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Development Of Mutant Reporter Mouse Models To Optimize And Evaluate CRISPR/Cas9 Therapeutic Base Editing

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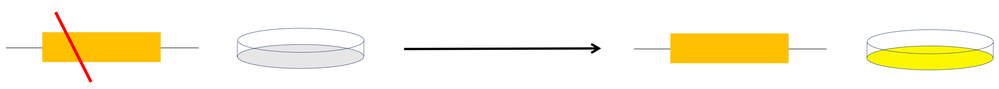
Abstract

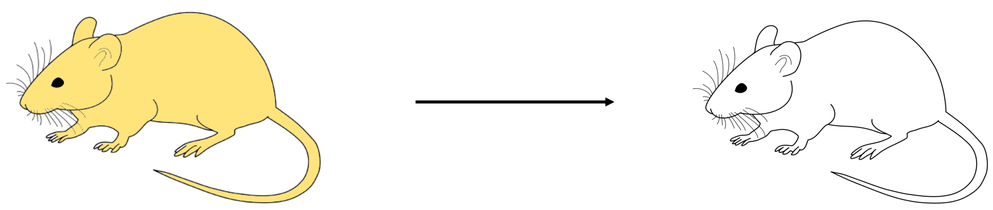
- There is still a great need to fully understand base editing *in vivo*
- We aim to develop and characterize two mutant reporter mouse models which allow us to easily and precisely quantify gene editing efficiency and analyze off-target effects
- Our mouse model is robust, sensitive and allows both live imaging and tissue-level imaging

Methods

- *In vitro* target identification and proof-of-principle



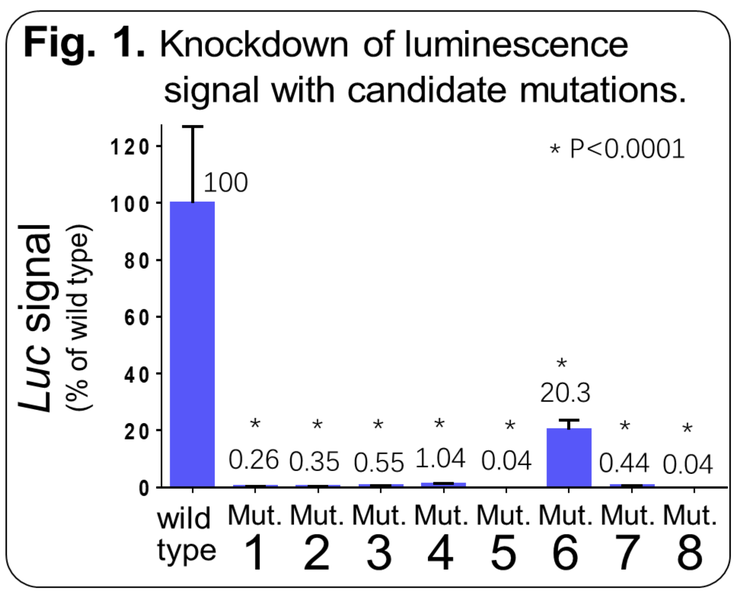
- Generation and characterization of mouse models

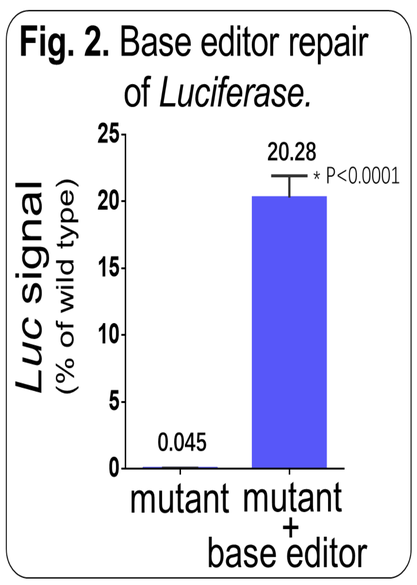


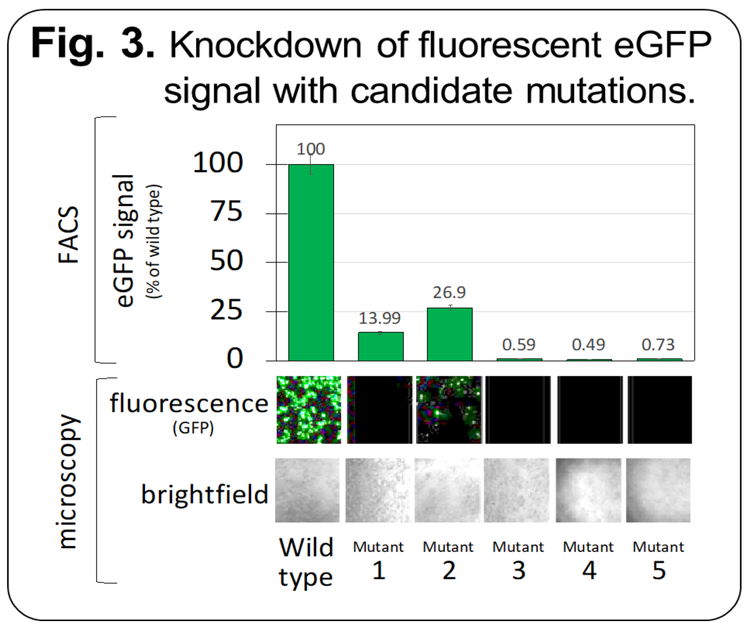
Background

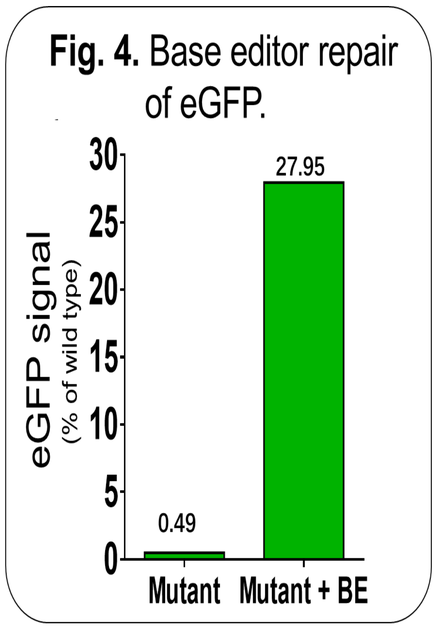
- Advances in genome sequencing has dramatically improved our ability to identify disease-causing mutations and diagnose genetic diseases
- New advances in CRISPR/Cas9 technologies, such as the base editors and prime editors, have provided a new therapeutic opportunity to directly repair those mutations in patients.
- However, there is still a great need to fully understand base editing *in vivo* in order to optimize and evaluate this approach before therapeutic applications.

Results









Conclusion

- These animal models can be used to monitor *in vivo* genome editing, to optimize delivery of genome-editing components into a variety of target tissues to aid many gene therapy applications, and to compare new generations of base editors.
- Our mouse model is robust, sensitive and allows both live imaging and tissue-level imaging

Research Aims

- Identify key mutations within luciferase and eGFP reporter genes which abolish its activity
- Develop and characterize two mutant reporter mouse models which allow us to easily and precisely quantify gene editing efficiency and analyze off-target effects.

Acknowledgment

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Photo Credit

Morse, M. (2012). TRANSGENIC MOUSE MODELS AS ALTERNATIVES TO THE 2-YEAR MOUSE BIOASSAY. [image] Available at: https://eureka.criver.com/transgenic-mouse-models-as-alternatives/ [Accessed 2 Feb. 2020].