

## Chapter 5

Effect of sitagliptin,  
melatonin and  
combination treatment on  
High Fat Diet (HFD)-  
induced T2D mouse model

## **5.1 Introduction**

Lifestyle changes, principally, calorie-rich diet intake and nocturnality contribute to increasing number of metabolic disorders, including obesity and Type 2 Diabetes (T2D) (Reutrakul et al., 2013). Disturbances in circadian rhythm are associated with metabolic dysregulation and glucose intolerance in humans (Scheer et al., 2009). T2D is characterized by insulin resistance, hyperinsulinemia, hyperleptinemia, oxidative stress, inflammation, metabolic and mitochondrial dysfunction. Impaired insulin action leads to hyperglycemia and dyslipidemia, which causes gluco-lipotoxicity to various cells, including pancreatic  $\beta$ -cells, further contributing to a reduction in  $\beta$ -cell mass and function (Lin et al., 2010). The prevalence of T2D is rapidly increasing worldwide. Researchers are coming up with many novel therapeutic approaches including incretin-based therapies that could suppress diabetic manifestations in different organs besides increasing  $\beta$ -cell mass.

Melatonin, a hormone of darkness, is known to reduce obesity and T2D (Pan et al., 2006; Peshchke et al., 2008; Stumpf et al., 2009) by regulating glucose metabolism (Peschke and Muhlbauer, 2010) and lipid metabolism (Rios-Lugo et al., 2010; Nduhirabandi et al., 2011) in both rodents and humans. When produced locally in several tissues, including the pancreas, melatonin acts as a free radical scavenger, a potent antioxidant and anti-inflammatory molecule (Galano et al., 2011; Korkmaz et al., 2009). It also has the potential to increase  $\beta$ -cell mass by proliferation/regeneration (Kanter et al., 2006). Pinealectomy leads to loss of melatonin which further causes hyperinsulinemia as melatonin keeps a check on insulin secretion (Nishida et al., 2003). It is shown that chronic administration of melatonin reduces insulin resistance and improves lipid metabolism in T2D rats (Nishida et al., 2002). Melatonin levels are reduced in Goto Kakizaki rats and T2D patients while they have hyperinsulinemia (Peschke et al., 2006). Recently, our study (Patel et al., 2018), along with other genome-wide association studies (GWAS) (Prokopenko et al., 2009; Bouatia-Naji et al., 2009), have shown that a variant of *melatonin receptor 1B* (*MTNR1B*) is associated with impaired FBG and T2D.

Sitagliptin, a dipeptidyl peptidase- IV (DPP-IV) inhibitor, is a second line drug for managing T2D. The therapeutic potential of sitagliptin has been assessed in various pre-clinical and clinical studies. It has been shown to reduce HbA1c and fasting blood glucose (FBG) in humans (Sakura et al., 2016). It enhances GLP-1 levels by two to three-fold following a meal (Herman et al., 2006). Sitagliptin preserves  $\beta$ -cell mass and function in T2D rodent model

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(Mu et al., 2006, Mu et al., 2009). Further, it also reduces inflammation in islets and adipose tissue of obese mice (Dobrian et al., 2011).

Hence, we aimed to investigate the therapeutic potential of melatonin combined with sitagliptin in the amelioration of T2D manifestations in high-fat diet (HFD) induced T2D.

### **5.2 Materials and Methods**

#### **5.2.1 Animals**

Forty young (6-8 weeks old) C57BL/6J male mice were procured from Advanced Centre for Treatment, Research and Education in Cancer (ACTREC), Navi-Mumbai, India. The animals were maintained on a 12hr light-dark cycle starting at 7:00 AM. Food and water were provided *ad libitum*. All the experimental procedures were performed according to the Purpose of Control and Supervision of Experiments on Animals (CPCSEA) guidelines which were approved by the Institutional Animal Ethical Committee (IAEC) (MSU/BC/13/2017).

#### **5.2.2 Development of Diet-Induced Obese T2D Mouse Model and Drug Treatment**

Thirty-two mice were fed with HFD for 25 weeks to develop a fully insulin-resistant Diet-Induced Obese (DIO) T2D mouse model. Simultaneously, eight mice were provided with a standard chow diet (NCD) for 25 weeks represented as NCD/control group. FBG was measured in mice after 6 hours fasting by tail snipping method using a Glucometer (TRUEresult, NIPRO Diagnostics, Pune, MH, India). Once the HFD fed mice turned diabetic (FBG>200mg/dL), mice were randomly divided into four groups: 1) HFD, 2) Sitagliptin (S) treated, 3) Melatonin (M) treated and 4) S+M treated. Melatonin (Sigma, St. Louis, MO, USA) was administered between 6 PM to 7 PM daily at a dose of 10 mg/kg BW i.p. dissolved in 0.1% ethanol and 0.9% saline. Sitagliptin (Januvia) (Merck & Co., Kenilworth, NJ, USA) was purchased in 100 mg tablets and was given at a dose of 5 g/kg diet. The drug treatment was given for four weeks. FBG levels and BW were recorded twice a week. Food and water intake were also monitored weekly.

#### **5.2.3 Glucose Tolerance Test and Insulin Tolerance Test**

The intraperitoneal glucose tolerance test (IPGTT) and intraperitoneal insulin tolerance test (IPITT) were performed post drug-treatment. For IPGTT and IPITT, all mice were fasted for 6 hours and were injected with glucose (2 g/kg BW, i.p.) and insulin (0.75 U/kg BW, i.p.),

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respectively. Blood glucose levels were measured immediately at 0, 15, 30, 90, and 120 minutes by tail snipping. The total area under the curve (AUC) was calculated.

### **5.2.4 Metabolic and Biochemical Parameters**

Before sacrificing mice, 1-2 ml blood from the orbital sinus was collected in K3 EDTA tubes and centrifuged at 6000 g for 5 minutes. Plasma was separated and stored at -20 °C for further analysis. Fasting plasma insulin, leptin and melatonin levels were estimated by commercially available mouse insulin, leptin (both from RayBiotech, GA, USA), and melatonin (Elabscience, Houston, TX, USA, Cat# E-EL-M0788) ELISA kits. Lipid profile (triglycerides, total cholesterol, HDL-c) was estimated by commercially available kits (Reckon Diagnostics Pvt. Ltd., Vadodara, GJ, India). Friedewald's (1972) formula was used for calculating low-density lipoprotein (LDL) levels.

### **5.2.5 Gene Expression Analysis**

Liver, skeletal muscle, and adipose tissue were harvested post euthanasia and stored in RNeasy Lysis Solution (Qiagen, Crawley, UK) for gene expression analysis. Total RNA was isolated by Trizol method. RNA integrity and purity were checked by 1.5% agarose gel electrophoresis/ethidium bromide staining and 260/280 absorbance ratio of 1.9, respectively. To avoid DNA contamination, RNA was treated with DNase I (Puregene, Genetix Biotech) before cDNA synthesis. Transcriptor High Fidelity cDNA Synthesis Kit (Roche Diagnostic GmbH, Mannheim, Germany) was used to prepare cDNA using one microgram of total RNA isolated, according to the manufacturer's instructions in the Eppendorf Mastercycler gradient (USA Scientific, Inc., Florida, USA). Transcript analysis was carried out for the key genes involved in glucoregulation (liver), mitochondrial biogenesis (skeletal muscle) and lipid metabolism (adipose tissue). *GAPDH* was used as a reference gene. Real-time PCR was performed using Light-Cycler® 480 SYBR Green I Master (Roche Diagnostics GmbH, Mannheim, Germany) and gene-specific primers (Eurofins, Bengaluru, KA India), and was carried out in the Light-Cycler® 480 Real-Time PCR (Roche Diagnostics GmbH, Mannheim, Germany). The forward and reverse primer (5'-3') details for gene expression study are as follows: *Glucokinase* (*GCK*), FP: AGGAGGCCAGTGTAAGATGT and RP: TCCCAGGTCTAAGGAGAGAAA; *Fructose-bisphosphatase 1* (*FBP1*), FP: GCATCGCACAGCTCTATGGT and RP: CTCAGGTTTCGATTATGATGGC; *Phosphoenolpyruvate carboxykinase* (*PEPCK*), FP: CTGCATAACGGTCTGGACTTC and RP: CAGCAACTGCCCGTACTCC; *Glucose-6-*

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phosphatase (G6Pase), FP: CTGTTTGGACAACGCCCCGTAT and RP: AGGTGACAGGGAAGTCTTTA; Glucose transporter 2 (GLUT2), FP: CTTGGAAGGATCAAAGCAATG and RP: CAGTCCTGAAATTAGCCCAC; Glycogen synthase (GS), FP: ACCAAGGCCAAAACGACAG and RP: GGGCTCACATTGTTCTACTTG; Glycogen phosphorylase (GP), FP: GAGAAGCGACGGCAGATCA and RP: CTTGACCAGAGTGAAGTGCA; Sirtuin 1 (SIRT1), FP: GATGAAGTTGACCTCCTCA and RP: GGGTATAGAAGTTGGAATTAG; Peroxisome proliferator-activated receptor gamma coactivator 1-alpha (PGC1- $\alpha$ ), FP: AGCCGTGACCACTGACAACGA and RP: GTAGCTGAGCTGAGTGTTGGC; Acetyl-CoA carboxylase 1 (ACCI), FP: ACGCTCAGGTCACCAAAAAGAAT and RP: GTAGGGTCCCGGCCACAT; Adipose triglyceride lipase (ATGL), FP: CAACGCCACTCACATCTACGG and RP: GGACACCTCAATAATGTTGGCAC; GAPDH, FP: AGGTCGGTGTGAACGGATTTG and RP: TGTAGACCATGTAGTTGAGGT. Real-time PCR was performed as described previously by determining  $2^{-\Delta\Delta C_t}$  (Patel et al., 2018).

### 5.2.6 Droplet Digital PCR (ddPCR)

Gene expression of *MTNR1B*, glucose transporter 4 (*GLUT4*), and tumor necrosis factor alpha (*TNF- $\alpha$* ) in mouse adipose tissue were monitored by ddPCR using EvaGreen dye (Bio-Rad, Hercules, CA, USA). Each ddPCR reaction contained 20  $\mu$ l of mastermix including 10  $\mu$ l of EvaGreen Supermix, 0.5  $\mu$ l (2.5 mM) forward primer and reverse primer each, 1  $\mu$ l cDNA (50 ng) and 8  $\mu$ l nuclease free water. This system was loaded in a droplet generator cartridge along with 70  $\mu$ l of droplet generation oil into oil well. QX200™ Droplet Generator was used for generating droplets and the droplets were loaded to 96 well PCR plate. The plate was heat-sealed with foil and was run in a thermal cycler. The PCR conditions for the assay were: 95 °C for 5 min; 40 cycles of 95 °C for 30s and 60 °C (depending on annealing temperature) for 1 min; and three final steps at 4 °C for 5 min, 90 °C for 5 min, and a 4 °C for 30 min to boost dye stabilization. The PCR was read in QX200™ Droplet Reader and was analyzed by QuantaSoft™ software. The results were plotted as Ch1Amplitude and copies/ $\mu$ l. Blue droplets show number of positive droplets for their respective target genes and grey droplets indicate negative droplets for the target genes. Non template control was run for each assay. The details of the forward and reverse primers (5'-3') for the target genes are as follows: *MTNR1B*, FP: TTGTGATGGGCCTGAGTGTC and RP:

AGCCAGACGAGGCTGATGTA; *GLUT4*, FP: TAGGAGCTGAGGGTTGGCTA and RP: TGCTCCAGTAGGCCGTAAAC; *TNF- $\alpha$* , FP: CCTCACTCACAAACCACCA and RP: ACAAGGTACAACCCATCGGC.

### **5.2.7 Glucoregulatory Enzymes Activity and Liver Glycogen Content**

The liver was harvested post euthanasia, snap frozen and stored at -80 °C for the enzyme activity assay. Liver tissue (50 mg) was homogenised, and the lysates were used for enzyme activity assays. Enzyme assays (GCK, FBPase, PEPCK and GP) and the estimation of glycogen content were carried out by commercially available kits (BioVision, Milpitas, CA, USA; Cat# K969-100, Cat# K590-100, Cat# K359-100, Cat# K179-100 and Cat# K646-100) according to the manufacturer's protocols.

### **5.2.8 Respiratory Control Ratio (RCR)**

For RCR studies, skeletal muscle was harvested post euthanasia and stored in mitochondrial respiration buffer at -80 °C. Mitochondria were isolated from skeletal muscle using a mitochondria isolation kit (Thermo Scientific™, Cat# 89801) using the manufacturer's protocol. The isolated mitochondria were resuspended in 100  $\mu$ l of mitochondria respiration buffer (110 mM Sucrose, 0.5 mM EGTA, 70 mM KCl, 0.1% FFA free BSA, 20 mM HEPES, 3 mM MgCl<sub>2</sub>, and 10 mM KH<sub>2</sub>PO<sub>4</sub>, 20 mM Taurine) (Butterick et al., 2016). RCR studies were carried out in Oxytherm+ System (Hansatech Instruments Ltd., Pentney, UK). Mitochondrial outer membrane integrity of the isolated mitochondria was assessed by impermeability to exogenous cytochrome c, which was consistently greater than 95%. The activities of respiratory chain complexes I-IV were monitored using 100  $\mu$ l of substrates [100 mM Pyruvate & 800 mM Malate (complex I), 1 M Succinate (complex II), 10 mM  $\alpha$ -glycerophosphate (complex III) and 0.8 M ascorbate (complex IV)] (Li and Graham, 2012), added to 90  $\mu$ l of mitochondria suspension. Other respiration reagents used were 100 mM adenosine diphosphate (100  $\mu$ l), 1 mM oligomycin (2  $\mu$ l), 1 mM rotenone (1  $\mu$ l), and 1 mM Antimycin (2.5  $\mu$ l). Protein concentration was estimated by the Bradford method (Stoscheck et al., 1990). All chemicals were purchased from Sigma-Aldrich, USA. OCR was determined by measuring the amount of oxygen (nmol) consumed, divided by the time elapsed (min) and the amount of protein present in the assay (Li and Graham, 2012). Data is represented as respiratory control ratio (RCR) of state 3/state 4 respiration.

### **5.2.9 Western Blot Analysis**

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Skeletal muscle was harvested post euthanasia and stored in lysis buffer at -80 °C for western blot analysis of key proteins involved in the insulin signalling pathway. The tissue was homogenised in liquid nitrogen and Laemmli buffer (1M Tris HCl, 10% SDS, 20% glycerol and 10%  $\beta$ -mercaptoethanol) containing 1 M urea (1:1), protease inhibitor cocktail, and phosphatase inhibitor cocktail 2 and 3 (both from Sigma, St. Louis, MO, USA). The homogenate was collected and sonicated twice in chilled condition and centrifuged to remove tissue/cell debris. The protein concentration in the lysates was estimated using the Bradford method (Stoscheck et al., 1990) and 25-40  $\mu$ g of the lysates were resolved on 8-10% sodium dodecyl sulphate–polyacrylamide gel electrophoresis (SDS-PAGE), followed by electrophoretic transfer to PVDF membrane. Membranes were blocked with 5% bovine serum albumin (Sisco Research Laboratories Pvt. Ltd., Mumbai, MH, India) for phosphorylated proteins and 5% blotting-grade blocker for non-phosphorylated proteins (Bio-Rad, Hercules, CA, USA) in Tris-buffered saline (pH 8.0) with 0.1% Tween-20 for 1 hour at room temperature. Immunoblot analysis was done with primary antibodies at a dilution of 1:1000 targeting rabbit anti-insulin receptor  $\beta$ , rabbit anti-insulin receptor substrate-1 (pIRS-1) Ser307 (both from Cell Signaling Technology, Cat# 3025 and Cat# 2381), rabbit anti-IRS1, rabbit anti-pAkt1 Ser473, rabbit anti-Akt1, mouse anti- $\beta$ -actin (all from ABclonal Technology; Cat# A0245, Cat# AP0140, Cat# A7270 and Cat# AC004), and rabbit anti-glucose transporter 4 (GLUT4) (Sigma, Cat#CBL243) incubated overnight at 4 °C. Blots were then incubated with goat anti-rabbit immunoglobulin G (IgG)-horseradish peroxidase (HRP) (Jackson ImmunoResearch, Cat# 111035144) or goat anti-mouse IgG-HRP (Genex, Cat# 105502) at 1:5000 – 1:10,000 dilution for one hour at room temperature. The membranes were visualised with clarity western ECL substrate (Bio-Rad Laboratories, USA) in the ChemiDoc™ Touch Imaging System. Blots were analysed in Image Lab™ software (Bio-Rad Laboratories, USA).

### **5.2.10 Immunohistochemistry-Immunofluorescence (IHC-IF)**

Pancreas was harvested post euthanasia and fixed in 10% neutral buffered formalin (NBF) for histological processing and paraffin embedding. 5 $\mu$ m sections were cut from the paraffin-embedded blocks. Immunofluorescence staining was carried out to study  $\beta$ -cell mass and islet number. The sections were deparaffinised in xylene and rehydrated in a series of graded ethanol. Antigen retrieval was performed using 1N HCL for 40 minutes at 37 °C. Sections were blocked in 5% normal donkey serum (Jackson ImmunoResearch, Cat# 017-000-121) in

PBST (PBS + 0.1% Tween 20) for 1 hour at room temperature and incubated with primary antibody prepared in blocking buffer at 37 °C in a humidified chamber for 2 hours [guinea pig anti-insulin (DAKO, Cat# A0564; 1:200). Sections were washed with PBS and were incubated with secondary antibody prepared in blocking buffer at room temperature for 45 minutes in the dark [donkey anti-guinea pig Alexa Fluor 488, Jackson ImmunoResearch, Cat# 706-545-148; 1:500]. Sections were washed with PBS and distilled water and were mounted with Slowfade® Gold Antifade mountant with DAPI (Thermo Fisher Scientific, USA), and the coverslips were sealed with nail varnish. Stained sections were observed under a confocal laser scanning microscope (Olympus FV10i, Tokyo, Japan). Image analysis was carried out in Image J software. Observations were made from three pancreatic sections per group from five different areas.  $\beta$ -cell mass (mg/pancreas) was calculated as (% insulin-positive area/ total insulin-positive area) x pancreas weight.

### **5.2.11 Statistical Analyses**

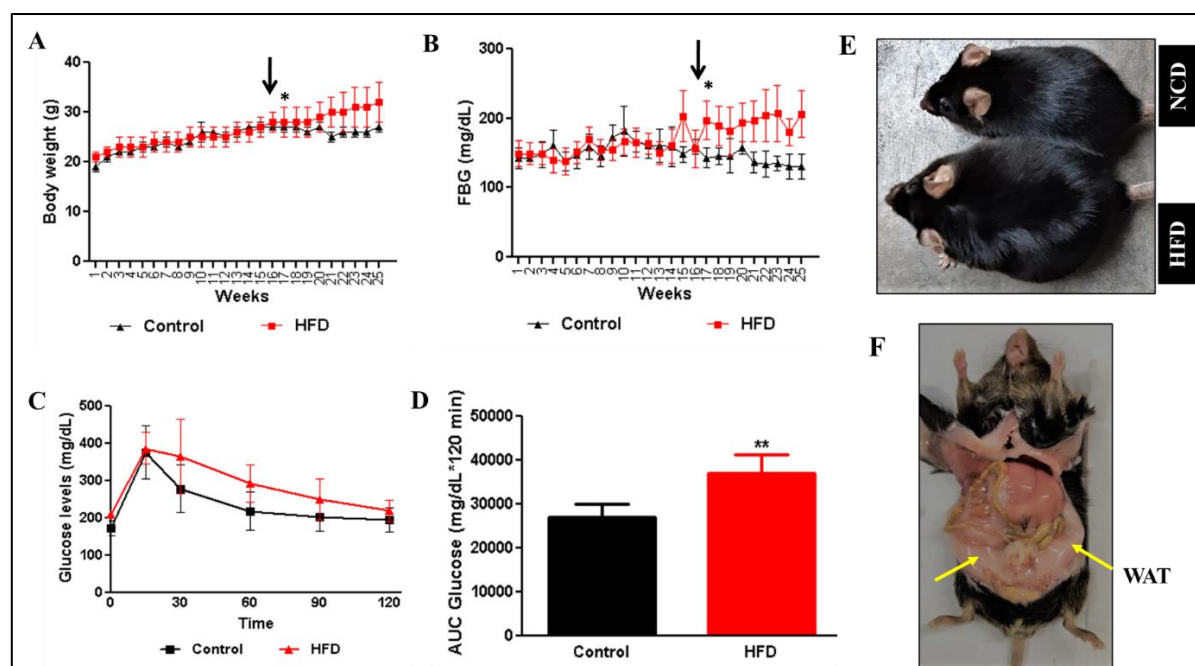
All results were confirmed in at least three independent experiments for the *in-vitro* study. Statistical comparisons of data were performed by one-way analysis of variance (ANOVA) and multiple group comparisons by Tukey's post hoc test in Prism 5 (GraphPad Software, San Diego, CA, USA). The significance level was set as  $p < 0.05$ . Results are expressed as mean  $\pm$  SEM.

## **5.3 Results**

### **5.3.1 Development of Diet-Induced Obese T2D Mouse Model**

Diet-induced obese (DIO) mouse T2D model was developed after 25 weeks of HFD feeding in C57BL/6J male mice. BW and FBG were measured once a week up to twenty-five weeks of HFD feeding for the model generation. Our data suggested that BW and FBG started increasing from 16<sup>th</sup> week of HFD feeding as compared to NCD. FBG levels were significantly increased  $\geq 200$  mg/dL at 25<sup>th</sup> week. Glucose tolerance test was carried out in the 25<sup>th</sup> week to check impaired glucose tolerance in HFD group. The results suggested that glucose tolerance was significantly reduced in HFD group as compared to NCD ( $p < 0.01$ ) along with BW and FBG levels, and a dissected open mouse shows increase in white adipose tissue indicating a successful model generation (Figure 5.1)

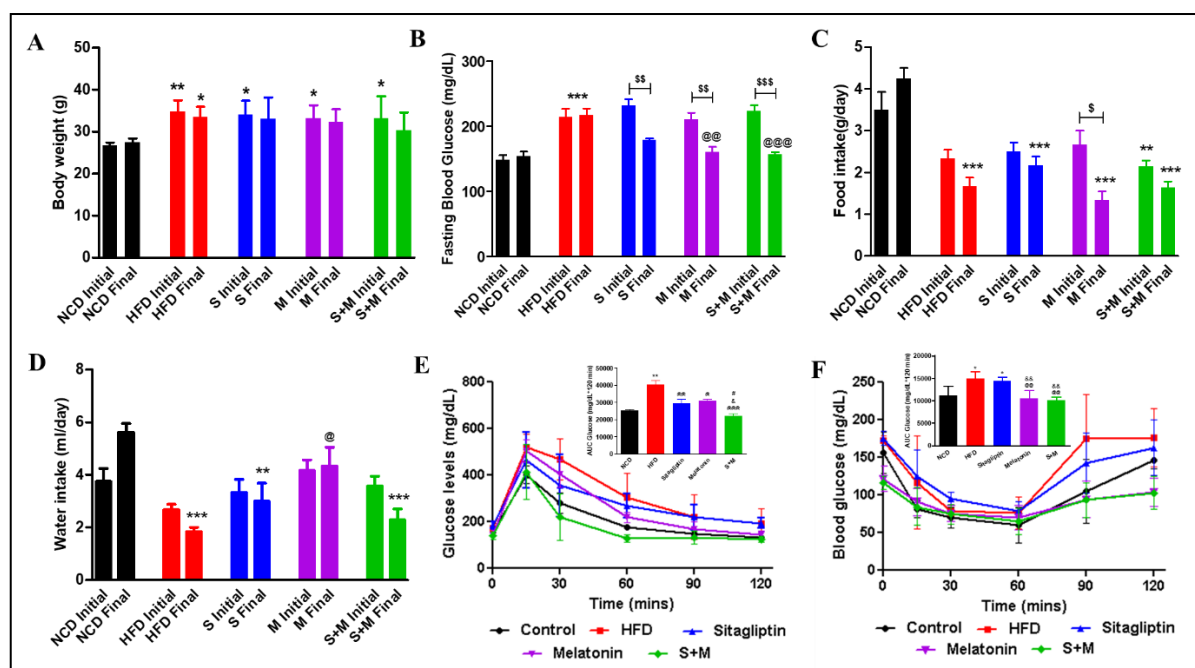




**Figure 5.1 Establishment of DIO T2D mouse model:** **A. Body weight.** HFD group showed significant increase in body weight as compared to control (NCD) at 25<sup>th</sup> week of HFD feeding. **B. Fasting blood glucose levels.** HFD group showed significant increase in FBG levels ( $\geq 200$  mg/dL) at 25<sup>th</sup> week. **C-D. IPGTT and AUC curve.** Glucose tolerance was significantly reduced in HFD group as compared to control at 25<sup>th</sup> week. **E-F. Body fat mass.** HFD fed mice showed increase in white adipose tissue (WAT) (\* $p < 0.05$ , \*\* $p < 0.01$ ) (NCD,  $n = 8$ ; HFD,  $n = 32$ ).

### 5.3.2 Analysis of Metabolic Parameters

Our results suggest that HFD group showed significant increase in BW ( $p < 0.01$ ) and FBG ( $p < 0.01$ ) levels as compared to NCD. In addition, the glucose tolerance ( $p < 0.01$ ) and insulin tolerance ( $p < 0.05$ ) were also reduced in HFD group. The combination therapy revealed that its effect was greater ( $p < 0.001$ ) as compared to the monotherapies (S,  $p < 0.01$ ; M,  $p < 0.01$ ) in reducing FBG levels, increasing glucose tolerance (S,  $p < 0.01$ ; M,  $p < 0.05$ ; S+M  $p < 0.001$ ) and insulin sensitivity (S,  $p > 0.05$ ; M,  $p > 0.01$ ; S+M,  $p < 0.001$ ). The monotherapies and combination therapy did not show any significant change in the final BW compared to their initial BW ( $p > 0.05$ ). Moreover, assessment of food and water intake revealed that there was a significant reduction in food (HFD, S, M, S+M;  $p < 0.001$ ) and water intake (HFD,  $p < 0.001$ ; S,  $p < 0.01$ ; S+M;  $p < 0.001$ ) after four weeks of the drug treatment as compared to NCD group. However, the water intake was significantly higher in M group as compared to HFD group ( $p < 0.05$ ) (Figure 5.2A-F).



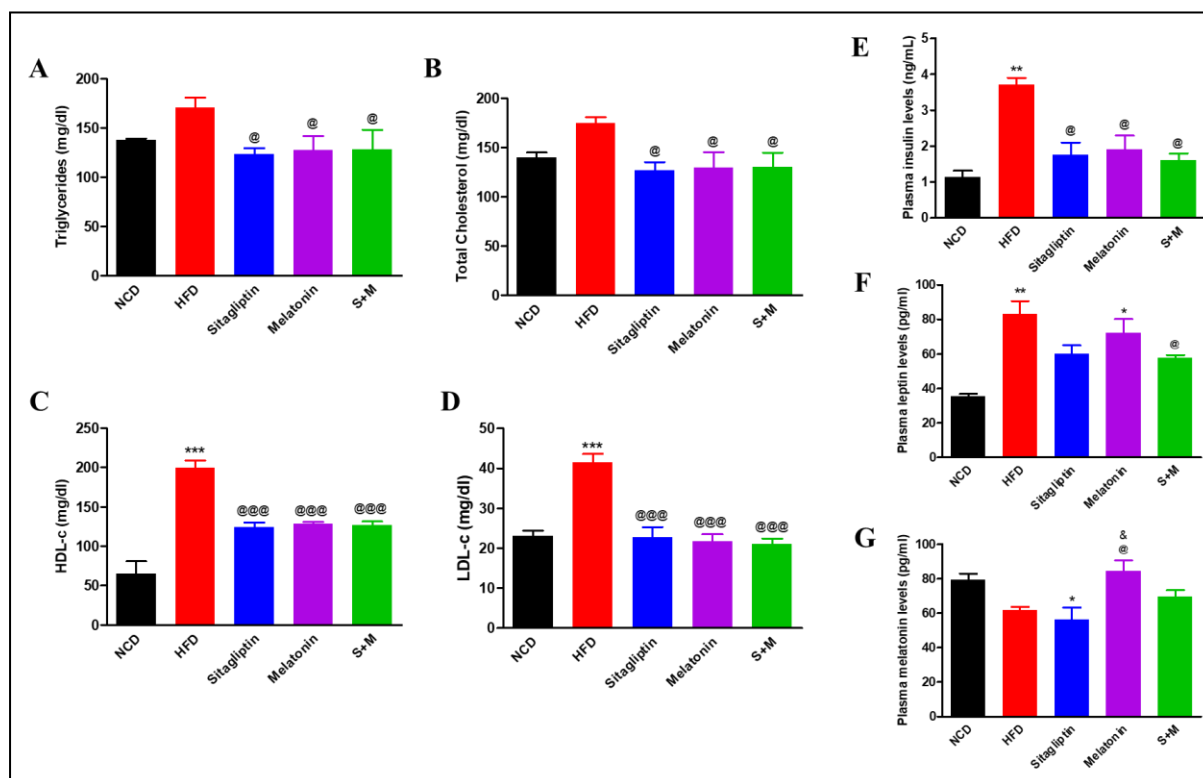
**Figure 5.2 Body weight, blood glucose levels, food and water intake, IPGTT and IPITT: A. Body weight.** A significant increase in body weight was observed in HFD fed mice as compared to NCD. No significant difference was observed in the body weight post drug treatment. **B. Fasting blood glucose levels.** A significant increase in FBG levels was observed in HFD fed mice and reduced in all the drug-treated groups 4 weeks post-treatment. **C. Food intake.** A significant reduction in food intake was observed in the melatonin group post-treatment, while HFD fed and other drug-treated groups showed reduction as compared to NCD. **D. Water intake.** A significant reduction in water intake was observed in HFD than in NCD, while the melatonin treated group showed a significant increase in water intake compared to HFD. **E. IPGTT.** Increased glucose clearance was observed in all the drug-treated groups as compared to HFD. **F. IPITT.** Melatonin and S+M treated groups showed significant increase in insulin sensitivity as compared to HFD. (\* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$  vs. NCD; @ $p < 0.05$ , @@ $p < 0.01$ , @@@ $p < 0.001$  vs. HFD; & $p < 0.05$ , && $p < 0.01$ , vs. Sitagliptin; # $p < 0.05$  vs. Melatonin) (n=6-8/group).

### 5.3.3 Analysis of Plasma Lipid Profile, Insulin, Leptin and Melatonin levels

Analysis of plasma lipid profile suggested that the levels of TG, TC were increased in HFD group but were not significant, but HDL-c and LDL-c were significantly increased in HFD group ( $p < 0.001$ ) as compared to NCD indicating dyslipidemia. Lipid levels were restored in the monotherapies and combination-treated groups as compared to HFD group (TG and TC: S, M, S+M,  $p < 0.05$ ; HDL-c and LDL-c: S, M, S+M,  $p < 0.01$ ). Analysis of plasma insulin, leptin and melatonin levels revealed that there was hyperinsulinemia and hyperleptinemia in the HFD group as compared to NCD ( $p < 0.01$ ), and the levels were restored in the drug-treated groups (insulin: S, M, S+M,  $p < 0.05$ ; leptin: S+M,  $p < 0.05$ ) as compared to HFD

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group. There was no change observed in melatonin levels. However, it was significantly increased in the M group ( $p<0.05$ ) (Figure 5.3A-G).

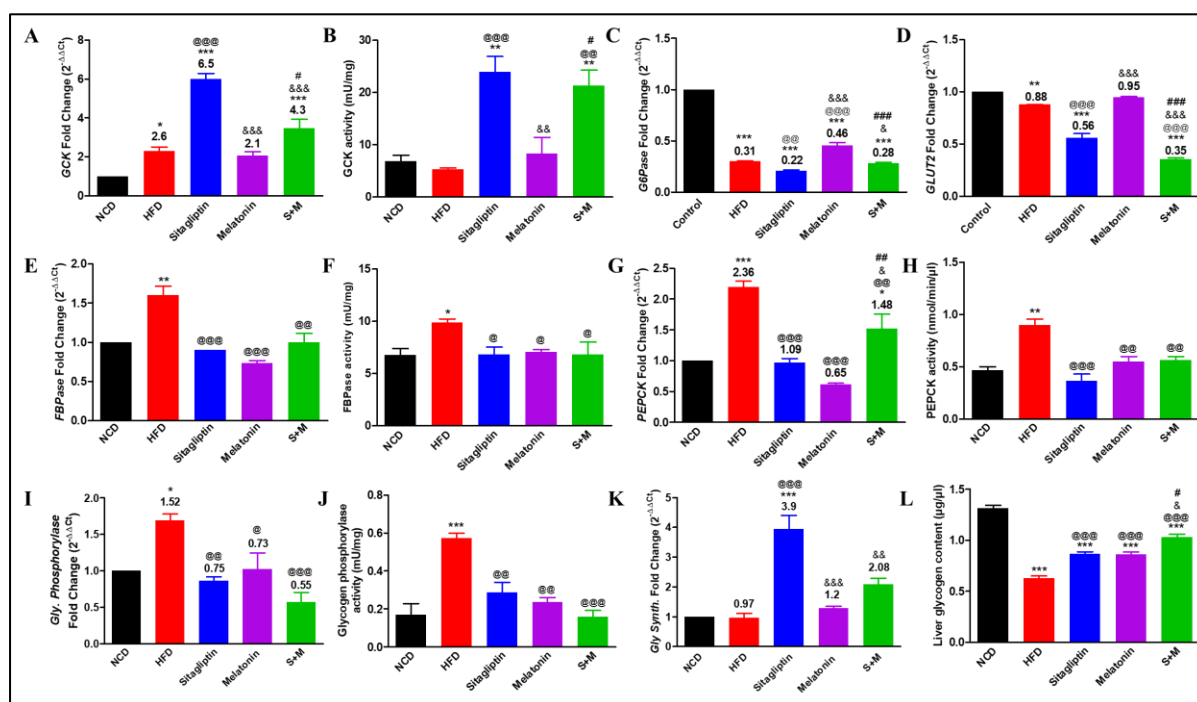


**Figure 5.3 Plasma lipid profile, insulin, leptin and melatonin levels:** A significant reduction of **A.** triglycerides, **B.** total cholesterol, **C.** HDL-c and **D.** LDL-c was observed in all the drug-treated groups as compared to HFD. **E. Fasting plasma insulin levels:** A significant reduction in plasma insulin was observed in the drug-treated groups as compared to HFD. **F. Fasting plasma leptin levels:** A significant reduction in plasma leptin was observed in the S+M treated group as compared to HFD. **G. Fasting plasma melatonin levels:** A significant increase in plasma melatonin was observed in the melatonin group as compared to HFD. (\* $p<0.05$ , \*\* $p<0.01$  vs. NCD; @ $p<0.05$ , @@@ $p<0.001$  vs. HFD; & $p<0.05$ , vs. Sitagliptin) (n=6-8/group).

### 5.3.4 Analysis of Glucoregulatory Enzyme Activity, Liver Glycogen Content and Gene Expression

Gene expression and specific activity of glucoregulatory enzymes in the liver were monitored. The data revealed that in HFD group, *GCK* expression ( $p<0.05$ ) along with *FBPase* expression ( $p<0.01$ ) and activity ( $p<0.05$ ), *PEPCK* expression ( $p<0.001$ ) and activity ( $p<0.01$ ), and *GP* expression ( $p<0.05$ ) and activity ( $p<0.001$ ) were significantly increased as compared to NCD, indicating dysregulated glucose metabolism. However, there was no change in the *GCK* activity ( $p>0.05$ ). In addition, there was a significant reduction in *G6Pase* ( $p<0.001$ ) and *GLUT2* ( $p<0.01$ ) expression besides reduced liver glycogen content ( $p<0.001$ )

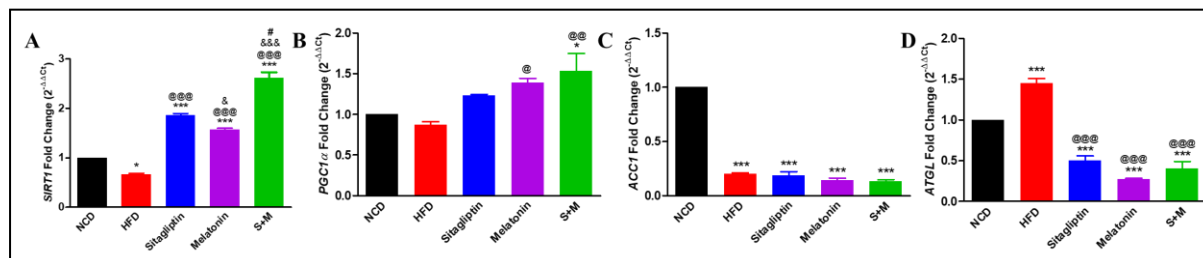
in HFD group as compared to NCD. With respect to the treatment groups, *GCK* expression was significantly increased in S ( $p<0.001$ ), and its enzyme activity was also significantly increased in the S+M group ( $p<0.01$ ) as compared to HFD group indicating increased glucose uptake. *G6Pase* was significantly reduced in S ( $p<0.01$ ) and increased in M group ( $p<0.001$ ), indicating increased glucose uptake while there was no change in S+M group. *GLUT2* expression was significantly reduced (S, S+M,  $p<0.001$ ). Furthermore, the gene expression and activity of *FBPase* and *PEPCK* were significantly increased in the HFD group ( $p<0.01$  and  $p<0.05$ , respectively) as compared to NCD groups, and significantly reduced in all the drug-treated groups (*FBPase*: S, M, S+M,  $p<0.05$ ; *PEPCK*: S, M, S+M,  $p<0.01$ ), indicating reduced gluconeogenesis. In addition, there was a significant reduction in the gene expression (S,  $p<0.01$ ; M,  $p<0.05$ ; S+M,  $p<0.001$ ) and activity of GP (S, M,  $p<0.01$ ; S+M,  $p<0.001$ ) in all the drug-treated groups as compared to HFD indicating reduced glycogenolysis. The GS expression was significantly increased in the S group as compared to HFD ( $p<0.001$ ) and the glycogen content in all the drug-treated groups (S, M, S+M,  $p<0.001$ ), indicating an increase in glycogenesis (Figure 5.4A-L).



**Figure 5.4 Gene expression and enzyme activities of glucoregulatory enzymes and glycogen content in the liver: A-B. GCK mRNA fold change and activity.** GCK expression was significantly increased in S while its activity in S and S+M groups. **C. G6Pase mRNA folds change.** *G6Pase* expression was significantly decreased in S and increased in the M group. **D. GLUT2 mRNA fold change.** A significant decrease in *GLUT2* expression was observed in the S, and S+M treated groups. **E-F. FBPase mRNA fold change and its activity.** *FBPase* gene expression and its activity were

significantly increased in HFD, whereas it was significantly reduced in all the drug-treated groups. **G-H. PEPCK mRNA fold change and activity.** PEPCK expression and activity were significantly reduced in all the drug-treated groups. **I-J. GP mRNA fold change and activity.** A significant decrease in GP expression and activity was observed in all the drug-treated groups. **K. GS mRNA fold change.** A significant increase in GS expression was observed in the sitagliptin treated group. **L. Liver glycogen content:** GC was significantly increased in all the drug-treated groups. (\* $p<0.05$ , \*\* $p<0.01$ , \*\*\* $p<0.001$  vs. Control; @ $p<0.05$ , @@ $p<0.01$ , @@@ $p<0.001$  vs. HFD; & $p<0.05$ , && $p<0.01$ , &&& $p<0.001$  vs. Sitagliptin; # $p<0.05$ , ## $p<0.01$ , ### $p<0.001$  vs. Melatonin) (n=6-8/group).

Furthermore, expression of *SIRT1* and *PGC1 $\alpha$* , which are involved in mitochondrial biogenesis pathway, showed a significant reduction in HFD group ( $p<0.05$ ) as compared to NCD, while it was increased in all the drug-treated groups as compared to HFD (*SIRT1*: S, M, S+M,  $p<0.001$ ; *PGC1 $\alpha$* : M,  $p<0.05$ , S+M,  $p<0.01$ ). Lipid metabolism markers viz. *ACCI* expression was reduced in both HFD and the drug-treated groups (S, M, S+M,  $p<0.001$ ) as compared to NCD with no change in the drug-treated groups (S, M, S+M,  $p>0.05$ ) as compared to HFD group. *ATGL* expression was significantly increased in HFD group as compared to NCD ( $p<0.001$ ), while it was significantly reduced in all the drug-treated groups (S, M, S+M,  $p<0.001$ ) as compared to HFD, showing improved lipid metabolism (Figure 5.5A-D).

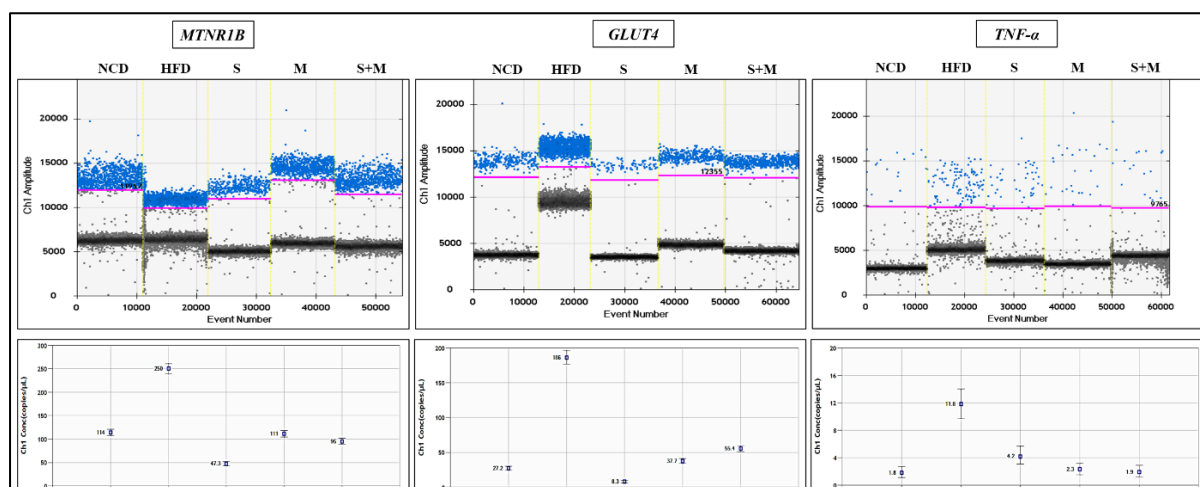


**Figure 5.5 Gene expression of mitochondrial biogenesis markers in skeletal muscle and lipid metabolism markers in adipose tissue. A-B. mRNA fold change of *SIRT1* and *PGC1 $\alpha$*  in skeletal muscle.** A significant increase in *SIRT1* and *PGC1 $\alpha$*  expression was observed in HFD (0.6-fold), whereas all the drug-treated groups showed a significant increase in *SIRT1* expression (1.8 to 2.5-fold). However, *PGC1 $\alpha$*  expression was significantly increased only in melatonin and S+M treated groups (1.4 to 1.6-fold). **C-D. mRNA fold change of *ACCI* and *ATGL* in adipose tissue.** There was no change in *ACCI* expression, whereas a significant reduction in *ATGL* gene expression was observed in all the drug-treated groups (50 to 70%). (\* $p<0.05$ , \*\*\* $p<0.001$  vs. NCD; @ $p<0.05$ , @@ $p<0.01$ , @@@ $p<0.001$  vs. HFD; & $p<0.05$  vs. Sitagliptin; # $p<0.05$  vs. Melatonin) (n=6-8/group).

### 5.3.5 Absolute Gene Quantification of *MTNR1B*, *GLUT4* and *TNF- $\alpha$* in Adipose Tissue

Furthermore, absolute gene expression of *MTNR1B*, *GLUT4*, and *TNF- $\alpha$*  in adipose tissue was studied by ddPCR. The results show an increased copy number/ $\mu$ l of the mentioned genes in the HFD group as compared to NCD group indicating higher expression and insulin

resistance. Moreover, in the treatment groups (monotherapies and combination), the copy number/ $\mu$ l were reduced suggesting reduced insulin resistance (Figure 5.6).

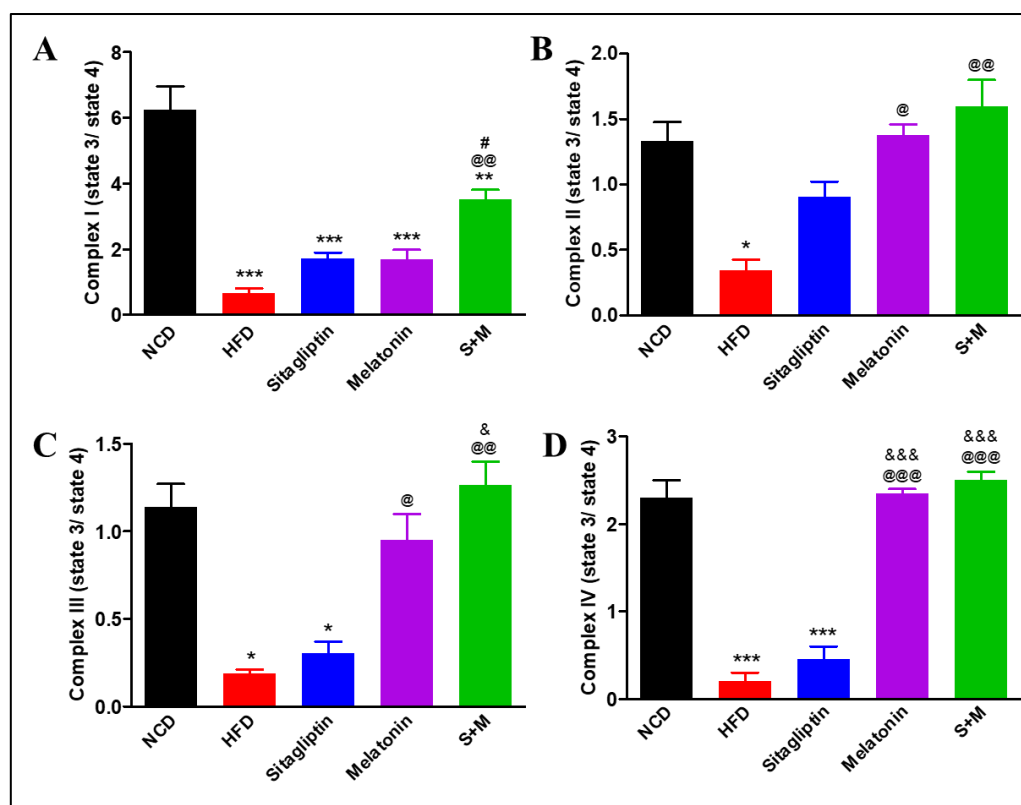


**Figure 5.6 Absolute gene quantification of *MTNR1B*, *GLUT4*, and *TNF- $\alpha$*  in adipose tissue.** Gene expression of *MTNR1B*, *GLUT4* and *TNF- $\alpha$*  was higher in HFD group as compared to NCD group whereas it was reduced in the all the treatment groups as compared to the HFD groups, as represented by change in amplitude of positive droplets (blue) and number of copies/ $\mu$ l. (n=3/group). Blue droplets: positive for the target gene; Grey droplets: negative for the target gene; Pink line: threshold intensity to discriminate positive and negative droplets.

### 5.3.6 Assessment of Mitochondrial Respiratory Control Ratio (RCR) of Complexes I-IV

The RCR of state 3/state 4 in the HFD group was significantly reduced as compared to NCD for the mitochondrial complexes I, II, III and IV ( $p<0.001$ ,  $p<0.05$ ,  $p<0.05$ ,  $p<0.001$ , respectively), while a significant increase in the RCR was observed in melatonin and S+M treated groups in CII (M,  $p<0.05$ ; S+M,  $p<0.01$ ) CIII (M,  $p<0.05$ ; S+M,  $p<0.01$ ), and CIV (M,  $p<0.001$ ; S+M,  $p<0.001$ ). However, the RCR of state 3/state 4 in complex I was significantly increased only in the S+M ( $p<0.01$ ) treated group (Figure 5.7A-D).

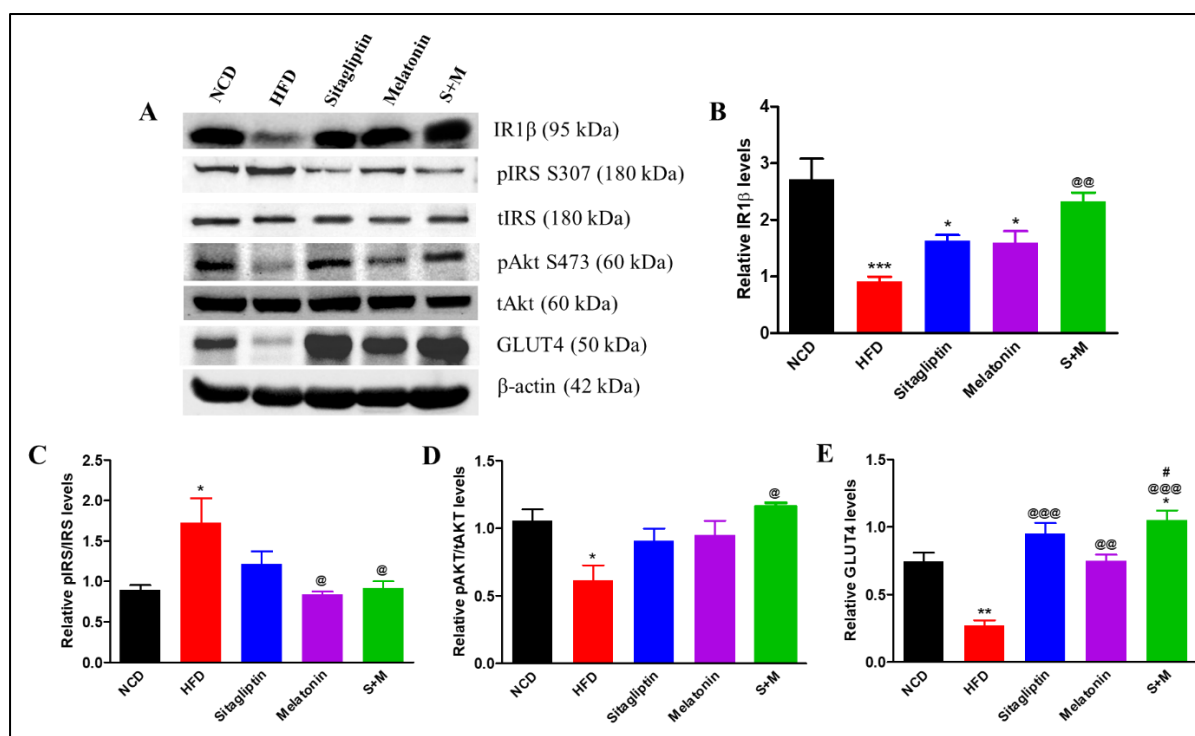




**Figure 5.7 Respiratory control ratio (state 3/state 4): A) Complex I.** RCR was significantly reduced in HFD group as compared to NCD and was significantly increased in the S+M treated group. **B-D) Complex II-IV.** RCR was significantly reduced in HFD group as compared to NCD and was significantly increased in the melatonin and S+M treated groups. (\* $p < 0.05$ , \*\*\* $p < 0.001$  vs. NCD; @ $p < 0.05$ , @@ $p < 0.01$ , @@@ $p < 0.001$  vs. HFD; & $p < 0.05$ , &&& $p < 0.001$  vs. Sitagliptin; # $p < 0.05$ , vs. Melatonin) (n=3/group).

### 5.3.7 Protein Expression Analysis for Insulin Signalling Pathway in Skeletal Muscle

Protein expression analysis of key proteins involved in insulin signalling pathway revealed that IR1 $\beta$  ( $p < 0.001$ ), pAkt Ser473/Akt ( $p < 0.05$ ) and GLUT4 ( $p < 0.01$ ) levels were significantly reduced in HFD fed mice while pIRS Ser307/IRS ( $p < 0.05$ ) was significantly increased in HFD ( $p < 0.05$ ) as compared to NCD, which is indicative of insulin resistance. With respect to the treatment groups, no significant change was observed in the levels of IR1 $\beta$  and pAkt/Akt in monotherapies ( $p > 0.05$ ), while a significant increase was observed in the S+M group ( $p < 0.01$ ,  $p < 0.05$ ) as compared to HFD group. Further, the levels of pIRS/IRS were significantly reduced in M and S+M groups (M,  $p < 0.05$ ; S+M,  $p < 0.05$ ) indicative of increased insulin sensitivity. Interestingly, GLUT4 levels were significantly increased in all the drug treated groups (S,  $p < 0.001$ ; M,  $p < 0.01$ ; S+M,  $p < 0.001$ ) as compared to HFD group. The results are shown in Figure 5.8A-D. These results indicate that the combination therapy showed significant effects as compared to monotherapies in improving insulin sensitivity.

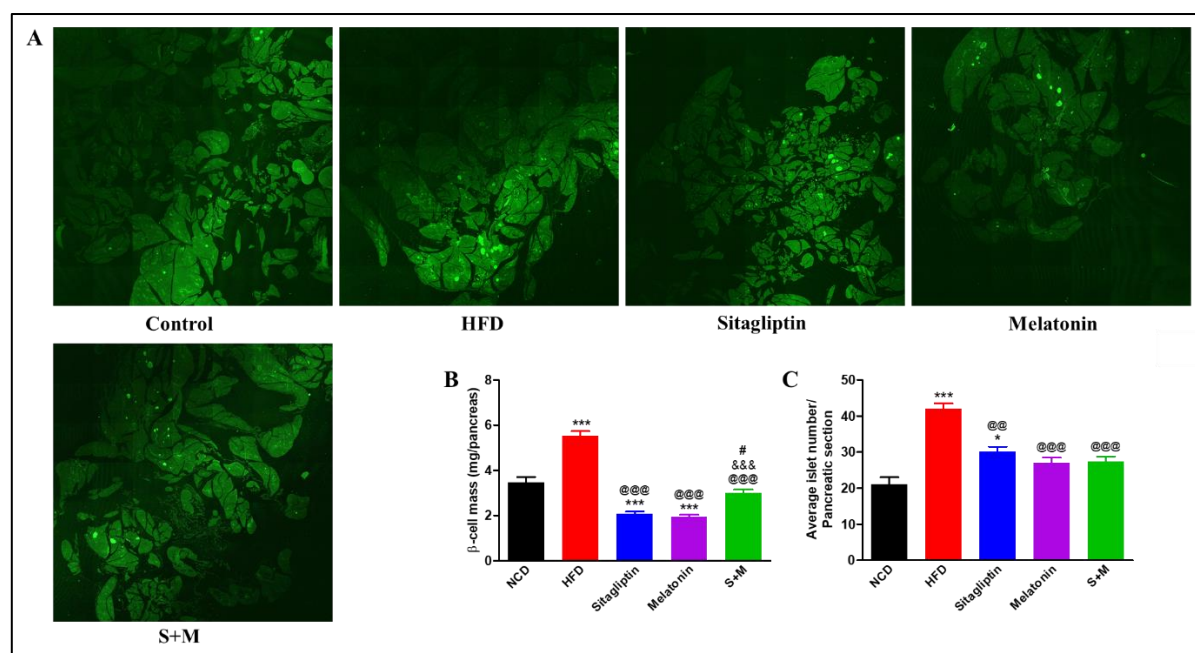


**Figure 5.8 Protein expression of the insulin signalling pathway in skeletal muscle: A.** Representative Western blot images. **B. Insulin Receptor 1β.** IR1β protein expression was significantly reduced in HFD compared to NCD, whereas a significant increase in IR1β was observed in S+M group. **B. pIRS/IRS.** pIRS/IRS levels were significantly increased in HFD and were significantly reduced in in M an S+M groups. **C. pAkt/Akt.** pAkt/tAkt protein expression was significantly decreased in HFD while it was significantly increased in S+M group. **D. GLUT4.** GLUT4 protein expression was significantly decreased in the HFD while it was significantly increased in all the drug treated groups. (\* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$  vs. NCD; @ $p < 0.05$ , @@ $p < 0.01$ , @@@ $p < 0.001$  vs. HFD; # $p < 0.05$ , vs. Melatonin) (n=4/group).

### 5.3.8 Assessment of β-cell Mass and Islet Number

Immunohistochemical analysis of the pancreas revealed that β-cell mass was significantly increased in the HFD group as compared to NCD ( $p < 0.001$ ). All the drug-treated groups showed significant decrease in β-cell mass as compared to HFD group (S, M, S+M,  $p < 0.001$ ). Interestingly, the islet number per pancreatic section was also significantly increased in HFD group ( $p < 0.001$ ) as compared to NCD while it was reduced in all the drug-treated groups as compared to HFD group (S,  $p < 0.01$ ; M,  $p < 0.001$ ; S+M,  $p < 0.001$ ), as shown in Figure 5.9A-C.





**Figure 5.9  $\beta$ -cell mass and Islet number.** A. Immunofluorescence staining for insulin (green) in mouse pancreatic tissue. Scale- 50 $\mu$ m. Magnification- 60X. B.  $\beta$ -cell mass in pancreas:  $\beta$ -cell mass was significantly increased in HFD group while it was significantly reduced in all the drug-treated groups as compared to HFD group. C. Number of islets per pancreatic section. Islet number was significantly increased in HFD group as compared to NCD group while it was reduced in all the drug-treated groups as compared to HFD group (\* $p$ <0.05, \*\*\* $p$ <0.001 vs. NCD; @@ $p$ <0.01, @@@ $p$ <0.001 vs. HFD; # $p$ <0.05 vs. Melatonin) (n=6-8/ group).

## 5.4 Discussion

T2D is a metabolic disorder with a reduced incretin effect and disturbed circadian rhythm (Scheer et al., 2009). Several studies have linked genetic variants of *MTNR1B* and reduced melatonin levels with T2D pathogenesis. T2D is a multifactorial disorder involving various factors like insulin resistance, leptin resistance, metabolic and mitochondrial dysfunction, and reduced  $\beta$ -cell mass and function. We have shown in Chapter 4 the effect combination therapy using sitagliptin and melatonin in the amelioration of T1D in mouse model by increasing  $\beta$ -cell mass. Here, we aimed to study the therapeutic potential of combination therapy of sitagliptin and melatonin in the amelioration of T2D manifestations in mouse model. Our results show that sitagliptin and melatonin alone and in combination can ameliorate hyperglycemia, hyperinsulinemia, hyperleptinemia, dyslipidemia and improve glucose and lipid metabolism. In addition, it preserves  $\beta$ -cell mass and islet number, increases mitochondrial biogenesis, and insulin sensitivity in skeletal muscle and adipose tissue.

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Apart from the pineal gland, melatonin is locally synthesized in various tissues like retina, pancreas, adipose tissue, etc. This pleiotropic hormone mediates its action via MTNR1A and MTNR1B receptors in central and peripheral tissues, regulating metabolic functions. These receptors are G protein-coupled receptors, and most of the signalling pathways are dependent on Gi proteins, which inhibit protein kinase A (PKA) - cAMP response element-binding protein (CREB) pathway. Gi proteins also inhibit other kinases such as protein kinase G (PKG), protein kinase C (PKC), phosphoinositide 3-kinase (PI3K), Akt, extracellular-signal-regulated kinase (ERK) and ion channels such as Kir3 and large-conductance Ca<sup>2+</sup>-activated potassium channels (BKCa) (Cecon et al., 2017). Alternatively, melatonin activates Gq-PKC-phospholipase C (PLC) pathway, which is shown to stimulate insulin secretion (Oishi et al., 2018). A few animal studies suggest modulatory effects of melatonin in peripheral tissues even though melatonin receptors are expressed at low levels in these tissues (Ha et al., 2006; Poon et al., 2001; Kemp et al., 2002; Muhlbauer et al., 2012; Zalatan et al., 2001; Stumpf et al., 2008). Reduced melatonin levels are observed in various T2D rodent models and T2D patients (Peschke et al., 2006). Pinealectomy leads to reduced GLUT4 levels, glucose intolerance and insulin resistance (Lima et al., 1998; Nogueira et al., 2011). Upon administration of melatonin, glucose metabolism is improved in HFD induced insulin-resistant mouse model (Sartori et al., 2009). Several reports suggest the role of melatonin in insulin secretion and glucose uptake. In HepG2 cells, melatonin stimulates glycogen synthesis via protein kinase C, zeta (PKC $\zeta$ ), Akt and glycogen synthase kinase-3 $\beta$  (GSK3 $\beta$ ) (Shieh et al., 2009) besides reducing gluconeogenesis in rats (Poon et al., 2001). The findings of melatonin regulating glucose metabolism via increased PI3K-Akt activity (Tuomi et al., 2016; Brydon et al., 2001) support our findings. Further, it is reported that melatonin activates IRS1-PI3K-PKC $\zeta$  pathway and stimulates glucose uptake in mouse skeletal muscle cells (Ha et al., 2006), while it is reduced in MT1 knockout mice (Owino et al., 2018). In addition, melatonin is reported to inhibit lipolysis and fatty acid transport by inhibiting the cAMP-PKA pathway in rat adipocytes (Zalatan et al., 2001). Melatonin seems to have differential effects in the adipose tissue under acute and chronic treatments. Acute treatment inhibits cAMP and cGMP production in PAZ6 human brown adipocyte cell line, while chronic treatment reduces GLUT4 and glucose uptake (Brydon et al., 2001). In rodents, melatonin reduces body weight and white adipose tissue in various experimental models (Cipolla-Neto et al., 2014). A few small-scale clinical studies of melatonin treatment showed a negligible effect on body weight reduction with opposite results on plasma lipids (Karamitri

and Jockers, 2019). Furthermore, melatonin inhibits insulin secretion in rodent  $\beta$ -cells via Gi-cAMP-PKA (Muhlbauer et al., 2012; Karamitri et al., 2013; Peshchke et al., 2013) or cGMP pathway (Stumpf et al., 2008). However, long-term melatonin administration, increases insulin release in our study. Similar results are reported in INS-1 cells (Kemp et al., 2002; Peshchke et al., 2013). Acute melatonin treatment in clinical trials show impaired glucose tolerance (Cagnacci et al., 2001; Rubio-Sastre et al., 2014). However, chronic treatment of melatonin up to five months reduces HbA1c levels and hyperglycemia (Garfinkel et al., 2011). Human islet studies have shown increased intracellular  $\text{Ca}^{2+}$  levels and insulin secretion in  $\beta$ -cells (Ramracheya et al., 2008), possibly by paracrine signalling. Melatonin signalling promotes  $\beta$ -cell survival by decreasing apoptosis and oxidative stress in T2D patients' islets (Karamitri et al., 2013; Costes et al., 2015). These findings corroborate with our results, where  $\beta$ -cell mass increases along with insulin secretion. Similar to our findings, a combination study of melatonin and insulin also showed promising results in achieving glycemic control and insulin sensitivity in the adipose tissue as compared to the monotherapies (Oliveira et al., 2018). A very recent meta-analysis of randomized clinical trials investigating effects of melatonin supplementation on diabetes patients suggest that it reduces diabetes parameters like FBG, HbA1c levels, and insulin resistance (Delino et al., 2021).

Sitagliptin is the first approved DPP-IV inhibitor and is used widely for the management of T2D. DPP-IV plays an essential role in energy metabolism apart from its antidiabetic property (Goldsmith et al., 2015). Adipose tissue secretes DPP-IV, which impairs insulin signalling causing insulin resistance. Sitagliptin is a GLP-1 secretagogue that mediates its action via cAMP and ERK1/2 signalling (Sangle et al., 2012). Sitagliptin via GLP-1 promotes insulin signalling by increasing PKB (Akt) activity (Buteau et al., 2004; Li et al., 2005). In obese diabetic patients, leptin resistance causes increased leptin and insulin levels. We observed reduced leptin and insulin levels in all drug-treated groups showing the drugs involvement in lowering inflammatory markers. In this context, Dobrian et al. (2011) have reported the effect of sitagliptin in reducing local inflammation in adipose tissue and pancreatic islets in obese mice in addition to its insulin stimulatory effects.

Further, GLP-1 effects on adipocytes revealed its lipogenic and lipolytic functions (Villanueva-Penacarrillo et al., 2001; Vendrell et al., 2011) and, interestingly, the GLP-1 receptors in the white adipose tissue are structurally and functionally different from those in

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the pancreas (Polakof et al., 2011). Sitagliptin treatment in diet-induced obesity reduces body weight (Lamont and Drucker, 2008). In clinical studies, similar results of reduced BW gain are seen in sitagliptin plus metformin-treated T2D patients (Raz et al., 2008; Bergenstal et al., 2010). Increasing GLP-1 levels reduces gluconeogenesis, promotes satiety and fat loss leading to insulin sensitivity (Green et al., 2006). It also controls metabolic abnormalities in HFD induced diabetic mice via peroxisome proliferator-activated receptor alpha (PPAR)- $\alpha$  activation in the liver (Souza-Mello et al., 2010). Our *in-vivo* studies are in agreement with these findings.

Furthermore, sitagliptin may slow down the progression of T2D by preserving  $\beta$ -cell mass, as observed by Yeom et al. (2011) in db/db mice. Our findings of increased  $\beta$ -cell mass seem to bring about glycemic control. However, it is essential to know if there is any different effect of sitagliptin on  $\beta$ -cell mass in lean subjects. We did not observe any significant change in food and water intake after sitagliptin treatment, as observed by Poucher et al. (2012). Nevertheless, we observed significant increase in insulin and glucose tolerance besides improved lipid profile, which supports studies by Akaslan et al. (2013) and Reimer et al. (2012), indicating improved lipid profile and insulin sensitivity in obese rats. Thus, sitagliptin shows its therapeutic effects on glycolipid metabolism in T2D (Yang et al., 2016).

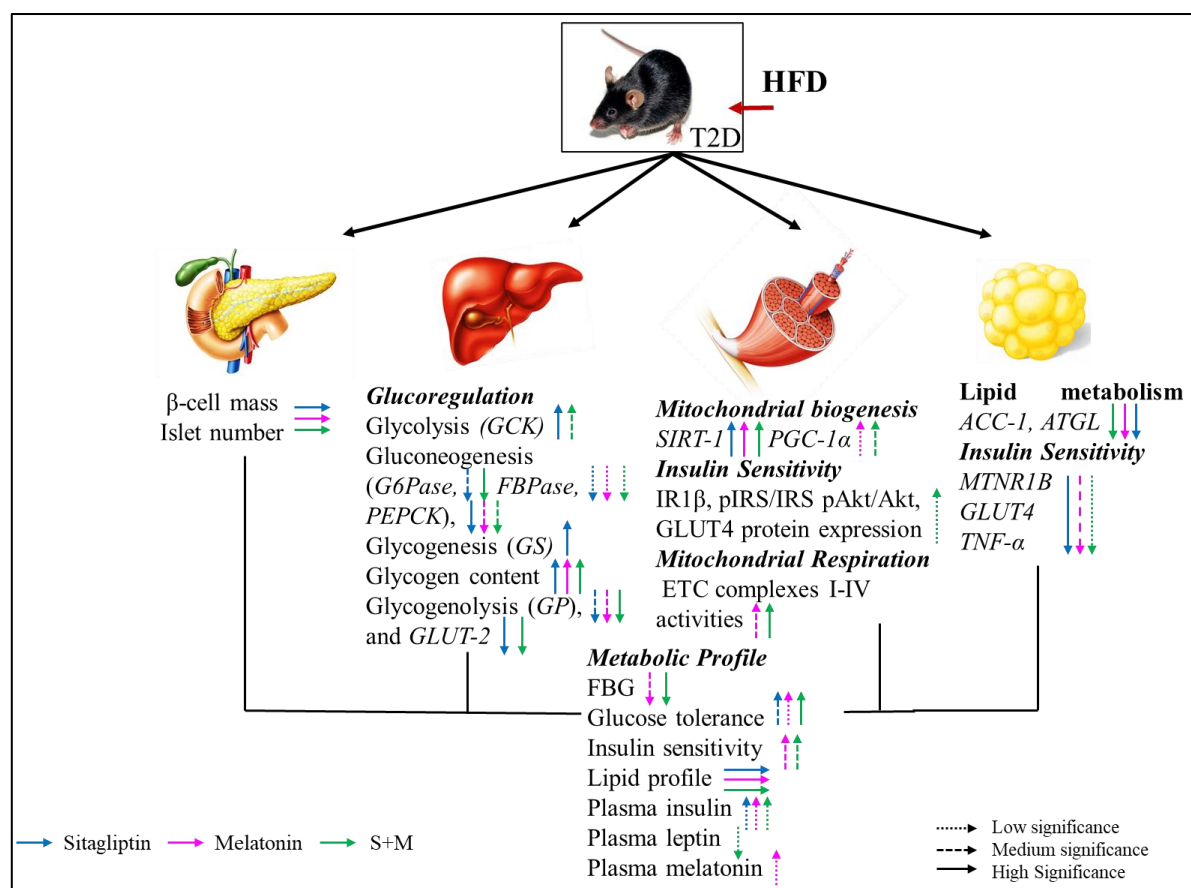
Interestingly, our study also reveals increased glycolysis, glycogen synthesis and glycogen content, and reduced gluconeogenesis, glycogenolysis and *GLUT2* expression in the liver, suggesting improved glucose metabolism in all drug-treated groups. Our mitochondrial studies suggest increased respiratory chain complexes I-IV activities in skeletal muscle in all drug treated groups. To our knowledge, there are no reports of the effects of sitagliptin treatment on mitochondrial function. However, Apaijai et al. (2013) showed improved cardiac mitochondrial function upon sitagliptin treatment in obese insulin-resistant rats. Defective insulin signalling leads to insulin resistance. Over nutrition causes activation of mTOR/S6K1 signalling and impairs insulin signalling by increased serine phosphorylation of IRS1 (Copps and White, 2012; Jia et al., 2014). A recent study showed decreased S6K1 activation and degradation of IRS1 and IRS2 upon sitagliptin treatment in obese mice (Qiao et al., 2018). We report a significant decrease in serine phosphorylation of IRS1 and increase in IR1 $\beta$ , pAKT and GLUT4 expression in all drug-treated groups. Sitagliptin activation of SIRT1- AMP-activated protein kinase (AMPK)/ adiponectin-AMPK/ PGC1- $\alpha$ -pAMPK pathway and downstream signalling are reported in liver, adipose tissue and skeletal muscle.

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Such activation leads to modulation of fatty acid metabolism and further reduces insulin resistance in T2D models (Shen et al., 2018; Prakash et al., 2020; Liu et al., 2020).

Similarly, we have observed decrease in *ATGL* (lipolytic) transcript levels in adipose tissue with no change in *ACCI* (lipogenic) in all the drug-treated groups. In addition, increased *SIRT1* and *PGC1- $\alpha$*  (mitochondrial biogenesis genes) in the drug-treated groups in skeletal muscle, indicating improved lipid metabolism and insulin sensitivity in the respective tissues. *ACCI* helps in fatty acid (FA) synthesis in liver and adipose tissue. Moreover, reduced *ACCI* expression decreases TG accumulation (Mao et al., 2006), as also observed in our study. However, the decreased expression of *ACCI* in HFD group could be due compensation as the TG levels are significantly higher. Furthermore, our ddPCR results revealed increased expression of *MTNR1B*, *GLUT4* and *TNF- $\alpha$*  in HFD group indicating insulin resistance whereas the levels were decreased in all the drug treated groups signifying increased insulin sensitivity in adipose tissue. There are various reports which suggest that overexpression of *GLUT4* increases insulin sensitivity and glucose tolerance in HFD fed mice (Atkinson et al., 2013), and that its expression changes with short term and long term HFD feeding (Kim et al., 2014). It is possible that the overexpression was to compensate for insulin resistance in HFD group which was then reduced in all drug-treated groups showing increased insulin sensitivity. Moreover, *TNF- $\alpha$* , a pro-inflammatory adipokine increases in obesity and T2D leading to insulin resistance (Patel et al., 2019). In addition, *MTNR1B* overexpression in adipose tissue leads to increased lipid levels in adipocytes (Owino et al., 2018) which is supported by our results showing increased TG levels and fat in HFD group while we observed decreased expression of *MTNR1B* expression and lipid levels in all drug-treated groups.

Thus, melatonin and sitagliptin in combination potentiate each other's action and improves glycolipid metabolism, insulin sensitivity, mitochondrial respiration and biogenesis, and preserves  $\beta$ -cell mass in HFD-induced T2D mouse model (Figure 5.10).



**Figure 5.10 Effect of sitagliptin, melatonin, and combination therapy in amelioration of HFD-induced T2D manifestations in a mouse model.** Combination of sitagliptin and melatonin shows greater therapeutic benefits than monotherapies in improving glyco-lipid metabolism in liver and adipose tissue, respectively; regulating mitochondrial biogenesis and mitochondrial respiration in skeletal muscle; increasing insulin sensitivity in skeletal muscle and adipose tissue; and maintaining  $\beta$ -cell mass and islet number in pancreas. These altogether brings about glucose homeostasis thereby ameliorating T2D manifestations.

As differences in the species play a significant role in influencing melatonin effects on glucose homeostasis, it is essential to consider acute/chronic melatonin treatment and paracrine interactions while translating its therapeutic effects in humans.

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