



UNIVERSITY OF
OXFORD

Weird gene in a weird mammal:

A highly divergent pancreatic duodenal homeobox 1 (*Pdx1*) gene in the fat sand rat

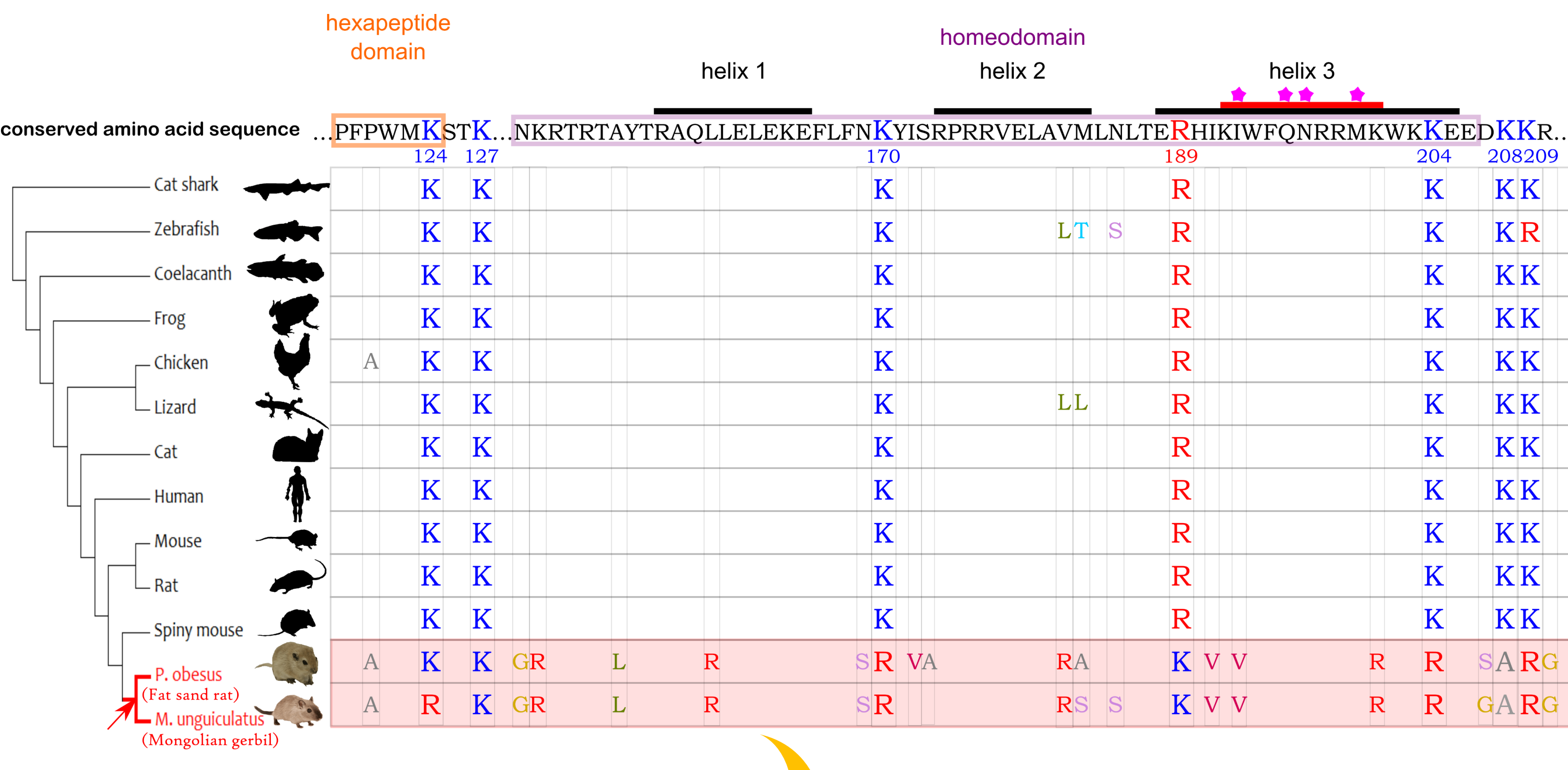
Yichen Dai (Serena), Peter WH Holland
Department of Zoology, University of Oxford
yichen.dai@stcatz.ox.ac.uk @DaiycSerena



Introduction

- Pancreatic duodenal homeobox 1 (PDX1) is a transcription factor necessary for pancreatic development during embryogenesis and a maintainer of β cell function in adults^{1, 2}.
- Mice without functional PDX1 fail to develop a pancreas, while mice with lower than normal levels of PDX1 form a pancreas but show type II diabetes symptoms^{1, 3}.
- The PDX1 homeodomain is highly conserved, with 100% similarity between mouse and frog, and changes in this region can cause pancreatic agenesis in humans^{2, 4}.
- Psammomys obesus* (fat sand rat) is a desert rodent that is prone to developing type II diabetes⁵.
- We have located the sand rat *Pdx1* gene in a genomic region with elevated GC-levels, and we show that sand rat PDX1 has a highly divergent amino acid sequence⁶.

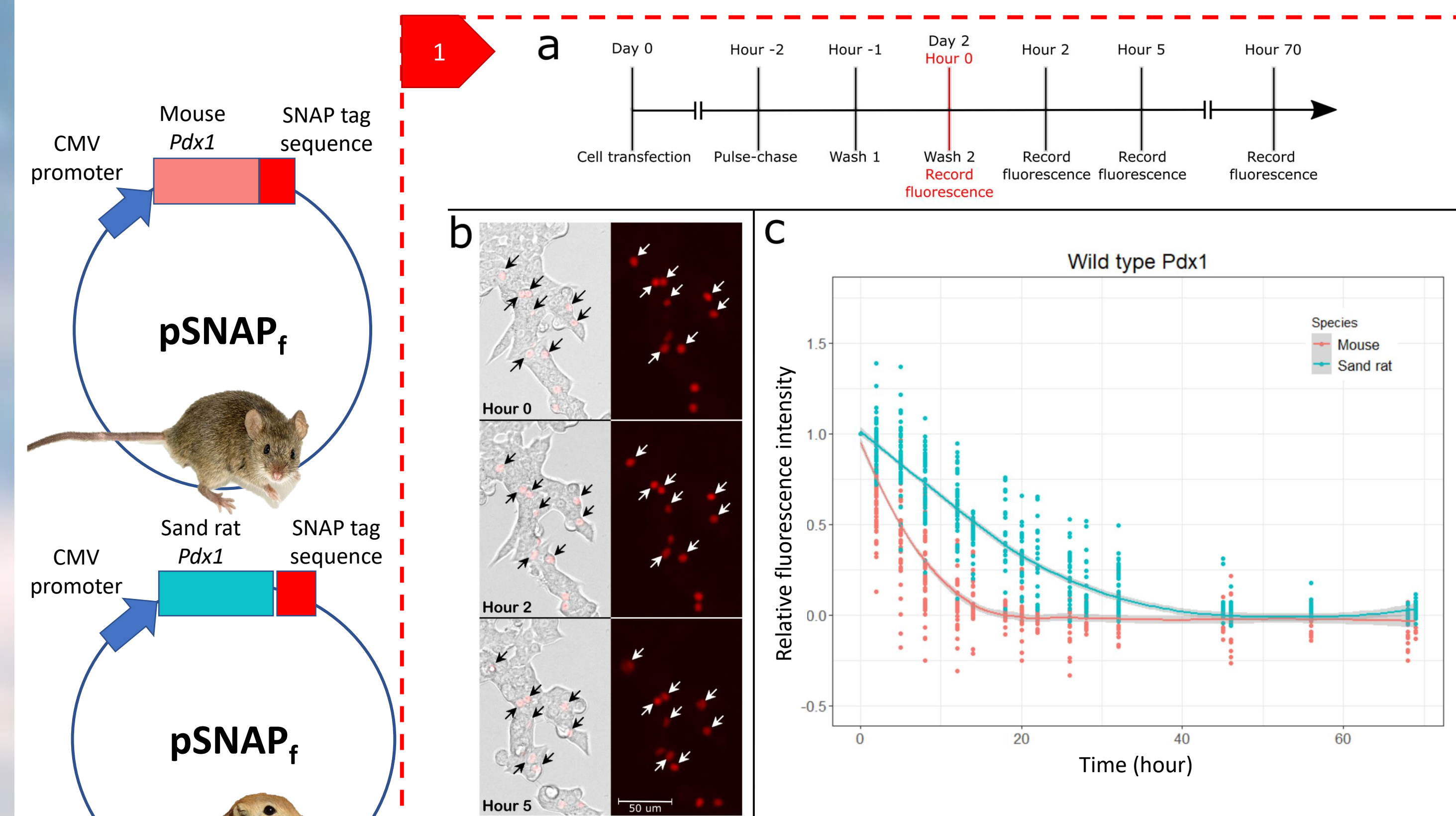
Result 1 The PDX1 homeodomain in gerbils is highly divergent



Questions

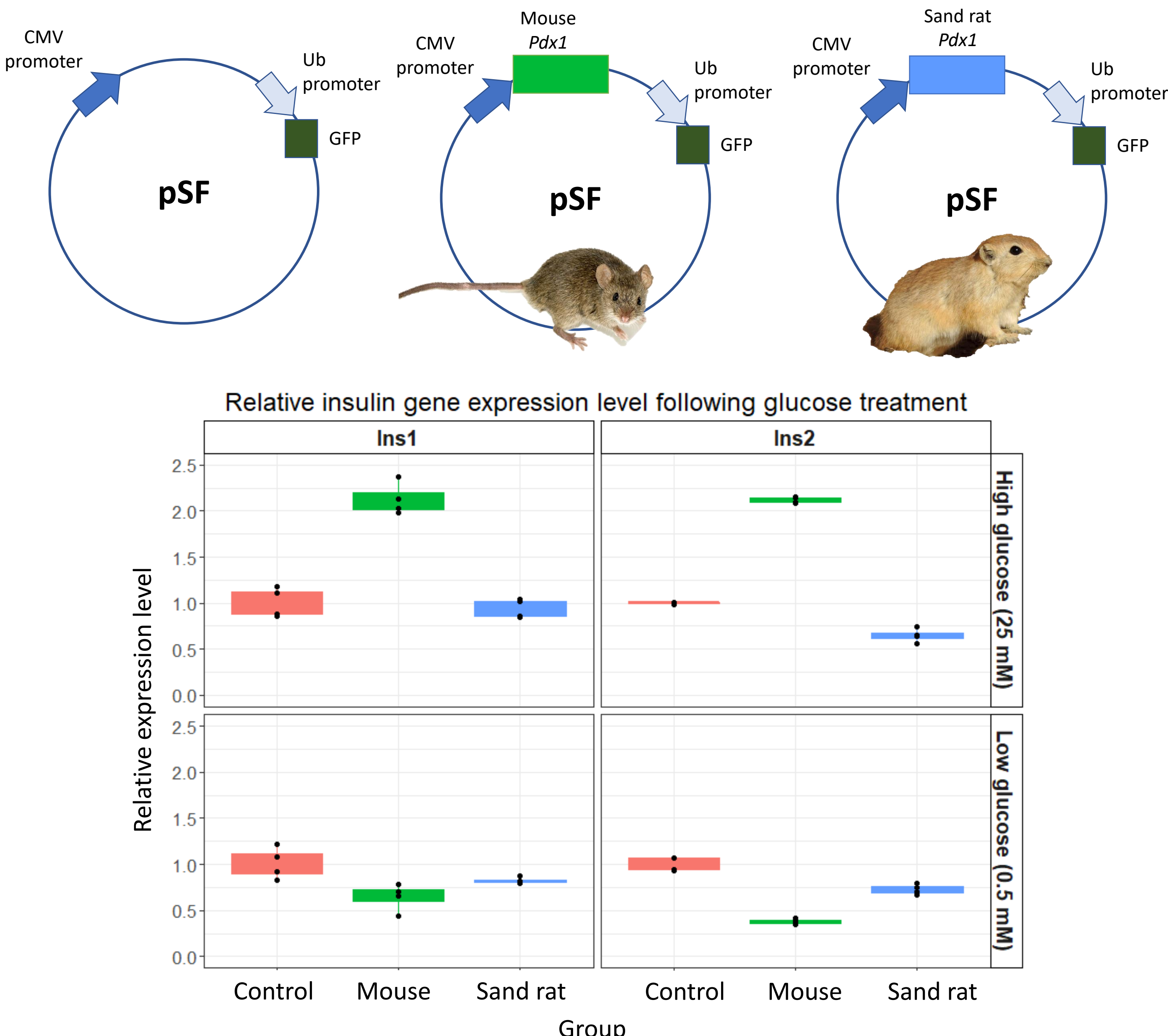
- How does this affect the biochemical properties of gerbil PDX1?
- How does this affect the biological function of gerbil PDX1?

Result 2 Due to loss of a conserved ubiquitination site in the homeodomain, gerbil PDX1 has a longer protein half-life



MG-132: a reversible inhibitor of the 26S proteasome. Cells were treated for 6 hours with MG-132

Result 3 Sand rat PDX1 is less capable of stimulating *insulin* expression

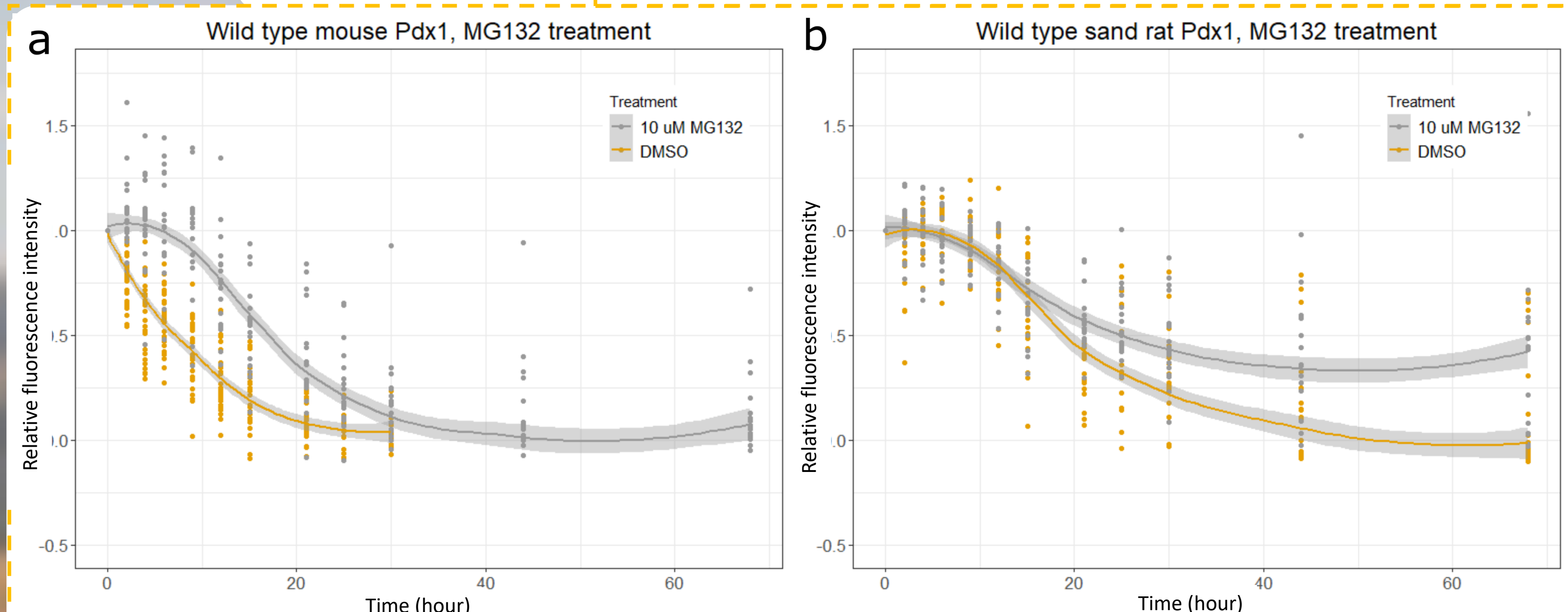


Functional differences exist

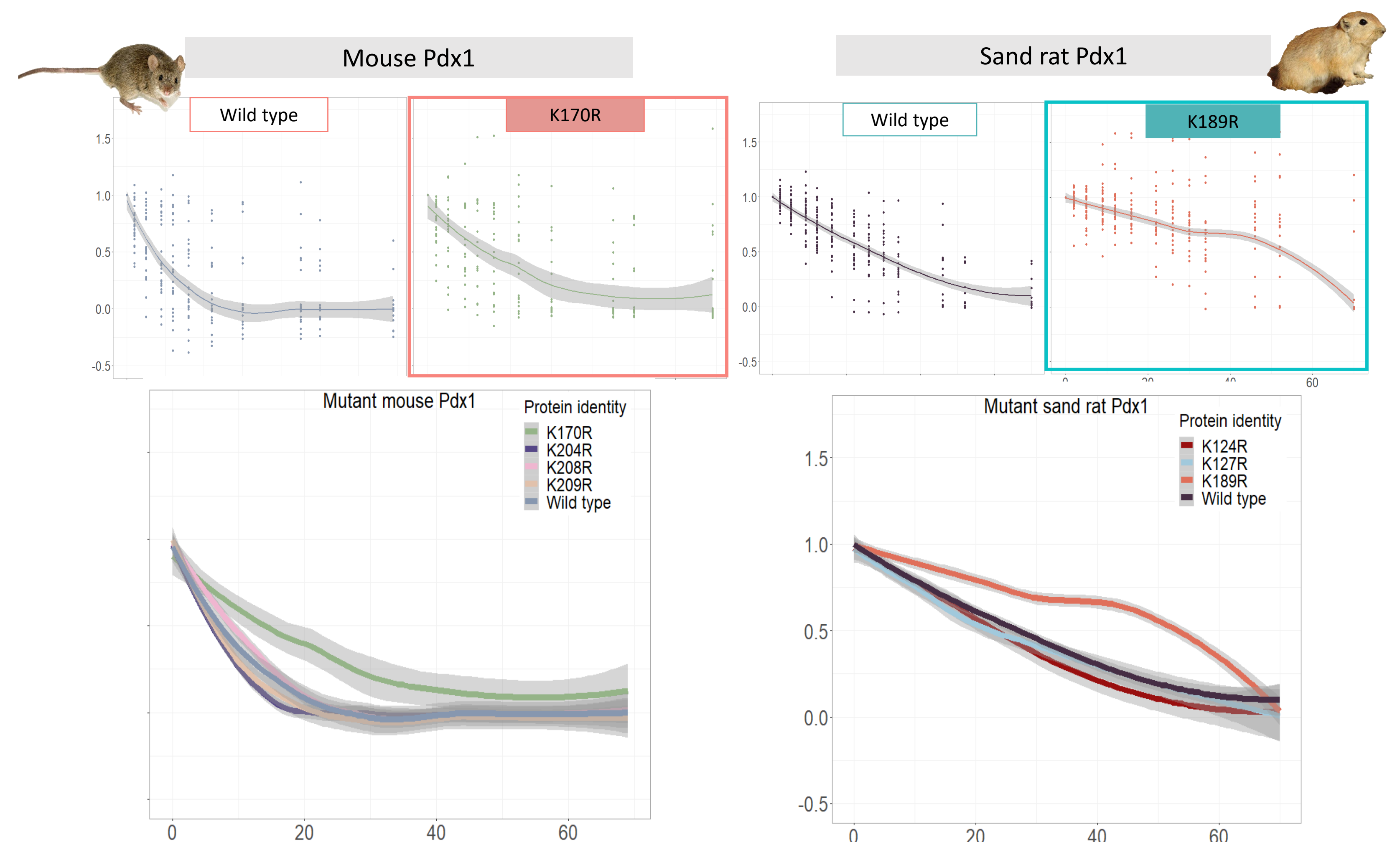
Sand rat PDX1 is significantly worse at stimulating rat insulin gene expression under high glucose levels

Conclusions

- The sand rat has the most divergent *Pdx1* gene in the entire vertebrate lineage. We infer this affects the entire gerbil subfamily.
- The loss of ubiquitination sites in sand rat PDX1 shows the impact of GC-skew in the local genomic region, while the presence of a new, gerbil-specific ubiquitination site indicates natural selection fighting back to retain basic protein functionality
- Sand rat PDX1 is less capable of stimulating insulin expression under high glucose conditions.
- The reason for the divergence remains unknown. However, it is possible that this region in the gerbil genome is fragile and susceptible to DNA breaks, thus leading to accumulation of mutations in the genes in this region.



In vitro mutagenesis: point mutations are indicated in the homeodomain alignment shown in Results 1.



Protein without lysine cannot be degraded

Conflict

GC-skew removes codons for lysine (AAA, AAG)

Natural selection vs GC-skew

Sand rat PDX1 has only one ubiquitination site, and this site is inferred to be a compensation for loss of other ubiquitination sites due to GC-rich mutation.



If you would like to read more about this work:

Dai, Y., & Holland, P. W. (2019). The interaction of natural selection and GC skew may drive the fast evolution of a sand rat homeobox gene. *Molecular biology and evolution*, **36**(7), 1473-1480.

Meeting attendance sponsored by:



This work and my study in Oxford were funded by:



References

- U. Ahlgren, J. Jonsson, L. Jonsson, K. Simu, H. Edlund, *Gene Dev.* **12**, 1763-1768 (1998).
- Offield, M. F. *et al.*, *Development* **122**, 983-995 (1996).
- J. Jonsson, L. Carlsson, T. Edlund, H. Edlund, *Nature* **371**, 606-609 (1994).
- V. M. Schwitzgebel *et al.*, *J. Clin. Endocrinol. Metab.* **88**, 4398-4406 (2003).
- M. Y. Donath *et al.*, *Diabetes* **48**, 738-744 (1999).
- A. D. Hargreaves *et al.*, *PNAS* **114**, 7677-7682 (2017).