concentration against the standard curve. For cholesterol, plasma samples (20ul) were measured
162 using a kit from Shanghai Westang Biotechnology, the absorbance was measured at 550nm. For
163 insulin, plasma samples were diluted (1:20) and measured using a kit from Crystal Chem, USA, and
164 the absorbance was measured at 450nm.

165 **2.4 Glucose tolerance test**

166 After 9 weeks of HFD feeding, a glucose tolerance test was carried out in all rats using published
167 methods. After 9 weeks of the diet, the rats were fasted for 5h before an intraperitoneal glucose
168 tolerance test (IPGTT) was performed as previously described (Chen et al., 2014;Chen et al.,
169 2018a;Chen et al., 2018b;Komalla et al., 2020). All mice were administered with D-glucose (2 g/kg,
170 ip). Tail tip blood was collected at time 0 prior to glucose injection (baseline), then at 15, 30, 60, and
171 90 min after glucose administration. Blood glucose levels were measured using a glucose meter
172 (AccuCheck®, Roche Diagnostics). The trapezoid method was used to calculate the area under the
173 curve (AUC) corresponding to the blood glucose levels over the monitoring period obtained for each
174 animal. At 13 weeks, samples were collected following the same protocol as mentioned above.

175 **2.5 Real-time PCR**

176 The major function of brown fat is non-shivering thermogenesis against the cold (Cedikova et al.,
177 2016), mainly relying on uncoupling proteins (UCPs), especially UCP1 (Argyropoulos and Harper,
178 2002). Mice lacking UCPs were cold intolerant (Enerback et al., 1997). Muscle contraction
179 contributes to shivering thermogenesis. mRNA expression of thermoregulator UCP1, mitochondrial
180 biogenesis marker peroxisome proliferator-activated receptor gamma coactivator 1-alpha (PGC1 α),
181 and insulin sensing marker Peroxisome proliferator-activated receptor gamma (PPAR γ) was
182 measured in brown and skeletal muscle using real-time PCR. Lipid metabolic marker Cholesterol 7
183 alpha-hydroxylase (CYP7A1) and gluconeogenesis marker Forkhead box protein O (FOXO)1 were
184 measured in the liver. The tissues (10-100mg) were extracted using mirVana™ miRNA Isolation Kit
185 (Life Technologies) following the manufacture's instructions.

186 Quantification was performed with a two-step reaction process: reverse transcription (RT) and PCR.
187 cDNA was synthesized using HiScript II Q RT SuperMix IIa (Vazyme Biotech Co. Ltd, Jiangsu,
188 China) in a GeneAmp® PCR System 9700 (Applied Biosystems, USA). The genes of interest were
189 measured by SYBR green primers using LightCycler® 480 II Real-time PCR Instrument (Roche,
190 Swiss). The primer sequences were designed in the laboratory and synthesized by Generay Biotech
191 (Generay, China) based on the mRNA sequences obtained from the NCBI database (CYP7A1 5'-
192 CCTGCCGGTACTAGACAGC -3', reverse 5'- AGGGTCTGGGTAGATTTTCAGGA -3'; FOXO1
193 forward 5'- TAGGAGTTAGTGAGCAGGCAAC -3', reverse 5'-TGCTGCCAAGTCTGACGAAA-
194 3'; PPAR γ forward 5'-ATCAAGAAGACGGAGACAGATA-3', reverse 5'-
195 GAAGGAACACTTTGTCAGCGA-3'; PGC1- α forward 5'- GGATATACTTTACGCAGGTCG -3',
196 reverse 5'-ATCGTCTGAGTTTGAATCTAGG-3'; UCP1 forward 5'- TCCGGGCTTAAAGAGCGA
197 -3', reverse 5'-TGGGTACCGAACTCTCAAC-3'; 18s forward 5'-
198 CGGCTACCACATCCAAGGAA-3', reverse 5'-GCTGGAATTACCGCGGCT-3'). At the end of the
199 PCR cycles, the melting curve analysis was performed to validate the specific generation of the
200 expected PCR product. mRNA expression was calculated using $2^{-\Delta\Delta Ct}$ methods using 18s as the
201 housekeeping gene. The Control group was assigned the calibrator against which all other results
202 were expressed as fold changes.

203 The mitochondrial number was measured using the mitochondrial DNA copy number. Genomic DNA
204 was extracted from tissues using the DNeasy Blood and Tissue kit according to the manufacturer's
205 instructions (Qiagen, Hilden, Germany). The content of mtDNA was calculated using real-time
206 quantitative PCR by measuring the threshold cycle ratio (ΔCt) of a mitochondrial-encoded gene
207 (COX1, forward 5'-ACTATACTACTACTAA-CAGACCG-3', reverse 5'-
208 GGTTCTTTTTTCCGGAGTA-3') versus a nuclear-encoded gene (cyclophilin A, forward 5'-

209 ACACGCCATAATGGCACTGG-3', reverse 5'-CAGTCTTGGCAGTGCAGAT-3') as we have
210 previously published (Stangenberg et al., 2015).

211 **2.6 Western blotting**

212 OXPHOS complexes, antioxidant manganese superoxide dismutase (MnSOD), Glutathione
213 peroxidase (GPx), phosphorylated (p)- and total insulin receptor substrate 1 (IRS1) and its
214 downstream protein kinase B (Akt) were measured by Western Blotting. Total and mitochondrial
215 protein was extracted from brown adipose tissue and skeletal muscle using our published method
216 (Chan et al., 2017a). Proteins of the whole tissue lysate and mitochondrial fraction were extracted by
217 the differential speed extraction method. The tissues were homogenized in 200 μ l of lysis buffer
218 (Shanghai West Tang Biotechnology Ltd., China). Whole cellular proteins and mitochondria
219 proteins were quantified using Bio-Rad DC protein assay (Bio-Rad Laboratories, California, USA)
220 according to the manufacturer's instructions. Proteins samples (2 μ g/ μ l) were loaded into each well
221 of NuPAGE® Novex 4-12% Bis-Tris protein gels (Life Technology, CA, USA) and separated on the
222 gel. The separated proteins were then transferred to PVDF membranes using either semi-dried or wet
223 transfer methods where applies (Thermo Scientific, Illinois, USA). The PVDF membrane was then
224 blocked with 5% skim milk for one hour at room temperature. Primary antibodies (OXPHOS
225 complexes 1:2500, MnSOD 1:5000, GPx-3 1:1000, p-IRS1 1:1000, IRS1 1:1000, p-Akt 1:1000, Akt
226 1:1000, GAPDH 1:1000, Abcam, Cambridge, UK; voltage-dependent anion channels (VDAC)
227 1:1000, Cell signaling technology, MA, USA) were incubated with the PVDF membrane at 4°C
228 overnight, followed by secondary antibodies (peroxidase-conjugated AffiniPure Goat Anti-Rabbit
229 IgG and Peroxidase-conjugated AffiniPure Goat Anti-Mouse IgG, 1:10000, Jackson Immuno
230 Research Laboratories, PA, USA) and SuperSignal™ West Pico Chemiluminescent Substrate
231 (ThermoFisher Scientific, NSW, Australia). The bands on the membrane were detected with LAS-
232 3000 Imaging system (Fujifilm, Tokyo, Japan). The results are expressed as a ratio of the intensity of
233 the protein of interest relative to the band intensity of VDAC for mitochondrial proteins (Wang et al.,
234 2020) or GAPDH for cytoplasmic proteins.

235 **2.7 Statistical methods**

236 The results are expressed as mean \pm SEM. The data between the 2 groups were analyzed by unpaired
237 t-test. The data between the 4 groups were analyzed by two-way ANOVA followed by post hoc
238 Fisher's LSD tests. The data of IPGTT were analyzed by ANOVA with repeated measures followed
239 by Fisher's LSD tests. Prism V9.0.1 (GraphPad Software, CA, USA) and Statistica (StatSoft, TIBCO
240 Software, CA, USA) were used for data analysis. $P < 0.05$ was considered statistically significant.

241 **3. Results**

242 **3.1 Baseline assessment in the KYD rats**

243 **3.1.1 *Biometric parameters***

244 Before pregnancy, KYD dams were 9% smaller than the controls ($P < 0.05$), consistent with weight
245 loss in patients with KYD (Lyttleton, 2013b). The litter size of KYD mothers (6.33 ± 0.88) was also
246 half of the Control group (13 ± 1.16 , $P < 0.05$). KYD dams seem to produce less female offspring in
247 each litter reflected by the sex ratio (female to male: KYD 1.57 ± 0.81 , Control 2.37 ± 1.20). However,
248 it did not have statistical significance. Thus, KYD dams showed issues of reproduction.

249 Male offspring from KYD dams had significantly smaller birth weight ($P < 0.01$ vs Control, Figure
250 1a), which was maintained in adulthood ($P < 0.05$ vs Control, Table 1). KYD offspring also had smaller
251 kidney mass ($P < 0.05$ vs Control) and white fat mass ($P < 0.01$ vs Control), however bigger muscle
252 mass at 13 weeks ($P < 0.05$ vs Control, Table 1). After standardizing for body weight, KYD rats had
253 a bigger percentage of liver and muscle weights (both $P < 0.05$ vs Control), and a smaller percentage
254 of white fat mass ($P < 0.01$, Table 1).

255 **3.1.2 *Serum metabolic markers***

256 To further confirm the human relevance of this rat model, we measured serum corticosterone and T3
257 levels. In KYD offspring, serum corticosterone levels were significantly lower than the Control group
258 ($P < 0.05$, Table 1), while T3 levels were only marginally reduced (Table 1).

259 We also measured blood glucose and lipid levels. The blood glucose level in the KYD offspring was
260 similar to the Control group (Table 1), whereas serum LDL and cholesterol levels were significantly
261 increased in KYD offspring ($P < 0.05$ and 0.01 vs Control, respectively, Table 1), suggesting lipid
262 metabolic disorders, which is also consistent with the risk in human patients.

263 **3.1.3 *Body temperature and warm/cold preference***

264 The hot plate test allows the rats to choose their preferred temperature by sitting or laying on either
265 of two plates set to temperatures of 25°C as cool and 40°C as warm. KYD rats showed a preference
266 for warm locations which was reflected in the rats spending twice as long as the Control rats on the
267 warm plate ($P < 0.05$ vs Control, Figure 1a), showing a preference for warm locations.

268 To investigate whether such preference was due to low core body temperature, we measured rectal
269 temperature and mRNA expression of uncoupling proteins (UCP)1 in BAT (non-shivering
270 thermogenesis) and muscle (shivering thermogenesis). However, there was no difference in body
271 temperature between the KYD offspring and Control offspring (Figure 1b). Not surprisingly, the
272 regulator of thermogenesis UCP1 expression was not significantly changed in both BAT and skeletal
273 muscle (Figure 1c,d).

274 **3.1.4 Mitochondrial metabolic markers in the BAT and muscle**

275 In BAT, ATP production was significantly lower in the KYD rats ($P < 0.01$ vs Control, Figure 2a).
276 Peroxisome proliferator-activated receptor gamma coactivator 1-alpha (PGC1a) is a multiple-
277 functional molecule, which also regulates mitochondrial biogenesis. PGC1 α in BAT was reduced in
278 KYD rats ($P < 0.05$, vs Control, Figure 2b), suggesting impaired ability to replenish mitochondrial
279 shortage. This is associated with reduced mitoDNA copy number ($P < 0.001$ vs Control, Figure 2c).
280 Results show that OXPHOS CI was nearly diminished in KYD rats, and OXPHOS CV was also
281 significantly lower in KYD rats (both $P < 0.05$ vs Control, Figure 2d,e). Endogenous antioxidants
282 MnSOD and GPx were not different between the groups (data not shown), suggesting oxidative stress
283 is not involved.

284 In the skeletal muscle, ATP levels were significantly higher in the KYD rats ($P < 0.05$ vs Control,
285 Figure 3a). Mitochondrial biogenesis and metabolic regulator PGC1 α was lower in the KYD rats
286 ($P = 0.07$ vs Control, Figure 3b), however mitochondrial DNA copy number was not different between
287 the groups (Figure 3c), suggesting impaired metabolic capacity in the muscle. OXPHOS CI was not
288 different between the groups (Figure 3d), however, OXPHOS CV was nearly depleted in the skeletal
289 muscle ($P < 0.01$, Figure 3e). Similarly, in BAT, mitochondrial endogenous antioxidant MnSOD and
290 GPx did not show any difference between the Control and KYD groups (not shown). Therefore, the
291 difference between mitochondrial biogenesis and functional units might not result from oxidative
292 stress.

293 **3.2 Effects of HFD consumption on metabolic profiles**

294 At weaning, the body weights were not significantly different among the groups (Table 2). At 13
295 weeks, KYD-chow rats were smaller than the Control-chow rats ($P < 0.05$, Table 2), consistent with
296 the first cohort. Interestingly, KYD-HFD rats gained less body weight by HFD consumption
297 compared with the Control rats ($P < 0.01$ KYD-HFD vs Control-HFD, Table 2) whose body weight
298 was similar to the Control-chow rats, although KYD rats had similar daily caloric intake as the
299 Control regardless of the diet (Table 2). HFD consumption significantly increased white fat mass in
300 both Control-HFD and KYD-HFD rats ($P < 0.05$, Table 2), but only increased liver mass in the KYD-
301 HFD rats ($P < 0.01$ vs KYD-chow, Table 2) both as net weight and percentage of body weight.

302 During the glucose tolerance test, it was expected that Control-HFD rats developed glucose
303 intolerance reflected by higher blood glucose levels at 30 min post glucose injection ($P < 0.01$, Figure
304 4a) and bigger AUC value ($P < 0.01$ vs Control-chow, Figure 4b); however, KYD-HFD rats showed
305 more severe glucose intolerance than Control HFD rats as shown by blood glucose level at 15 min
306 and 30 min post glucose injection (Figure 4a) and AUC value ($P < 0.01$ KYD-HFD vs KYD-chow
307 and Control-HFD, Figure 4b) albeit smaller body weight and fat mass. This may be due to insulin

308 insufficiency, as serum insulin level ($P < 0.01$ Control-HFD vs Control-chow and KYD-HFD) was
309 significantly increased in the Control-HFD group, but remained unchanged in the KYD-HFD rats.
310 Interestingly, hyperlipidemia was worsened in KYD rats after HFD consumption, especially the LDL
311 which was increased in the KYD-HFD group ($P < 0.01$ KYD-HFD vs KYD-chow and Control-HFD,
312 Table 2), not the Control-HFD group. Cholesterol was increased in Control-HFD group ($P < 0.05$ vs
313 Control-chow Table 2), which was further increased in the KYD-HFD group ($P < 0.05$ vs Control-
314 HFD, $P < 0.01$ vs KYD-chow group, Table 2)

315 To further investigate the molecular pathway, we found in the muscle, the energy regulator PGC-1 α
316 was significantly downregulated in the KYD-chow rats ($P < 0.05$ vs Control-chow, Figure 4c), which
317 was less reduced in the Control-HFD and KYD-HFD rats, suggesting diet and phenotype may
318 independently affect this marker. The insulin sensing marker PPAR γ expression was only reduced by
319 HFD consumption ($P < 0.01$ Control-HFD vs Control-chow, KYD-HFD vs KYD-chow, Figure 4d).
320 The ratio between p-IRS1 and total IRS1 was reduced in KYD-chow rats and by HFD consumption
321 (both $P < 0.01$, Figure 4e). However, there was some increase in p-IRS1/IRS1 in KYD-HFD rats
322 compared with their chow-fed littermates ($P < 0.01$). The downstream signaling p-Akt/Akt ratio was
323 only reduced in KYD rats independent of the diet ($P < 0.01$ vs Control rats fed the same diet, Figure
324 4f). In the liver, FOXO1 expression was suppressed in the KYD-chow rats ($P < 0.01$ vs Control-chow,
325 Figure 4g), and to a less extent in the Control-HFD-rats ($P < 0.01$ vs Control-chow); however, FOXO1
326 was significantly upregulated by HFD feeding in KYD rats ($P < 0.05$ KYD-HFD vs KYD-chow,
327 Figure 4g). The lipid metabolic marker CYP7A1 was more than halved in the liver of the KYD-rats
328 albeit without statistical significance (Figure 4h). CYP7A1 mRNA was however increased in
329 Control-HFD ($P < 0.01$ vs Control-chow), which was at a normal level in KYD-HFD rats ($P < 0.01$ vs
330 Control-HFD).

331 4. Discussion

332 As the kidney in Chinese Medicine is considered the ‘powerhouse’, the condition of KYD is mostly
333 caused by mitochondrial dysfunction. In this study, we used a clinically relevant rat model to
334 demonstrate that in KYD, markers of the mitochondrial number, biogenesis, and function are
335 differentially regulated in different key heat production organs, which may contribute to the warm
336 preference but unchanged core body temperature. Reduced metabolic main regulator PGC1 α may
337 contribute to blood hyperlipidemia.

338 The KYD rats showed a similar phenotype as the humans with KYD (Sheng et al., 1979; Shen,
339 1999; Lyttleton, 2013b;a; Zhao et al., 2013; Malikov, 2016; Tang et al., 2018), including warm
340 preference, issues of reproduction small birth weight, slow postnatal growth, impaired fertility

341 function, hyperlipidemia, and reduced corticosterone levels, suggesting its clinical relevance.
342 According to the theory of Chinese medicine, KYD is closely related to lifestyle or environment, such
343 as living and working in icy climates (Lyttleton, 2013b). However, the dietary supplement Huang
344 Bai is not known to suppress T3, rather its anti-inflammatory and gonadotropin-releasing hormone
345 suppressing effects (Xian et al., 2011; Lee et al., 2016; Sun et al., 2019). This may explain reduced
346 corticosterone levels, which is also anti-inflammatory hormone. However, reduced T3 levels in some
347 patients with KYD may be secondary to reduced energy supply, which is not seen in this rat model.

348 As the cellular powerhouse in modern science, electron respiration within the mitochondrial
349 OXPHOS complex generate both ATP to fuel the cells, and heat to warm the body. In small rodents
350 and infants, BAT is a discrete organ for heat production; whereas in adult humans, brown adipocytes
351 diffuse into white fat tissue, skeletal muscles, and around major arteries to maintain core temperature
352 (Ravussin and Galgani, 2011). Here in the KYD rats, ATP production is significantly reduced in BAT,
353 and somehow it was partially compensated by muscle ATP production. In Chinese medicine, Kidney-
354 yang is the source of energy to promote blood movement. Therefore KYD can affect microcirculation
355 in the limbs resulting in cold extremities (Shu et al., 2000). In humans, cold intolerance in KYD
356 patients mainly occurs in the low limbs and not in the whole body, which may explain why KYD rats
357 prefer warm places although the core body temperature did not change.

358 ATP reduction in BAT may directly attribute to reduced mitochondrial number and biogenesis,
359 reflected by mitoDNA number and PGC1 α expression, respectively. In addition, OXPHOS
360 complexes, where electron enters the inner membrane OXPHOS CI and ATP is produced in
361 OXPHOS CV, were both reduced contributing to reduced ATP production. In the muscle, we
362 observed significantly increased ATP production. However, although the mitochondrial number and
363 OXPHOS CI seem to be unchanged, OXPHOS CV was depressed in the muscle. It is unclear whether
364 this is an outcome of the overproduction of ATP, or it is an outcome of KYD, which requires further
365 investigation. Reactive oxygen species (ROS) are released as a by-product during ATP production,
366 which is normally consumed by endogenous antioxidants, such as MnSOD and GPx. Thus if MnSOD
367 and GPx are overconsumed, increased oxidative stress can damage the mitochondria and cells.
368 Mitochondrial antioxidant MnSOD and GPx did not show any difference between the Control and
369 KYD groups in both BAT and muscle. Therefore, the differences between mitochondrial biogenesis
370 and functional units are unlikely to be due to oxidative stress.

371 Mitochondria have been implicated as key factors regulating reproductive processes (Kumar and
372 Sangeetha, 2009; Cecchino et al., 2018). The downregulation of mitochondrial biogenesis marker
373 PGC1 α and OXPHOS CV may play some role in reduced litter size in KYD dams. In addition, the
374 healthy mitochondrial function also plays a key role in maintaining nutrient homeostasis, and is the

375 main regulator for both glucose and lipid metabolism (Gerhart-Hines et al., 2007; Handschin et al.,
376 2007). However, reduced PGC1 α seems to only affect the blood lipid profile, maybe because of the
377 need for glucose being used to produce ATP in the muscle. Therefore, we postulate that mitochondrial
378 insufficiency and dysfunction is the underlying mechanism of hyperlipidemia observed in patients
379 with KYD (Zhang et al., 1989; Liu and Shan, 2017).

380 The highlight of this study is the introduction of a second insult, *ad libitum* HFD feeding, which
381 confirmed our hypothesis that KYD rats are prone to glucose and lipid metabolic disorders when the
382 obesogenic environment is present. KYD and control rats had similar body weights at weaning. We
383 think the recovery of body weight at weaning is related to breastmilk, which is full of antioxidants
384 and nutrients. Thus, breastfeeding may promote catch growth in rats with in-utero underdevelopment.
385 After weaning, the loss of protection from breastmilk and dysfunctional mitochondrial function
386 resulted in retarded growth in KYD rats after weaning. However, KYD rats did not gain as much
387 weight as the Control rats, yet exhibit more severe glucose and lipid disorders, suggesting underlying
388 dysfunction in tissue nutrient metabolism. The unchanged serum insulin in the KYD-HFD group,
389 suggesting the inability of the pancreas to produce more insulin in response to increased energy influx,
390 eg. rising in blood glucose level after meals. Muscle is a major organ for insulin-stimulated glucose
391 deposition. Therefore, we investigated markers related to glucose metabolism in the muscle.
392 Previously, we have found that in rats with glucose intolerance, PGC1 α is the main switch for energy
393 sensing and metabolism. Its expression is significantly reduced in skeletal muscle (Simar et al.,
394 2011; Chan et al., 2015), which was only displayed in KYD-chow rats, whereas there was only a
395 marginal reduction in Control-HFD rats. The change in KYD-chow rats may already determine their
396 poor metabolic capability. Insulin sensing marker PPAR γ was suppressed by HFD consumption in
397 both HFD and KYD-HFD rats, which can only explain increased insulin resistance by HFD
398 consumption, which can't explain why KYD-HFD had more severe glucose intolerance. Then, we
399 further investigated the liver, which plays a key role in both glucose homeostasis and lipid metabolism
400 (especially in the synthesis of cholesterol and major lipoproteins, eg. LDL). What needs to be noted
401 here is the increased gluconeogenesis marker FOXO1 in KYD-HFD rats compared with their chow-
402 fed littermates. Although the level is comparable to a normal level as reflected in the Control-chow
403 rats, such an increase is perhaps sufficient to cause higher blood glucose levels during glucose
404 tolerance test thereafter more severe glucose intolerance in KYD-HFD rats compared with Control-
405 HFD rats, whose FOXO1 was actually suppressed by HFD feeding.

406 Another worsened profile in KYD-HFD rats is the blood lipids, ie. LDL and cholesterol. CYP7A1 is
407 an important enzyme to regulate cholesterol metabolism. In humans, CYP7A1 deficiency is directly
408 related to increased circulating cholesterol and LDL levels (Pullinger et al., 2002). Overexpression

409 of CYP7A1 in the liver can protect against HFD-induced obesity (Li et al., 2010). Here, we observed
410 a marked increase in this enzyme in HFD-fed mice, which may be an adaptive change to prevent
411 further increase in circulating cholesterol and LDL levels. Interestingly, such adaptation was lost in
412 KYD rats when they consumed the HFD diet, attribute to its low baseline level in the KYD-chow rats.
413 As such, dyslipidemia seems more problematic in KYD-HFD rats. Future studies can follow up on
414 the cardiovascular consequence in these rats.

415 We need to acknowledge the limitation of using rats to model a condition with no clear origins, which
416 represents a partial match to the phenotype of human patients. However, it may still be useful to
417 determine the risk of other conditions, such as vascular damage, and investigate the efficacy of certain
418 treatments to improve mitochondrial function.

419

420 **5. Conclusion**

421 The ‘kidney yang’ in Chinese Medicine seems to be closely related to abnormal mitochondrial
422 function. This study showed abnormal mitochondrial functional units in both BAT and skeletal
423 muscle with impaired ATP production in BAT. There seems to be an adaptive increase in muscle
424 ATP production, KYD rats still showed abnormal temperature sensation and hyperlipidemia,
425 suggesting impaired mitochondrial metabolic function (summarized in Figure 5). This may contribute
426 to exacerbated glucose and lipid metabolic disorders when HFD was introduced in KYD rats.

427

428 **6. Conflict of interests**

429 The authors declare that they have no competing interests.

430 **7. Author’s contribution**

431 YC, BGO, and HChen designed the study. HCai and HL performed the animal studies and collected
432 the tissues. Hcai, XH, JE, YS, WL analyzed the tissues. HChen drafted the manuscript. All authors
433 contributed to the final manuscript and approved the submission.

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441 NA

442 10. References

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625

626 **Table 1: Biometric parameters and blood metabolic markers in male offspring at 13 weeks.**

	Control	KYD
Birth weight at birth (g)	7.80 ± 0.20	4.78 ± 0.29**
Body weight at 13 weeks (g)	322 ± 70	286 ± 96*
Liver (g)	10.28±0.24	10.68±0.21
Liver %	2.88±0.06	3.32±0.13*
Kidney (g)	2.46±0.10	2.06±0.06*
Kidney %	0.71±0.02	0.64±0.03
Brown adipose tissue (g)	0.50±0.05	0.47±0.05
Brown adipose tissue %	0.14±0.01	0.15±0.02
White adipose tissue (g)	4.96±0.32	2.80±0.31**
White adipose tissue%	1.39±0.09	0.86±0.08**
Sketeal muscle (g)	0.53±0.04	0.69±0.04*
Sketeal muscle %	0.15±0.01	0.22±0.02*
Serum corticosterone (ng/ml)	22.2 ± 0.8	15.2 ± 1.4*
Serum T3 (ng/ml)	3.84 ± 0.15	3.68 ± 0.11
Blood glucose (mM)	8.05 ± 0.37	7.83 ± 0.51
Serum LDL (mM)	1.11 ± 0.06	1.26 ± 0.03*
Serum Cholesterol (mM)	2.21 ± 0.08	2.76 ± 0.12**

627 Results are expressed as mean ± SEM, n=10. * P < 0.05, ** P< 0.01.

628 LDL: Low-Density Lipoprotein; T3: triiodothyronine.

629 **Table 2: Biometric parameters and blood metabolic markers in male offspring fed a HFD.**

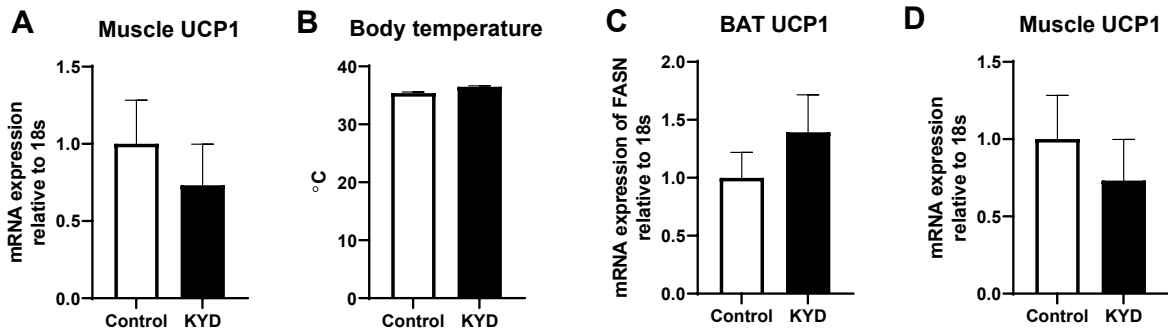
	Control-chow	KYD-chow	Control-HFD	KYD-HFD
Body weight before the diet (g)	53.0 ± 0.5	50.8 ± 1.4	52.0 ± 1.3	53.0 ± 0.7
Body weight at endpoint (g)	375 ± 9	323 ± 15*	442 ± 12**	380 ± 9 ^{##δ}
Caloric intake (kJ/day/rat)	271 ± 16	275 ± 14	348 ± 12*	403 ± 35 ^{δδ}
Liver (g)	11.4 ± 0.5	10.7 ± 0.75	13.7 ± 0.9	14.2 ± 0.7 ^{δδ}
Liver %	2.97 ± 0.20	3.01 ± 0.07	3.16 ± 0.15	3.71 ± 0.09 ^{δδ}
White adipose tissue (g)	4.99 ± 0.82	3.56 ± 0.48	9.76 ± 1.71 *	8.47 ± 0.90 ^δ
White adipose tissue%	1.28 ± 0.20	0.89 ± 0.07	1.88 ± 0.22 *	2.20 ± 0.20 ^{δδ}
Sketeal muscle (g)	0.71 ± 0.04	0.74 ± 0.05	0.82 ± 0.03	0.78 ± 0.02
Sketeal muscle %	0.18 ± 0.01	0.19 ± 0.00	0.20 ± 0.01	0.20 ± 0.01
Blood insulin (ng/ml)	0.15 ± 0.03	0.12 ± 0.01	0.29 ± 0.05**	0.15 ± 0.03 ^{##}
Serum LDL (mM)	1.20 ± 0.07	1.41 ± 0.05*	1.49 ± 0.08**	2.01 ± 0.08 ^{##δδ}
Serum Cholesterol (mM)	2.51 ± 0.05	2.71 ± 0.08	3.00 ± 0.18*	3.52 ± 0.17 ^{##δδ}

630 Results are expressed as mean ± SEM, n=6. * P < 0.05, ** P< 0.01 vs Control-chow; # P < 0.05, ##

631 P < 0.01 vs Control-HFD; δ P < 0.05, δδ P < 0.01 vs KYD-chow.

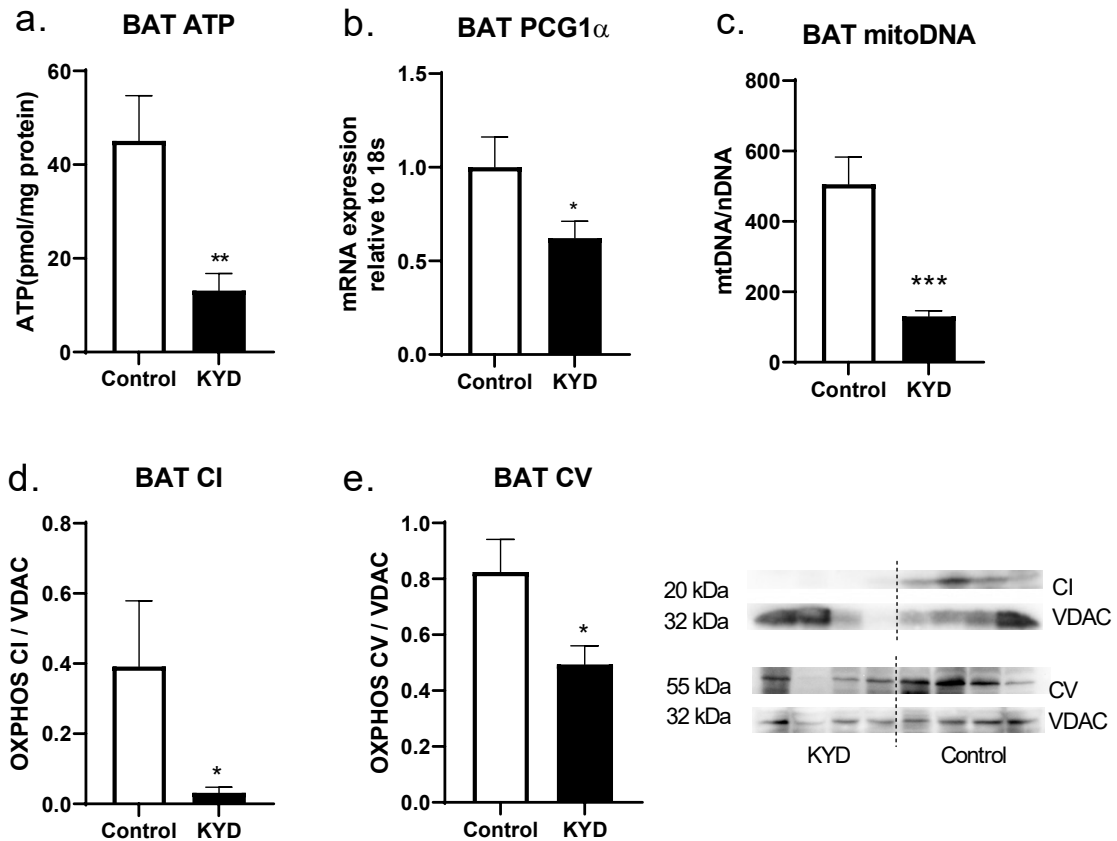
632 HFD: high-fat diet; KYD: kidney yang deficiency; LDL: Low-Density Lipoprotein.

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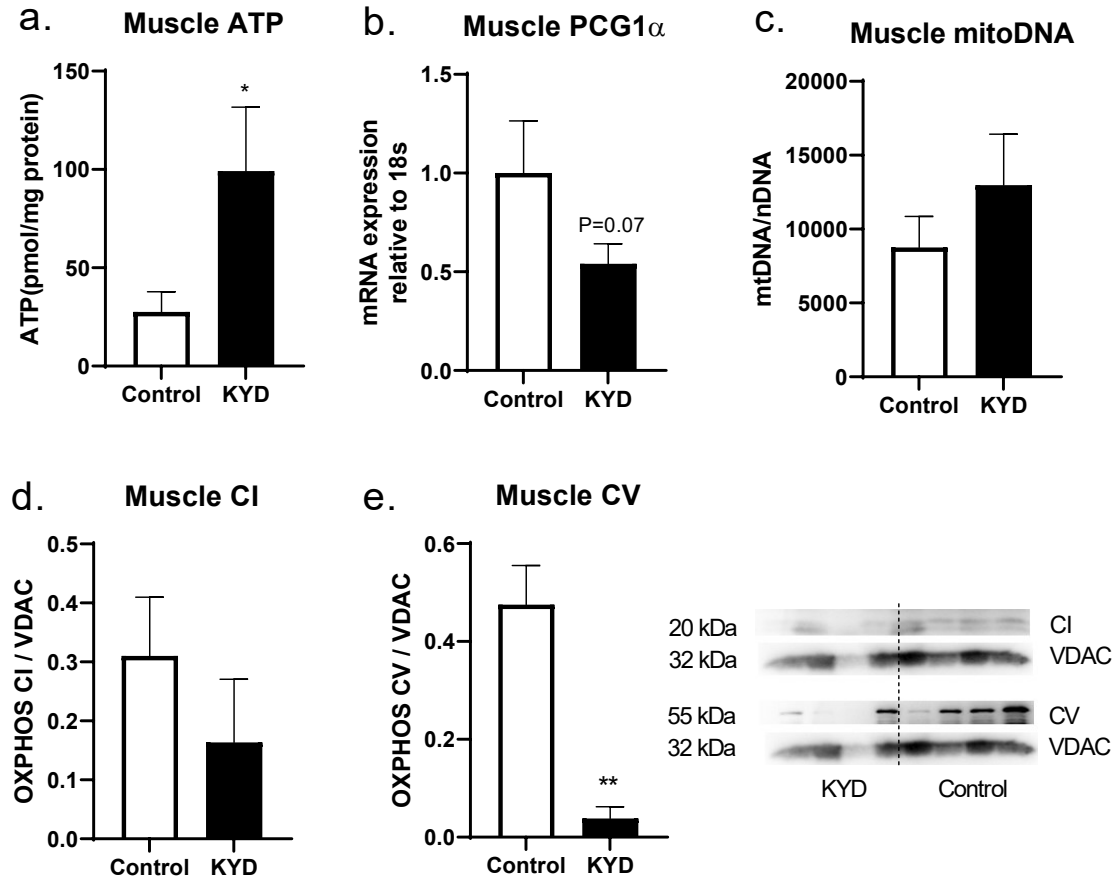
635

636 **Figure 1:** Hot plate test (a), body temperature (b), mRNA expression of uncoupling protein 1 (UCP1)
 637 in the brown adipose tissue (BAT, c) and skeletal muscle (d) in male offspring at 13 weeks. Results
 638 are expressed as mean \pm SEM, n=6-10. * $P < 0.05$, ** $P < 0.01$. KYD: kidney yang deficiency;



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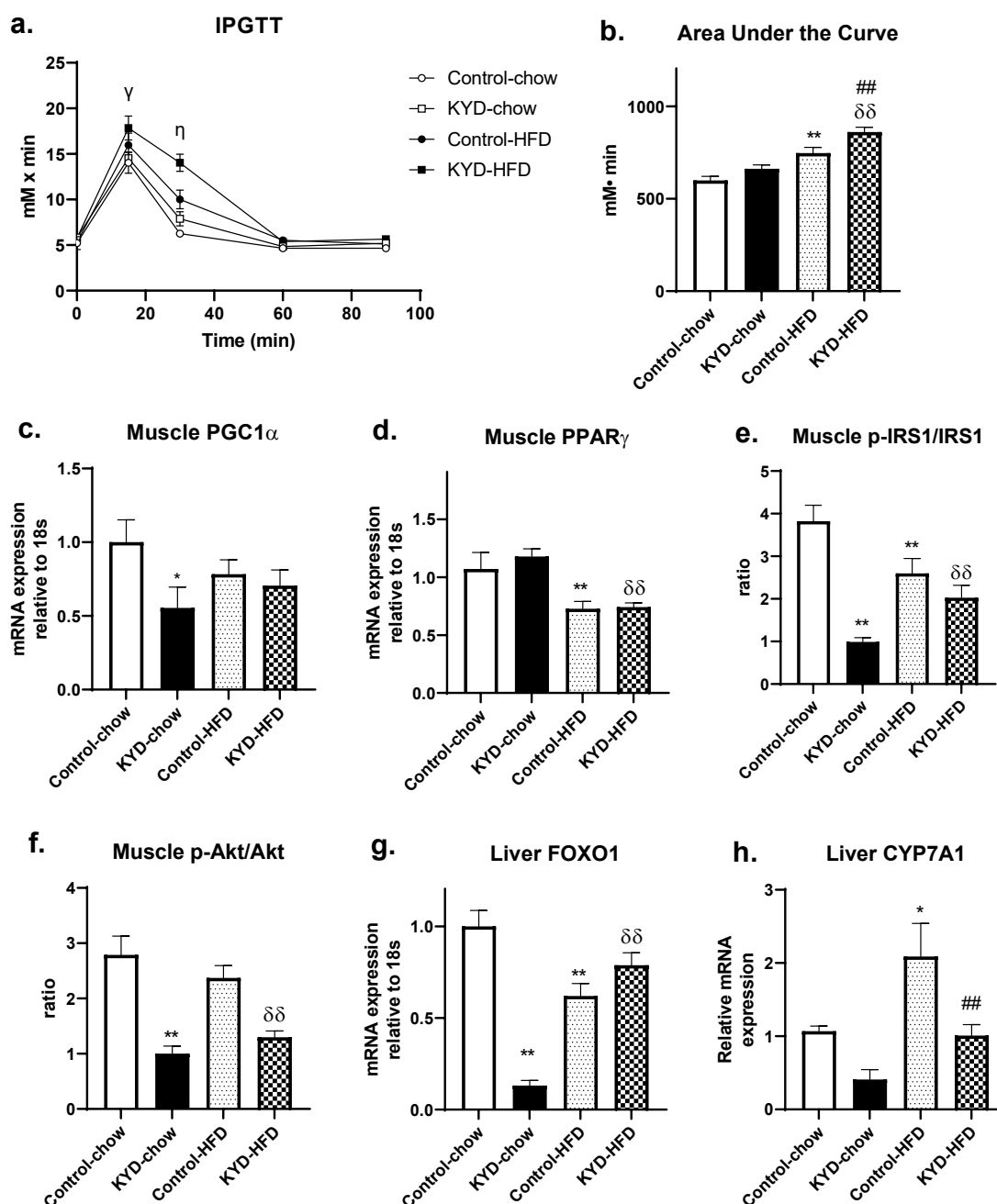
640 **Figure 2:** ATP levels (a), peroxisome proliferator-activated receptor gamma coactivator 1-alpha
 641 (PCG1 α) mRNA expression (b), Mitochondrial DNA (mitoDNA) copy number (c), oxidative
 642 phosphorylation complexes CI (d) and CV (e) in the brown adipose tissue (BAT) in male offspring
 643 at 13 weeks. Results are expressed as mean \pm SEM, n = 4-6. * $P < 0.05$, ** $P < 0.01$. KYD: kidney
 644 yang deficiency;



645

646 **Figure 3:** ATP levels (a), peroxisome proliferator-activated receptor gamma coactivator 1-alpha
 647 (PCG1 α) mRNA expression (b), Mitochondrial DNA (mitoDNA) copy number (c), oxidative
 648 phosphorylation complexes CI (d) and CV (e) in the skeletal muscle in male offspring at 13 weeks.
 649 Results are expressed as mean \pm SEM, n = 4-6. * P < 0.05, ** P < 0.01. KYD: kidney yang deficiency;

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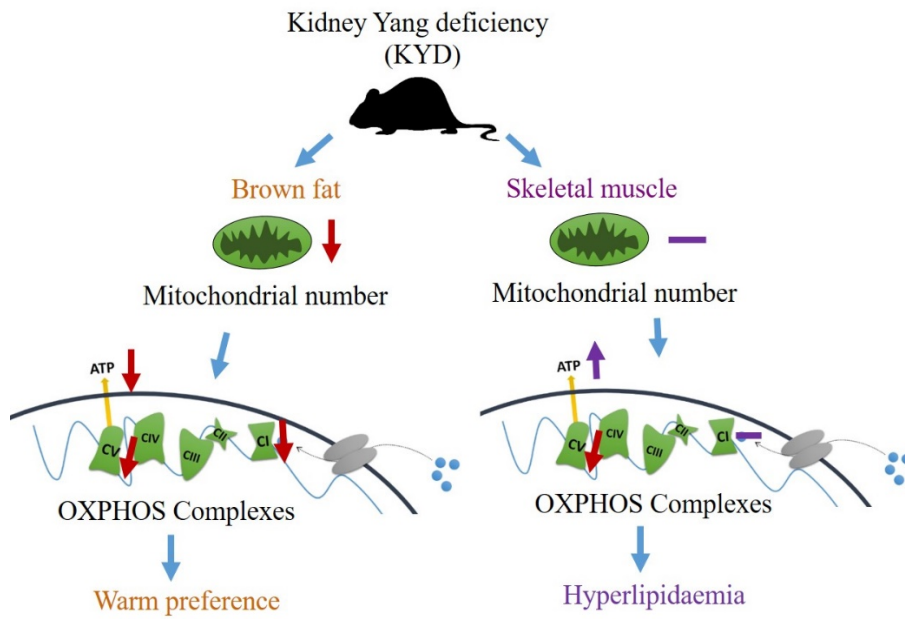


651

652 **Figure 4** Blood glucose level change during intraperitoneal glucose tolerance test (IPGTT, a) and
 653 area under the curve (b) of (a) in male offspring at 12 weeks. Peroxisome proliferator-activated
 654 receptor gamma coactivator 1-alpha (PGC1 α , c) and Peroxisome proliferator-activated receptor
 655 gamma (PPAR γ , d) mRNA expression, and ratios between p-insulin receptor substrate (IRS)1 and
 656 total IRS1 (e) and between p-protein kinase B (Akt) and total Akt (f) in the skeletal muscle, as well
 657 as mRNA expression of Forkhead box protein O (FOXO)1 (g) and Cholesterol 7 alpha-hydroxylase
 658 (CYP7A1, h) in the liver in chow and HFD-fed rats at 13 weeks. Results are expressed as mean \pm
 659 SEM, n=6. γ P<0.05 KYD-chow vs KYD-HFD; η P< 0.01 Control-chow vs Control-HFD, KYD-
 660 chow vs KYD-HFD, Control-HFD vs KYD-HFD; * P < 0.05, ** P< 0.01 vs Control-chow; # P <
 661 0.05, ## P < 0.01 vs Control-HFD; δ P < 0.05, $\delta\delta$ P < 0.01 vs KYD-chow. HFD: high-fat diet; KYD:
 662 kidney yang deficiency;

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665

666 **Figure 5:** Working mechanism of the phenotype in Kidney Yang Deficiency (KYD). Mitochondrial
667 disorder in the brown fat leads to warm preference, whereas the compensation of mitochondrial
668 function in the skeletal muscle maintained body temp.

669