DNA Methylation: A New Method for the Quantitative Predictor Of Age In Dogs

Tech ID: 30053 / UC Case 2017-369-0

BACKGROUND

The ability to properly estimate the age of dogs would be quite useful in a variety of ways. For example, proper age estimation is important because age often plays a significant role when making medical decisions for pets. Currently, the accepted method to estimate age in dogs is based on the quality of teeth as well as ocular features. Estimating age based on tooth-wear (the commonly used metric in shelters) is very inaccurate after the teeth have fully erupted, generally by 6-7 months of age in dogs. Unfortunately, these methods have an accuracy of ~50% at best for domesticated pets and is error-prone for dogs between 2-8 years, encompassing a large portion of a dog's adult life. Thus, shelters commonly underestimate the ages of these dogs to increase the likelihood of dogs being adopted, as people generally have a preference for younger pets.

TECHNOLOGY DESCRIPTION

Researchers at UC San Diego have developed a more precise method to quantitatively measure the age of an animal subject based upon the methylation status of select epigenetic predictors.

APPLICATIONS

Provides a quantitative measure of age in dogs, with an error of +/- 8 months.

ADVANTAGES

This invention is particularly useful for typing the age of dogs that were adopted from shelters, which is the case for the vast majority of dogs in the United States and other developed countries. This technology will inform owners and help them prepare for health-related issues that may arise as dog's age. It could also be used to assess the 'aging rate' of their pet and help prepare for future medical expenses when caring for their adopted dog.

STATE OF DEVELOPMENT

A study has been completed for which there is data on 104 dogs.

INTELLECTUAL PROPERTY INFO

This technology is patent pending and available for licensing and/or research sponsorship.

RELATED MATERIALS

- Adam E. Field, Neil A. Robertson,Tina Wang,Aaron Havas, Trey Ideker,and Peter D. Adams. DNA Methylation Clocks in Aging: Categories, Causes, and Consequences. Molecular Cell. 2018 - 09/20/2018
- Tina Wang, Brian Tsui, Jason F. Kreisberg, Neil A. Robertson, Andrew M. Gross, Michael Ku Yu, Hannah Carter, Holly M. Brown-Borg, Peter D. Adams and Trey Ideker. Epigenetic aging signatures in mice livers are slowed by dwarfism, calorie restriction and rapamycin treatment. Genome Biology. 2017 18:57 DOI 10.1186/s13059-017-1186-2 - 03/28/2017

PATENT STATUS

Country	Type	Number	Dated	Case
Patent Cooperation Treaty	Published Application	2019046725	03/07/2019	2017-369

Additional Patent Pending

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OTHER INFORMATION

KEYWORDS

DNA methylation, epigenomics, aging, epigenetic aging, mammalian DNA methylome

CATEGORIZED AS

- **Agriculture & Animal Science**
  - Animal Science
- **Research Tools**
  - Screening Assays
- **Veterinary**
  - Other

RELATED CASES

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