Modified aging of elite athletes revealed by analysis of epigenetic age markers

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ABSTRACT

Recent progress in epigenomics has led to the development of prediction systems that enable accurate age estimation from DNA methylation data. Our objective was to track responses to intense physical exercise of individual age-correlated DNA methylation markers and to infer their potential impact on the aging processes. The study showed accelerated DNA hypermethylation for two CpG sites in *TRIM59* and *KLF14*. Both markers predicted the investigated elite athletes to be several years older than controls and this effect was more substantial in subjects involved in power sports. Accordingly, the complete 5-CpG model revealed age acceleration of elite athletes (P=1.503x10^{-7}) and the result was more significant amongst power athletes (P=1.051x10^{-9}). The modified methylation of *TRIM59* and *KLF14* in top athletes may be accounted for by the biological roles played by these genes. Their known anti-tumour and anti-inflammatory activities suggests that intense physical training has a complex influence on aging and potentially launches signalling networks that contribute to the observed lower risk of elite athletes to develop cardiovascular disease and cancer.

INTRODUCTION

Aging is a complex process associated with various molecular modifications in cells including epigenetic transitions that create changes in gene expression. Many studies have indicated DNA methylation (DNAmet) is an important component of aging. In addition to inherit-ed, genetically driven DNAmet changes, a broad spectrum of environmental factors can influence the methylation status of many sites making the human DNA methylome a sensitive marker set of epigenetic drift rather than a stable imprint [1, 2, 3]. Therefore, age predicted with epigenetic markers better reflects the biological age than the chronological age of an indivi-