

An epigenetic aging clock for cattle using portable long read sequencing technology

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Abstract:

Extensively grazed cattle are often gathered once yearly. Therefore, birthdates are typically unknown or inaccurate. Birthdates would be useful for deriving important traits (growth rate; calving interval), breed registrations, and making management decisions. Epigenetic clocks use methylation of DNA to predict an individual's age. An epigenetic clock for cattle could provide a solution to the challenges of industry birthdate recording. Here we derived the first epigenetic clock for tropically adapted cattle using portable sequencing devices from tail hair, a tissue which is widely used in industry for genotyping. Cattle ($n = 66$) with ages ranging from 0.35 to 15.7 yrs were sequenced using Oxford Nanopore Technologies MinION and methylation was called at CpG sites across the genome. Sites were then filtered and used to calculate a covariance relationship matrix based on methylation state. Best linear unbiased prediction was used with 5-fold cross validation to predict age. A second methylation relationship matrix was also calculated that contained sites associated with genes used in the dog and human epigenetic clocks. The correlation between predicted age and actual age was 0.71 for all sites and 0.60 for dog and human gene epigenetic clock sites. The mean absolute deviation was 1.4 yr for animals aged less than 3 yr of age, and 1.5 yr for animals aged 3-10 yr. This is the first reported epigenetic clock using industry relevant samples in cattle.