Background Primary hepatocellular carcinoma (HCC) is one of the most common malignancies all over the world. However, the mechanism of HCC initiation and development remains unclear. In our previous work, high-throughput microarray assay in HCC samples followed by bioinformatic analysis suggested that Metallothionein1G (MT1G) might be one of the key factors in HCC. In this study, we aim to clarify the biological function of MT1G and validate its potential to be utilised as a biomarker in HCC.

Methods We detected the MT1G expression in paired HCC samples and cell lines by both RT-qPCR and Western blot. MSP (Methylation specific PCR) and BGS (Bisulfite genomic sequencing) were performed to evaluate methylation status of MT1G in HCC. TCGA (The Cancer Genome Atlas) data analysis was used to validate the results from our samples. Kaplan-Meier survival analysis was performed using TCGA data to estimate the clinical value of MT1G expression and methylation status in HCC.

Results MT1G was inactivated in 4 of 6 HCC cell lines. The expression of MT1G was downregulated in cancer tissues compared with the adjacent non-tumour tissues (p<0.001). The gene expression of MT1G was closely correlated to the promoter methylation status. The MT1G expression in silenced HCC cell lines could be restored by demethylation agent. Ectopic re-expression of MT1G by stable transfection in SMCC7721 and Hep3B cells inhibited colony formation (p<0.001), suppressed cell motility and invasiveness (p<0.05), accompanying with up-regulation of E-cadherin; and down-regulation of PCNA, MMP2, MMP13 and Vimentin. Xenograft tumour assay in nude mice also revealed that MT1G could markedly decrease tumour weights and volumes in vivo (p<0.001). Survival analysis revealed that hypermethylation of MT1G predicts good outcomes of HCC patients.

Conclusions Our results demonstrate that MT1G promoter methylation directly mediates the transcription down-regulation and commonly occurs in HCC. MT1G gene can act as a functional tumour suppressor in liver carcinogenesis by playing an important role in the depression of cell proliferation, migration and invasion.

Background Metabolic reprogramming in cancer cells is likely to interact with the epigenetic landmarks, which may modulate tumorigenesis. However, the exact mechanism is still largely unknown. In our previous study, inhibition of activity of mechanistic target of rapamycin (mTORC1), a nutrient sensor that affects cellular metabolism, was able to attenuate the DNA methylation level. In this study, we aim to clarify the correlation between the metabolism and DNA methylation and evaluate their interactive roles in the pathogenesis of hepatocellular carcinoma (HCC).

Methods We treated HCC cell lines with rapamycin to inhibit mTORC1 activity and performed immunofluorescence (IF) and Enzyme-linked immune sorbent assay (ELISA) to detect the levels of 5-methylcytosine (5-mC). Western-blot and IF assays were used to detect the protein levels of DNA methyltransferases (DNMTs) and RT-PCR was performed to test transcription of DNMTs. Cycloheximide was used to suppress the protein translation. Moreover, MG132 and BafA1 were used to inhibit the functions of ubiquitin-proteasome and autophagy-lysosome respectively to evaluate the effect of posttranslational modification for DNMTs degradation. Finally, we selected twenty liver cancer cell lines and combined western-blot and CCK8 assays to observe the association between mTORC1 inhibition-induced DNMTs degradation and cell viabilities.

Results Rapamycin treatment reduced 5 mC levels in HCC cell lines. In parallel, mTORC1 inhibition attenuated the expressions of DNMT1. The subsequent experiments revealed that transcriptional regulation and posttranslational modification is not likely to participate in the process of DNMT1 degradation induced by mTORC1 inhibition. However, cycloheximide half-life assay indicated that mTORC1 might adjust the expression DNMT1 through regulating initial translational efficiency. We found that mTORC1-mediated DNMT1 degradation is closely linked to cell proliferation.

Conclusions In conclusion, we demonstrated that mTORC1 could affect DNA methylation levels in HCC probably through regulating DNMTs expression. Besides, this interactive role seems to be closely linked to HCC cell viability. Investigation of the relationship between mTORC1 signalling and DNA methylation will deepen our insight on the pathogenesis of HCC and develop a novel therapeutic strategy for HCC patients.
candida circRNA was performed in vitro and in vivo, including cell viability assay, colony formation assay, cell cycle analysis, apoptosis assay, and Matrigel migration and invasion assay. Differences between experimental groups and control groups were analysed using the paired t-test and Wilcoxon test.

**Results** Of the seven-candidate circRNAs, Circ5379-6 was verified to be correlated positively to PPARα. Overexpression of Circ5379-6 lead to up-regulation of PPARα and it thereby suppressed the cell proliferation, inhibited the cell migration and invasion. The most obvious effect of circ5379-6 expression should be the induction of cell apoptosis in the HCC cell lines. Matrix metalloprotein 9 (MMP-9) was down-regulated expressed while Vimentin, N-Cadherin and E-Cadherin were up-regulated expressed in the tumour generated by the cells with circ5379-6 overexpression. Furthermore, the overexpression of circ5379-6 effectively inhibited the tumorigenesis and metastasis of HCC according to the in vivo studies in nude mice.

**Conclusions** Circ5379-6 acts as an effective tumour inhibitor of HCC via regulating the level of PPARα. It suggests that induction of Circ5379-6 expression may utilise as a potential therapeutic method for HCC.

### Abstracts

#### IDDF2018-ABS-0210

**POKEMON OVER-EXPRESSION ACCELERATES THE PROGRESSION OF NAFLD VIA INCREASING LIPID DROPLET DEPOSIT IN HEPATOCYTE**

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**Background** Non-alcoholic fatty liver disease (NAFLD) is considered as the hepatic manifestation of metabolic syndrome and is characterised by the accumulation of lipid droplets. Pokemon (FBI-1/ZATB7A) is an important proto-oncogene which is involved in cancer development and adipogenic gene expression. The aim of our study is to explore the role of Pokemon in the development and progression of NAFLD.

**Methods** C57BL/6 mice were fed with normal chow (NC) or high-fat diet (HFD) for 16 weeks to induce NAFLD. Pokemon mRNA and protein were detected by RT-PCR and Western blot as well as immunohistochemistry. NAFLD cell models were established by oleic acid, and si-Pokemon hepatic cancer cell lines were also constructed by plko lentiviral system. NAFLD models were established by oleic acid, and si-Pokemon hepatic cancer cell lines. Matrix metalloprotein 9 (MMP-9) was down-regulated expressed while Vimentin, N-Cadherin and E-Cadherin were up-regulated expressed in the tumour generated by the cells with circ5379-6 overexpression. Furthermore, the overexpression of circ5379-6 effectively inhibited the tumorigenesis and metastasis of HCC according to the in vivo studies in nude mice.

**Conclusions** Circ5379-6 acts as an effective tumour inhibitor of HCC via regulating the level of PPARα. It suggests that induction of Circ5379-6 expression may utilise as a potential therapeutic method for HCC.

#### IDDF2018-ABS-0216

**ANTIDIABETIC EFFECTS OF SODIUM ORTHOVANADATE AND TRIGONELLA FOENUM GRAECUM SEED POWDER IN LIVER OF RAT MODEL**

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**Background** Diabetes has been considered as one of the fastest growing epidemic worldwide; the number of people with diabetes is estimated to increase from 381.8 million in 2013 to 591.9 million in 2030. Oxidative stress in diabetic tissues is accompanied by high level of free radicals and the simultaneously declined antioxidant enzymes status leading to cell membrane damage. In the present study, the effect of sodium orthovanadate (SOV) and Trigonella foenum graecum seed powder (TSP) administration has been studied on blood glucose and insulin levels, antioxidant enzymes, enzyme peroxidation, lipofuscin and DNA degradation, distribution of glucose transporter (glut 2, glut4) in liver tissues of the alloxan-induced diabetic rats and to see whether the treatment with SOV and TSP is capable of reversing these effects.

**Materials and methods** Diabetes was induced by administration of alloxan monohydrate (15 mg/100 gm b.wt.) and rats were treated with 2IU insulin, 0.6 mg/ml SOV, 5% TSP in the diet and a combination of 0.2 mg/ml SOV with 5% TSP separately for 21 days. Control animals were given only the vehicle.

**Results** Diabetic rats showed hyperglycaemia with almost fourfold high blood glucose levels. Hyperglycemia increases lipid peroxidation and DNA degradation, causing decreased activities of membrane-bound ATPases, antioxidant enzymes and glucose transporter expression with diabetes in the rat liver. Rats treated with a combined dose of SOV and TSP had glucose levels comparable to controls, similar results were obtained with the activities of antioxidant enzymes, membrane-bound ATPases, DNA degradation, lipid peroxidation and glucose transporter in the liver of diabetic rats.

**Conclusions** Our results showed that lower doses of vanadate (0.2 mg/ml) could be used in combination with Trigonella to effectively counter diabetic alterations without any toxic side effects. Therefore combined therapy can indeed be considered a better alternative to being explored further as a means of diabetic control.

#### IDDF2018-ABS-0232

**WEARABLE TECHNOLOGY (MI BAND AND YU BAND) A BOON FOR PATIENTS WITH CHRONIC KIDNEY DISEASE**

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**Background** New wearable sensor networks together with smartphone applications are being examined and tested for their potential to monitor and manage patients with chronic kidney disease (CKD). To develop methods for analyses and