



## METHODOLOGY

The 269 patients (onset age  $\leq 35$  years) enrolled were subjected to the EQ-5D-5L questionnaire upon recruitment. EQ-5D-5L consists of a descriptive page, which comprises 5 dimensions: mobility, self-care, usual activities, pain/discomfort, anxiety/depression with 5 response levels, and an EQ-VAS scale (0-100), which evaluates health status and health preference. Health states were validated against the Singapore valuation set.

## RESULTS

Majority (72.1%) of the patients (mean  $\pm$  SD age:  $33.7 \pm 13.8$ , diabetes duration:  $10.5 \pm 10.6$ ) reported a full health state of "11111". Of the remaining patients, 15.2% and 14.9% reported problems of varying severity under pain/discomfort and anxiety/depression, respectively. Mean VAS score was 79.3 (range 30-100) with 29% reporting a score of  $\leq 70$ . A longer duration of diabetes was found to be associated with lower VAS scores ( $\leq 70$  or  $>70$ ) (OR=1.04, 95% CI: 1.01-1.09,  $p=0.028$ ) after adjusting for age, gender, ethnicity, BMI and HbA1c.

## CONCLUSION

Our results suggest that patients with younger-onset and longer diabetes duration have lower self-rated quality of life. We identified pain/discomfort and anxiety/depression as two areas of concern that clinical care providers can focus on to better support patients in their diabetes care.

## PP-D-12

### RNA-SEQ ANALYSIS OF LIVER FROM NASH-HCC MODEL MOUSE TREATED WITH STREPTOZOTOCIN-HIGH FAT DIET

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## OBJECTIVES

NASH is a chronic liver disease, often associated with type II diabetes, which sometimes progresses to more serious conditions such as liver fibrosis and hepatocellular carcinoma (HCC). The STAM<sup>TM</sup> mouse shows the same pathological progression as human NASH patients, and has been widely used for both drug efficacy and basic research. In this study, we analyzed the RNA-seq data of STAM<sup>TM</sup> mouse at each pathological stage (steatosis, steatohepatitis, liver fibrosis and HCC) and examined the clinical correlation at the genetic level.

## METHODOLOGY

NASH was induced in male mice by a single subcutaneous injection of streptozotocin 2 days after birth and feeding with high fat diet after 4 weeks of age. The mice were sacrificed and livers collected at 6, 8, 12 and 20 weeks of age. For liver samples, the left lateral lobe was snap frozen in liquid nitrogen and stored at  $-80^{\circ}\text{C}$  for RNA-seq analysis. Total RNA of the cells was isolated using RNeasy mini kit.

## RESULTS

The gene expression of the canonical pathways in NASH progression from steatosis to HCC were analyzed, such as immune system process, oxidation-reduction process and lipid metabolic process. Moreover, since it has been reported that genetic traits are involved in the development of NASH-HCC, we subsequently analyzed the genetic mutations in the STAM<sup>TM</sup> mice. The number of individual genes showing mutations in mTOR involved in Insulin signalling increases as the disease progresses, especially in the liver cancer phase.

## CONCLUSION

These results indicate that gene profiles in the STAM<sup>TM</sup> mouse are clinically correlated.

## PP-D-13

### CLINICAL EFFECTIVENESS OF ONCE-WEEKLY DULAGLUTIDE AS ADD-ON TO SGLT2i IN THAI PATIENTS WITH T2DM: RETROSPECTIVE STUDY IN A REAL-WORLD SETTING

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## OBJECTIVES

Both GLP-1 receptor agonists (GLP-1 RA) and SGLT2 inhibitors (SGLT2i) reduce the risk of cardiovascular and renal complications when included as part of usual care in T2DM patients with established atherosclerotic cardiovascular disease (ASCVD) or multiple risk factors for ASCVD. Dulaglutide is a once-weekly GLP1-RA which became available in Thailand in 2018. This study aimed to show the real-world use of dulaglutide as add-on to SGLT2i among Thai patients with T2D in a specialized tertiary diabetes center.