



King's Research Portal

DOI:

[10.1016/j.mad.2016.02.001](https://doi.org/10.1016/j.mad.2016.02.001)

Document Version

Publisher's PDF, also known as Version of record

[Link to publication record in King's Research Portal](#)

Citation for published version (APA):

Spiers, H., Hannon, E., Wells, S., Williams, B., Fernandes, C., & Mill, J. (2016). Age-associated changes in DNA methylation across multiple tissues in an inbred mouse model. *Mechanisms of Ageing and Development*, 154, 20-23. <https://doi.org/10.1016/j.mad.2016.02.001>

Citing this paper

Please note that where the full-text provided on King's Research Portal is the Author Accepted Manuscript or Post-Print version this may differ from the final Published version. If citing, it is advised that you check and use the publisher's definitive version for pagination, volume/issue, and date of publication details. And where the final published version is provided on the Research Portal, if citing you are again advised to check the publisher's website for any subsequent corrections.

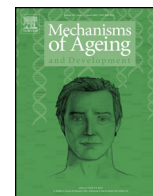
General rights

Copyright and moral rights for the publications made accessible in the Research Portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognize and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the Research Portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the Research Portal

Take down policy

If you believe that this document breaches copyright please contact librarypure@kcl.ac.uk providing details, and we will remove access to the work immediately and investigate your claim.



Short communication

Age-associated changes in DNA methylation across multiple tissues in an inbred mouse model



Helen Spiers^a, Eilis Hannon^b, Sara Wells^c, Brenda Williams^d, Cathy Fernandes^{a,1}, Jonathan Mill^{a,b,*,1}

^a Social, Genetic and Developmental Psychiatry Centre, Institute of Psychiatry, Psychology and Neuroscience, King's College London, London SE5 8AF, UK

^b University of Exeter Medical School, University of Exeter, Exeter EX2 5DW, UK

^c Mary Lyon Centre, Harwell, Didcot, Oxfordshire OX11 0RD, UK

^d Department of Basic and Clinical Neuroscience, Institute of Psychiatry, Psychology and Neuroscience, King's College London, London SE5 8AF, UK

ARTICLE INFO

Article history:

Received 15 January 2016

Received in revised form 3 February 2016

Accepted 4 February 2016

Available online 6 February 2016

Keywords:

Aging

Epigenetics

DNA methylation

Inbred mouse

Cross-tissue

ABSTRACT

Epigenetic disruption has been implicated in many diseases of aging, and age-associated DNA methylation changes at specific genomic loci in humans are strongly correlated with chronological age. The aim of this study was to explore the specificity of selected age-associated differentially methylated positions (aDMPs) identified in human epidemiological studies by quantifying DNA methylation across multiple tissues in homologous regions of the murine genome. We selected four high-confidence aDMPs (located in the vicinity of the *ELOVL2*, *GLRA1*, *MYOD1* and *PDE4C* genes) and quantified DNA methylation across these regions in four tissues (blood, lung, cerebellum and hippocampus) from male and female C57BL/6J mice, ranging in age from fetal (embryonic day 17) to 630 days. We observed tissue-specific age-associated changes in DNA methylation that was directionally consistent with those observed in humans. These findings lend further support to the notion that changes in DNA methylation are associated with chronological age and suggest that these processes are often conserved across tissues and between mammalian species. Our data highlight the relevance of utilizing model systems, in which environmental and genetic influences can be carefully controlled, for the further study of these phenomena.

© 2016 The Authors. Published by Elsevier Ireland Ltd. This is an open access article under the CC BY license (<http://creativecommons.org/licenses/by/4.0/>).

Aging, the progressive decline in physiological and psychological functioning that occurs across the lifespan, involves a complex suite of molecular changes (Lopez-Otin et al., 2013) including perturbations to the epigenetic processes regulating gene transcription (Jones et al., 2015). A growing literature, for example, describes robust age-associated DNA methylation changes at specific genomic loci in humans, representing a so-called “epigenetic clock” that is strongly correlated with chronological age (Horvath, 2013). Notably, some changes in DNA methylation associated with age are cell-type specific (Day et al., 2013) while others occur across multiple tissues (Horvath, 2013). Epigenetic changes have been implicated in many diseases of aging including cancer (Bergman and Cedar, 2013) and dementia (Lunnon et al., 2014), and it has

been hypothesized that accelerated aging of the “epigenetic clock” is associated with mortality-linked markers of physical and mental fitness (Marioni et al., 2015). Our knowledge about the origins and function of age-associated epigenetic variation remains limited, in part because of the difficulties inherent in studying such dynamic and tissue-specific processes in human cohorts (Heijmans and Mill, 2012). The aim of this study was to explore the specificity of selected age-associated differentially methylated positions (aDMPs) identified in human epidemiological studies by quantifying DNA methylation across multiple tissues in homologous regions of the murine genome.

We aged a colony of inbred C57BL/6J mice and sequentially collected four tissues (whole blood, lung, cerebellum and hippocampus (Table C.1 of Supplementary material) from fetal (embryonic (E) 17, -4 days old) to elderly (630 days old) individuals (Fig. B.1 of Supplementary material). Targeted assays were designed to quantify DNA methylation across regions of the murine genome homologous to four robustly-associated human aDMPs in the vicinity of the genes *ELOVL2*, *GLRA1*, *MYOD1* and *PDE4C* (Table C.2, Figs. B.2–B.5 of Supplementary material) that have been previously associated with chronological age (Bell et al., 2012;

* Corresponding author at: University of Exeter Medical School, RILD Building, Royal Devon and Exeter Hospital, Barrack Road, Exeter EX2 5DW, UK.

E-mail addresses: helen.h.spiers@kcl.ac.uk (H. Spiers), e.j.hannon@exeter.ac.uk (E. Hannon), s.wells@har.mrc.ac.uk (S. Wells), brenda.p.williams@kcl.ac.uk (B. Williams), catherine.fernandes@kcl.ac.uk (C. Fernandes), j.mill@exeter.ac.uk (J. Mill).

¹ These authors contributed equally.

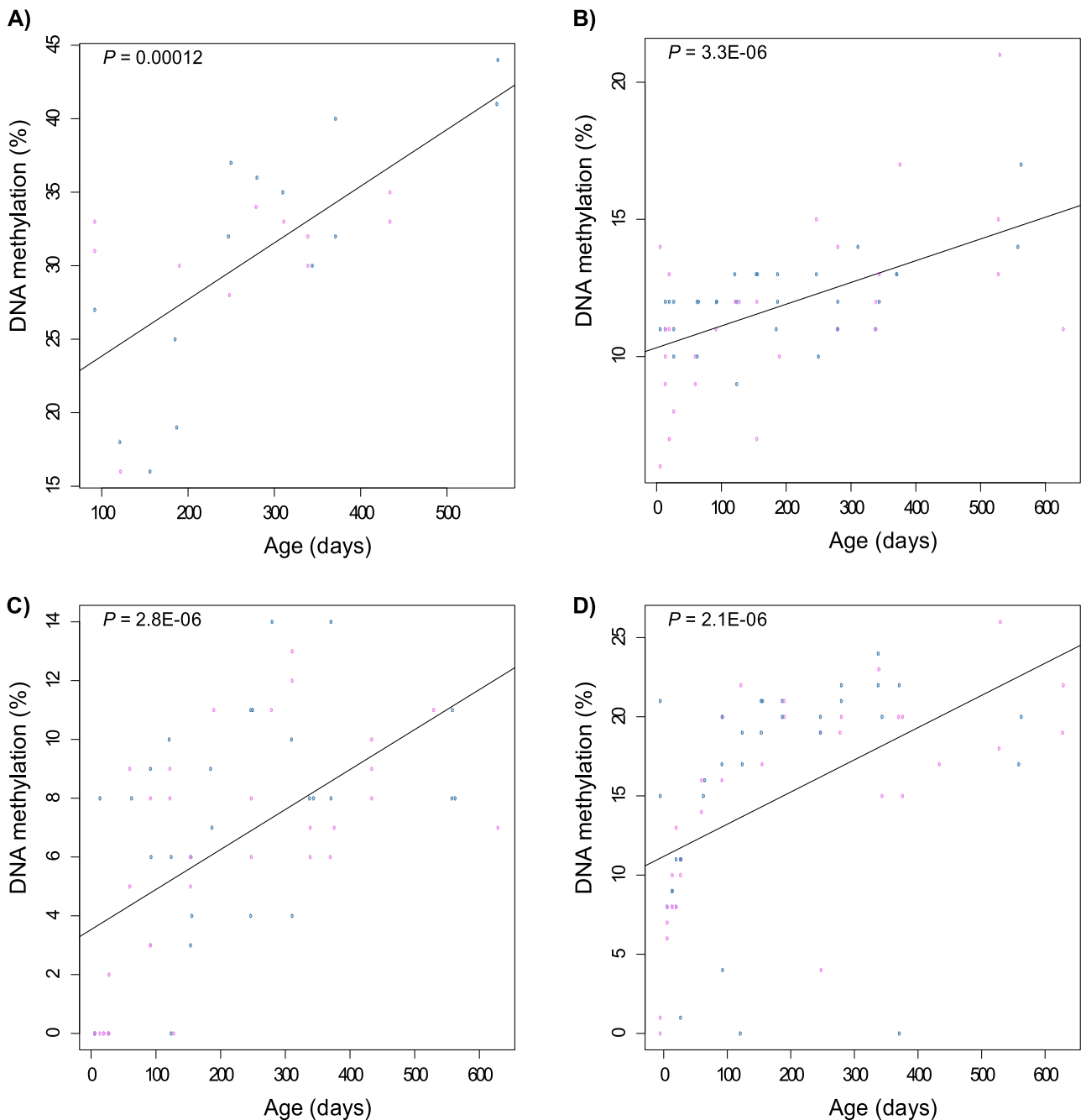


Fig. 1. DNA methylation across regions homologous to human aDMP is associated with chronological age in mouse. For each of the amplicons the most significantly age associated CpG site across the four tissues assessed is shown. (A) ELOVL2 – CpG sites 2/3 – blood ($P = 1.15E - 04$). (B) GLRA1 – CpG sites 13/14 – blood ($P = 3.31E - 06$). (C) MYOD1 – CpG site 1 – blood ($P = 2.82E - 06$). (D) PDE4C – CpG sites 21/21 – cerebellum ($P = 2.14E - 06$). Blue dots depict male samples, pink dots depict female samples (see also Tables C.7–C.10 of Supplementary material). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

Bocklandt et al., 2011; Florath et al., 2014; Garagnani et al., 2012; Hannum et al., 2013; Hernandez et al., 2011; Johansson et al., 2013; Koch and Wagner, 2011; Rakyan et al., 2010; Teschendorff et al., 2010; Weidner et al., 2014). Briefly, genomic DNA was treated with sodium bisulfite, and DNA methylation was quantified across multiple CpG sites using the Sequenom EpiTYPER system following bisulfite-PCR amplification. A full description of experimental methods is given in Appendix A.

Average and CpG site-specific DNA methylation across the four amplicons in each tissue is shown in Tables C.3–C.6 of Supplementary material. Age-associated changes in DNA methylation were identified using a linear model for each of the four tissues

(Table 1 and Tables C.7–C.10 of Supplementary material). Our initial analyses focused on whole blood, the predominant tissue used for epigenetic aging studies in human populations. Average DNA methylation across two amplicons (ELOVL2, $P = 0.01$; GLRA1, $P = 3.86E - 05$) was found to be significantly associated with age in the same direction as reported in human data, with individual CpG units within each amplicon being strongly associated with age (Fig. 1 and Tables C.7–C.8 of Supplementary material). Although amplicon-average DNA methylation across the other two regions was not significantly associated with age in whole blood (MYOD1, $P = 0.09$; PDE4C, $P = 0.83$), multiple CpG units within both amplicons were significantly correlated with age in the direction predicted

Table 1
Tissue-specific age-associated changes in DNA methylation were observed candidate regions in an inbred strain of mouse. B = blood; L = lung; C = cerebellum; H = hippocampus.

Amplicon	ELOVL2				GLRA1				MYOD1				PDE4C			
Human aDMP (corresponding illumina 450 K array probe) Human Feb. 2009 (GRCh37/hg19) Homologous mouse target region Mouse July 2007 (NCBI37/mm9) CpG units passing QC (n) Tissue	cg16867657 Chr6: 11044877				cg00059225 Chr5: 151304357				cg18555440 Chr11: 17741687cg17861230 Chr19: 18343901							
	Chr13: 41316038–41316469				Chr11: 55421383–55421670				Chr7: 53632317–53632673				Chr8: 73253999–73254240			
	8				10				19				11			
	B	L	C	H	B	L	C	H	B	L	C	H	B	L	C	H
Amplicon average P-value	0.01*	0.02*	0.18	0.53	3.86E–05*	0.01*	0.16	0.59	0.09	0.45	0.02*	0.97	0.83	0.89	5.74E–06*	0.59
Age-associated CpG units (n) P < 0.05 in same direction as human	3	3	1	0	6	4	0	1	5	0	1	0	1	0	6	0

from human studies (Tables C.9–C.10 of Supplementary material). Together, these data provide evidence that human blood aDMPs are also associated with chronological age in mouse.

We next examined changes in DNA methylation with age at these four loci in three additional tissues dissected from the same individual animals. Amplicon average DNA methylation was associated with age in lung across both the ELOVL2 and GLRA1 amplicons, reflecting the patterns seen in whole blood (ELOVL2, $P=0.02$; GLRA1, $P=0.01$), although not in cerebellum or hippocampus (Tables C.7–C.8 of Supplementary material). In contrast, cerebellum-specific associations with age were observed for amplicon-average DNA methylation across the two other amplicons (MYOD1, $P=0.02$; PDE4C, $P=5.74E-06$) (Tables C.9–C.10 of Supplementary material).

These findings lend further support to the notion that changes in DNA methylation are associated with chronological age and suggest that these processes may often be conserved across tissues and between species (Polanowski et al., 2014). Characterization of the molecular mechanisms underpinning normative aging processes has the potential to facilitate the development of novel therapeutic interventions targeting diseases of aging, potentially increasing the health-span of our aging population. Our data highlight the relevance of utilizing model systems, in which environmental and genetic influences can be carefully controlled, for the further study of these phenomena.

Author contributions

JM and HS conceived the project. CF, SW and BP performed mouse work. HS performed DNA methylation quantification and analysis with advice from EH. HS and JM wrote manuscript. All authors approved the manuscript before submission.

Conflict of interest

We certify that there is no conflict of interest with any financial organization regarding the material discussed in the manuscript.

Acknowledgements

This project was in part supported by research funds provided by the University of Exeter Medical School. HS is supported by a MRC studentship.

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at <http://dx.doi.org/10.1016/j.mad.2016.02.001>.

References

Bell, J.T., Tsai, P.C., Yang, T.P., Pidsley, R., Nisbet, J., Glass, D., Mangino, M., Zhai, G., Zhang, F., Valdes, A., Shin, S.Y., Dempster, E.L., Murray, R.M., Grundberg, E., Hedman, A.K., Nica, A., Small, K.S., Dermitzakis, E.T., McCarthy, M.I., Mill, J., Spector, T.D., Deloukas, P., 2012. Epigenome-wide scans identify differentially methylated regions for age and age-related phenotypes in a healthy ageing population. *PLoS Genet.* 8, e1002629.

Bergman, Y., Cedar, H., 2013. DNA methylation dynamics in health and disease. *Nat. Struct. Mol. Biol.* 20, 274–281.

Bocklandt, S., Lin, W., Sehl, M.E., Sanchez, F.J., Sinsheimer, J.S., Horvath, S., Vilain, E., 2011. Epigenetic predictor of age. *PLoS One* 6, e14821.

Day, K., Waite, L.L., Thalacker-Mercer, A., West, A., Bamman, M.M., Brooks, J.D., Myers, R.M., Absher, D., 2013. Differential DNA methylation with age displays both common and dynamic features across human tissues that are influenced by CpG landscape. *Genome Biol.* 14, R102.

Florath, I., Butterbach, K., Muller, H., Bewerunge-Hudler, M., Brenner, H., 2014. Cross-sectional and longitudinal changes in DNA methylation with age: an epigenome-wide analysis revealing over 60 novel age-associated CpG sites. *Hum. Mol. Genet.* 23, 1186–1201.

Garagnani, P., Bacalini, M.G., Pirazzini, C., Gori, D., Giuliani, C., Mari, D., Di Blasio, A.M., Gentilini, D., Vitale, G., Collino, S., Rezzi, S., Castellani, G., Capri, M., Salvioli, S., Franceschi, C., 2012. Methylation of ELOVL2 gene as a new epigenetic marker of age. *Aging Cell* 11, 1132–1134.

Hannum, G., Guinney, J., Zhao, L., Zhang, L., Hughes, G., Sada, S., Klotzle, B., Bibikova, M., Fan, J.B., Gao, Y., Deconde, R., Chen, M., Rajapakse, I., Friend, S., Ideker, T., Zhang, K., 2013. Genome-wide methylation profiles reveal quantitative views of human aging rates. *Mol. Cell* 49, 359–367.

Heijmans, B.T., Mill, J., 2012. Commentary: the seven plagues of epigenetic epidemiology. *Int. J. Epidemiol.* 41, 74–78.

Hernandez, D.G., Nalls, M.A., Gibbs, J.R., Arepalli, S., van der Brug, M., Chong, S., Moore, M., Longo, D.L., Cookson, M.R., Traynor, B.J., Singleton, A.B., 2011. Distinct DNA methylation changes highly correlated with chronological age in the human brain. *Hum. Mol. Genet.* 20, 1164–1172.

Horvath, S., 2013. DNA methylation age of human tissues and cell types. *Genome Biol.* 14, R115.

Johansson, A., Enroth, S., Gyllenstein, U., 2013. Continuous aging of the human DNA methylome throughout the human lifespan. *PLoS One* 8, e67378.

Jones, M.J., Goodman, S.J., Kobor, M.S., 2015. DNA methylation and healthy human aging. *Aging Cell.*

Koch, C.M., Wagner, W., 2011. Epigenetic-aging-signature to determine age in different tissues. *Aging* 3, 1018–1027.

Lopez-Otin, C., Blasco, M.A., Partridge, L., Serrano, M., Kroemer, G., 2013. The hallmarks of aging. *Cell* 153, 1194–1217.

Lunnion, K., Smith, R., Hannon, E., De Jager, P.L., Srivastava, G., Volta, M., Troakes, C., Al-Sarraj, S., Burrage, J., Macdonald, R., Condliffe, D., Harries, L.W., Katsel, P., Haroutunian, V., Kaminsky, Z., Joachim, C., Powell, J., Lovestone, S., Bennett, D.A., Schalkwyk, L.C., Mill, J., 2014. Methyloomic profiling implicates cortical deregulation of ANK1 in Alzheimer's disease. *Nat. Neurosci.* 17, 1164–1170.

Marioni, R.E., Shah, S., McRae, A.F., Ritchie, S.J., Muniz-Terrera, G., Harris, S.E., Gibson, J., Redmond, P., Cox, S.R., Pattie, A., Corley, J., Taylor, A., Murphy, L., Starr, J.M., Horvath, S., Visscher, P.M., Wray, N.R., Deary, I.J., 2015. The epigenetic clock is correlated with physical and cognitive fitness in the Lothian Birth Cohort 1936. *Int. J. Epidemiol.*

Polanowski, A.M., Robbins, J., Chandler, D., Jarman, S.N., 2014. Epigenetic estimation of age in humpback whales. *Mol. Ecol. Resour.* 14, 976–987.

- Rakyan, V.K., Down, T.A., Maslau, S., Andrew, T., Yang, T.P., Beyan, H., Whittaker, P., McCann, O.T., Finer, S., Valdes, A.M., Leslie, R.D., Deloukas, P., Spector, T.D., 2010. [Human aging-associated DNA hypermethylation occurs preferentially at bivalent chromatin domains.](#) *Genome Res.* 20, 434–439.
- Teschendorff, A.E., Menon, U., Gentry-Maharaj, A., Ramus, S.J., Weisenberger, D.J., Shen, H., Campan, M., Noushmehr, H., Bell, C.G., Maxwell, A.P., Savage, D.A., Mueller-Holzner, E., Marth, C., Kocjan, G., Gayther, S.A., Jones, A., Beck, S., Wagner, W., Laird, P.W., Jacobs, I.J., Widschwendter, M., 2010. [Age-dependent DNA methylation of genes that are suppressed in stem cells is a hallmark of cancer.](#) *Genome Res.* 20, 440–446.
- Weidner, C.I., Lin, Q., Koch, C.M., Eisele, L., Beier, F., Ziegler, P., Bauerschlag, D.O., Jockel, K.H., Erbel, R., Muhleisen, T.W., Zenke, M., Brummendorf, T.H., Wagner, W., 2014. [Aging of blood can be tracked by DNA methylation changes at just three CpG sites.](#) *Genome Biol.* 15, R24.