

Investigating the molecular pathomechanism of diabetes in an *in vivo* mouse model



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INTRODUCTION

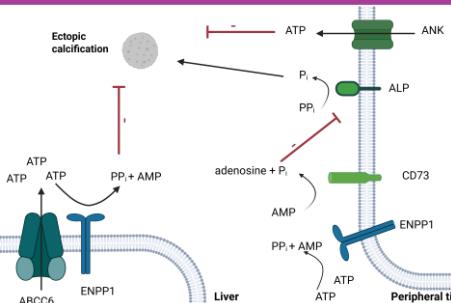


Fig.1: Molecular mechanism of calcification

Diabetes mellitus is the most common chronic metabolic disease worldwide. **Type 1 diabetes** is triggered by the autoimmune destruction of pancreatic β -cells. It is characterized by persistent hyperglycemia, increased oxidative stress, and chronic inflammation. [1,2] Complications include **soft tissue calcification**, contributing to chronic kidney disease and vascular damage.[3] Pyrophosphate is an endogenous inhibitor of calcification.[4]

METHODS

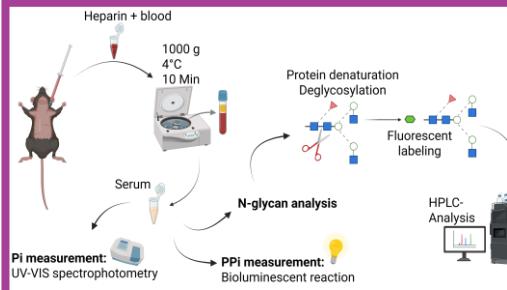


Fig.2: Measurement methods

RESULTS

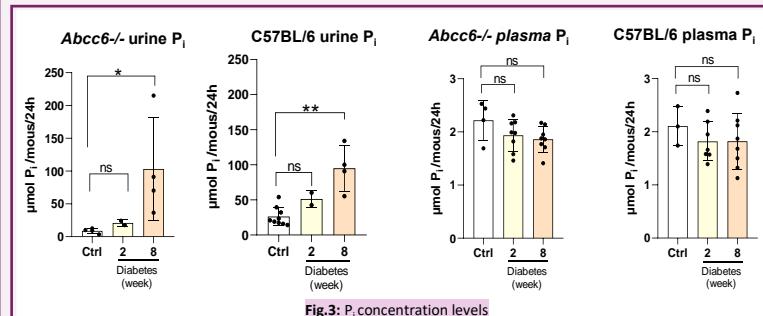


Fig.3: Pi concentration levels

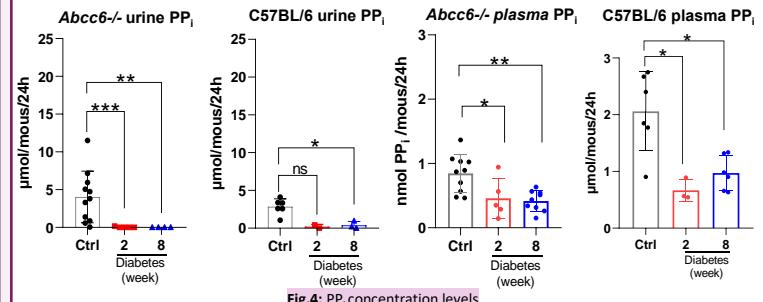


Fig.4: PPi concentration levels

Statistical analysis was performed using the Kruskal Wallis test. Significance is indicated as follows: * = $p < 0.05$, ** = $p < 0.01$, *** $p < 0.001$.

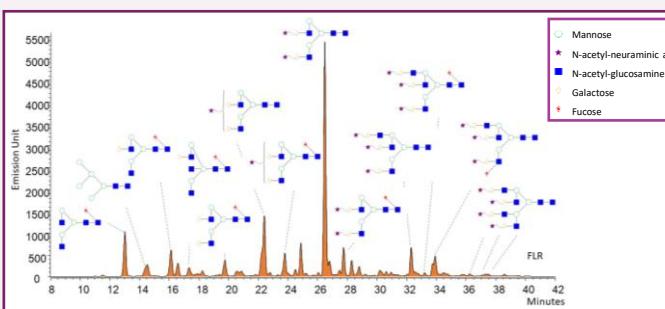


Fig.5: Fluorescence Chromatogram of Detected Sugar Structures

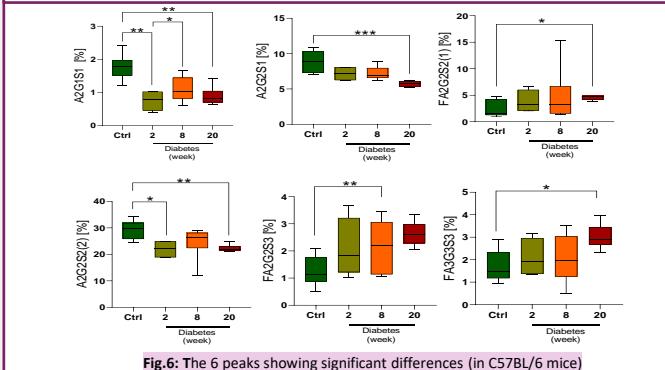


Fig.6: The 6 peaks showing significant differences (in C57BL/6 mice)

CONCLUSION

Serum Pi \rightarrow constant
Urinary Pi \uparrow (week 8)
Hyperphosphatemia
Literature supported

HPLC glycan profiling
6 altered peaks ($p < 0.05$)
Altered glycosylation pattern
Potential biomarkers

FUTURE PLANS

Abcc6^{-/-} mice and human samples
HPLC analysis, Biomarker validation

ACKNOWLEDGEMENTS

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