ing treatments (tx), offering effective glycemic control without increasing the risk of hypoglycemia. Considering patients' (pts) preference is crucial to ensure tx adherence.

Aim: To understand the pts tx preference for T2DM in Asian countries between medication profiles resembling SGLT2I (medication A) and DPP4I (medication B).

Method: In this cross-sectional study (Nov 2021–Nov 2022) adult T2DM patients across India, Philippines and Taiwan, completed a survey to identify their preferred medication profile. Descriptive statistics and Chi-squared/Fisher's exact tests were employed to detect differences in pts baseline characteristics and choice between the two profiles across three regions.

Results: The study included 1224 pts (Philippines-34.8 %, India-32.7 %, Taiwan-32.5 %), with a mean age of 59.3 years. Philippines had highest proportion of females (64.8 %) and greater prevalence of hypertension (73.7 %) and dyslipidemia (81.2 %) vs India (46.5 %, 58.3 %,59.3 %) and Taiwan (45.2 %, 55.5 %, 76.9 %). Compared to Philippines and Taiwan, India had high proportion of overweight/obese pts (64.8 %) and pts with uncontrolled glycated hemoglobin (HbA 1c , 70.8 % vs. 53.3 % [Philippines] and 48.7 % [Taiwan], p<.001); but low prevalence of chronic kidney disease (8.5 %) and dyslipidemia (60.3 %). Philippines showed lowest use of biguanides (74.6 %) compared to India (90.3 %) and Taiwan (87.4 %); while India reported high use of sulfonylureas ([73.5 % vs 26.8 %: Philippines and 36.2 %: Taiwan).SGLT2I was significantly preferred over DPP4I (64.5 % vs 35.5 %; p<0.001) with Philippines reporting highest preference (80 %), followed by Taiwan (58 %) and India (54.5 %).

Conclusion: Among Asian pts with T2DM, SGLT2I was preferred over DPP4I. Knowledge of pts preference and factors influencing the tx choices, may help optimize tx adherence and clinical outcomes.

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Exploring islet macrophage-stellate cell interactions using single-cell sequencing

G. Yan, Z. Sun

Institute of Diabetes, School of Medicine, Southeast University, Department of General Practice, Zhongda Hospital, Nanjing, Jiangsu, China

Background: Islet fibrosis is an end-stage alteration in type 1 and type 2 diabetes. Islet fibrosis in diabetic patients may affect insulin secretion and accelerate disease progression. Platelet-derived growth factor (PDGF) is an essential mitogenic factor secreted by macrophages, to promote cell proliferation and migration when the organism is injured. As one of the crucial mediators of fibrotic diseases, the PDGF/PDGFR pathway regulates multi-organ fibrosis. However, the role and mechanism of PDGF/PDGFR in promoting islet fibrosis are not yet understood.

Aim: Explore the interactions between pancreatic islet macrophages and stellate cells in mice amidst the influence of a high-fat diet.

Method: Data were quality controlled and normalised in normal and high-fat diet mice imported into the Seurat R toolkit. Annotated clustering of immune cells was performed for T cells, B cells, macrophages, and monocytes, respectively, and clustering and downscaling of islet stellate cells was performed. Interactions between immune cells and islet stellate cells were analysed using CellChatDB.mouse. Multiplex immunofluorescence was used to detect PDGF and PDGFR expression in pancreatic islet macrophages and stellate cells from normal mice and mice with high-fat diets.

Results: Using GO enrichment analysis, which revealed that PDGFRA^{hi}PDGFRB^{lo} stellate cells have higher extracellular matrix remodelling phenotype and were able to secrete more collagen. Multiplex immunofluorescence revealed that PDGFRA^{hi}PDGFRB^{lo} stellate cells predominantly aggregated around pancreatic islets and promoted peri-islet fibrosis in high-fat diet mice. Exploration of interactions between immune cells and stellate cell subpopulations using CellChatDB.mouse revealed significant interactions between macrophages and stellate cells, in which macrophages could act on PDGFRA and PDGFRB of stellate cells to promote cell proliferation.

Conclusion: Islet macrophages in high-fat mice release PDGF, promoting islet stellate cell proliferation, migration, and islet fibrosis.

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Profiling of plasma-derived exosomal miRNAs in individuals with type 2 diabetes: deeper insights from the RICH study

Y.L. Sou[a], H.C. Low[a], N.A. Muhamad Hendiri[b], J.H. Lim[c], C.K.Y. Ong[d], Y.Q. Chin[e], C.K.M. Lim[c], W. Ratnam[f], T. Karupaiah[d], F. Daud[g], Z.A.M. Daud[c], Y.F. Pung[a]

[a] *University of Nottingham Malaysia, Division of Biomedical Science, Faculty of Science and Engineering, Semenyih, Selangor, Malaysia*
[b] *National Institutes of Health, Department of Electron Microscopy-Institute of Medical Research, Shah Alam, Selangor, Malaysia*
[c] *Universiti Putra Malaysia, Department of Dietetics, Faculty of Medicine and Health Sciences, Serdang, Selangor, Malaysia*
[d] *Taylor's University, School of Biosciences, Faculty of Health and Medical Sciences, Subang Jaya, Selangor, Malaysia*
[e] *Taylor's University, School of Food Studies and Gastronomy, Faculty of Social Sciences and Leisure Management, Subang Jaya, Selangor, Malaysia*
[f] *Nomatech Sdn Bhd, UKM-MTDC Technology Centre, Bangi, Selangor, Malaysia*
[g] *Universiti Kebangsaan Malaysia, Department of Community Health, Faculty of Medicine, Kuala Lumpur, Malaysia*

Background: Exosomes are small extracellular vesicles found in human biofluids such as plasma and urine [1]. The microRNAs (miRNAs) transported within exosomes play important roles in the initiation and development of type 2 diabetes (T2D) [2]. While dietary interventions have been shown to improve T2D and influence the exosomal miRNA expression, the exosomal miRNA profiles for T2D patients in the Asian population have not been reported [3].

Aim: This study aimed to compare the exosomal miRNA profiles between clinically diagnosed T2D patients as compared to non-T2D controls (HbA1c< 6.3 %). Secondly, it also evaluated the changes in exosomal miRNA profiles in T2D patients after a 24-week intervention with UKMRC9.

Method: Plasma exosomes were isolated from 72 Rice Intervention in Chronic Healthy (RICH) participants and characterized using transmission electron microscopy (TEM), nanoparticle tracking analysis (NTA), and western blotting. Total RNAs from exosomes were extracted to construct miRNA libraries for next-generation sequencing (NGS). Lastly, the Gene Ontology (GO) and Kyoto Encyclopaedia Genes and Genomes (KEGG) analyses were conducted to predict the downstream targets of the dysregulated genes.

Results: TEM and NTA analyses revealed no significant differences in exosome size and concentration between T2D patients and non-T2D controls. However, the bioinformatics analyses of NGS data identified 12 differentially expressed exosomal miRNAs in T2D patients as compared to non-T2D controls, with 6 miRNAs upregulated and 6 downregulated (log fold change >1, FDR $p < 0.05$). After the UKMRC9 intervention, a subset of exosomal miRNAs in T2D patients returned to levels similar to non-T2D controls. GO and KEGG pathway analyses linked these exosomal miRNAs to several T2D-related pathways.

Conclusion: Consumption of UKMRC9 altered the exosomal miRNA profiles in T2D patients to levels similar to non-T2D controls. Thus, UKMRC9 could serve as an alternative approach to manage, and potentially reverse T2D.

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IL-6 knockout mice nutri-stressed with high-fat diet show improved glucose tolerance and insulin resistance

S. Al-Beloushi[a], A. Hasan[b], F. Bahman[a], S. Sindhu[c], S. Kochumon[a], F. Al-Mulla[b], R. Ahmad[a]

[a] *Dasman Diabetes Institute, Immunolog, Dasman, Kuwait*
[b] *Dasman Diabetes Institute, Translational Research, Dasman, Kuwait*
[c] *Dasman Diabetes Institute, Animal Facility, Dasman, Kuwait*

Background: Interleukin-6 (IL-6) is a major cytokine that plays a role in inflammation and metabolism. Its role in adipose tissue, as well as in obesity-induced impairment in glucose homeostasis and insulin resistance, remains elusive.

Aim: We aimed to investigate the effect of a global knockout of IL-6 (IL-6 $^{-/-}$) on glucose homeostasis in mice fed with high-fat diets.

Method: C57BL/6 male mice (n = 20) and IL-6 $^{-/-}$ male mice (n = 20) were randomly assigned to two dietary interventions, including Chow (n=10) or HFD (n = 10), for 22 weeks. Intraperitoneal glucose tolerance tests (IP-GTT) and intraperitoneal insulin tolerance tests (IP-ITT) were performed. Blood samples were collected for metabolic hormone measurements.

Results: IL-6 $^{-/-}$ mice fed with a high-fat diet showed significantly ($P > 0.0001$) lower fasting blood glucose concentrations (6.3 ± 0.2 mmol.L^{-1}) than wild-type mice fed on the same high-fat diet (8.9 ± 0.4 mmol.L^{-1}). During IP-GTT and IP-ITT, IL-6 $^{-/-}$ mice fed with a high-fat diet showed significantly ($P = 0.007$ and $P > 0.0001$, respectively) lower area-under-the-curve (AUC: 1610 ± 140 and 493 ± 62.2, respectively) than wild-type mice fed on the same high-fat diet (2203 ± 120 and 956 ± 45, respectively). IL-6 $^{-/-}$ mice fed a high-fat diet showed significantly ($P = 0.037$ and $P = 0.045$, respectively) lower serum leptin and MCP-1 concentrations (9820 ± 1174 and 322 ± 113 pg.mL^{-1}, respectively) than wild-type mice fed the same high-fat diet (13196 ± 940 and 344 ± 99 pg.mL^{-1}, respectively). Fasting insulin concentrations were significantly ($P = 0.027$) higher in IL-6 $^{-/-}$ mice fed with a high-fat diet (8427 ± 746 pg.mL^{-1}) than in wild-type mice fed the same high-fat diet (6349 ± 438 pg.mL^{-1}).

Conclusion: Our findings suggest that a global knockout of the IL-6 might improve insulin resistance and glucose intolerance in mice nutri-stressed with a high-fat diet.

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Global and mitochondrial epigenetic profiles in type 2 diabetes: Findings from the RICH study

H.C. Low[a], H.L. Cheah[b], J.H. Lim[c], C.K.Y. Ong[d], Y.Q. Chin[e], C.K.M. Lim[c], Q. Ayub[b], W. Ratnam[f], T. Karupaiah[d], F. Daud[g], Z.A.M. Daud[c], Y.F. Pung[a]

[a] *University of Nottingham Malaysia, Division of Biomedical Science, Semenyih, Malaysia*
[b] *Monash University Malaysia, Monash University Malaysia Genomics Platform, Bandar Sunway, Malaysia*
[c] *Universiti Putra Malaysia, Department of Dietetics, Serdang, Malaysia*
[d] *Taylor's University, School of Biosciences, Subang Jaya, Malaysia*
[e] *Taylor's University, School of Food Studies and Gastronomy, Subang Jaya, Malaysia*
[f] *Nomatech Sdn Bhd, UKM-MTDC Technology Centre, Bangi, Malaysia*
[g] *Universiti Kebangsaan Malaysia, Department of Community Health, Kuala Lumpur, Malaysia*

Background: With more than 500 million adults afflicted with type 2 diabetes (T2D) globally, studies have shown that T2D could be managed with lifestyle and dietary interventions [1,2]. The inherent plasticity of epigenetics presents another perspective on the development, progression and management of T2D [3]. While numerous studies link epigenetic changes to improved outcomes in T2D patients, the epigenetic profile of T2D patients in Asian populations is not fully elucidated.